Ovation® Ultralow Library System V2

www.nugen.com

A single workflow for all of your DNA samples

Ovation® Ultralow Library System V2 provides a simple and fast solution for producing libraries that can be used in a broad range of next generation sequencing applications. Using our proprietary **DimerFree** technology allows for efficient library preparation with virtually no adaptor dimers at input levels ranging from 10 pg to 100 ng.

The Ovation Ultralow V2 System is well published across a wide variety of sample types including purified DNA generated from cell lines, fresh and FFPE tissue, liquid biopsy and cell-free DNA. The kit is compatible with most commercially available hybrid capture methods.

Why use Ovation Ultralow Library System V2?

Ultralow V2 offers several unique features:

1. **Short, simple, automatable workflow:** library construction in as little as 3 hours (2 hours for PCR-free).
2. **Broad range of input for any sample type:** **DimerFree** technology enables one method to sequence all DNA samples from low to high input, intact or fragmented DNA.
3. **Accurate variant detection:** 96 Unique Dual Indexes using 192 unique sequences and edit-3 design.
4. **Simpler workflow:** no hidden sample normalization or adaptor dilution steps required.
5. **No adaptor dimers:** get more informative reads compared to competitors without multiple bead clean-ups.
6. **Obtain broad coverage:** high fidelity amplification across a broad range of GC content.

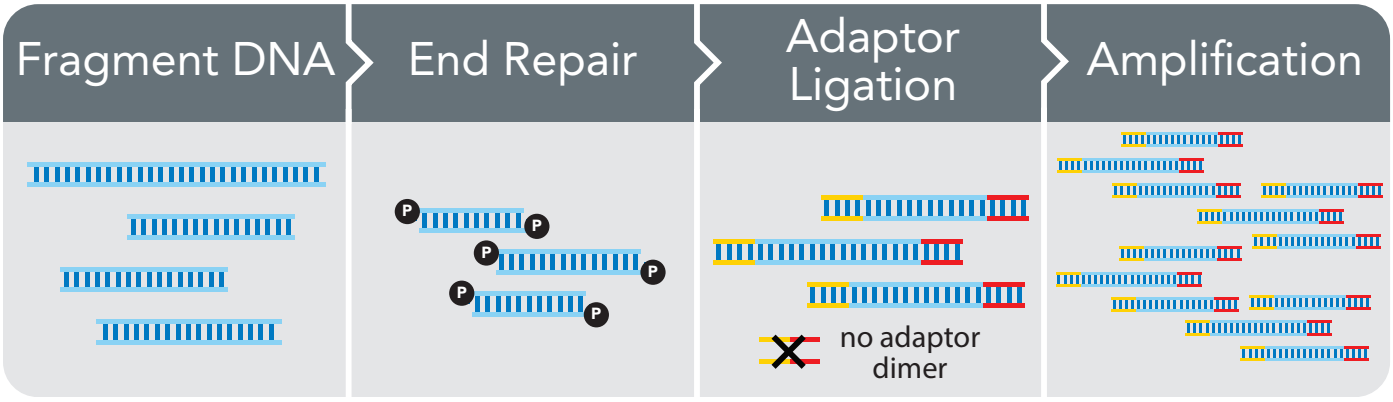

Figure 1. Ovation Ultralow System V2 is a simple, fast and scalable workflow that produces clean libraries with no adaptor dimers.

NuGEN®

Applications and Sample Types

- Whole genome sequencing
- Exome sequencing
- ChIP-Seq
- Microbiome
- Liquid biopsy
- FFPE DNA
- cDNA

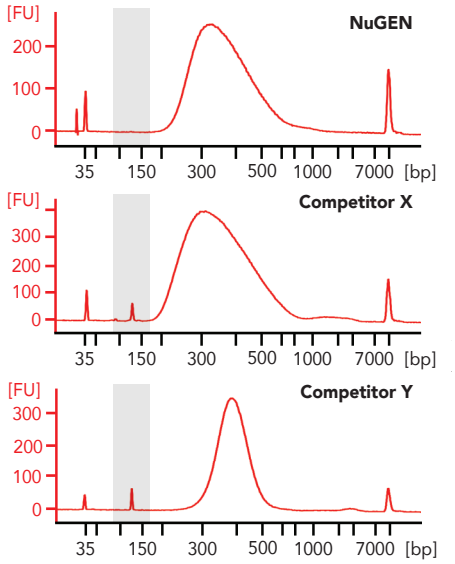

Figure 2. No detectable adaptor dimers. 1 ng gDNA created from Ultralow System V2 vs. Competitors X and Y analyzed on Agilent Bioanalyzer. Adaptor dimers are highlighted in the grey box.

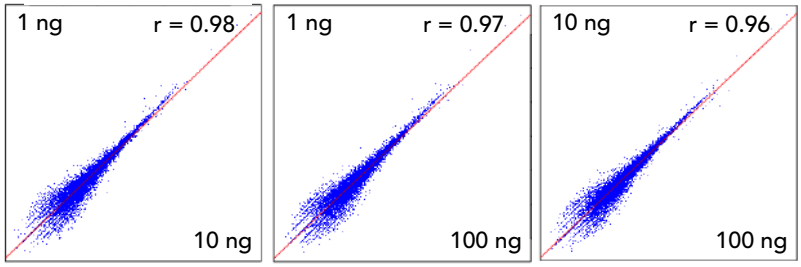

Figure 3. High concordance across a broad input range without the need to adjust adaptor concentrations. Scatterplots of the log FPKM and corresponding pearson R values are shown for Ultralow Library Systems V2 libraries constructed from 1, 10 or 100 ng of double-stranded cDNA made from Human Brain reference RNA.

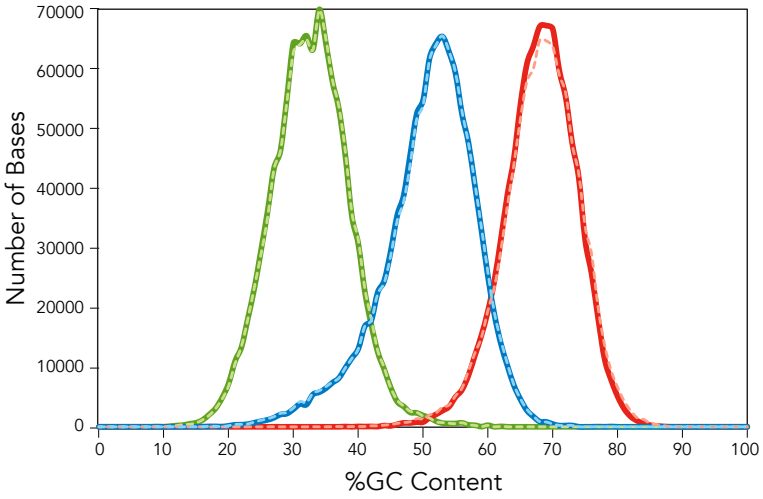

Figure 4. Even read distribution across a broad GC range. 1 ng of gDNA from *E. coli* (blue, 51% GC), *R. sphaeroides* (red, 69% GC) or *S. aureus* (green, 33% GC) were sequenced with Ultralow Library Systems V2. Experimental GC distribution (solid lines) closely matches theoretical distribution (dashed lines) from a GC of less than 20% to greater than 80%.

Ordering Information	No. of Reactions	Part No.
Ovation Ultralow System V2	8	0344NB-08
Ovation Ultralow System V2, includes purification beads	32	0344-32
Ovation Ultralow System V2	32	0344NB-32
Ovation Ultralow System V2 1-96	96	0344NB-A01
Ovation Ultralow System V2 with Unique Dual Indexes	96	9149-A01

NuGEN Technologies, Inc.

Headquarters USA
201 Industrial Road, Suite 310
San Carlos, CA 94070 USA
Toll Free Tel: 888.654.6544
Toll Free Fax: 888.296.6544
custserv@nugen.com
techserv@nugen.com

Europe
P.O. Box 109,
9350 AC Leek
The Netherlands
Tel: +31-13-5780215
Fax: +31-13-5780216
europe@nugen.com

Worldwide
For our international distributors contact information, visit our website.
worldwide@nugen.com

www.nugen.com

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