



NEXTFLEX™ NGS library preparation reagents

Selection guide

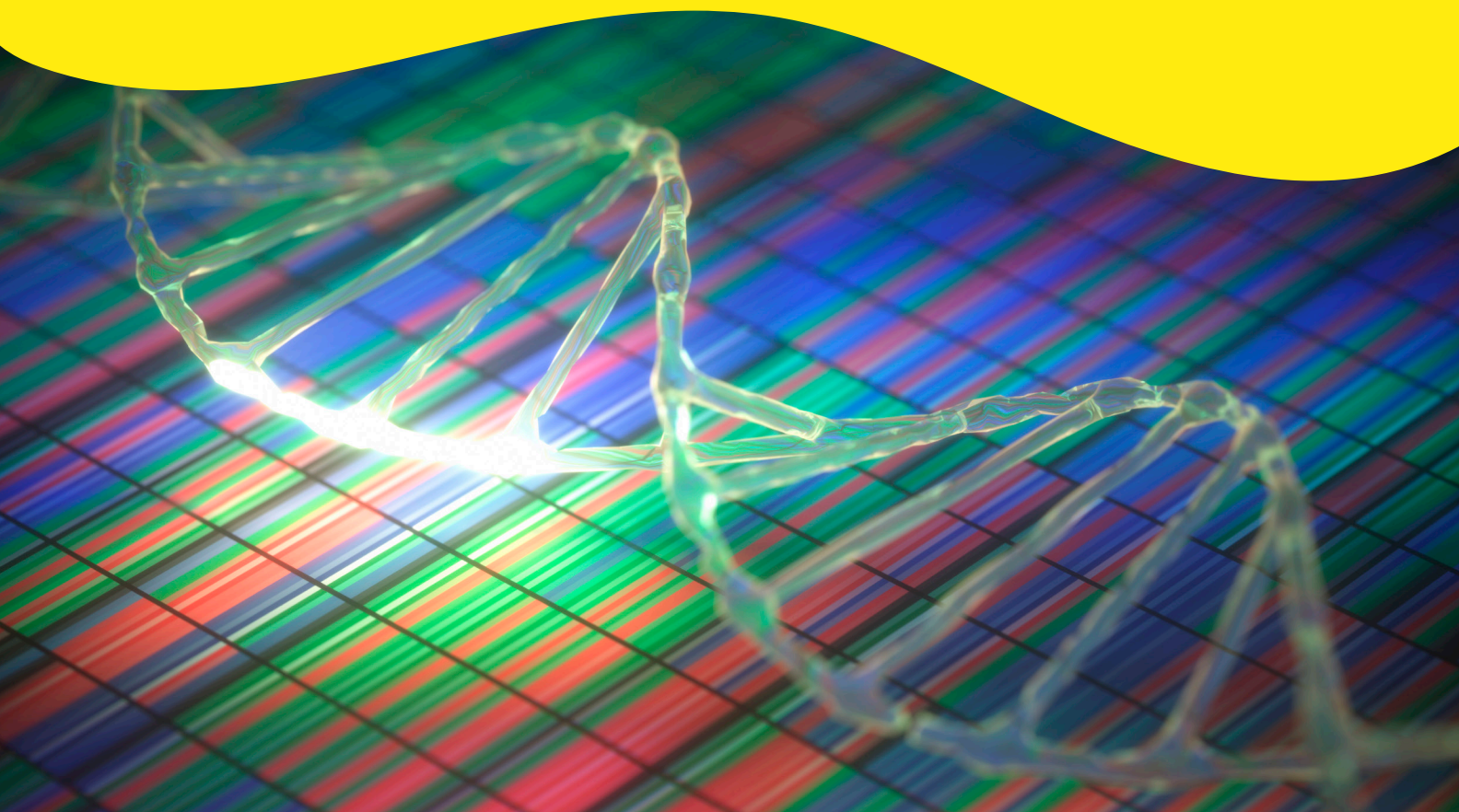


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NEXTFLEX NGS library preparation reagents selection guide

Application	Product features	Library preparation kit
DNA-seq		
Whole-genome sequencing	Enzymatic fragmentation	NEXTFLEX Rapid XP v3 DNA-Seq Kit NEXTFLEX HT Agrigenomics Low-pass WGS Kit
	Mechanical fragmentation	NEXTFLEX Rapid DNA-Seq Kit 2.0
	No fragmentation (Cell-free DNA)	NEXTFLEX Cell Free DNA-Seq Kit 2.0
	Unique Dual Index, up to 384 samples	NEXTFLEX Unique Dual Index Barcodes (1-384)
	Unique Dual Index, up to 1,536 samples	NEXTFLEX Unique Dual Index Barcodes (1-1536)
	Unique Dual Index + UMI, up to 96 samples	NEXTFLEX UDI-UMI Barcodes (1-96)
Metagenomics (16S sequencing)	V1-V4 hypervariable regions of microbial 16S ribosomal RNA genes	NEXTFLEX 16S V4 Amplicon-Seq Kit 2.0 NEXTFLEX 16S V3-V4 Amplicon-Seq Kit NEXTFLEX 16S V1-V3 Amplicon-Seq Kit
Accessories	Universal blockers for hybridization enrichment workflows	NEXTFLEX Universal Blockers
	Cleanup and size selection beads	NEXTFLEX NGS Cleanup Beads
RNA-seq		
RNA sequencing	High-throughput RNA sequencing with no RNA extraction required	MERCURIUS DRUG-seq MERCURIUS Total DRUG-seq
	Strand-specific, total RNA sequencing	NEXTFLEX Rapid Directional RNA-Seq Kit 2.0
	Poly(A) beads for mRNA enrichment	NEXTFLEX Poly(A) Beads 2.0
	Bead-based rRNA depletion	NEXTFLEX RiboNaut rRNA Depletion Kit
	CRISPR-based RNA depletion	NEXTFLEX Cas9-gRNA rRNA Depletion Enzyme NEXTFLEX Cas9-gRNA Globin Depletion Enzyme NEXTFLEX Cas9-gRNA Mito Depletion Enzyme
	Unique Dual Index, up to 384 samples	NEXTFLEX RNA-Seq 2.0 UDI Barcodes (1-384)
	Unique Dual Index + UMI, up to 96 samples	NEXTFLEX UDI-UMI Barcodes (1-96)
Small RNA sequencing	Gel-free workflow with improved detection rate	NEXTFLEX Small RNA-seq Kit v4
	Removal of abundant miRNAs from human whole blood samples	NEXTFLEX miRNA Blood Blockers
	Removal of unwanted small RNAs from samples	NEXTFLEX Custom Small RNA Blockers
	Ribosome Profiling (Ribo-Seq)	RiboLace Pro

Revvity NGS library preparation reagents are compatible with Illumina® and Element® Biosciences platforms

NEXTFLEX NGS barcode adapters

All Revvity NGS adapters include unique dual indexes (UDI) and are compatible with Illumina®, Watchmaker, Twist, and many other TruSeq-style library preparation kits. Adapters containing both UDI and unique molecular identifiers (UMI) are also available.

- Functional validation and sequencing-based index purity testing are performed for every lot
- All NEXTFLEX NGS adapters include UDI
- UMI + UDI adapters are also available
- Compatible with DNA-seq and RNA-seq applications
- Compatible with Illumina and Element sequencing platforms

Example of NEXTFLEX adapter structure

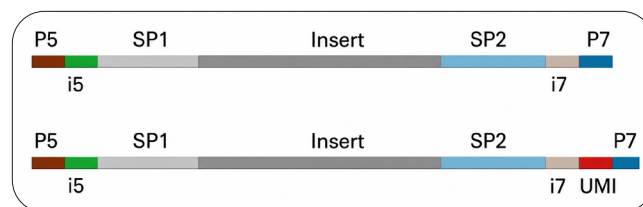
Insert: DNA or RNA fragment derived from the sample

P5, P7: Flow-cell binding sites for Illumina platforms

SP1, SP2: Sequencing primer binding sites

i5, i7: Short sequences (8 or 10 nt) used to identify each sample (UDI)

UMI: 9-nt unique molecular identifier used to tag individual molecules in the library



Unique Dual Indexes (UDI)

UDIs (i5 and i7 in the diagram) are added to both ends of library molecules. This enables parallel multiplex processing of multiple samples and minimizes index hopping, where reads are incorrectly assigned to the wrong index.

- 384-adapter set (8-nt indexes)
- 1,536-adapter set (10-nt indexes)

Unique Molecular Identifiers (UMI)

A 9-nt UMI is incorporated into each library molecule, providing 262,144 possible UMI sequences for molecular tagging.

UMIs are useful for

- Identifying PCR duplicates and distinguishing them from independently derived library molecules
- Supporting error suppression by distinguishing technical errors from true variants

Configuration	Index length	Multiplex options	Library compatibility	Kit
UDI	8	Up to 384 samples	Ligation-based (TruSeq®-style adapters)	NEXTFLEX UDI Barcodes (1-384)
UDI	10	Up to 1536 samples		NEXTFLEX UDI Barcodes (1-1536)
UDI-UMI	10	Up to 96 samples		NEXTFLEX UDI-UMI Barcodes

DNA-Seq barcode adapters

Barcoded adapters for multiplex sequencing

High-quality barcode adapters are essential for successful multiplex sequencing. All adapters not only pass oligonucleotide-level QC, but are also

sequence-verified and undergo quality testing through library preparation, giving you confidence in their performance.

Part no.	Product name	Index length	Reactions	Barcode
NOVA-514150-EVAL16	NEXTFLEX Unique Dual Index Barcodes	8 nt	16	UDI 1-8
NOVA-514150-EVAL48			48	UDI 1-24
NOVA-514150			192	UDI 1-96
NOVA-514151			192	UDI 97-192
NOVA-514152			192	UDI 193-288
NOVA-514153			192	UDI 289-384
NOVA-634100-EVAL16	NEXTFLEX UDI Barcodes	10 nt	16	UDI 1-16
NOVA-634100-EVAL24			24	UDI 1-24
NOVA-634100-EVAL48			48	UDI 1-48
NOVA-634101			96	UDI 1-96
NOVA-634102			96	UDI 97-192
NOVA-634103			96	UDI 193-288
NOVA-634104			96	UDI 289-384
NOVA-634105			96	UDI 385-480
NOVA-634106			96	UDI 481-576
NOVA-634107			96	UDI 577-672
NOVA-634108			96	UDI 673-768
NOVA-634109			96	UDI 769-864
NOVA-634110			96	UDI 865-960
NOVA-634111			96	UDI 961-1,056
NOVA-634112			96	UDI 1,057-1,152
NOVA-634113			96	UDI 1,153-1,248
NOVA-634114			96	UDI 1,249-1,344
NOVA-634115			96	UDI 1,345-1,440
NOVA-634116			96	UDI 1,441-1,536
NOVA-534100			3,072	UDI 1-1,536
NOVA-534101			768	UDI 1-384
NOVA-534102			768	UDI 385-768
NOVA-534103			768	UDI 769-1,152
NOVA-534104			768	UDI 1,153-1,536
NOVA-734100	NEXTFLEX UDI-UMI Barcodes	UDI 10 nt, UMI 9 nt	8	UDI-UMI 1-8
NOVA-734101			24	UDI-UMI 1-24
NOVA-734102			48	UDI-UMI 1-48
NOVA-734103			96	UDI-UMI 1-96

Storage: -20 °C; stable for 12 months under appropriate conditions

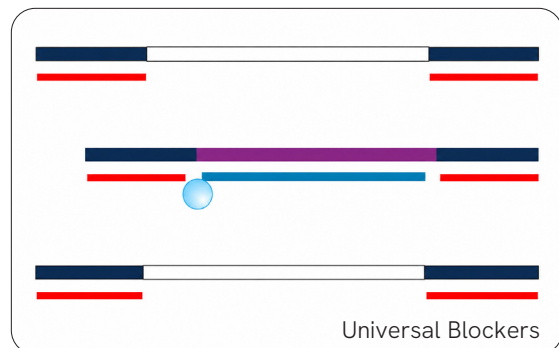
NEXTFLEX universal blockers

During target enrichment, adapters may interact with complementary adapter-sequence strands present on other library molecules.

NEXTFLEX Universal Blockers are short DNA oligos that block non-specific hybridization between adapter sequences.

By preventing adapter-sequence interactions, they improve specificity and help reduce sequencing costs.

NEXTFLEX Universal Blockers are compatible with all NEXTFLEX barcodes and can be used in ligation-based and tagmentation-based workflows for Illumina® and Element® platforms.



- Equivalent enrichment efficiency and data quality to xGen® Universal Blockers at up to 1/15 of the cost
- Compatible with single-index, dual-index, and UMI-containing libraries
- Usable in ligation-based and tagmentation-based Illumina® sequencing workflows
- Easily integrates into existing hybrid-capture protocols with minimal or no changes

NEXTFLEX universal blocker design

Composed of a proprietary mixture of modified oligos designed to bind the P5, P7, SP1, and SP2 sites

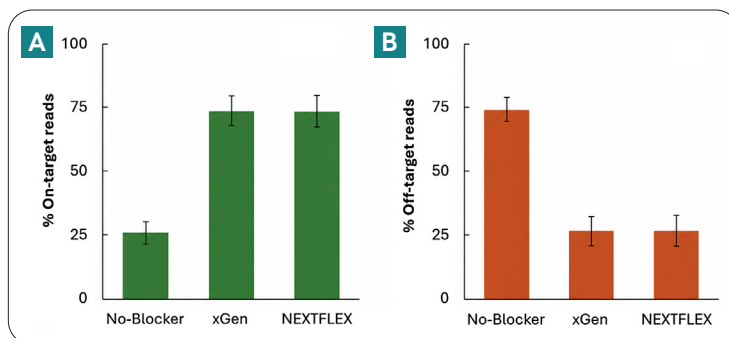
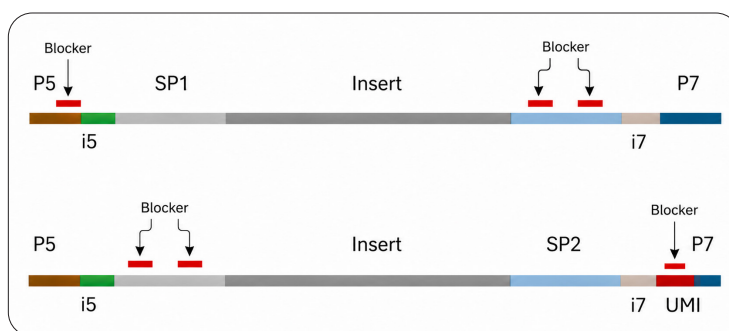


Figure 1: Performance comparison of xGen® Universal Blockers and NEXTFLEX Universal Blockers using the xGen® AML Cancer Panel.

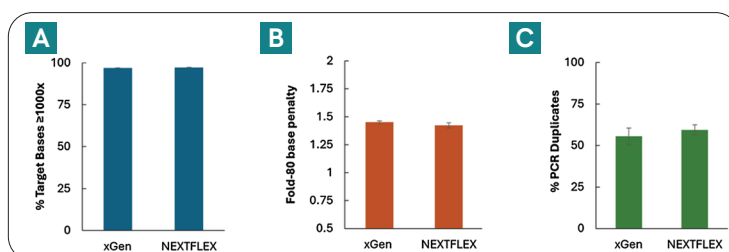


Figure 2: Libraries prepared with the xGen® AML Cancer Panel were enriched using a standard hybridization workflow. Key performance metrics are shown, including the percentage of target bases achieving $\geq 1,000\times$ coverage (A), Fold-80 Base Penalty (B), and PCR duplicate rate (C). Similar read depths were used for each condition.

Part no.	Product name	Reactions
NOVA-5143231	NEXTFLEX Universal Blockers	8
NOVA-5143232		48
NOVA-5143233		96

Storage: -20 °C; stable for 12 months under appropriate conditions

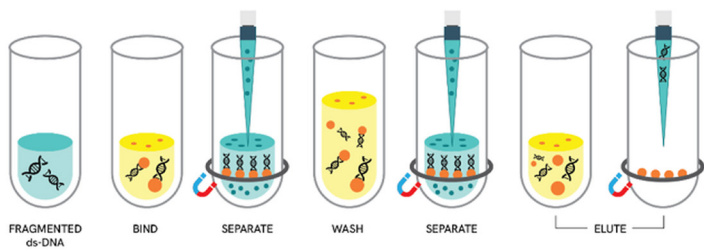
NEXTFLEX NGS Cleanup Beads

NEXTFLEX NGS Cleanup Beads are solid-phase reversible immobilization (SPRI) beads that use reversible magnetic binding to efficiently purify nucleic acids for NGS library preparation, at a fraction of the cost of standard SPRI beads.

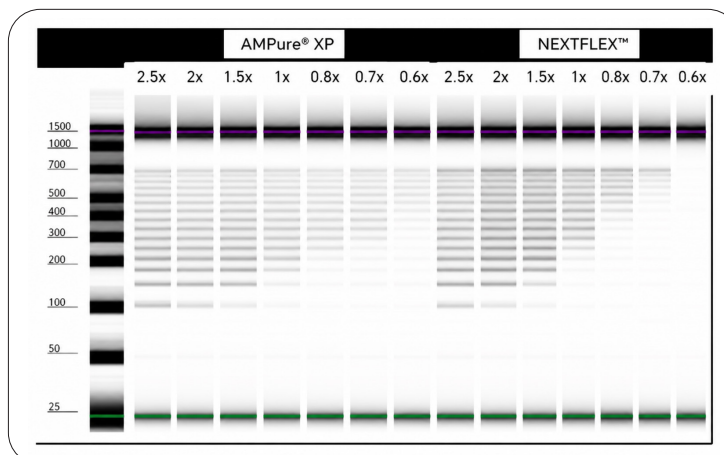
SPRI technology:

- Uses paramagnetic beads to efficiently purify DNA
- In the presence of polyethylene glycol (PEG) and salt, carboxyl groups on the bead surface bind DNA
- Binding is reversible, enabling controlled DNA capture and release
- Size selection is possible by adjusting the bead/sample ratio
- Optimized bead composition provides high recovery and purity
- Compatible with manual and automated workflows
- Drop-in replacement for most SPRI beads (no protocol changes required)

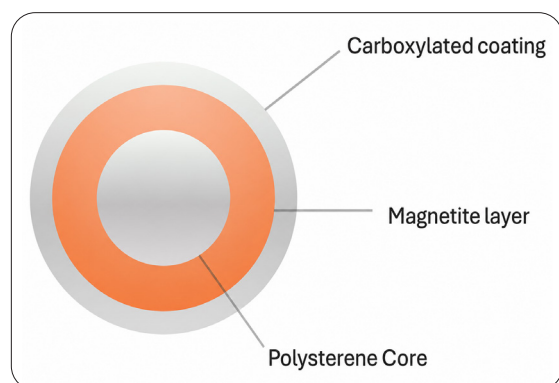
NEXTFLEX NGS Cleanup Beads

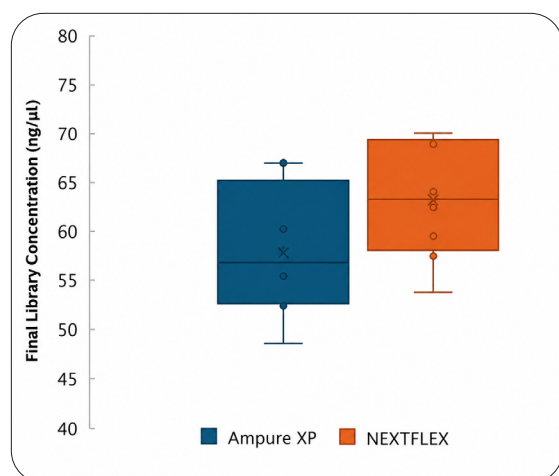


1. Capture DNA using magnetic beads.
2. Isolate beads from impurities.
3. Rinse magnetic beads with 70 % ethanol solution to eliminate impurities.
4. Release DNA from magnetic beads.
5. Transfer eluted DNA to a fresh plate.



NEXTFLEX NGS Cleanup Beads (right) show size-selection behavior equivalent to AMPure® XP beads (left) when purifying 150 ng of a 50 bp Promega DNA ladder, confirming drop-in replacement compatibility.





Final yields obtained when NEXTFLEX NGS Cleanup Beads or a competitor product were used at the same bead-to-sample ratio for cleanup of libraries prepared with the NEXTFLEX 16S V4 2.0 Kit. No significant difference in yield was observed.

Part no.	Product name	Volume
NOVA-BEADS-1ML	NEXTFLEX NGS Cleanup Beads	1 mL
NOVA-BEADS-5ML		5 mL
NOVA-BEADS-50ML		50 mL
NOVA-BEADS-500ML		500 mL

Storage: 4 °C; stable for 6 months under appropriate conditions

DNA library preparation reagents

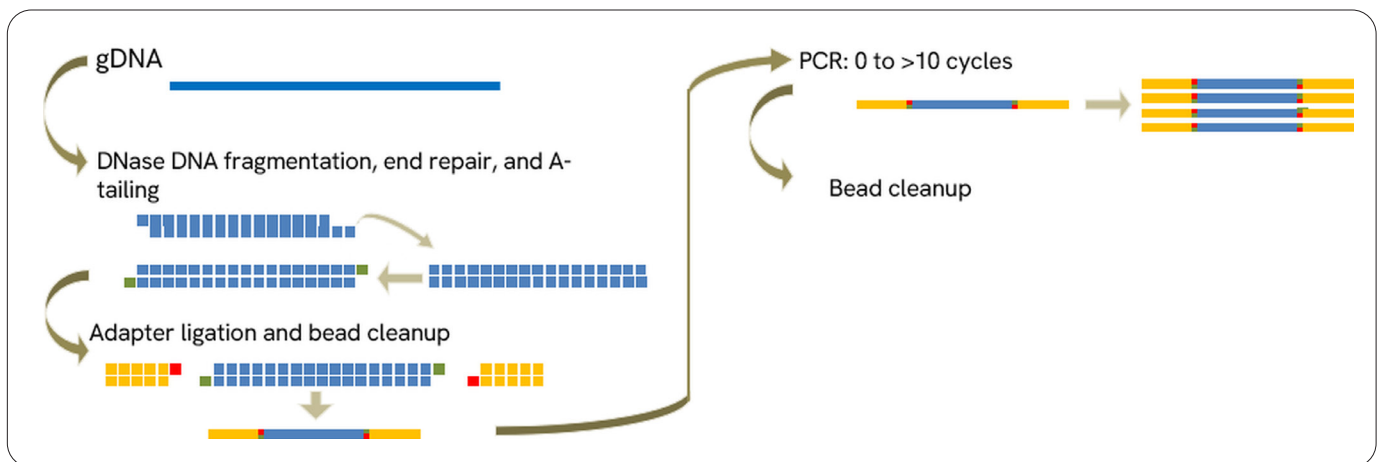
Revvity offers different library preparation kits to support WGS for customers with different requirements

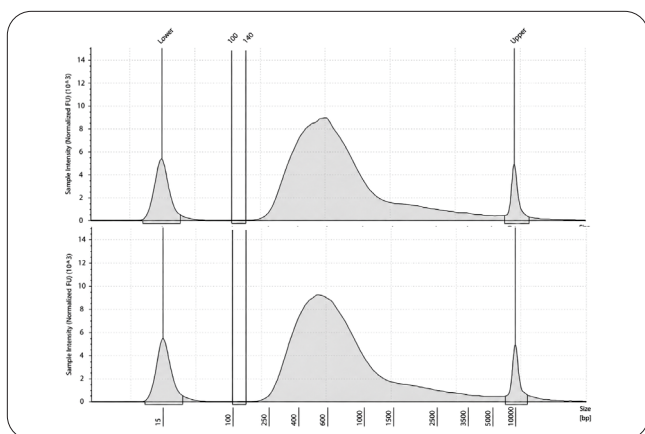
WGS library preparation kit with enzymatic DNA fragmentation: NEXTFLEX Rapid XP v3 DNA-Seq Kit

The new NEXTFLEX Rapid XP v3 DNA-seq Kit uses DNase to randomly cut DNA into sizes suitable for sequencing. It supports library preparation from a wide range of sample types, including low-input DNA and FFPE DNA.

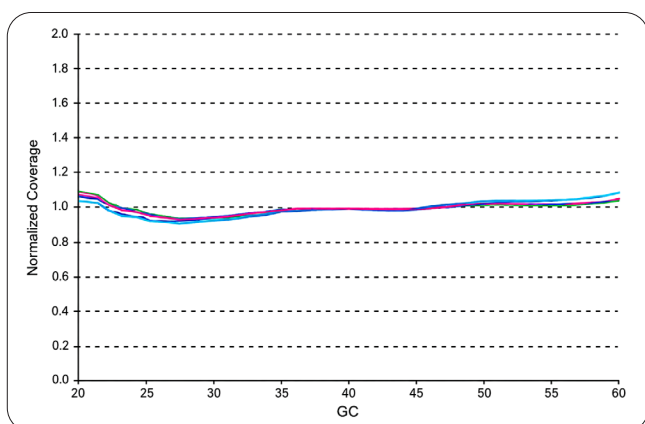
The kit is optimized to efficiently convert both high- and low-quality DNA into Illumina®- and Element®-compatible libraries, delivering improved yield, reduced sequencing artifacts, and uniform coverage. It also adapts easily to high-throughput workflows and automation. A miniaturized protocol is available for cost-sensitive applications.

- Supports a broad DNA input range from <1 ng to 500 ng
- High-efficiency ligation and uniform-coverage preparation completed in 4 hours
- PCR-free preparation possible with ≥ 75 ng DNA (under 90 minutes)
- Automatable on Sciclone G3 NGSx, Sciclone G3 NGSx iQ, and Fontus NGS workstations
- Miniaturized protocols available for the FlexDrop Plus Dispenser (Revvity) and I.DOT Liquid Handler (Dispensix)
- Compatible with NEXTFLEX Normalization Beads to reduce the time needed for final library quantification and pooling





The NEXTFLEX Rapid XP v3 DNA-seq Kit delivers consistent yield and low adapter-dimer formation. Multiple replicate libraries were prepared using 25 ng of human genomic DNA with reaction volumes reduced to one-quarter of the standard volume. Adapter dimers are detected as a peak at approximately 140 bp.



GC-bias analysis of replicate libraries prepared with the NEXTFLEX Rapid XP v3 DNA-Seq Kit. Consistent coverage is obtained across the 20-60 % GC-content range, which represents 95 % of the human genome.

Part no.	Product name	Reactions	Barcode
NOVA-5249-21	NEXTFLEX Rapid XP v3 DNA-Seq Kit	8	Sold separately
NOVA-5249-22		48	Sold separately
NOVA-5249-23		96	Sold separately

Kit contents (storage: *-20 °C, **4 °C, ***room temperature)

- NEXTFLEX Frag Buffer V3*
- NEXTFLEX Frag Enzyme V3*
- NEXTFLEX Ligation Mix V3*
- NEXTFLEX PCR Mix V3*
- NEXTFLEX Primer Mix V2*
- Nuclease-free Water***
- NEXTFLEX NGS Cleanup Beads**

WGS library preparation kit with enzymatic DNA fragmentation: NEXTFLEX HT Agrigenomics Low-pass WGS Kit

This workflow is designed for plant and animal breeding applications using low-pass whole-genome sequencing (LP-WGS). LP-WGS is a cost-effective method that sequences the whole genome at 0.1× to 10× coverage. When combined with imputation, it is becoming a key genotyping approach in plant and animal breeding. Compared with SNP arrays, LP-WGS captures a broader range of genetic variation and is not limited by fixed probe designs, helping accelerate selection and improve prediction accuracy. After sequencing data upload, CURIO* is recommended to generate analysis results within minutes with one click. This solution provides advanced imputation analysis for both plant and animal breeding, from early research to large-scale routine analysis.

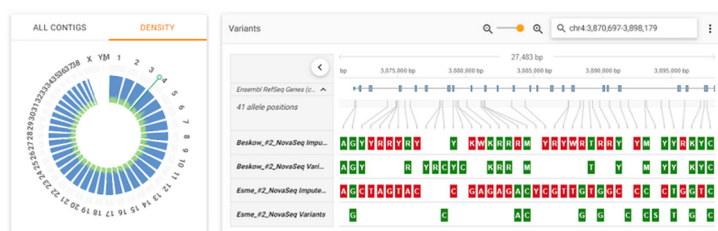
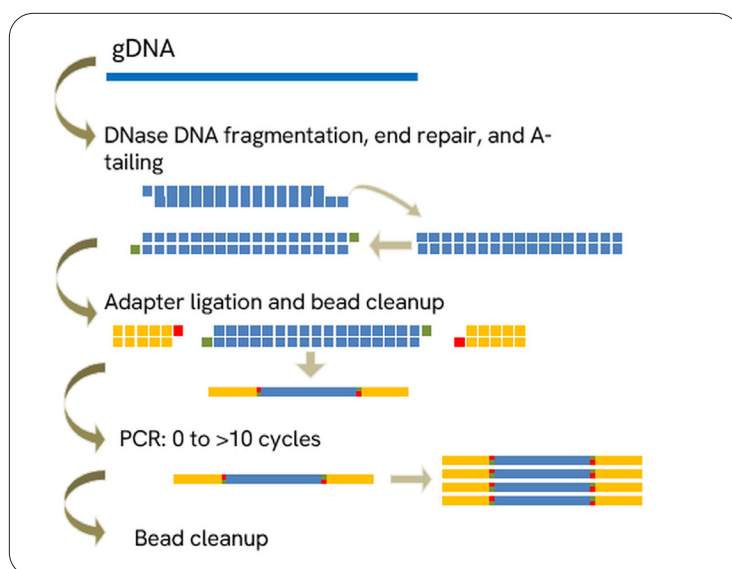
*CURIO analysis is not included with this kit.

- DNA input: 1-500 ng
- Supports high-throughput analysis with up to 1,536 UDI barcodes
- Supports 24- and 384-plate formats and is automation-compatible
- Compatible with Illumina and Element platforms and integrates seamlessly with CURIO analysis

A Revvity authorized collaborator.



From early research to large-scale daily operations of breeders, CURIO provides best-in-class imputation analysis for plant and animal breeders with speed and scalability found in no other agrigenomics platform.



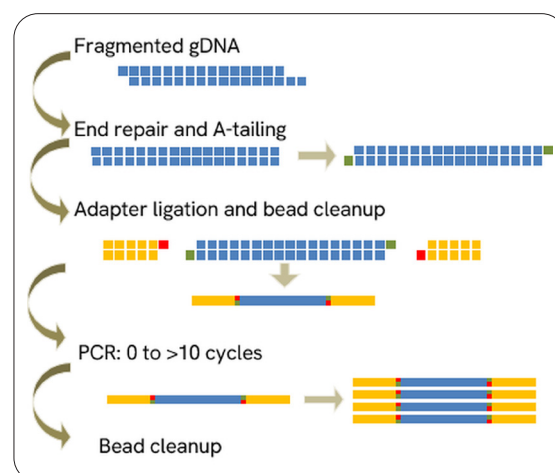
Part no.	Product name	Reactions	Barcode
NOVA-5141-70	NEXTFLEX HT AgriGenomics Low-pass WGS Kit	24	UDI 1-24
NOVA-5141-71		384	UDI 1-384
NOVA-5141-72		384	UDI 385-768
NOVA-5141-73		384	UDI 769-1152
NOVA-5141-74		384	UDI 1153-1536

Kit contents (storage: *-20 °C, **4 °C, ***Room temperature)

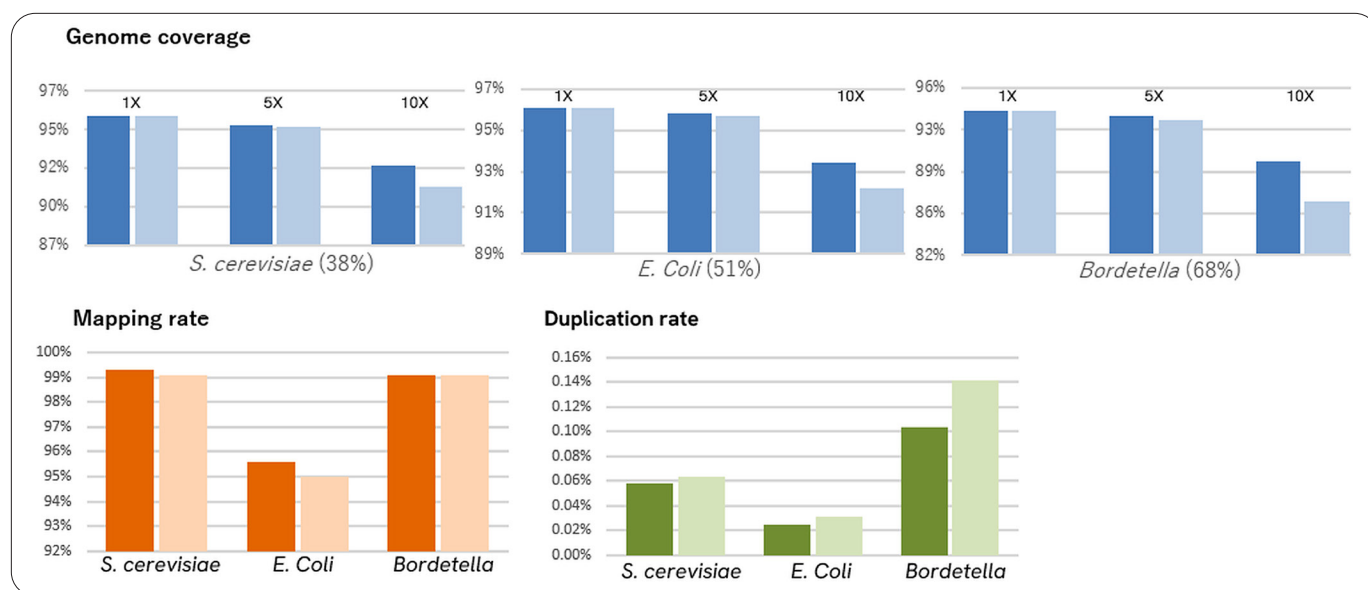
- NEXTFLEX HT Agri Frag Buffer*
- NEXTFLEX HT Agri Frag Enzyme*
- NEXTFLEX HT Agri Ligation Mix*
- NEXTFLEX HT Agri PCR Mix*
- NEXTFLEX HT Agri Primer Mix*
- NEXTFLEX UDI Barcodes (25 µM)*
- Nuclease-free Water***
- NEXTFLEX NGS Cleanup Beads**

WGS library preparation kit for mechanically fragmented DNA: NEXTFLEX Rapid DNA-Seq Kit 2.0

A conventional method in which DNA is fragmented by physical methods (e.g., sonication or nebulization) when random fragmentation is required or enzymatic bias is a concern. It can also be used to sequence amplicons of different sizes.



- For mechanically fragmented DNA (e.g., Covaris® or Bioruptor®)
- Preparation completed in 3 hours
- Minimum input: 1 ng
- PCR-free preparation possible with 250 ng input
- Low GC bias (<3 %) and low duplication rate deliver uniform coverage even for GC-rich genomes and moderately degraded genomes
- Automation-verified on Sciclone™ G3 NGSx and Zephyr™ G3 NGS systems



Part no.	Product name	Reactions	Barcode
NOVA-5188-01	NEXTFLEX Rapid DNA-Seq Kit 2.0	8	Sold separately
NOVA-5188-02		48	Sold separately
NOVA-5188-03		96	Sold separately

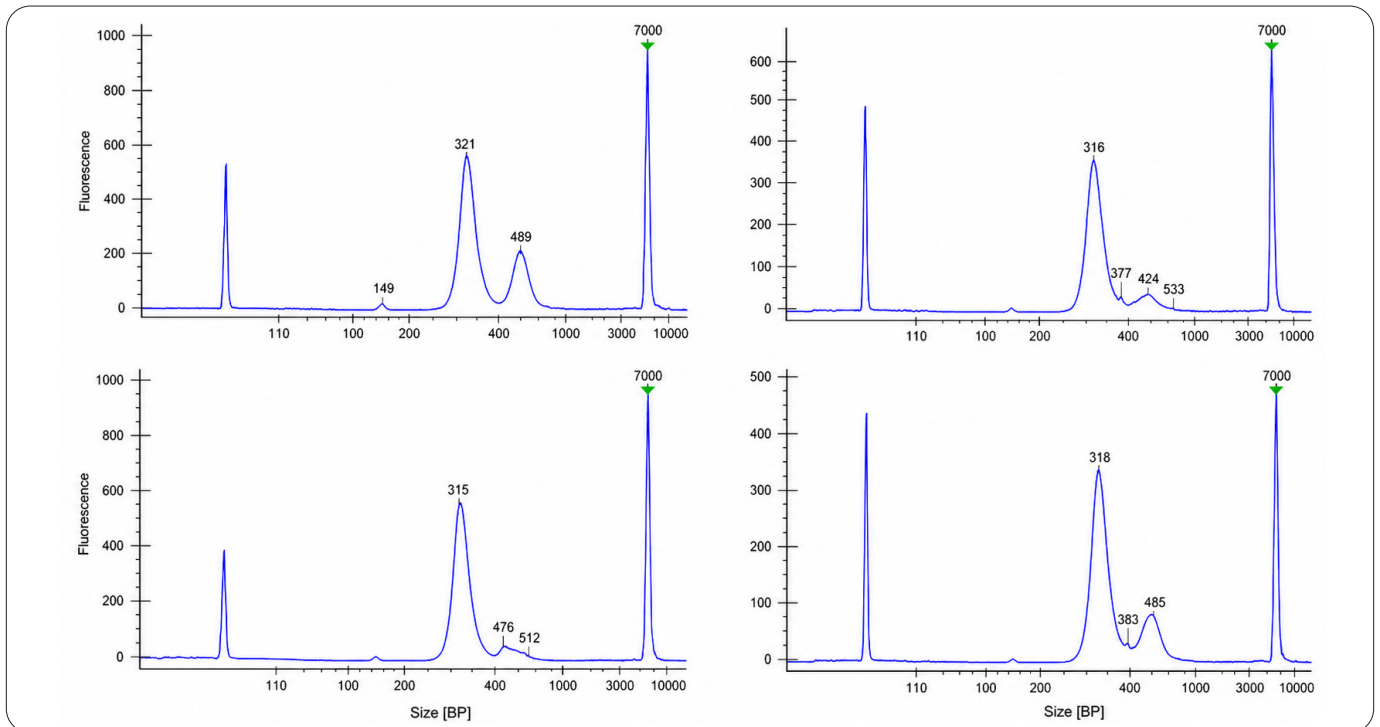
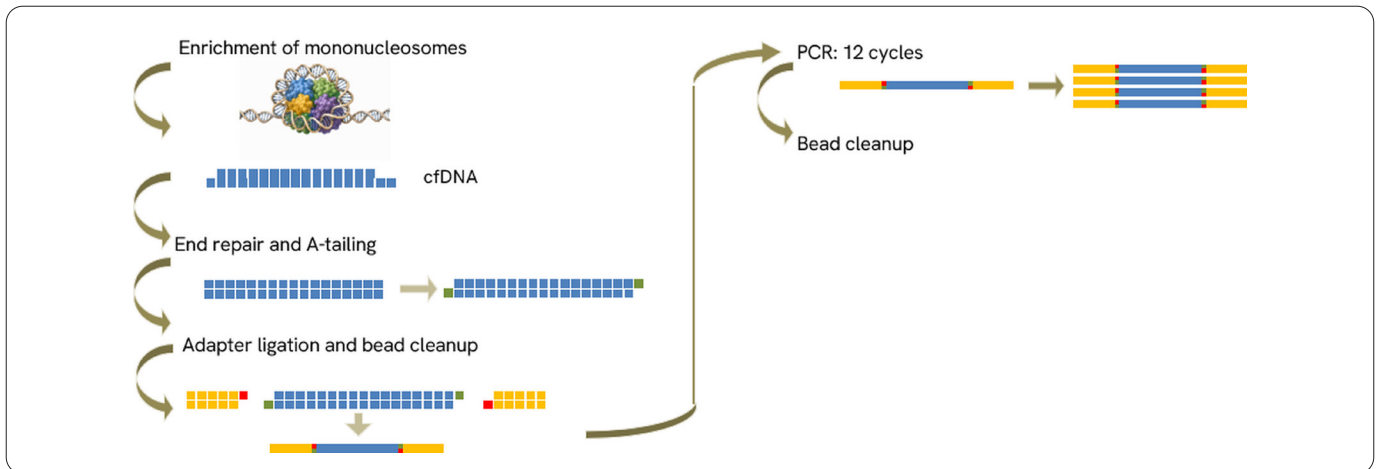
Kit contents (storage: *-20 °C, **4 °C, ***Room temperature)

- NEXTFLEX End-Repair & Adenylation Buffer Mix 2.0*
- NEXTFLEX End-Repair & Adenylation Enzyme Mix*
- NEXTFLEX Ligation Buffer Mix 2.0
- NEXTFLEX Ligation Master Mix 2.0*
- NEXTFLEX PCR Master Mix 2.0*
- NEXTFLEX Primer Mix 2.0 (50 mM)*
- Nuclease-free Water***
- Resuspension Buffer***
- NEXTFLEX Cleanup Beads 2.0**

WGS library preparation kit for cell-free DNA: NEXTFLEX Cell Free DNA-Seq Kit 2.0

Cell-free DNA (cfDNA) present in blood offers advantages as a biological sample because it is relatively easy to obtain and prepare and places a low burden on patients. Prenatal cfDNA testing is widely used to screen for common fetal chromosomal abnormalities, including trisomies. In oncology research, cfDNA analysis can be used to study circulating tumor DNA and tumor-associated genomic alterations. Library preparation kits and cfDNA extraction kits are available.

- Robust performance from 10 ng cfDNA
- A complete workflow in only 2 hours with minimal hands-on time
- Uniform genome coverage with minimized bias
- 1,536 UDI or 96 UDI-UMI options to suppress index hopping and enable error correction



Electropherograms of cfDNA libraries prepared with the NEXTFLEX Cell Free DNA-Seq Kit 2.0 using 10 ng plasma cfDNA show a clear peak at approximately 320 bp, negligible adapter dimers, and high reproducibility under low-input conditions.

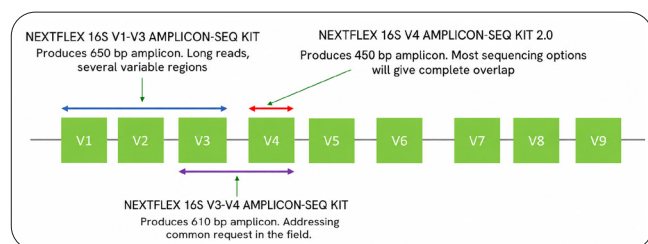
Part no.	Product name	Reactions	Barcode
NOVA-5150-01	NEXTFLEX Cell Free DNA-Seq Kit 2.0	8	Sold separately
NOVA-5150-02	NEXTFLEX Cell Free DNA-Seq Kit 2.0	48	Sold separately
Related products (cfDNA isolation kit)			
CMG-134	chemagic cfDNA 5k Kit (Manual)	40	

Kit contents (storage: *-20 °C, **4 °C, ***Room temperature)

- NEXTFLEX End-Repair & Adenylation Buffer Mix 2.0*
- NEXTFLEX End-Repair & Adenylation Enzyme Mix*
- NEXTFLEX Ligation Buffer Mix 2.0
- NEXTFLEX Ligation Master Mix 2.0*
- NEXTFLEX PCR Master Mix 2.0*
- NEXTFLEX Primer Mix 2.0 (50 mM)*
- Nuclease-free Water***
- Resuspension Buffer***
- NEXTFLEX Cleanup Beads 2.0**

16S rRNA sequencing library preparation kit for metagenomic analysis: NEXTFLEX 16S Amplicon-Seq Kits

The three 16S library preparation kits available cover different regions of the 16S rRNA gene, enabling microbial community profiling.



Kit name	Target region	Features
NEXTFLEX 16S V4 Amplicon-Seq Kit 2.0	V4	Rich reference databases such as SILVA are available. Supports genus-level identification and, in some cases, species-level identification depending on the organism and reference database. The relatively short V4 amplicon is well suited to paired-end short-read sequencing.
NEXTFLEX 16S V3-V4 Amplicon-Seq Kit	V3-V4	Widely used V3-V4 region. PCR I primers include random bases up to 10 nt to increase base diversity and improve sequencing quality, enabling sequencing with little to no PhiX.
NEXTFLEX 16S V1-V3 Amplicon-Seq Kit	V1-V3	Provides high taxonomic resolution for specific microbial taxa. The trade-off between taxonomic resolution and comprehensive community profiling should be considered.

Part no.	Product name	Reactions	Barcode
NOVA-4202-02	NEXTFLEX 16S V1-V3 Amplicon-Seq Kit	24	UDI 1-12
NOVA-4202-03		96	UDI 1-48
NOVA-4202-04		192	UDI 1-96
NOVA-4202-05		192	UDI 97-192
NOVA-4202-06		192	UDI 193-288
NOVA-4202-07		192	UDI 289-384
NOVA-4202-02S		24	UDI 1-12
NOVA-4202-03S		96	UDI 1-48
NOVA-4202-04S		192	UDI 1-96
NOVA-4202-05S		192	UDI 97-192
NOVA-4202-06S		192	UDI 193-288
NOVA-4202-07S		192	UDI 289-384
NOVA-4203-02	NEXTFLEX 16S V4 Amplicon-Seq Kit 2.0	24	UDI 1-12
NOVA-4203-03		96	UDI 1-48
NOVA-4203-04		192	UDI 1-96
NOVA-4203-05		192	UDI 97-192
NOVA-4203-06		192	UDI 193-288
NOVA-4203-07		192	UDI 289-384
NOVA-4203-02S		24	UDI 1-12
NOVA-4203-03S		96	UDI 1-48
NOVA-4203-04S		192	UDI 1-96
NOVA-4203-05S		192	UDI 97-192
NOVA-4203-06S		192	UDI 193-288
NOVA-4203-07S		192	UDI 289-384
NOVA-4204-03	NEXTFLEX 16S V3-V4 Amplicon-Seq Kit	96	UDI 1-48
NOVA-4204-04		192	UDI 1-96
NOVA-4204-03S		96	UDI 1-48
NOVA-4204-04S		192	UDI 1-96

Part numbers ending in “S” include access to Cosmos-Hub for efficient 16S analysis. FASTQ files are processed using a standardized, version-controlled DADA2 pipeline with SILVA taxonomy, generating ASV tables plus clear QC summaries and interactive visualizations.



Tables, heat maps, bar and stacked plots, alpha- and beta-diversity metrics, abundance distributions, differential abundance analysis, and statistical comparisons between groups are available. Analysis results can be exported as tab-delimited files and PDFs, and plots can be downloaded in PNG or SVG format.

Kit contents (storage: *-20 °C, **4 °C, ***Room temperature)

- NEXTFLEX PCR Master Mix*
- NEXTFLEX 16S PCR I Primer Mix*
- NEXTFLEX PCR II Barcoded Primer Mix*
- Resuspension Buffer**
- Nuclease-free Water***
- NEXTFLEX NGS Cleanup Beads**

RNA library preparation reagents

High-throughput RNA sequencing library preparation kit: MERCURIUS™ DRUG-seq and Total DRUG-seq

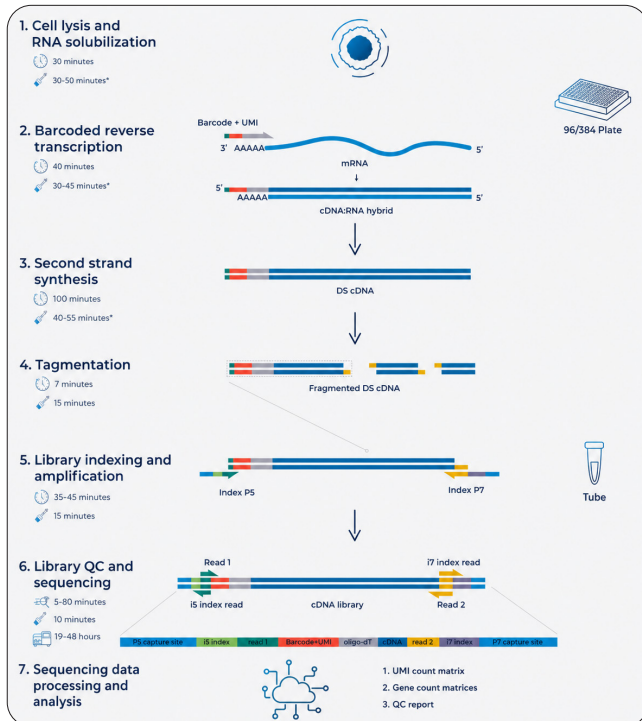
A high-throughput library preparation kit for screening-scale gene-expression profiling. It generates large-scale gene-expression signatures useful for drug-target discovery, functional genomics, hit prioritization, and mechanism-of-action (MoA) analysis.

DRUG-seq can be combined with high-content imaging, cell painting, and Dharmacon™ RNAi and CRISPR screens to add transcriptomic information for deeper MoA analysis.

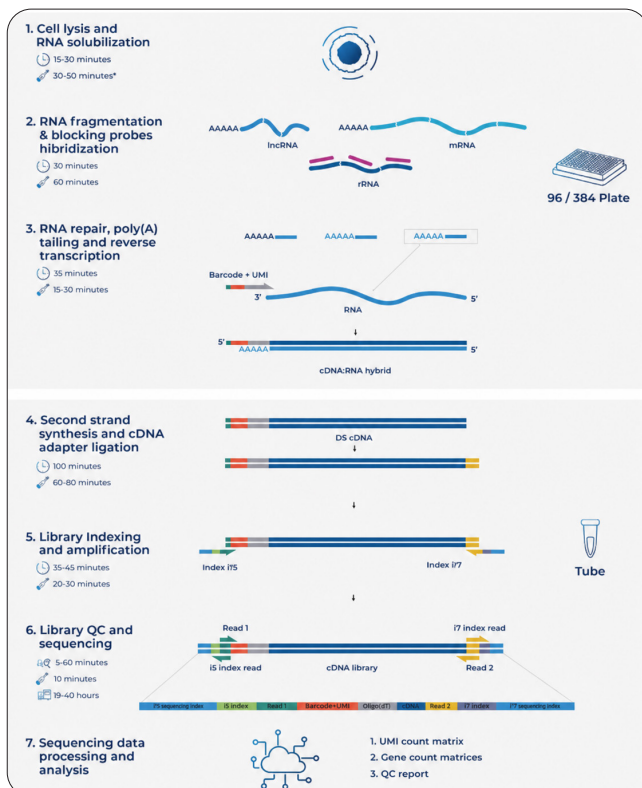
- Library preparation directly from cell lysates
- Extraction-free workflow reduces hands-on time and simplifies sample processing
- Early barcoding supports high-throughput multiplexing of up to 1,536 samples.
- Supports 96-, 384-, and 1,536-well formats
- Substantial cost savings compared with conventional methods



DRUG-seq



Total DRUG-seq



The DRUG-seq workflow uses a proprietary lysis buffer, added directly to cells in pre-washed and frozen 96- or 384-well plates.

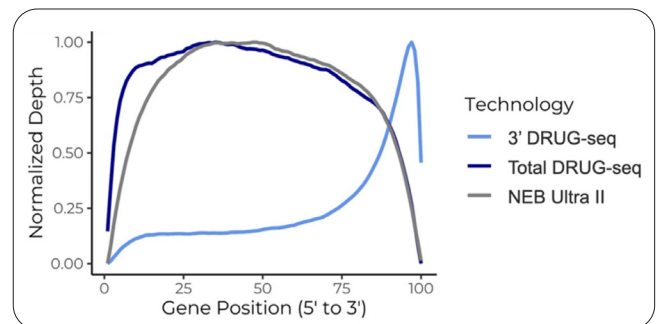
The resulting lysate is transferred directly to the DRUG-seq reverse-transcription reaction plate. The plate contains primers, and each well's RNA sample is tagged with a specific barcode while also receiving a unique molecular identifier (UMI).

All samples are then pooled into a single tube and purified. Library amplification uses unique dual indexes (UDI) to maximize library demultiplexing efficiency in next-generation sequencing. In Total DRUG-seq, after cell lysis, RNA is fragmented and hybridized with oligonucleotides for rRNA depletion. The RNA is then repaired and poly(A)-tailed, and the workflow proceeds similarly to DRUG-seq.

~384
preps in a
single tube

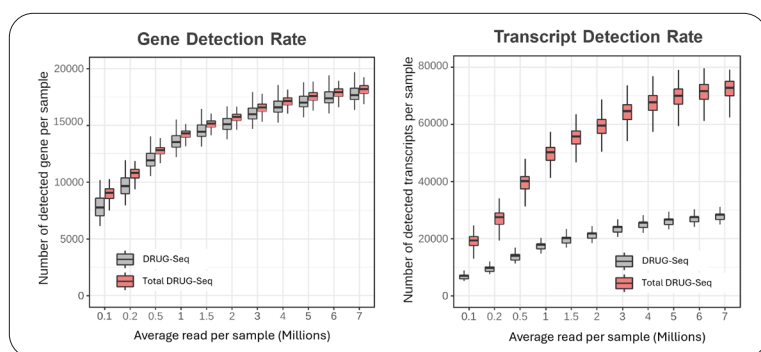
13,000+
genes detected
at 1M reads/
sample

No RNA
extraction
required



Total DRUG-seq shows uniform coverage across the full length of transcripts and performance equivalent to NEB Ultra II Total RNA preparation.

DRUG-seq shows characteristic 3' enrichment, reflecting its 3'-end capture design.



Both protocols detect similar numbers of genes at all read depths. At the transcript level, Total DRUG-seq detects up to approximately 2.5× more transcripts than 3' DRUG-seq at equivalent sequencing depth, demonstrating its ability to cover full-length RNA and distinguish isoforms.

	Output	RNA captured	Transcript coverage	Reads/sample	Required cell number
DRUG-seq	Gene level	mRNA	3'-end gene	Approx. 1-2 million reads	15,000-50,000 (96 well) 2,000-10,000 (384 well)
Total DRUG-seq	Whole transcriptome	Total RNA (mRNA + non-coding RNA)	Full transcript length	Approx. 2-5 million reads	5,000-25,000 (96 well) 2,000-10,000 (384 well)

Please contact us for a list of validated cell lines/tissues.

Part no.	Product name	Reactions	Plate format
NOVA-10841	MERCURIUS DRUG-seq	96	1 x 96
NOVA-11041		384	4 x 96
NOVA-10851		384	1 x 384
NOVA-11051		1536	4 x 384
NOVA-10705	MERCURIUS Total DRUG-seq	96	1 x 96
NOVA-11661		384	4 x 96
NOVA-10706		384	1 x 384
NOVA-11662		1536	4 x 384

Kit contents (storage: -20 °C)

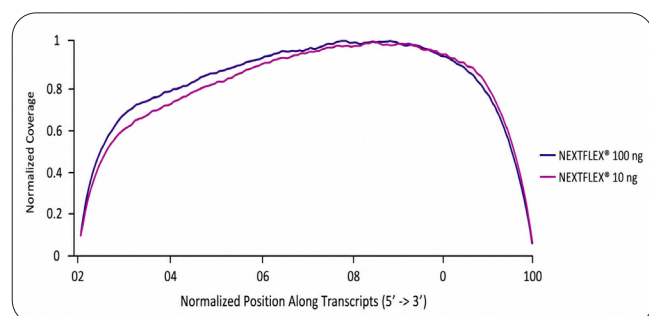
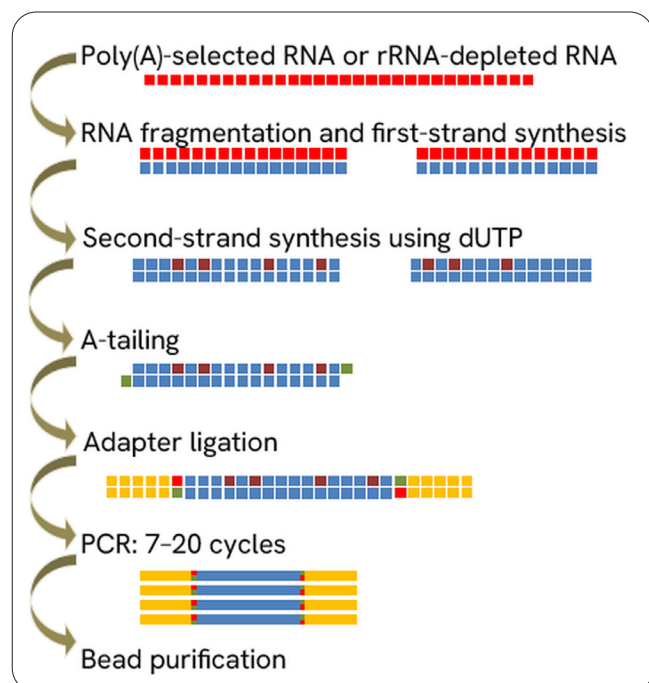
- Barcoded oligo-dT adapter plate
- Library preparation components
 - RT Enzyme, Buffer
 - rRNA Depletion Mix**
 - Repair/RI Enzyme, Solution**
 - Exonuclease I Enzyme, Buffer
 - Second Strand Enzyme, Buffer
 - Tagmentation Enzyme, Buffer*
 - Adapter Ligation Buffer**
 - BRB-compatible Adapter**
 - Library Amplification Mix
- UDI Adapter Mix
- Cell Lysis Buffer
- RNase Inhibitor
- Aluminum seal

*DRUG-seq only

**Total DRUG-seq only

Library preparation kit for RNA sequencing: NEXTFLEX Rapid-Directional RNA-Seq Kit 2.0

Generates strand-specific data with highly uniform coverage and low duplication rates. Poly(A) beads for mRNA capture and reagents for rRNA depletion are also available.



NEXTFLEX Rapid Directional RNA-Seq Kit 2.0 shows uniform coverage across transcripts using 100 ng and 10 ng of human total RNA.

- Supports an input range of 5 ng-5 µg of total RNA
- Validated for use with NEXTFLEX Poly(A) Beads 2.0 and NEXTFLEX RiboNaut rRNA Depletion
- Strand-specific detection of coding transcripts and non-coding transcripts including lncRNAs

Part no.	Product name	Reactions	Barcode
NOVA-5198-01	NEXTFLEX Rapid Directional RNA-Seq Kit 2.0	8	Sold separately
NOVA-5198-02		48	Sold separately
NOVA-5198-03		96	Sold separately
NOVA-5198-43	Automation Friendly Volumes	48	Sold separately
NOVA-5198-53		96	Sold separately

Kit contents (storage: *-20 °C, **4 °C, ***Room temperature)

- NEXTFLEX RNA-Seq Fragmentation Buffer Mix 2.0*
- NEXTFLEX RNA-Seq Directional First Strand Synthesis Buffer Mix 2.0*
- NEXTFLEX RNA-Seq Rapid Reverse Transcriptase 2.0*
- NEXTFLEX RNA-Seq Directional Second Strand Synthesis Mix 2.0*
- NEXTFLEX RNA-Seq Adenylation Buffer Mix 2.0*
- NEXTFLEX RNA-Seq Adenylation Enzyme 2.0*
- NEXTFLEX RNA-Seq Ligase Buffer Mix 2.0*
- NEXTFLEX RNA-Seq Ligase Enzyme 2.0*
- NEXTFLEX RNA-Seq PCR Master Mix 2.0*
- NEXTFLEX RNA-Seq Primer Mix 2.0*
- Nuclease-free Water***
- Resuspension Buffer***
- NEXTFLEX Cleanup Beads XP**

RNA-Seq barcode adapters: Barcoded adapters for multiplex sequencing

High-quality barcode adapters are essential for successful multiplex sequencing. All adapters not only pass oligonucleotide QC but are also sequence-confirmed and pass quality checks through library preparation, providing confidence in use.

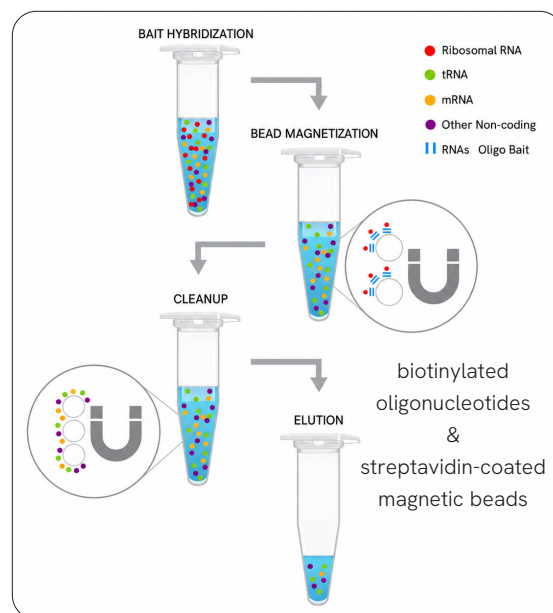
Note: Both the i5 and i7 indexes are 8 nt.

Part no.	Product name	Reactions	Barcode
NOVA-512920-eval16	NEXTFLEX RNA-Seq 2.0 Unique Dual Index Barcodes	16	UDI 1-8
NOVA-512920-eval48		48	UDI 1-24
NOVA-512920		192	UDI 1-96
NOVA-512921		192	UDI 97-192
NOVA-512922		192	UDI 193-288
NOVA-512923		192	UDI 289-384

Bead-based ribosomal RNA depletion kit: NEXTFLEX RiboNaut rRNA Depletion Kit

Uses subtractive hybridization with biotinylated probes and magnetic-bead capture of ribosomal RNA to generate RNA depleted of ribosomal RNA for downstream RNA-seq library preparation.

- Removes cytoplasmic and mitochondrial ribosomal RNA from human, mouse, and rat total RNA
- Broad transcript detection: retains mRNA and non-poly(A) RNA
- Compatible with almost all short-read bulk RNA-seq library preparation workflows. Prepared libraries can be analyzed on compatible sequencing platforms.
- Automated on the Sciclone and Zephyr workstations



Part no.	Product name	Reactions
NOVA-512961	NEXTFLEX RiboNaut rRNA	8
NOVA-512962	Depletion Kit (Human / Mouse	48
NOVA-512963	/ Rat)	96

Kit contents (storage: *-20 °C, **4 °C, ***Room temperature)

- NEXTFLEX Bait Hybridization Buffer***
- NEXTFLEX Cleanup Buffer**
- NEXTFLEX RiboNaut Bait Mix*
- NEXTFLEX Cleanup Beads XP**
- NEXTFLEX RiboNaut Beads**
- Nuclease-free water***
- NEXTFLEX RiboNaut Beads Wash Buffer***

Bead-based mRNA enrichment: NEXTFLEX poly(A) beads 2.0

Selectively captures poly(A)-tailed mRNA to reduce ribosomal RNA and background, improving detection efficiency in RNA-seq. Use when targeting poly(A)-tailed mRNA and RNA quality is high. If RNA is degraded or non-poly(A) transcripts such as lncRNAs are targets, an rRNA depletion kit can be selected.

- Capture with oligo(dT) magnetic beads enables elution of intact mRNA even from low RNA amounts.
- Compatible with almost all short-read bulk RNA-seq library preparation workflows. Prepared libraries can be analyzed on any sequencing platform.
- Simple magnetic separation reduces variability and shortens hands-on time

Part no.	Product name	Reactions
NOVA-512991	NEXTFLEX Poly(A) Beads 2.0	8
NOVA-512992		48
NOVA-512993		96
NOVA-512994	Automation Friendly Volumes	48
NOVA-512995		96

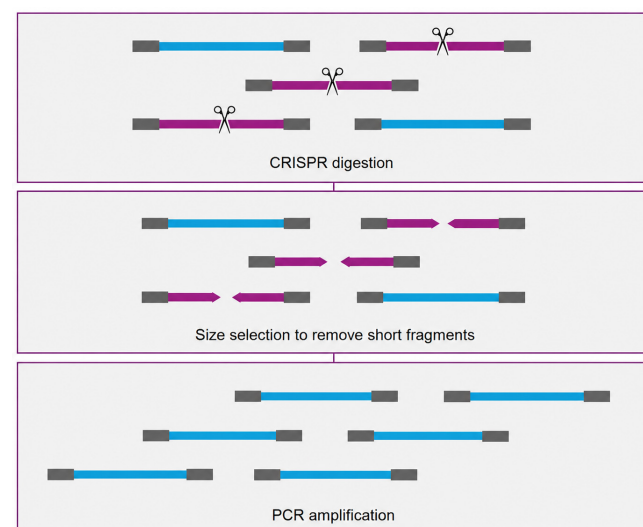
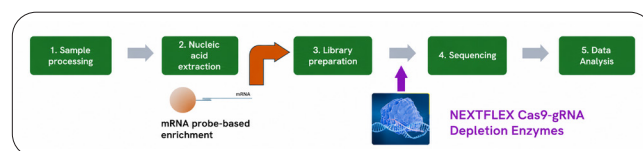
Kit contents (storage: 4 °C)

- NEXTFLEX Poly(A) Beads 2.0
- NEXTFLEX Poly(A) Elution Buffer 2.0
- NEXTFLEX Poly(A) Binding Buffer 2.0
- NEXTFLEX Poly(A) Washing Buffer 2.0

CRISPR-based RNA depletion solutions: NEXTFLEX Cas9-gRNA RNA depletion enzymes

Jumpcode's DepleteX™ technology uses Cas9 and guide RNAs to selectively cleave unwanted RNA-derived sequences, such as ribosomal RNA, after conversion to double-stranded DNA. This depletion step can be performed either after second-strand synthesis or after library preparation.

By reducing non-informative reads, these enzymes increase the proportion of reads assigned to relevant transcripts, improving transcriptome coverage and supporting higher-quality clustering, differential expression analysis, and downstream biological interpretation.



The Cas9-guide RNA complex targets and cuts dsDNA sequences corresponding to unwanted RNA-derived targets, increasing the proportion of informative reads.

- Depletion is performed after conversion to DNA, leaving the input RNA untouched
- Digestion time is approximately 1 hour, with only 5 minutes of hands-on time
- Easily integrated into any library preparation workflow
- Compatible with both short-read and long-read sequencing
- Compatible with bulk and single-cell sequencing

CRISPR-based ribosomal RNA depletion: NEXTFLEX Cas9-gRNA rRNA depletion enzyme

- Uses 435 guide RNAs targeting GRCh38-annotated nuclear ribosomal RNA loci (5S, 5.8S, 18S, 28S, and 45S) and mitochondrial rRNA loci (12S and 16S).
- Functionally validated to provide good ribosomal RNA depletion performance in human, mouse, rat, dog, and chicken libraries

Part no.	Product name	Units
NOVA-801100	NEXTFLEX Cas9-gRNA	6-10
NOVA-801500	rRNA Depletion Enzyme	30-500

One unit is the amount required to deplete the recommended input of 1–10 ng dsDNA (corresponding to library size ≥ 400 bp and insert size approximately ≥ 300 bp).

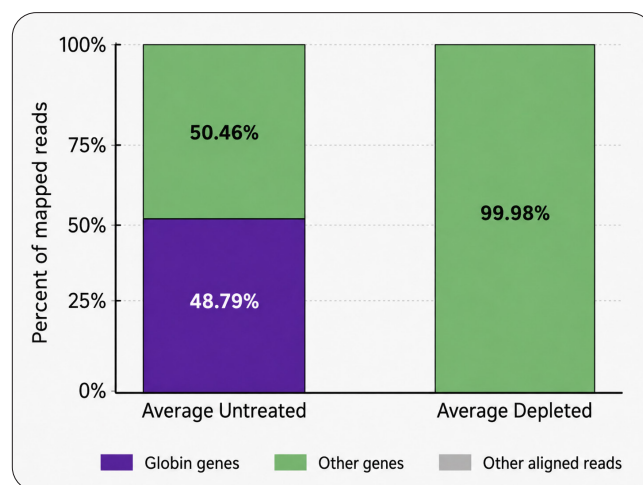
Kit contents (storage: -80°C)

- NEXTFLEX Cas9-gRNA Depletion Enzyme
- NEXTFLEX 10x Cas9 Buffer

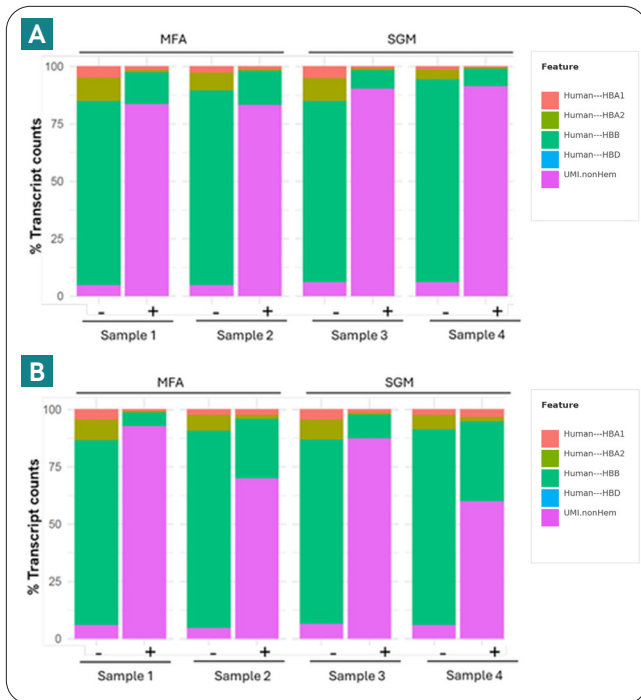
CRISPR-based globin mRNA depletion: NEXTFLEX Cas9-gRNA globin depletion enzyme

Designed to remove globin-derived sequences from RNA-seq libraries derived from human blood, reducing hemoglobin-derived background.

- Uses 30 guide RNAs targeting the HBA1, HBA2, HBB, and HBD genes.



Percentage of mapped reads assigned to globin genes (purple) and non-globin genes (green) in untreated and Cas9-treated libraries. In untreated libraries, globin transcripts account for almost half of the reads; after Cas9 globin depletion, most reads align to non-globin genes.

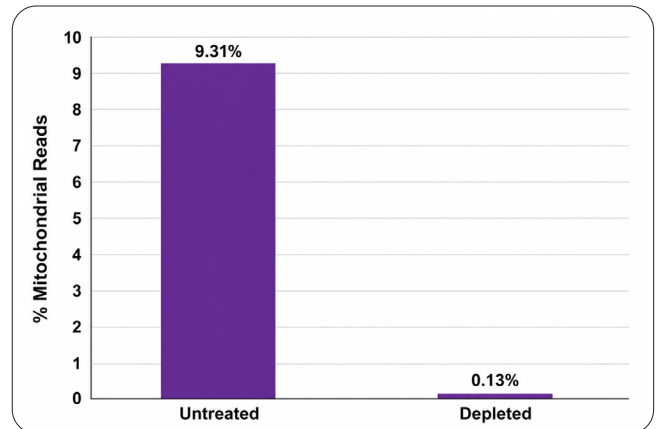


Single-cell RNA-seq (10x Genomics) results from malaria parasite-infected blood cells (A) or infected bone marrow cells (B). In globin-depleted samples (+), the percentage of UMI counts mapped to target globin genes is reduced compared with untreated samples (-). MFA: Minimal Fatty Acid Media; SGM: Standard Growth Media

CRISPR-based mitochondrial depletion: NEXTFLEX Cas9-gRNA mito depletion enzyme

Cuts mitochondrial-derived sequences at the double-stranded DNA stage, reducing mitochondrial background in NGS libraries. In ATAC-seq, it removes mitochondrial peaks that can account for a large fraction of reads, producing clearer nuclear open-chromatin profiles in mitochondria-rich tissues such as heart, muscle, and brain. Removal of excess mitochondrial reads is also useful for single-cell RNA sequencing.

- Can be applied to completed libraries with excessive mitochondrial reads to reduce mitochondrial background and increase the fraction of reads available for nuclear targets
- Uses 657 guide RNAs.



Comparing the percentage of reads mapped to the mitochondrial genome before and after depletion of the same library shows a strong reduction from 9.31 % to 0.13 %.

Part no.	Product name	Units
NOVA-802100	NEXTFLEX Cas9-gRNA	6-10
NOVA-802500	Globin Depletion Enzyme	30-500
NOVA-803100	NEXTFLEX Cas9-gRNA	6-10
NOVA-803500	Mito Depletion Enzyme	30-500

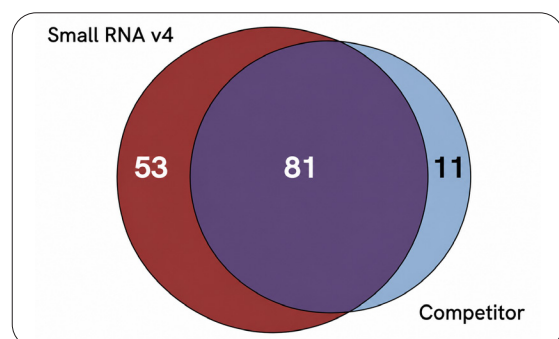
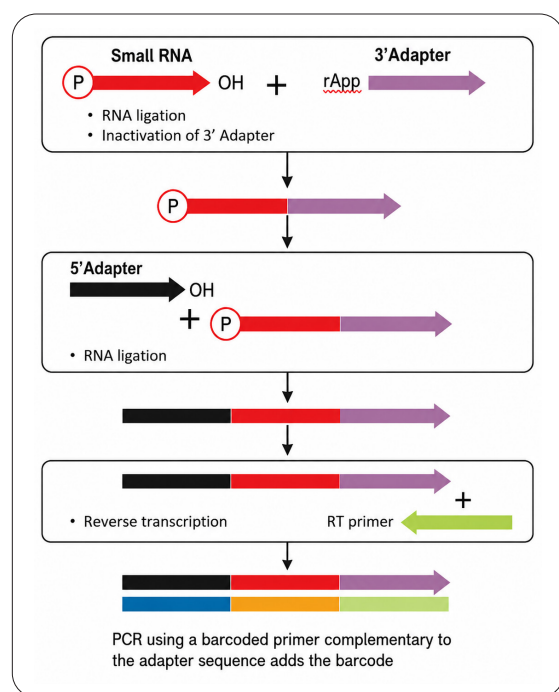
One unit is the amount required to deplete the recommended input of 1-10 ng dsDNA.

Kit contents (storage: -80 °C)

- NEXTFLEX Cas9-gRNA Depletion Enzyme
- NEXTFLEX 10x Cas9 Buffer

Library preparation kit for small RNA sequencing: NEXTFLEX Small RNA-Seq Kit v4

Small RNA library preparation requires direct ligation of single-stranded small RNA to adapters. This kit optimizes reaction conditions to achieve highly efficient ligation of small RNAs while reducing adapter-dimer formation. As a result, small RNA abundance can be accurately analyzed even from low-concentration samples without gel-based size selection.



Comparison of detected miRNA species. More than 45 % more miRNAs were detected with NEXTFLEX than with the competitor kit.

- Gel-free protocol (no PAGE purification) usable from as little as 1 ng total RNA.
- Automation-compatible
- Low-bias ligation and dimer-reduction chemistry improve data quality from challenging samples such as body fluids and extracellular vesicles
- Library preparation completed in approximately 6 hours
- 384 UDI barcodes support high-throughput multiplexing and minimize index hopping on Illumina/Element platforms
- Every lot is rigorously tested to ensure quality

Part no.	Product name	Reactions	Barcode
NOVA-5132-31	NEXTFLEX Small RNA-Seq Kit v4	8	UDI 1-8
NOVA-5132-32		48	UDI 1-48
NOVA-5132-41		96	UDI 1-96
NOVA-5132-42		96	UDI 97-192
NOVA-5132-43		96	UDI 193-288
NOVA-5132-44		96	UDI 289-384

Kit contents (storage: *-20 °C, **4 °C, ***Room temperature)

- NEXTFLEX 3' Adenylated Adapter v4*
- NEXTFLEX 3' Ligation Buffer v4*
- NEXTFLEX 3' Ligation Enzyme Mix v4*
- NEXTFLEX Adapter Depletion Solution***
- NEXTFLEX tRNA/YRNA Blockers v4*
- NEXTFLEX Adapter Inactivation Mix v4*
- NEXTFLEX 5' Adapter v4*
- NEXTFLEX 5' Ligation Buffer v4*
- NEXTFLEX 5' Ligation Enzyme Mix v4*
- NEXTFLEX RT Enzyme Mix v4*
- NEXTFLEX RT Buffer v4*
- NEXTFLEX RT Primer v4*
- NEXTFLEX UDI Barcoded Primer Mix v4*
- NEXTFLEX Small RNA PCR Master Mix v4*
- Resuspension Buffer***
- Nuclease-free Water***
- microRNA Control*
- NEXTFLEX Cleanup Beads**

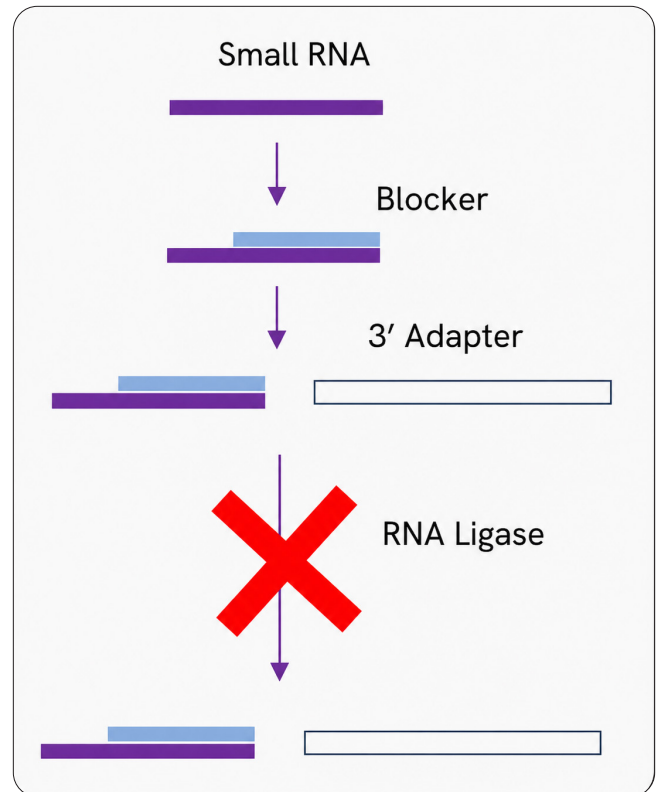
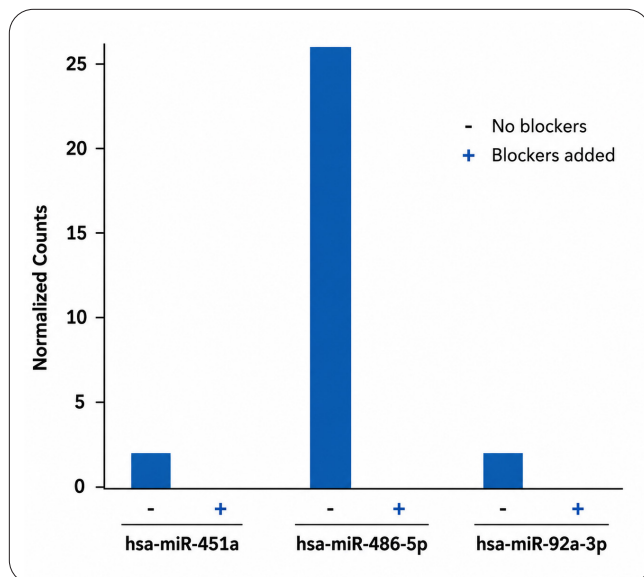
Library preparation-related reagents for small RNA sequencing: NEXTFLEX blood miRNA blockers

NEXTFLEX blood miRNA blockers are a mixture of oligonucleotides that reduce the abundance of specific highly abundant microRNAs (miRNAs) in small RNA libraries prepared from total RNA extracted from human whole blood and plasma.

Blocking of these species has been reported to enable detection of 100 additional miRNAs in a sample and increase the number of detectable miRNA species by approximately 20 %⁽¹⁾.

(1) NAR Genom Bioinform. 2020 Feb 12;2(1):lqaa008. doi: 10.1093/nargab/lqaa008

- Removes miRNAs highly abundant in whole blood and plasma (50-70 % of small RNA), such as hsa-miR-451a, hsa-miR-486-5p, and hsa-miR-92a-3p
- Compatible with the NEXTFLEX Small RNA-Seq Kit v4



NEXTFLEX blood miRNA blockers effectively remove the three major highly expressed miRNAs in human whole blood and plasma.

Part no.	Product name	Reactions
NOVA-513103	NEXTFLEX blood miRNA blockers	96

Storage: -20 °C

Library preparation-related reagents for small RNA sequencing: NEXTFLEX custom small RNA blockers

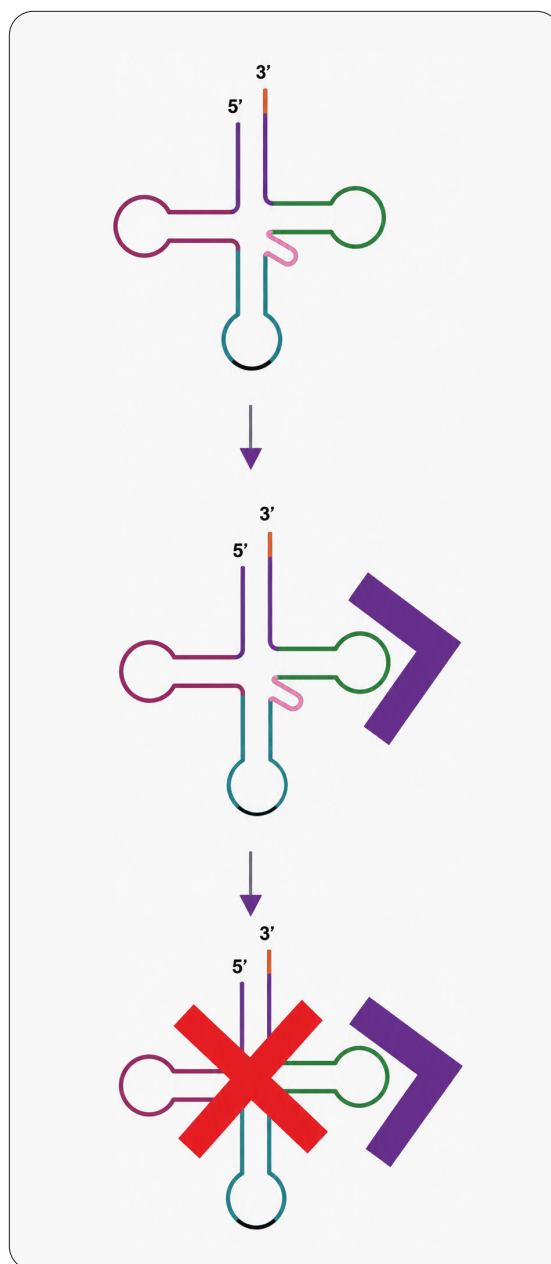
Small RNA sequencing can analyze diverse RNA molecules shorter than 200 nucleotides. However, in most samples, a small number of highly abundant RNAs, such as tRNA fragments, Y RNA fragments, and some overexpressed miRNAs, account for a large proportion of sequencing reads. This reduces sensitivity for detecting low-abundance RNAs that may provide important biological insights. Blocking highly abundant miRNAs has been reported to enable detection of 100 additional miRNAs in a sample and increase the number of detectable miRNA species by approximately 20 %⁽¹⁾.

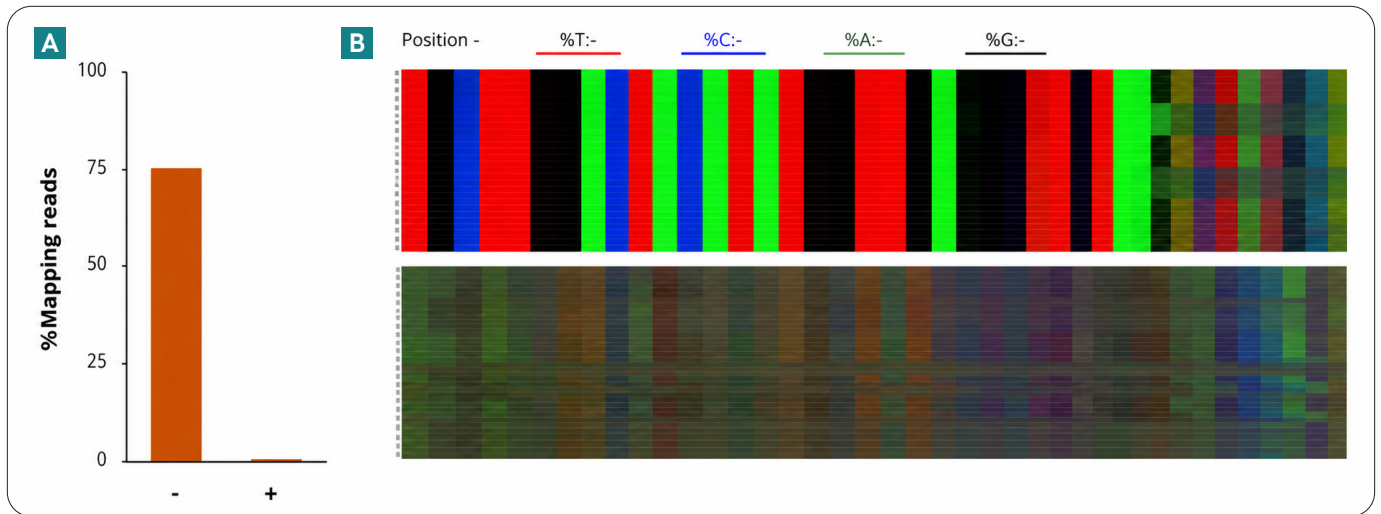
With NEXTFLEX Custom Small RNA Blockers, up to 10 user-selected highly abundant sequences can be selectively removed. This allocates more sequencing depth to biologically important transcripts. The blockers support flexible designs based on species, tissue, and study design and can be used for small RNA analysis in non-human species or to block specific miRNAs or rRNAs.

(1). *NAR Genom Bioinform.* 2020 Feb 12;2(1):lqaa008. doi: 10.1093/nargab/lqaa008

- Affordable and customizable
- Targets up to 10 user-selected sequences
- Selectively reduces targeted unwanted sequences
- Used during 3' adapter ligation in the NEXTFLEX Small RNA-Seq Kit v4. Hybridized RNA cannot undergo 3' adapter ligation, preventing subsequent PCR amplification
- Compatible with tRNA/Y RNA blockers* and blood miRNA blockers

*Included in the NEXTFLEX Small RNA-Seq Kit v4





In *Drosophila melanogaster* small RNA libraries, 2S rRNA may account for the majority of reads. A. Percentage of reads mapped to 2S rRNA in libraries prepared from RNA extracted from whole adult males, without blockers (-) and with blockers (+). B. Per-base sequence composition (FastQC). In the no-blocker sample (top), base composition is dominated by the 2S rRNA sequence, causing strong position-dependent bias. In the blocker-added sample (bottom), this bias is greatly reduced, consistent with effective removal of 2S rRNA.

Part no.	Product name	Reactions
NOVA-51313-01	NEXTFLEX Custom Small RNA Blockers	96

When contacting us, please provide sample information such as serum, plasma, tissue, cells, plants, EVs, etc. Supported blocker lengths are 20-60 nt.

Library preparation-related reagents for small RNA analysis: RiboLace® Pro

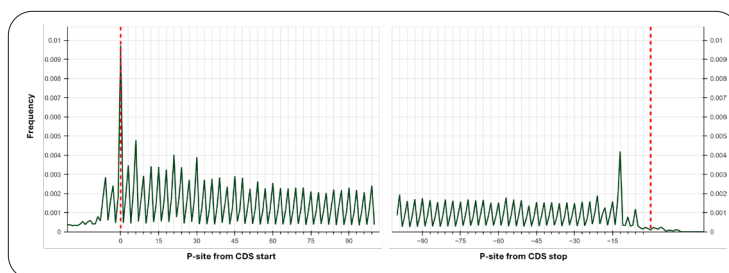
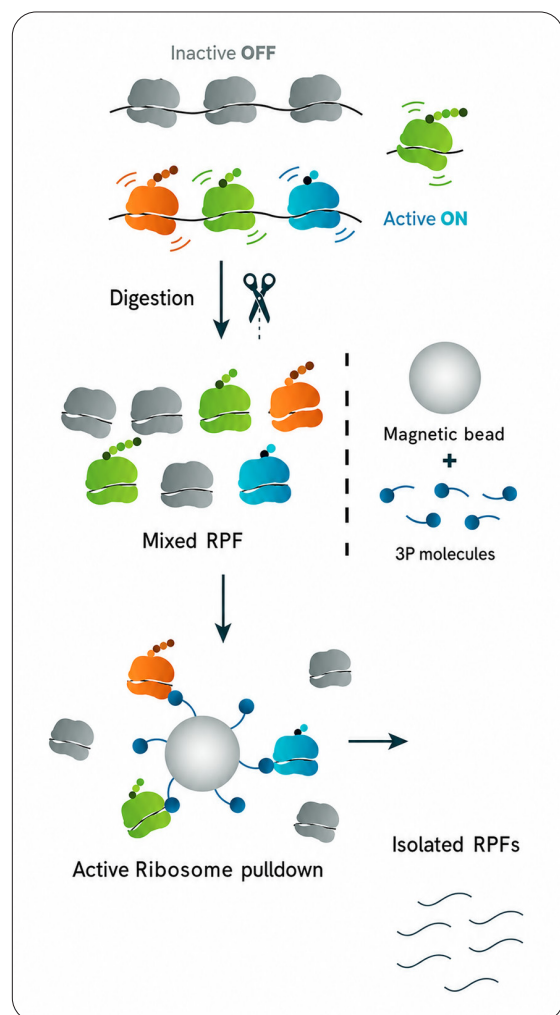
Ribosome profiling (Ribo-Seq) captures a snapshot of mRNAs being translated in cells at a given point in time. In recent years, the need to study translation accurately has increased⁽²⁾, and the technology is becoming increasingly important in cancer research and drug discovery.

In Ribo-Seq, ribosome-protected fragments (RPFs, or ribosome footprints) must be isolated to determine the positions of translating ribosomes at nucleotide resolution. RPFs are approximately 28-30 nucleotides long and are analyzed by small RNA-seq. RiboLace Pro is a kit for selectively enriching actively translating ribosomes for Ribo-Seq.

(2). *Nat Methods*. 2025 Oct;22(10):2002-2006. doi: 10.1038/s41592-025-02810-3.

- Uses magnetic beads immobilized with a puromycin-derived molecule (3P) to selectively capture actively translating ribosomes and enrich ribosome-protected fragments (RPFs) suitable for ribosome profiling analysis
- Antibody- and tag-free enrichment process
- No sucrose density gradient or cushion ultracentrifugation required
- Compatible with primary cultured cells, immortalized eukaryotic cell lines, and tissue samples
- Required cell input: >35,000 cells
- Validated with the NEXTFLEX Small RNA-Seq Kit

The puromycin-derived molecule (3P) immobilized on magnetic beads selectively binds to the A site of ribosomes during peptide elongation, pausing peptide elongation. After RNase treatment, ribosome-protected fragments (RPFs) captured on the magnetic beads are purified and enriched.



The metagene profile summarizes average ribosome occupancy (P-site frequency) across all transcripts and provides an overview of ribosome behavior around translation start and stop sites. P-site positions were aggregated within ± 100 nt around start and stop sites. The data suggest accurate P-site assignment and consistent ribosome positioning during translation initiation and termination. RPFs were isolated with RiboLace Pro, and sequencing libraries were prepared with the NEXTFLEX Small RNA-Seq Kit.

Part no.	Product name	Reactions
RL00P-12	RiboLace Pro	12

Kit contents (storage: *-20 °C, **4 °C)

- Lysis buffer*
- B-Buffer**
- RiboLace Magnetic Beads v2.1**
- OH-buffer**
- mPEG*
- RiboLace smart probe*
- W-buffer**
- Nuclease*
- Nux Enhancer*
- Proteinase K*
- SDS 10 %**

Library preparation automation

Fontus NGS automated liquid handler

Fontus NGS is an automated liquid handler that fully automates NGS library preparation for 96 DNA/RNA samples. It includes reagent-cooling units and a thermal cycler required for library preparation. Fontus NGS has a dual-arm configuration consisting of an 8-channel variable-span pipette (Varispan) and a 96-channel multichannel dispensing arm, enabling automated library preparation while reducing reagent dead volume.

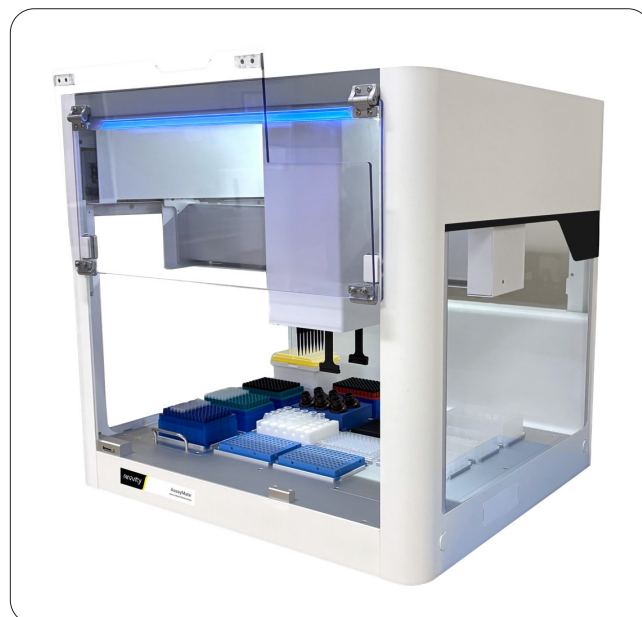
- Supports library preparation for 96 samples
- Integrated thermal cycler
- Integrated reagent-cooling unit
- Also supports normalization and pooling



AssayMate automated liquid handler

AssayMate is a compact liquid handler composed of an 8-channel fixed pipette and a gripper arm. Users can easily create protocols, and a thermal cycler option is available to support automated library preparation.

- Supports library preparation for 24-32 samples
- Thermal cycler option available
- Reagent-cooling unit option available
- Also supports one-sample-at-a-time normalization and pooling by attaching a single tip



NGS-related instruments

Omni Bead Ruptor Elite homogenizer

A bead-based homogenizer can be used for preprocessing samples such as tissue samples that require disruption. Processes 24 samples in 2 mL tubes simultaneously.



VICTOR Nivo plate reader

Compact plate reader supporting absorbance, luminescence, and fluorescence measurements. Can be used for nucleic acid quantification.



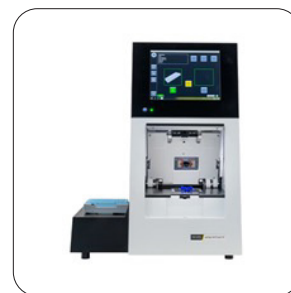
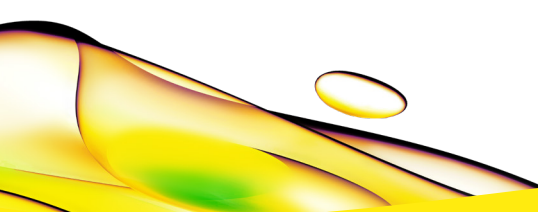
chemagic 360 nucleic acid extraction instrument

Automatically extracts DNA/RNA from up to 96 samples of various types using proprietary magnetic beads. A built-in dispenser eliminates the need for users to prepare wash buffers and similar reagents.



LabChip GX Touch automated electrophoresis

Fully automated electrophoresis system supporting up to 384 samples. Analysis in as little as 28 seconds per sample.

revvity

www.revvity.com