

FROM SEQUENCING TO INSIGHT

Real-world applications powered by NEBNext®



HUMAN HEALTH



POPULATION GENOMICS

Recent advances in sequencing technology have made human whole-genome and whole-transcriptome sequencing suitable for understanding genomic variation and expression at population scale. These projects require flexible solutions for processing tens of thousands of samples, including automation compatibility, enzymatic fragmentation and modular kit formats.

NEBNext Solutions

- Streamline and scale library prep with NEBNext UltraExpress® FS DNA
- Build libraries in 3 hours with NEBNext UltraExpress RNA
- Analyze the methylome at population scale with Enzymatic Methyl-seq (EM-seq™) v2



AGRICULTURAL BIOLOGY

Genomic technologies are being employed to address global food shortage concerns. Development of crops with resistance to pathogens, drought and environmental extremes requires structured approaches to measure and monitor key polymorphisms at scale, in a cost-effective manner.

NEBNext Solutions

- Harvest libraries faster with streamlined workflows with NEBNext UltraExpress FS DNA
- Analyze the spectrum of non-coding sequences with NEBNext Low-bias Small RNA
- Read the epigenome with NEBNext Enzymatic Methyl-seq (EM-seq) v2

ENVIRONMENTAL



TRANSLATIONAL & CLINICAL RESEARCH

Defining the clinical relevance of genomic variation towards predictive biomarkers, translational research pushes the limits of NGS library prep. Building high-confidence clinical evidence requires solutions for damaged and degraded samples of limited quantities, including those derived from formalin-fixed, paraffin-embedded (FFPE) tissues, circulating cell-free DNA and fresh-frozen tissue samples.

NEBNext Solutions

- Repair damaged DNA with NEBNext DNA Repair v2 & NEBNext UltraShear FFPE
- Discover novel biomarkers with NEBNext Low-bias Small RNA
- Generate libraries from rare or precious samples with NEBNext Ultra™ II DNA



TRANSCRIPTOMICS

RNA sequencing provides insights into quantitative gene expression, novel transcripts, and gene annotation. Researchers must be able to generate accurate, full-length representations of RNA transcripts from low input amounts. NEBNext continues to push the limits of RNA-seq libraries, expanding the utility and flexibility of transcriptomics.

NEBNext Solutions

- Produce same-day libraries with NEBNext UltraExpress RNA
- Overcome sample limitations with NEBNext Single-cell/Low-input RNA
- See the full spectrum of small RNAs with NEBNext Low-bias Small RNA
- Reveal full-length B- or T-cell transcripts with NEBNext Immune Sequencing

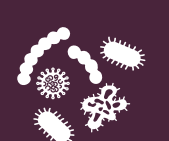


EPIGENETICS

Sequencing is routinely used to detect genomic modifications, offering insight into the factors controlling gene expression. These can be brought to bear in the monitoring of inherited and environmental states associated with human health and developmental biology for diagnostic decision making.

NEBNext Solutions

- Profile genome-wide methylation with NEBNext Enzymatic Methyl-seq (EM-seq) v2
- Detect 5hmC with NEBNext Enzymatic 5hmC-seq (E5hmC-seq™)
- Enhance measurement with EpiMark® Methylated DNA Enrichment



METAGENOMICS

Underpinning the interdependency of environmental and organismal health are the relationships between metagenomic communities and their hosts. Understanding these relationships necessitates tools for isolation of microbial nucleic acids from mixed eukaryotic samples. Samples must also be prepped into sequencer-ready libraries despite extreme nucleotide representation, often without an available reference sequence.

NEBNext Solutions

- Isolate prokaryotic DNA with NEBNext Microbiome DNA Enrichment
- Prepare long-read libraries with NEBNext Companion Module v2 for Oxford Nanopore Technologies' Ligation Sequencing
- Deplete host RNA with NEBNext rRNA Depletion v2 (H/M/R)
- Remove unwanted ribosomal RNA with NEBNext rRNA Depletion (Bacteria)

PATHOGEN SURVEILLANCE

The emergence and evolution of pathogens demands high-quality tools to monitor viral and bacterial genomes at single-nucleotide resolution. Advances in short- and long-read whole genome sequencing facilitate rapid elucidation of pathogen genomes, enabling global researchers to detect and react to emerging pathogen threats.

NEBNext Solutions

- Amplicon-based whole genome sequencing with NEBNext ARTIC Kits for SARS-CoV-2
- Prepare long-read libraries with NEBNext Companion Module v2 for ONT® Sequencing
- Monitor viral evolution with NEBNext RSV and Flu A Primers

Find your solution at [NEBNext.com](https://www.neb.com)