gBLOCKS™ HiFi GENE FRAGMENTS

Pure confidence

Industry's lowest error rate

Reliable delivery times

NGS-verified

HIGH-QUALITY GENE FRAGMENTS

gBlocks HiFi Gene Fragments are double-stranded DNA fragments with sizes of 1000–3000 bp (Table 1). They are NGS verified with a median error rate less than 1:12,000. These high-quality, high-fidelity constructs facilitate the assembly of large and complex sequences, matching both the length and accuracy needed to minimize the introduction of unwanted substitution or deletion errors. gBlocks HiFi Gene Fragments are best suited for applications like gene assembly, pathway development, and microbe design.

gBlocks HiFi Gene Fragments are manufactured utilizing over 30 years of industrial knowledge at Integrated DNA Technologies (IDT). As innovators of double-stranded DNA fragments, our goal is to provide efficient, cost-effective, and reliable solutions for genomics and molecular biology.

BENEFITS

- High fidelity and DNA purity for gene assembly
- Flexible for all downstream cloning methods
- No universal linkers to remove

Table 1. Product specifications.

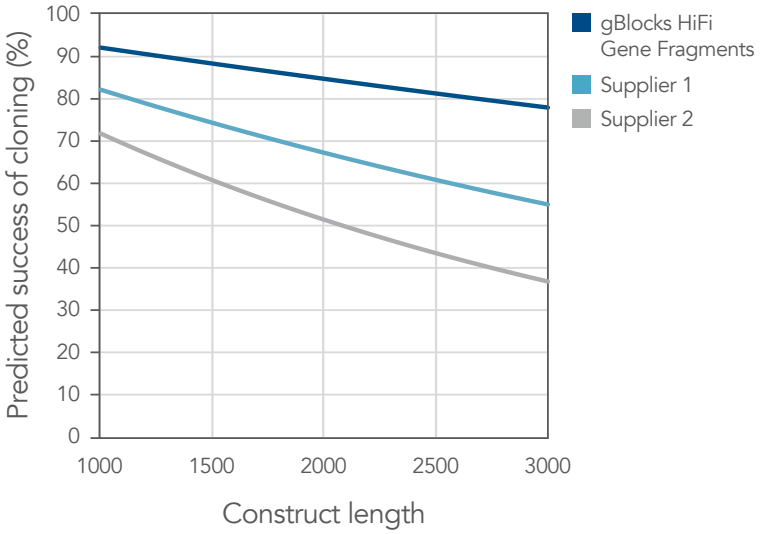
Product type	dsDNA fragments
Verification method	next generation sequencing (NGS)
Error rate	1:12,000
Shipping time	6–10 business days
Formats available	tubes and plates
Minimum order for tube format	none
Minimum order for plate format	24 fragments

FLEXIBLE AND ADAPTABLE TO ALL CLONING METHODS

gBlocks HiFi Gene Fragments demonstrate consistently high sequence fidelity and purity across various lengths (Figure 1). They are compatible with all cloning methods that require double-stranded DNA as a starting material, allowing easy assembly of your desired construct sequence into your favorite cloning system (Table 2). Examples of cloning methods that are compatible with gBlocks HiFi Gene Fragments include traditional cloning, Gibson Assembly™, Golden Gate, Gateway™, TOPO™/TA cloning, and blunt-end cloning.

Table 2 demonstrates the approximate number of colonies needed to be picked to identify the correct clone. Cloning efficiency is affected by many factors. The results noted here represent screening using a seamless assembly method with our preferred vector and reagents. Results may vary based on sequence composition, cloning method, and reagents used.

A. Effect of construct length on predicted success of cloning



B. Demonstrated cloning efficiency

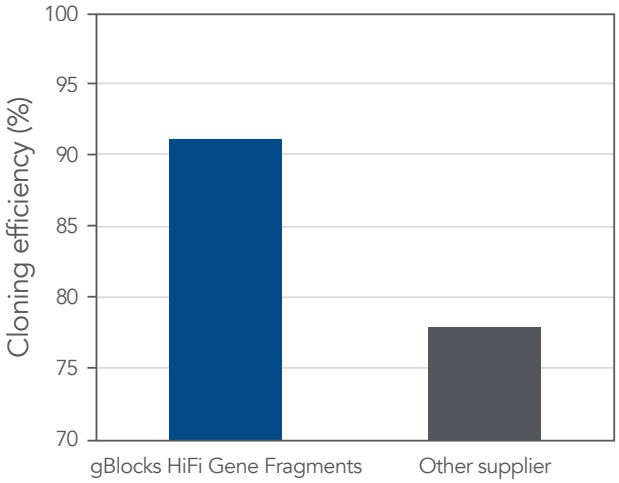


Figure 1. A) Predicted cloning efficiency. As construct length is increased, predicted success decreases. However, because of the exceptionally low error rates in the production of gBlocks HiFi Gene Fragments, the predicted success of cloning is higher than when similar fragments are used from other suppliers. **B) Demonstrated cloning efficiency.** Based on NGS sequencing of ~500 clones, gBlocks HiFi Gene Fragments exhibited a high degree of cloning success. Compared to dsDNA strands from a leading provider, gBlocks HiFi Gene Fragments showed a significant improvement in cloning efficiency, leading to a reduction in the time and cost to find a correct clone.

Table 2. Pick fewer colonies with gBlocks HiFi Gene Fragments.

Length (bp)	gBlocks HiFi Gene Fragments	Other supplier
1000–2000	2	6–10
2001–3000	2	N/A

> For more information and to order, visit **www.idtdna.com/gBlocks**.