repliQa™ HiFi Assembly Mix

Seamless assembly of multiple DNA fragments for high efficiency cloning

FEATURES & BENEFITS:

- Formulated to increase number of transformants
- Assemble up to 6 fragment inserts without the need for restriction enzymes
- Flexibility in design with 10x master mix enabling assembly of low concentration DNA samples
- Eliminates dilution step resulting in easier workflow and 1 hr assembly
- Includes DpnI to reduce background when using plasmid templates for PCR

DESCRIPTION:

The repliQa™ HiFi Assembly Mix simplifies the construction of recombinant DNA through seamless assembly of multiple DNA fragments in a single, isothermal reaction.

Similar in principle to the Gibson Assembly® Method, the high efficiency repliQa HiFi Assembly Mix is ideal for a range of genetic engineering applications including:

- Routine molecular cloning
- Site-directed mutagenesis
- Synthetic biology
- Construction of libraries for directed evolution studies

The concentrated (10x), two component format allows flexibility in design of assembly reactions and compatibility with less concentrated DNA samples. The repliQa Mix has been optimized for use with a total input quantity of DNA fragments in the range of 0.03 to 0.5 pmols. Assembly of up to six DNA fragments is recommended, though the repliQa Mix has been used successfully for more complex assemblies. The mix supports assembly of multiple DNA fragments in a single 1-hr reaction.

For more info visit: www.quantabio.com
Speed up your workflow and increase transformation efficiency

repliQa HiFi Assembly Mix increases transformation efficiency without the need for diluting or purifying the assembly reaction prior to transformation of competent cells, resulting in less hands-on time and faster workflows.

Low DNA amounts can be used and will efficiently generate high amounts of transformats.

Assemble larger number of fragments

repliQa HiFi Assembly Mix allows for large inserts to be cloned at a very high efficiency resulting in significantly more positive clones eliminating the need to repeat experiments due to erroneous or insufficient clones.

1.1 Three DNA fragments containing 23 bp overlaps were generated by PCR, DpnI treated and purified. The three fragments, 4.2 kb, 3.1 kb, and 400 bp in size, were combined in a 1:1.4:5 molar ratio. Total DNA quantities used are indicated (x-axis) and reacted at 50 °C for 60 minutes according to the protocol. One microliter of the undiluted assembled products or one microliter of a 4-fold dilution of the assembled products was used to transform 30 μl of chemically competent cells.

1.2 PCR fragments containing 30 bp overlaps were DpnI treated, purified, and assembled according to the protocol. Reactions contained the indicated number of DNA fragments (0.1 pmol each) and were incubated at 50 °C for 60 minutes. 1 µl of the reactions were used to transform 30 µl of chemically competent cells.

ORDER INFO

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