Expand your metagenomic sequencing options with AVITI™ compatibility

Combine the xGen™ DNA Library Prep EZ Kit with the Element Adept™ Library Compatibility Kit for an efficient and flexible approach to microbial community sequencing on the AVITI System

AVITI Compatibility

High-quality NGS data

Uniform GC coverage

Compatibility of xGen DNA Library Prep EZ Kit with AVITI sequencing

The AVITI System is a new next generation sequencing (NGS) platform from Element Biosciences, that is well-suited for metagenomic applications. xGen DNA Library Prep EZ Kits, which use enzymatic fragmentation for streamlined preparation of NGS libraries, can be seamlessly paired with the Element Adept Library Compatibility Kit for library circularization and downstream sequencing on the AVITI System. Together, this combination of NGS technologies provides an efficient solution for users with needs outside of traditional benchtop sequencing options.

Benefits

- Complete, streamlined library preparation using the xGen DNA Library EZ Kit and xGen UDI Primer Pairs
- High multiplex capacity with up to 1536 unique dual indexes ready-made in single use plates
- Easy-to-use Adept Library Compatibility Kit pairs with any xGen DNA Library Prep EZ Kit for downstream AVITI sequencing

Quality sequencing data generated on the AVITI platform

Pair the xGen DNA Library Prep EZ Kit with the Adept Library Compatibility Kit to gain a streamlined NGS workflow for high-complexity libraries and take advantage of the flexibility, quality (run metrics: Q30: 93.6%, Index Assignment: 95.7%), and speed of the AVITI System. Key NGS metrics demonstrating quality and reproducibility across 24 metagenomic libraries are summarized below (Table 1).

Estimated library size (unique molecules)	Duplicate rate (%)	Reads mapping to genome (%)	Mean Insert Size (bp)
3.15 x 10^9 (6.13 x10^8)	0.094 (0.03)	99.8 (<0.007)	253 (7.7)

Table 1. Sequencing metrics. Libraries (n = 24) were prepared with the xGen Library Prep EZ Kit using 8 ng of DNA input from a mock microbial community (ATCC MSA-1000) containing 10 different strains. Each library was normalized and pooled into a single reaction for circularization by the Adept Library Compatibility Kit. qPCR was performed after circularization and final libraries were sequenced with the Element AVITI System using 2 x 150 paired end reads. Sequencing reads were subsampled to 8 million reads per library. Analysis was performed using CollectWgsMetrics (Picard). Values in the table represent the mean of the 24 replicates with standard deviations noted in parentheses.

Metagenomic sequencing performance

AVITI sequencing of NGS libraries prepared with the xGen Library Prep EZ Kit and Adept Library Compatibility workflow identified all expected members of a mock microbial community and generated uniform coverage across a wide GC content range.

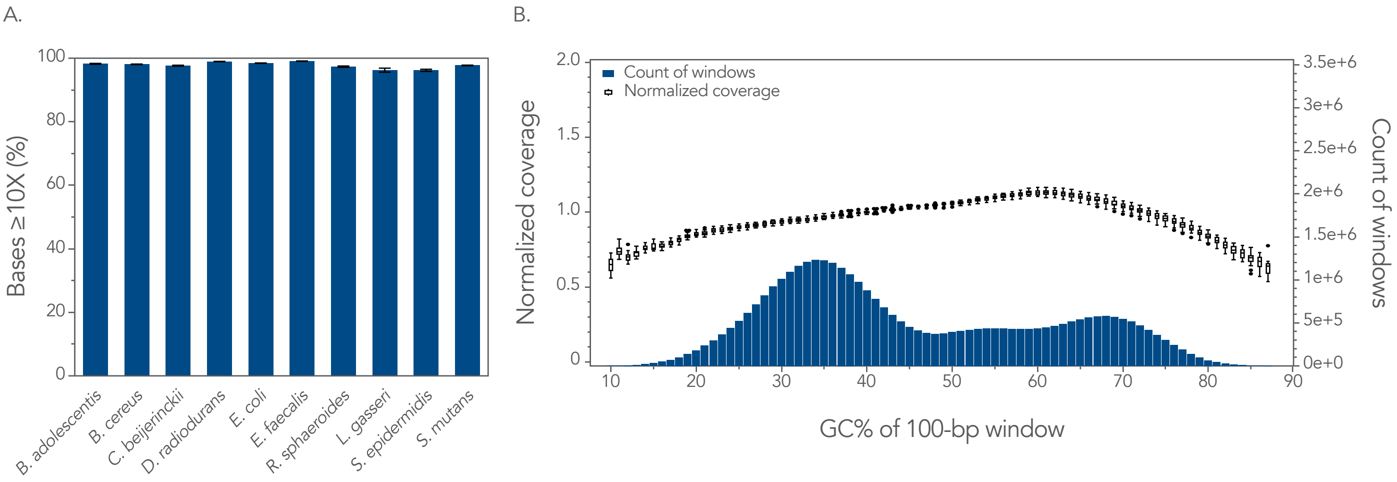

Figure 1. NGS sequencing results using the xGen DNA Library Prep EZ Kit and Adept Library Compatibility workflow for the AVITI System. (**A**) All 10 of the expected bacterial strains were identified in each library (*n* = 24). Sequencing resulted in a mean of >96% bases covered at ≥10X per strain, with a mean coverage of 24X (Std Dev 4.2). Analysis was performed using CollectWgsMetrics (Picard). (**B**) Sequencing prepared libraries (*n* = 24) resulted in even coverage across the range of GC content.* The histogram represents the number of windows for each GC 100 bp-sequence window within the mixture (right Y-axis). The box plots indicate the normalized read depth for a given GC window (left Y-axis). Analysis was performed using CollectGCBiasMetrics (Picard). (**A–B**) Libraries were prepared with the xGen Library Prep EZ Kit using 8 ng of DNA input from a mock microbial community (ATCC MSA-1000) containing 10 different bacterial strains with varying GC content (GC range = 29.9%–68.9%) and genome size. Each library was normalized and pooled into a single reaction for circularization by the Adept Library Compatibility Kit. qPCR was performed after circularization and final libraries were sequenced with the Element AVITI System using 2 x 150 paired end reads. Sequencing was subsampled to 8 million reads per library.

* Standardized 10-strain microbial sample contains fewer GC-windows for 0–20% and 80–100% ranges, which may lead to lower normalized coverage across those windows.

ORDERING INFORMATION

Product	Catalog #	URL
xGen DNA Library Prep EZ 16rxn	10009863	www.idtdna.com/xGen-library-prep-EZ
xGen DNA Library Prep EZ 96rxn	10009821	
xGen UDI Primer Pairs	Varies	www.idtdna.com/xGen-UDI-primer-pairs
Element AVITI System	880-00001	www.elementbiosciences.com/products/aviti
Element AVITI 2x150 Sequencing Kit	860-00001	
Element Adept Library Compatibility Kit	830-00003	www.elementbiosciences.com/products/adept

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