WGS Fragmentation Mix

Key benefits

- Fragmentation, end-repair and dA-tailing in a single reaction step
- Ligation in the same tube simplifies the workflow, reducing total reaction and hands-on time
- Matches Covaris fragmentation and sequencing performance
- Suitable for high throughput and automation
- Fragment size is easily tuned (200–800 bp) for different sequencing applications
- Broad input amount (1 ng to 1 µg)
- PCR-free library construction from as low as 50 ng input DNA
- High library efficiency and yield; reproducible and consistent

A better method of library construction

WGS (Whole Genome Sequencing) Fragmentation Mix is a single-tube library construction method for Illumina® platforms. The protocol supports fragmentation, end-repair and dA-tailing in a single reaction step. The subsequent ligation step occurs in the same reaction tube, thereby greatly simplifying the workflow. Total reaction time is reduced, and hands-on time is minimized. The fragmentation profiles are similar to mechanically sheared profiles and the size can be easily tuned to accommodate different sequencing applications. The sequencing qualities, including mapping statistics, coverage, bias and uniformity, are equivalent to fragments generated by the Covaris AFA® (Adaptive Focused Acoustics) shearing process. For an unmatchable library workflow from QIAGEN, combine WGS Fragmentation Mix with our high efficiency ligation reagents and optimized library amplification with 2X HiFi PCR Master Mix.

The simplest workflow

By combining DNA fragmentation, end-repair and dA-tailing reactions in one step, WGS Fragmentation Mix provides the simplest workflow for enzyme-based DNA fragmentation and library construction. With an uncompromising approach to sequencing quality comparable to Covaris shearing, the easy workflow is adaptable to different throughputs (individual use and automation) and can accommodate various sequencing applications.

	Illumina TruSeq®	NEBnext® Fragmentase/Ultra™	Illumina Nextera® XT	QIAGEN workflow
Total/ Hands-on time	3.5 h/1 h	3.5 h/45 min	1.5 h/15 min	2.5 h/30 min
Pros	Good sequencing performance	Enzyme-based fragmentation	Tagmentation; short time	High sequencing quality; simple workflow; flexible
Cons	Relies on Covaris; long process	Known bias; poor reproducibility	Known bias; loss of complexity; distal effect; fixed input amount	

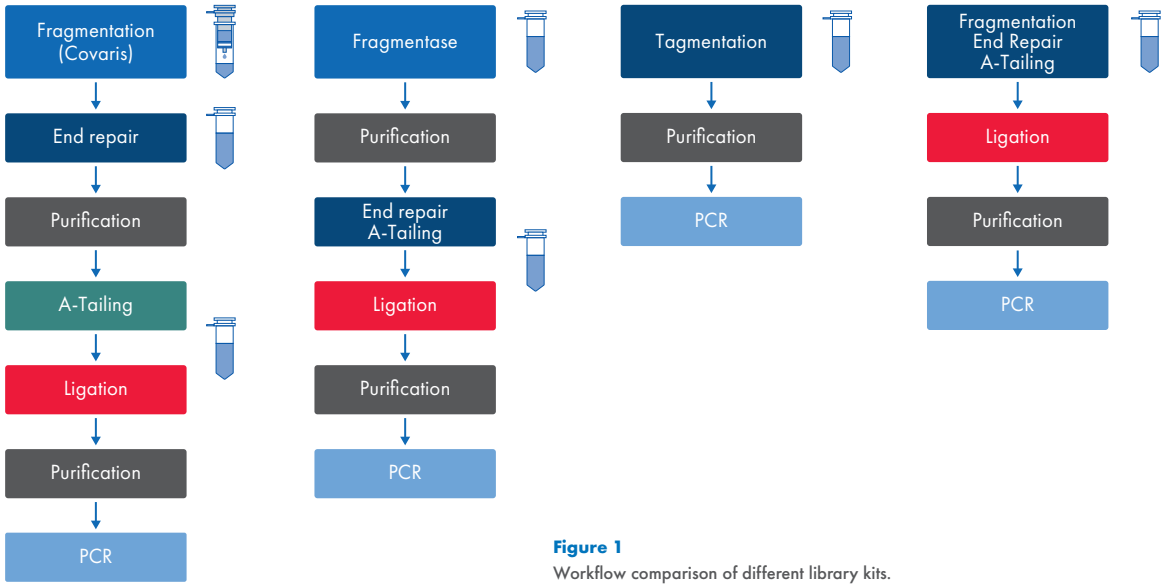

Figure 1
Workflow comparison of different library kits.

Features and benefits for a better library solution

In addition to offering the uncompromised sequencing quality compared to Covaris shearing, the combined steps and easy workflow make our solution adaptable to different throughputs (individual use and automation) and can accommodate various sequencing applications.

Table 1
Features and benefits of WGS Fragmentation Mix

Quality	Workflow	Flexibility
Covaris-matching fragmentation and sequencing performance	Single tube library prep; multiple reactions in single step	Tunable size range (200–800 bp)
High library efficiency and yield	Time saving (total and hands-on)	Broad input amount (1 ng to 1 µg)
Reproducibility and consistency	High-throughput and automation friendly	PCR-free (≥50 ng)

Tunable size range for different input DNA

The range and average fragment size can be tuned by simply changing the reaction time (Figure 2). WGS Fragmentation Mix can generate consistent DNA fragments from a wide range of input DNA (1 ng to 1 µg) with various GC contents.

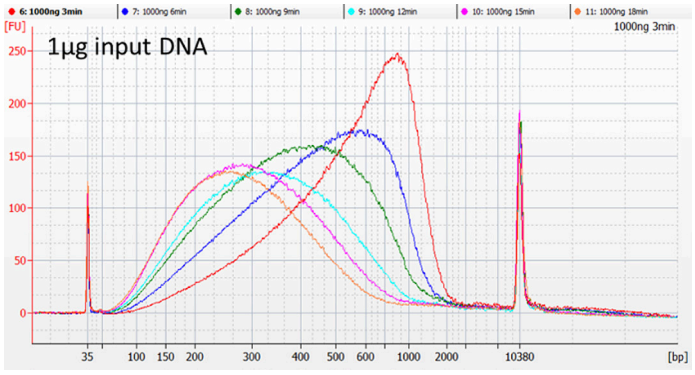

Figure 2
Fragmentation size is tunable. Agilent® Bioanalyzer profile of reference human DNA (Coriell Institute for Medical Research) fragmented to various sizes. Genomic DNA (1 µg) was subjected in-house to fragmentation with different reaction time points (3–18 minutes). After fragmentation, DNA samples were purified and then visualized using Agilent High Sensitivity DNA Kit. Similar fragment profiles can be achieved for other input amounts (data not shown).

Sequence coverage performance equivalent to Covaris shearing

When WGS Fragmentation Mix was challenged in-house with a DNA mix of varying GC contents, the system maintained even sequence coverage compared to Covaris, Tagmenation and other enzyme-based DNA fragmentation methods (Figure 3). No coverage bias was introduced with DNA input as low as 1 ng (Figure 4).

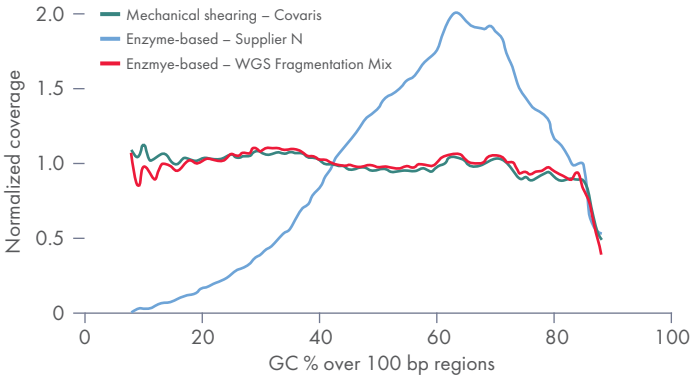

Figure 3
Genome coverage analysis of 100 ng input DNA from 3 bacterial genomes with different GC content in an equal molar mix: *Fusobacterium nucleatum* (27% GC); *Bordetella pertussis* (67% GC) and *E. coli* (50% GC).

Uniform coverage

The WGS Fragmentation Mix protocol provides similar coverage uniformity compared to a Covaris-sheared library, and superior performance compared to other non-Covaris library methods (Figure 5). All major mapping statistics and duplication rates are equivalent or similar to Covaris-based library methods (data not shown).

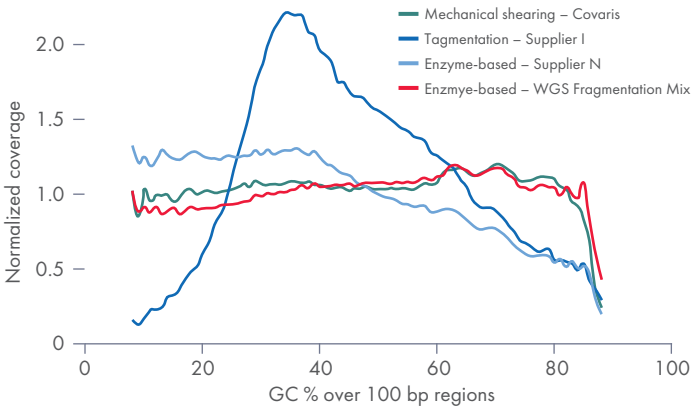

Figure 4
Genome coverage analysis of 1 ng input DNA from 3 bacterial genomes with different GC content in an equal molar mix: *Fusobacterium nucleatum* (27% GC); *Bordetella pertussis* (67% GC) and *E. coli* (50% GC).

PCR-free genome coverage performance

The WGS Fragmentation Mix reaction in a single-tube and high efficiency library chemistry enables PCR-free library construction from as low as 50 ng input DNA (Figure 6).

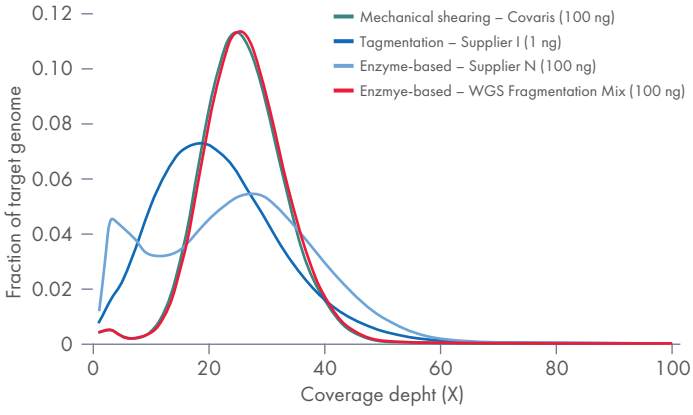

Figure 5
Comparison in-house of coverage distribution for mechanical shearing (Covaris) and non-Covaris library methods.

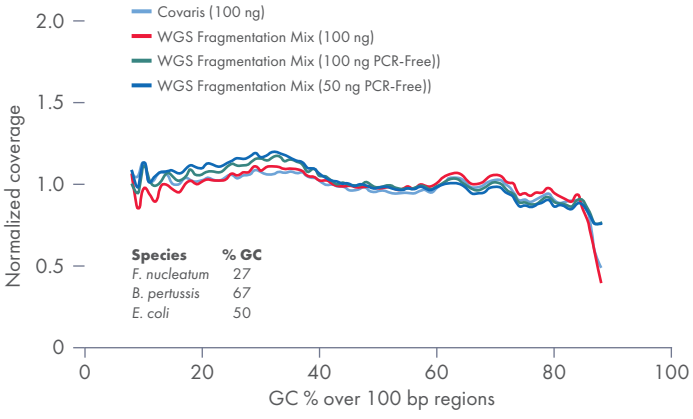

Figure 6
Genome coverage analysis comparing library preparation with a mechanical shearing method (Covaris) (PCR) and WGS Fragmentation Mix (PCR and PCR-free). Input DNA was from 3 bacterial genomes with different GC content.

Quality and service you can count on

QIAGEN manufactures pure, highest quality enzymes and reagents for molecular biology and other applications. The company strives to resolve customers' challenges by providing high quality materials, an unbreakable supply chain and excellent service. With a manufacturing record unmatched in commercial enzyme production, QIAGEN designs analytical grade quality into all its products to meet the most rigorous specifications. WGS Fragmentation Mix is evidence of our commitment to identifying, developing, and delivering the very best enzyme technologies. WGS Fragmentation Mix is evidence of our commitment to identifying, developing and delivering the very best enzyme technologies. If your company requires products and a service partner that stand above the crowd, we'd love to hear from you.

WGS Fragmentation Mix is intended for molecular biology applications. This product is not intended for the diagnosis, prevention, or treatment of a disease.

Ordering Information

Product	Contents	Cat. no.
WGS Fragmentation Mix, 5x	For 24 reactions: 5x WGS Fragmentation Mix (1 x 0.24 mL), 10X Fragmentation Buffer (1 x 0.25 mL) and Enhancer (1 x 0.25 mL)	Y9410L
WGS Ligase (24 reactions)	144,000 U of T4 DNA Ligase (600,000 U/ml) and 5X Rapid Ligation Buffer	L6030-W-L
2X HiFi PCR Master Mix	2X HiFi PCR Master Mix is a high efficiency, high fidelity, and low bias PCR master mix for NGS DNA library amplification	P7670L

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