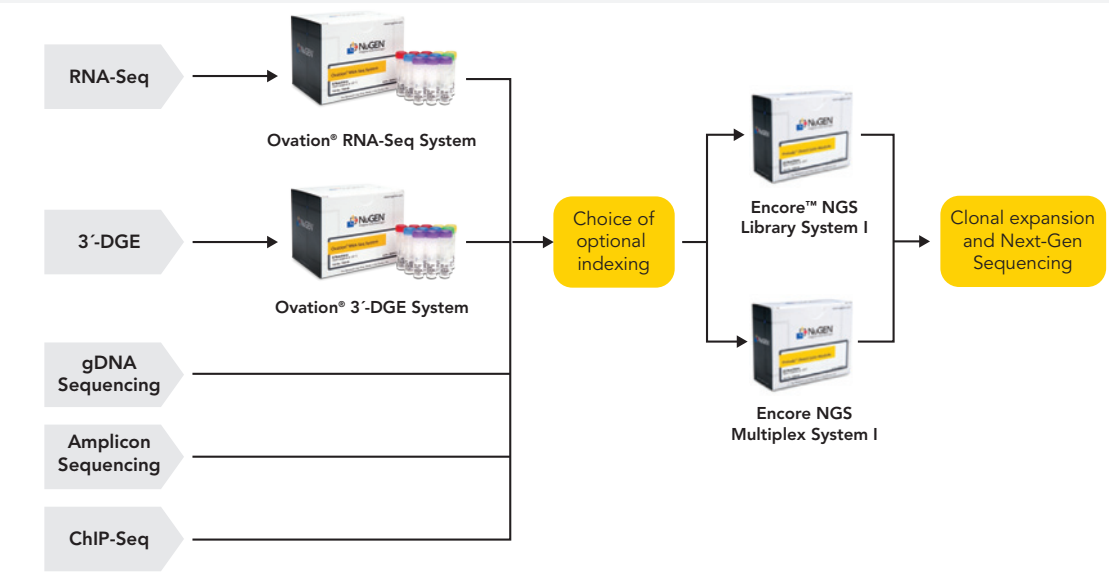
Power Your Next-Generation Sequencing with Innovative Sample Preparation Solutions from NuGEN®

Advances in Next-Generation Sequencing (NGS) have increased both the throughput and capacity of sequencing platforms, calling for increased efficiency in sample preparation and the ability to work with small and precious samples. NuGEN's portfolio of NGS products meets this challenge by enabling simple, rapid and affordable sample preparation workflows for key applications on leading NGS platforms.

Unleash the power of your sequencing platforms with NGS reagent solutions from NuGEN!

NuGEN's portfolio of NGS products enables simple, rapid and affordable sample preparation workflows.



Ovation® RNA-Seq System

- Preparation of ds-cDNA for RNA-Seq library construction, eliminating rRNA reduction or poly(A) selection
- Simple, fast, automatable workflow—coupled with the optional indexing capability of the Encore NGS Library Systems for improved sample throughput and reduced overall costs
- Input of total RNA as low as 500 pg
- Compatibility with all leading commercial NGS platforms

Ovation 3′-DGE System

- Suitable solution for DGE analysis of any eukaryotic transcriptome—accurate expression profiling without the need for prior sequence knowledge for array design
- Simple, fast, automatable workflow—coupled with the optional indexing capability of the Encore NGS Library Systems, offering the advantages of NGS with the throughput and cost of microarrays
- Total RNA input as low as 10 ng.
- Compatibility with all leading commercial NGS platforms

Encore™ NGS Library System I

- Simple, fast, automatable workflow—Library construction in as little as three hours, with only two purification steps and no gel purification required
- Complete solution for a range of NGS applications such as RNA-Seq, genomic DNA sequencing, ChIP-Seq or DGE
- Affordable and scalable system—Optional indexing capability for multiplex sequencing up to eight samples to improve sample throughput and reduce sequencing costs
- Seamless integration with the Ovation RNA-Seq and 3′-DGE Systems
- Primers and adaptors included are compatible with Illumina NGS systems

NuGEN®
imagine more from less™

NuGEN Customer Success Stories, accessible at www.nugeninc.com

1. **Shawn Levy, Ph.D., HudsonAlpha Institute for Biotechnology** *(NuGEN webinar, and presented at ABRF 2010)*
   - RNA-Seq was performed using a small amount of total RNA from cardiac clinical biopsies, a precious and non-renewable sample type.
   - The Ovation RNA-Seq System enabled quantification of transcriptome expression as well as the discovery of expressed sequence variants (SNPs) in the transcript population.
   - The researchers were able to successfully characterize four candidate genes for altered expression levels, alternative splicing and SNPs related to the phenotype of the patient.
2. **Stephanie Willerth, Ph.D., University of California at Berkeley** *(NuGEN webinar, and presented at ASGT 2010)*
   - The researchers were challenged by sequencing the HIV genome from infected HIV+ patients having a highly heterogeneous viral population, which made it difficult to obtain sufficient virus for analysis.
   - The Ovation RNA-Seq System allowed them to amplify the entire HIV genome and obtain good sequencing results from CD4+ T cells without the use of any HIV specific primers.
3. **Jennifer Beane, Ph.D., Boston University** *(presented at AACR 2010)*
   - RNA-Seq was performed using total RNA from airway epithelial cells harvested from patients that were either smokers or never smokers to predict gene expression changes associated with the early onset of lung cancer.
   - The results showed good correlation between GeneChip® Exon 1.0 ST Arrays and RNA-Seq results using the Ovation RNA-Seq System, with more differentially expressed genes detected by RNA-Seq due to expanded dynamic range.
4. **Dan Salomon, Ph.D., The Scripps Research Institute** *(Ovation RNA-Seq Early Access User)*
   - The study utilized total RNA from CD4+ T cells obtained from six human donors and the Ovation RNA-Seq system to prepare samples for NGS library construction.
   - Illumina sequencing resulted in consistent RNA expression profiles and measurement of differential expression between control cells and CD3/CD28-activated cells.
   - The RNA-Seq results were highly reproducible, and results showed good correlation with GeneChip Gene 1.0 ST Arrays using samples prepared with the Applause™ WT-Amp ST System.
5. **Stephen Tsoi, Ph.D., University of Alberta** *(presented at Plant & Animal Genome 2009)*
   - The researchers performed RNA-Seq using total RNA isolated from pig embryos (Day 5–6 blastocysts) and amplified with the Ovation RNA-Seq System. Following library construction, sequencing was performed using the Roche 454 platform.
   - The results lead to the discovery of 15 new genes that appear to be blastocyst specific, as well as several uncharacterized transcript forms related to early embryogenesis.

ORDERING INFORMATION

Part No.	Product Name
Next-Generation Sequencing Library Kit Products	
300	Encore™ NGS Library System I
301	Encore™ NGS Multiplex System I
3′-DGE Products	
7200	Ovation® 3′-DGE System
RNA-Seq Products	
7100	Ovation® RNA-Seq System
Complete Workflow for RNA-Seq and 3′-DGE	
350	RNA-Seq Complete Solution
351	RNA-Seq Multiplex Complete Solution
360	3′-DGE Complete Solution
361	3′-DGE Multiplex Complete Solution
Prelude™ Systems	
1400	Prelude™ Direct Lysis Module

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