

DNA MODIFYING ENZYMES

Gibson Assembly™ Cloning Kit

Instruction Manual

NEB #E5510S
10 reactions

 NEW ENGLAND
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enabling technologies in the life sciences



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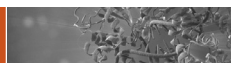


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Components:

Important Note: Upon arrival, store the kit components at indicated temperatures. Store the Gibson Assembly Master Mix and positive controls at -20°C . Store the competent cells at -80°C . Store the SOC Outgrowth Medium at room temperature. Before use, thaw and vortex the master mix thoroughly and keep on ice.

Gibson Assembly Master Mix (2X)

NEB 5-alpha Competent *E. coli* (High Efficiency)

SOC Outgrowth Medium

Positive Controls:

Gibson Assembly Positive Control

2 overlapping dsDNA fragments for control assembly

pUC19 Control DNA

Required Materials Not Included:

DNA Polymerase (for generating PCR products):

We recommend Q5™ High-Fidelity DNA Polymerase (NEB #M0491) or related products, such as Q5 Hot Start High-Fidelity DNA Polymerase (NEB #M0493) or Q5 Hot Start High-Fidelity 2X Master Mix (NEB #M0494).

LB (Luria-Bertani) plates with appropriate antibiotic.

Introduction:

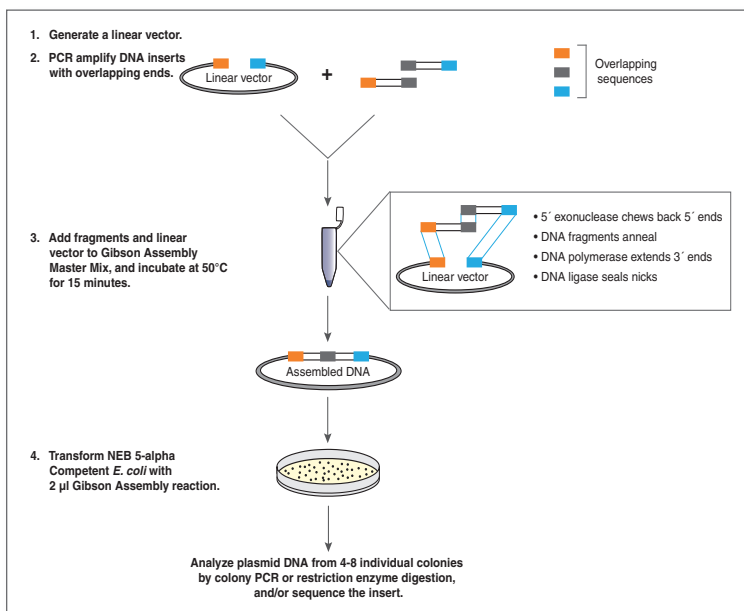
Gibson Assembly was developed by Dr. Daniel Gibson and his colleagues at the J. Craig Venter Institute and licensed to New England Biolabs by Synthetic Genomics, Inc. The method allows for successful assembly of multiple DNA fragments, regardless of fragment length or end compatibility. The method has been successfully used by Gibson's group to assemble oligonucleotides, DNA with varied overlaps (15–80 bp) and fragments hundreds of kilobases long (1–2) and has been rapidly adopted by the synthetic biology community due to its ease-of-use, flexibility and suitability for large DNA constructs.

The Gibson Assembly Cloning Kit has been further optimized to increase the efficiencies for simultaneous assembly and cloning of one or two fragments into any vector. A single-tube isothermal assembly reaction features three different enzymatic activities that perform in the same buffer:

- The exonuclease creates single-stranded 3' overhangs that facilitate the annealing of fragments that share complementarity at one end (overlap region).
- The proprietary DNA polymerase fills in gaps within each annealed fragment.
- The DNA ligase seals nicks in the assembled DNA.

The end result is a circular, double-stranded, fully-sealed DNA molecule that can be used to transform NEB 5-alpha Competent *E. coli*, provided with the kit.

Figure 1: Overview of the Gibson Assembly Cloning Method



Overview of Gibson Assembly Cloning Kit Protocol:

- Design primers to amplify fragments (and/or vector) with appropriate overlaps (see pages 4–9).
- PCR amplify fragments using a high-fidelity DNA polymerase.
- Prepare linearized vector by PCR amplification using a high-fidelity DNA polymerase or by restriction digestion.
- Confirm and determine concentration of fragments and linearized vector using agarose gel electrophoresis, a NanoDrop™ instrument or other method.
- Add PCR fragments and linearized vector to Gibson Assembly Master Mix and incubate at 50°C for 15 minutes.
- Transform into NEB 5-alpha Competent *E. coli*.

Design and PCR Amplification of Fragments for Gibson Assembly:

Note: We highly recommend using our web tool, NEBuilder™, available at www.NEBGibson.com, to design PCR primers with overlapping sequences between the adjacent DNA fragments and for their assembly into a cloning vector.



NEBuilder is the fastest and easiest approach to obtain ready-to-use sequences for overlapping primers. However, it does not give details about the primer design workflow. In some cases, it might be appropriate to further manually alter primer sequences in order to adapt them for the use in more complex assemblies, such as those that include site-specific mutagenesis. For this purpose, it is absolutely necessary to understand the general requirements and rules that apply to PCR primers used in conjunction with Gibson Assembly. The sections below offer step-by-step directions and recommendations for the manual design of primers for the assembly of two or more PCR fragments, as well as primer design for assembly of PCR fragments into a cloning vector prepared either by PCR or by restriction digestion.

Structure of the Overlapping Primers

PCR primers for use in Gibson Assembly must have two sequence components:

- an overlap sequence, required for the assembly of adjacent fragments;
- a gene-specific sequence, required for template priming during PCR amplification;

The non-priming overlap sequence is added at the 5'-end of the primer. This sequence is homologous to the 5'-terminal sequence of the adjacent fragment. The length of overlap sequence is dependent on the GC content of the sequences.

The priming gene-specific sequence is added at the 3'-end of the primer after the overlap sequence. The priming sequence should meet the criteria required for template annealing during PCR amplification.



The T_m of the 3' gene-specific sequence of the primer can be calculated using the T_m calculator found on the NEB website at <http://www.neb.com/TmCalculator>.

General Recommendations for Design of Overlapping Primers

To achieve efficient assembly of PCR fragments into a vector, we suggest using a 15–25 nt overlap with a T_m equal to or greater than 48°C (assuming A-T pair = 2°C and G-C pair = 4°C). To prevent errors in primer design it is highly recommended to first perform DNA fragment assembly *in silico* and create a final sequence file displaying both DNA strands (Fig. 2A, Step I). This virtual sequence may then be used as a template to design overlapping primers. Figure 2A shows the workflow for overlapping primer design by using an *in silico*-created DNA sequence file. First, mark the junctions between the adjacent fragments 1, 2 and 3 (Fig. 2A, step II). Next, at or near each junction choose 15–25 nucleotide sequences to serve as the overlap region between the two adjacent fragments (Fig. 2A, step III). For the best fit, in terms of length and T_m , the overlap sequence can be composed of nucleotides which belong to only one fragment (overlap shown in blue) or it can be split between the two adjacent fragments in any combination (overlap shown in orange). Mark the first 5' and the last 3' nucleotide of the overlap sequence on both DNA strands (boxed sequence). Finally, starting from the first 5' nucleotide, copy the entire overlap sequence in the 5' to 3' direction and, if necessary, continue to add additional nucleotides to the 3' end until the gene-specific priming sequence length is reached (Fig. 2A, step IV). The reverse overlapping primer is designed following the same steps as described above but copying the sequence from the complementary DNA strand in the 5' to 3' direction. Keep in mind that the two primers sharing the same overlap sequence are always used in separate PCR reactions, each in combination with the primer, which primes the complementary sequence on the opposite end of the respective DNA fragment (Fig. 2A, step V).

Figure 2A: Primer design using *in silico* created final DNA sequence file.

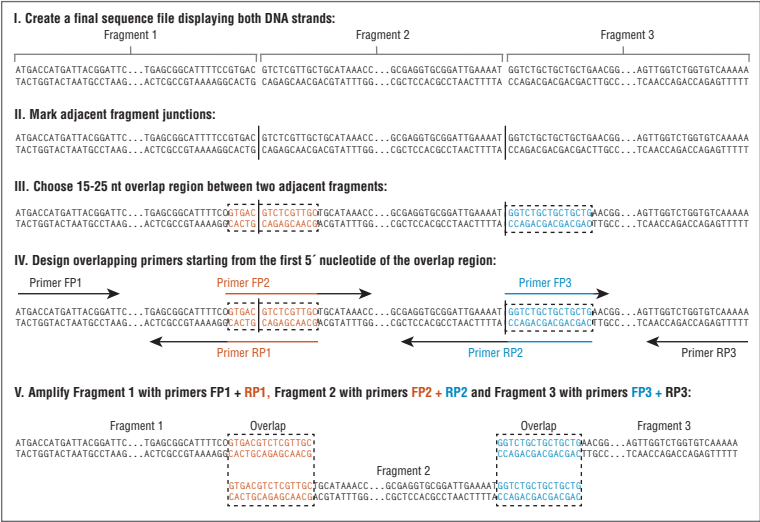
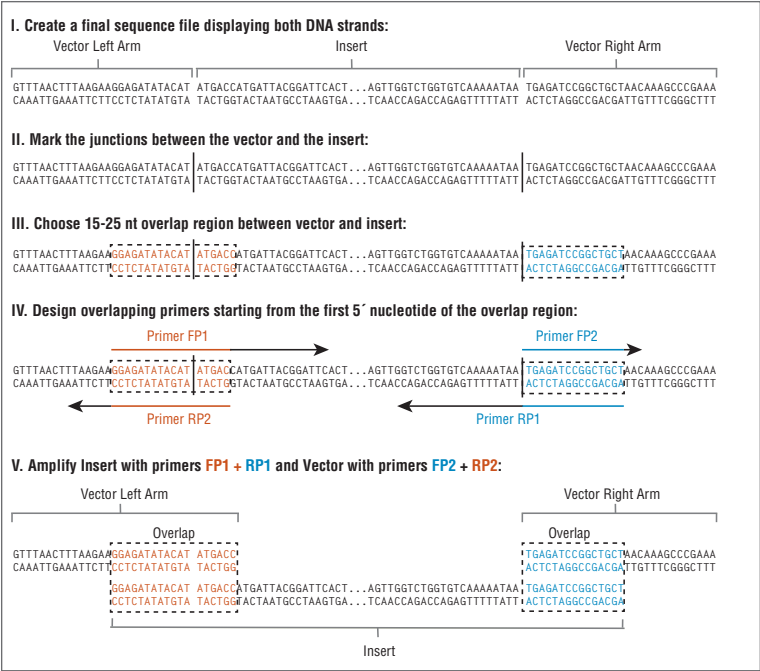


Figure 2B: Primer design for PCR-generated vector and insert using *in silico* created final DNA sequence file.



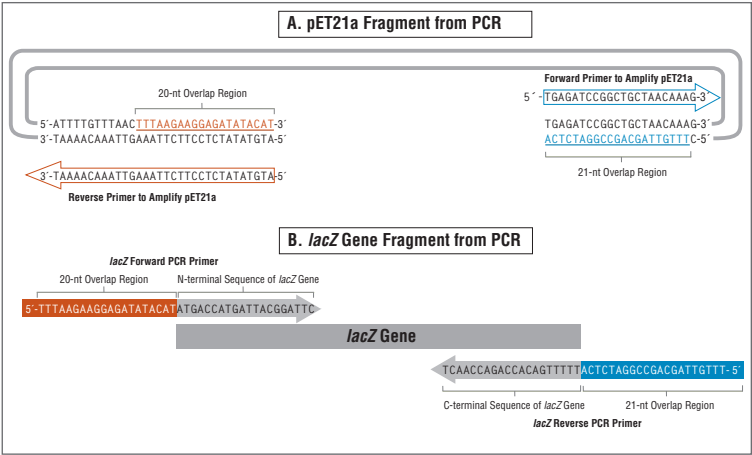
Primer Design for PCR-Generated Vector and Insert

For the purposes of primer design, the vector and the insert may be viewed as two PCR fragments that have to be assembled into a circular DNA molecule. This means that the primer design rules described above may also be applied for generation of the vector fragment and the insert fragment sharing overlapping ends. Use the *in silico*-created final sequence file as a template to design overlapping primers between the vector and the insert by accomplishing the same steps as described above, and as shown in Figure 2B.

If you intend to use PCR-generated vector for one specific insertion, then the overlap sequence may be split between the vector and the insert in any combination to make shorter primers (Figure 2B, step III, overlap shown in orange). However, if the same PCR-generated vector will be used for assembly of various inserts, then the entire overlap sequence must originate from the vector sequence and must be added to primers that will be used to amplify the insert (Figure 2B, step III, overlap shown in blue). The latter case is also illustrated in Figure 3 for assembly of the *lacZ* gene into a pET21a vector. The pET21a forward primer (orange arrow) and the reverse primer (blue arrow) start at the position where the *lacZ* gene must be inserted. Both vector-specific primers completely match the vector sequence on the respective strands. This inverse PCR strategy yields a linear vector fragment. Generally, 10–100 pg of a vector is recommended as a template in the inverse PCR reaction.

To amplify the *lacZ* gene, both forward and reverse *lacZ*-specific priming sequences (gray) at their 5′ end are fused with the respective vector sequences to be used as overlap sequences in assembly with the vector. Within the *lacZ* Forward PCR primer, the overlap sequence (orange) is identical to the 20-nt terminal sequence on the top strand (orange) of the vector's left-arm (in the 5′→3′ direction). Within the *lacZ* Reverse PCR primer, the overlap sequence (blue) is identical to the 21-nt terminal sequence on the bottom strand (blue) of the vector's right-arm (in the 5′→3′ direction). The length of the overlap sequence is determined by the number of nucleotides needed to reach a $T_m \geq 48^\circ\text{C}$. If necessary, one may add additional nucleotides between the overlap sequence and the *lacZ*-specific sequence, for example, to introduce a unique restriction site.

Figure 3: Primer Design for Vector pET21a and *lacZ* Gene Assembly.



Primer Design for Assembly of Restriction Enzyme Digested Vector and PCR-Generated Insert.

Restriction enzyme-treated vectors can have 5'-overhangs, 3'-overhangs or blunt ends. When vector is linearized by restriction digestion, the entire overlap sequence must originate from the vector sequence and must be added to primers that will be used to amplify the insert. The overlap region of the forward primer for the gene of interest (orange) should line up with the 3' end of the overhang on the vector's left arm and extend back until the $T_m \geq 48^\circ\text{C}$ (Fig.4A, Left side). This primer also includes gene-specific sequence at the 3'-end (gray). Keep in mind that the restriction site, which was used to digest the vector, will be lost in the assembled product. However, additional nucleotides may be added between the overlap region and gene-specific sequence region to restore the pre-existing restriction site, or to introduce a new, unique restriction site. A similar principle is applied to the design of the reverse primer for the gene of interest (Fig. 4A, Right side).

Figure 4A: Assembly of Restriction Enzyme-Digested Vector and PCR-derived Insert

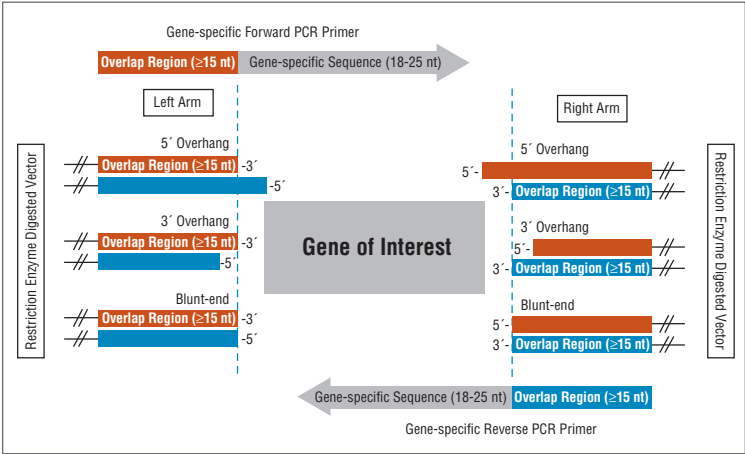
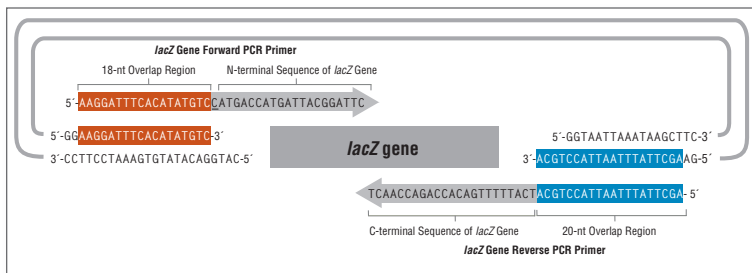


Figure 4B shows primer design for assembly of the *lacZ* gene and pMAL-c5X, digested with NcoI and SbfI. In this example, the forward primer of the gene has a "C" nucleotide (underlined) inserted between the 18-nt overlap and the N-terminal sequence of the *lacZ* gene to ensure the *lacZ* protein is in frame with the maltose binding protein.

Figure 4B: Primer Design for *lacZ* Gene and NcoI/SbfI-cut pMAL-c5X Assembly



Useful Recommendations for Vector Digestion with Restriction Enzymes

In general, the cloning vector can be linearized by any restriction endonuclease or by any combination of two restriction endonucleases displaying unique site(s) at the desired locations within the vector sequence.

Note: Double-digestion of vector DNA with two restriction endonucleases is the best approach to reduce the uncut vector background.

- Some restriction endonucleases cannot efficiently digest supercoiled DNA and thus may leave behind different amounts of uncut vector DNA. If not gel-purified, the uncut vector is transformable and will show up after transformation of the Gibson Assembly reaction, thereby, reducing the overall fraction of recombinant clones. A table “Cleavage of Supercoiled DNA” found at www.neb.com/nebecomm/tech_reference/restriction_enzymes/ may be used as a reference for choosing the most suitable restriction endonucleases and the number of activity units required for complete digestion of plasmid vector.
- Restriction endonucleases might have a reduced activity on plasmid DNA purified using various plasmid purification kits. In such cases, the extended restriction time or increased enzyme concentration may be necessary to digest plasmid vector to completion (or as nearly as possible to completion). When applicable, NEB highly recommends using High-Fidelity (HF™) restriction endonucleases to avoid star activity which may occur when digesting DNA for extended periods of time with elevated amounts of regular restriction endonuclease.
- Purification of restriction endonuclease-digested vector is not necessary unless the same restriction site is present in insert DNA. In such cases, either heat-inactivate restriction endonuclease before Gibson Assembly reaction or purify the linearized vector, either by phenol-chloroform extraction/alcohol precipitation or by electrophoresis on an agarose gel.

Useful Recommendations for PCR Amplification

NEB recommends using Q5 High-Fidelity DNA polymerase (NEB #M0491) or related products (NEB #M0493 or NEB #M0494) to amplify fragments of interest prior to assembly. The use of this high-fidelity DNA polymerase yields PCR products with blunt ends, thereby reducing the error rates at the fragment junctions.

- When using circular plasmid DNA as a template, it is important to use a minimal amount of DNA (usually recommended 0.1–0.5 ng of plasmid template per 50 µl PCR reaction) in order to reduce the template background after transformation. If higher amounts of plasmid template must be used in PCR reaction or higher amounts of PCR product must be used in the Gibson Assembly reaction, it is recommended to digest the PCR product with DpnI restriction endonuclease in order to destroy plasmid template before setting up the Gibson Assembly reaction (for protocol see below).
- Verify PCR product purity and yield by gel electrophoresis. If non-specific DNA fragments are obtained, you will need to purify the target fragment from the agarose gel to ensure the correct product assembly during the Gibson Assembly reaction.
- PCR product purification is not necessary as long as the product is > 90% pure. You can add unpurified PCR product directly from the PCR reaction into the Gibson Assembly for up to 20% of the total Gibson Assembly reaction volume (i.e. PCR products should account for 4 µl, or less, in a 20 µl Gibson Assembly reaction). Larger volumes of unpurified PCR products could significantly inhibit both the Gibson Assembly and the transformation. In such cases, it is recommended to column purify PCR products and, if necessary, to concentrate DNA by ethanol precipitation.

(Optional) DpnI Digestion Protocol

When higher amounts of plasmid template must be used in the PCR reaction, it is recommended to digest the PCR product with DpnI (NEB #R0176) in order to destroy plasmid template before setting up the Gibson Assembly reaction. DpnI cleaves only *E. coli* Dam methylase-methylated plasmid DNA, but does not cleave the PCR product since it is not methylated.

DpnI Digestion Protocol:

1. In a total 10 µl reaction, mix 5–8 µl of PCR product with 1 µl of 10X NEBuffer 4 and 1 µl (20 units) of DpnI.
2. Incubate at 37°C for 30 minutes.
3. Heat-inactivate DpnI by incubating at 80°C for 20 minutes.
4. Proceed with the Gibson Assembly Cloning procedure, described on page 11.

Gibson Assembly Reaction:

Optimal Quantities

NEB recommends a total of 0.02–0.5 pmols of DNA fragments when 1 or 2 fragments are being assembled into a vector. Efficiency of assembly decreases as the number or length of fragments increases. To calculate the number of pmols of each fragment for optimal assembly, based on fragment length and weight, we recommend the following formula:

$$\text{pmols} = (\text{weight in ng}) \times 1,000 / (\text{base pairs} \times 650 \text{ daltons})$$

50 ng of 5000 bp dsDNA is about 0.015 pmols.

50 ng of 500 bp dsDNA is about 0.15 pmols.

The mass of each fragment can be measured using the NanoDrop instrument, absorbance at 260 nm or estimated from agarose gel electrophoresis followed by ethidium bromide staining.

Assembly Protocol

Please note that this protocol has been optimized for the assembly and cloning of one or two fragments into any vector. For the cloning of larger assemblies, we recommend using the standard protocol provided with the Gibson Assembly Master Mix (NEB #E2611).

1. Set up the following reaction on ice:

	Gibson Assembly Reaction Setup	
	Amount per Reaction	Positive Control**
PCR Fragment(s) + linearized vector	2–10 µl (0.02–0.5 pmols)*	10 µl
Gibson Assembly Master Mix (2X)	10 µl	10 µl
Deionized H ₂ O	xx µl	0
Total Volume	20 µl	20 µl

* Optimized cloning efficiency requires about 25–100 ng of vector and at least 2-fold excess inserts. Use 5–10X more insert if the size is less than 200 bp. Total volume of unpurified PCR fragments in Gibson Assembly reaction should not exceed 20%.

** Control reagents are provided for two reactions.

2. Incubate samples in a thermocycler at 50°C for 15 minutes. After incubation, store the samples on ice or at –20°C for subsequent transformation.
3. Transform NEB 5-alpha Competent *E. coli* cells (provided with the kit) with 2 µl of the assembly reaction, following the transformation protocol on page 12.

Gibson Assembly Transformation Protocol

1. Thaw competent cells on ice.
2. Add 2 μ l of the chilled assembly product to the competent cells. Mix gently by pipetting up and down or by flicking the tube 4–5 times. Do not vortex.
3. Place the mixture on ice for 30 minutes. Do not mix.
4. Heat shock at 42°C for 30 seconds. Do not mix.
5. Transfer tubes to ice for 2 minutes.
6. Add 950 μ l of room-temperature SOC media to the tube.
7. Incubate the tube at 37°C for 60 minutes. Shake vigorously (250 rpm) or rotate.
8. Warm selection plates to 37°C.
9. Spread 100 μ l of the cells onto the selection plates. Use Amp plates for positive control sample.
10. Incubate overnight at 37°C.

Usage Notes:

To ensure the successful assembly and subsequent transformation of assembled DNAs, NEB recommends the following:

- *DNA*: PCR product purification is not necessary if the total volume of all PCR products in the Gibson Assembly reaction is 20% or less of the Gibson Assembly reaction volume. Higher volumes of PCR products may reduce the efficiency of Gibson Assembly and transformation due to the elevated carryover amounts of PCR reaction buffer and unused primers present in the PCR product. Column purification of PCR products may increase the efficiency of both Gibson Assembly and transformation by 2–10 fold and is highly recommended when performing assemblies of three or more PCR fragments or assembling longer than 5 kb fragments. Purified DNA for assembly can be dissolved in ddH₂O (Milli-Q® water or equivalent is preferable), TE or other dilution buffers.
- *Insert*: When directly assembling fragments into a cloning vector, the concentration of assembly fragments should be at least 2–3 times higher than the concentration of vector. For assembly of multiple fragments into a vector, we recommend using equimolar ratio of fragments.
- *Transformation*: NEB 5-alpha Competent *E. coli* (High Efficiency, NEB #C2987) provided with the kit are recommended for use for assembled products of less than 20 kb in size.
- *Biology*: Some DNA structures, including inverted and tandem repeats, are selected against by *E. coli*. Some recombinant proteins are not well tolerated by *E. coli* and can result in poor transformation or small colonies.

Frequently Asked Questions (FAQs):

What are the advantages of this method compared to traditional cloning methods?

Gibson Assembly allows insertion of one or more DNA fragments into virtually any position of the linearized vector and does not rely on the presence of restriction sites within a particular sequence to be synthesized or cloned. Therefore, the user has complete control over what is assembled and insertion of unwanted additional sequence, often used to facilitate the manipulation of multiple DNA sequences, can be avoided. Furthermore, the Gibson Assembly method is fast relative to standard restriction enzyme-based cloning. Lastly, a greater number of DNA fragments can be joined in a single reaction with greater efficiency than conventional methods.

How large of a DNA fragment can I assemble?

Gibson Assembly Cloning Kit has been used to clone a 15 kb DNA fragment into a 5.4 kb plasmid in *E. coli*, totaling up to 20.4 kb in length. For assembled products greater than 15 kb, NEB recommends NEB 10-beta Competent *E. coli* (High Efficiency, NEB #C3019) or NEB 10-beta Electrocompetent *E. coli* (NEB #C3020).

Can I use electroporation instead of chemical transformation?

Yes, but it is necessary to dilute the Gibson Assembly reaction product 3-fold, and use only 1 μ l for electroporation.

How many fragments of DNA can be assembled in one reaction?

The Gibson Assembly Cloning kit is formulated to work best when assembling 1–2 fragments into a cloning vector. Assembly efficiency drops by 5–10-fold for 3-fragment assembly into a cloning vector when compared to one-fragment assembly into a vector. We recommend using the standard protocol provided with the Gibson Assembly Master Mix (NEB #E2611) for the assembly of three or more inserts into a vector in one reaction in order to produce a clone with the correct insert. A strategy involving sequential assembly can be used if all of the fragments cannot be assembled in a single reaction.

Can I PCR-amplify the assembled product?

Yes. The assembled DNA molecule is covalently joined and may be PCR-amplified. Additionally, if the final product is a closed circular DNA molecule, it may be used as a template in rolling-circle amplification (RCA).

Is this method applicable to the assembly of repetitive sequences?

Yes. However, one must ensure that each DNA fragment includes a unique overlap so that the sequences may anneal and are properly arranged. The repetitive sequence can also be internalized in the first stage of a two-stage assembly strategy. If having repetitive sequences at the ends of each fragment is unavoidable, the correct DNA assembly may be produced, albeit at lower efficiency than other, unintended assemblies.

What are the shortest overlaps that can be used with this assembly method?

Productive assembly has been shown for DNA fragments with as little as a 12 bp overlap, however, it depends on the GC content of the overlap. We recommend using 15 bp overlaps, or more, for dsDNA assembly with a $T_m \geq 48^\circ\text{C}$ (AT pair = 2°C and GC pair = 4°C).

What are the longest overlaps that can be used with this method?

The quantity of 5' exonuclease in the Gibson Assembly Master Mix and a 15 minute assembly reaction time have been optimized for the assembly of DNA molecules with ≤ 25 -bp overlaps. If assembly reaction time is increased to 60 minutes, overlaps up to 40-bp may be used with the Gibson Assembly Cloning Kit.

Can I use a 15-nt overlap that is entirely composed of His-tag repeats (i.e. CACCACCACCACCAC)?

No, you must flank the His-tag sequence on both sides with at least 2 nucleotides, that are not part of the His-tag repeating sequence. You should avoid repeating sequences at the end of an overlap.

Is it necessary to inactivate restriction enzymes after vector digestion?

Inactivation of restriction endonucleases is generally not necessary, but in some cases it might increase the transformation efficiency. If the insert also carries the restriction site that was used to linearize the vector it is necessary to heat inactivate the restriction enzyme before mixing the linearized vector with the insert in Gibson Assembly. If a heat-resistant restriction enzyme was used to linearize the vector, then vector should be purified by phenol-chloroform extraction or extracted from agarose gel after electrophoresis, before coming into contact with the insert.

Is it necessary to purify PCR products?

Purification of PCR products is generally not necessary. You can use unpurified PCR products directly, as long as the total volume of PCR products in the Gibson Assembly reaction is 20% or less. If greater amounts of PCR products are used, a column cleanup kit is sufficient. It is advantageous to gel-purify the target DNA fragment if the PCR product is contaminated by either non-specific amplification products, primer-dimers or large quantities of unused PCR primers.

Can ≤ 200 bp dsDNA fragments be assembled by this method?

Yes. For optimal results, use these fragments in ≥ 5-fold excess.

Can longer or shorter incubation times be used?

The Gibson Assembly Cloning Kit has been optimized for assembly in 15 minutes at 50°C. Reaction times less than 15 minutes are generally not recommended. Extended incubation times (e.g., 60 minutes) have been shown to improve assembly efficiencies in some cases. Do not incubate the Gibson Assembly reaction overnight.

Will the reaction work at other temperatures?

The reaction has been optimized at 50°C, but it has been shown to work at temperatures between 40°C and 50°C.

I would like to produce overlapping dsDNA fragments by PCR. Do I need to use PCR primers that have been purified by PAGE or HPLC?

No. Standard, desalted primers may be used.

Are there any differences between the Gibson Assembly Master Mix (NEB #E2611) and Gibson Assembly Master Mix included in the Gibson Assembly Cloning Kit (NEB #E5510)?

Although the Gibson Assembly Master Mix included with both kits is the same, the protocol for the Gibson Assembly Cloning Kit (NEB #E5510) is optimized to perform one to two fragment assembly and cloning into a vector, while the protocol for Gibson Assembly Master Mix (NEB #E2611) is optimized to perform multiple-fragment assemblies (up to six fragments). The major differences between the two protocols are the length of overlapping sequences between the adjacent fragments and the incubation time of the assembly reaction. The 15 minute assembly reaction protocol provided with the Gibson Assembly Cloning Kit (NEB #E5510) is recommended for assembly of fragments that are flanked by 15-25 nt overlaps. The Gibson Assembly Master Mix (NEB #E2611) is recommended for assembly of up to six fragments that are flanked by 20-80 nt overlaps, and requires a 60 minute reaction time.

Troubleshooting

Positive Control Yields No Colonies Following Transformation into *E. coli*

- Be sure to perform a positive control assembly reaction with Gibson Master Mix, as described on page 11.
- Use the competent cells provided with the kit (NEB 5-alpha, NEB #C2987). The components of the Gibson Master Mix may inhibit the functionality of competent cells from other companies.
- Perform the transformation procedure exactly as described on page 12.
- Competent cells may be thawed only once and cannot be repeatedly frozen and thawed without extreme loss in competency. Cells are best thawed on ice and DNA added as soon as the last bit of ice in the tube disappears.
- Do not vortex competent cells. Mix cells and DNA by gently pipetting up and down. Check cell competency by transforming 100 pg of pUC19 plasmid provided with the kit. Expect $1-3 \times 10^9$ colonies formed/ μ g DNA after overnight incubation on LB-ampicillin plates at 37°C.

Gibson Assembly Reaction Yields No Colonies Following Transformation into *E. coli*.

- Assemble and transform the positive control provided with the Gibson Assembly Cloning Kit. Successful assembly of a positive control will demonstrate that the Gibson Assembly Master Mix is functional and the transformation conditions are suitable.
- Check the primer design of the overlapping DNA fragments to ensure that there is sufficient and correct overlap to facilitate assembly.
- Avoid overlaps with highly palindromic sequences as they may cause up to a 10-fold reduction in recombinant colonies. When assembling fragments into a multiple cloning site (MCS) of a cloning vector, it is strongly recommended to use restriction sites that are located on the edges of the MCS to avoid overlap regions with highly palindromic sequences. Plate higher amounts of transformation reaction when using restriction sites that are located in the middle of the MCS of the cloning vector.
- Repeat the Gibson Assembly reaction using higher concentrations of fragments and/or vector. Make sure that the total volume of PCR-amplified products does not exceed 20% of Gibson Assembly reaction. If necessary, purify PCR fragments and/or PCR-amplified vector before the assembly reaction.
- Some DNA structures, including inverted and tandem repeats, are selected against by *E. coli*. Some recombinant proteins are not well tolerated by *E. coli* and can result in poor transformation.

- Test the success of the Assembly by performing PCR with primers that flank the assembled product.
- Consider whether the cloned insert may be toxic to *E. coli*, and a low-copy vector, such as a BAC, should be used. Because the assembled product is a covalently-closed molecule, it may be alternatively amplified by PCR or rolling-circle amplification (RCA).

Gibson Assembly Reaction Yields High Number of Clones with Incorrect Inserts

- Make sure that your PCR product is a single band of the correct size. If the PCR product is contaminated with non-specific bands, it is necessary to gel-purify the PCR product to ensure cloning of the correct insert.
- Consider whether the cloned insert may be toxic to *E. coli* and a low-copy vector, such as a BAC, should be used. Because the assembled product is a covalently closed molecule, it may be alternatively amplified by PCR or RCA.

Gibson Assembly Reaction Yields High Number of Small Colonies

- Some recombinant proteins are not well-tolerated by *E. coli* and can result in poor transformation efficiency or small colonies. Use a low copy number vector (i.e. pACYC184) or a vector with tight control of protein expression. When assembling into the pUC19 vector, make sure that your gene is not in frame with *lacZ* alpha fragment.

Gibson Assembly Reaction Yields a High Number of Clones without the Insert

- PCR products may carry over large quantities of uncut plasmid template. To remove plasmid template, treat PCR products with DpnI restriction endonuclease before performing Gibson Assembly. Protocol for DpnI digestion can be found on page 10.
- Restriction enzyme digested vector may carry over large quantities of uncut plasmid. Some restriction enzymes do not cut supercoiled plasmids to completion. The best way to reduce uncut vector background is to digest the vector with two different restriction endonucleases. If a single enzyme must be used, avoid restriction enzymes that leave four-base single-stranded overhangs rich in C/G (i.e. CCGG overhang). These overhangs may self-anneal to form the transformable form of the vector molecule. Also, increase units and/or incubation time and/or purify the linear vector from agarose gel.

Appendix A

NEB 5-alpha Competent *E. coli* (High Efficiency, NEB #C2987)

Store at -80°C

Genotype: *fhuA2 D(argF-lacZ)U169 phoA glnV44 f80D(lacZ)M15 gyrA96 recA1 relA1 endA1 thi-1 hsdR17*

CAUTION: This product contains DMSO, a hazardous material. Review the MSDS before handling.

Quality Control Assays

Transformation Efficiency:

100 pg of pUC19 plasmid DNA was used to transform NEB 5-alpha Competent *E. coli* (High Efficiency) following the protocol provided. 1–3 x 10⁹ colonies formed/μg after an overnight incubation on LB-ampicillin plates at 37°C.

Untransformed cells were also tested for resistance to phage φ80, a standard test for resistance to phage T1 and sensitivity to ampicillin, chloramphenicol, kanamycin, nitrofurantoin, spectinomycin, streptomycin and tetracycline. The cells were shown to be suitable for blue/white screening by α-complementation of the β-galactosidase gene using pUC19.

Transformation Protocol Variables:

- **Thawing:** Cells are best thawed on ice and DNA added as soon as the last bit of ice in the tube disappears. Cells can also be thawed by hand, but warming above 0°C will dramatically decrease the transformation efficiency.
- **Incubation of DNA with Cells on Ice:** For maximum transformation efficiency, cells and DNA should be incubated together on ice for 30 minutes. Expect a 2-fold loss in transformation efficiency for every 10 minutes this step is shortened.
- **Heat Shock:** Both the temperature and the timing of the heat shock step are important and specific to the transformation volume and vessel. Using the transformation tube provided, 30 seconds at 42°C is optimal.
- **Outgrowth:** Outgrowth at 37°C for 1 hour is best for cell recovery and for expression of antibiotic resistance. Expect a 2-fold loss in transformation efficiency for every 15 minutes this step is shortened. SOC gives 2-fold higher transformation efficiency than LB medium; and incubation with shaking or rotating the tube gives 2-fold higher transformation efficiency than incubation without shaking.

- *Plating*: Selection plates can be used warm or cold, wet or dry, without significantly affecting the transformation efficiency. However, warm, dry plates are easier to spread and allow for the most rapid colony formation.

Antibiotics for Plasmid Selection

Antibiotics	Working Concentration
Ampicillin	100 µg/ml
Carbenicillin	100 µg/ml
Chloramphenicol	33 µg/ml
Kanamycin	30 µg/ml
Streptomycin	25 µg/ml
Tetracycline	15 µg/ml

References:

1. Gibson, D.G. et.al. (2009) *Nature Methods*, 343–345.
2. Gibson, D.G. et al. (2010) *Nature Methods*, 901–903.

For additional references and information on Gibson Assembly Master Mix, visit www.syntheticgenomics.com. and www.jcvi.org.

Ordering Information

PRODUCT	NEB #	SIZE
Gibson Assembly Cloning Kit	E5510S	10 reactions
COMPANION PRODUCTS		
Gibson Assembly Master Mix	E2611S/L	10/50 reactions
Q5 High-Fidelity DNA Polymerase	M0491S/L	100/500 units
Q5 Hot Start High-Fidelity DNA Polymerase	M0493S/L	100/500 units
Q5 High-Fidelity 2X Master Mix	M0492S/L	100/500 rxns
NEB5-alpha Competent <i>E. coli</i> (High Efficiency)	C2987I/H	6 x 0.2 ml/ 20 x 0.05 ml
NEB 10-beta Competent <i>E. coli</i> (High Efficiency)	C3019I/H	6 x 0.2 ml/ 20 x 0.05 ml
NEB 10-beta Electrocompetent <i>E. coli</i>	C3020K	6 x 0.1 ml
SOC Outgrowth Medium	B9020S	4 x 25 ml



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