



xGen™ NGS — MADE FOR YOU

Uncover a comprehensive, flexible range of solutions designed to help you sequence samples and generate research data you never thought you could.



Flexible solutions for various applications and sample types



Rapid, high-quality custom panels that can be combined with other predesigned solutions



Achieve high coverage uniformity at scale



Automation compatible solutions to increase your lab workflow efficiency

We understand your next generation sequencing (NGS) workflow needs are unique. With reliable and flexible workflows, xGen NGS products provide solutions for various applications and sample types so that you can discover faster.

LIBRARY PREPARATION SOLUTIONS

With xGen NGS, a flexible and automatable library preparation workflow provides cost-effective solutions. Wherever your research journey takes you, trust that xGen NGS will assist you.

DNA Library Preparation Kits

xGen DNA Library Prep Kit EZ

A fast and flexible enzymatic library preparation workflow compatible with our suite of custom adapters and xGen hybridization capture products.

xGen ssDNA & Low-Input DNA Library Prep Kit

This kit enables the preparation of libraries from degraded and damaged ssDNA and dsDNA samples in a single reaction. This kit allows users to sequence the difficult-to-process samples using proprietary Adaptase™ technology.

xGen Methyl-Seq Library Prep Kit

Utilizes Adaptase technology for capturing bisulfite-converted ssDNA molecules for epigenetic research studies. The resultant libraries represent a sample base composition of the genome.

xGen DNA Library Prep Kit MC

This kit converts mechanically sheared DNA into libraries suitable for PCR-free, PCR-amplified, and targeted sequencing research applications.

xGen cfDNA & FFPE DNA Library Prep Kit

The unique, single-stranded ligation strategy and workflow converts a high number of low-input DNA molecules into sequencing data.

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



custom oligos • next generation sequencing • CRISPR genome editing • qPCR & PCR • synthetic biology • functional genomics



RNA Library Preparation Kits

xGen DNA Library Prep Kit

A fast RNA-seq workflow creates libraries that use random primers that attach the R1 Stubby Adapters and ligation of R2 Stubby Adapters during the Adaptase step. IDT supplies a variety of index configurations and strategies.

xGen Broad-Range RNA Library Prep Kit

Compatible with a range of RNA input and various indexing options for manual or automated systems. Assemble RNA-seq libraries from 1st strand cDNA synthesis.

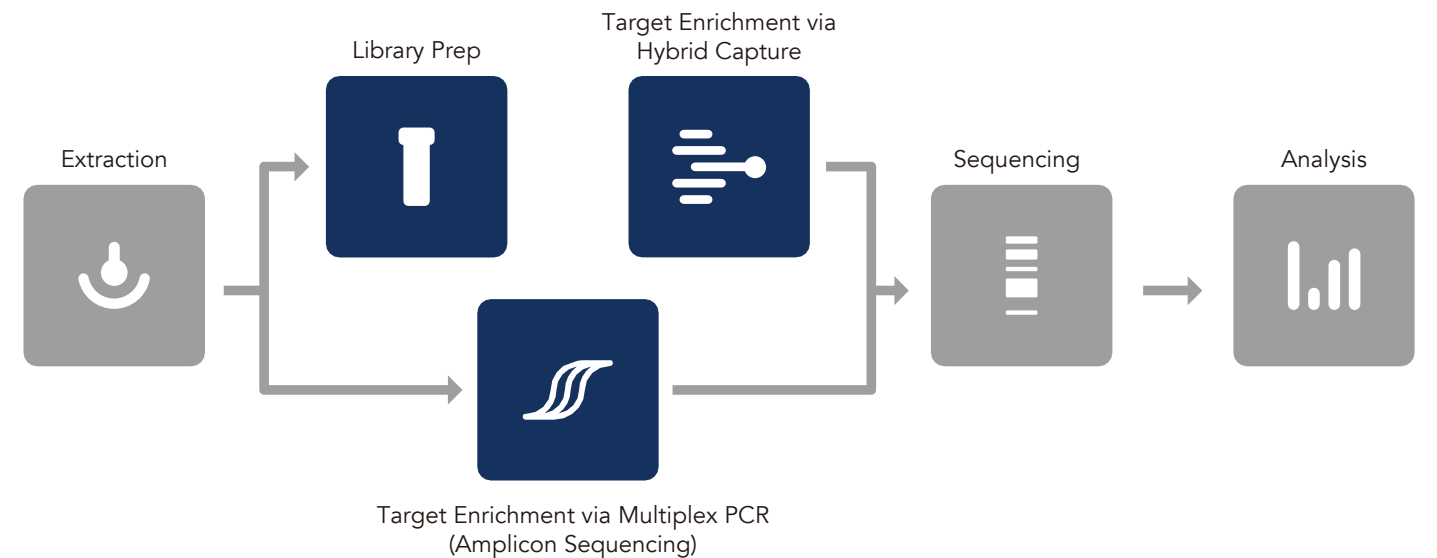
Adapter and indexing primer solutions

IDT provides comprehensive solutions for stocked indexing primers and adapters. Stocked indexing primers are available with single or dual indexes (unique/UDI or combinatorial/CDI) compatible with the Normalase™ workflow. Full-length adapters are available as a dual index (UDI) with an in-line UMI (molecular) barcode (Table 1). In addition to the stocked products, IDT provides you even greater flexibility and control by using the online Custom Adapter Configurator Tool to guide you through designing your own custom NGS adapters.

Table 1. Recommended adapters and indexing primers compatibility based on library prep method.

	Full-length adapters	Indexing primer options				
Indexing strategy	UDI + UMI	UDI	UDI + stubby	CDI	Normalase-UDI	Normalase-CDI
xGen RNA Library Prep		•		•	•	•
xGen Broad-Range RNA Library Prep		•		•	•	•
xGen DNA Library Prep EZ or MC		•		•	•	•
xGen DNA Library Prep EZ or MC UNI	•		•			
xGen ssDNA & Low-Input DNA Library Prep		•		•	•	•
xGen Methyl-Seq Library Prep		•		•	•	•
xGen cfDNA & FFPE Library Prep		•				

ENRICHMENT METHODS



Targeted NGS focuses on sequencing specific areas of the genome. Select an appropriate enrichment method for a particular application, including the most popular methods, which are xGen Hybridization Capture and xGen Amplicon Sequencing.

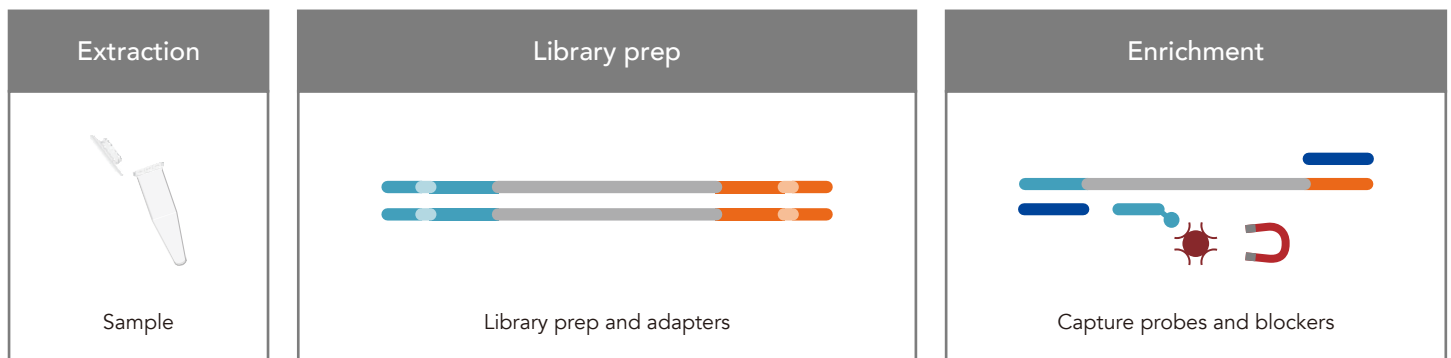
Hybridization capture

This targeted NGS method uses biotinylated oligonucleotides (probes) to hybridize to the regions of interest, which is helpful for genotyping, detecting rare variants, and exome sequencing. In contrast to amplicon sequencing, where PCR primers are designed to avoid mismatched bases due to single nucleotide variations (SNVs) or indels, capture with hybridization probes is likely to perform better due to sequence complexity. Hybridization capture's capacity for mutation discovery makes it particularly suited to cancer research. Since it can be designed for sequence complexity and scalability, this methodology is better for exome sequencing.

The IDT xGen hybridization capture products include a variety of predesigned and custom panels available in various sizes. An updated, automation-friendly protocol is available for high-throughput applications.

xGen Custom Hyb Panel

- **xGen Custom Hyb Panel—Accel** provides the fastest turnaround times for customers (<5 days)
- **xGen Custom Hyb Panel** provides the best trade-off between speed and value (includes NGS functional testing report)
- **xGen Custom Hyb Panel—Production** provides additional quality and NGS functional testing documentation



Feature	xGen Custom Hyb Panel— Accel	xGen Custom Hyb Panel	xGen Custom Hyb Panel— Production
Custom design service	•	•	•
Quality synthesis	•	•	•
xGen NGS Functional Test Report		•	•
Quality documentation			•
Stock custom panel	•	•	•
Reactions	16, 96, custom	16, 96, custom	16, 96, custom
Turnaround time	Within 5 business days*	Within 3 weeks*	Variable

* Turnaround time after design finalization for up to 50,000 probes

Predesigned xGen Hyb Capture Panels

- Exome Hyb Panel v2
- Inherited Diseases Hyb Panel
- Human CNV Backbone Hyb Panel
- Human ID Hyb Panel
- AML Cancer Hyb Panel
- Human mtDNA Hyb Panel
- Pan-Cancer Hyb Panel
- SARS-CoV-2 Hyb Panel

Amplicon sequencing

Amplicon sequencing is a targeted NGS method that enables researchers to analyze genetic variation in specific genomic regions. The xGen amplicon sequencing technology uses multiple overlapping amplicons in a single tube, using a two-hour workflow to prepare ready-to-sequence libraries for research studies (**Figure 1**). xGen NGS amplicon panels provide high-quality primers for target enrichment, increasing your lab workflow efficiency for sequencing while achieving high-quality sequencing coverage.

xGen Custom Amplicon Panels have a single tube workflow performed in as little as 2 hours.

Multiplex PCR

70 minutes

Adapter attachment & indexing PCR

35 minutes

Library normalization with Normalase™ technology (optional)

35 minutes

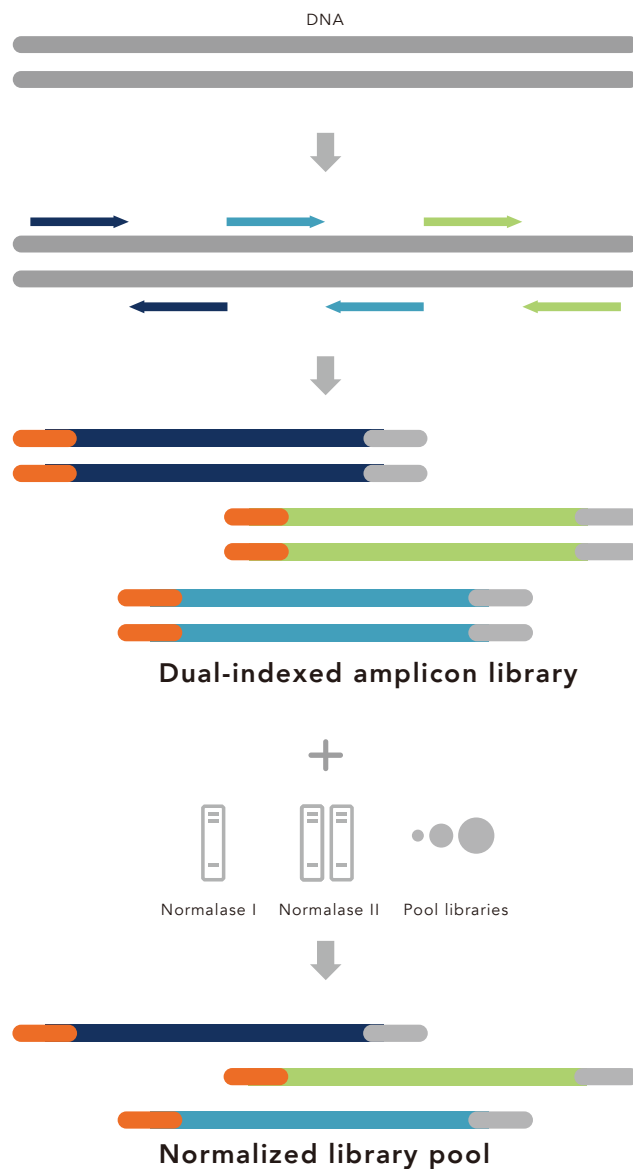


Figure 1. Creating an NGS library starts with a multiplex PCR reaction of a DNA sample to amplify the targets of interest. The samples are then amplified with indexing primers to create a functional dual indexed library. As an optional step, the xGen Normalase reagent is used to normalize the library input concentrations when pooling multiple libraries in a single tube.

Key benefits of the IDT xGen amplicon sequencing technology:

- Amplify hundreds to thousands of targets in single tube PCR
- Amenable for low-input samples such as cell-free DNA
- Simple, fast 2-hour workflow
- Supports high-throughput methods
- Compatible with Illumina® sequencing platforms with the correct adapter and index sequences

Predesigned amplicon sequencing panels

Ready-to-use panels for research on COVID-19, oncology, inherited diseases, metagenomics, or sample ID.

SARS-CoV-2 solutions	<ul style="list-style-type: none"> • SARS-CoV-2 Amplicon Panel
	<ul style="list-style-type: none"> • SARS-CoV-2 ARTIC Panel
	<ul style="list-style-type: none"> • SARS-CoV-2 Midnight Amplicon Panel
	<ul style="list-style-type: none"> • SARS-CoV-2 S Gene Panel
	<ul style="list-style-type: none"> • ACE2 Panel
Oncology/ inherited disease solutions	<ul style="list-style-type: none"> • BRCA1/2 Amplicon Panel
	<ul style="list-style-type: none"> • CFTR Amplicon Panel
	<ul style="list-style-type: none"> • EGFR Pathway Amplicon Panel
	<ul style="list-style-type: none"> • Lynch Syndrome Amplicon Panel
	<ul style="list-style-type: none"> • TP53 Amplicon Panel
	<ul style="list-style-type: none"> • 57G Pan-Cancer Amplicon Panel
	<ul style="list-style-type: none"> • 56G Onco Amplicon Panel v2
	<ul style="list-style-type: none"> • BRCA1/2 PALB2 Amplicon Panel
	<ul style="list-style-type: none"> • Colorectal Amplicon Panel
Metagenomics solutions	<ul style="list-style-type: none"> • 16S Amplicon Panel v2
	<ul style="list-style-type: none"> • ITS1 Amplicon Panel
Other solutions	<ul style="list-style-type: none"> • Human Sample ID Amplicon Panel
	<ul style="list-style-type: none"> • HS EGFR Pathway Amplicon Panel

Custom amplicon sequencing panels

Start from scratch. We'll help you through the design process to create a unique panel for you for your research inquiries. Submit your request to get started.

LIBRARY NORMALIZATION

The xGen Normalase Module offers a novel enzymatic library normalization technology that equalizes DNA or RNA library samples after pooling for loading on Illumina® systems in research studies. The Normalase workflow eliminates the need for library concentration determination before library pooling. With Normalase treatment, there is better cluster density and library balance.

DNA Library Preparation Kits

The xGen Normalase Module can easily be integrated into standard library preparation protocols to improve turnaround time and loading accuracy for NGS laboratories. The library selection and enzymatic normalization steps of the Normalase workflow are designed for consistent amplified library yields 3X the target normalization amount which is achieved with library amplification using Normalase primers.

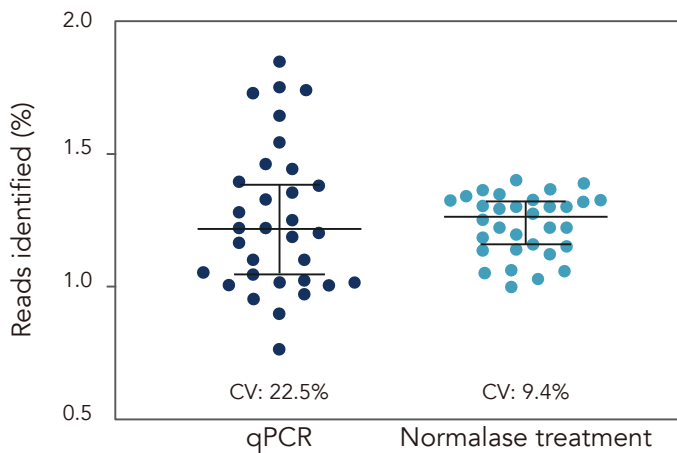


Figure 2. qPCR vs. Normalase treatment. xGen DNA libraries (N=32) were generated with full-length indexed adapters between two users (n=16/user) with 1–250 ng inputs of NA12878 gDNA. Normalase PCR libraries were quantified with qPCR to ensure the libraries met the minimum threshold. Libraries were either quantified by qPCR and then pooling or normalized using the Normalase treatment. Both sets were sequenced to determine percent Reads Identified of each index (MiSeq V2 50 cycle Nano). The coefficient of variation (CV) for the qPCR pool was 22.5% across the two users, while the CV for the Normalase pool was 9.4%. Lines are median and 95% confidence interval.

> FOR MORE INFORMATION, VISIT WWW.IDTDNA.COM/NGS.

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