ELLIS BIO | Your Experts In DNA Methylation

The New Standard in Low-Input Methylation Detection

Gentle, Reproducible, Enzyme-Free

SuperMethyl™ Max Bisulfite Conversion

Ultra-Mild Bisulfite Conversion for results that beat enzymes for low-input DNA

Compared to enzyme-based methods:

- Lower input: down to 100pg
- Up to 6X fewer false positives
- 3X faster, 5x less hands-on time
- 99.8% C-to-U conversion
- Comparable yields

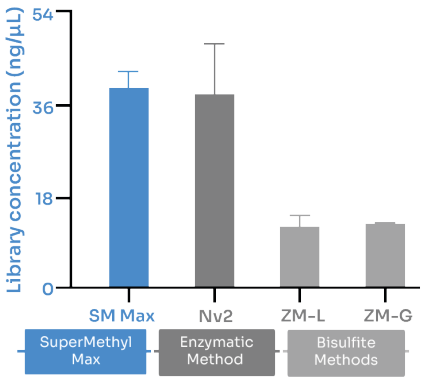
Excels in analysis of:

- cfDNA/ liquid biopsy
- FFPE-derived DNA
- Single-cells
- Forensic trace DNA
- Ancient/archival DNA

Ultra-Mild Bisulfite Conversion Preserves DNA like Enzymes

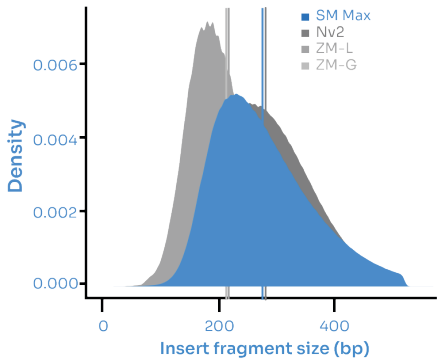
1.A

Max maximizes library yields



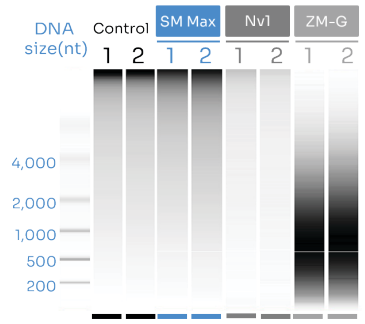
1.B

Max achieves longer insert sizes



2.

Max is gentle on DNA



1) 10ng mouse embryonic stem cell gDNA + unmethylated lambda DNA and 1% methylated pUC19 DNA spike-in controls. Yield quantified post library prep (A); insert size determined post-sequencing (B).

2) 100ng intact lambda DNA subjected in duplicate to methylconversion.

Request a free sample kit

sales@ellisbio.com

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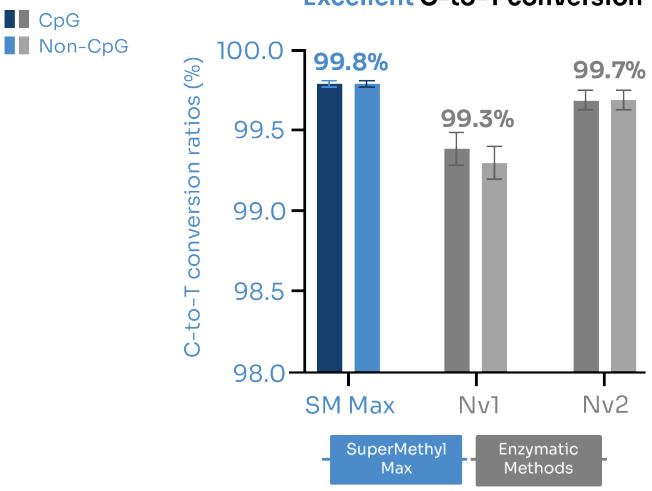
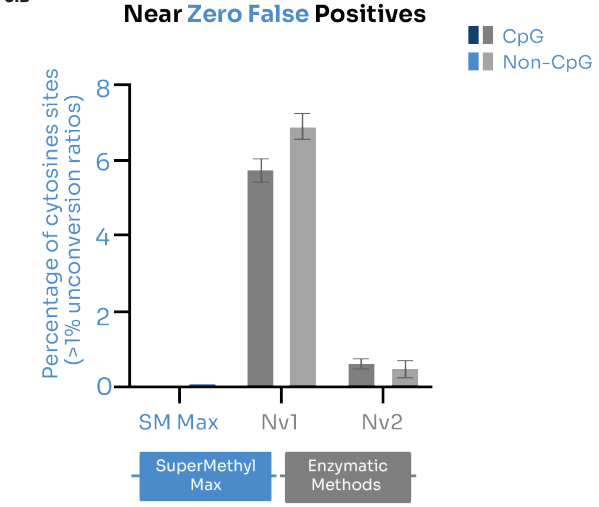
Accuracy that Beats Enzymes for Reliable Methylation

3.A



3.B



3) 10ng DNA + unmethylated lambda DNA and 1% methylated pUC19 DNA spike-in controls. C-to-T conversion rate and false positive rates were determined post-sequencing.

How it works

SuperMethyl Max incorporates Ultra-Mild Bisulfite technology (Nature Communications Publication In Press) for optimal reaction conditions.

The gentle conversion condition and shortened conversion time minimizes DNA degradation, while the greater conversion efficiency improves accuracy.

Max-24R (Bead Purification)

In a simple efficient, workflow

SuperMethyl Max — 2-3 hours

Enzymatic Methods Nv1/Nv2 — 7.5-9+ hours

Time reflects total end-to-end workflow time for conversion modules Nv1/Nv2 under standard bench conditions.

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