

Sequencing Fidelity Begins at the Molecule

When native molecules are preserved, NGS reveals true biology

Enzymatic end repair has long been a foundational step in NGS library preparation, standardizing DNA termini for adaptor ligation but often introducing artifacts that obscure authentic mutational and methylation signals. TrueLink™ eliminates the need for end repair via a novel dual-independent ligation architecture that preserves native fragment termini while enabling efficient capture of both double- and single-stranded DNA templates, resulting in higher-fidelity sequencing data and more biologically faithful interpretation.

End Repair Rewrites DNA. TrueLink™ Preserves It.

Higher Fidelity Sequencing

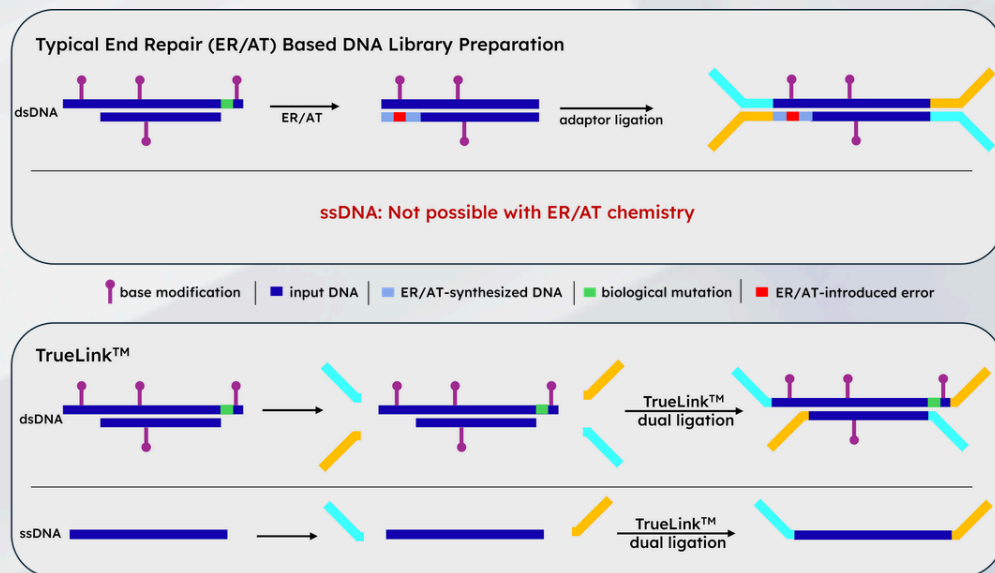
- ~80% reduction in chimeric reads
- Elimination of ER/AT substitution artifacts

Native Molecular Preservation

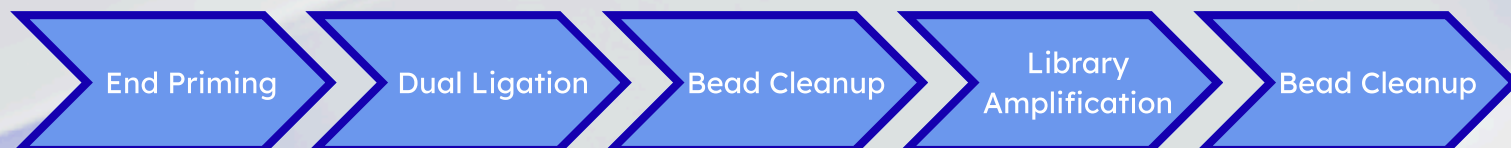
- Authentic cfDNA fragmentation
- Unified ss + ds DNA capture

Workflow Compatibility

- Comparable yield/diversity
- Drop-in replacement for ER/AT



Drop-In Replacement. No Workflow Disruption.



Where Native Molecules Matter Most...

TrueLink™ enhances applications where sequencing accuracy, molecular authenticity, and artifact suppression are critical:

- 🔒 **Precision oncology sequencing**— including MRD detection, liquid biopsy, and cfDNA analysis
- 🔒 **Methylome profiling** — preserving native fragmentation and epigenetic signal integrity
- 🔒 **Single-stranded DNA sequencing** — supporting challenging templates, including viral vector QC
- 🔒 **Rare variant detection** — improving confidence at the limits of detection
- 🔒 **Structural rearrangement analysis** — maintaining authentic breakpoint representation
- 🔒 **Fragmentomics** — revealing biologically meaningful fragmentation patterns



SCAN ME

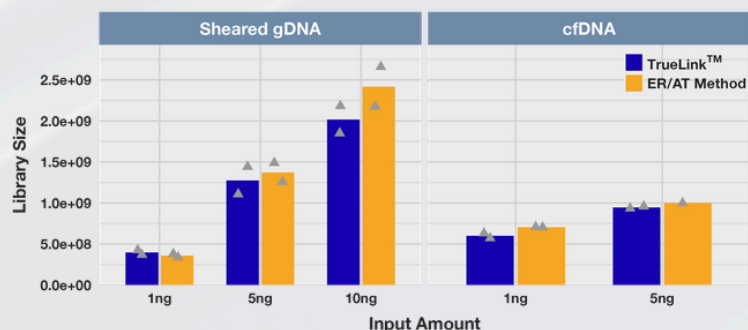
to learn more about TrueLink™

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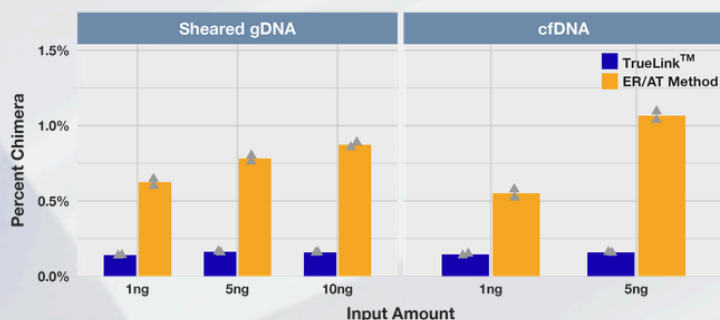
Native Molecule Preservation Produces Measurably Higher-Fidelity Data

Comparable Library Yield and Diversity



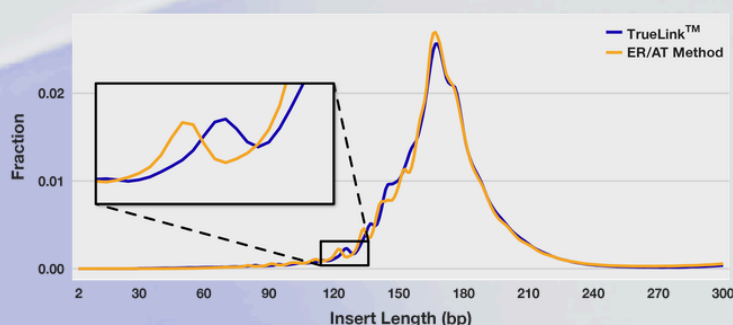
Across gDNA and cfDNA inputs, TrueLink™ produces high-diversity libraries comparable to ER/AT from a leading provider (Supplier N). Library size was estimated using Picard MarkDuplicates. Inputs included mechanically sheared NA12878 human gDNA and single-donor plasma cfDNA (MagMAX™-extracted). All libraries were sequenced on 2x150 on NovaSeq X flowcells.

~80% Reduction in Chimeric Reads



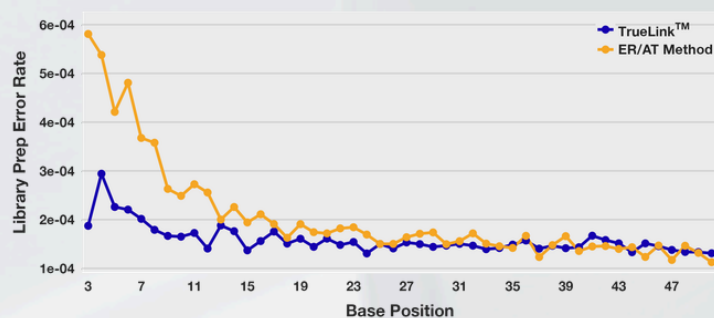
TrueLink™ libraries result in markedly fewer chimeric reads, regardless of input amount, whereas ER/AT samples show high chimera rates which rise with increasing input. Chimera rate was reported by Picard CollectAlignmentSummaryMetrics. Reduced chimeras may improve robustness for indel and structural-variant detection.

Retains Authentic cfDNA Fragmentation Pattern



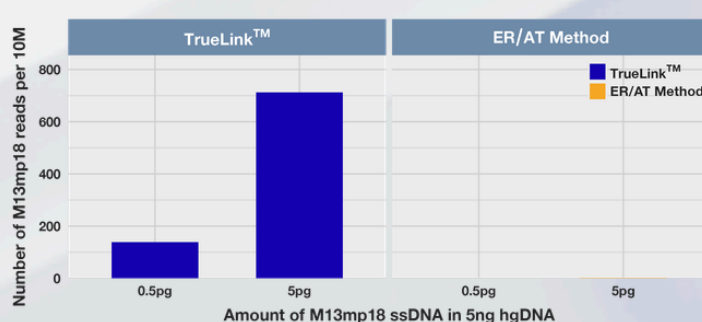
TrueLink™ retains the native cfDNA fragmentation pattern. cfDNA was extracted from a healthy donor sample and used as input for both methods. TrueLink™ fragments show a small shift in insert length, specifically cfDNA's characteristic "saw tooth" 10.4 bp periodicity peaks, while ER/AT fragment peaks are 1-4 bp shorter. This suggests that, on average, cfDNA fragments are shortened by ER/AT, whereas TrueLink™ is capturing the true native ends of the cfDNA fragments.

Elimination of ER/AT Substitution Artifacts



TrueLink™ libraries exhibit significantly lower substitution error rates at the start of Read 2 as compared to ER/AT-prepared libraries, consistent with the absence of DNA polymerase-driven resynthesis of 3' template termini. Bases 1 and 2 were trimmed from TrueLink™ and ER/AT libraries.

Simultaneous ssDNA and dsDNA Capture



TrueLink™ converts single-stranded DNA in the input sample, while the ER/AT-based method cannot. M13mp18 ssDNA was spiked into 5ng of sheared hgDNA and used as input DNA. Comparison is based on the number of reads mapped to the M13mp18 genome per 10M total reads.

Conclusion

Sequencing accuracy begins at the molecule. By eliminating end repair and preserving native fragment structure, TrueLink™ establishes a new foundation for sequencing — one built on molecular authenticity rather than enzymatic correction. The result is more faithful data, deeper biological insight, and a platform engineered for even the most demanding sequencing applications.

TrueLink™ Products

TL0001-24: TrueLink™ DNA Library Prep Kit (24 Samples)
TL0001-96: TrueLink™ DNA Library Prep Kit (96 Samples)

COMING SOON:

- TrueLink™ True Methylome Library Prep Kit
- TrueLink™ PCR-Free Library Prep Kit



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No Molecular Rewriting. No Performance Tradeoffs.
TrueLink™. Library Prep without Compromise.

