



Double Strand DNA Sequencing Analysis

Objective

To sequence the DNA sample in full-length by primer walking method in double strand to confirm the known sequences

Starting Materials

1. 5µg of PCR DNA.
2. The predicted sequence of the 3.7kb region.

Methods

1. Design and synthesis of 12 internal sequencing primers every 500 - 550 bases.
2. Sequencing the plasmid with the designed primers and two universal primers.
3. Assembly of the sequencing results by Sequencher 4.2.
4. Determination of consensus sequences

Results

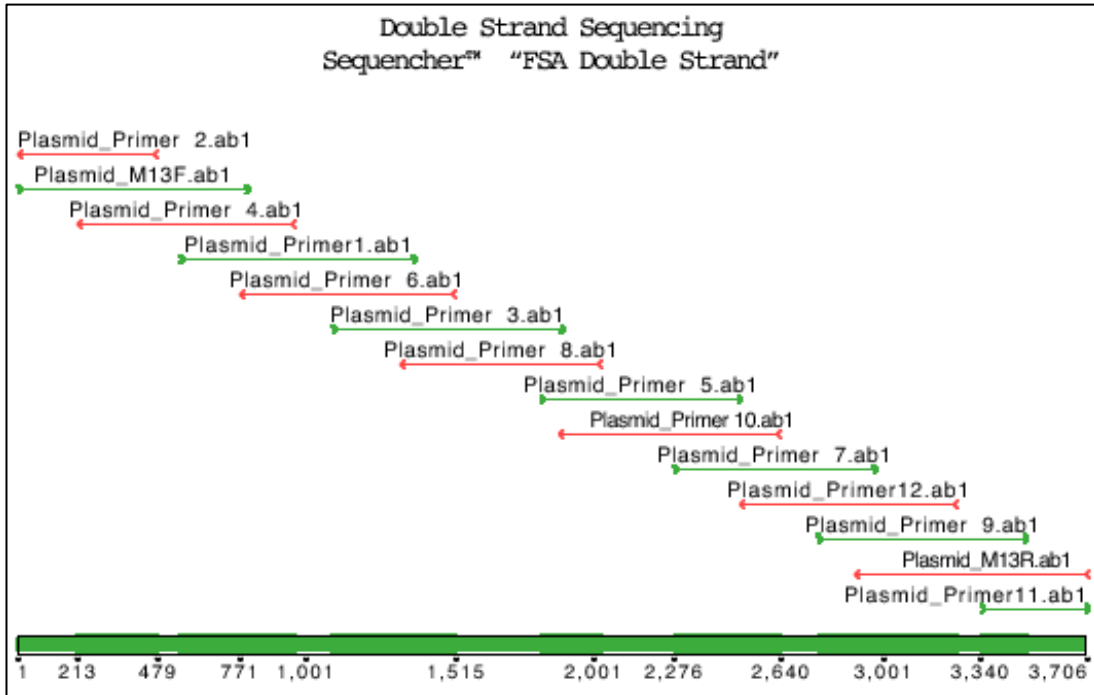
1. All 12 designed internal primers and two universal primers generated clean sequencing data.
2. After assembly by Sequencher and proofreading, a consensus file had been generated.
3. All primers information, chromatograms, and consensus sequence are available at our secure website.

Primer Information

Primer Name	Primer Sequences
M13F	5' (GTA AAA CGA CGG CCA GT) 3'
M13R	5' (GGA AAC AGC TAT GAC CAT G) 3'
Primer 1	5' (ACG GGA CGT CGG TGA CAT CA) 3'
Primer 2	5' (AGA CAC GGG ACC GTA CGT CG) 3'
Primer 3	5' (GGA CGT CGG TTA TGA TGA CGT) 3'
Primer 4	5' (ACG GGA CGT CGT CGG TGA CA) 3'
Primer 5	5' (ACG GGA ACT CGG GCG GGA AT) 3'
Primer 6	5' (CGT CGT CGA CAT TTG CGG C) 3'
Primer 7	5' (TTG CAT CGT CGG TGA CAT TTG) 3'
Primer 8	5' (TGA CAT CGA CGT CGA TGA CAT T) 3'
Primer 9	5' (ACT CGT CGT CCT CGT GAA CT) 3'
Primer 10	5' (TTG CGA GAC CAT TTG CAT CA) 3'
Primer 11	5' (ACA CGT CGA AGG TGA CAT TTG) 3'
Primer 12	5' (ATG GTA GTT ACA CAT TTG GC) 3'

800.557.ACGT (2248)
847.520.9162 phone
847.520.9163 fax
www.acgtinc.com

35 Waltz Drive
Wheeling, Illinois 60090
dnaseq@acgtinc.com



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