The MiniSeq™ System. Explore the possibilities.

Discover demonstrated NGS workflows for molecular biology applications.

For Research Use Only. Not for use in diagnostic procedures.

illumina®

Let your work flow with Illumina NGS.

The MiniSeq System delivers powerful and cost-effective methods for DNA and RNA sequencing in a highly accurate benchtop solution. Its convenient and streamlined library-to-results workflow enables rapid sequencing for analysis of a single gene or entire pathways in 1 run. Supported by a full suite of Illumina library preparation solutions, the MiniSeq System features an intuitive, touch-screen user interface, integrated data analysis, and a small footprint. Every aspect is designed for easy, everyday use. Finally, next-generation sequencing (NGS) that fits your budget, your bench, and your research needs.

NGS is redefining scientific research every day. Researchers no longer have to rely on methods of genetic analysis that require multiple iterations to study genes, gene families, or signaling pathways. This iterative approach can consume substantial time and does not always result in comprehensive findings. Now, with the power of NGS, researchers can assess multiple genes or entire pathways simultaneously for a more complete view of biology, in a single run. Explore the many demonstrated workflows for molecular biology applications.

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Targeted DNA sequencing | Targeted RNA sequencing | Small RNA sequencing | Small Genome sequencing

TruSeq® Custom Amplicon Low Input

Target more breakthroughs.

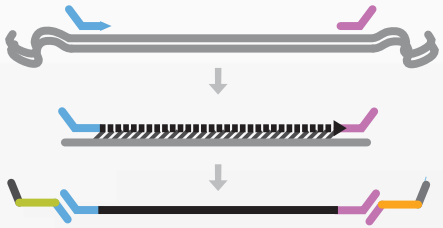
The TruSeq Custom Amplicon Low Input workflow is a highly targeted approach to efficiently discover, validate, and screen genetic variants, even from limited and challenging samples. Following whole-genome or exome sequencing, deep sequencing lets you interrogate your specific areas of interest for higher coverage and greater resolution.

Access discovery power.

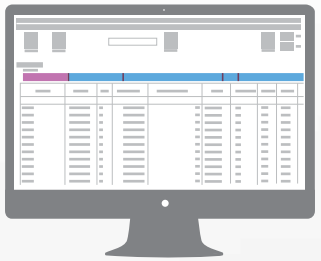
- Study and deeply interrogate specific areas of interest, following whole-genome sequencing (WGS), whole-exome sequencing (WES), array, or fine mapping studies.
- Analyze variants across a wide range of applications, including population genetics, genetic disease, and cancer studies.
- Utilize a cost-effective alternative to broader methods, such as WGS.

Highlights

- Achieve accurate variant detection from as little as 10 ng of DNA.
- Experience a completely customizable solution using the DesignStudio™ Tool for your genes and targets of interest.
- Leverage Illumina Concierge for additional design assistance and optimization.
- Sequence up to 1536 amplicons in a single reaction using a simple workflow.
- Rely on a fully supported, optimized workflow solution that includes simple onboard or cloud-based data analysis.



TruSeq Custom Amplicon Low Input Kit
www.illumina.com/ampliconseq



On System: Local Run Manager—Amplicon
On Cloud: BaseSpace® Platform—TruSeq Amplicon
On Site: BaseSpace® Platform—TruSeq Amplicon VariantStudio
www.illumina.com/basespace

Prepare library → Sequence → Analyze data

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TruSeq Custom Amplicon Low Input Dual Strand

Challenge the limits.

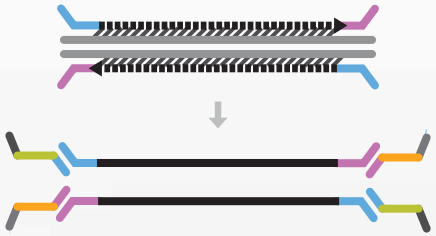
The TruSeq Custom Amplicon Low Input Dual Strand workflow interrogates each complementary strand with a mirror probe design. This can further enhance the ability to filter actual variants from systemic “noise,” providing variant identification confidence. Overcome sequencing artifacts caused by DNA damage such as deamination and oxidation, and sequence context challenges, such as repeats and base-read errors.

Access discovery power.

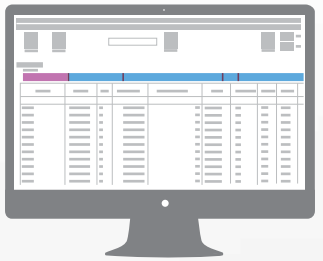
- Filter false positives from true variants for accuracy and confidence.
- Deeply interrogate and study specific areas of interest, following WGS, WES, array, or fine mapping studies.
- Analyze variants across a wide range of applications, including population genetics, genetic disease, and cancer studies.
- Search for pathways or disease-causing variants more cost effectively than you can using other methods, such as WGS.

Highlights

- Experience a completely customizable solution, using the DesignStudio tool for your genes and targets of interest.
- Leverage Illumina Concierge for personal design assistance and optimization.
- Achieve accurate variant detection from as little as 20 ng of DNA.
- Sequence up to 1536 amplicons in 2 pool reactions using a simple workflow.
- Rely on a fully supported, optimized workflow solution that includes simple onboard or cloud-based data analysis.



TruSeq Custom Amplicon Low Input Kit
www.illumina.com/ampliconseq



On System: Local Run Manager—Amplicon DS
On Cloud: BaseSpace Platform—Amplicon DS
On Site: BaseSpace Platform—Amplicon DS VariantStudio
www.illumina.com/basespace

Prepare library → Sequence → Analyze data

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TruSeq Custom Amplicon 1.5

Challenge the limits.

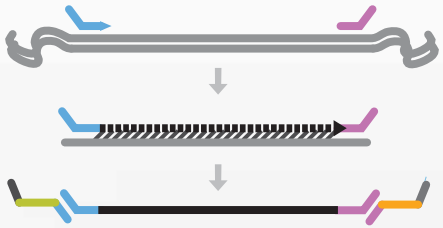
The TruSeq Custom Amplicon v1.5 workflow is a highliy targeted approach to efficiently discover, valildate, and screen genetic variants, even from challenging samples. Following whole-genome or exome sequencing, deep sequencing lets you interrogate your specific areas of interest for higher coverage and greater resolution.

Access discovery power.

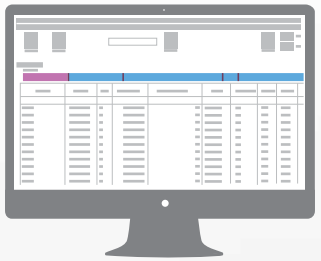
- Deeply interrogate and study specific areas of interest, following WGS, WES, array, or fine mapping studies.
- Analyze variants across a wide range of applications, including population genetics, genetic disease, and cancer studies.
- Access up to 4.25Mb across 10,000 multiplexed amplicons to broaded your discovery power.
- Utilize a cost-effective alternative to broader methods, such as WGS.

Highlights

- Achieve accurate variant detection from as little as 50 ng of gDNA, or 150 ng of FFPE DNA.
- Experience a completely customizable solution, using the DesignStudio tool for your genes and targets of interest.
- Leverage Illumina Concierge for personal design assistance and optimization.
- Sequence up to 10,000 amplicons in a single reaction using a simple workflow.
- Rely on a fully supported, optimized workflow solution that includes simple onboard or cloud-based data analysis.



TruSeq Custom Amplicon v1.5 Kit
www.illumina.com/ampliconseq



On System: Local Run Manager—Amplicon
On Cloud: BaseSpace Platform—TruSeq Amplicon
On Site: BaseSpace Platform—TruSeq Amplicon
VariantStudio
www.illumina.com/basespace

Prepare library → Sequence → Analyze data

For Research Use Only. Not for use in diagnostic procedures.

TruSeq ChIP

Further your understanding.

The TruSeq ChIP workflow provides a simple, cost-effective solution for chromatin immunoprecipitation sequencing (ChIP-Seq). ChIP-Seq leverages next-generation sequencing (NGS) to quickly and efficiently determine the distribution and abundance of protein-bound DNA targets of interest across the genome. It enables researchers to identify binding sites of a broad range of targets across the entire genome, reliably and simultaneously, with high resolution and without constraints.

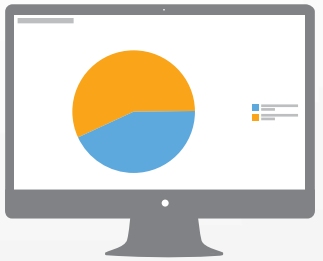
Highlights

- Proven TruSeq data quality
- Low DNA input requirement > 5ng
- Simple, streamlined workflow
- Multiplexed sequencing with 24 available indexes.

Access vdiscovery power.

- Obtain a complete and accurate profile of target protein DNA interactions.
- Get robust results from just 5ng DNA from a range of sample sources.
- Enhance scalability with an easy-to-use, simplified workflow.
- Optimize sequencing output distribution across samples, reducing cost per sample.

TruSeq ChIP Library Preparation Kit
www.illumina.com/ChIP



On System: Local Run Manager—Not available
On Cloud: BaseSpace Platform—ChIPSeq
On Site: BaseSpace Platform—Not available
www.illumina.com/basespace

Prepare library → Sequence → Analyze data

For Research Use Only. Not for use in diagnostic procedures.

TruSight® Inherited Disease

Challenge the limits.

The TruSight Inherited Disease Sequencing Panel focuses on severe, recessive pediatric onset diseases. It targets 552 genes, including coding exons, intron-exon boundaries, and regions known to harbor pathogenic variants. The panel set includes custom oligos targeting identified regions of interest and enough product for 4 enrichment reactions. It features compatibility with TruSight Rapid Capture and libraries prepared with this panel can be run on the MiniSeq System.

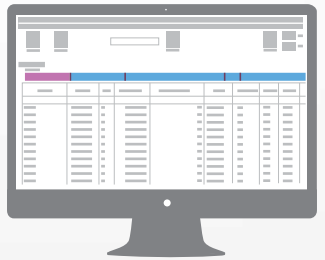
Access discovery power.

- Comprehensive Coverage – Focus on genes with potential involvement in severe, recessive pediatric-onset diseases with
- comprehensive coverage and optimized probe set.
- Data Analysis – On instrument software analyzes sequence data generated from TruSight Inherited Disease libraries.
- High Data Quality – Each sample is sequenced with high coverage uniformity across the target region with > 95% of exons covered at minimum coverage of 20x.

Highlights

- Expert-defined content targeting 552 genes, including coding exons, intron-exon boundaries, and regions harboring pathogenic mutations.
- Low input DNA requirements allow for excellent data quality with as little as 50 ng DNA to preserve precious samples.
- Fast and simple workflow enables complete library preparation and enrichment in 1.5 days.

TruSight Inherited Disease
www.illumina.com/inherited_disease



On System: Local Run Manager—Isaac/BWA Enrichment
On Cloud: BaseSpace Platform—Isaac/BWA Enrichment
On Site: BaseSpace Platform—Isaac/BWA Enrichment
www.illumina.com/basespace

Prepare library → Sequence → Analyze data

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TruSeq Targeted RNA Expression

Explore regions of interest.

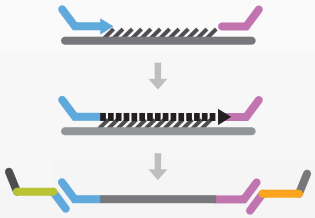
The TruSeq Targeted RNA Expression workflow allows you to profile the expression of select target genes to assess the functional impact of disease-associated variants and epigenetic alterations. Leveraging cost and workflow advantages over existing techniques such as quantitative polymerase chain reaction (qPCR), this workflow offers custom panel design in addition to a range of fixed panels for commonly studied pathways.

Access discovery power.

- Focus on transcripts of interest with accuracy and specificity.
- Achieve differential expression analysis, allele-specific expression measurement, and fusion gene verification utilizing qualitative and quantitative information.
- Measure dozens to thousands of targets simultaneously.

Highlights

- Work with low-quality or formalin-fixed, paraffin-embedded (FFPE)-derived RNA samples.
- Start with as little as 50 ng of total RNA.
- Leverage RNA fixed panels, including apoptosis, cardiotoxicity, cell cycle, hedgehog pathway, neurodegeneration, NFKB pathway, P450 pathway, P53 pathway, stem cells, Wnt pathway panels.
- Rely on a fully supported, optimized workflow solution that includes simple onboard or cloud-based data analysis.



TruSeq Targeted RNA Kit
www.illumina.com/targetedexpression

On System: Local Run Manager—Targeted RNA
On Cloud: BaseSpace Platform—TruSeq Targeted RNA
On Site: BaseSpace Platform—TruSeq Targeted RNA
www.illumina.com/basespace

Prepare library → Sequence → Analyze data

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Targeted RNA sequencing

TruSeq Small RNA

Further your understanding.

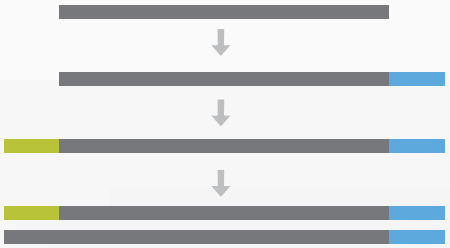
The TruSeq Small RNA workflow allows you to accelerate your research by studying thousands of microRNA and other small RNA sequences. No prior knowledge of the transcriptome is needed. Benefit from high sensitivity and dynamic range for small RNA discovery and profiling across a wide range of organisms.

Access discovery power.

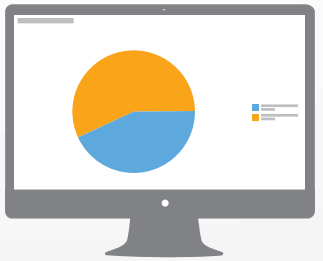
- Gain an understanding of how post-transcriptional regulation contributes to phenotype.
- Drive discovery of novel small RNA species and biomarkers.
- Capture the complete microRNA transcriptome.

Highlights

- Experience a simple, cost-effective solution for generating small RNA libraries directly from total RNA.
- Target microRNAs with the modified adapters included in the kit.
- Rely on a fully supported, optimized workflow solution that includes simple onboard or cloud-based data analysis.



TruSeq Small RNA Kit
www.illumina.com/mirna



On System: Local Run Manager—Small RNA
On Cloud: BaseSpace Platform—Small RNA
On Site: BaseSpace Platform—Small RNA
www.illumina.com/basespace

Prepare library → Sequence → Analyze data

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Small RNA sequencing

Nextera® XT

Challenge the limits.

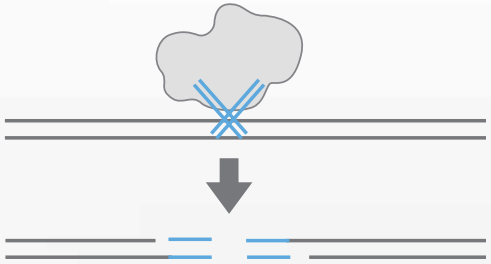
The Nextera XT workflow enables high quality and efficient sequencing for small genomes (bacteria, archaea, viruses), amplicons, and plasmids. Sequencing small microbial genomes provides valuable insights for food testing in public health, infectious disease surveillance, molecular epidemiology studies, and environmental metagenomics. For small genomes, DNA libraries can be prepared, sequenced, and analyzed in as little as 2 days.

Access discovery power.

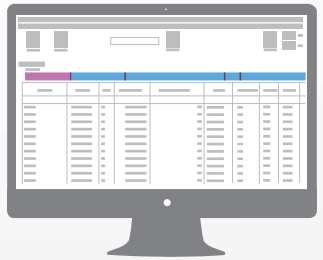
- Characterize microbial communities without cultures.
- Discover entirely new viruses.
- Monitor host-pathogen interactions.
- Investigate of all genes from single organism culture.
- Sequence thousands of organisms in parallel.
- Conduct comprehensive analysis of the microbial or viral genome.

Highlights

- Ultra-low DNA input of only a single nanogram for a wide variety of samples types.
- Prepare libraries in less than 90 minutes with only 15 minutes of hands-on time.
- Simultaneously fragments and tags with sequencing adapters in a single tube enzymatic reaction.
- Rely on a fully supported, optimized workflow solution that includes simple onboard or cloud-based data analysis.



www.illumina.com/nextera



On System: Local Run Manager
On Cloud: BaseSpace Platform—SPAdes
On Site: Genome Assembler BaseSpace

www.illumina.com/basespace

Prepare library → Sequence → Analyze data

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Committed to your success with services, training, and personalized consulting.

We provide accurate and expedient solutions to match your evolving needs. Whether you are just beginning to evaluate your NGS options, or you are an experienced NGS user looking to access strategic consulting alternatives, we have services to support you every step of the way.

Our offerings are flexible and customizable to fit your lab's unique needs.

Product care services

- Tiered service plans, plus add-on options
- Compliance and on-demand services to meet your evolving needs

Illumina University training

- Instructor-led training for the entire workflow
- Online courses
- Webinars

Personalized consulting

- Bioinformatics guidance for ease of adoption
- Proof-of-concept services for instrument and library prep testing
- Concierge services for design assistance and product optimization

Cluster generation and sequencing.

MiniSeq System High-Output Kit*

Cycles	Output
300	7.5 Gb
150	3.75 Gb
75	1.875 Gb

MiniSeq System Mid-Output Kit*

Cycles	Output
300	2.4 Gb

Reads passing filter

MiniSeq System High-Output Kit	
Single reads	Up to 25 million
Paired-end reads	Up to 50 million

MiniSeq System Mid-Output Kit	
Single reads	Up to 8 million
Paired-end reads	Up to 16 million

* Install specifications based on the Illumina PhiX Control Library at supported cluster densities (between 129 and 165 k/mm^2 clusters passing filter). Actual performance parameters may vary based on sample type, sample quality, and clusters passing filter. All MiniSeq System library prep kits are paired-end compatible.

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Industry-leading solutions.
A community of support.

From library prep, arrays, and sequencing to informatics, Illumina genomic solutions empower researchers and clinical researchers across the globe to find the answers they seek.

When you join the Illumina community, you become part of a dynamic scientific movement that includes thousands of researchers and industry thought leaders. Throughout the year, we host user group meetings, symposia, consortia, online forums, and other initiatives—all designed to bring the best minds together to share ideas and advance science.

In addition to on-site training, ongoing support, and phone consults, we offer webinars and courses at various Illumina locations. We're here with all the resources you need to accelerate progress.

The MiniSeq System is a small, robust sequencer, perfect for everyday sequencing. Incorporating the latest advancements in sequencing by synthesis (SBS) chemistry, the flexible MiniSeq System features push-button operation and a streamlined library-to-results workflow.

Learn more about the MiniSeq System at **www.illumina.com/miniseq**.

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A global genomics leader, Illumina provides complete next-generation sequencing workflow solutions to the basic and translational research communities. Illumina technology is responsible for generating more than 90% of the world's sequencing data.* Through collaborative innovation, Illumina is fueling groundbreaking research in the fields of oncology, reproductive health, genetic disease, microbiology, agriculture, and forensic science.

*Data calculations on file. Illumina, Inc., 2015.

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