

Description

Title of Invention: METHOD FOR PRODUCING DNA PROBE AND METHOD FOR ANALYZING GENOMIC DNA USING THE DNA PROBE

Technical Field

[0001] The present invention relates to a method for producing a DNA library that can be used for analyzing a DNA marker or other purposes and a method for gene analysis using such DNA library.

Background Art

[0002] In general, genomic analysis is performed to conduct comprehensive analysis of genetic information contained in the genome, such as nucleotide sequence information. However, an analysis aimed at determination of the nucleotide sequence for whole genome is disadvantageous in terms of the number of processes and the cost. In cases of organisms with large genomic sizes, in addition, genomic analysis based on nucleotide sequence analysis has limitations because of genome complexity.

Patent Literature 1 discloses an amplified fragment length polymorphism (AFLP) marker technique wherein a sample-specific marker is incorporated into a restriction-enzyme-treated fragment that had been ligated to an adaptor and only a part of the sequence of the restriction-enzyme-treated fragment is to be determined. According to the technique disclosed in Patent Literature 1, the complexity of genomic DNA is reduced by treating genomic DNA with a restriction enzyme, the nucleotide sequence of a target part of the restriction-enzyme-treated fragment is determined, and the target restriction-enzyme-treated fragment is thus determined sufficiently. The technique disclosed in Patent Literature 1, however, requires processes such as treatment of genomic DNA with a restriction enzyme and ligation reaction with the use of an adaptor. Thus, it is difficult to achieve a cost reduction.

[0003] Meanwhile, Patent Literature 2 discloses as follows. That is, a DNA marker for identification that is highly correlated with the results of taste evaluation was found from among DNA bands obtained by amplifying DNAs extracted from a rice sample via PCR in the presence of adequate primers by the so-called RAPD (randomly amplified polymorphic DNA) technique. The method disclosed in Patent Literature 2 involves the use of a plurality of sequence-tagged sites (STSs, which are primers) identified by particular sequences. According to the method disclosed in Patent Literature 2, a DNA marker for identification amplified with the use of an STS primer is detected via electrophoresis. However, the RAPD technique disclosed in Patent Literature 2 yields significantly poor reproducibility of PCR amplification, and, accordingly, such technique

cannot be generally adopted as a DNA marker technique.

- [0004] Patent Literature 3 discloses a method for producing a genomic library wherein PCR is carried out with the use of a single type of primer designed on the basis of a sequence that appears relatively frequently in the target genome, the entire genomic region is substantially uniformly amplified, and a genomic library can be thus produced. While Patent Literature 3 describes that a genomic library can be produced by conducting PCR with the use of a random primer containing a random sequence, it does not describe any actual procedures or results of experimentation. Accordingly, the method described in Patent Literature 3 is deduced to require nucleotide sequence information of the genome so as to identify the genome appearing frequency, which would increase the number of procedures and the cost. According to the method described in Patent Literature 3, in addition, the entire genome is to be amplified, and complexity of genomic DNA cannot be reduced, disadvantageously.
- [0005] Patent Literature 4 discloses a high-throughput technique associated with markers that involves reduction in genome complexity by restriction enzyme treatment in combination with an array technique. According to the technique associated with markers disclosed in Patent Literature 4, genomic DNA is digested with restriction enzymes, an adaptor is ligated to the resulting genomic DNA fragment, a DNA fragment is amplified with the use of a primer hybridizing to the adaptor, and a DNA probe used for detection of such DNA fragment is then designed on the basis of the nucleotide sequence of the amplified DNA fragment.
- [0006] In addition, Non-Patent Literature 1 discloses the development of high-density linkage map containing several thousands of DNA markers for sugarcane and wheat by making use of the technique disclosed in Patent Literature 4. Also, Non-Patent Literature 2 discloses the development of a high-density linkage map containing several thousands of DNA markers for buck wheat by making use of the technique disclosed in Patent Literature 4.
- [0007] Further, Patent Literature 5 discloses a method involving the use of a random primer as a sample to be reacted with an array on which a probe is immobilized. However, Patent Literature 5 does not disclose a method in which a random primers is used to obtain an amplified fragment and the resulting amplified fragment is used to construct a DNA library.

Citation List

Patent Literature

- [0008] PTL 1: JP Patent No. 5389638
PTL 2: JP 2003-79375 A
PTL 3: JP Patent No. 3972106

PTL 4: JP Patent No. 5799484

PTL 5: JP 2014-204730 A

Non Patent Literature

[0009] NPL 1: DNA Research 21, 555-567, 2014

NPL 2: Breeding Science 64: 291-299, 2014

Summary

Technical Problem

[0010] A technique for genome information analysis, such as genetic linkage analysis conducted with the use of a DNA marker, is desired to produce a DNA library in a more convenient and highly reproducible manner. In addition, such technique is desired to produce a DNA probe capable of detecting a DNA fragment contained in a DNA library with high accuracy. As described above, a wide variety of techniques for producing a DNA library and a DNA probe are known. To date, however, there have been no techniques known to be sufficient in terms of convenience and/or reproducibility. Under the above circumstances, it is an object of the present invention to provide a method for producing a DNA probe that is applicable to a DNA library produced by a method with more convenience and higher reproducibility, and it is another object to provide a method for analyzing genomic DNA with the use of such DNA probe.

Solution to Problem

[0011] The present inventors have conducted concentrated studies in order to attain the above objects. As a result, they discovered that a DNA library could be produced with high reproducibility by conducting PCR with the use of a random primer while designating the concentration of such random primer within a designated range in a reaction solution and that a DNA probe could be easily designed on the basis of the nucleotide sequences of the DNA library to be produced. This has led to the completion of the present invention.

In one aspect, the present disclosure refers to a method for producing a DNA probe comprising steps of: conducting a nucleic acid amplification reaction in a reaction solution containing genomic DNA and a random primer having 9-30 bases using genomic DNA as a template to obtain DNA fragments, wherein when the random primer comprises 9 to 10 bases, the concentration of the random primer is 40 to 60 microM; when the random primer comprises 10 to 14 bases, the concentration of the random primer satisfy the conditions defined by an inequation: $y > 3E + 08x^{-6.974}$ and be 100 microM or less, provided that the nucleotide length of the random primer is represented by "x" and the concentration of the random primer is represented by "y"; when the random primer comprises 14 to 18 bases, the concentration of the random primer is 4 to 100 microM; when the random primer comprises 18 to 28 bases, the concentration of such random primer be 4 microM or more and satisfy the conditions defined by an inequation: $y < 8E + 08x^{-5.533}$; when the random

primer comprises 28 to 29 bases, the concentration of the random primer is 6 to 10 microM; when the random primer comprises 30 bases, the concentration of the random primer is 6 microM; determining the nucleotide sequence of the obtained DNA fragments; and designing a DNA probe used for detecting a DNA fragment obtained in the above step on the basis of the nucleotide sequence of the DNA fragments, the DNA probe comprising a nucleotide sequence complementary to the nucleotide sequence the DNA fragment. In another aspect, the present disclosure refers to a method for analyzing genomic DNA comprising steps of: conducting a nucleic acid amplification reaction with the use of the genomic DNA subjected to analysis and the random primer of claim 1 to obtain a DNA fragment; bringing the DNA probe produced by the method for producing a DNA probe as described herein into contact with the DNA fragment derived from the genomic DNA subjected to analysis; and detecting hybridization occurring between the DNA probe and the DNA fragment.

In another example, the present disclosure refers to an apparatus for DNA analysis comprising the DNA probe produced by the method for producing a DNA probe as described herein and a support comprising the DNA probe immobilized thereon.

The present invention includes the following.

- (1) A method for producing a DNA probe comprising steps of: conducting a nucleic acid amplification reaction in a reaction solution containing genomic DNA and a random primer at a high concentration using genomic DNA as a template to obtain DNA fragments; determining the nucleotide sequences of the obtained DNA fragments; and designing a DNA probe used for detecting a DNA fragment obtained in the above step on the basis of the nucleotide sequences of such DNA fragments.
- (2) The method for producing a DNA probe according to (1), wherein DNA fragments are obtained from a plurality of different genomic DNAs with the use of the random primers and, on the basis of the nucleotide sequences of the DNA fragments,

the DNA probe containing regions different between such genomic DNAs is designed.

(3) The method for producing a DNA probe according to (1), wherein the nucleotide sequence of the DNA fragment is compared with a known nucleotide sequence and the DNA probe containing a region different from that of the known nucleotide sequence is designed.

(4) The method for producing a DNA probe according to (1), wherein the reaction solution contains a random primer at a concentration of 4 to 200 microM.

(5) The method for producing a DNA probe according to (1), wherein the reaction solution contains a random primer at a concentration of 4 to 100 microM.

(6) The method for producing a DNA probe according to (1), wherein the random primers each contain 9 to 30 nucleotides.

(7) The method for producing a DNA probe according to (1), wherein the DNA fragments contain 100 to 500 nucleotides.

(8) A method for analyzing genomic DNA comprising steps of: bringing the DNA probe produced by the method for producing a DNA probe according to any of (1) to (7) into contact with a DNA fragment derived from genomic DNA subjected to analysis; and detecting hybridization occurring between the DNA probe and the DNA fragment.

(9) The method for analyzing genomic DNA according to (8), which further comprises a step of conducting a nucleic acid amplification reaction with the use of the genomic DNA subjected to analysis and the random primer to obtain the DNA fragment.

(10) The method for analyzing genomic DNA according to (8), wherein the DNA fragment derived from genomic DNA is a DNA marker and the presence or absence of the DNA marker is detected with the use of the DNA probe.

(11) An apparatus for DNA analysis comprising the DNA probe produced by the method for producing a DNA probe according to any of (1) to (7) and a support comprising the DNA probe immobilized thereon.

(12) The apparatus for DNA analysis according to (11), wherein the support is a substrate or bead.

Advantageous Effects of Invention

[0012] In the method for producing a DNA probe according to the present invention, a nucleotide sequence of a DNA probe is designed based on the nucleotide sequence of DNA fragments produced by the method of nucleic acid amplification using a random primer at a high concentration. According to the method of nucleic acid amplification using a random primer at a high concentration, DNA fragments can be amplified with excellent reproducibility. According to the present invention, therefore, a DNA probe applicable to a DNA fragment that can be obtained while achieving excellent repro-

ducibility can be produced in a simple manner.

[0013] According to the method for producing a DNA probe according to the present invention, also, a DNA probe applicable to a DNA fragment can be produced while achieving excellent reproducibility, and the resulting DNA probe can be used for genetic analysis, such as genetic linkage analysis, involving the use of a DNA fragment of interest as a DNA marker.

[0014] The method for analyzing genomic DNA with the use of a DNA probe according to the present invention involves the use of a DNA probe applicable to a DNA fragment produced in a simple manner with excellent reproducibility. Accordingly, genomic DNA can be analyzed in a cost-effective manner with high accuracy.

Brief Description of Drawings

[0015] [fig.1]Fig. 1 shows a flow chart demonstrating a method for producing a DNA library and a method for genetic analysis with the use of the DNA library.

[fig.2]Fig. 2 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified via PCR using DNA of the sugarcane variety NiF8 as a template under general conditions.

[fig.3]Fig. 3 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template at an annealing temperature of 45 degrees C.

[fig.4]Fig. 4 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template at an annealing temperature of 40 degrees C.

[fig.5]Fig. 5 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template at an annealing temperature of 37 degrees C.

[fig.6]Fig. 6 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 2.5 units of an

enzyme.

[fig.7]Fig. 7 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 12.5 units of an enzyme.

[fig.8]Fig. 8 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and MgCl_2 at the concentration doubled from the original level.

[fig.9]Fig. 9 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and MgCl_2 at the concentration tripled from the original level.

[fig.10]Fig. 10 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and MgCl_2 at the concentration quadrupled concentration.

[fig.11]Fig. 11 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 8 bases.

[fig.12]Fig. 12 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 9 bases.

[fig.13]Fig. 13 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 11 bases.

[fig.14]Fig. 14 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified

fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 12 bases.

[fig.15]Fig. 15 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 14 bases.

[fig.16]Fig. 16 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 16 bases.

[fig.17]Fig. 17 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 18 bases.

[fig.18]Fig. 18 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 20 bases.

[fig.19]Fig. 19 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 2 microM.

[fig.20]Fig. 20 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 4 microM.

[fig.21]Fig. 21 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 6 microM.

[fig.22]Fig. 22 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 6 microM.

[fig.23]Fig. 23 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 8 microM.

[fig.24]Fig. 24 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 8 microM.

[fig.25]Fig. 25 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 10 microM.

[fig.26]Fig. 26 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 10 microM.

[fig.27]Fig. 27 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 20 microM.

[fig.28]Fig. 28 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 20 microM.

[fig.29]Fig. 29 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the

first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 40 microM.

[fig.30]Fig. 30 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 40 microM.

[fig.31]Fig. 31 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 60 microM.

[fig.32]Fig. 32 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 60 microM.

[fig.33]Fig. 33 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 100 microM.

[fig.34]Fig. 34 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 100 microM.

[fig.35]Fig. 35 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 200 microM.

[fig.36]Fig. 36 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 200 microM.

[fig.37]Fig. 37 shows a characteristic diagram demonstrating a correlation between an

amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 300 microM.

[fig.38]Fig. 38 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 300 microM.

[fig.39]Fig. 39 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 400 microM.

[fig.40]Fig. 40 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 400 microM.

[fig.41]Fig. 41 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 500 microM.

[fig.42]Fig. 42 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 500 microM.

[fig.43]Fig. 43 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 600 microM.

[fig.44]Fig. 44 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer

at a concentration of 700 microM.

[fig.45]Fig. 45 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 800 microM.

[fig.46]Fig. 46 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 900 microM.

[fig.47]Fig. 47 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer at a concentration of 1000 microM.

[fig.48]Fig. 48 shows a characteristic diagram demonstrating the results of MiSeq analysis of a DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer.

[fig.49]Fig. 49 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the rice variety Nipponbare as a template and a random primer.

[fig.50]Fig. 50 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the rice variety Nipponbare as a template and a random primer.

[fig.51]Fig. 51 shows a characteristic diagram demonstrating the results of MiSeq analysis of a DNA library amplified using DNA of the rice variety Nipponbare as a template and a random primer.

[fig.52]Fig. 52 shows a characteristic diagram demonstrating positions of MiSeq read patterns in the genome information of the rice variety Nipponbare.

[fig.53]Fig. 53 shows a characteristic diagram demonstrating the frequency distribution of the number of mismatched nucleotides between the random primer and the rice genome.

[fig.54]Fig. 54 shows a characteristic diagram demonstrating the number of reads of

the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the marker N80521152.

[fig.55]Fig. 55 shows a photograph demonstrating electrophoretic patterns of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the PCR marker N80521152.

[fig.56]Fig. 56 shows a characteristic diagram demonstrating the number of reads of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the marker N80997192.

[fig.57]Fig. 57 shows a photograph demonstrating electrophoretic patterns of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the PCR marker N80997192.

[fig.58]Fig. 58 shows a characteristic diagram demonstrating the number of reads of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the marker N80533142.

[fig.59]Fig. 59 shows a photograph demonstrating electrophoretic patterns of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the PCR marker N80533142.

[fig.60]Fig. 60 shows a characteristic diagram demonstrating the number of reads of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the marker N91552391.

[fig.61]Fig. 61 shows a photograph demonstrating electrophoretic patterns of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the PCR marker N91552391.

[fig.62]Fig. 62 shows a characteristic diagram demonstrating the number of reads of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the marker N91653962.

[fig.63]Fig. 63 shows a photograph demonstrating electrophoretic patterns of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the PCR marker N91653962.

[fig.64]Fig. 64 shows a characteristic diagram demonstrating the number of reads of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the marker N91124801.

[fig.65]Fig. 65 shows a photograph demonstrating electrophoretic patterns of the sugarcane varieties NiF8 and Ni9 and hybrid progeny lines thereof at the PCR marker N91124801.

[fig.66]Fig. 66 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the

first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 9 bases.

[fig.67]Fig. 67 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 9 bases.

[fig.68]Fig. 68 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 10 bases.

[fig.69]Fig. 69 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 10 bases.

[fig.70]Fig. 70 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 11 bases.

[fig.71]Fig. 71 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 11 bases.

[fig.72]Fig. 72 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 12 bases.

[fig.73]Fig. 73 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 12 bases.

[fig.74]Fig. 74 shows a characteristic diagram demonstrating a correlation between an

amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 14 bases.

[fig.75]Fig. 75 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 14 bases.

[fig.76]Fig. 76 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 16 bases.

[fig.77]Fig. 77 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 16 bases.

[fig.78]Fig. 78 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 18 bases.

[fig.79]Fig. 79 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 18 bases.

[fig.80]Fig. 80 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer comprising 20 bases.

[fig.81]Fig. 81 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8

as a template and a random primer comprising 20 bases.

[fig.82]Fig. 82 shows a characteristic diagram demonstrating the results of investigating the reproducibility of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and random primers each comprising 8 to 35 bases used at a concentration of 0.6 to 300 microM.

[fig.83]Fig. 83 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a single type of random primer.

[fig.84]Fig. 84 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a single type of random primer.

[fig.85]Fig. 85 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 2 types of random primers.

[fig.86]Fig. 86 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 2 types of random primers.

[fig.87]Fig. 87 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 3 types of random primers.

[fig.88]Fig. 88 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 3 types of random primers.

[fig.89]Fig. 89 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the

first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 12 types of random primers.

[fig.90]Fig. 90 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 12 types of random primers.

[fig.91]Fig. 91 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 24 types of random primers.

[fig.92]Fig. 92 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 24 types of random primers.

[fig.93]Fig. 93 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 48 types of random primers.

[fig.94]Fig. 94 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and 48 types of random primers.

[fig.95]Fig. 95 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer B comprising 10 nucleotides.

[fig.96]Fig. 96 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer B comprising 10 nucleotides.

[fig.97]Fig. 97 shows a characteristic diagram demonstrating a correlation between an

amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer C comprising 10 nucleotides.

[fig.98]Fig. 98 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer C comprising 10 nucleotides.

[fig.99]Fig. 99 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer D comprising 10 nucleotides.

[fig.100]Fig. 100 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer D comprising 10 nucleotides.

[fig.101]Fig. 101 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer E comprising 10 nucleotides.

[fig.102]Fig. 102 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer E comprising 10 nucleotides.

[fig.103]Fig. 103 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using DNA of the sugarcane variety NiF8 as a template and a random primer F comprising 10 nucleotides.

[fig.104]Fig. 104 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using DNA of the sugarcane variety NiF8

as a template and a random primer F comprising 10 nucleotides.

[fig.105]Fig. 105 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the first time) of the DNA library amplified using human genomic DNA as a template and a random primer A comprising 10 nucleotides.

[fig.106]Fig. 106 shows a characteristic diagram demonstrating a correlation between an amplified fragment length and a fluorescence unit (FU) in which the amplified fragment length is determined based on an electrophoretic pattern (appeared for the second time) of the DNA library amplified using human genomic DNA as a template and a random primer A comprising 10 nucleotides.

[fig.107]Fig. 107 shows a flow chart demonstrating a process for producing a DNA microarray with the application of the method for producing a DNA probe according to the present invention.

[fig.108]Fig. 108 shows a characteristic diagram demonstrating the results of assaying signals obtained from a DNA probe concerning the DNA library amplified using genomic DNAs of NiF8 and Ni9 as templates and a random primer at a high concentration.

[fig.109]Fig. 109 shows a characteristic diagram demonstrating the results of comparison of signals obtained through repeated measurements concerning the DNA library amplified using genomic DNA of Ni9 as a template and a random primer at a high concentration.

[fig.110]Fig. 110 shows a characteristic diagram demonstrating the results of assaying signal levels obtained from the DNA probe reacting with the marker N80521152.

[fig.111]Fig. 111 shows a characteristic diagram demonstrating the results of assaying signal levels obtained from the DNA probe reacting with the marker N80997192.

[fig.112]Fig. 112 shows a characteristic diagram demonstrating the results of assaying signal levels obtained from the DNA probe reacting with the marker N80533142.

[fig.113]Fig. 113 shows a characteristic diagram demonstrating the results of assaying signal levels obtained from the DNA probe reacting with the marker N91552391.

[fig.114]Fig. 114 shows a characteristic diagram demonstrating the results of assaying signal levels obtained from the DNA probe reacting with the marker N91653962.

[fig.115]Fig. 115 shows a characteristic diagram demonstrating the results of assaying signal levels obtained from the DNA probe reacting with the marker N91124801.

Description of Embodiments

[0016] Hereafter, the present invention is described in detail.

[0017] According to the method for producing a DNA probe of the present invention, a

nucleic acid amplification reaction is carried out in a reaction solution, which is prepared to contain a primer having an arbitrary nucleotide sequence (hereafter, referred to as a "random primer") at a high concentration, and a nucleotide sequence of a DNA probe used for detecting an amplified nucleic acid fragment (i.e., a DNA fragment) is designed based on the nucleotide sequence of such DNA fragment. By conducting a nucleic acid amplification reaction in a reaction solution containing a random primer at a high concentration, a DNA fragment of interest can be amplified with excellent reproducibility. Hereafter, the obtained DNA fragment is referred to as a "DNA library."

When a reaction solution contains a random primer at a high concentration, such concentration is higher than the concentration of a primer used in a general nucleic acid amplification reaction. When producing a DNA library, specifically, a random primer is used at a higher concentration than a primer used in a general nucleic acid amplification reaction. As a template contained in a reaction solution, genomic DNA prepared from a target organism for which a DNA library is to be produced can be used. A target organism species is not particularly limited, and a target organism species can be, for example, an animal including a human, a plant, a microorganism, or a virus. That is, a DNA library can be produced from any organism species.

[0018] When producing a DNA library, the concentration of a random primer may be prescribed as described above. Thus, a nucleic acid fragment (or nucleic acid fragments) can be amplified with high reproducibility. The term "reproducibility" used herein refers to an extent of concordance among nucleic acid fragments amplified by a plurality of nucleic acid amplification reactions carried out with the use of the same template and the same random primer. That is, the term "high reproducibility (or the expression "reproducibility is high")" refers to a high extent of concordance among nucleic acid fragments amplified by a plurality of nucleic acid amplification reactions carried out with the use of the same template and the same random primer.

[0019] The extent of reproducibility can be evaluated by, for example, conducting a plurality of nucleic acid amplification reactions with the use of the same template and the same random primer, calculating the Spearman's rank correlation coefficient for the data of the nucleotide sequences of the resulting amplified fragments, and evaluating the extent of reproducibility on the basis of such coefficient. The Spearman's rank correlation coefficient is generally represented by the symbol ρ (rho). When ρ (rho) is greater than 0.9, for example, the reproducibility of the amplification reaction of interest can be evaluated to be sufficient.

Random primer

[0020] A sequence constituting a random primer that can be used for producing a DNA library is not particularly limited. For example, a random primer comprising nu-

cleotides having 9 to 30 bases can be used. In particular, a random primer may be composed of any nucleotide sequence comprising 9 to 30 bases, a nucleotide type (i.e., a sequence type) is not particularly limited, and a random primer may be composed of 1 or more types of nucleotide sequences, preferably 1 to 10,000 types of nucleotide sequences, more preferably 1 to 1,000 types of nucleotide sequences, further preferably 1 to 100 types of nucleotide sequences, and most preferably 1 to 96 types of nucleotide sequences. With the use of nucleotides (or a group of nucleotides) within the range mentioned above for a random primer, an amplified nucleic acid fragment can be obtained with higher reproducibility. When a random primer comprises a plurality of nucleotide sequences, it is not necessary that all nucleotide sequences comprise the same number of bases (9 to 30 nucleotides). A random primer may comprise a plurality of nucleotide sequences composed of a different number of bases.

[0021] When designing a plurality of types of nucleotide sequences for a random primer, 30% or more, preferably 50% or more, more preferably 70% or more, and further preferably 90% or more of the entire such sequences exhibit 70% or less, preferably 60% or less, more preferably 50% or less, and most preferably 40% or less identity. By designing a plurality of types of nucleotides for a random primer exhibiting the identity within such range, an amplified fragment can be obtained over the entire genomic DNA of the target organism species. Thus, uniformity of the amplified fragment can be enhanced.

[0022] A nucleotide sequence constituting a random primer is preferably designed to have a G-C content of 5% to 95%, more preferably 10% to 90%, further preferably 15% to 80%, and most preferably 20% to 70%. With the use of an aggregate of nucleotides having the G-C content within the aforementioned range as a random primer, amplified nucleic acid fragments can be obtained with higher reproducibility. G-C content is the percentage of guanine and cytosine contained in the whole nucleotide chain.

[0023] In particular, a nucleotide sequence used as a random primer is preferably designed to comprise continuous bases accounting for 80% or less, more preferably 70% or less, further preferably 60% or less, and most preferably 50% or less of the full-length sequence. Alternatively, the number of continuous bases in a nucleotide sequence used as a random primer is preferably 8 or less, more preferably 7 or less, further preferably 6 or less, and most preferably 5 or less. With the use of an aggregate of nucleotides comprising the number of continuous bases within the aforementioned range as a random primer, amplified nucleic acid fragments can be obtained with higher reproducibility.

[0024] In addition, it is preferable that a nucleotide sequence used as a random primer be designed to not comprise a complementary region of 6 or more, more preferably 5 or more, and further preferably 4 or more bases in a molecule. Thus, double strand

formation occurring in a molecule can be prevented, and amplified nucleic acid fragments can be obtained with higher reproducibility.

[0025] When a plurality of types of nucleotide sequences are designed as random primers, in particular, it is preferable that a plurality of nucleotide sequences be designed to not comprise complementary regions of 6 or more, more preferably 5 or more, and further preferably 4 or more bases among a plurality of types of nucleotide sequences. Thus, double strand formation occurring between nucleotide sequences can be prevented, and amplified nucleic acid fragments can be obtained with higher reproducibility.

[0026] When a plurality of nucleotide sequences are designed as random primers, in addition, it is preferable that such sequences be designed to not comprise complementary regions of 6 or more, more preferably 5 or more, and further preferably 5 or more bases at the 3' terminus. Thus, double strand formation occurring between nucleotide sequences can be prevented, and amplified nucleic acid fragments can be obtained with higher reproducibility.

[0027] The terms "complementary regions" and "complementary sequences" refer to, for example, regions and sequences exhibiting 80% to 100% identity to each other (e.g., regions and sequences each comprising 5 bases in which 4 or 5 bases are complementary to each other) or regions and sequences exhibiting 90% to 100% identity to each other (e.g., regions and sequences each comprising 5 bases in which 5 bases are complementary to each other).

[0028] Further, a nucleotide sequence used as a random primer is preferably designed to have a T_m value suitable for thermal cycling conditions (in particular, an annealing temperature) of a nucleic acid amplification reaction. A T_m value can be calculated by a conventional method, such as the nearest neighbor base pair approach, the Wallace method, and the GC% method, although a method of calculation is not particularly limited thereto. Specifically, a nucleotide sequence used as a random primer is preferably designed to have a T_m value of 10 to 85 degrees C, more preferably 12 to 75 degrees C, further preferably 14 to 70 degrees C, and most preferably 16 to 65 degrees C. By designing a random primer to have a T_m value within the aforementioned range, amplified nucleic acid fragments can be obtained with higher reproducibility under given thermal cycling conditions (in particular, at a given annealing temperature) of the nucleic acid amplification reaction.

[0029] When a plurality of nucleotide sequences are designed as random primers, in addition, a variation for T_m among a plurality of nucleotide sequences is preferably 50 degrees C or less, more preferably 45 degrees C or less, further preferably 40 degrees C or less, and most preferably 35 degrees C or less. By designing random primers while adjusting a variation for T_m among a plurality of nucleotide sequences within the range mentioned above, amplified nucleic acid fragments can be obtained with

higher reproducibility under given thermal cycling conditions (in particular, at a given annealing temperature) of the nucleic acid amplification reaction.

Nucleic acid amplification reaction

[0030] When producing a DNA library, many DNA fragments are obtained via the nucleic acid amplification reaction carried out with the use of random primers and genomic DNA as a template described above. At the time of the nucleic acid amplification reaction, in particular, the concentration of random primes in a reaction solution is prescribed higher than the concentration of primers in a conventional nucleic acid amplification reaction. Thus, many DNA fragments can be obtained with the use of genomic DNA as a template while achieving high reproducibility. Such many DNA fragments can be used for a DNA library that can be used for genotyping and other purposes.

[0031] A nucleic acid amplification reaction is aimed at synthesis of amplified fragments in a reaction solution containing genomic DNA as a template, the random primers, DNA polymerase, deoxynucleoside triphosphates as a substrate (i.e., dNTP, which is a mixture of dATP, dCTP, dTTP, and dGTP), and a buffer under the given thermal cycling conditions. It is necessary that a nucleic acid amplification reaction be carried out in a reaction solution containing Mg^{2+} at a given concentration. In the reaction solution of the composition described above, the buffer contains $MgCl_2$. When the buffer does not contain $MgCl_2$, the reaction solution of the composition described above further contains $MgCl_2$.

[0032] In a nucleic acid amplification reaction, in particular, it is preferable that the concentration of random primers be adequately determined in accordance with the base lengths of the random primers. When a plurality of types of nucleotide sequences having different numbers of bases are used as random primers, the number of bases constituting the random primers may be the average of such plurality of nucleotide sequences (the average may be a simple average or the weight average taking the amount of nucleotides into account).

[0033] Specifically, a nucleic acid amplification reaction is carried out with the use of a random primer comprising 9 to 30 bases at a concentration of 4 to 200 μM , and preferably at 4 to 100 μM . Under such conditions, many amplified fragments, and, in particular, many amplified fragments comprising 100 to 500 bases, can be obtained via a nucleic acid amplification reaction while achieving high reproducibility.

[0034] When a random primer comprises 9 to 10 bases, more specifically, the concentration of such random primer is preferably 40 to 60 μM . When a random primer comprises 10 to 14 bases, it is preferable that the concentration of such random primer satisfy the conditions defined by an inequation: $y > 3E + 08x^{-6.974}$ and be 100 μM or less, provided that the nucleotide length of the random primer is represented by "x" and

the concentration of the random primer is represented by "y." When a random primer comprises 14 to 18 bases, the concentration of such random primer is preferably 4 to 100 microM. When a random primer comprises 18 to 28 bases, it is preferable that the concentration of such random primer be 4 microM or more and satisfy the conditions defined by an inequation: $y < 8E + 08x^{-5.533}$. When a random primer comprises 28 to 29 bases, the concentration of such random primer is preferably 6 to 10 microM. By designating the random primer concentration in accordance with the number of bases constituting the random primer as described above, many amplified fragments can be obtained with more certainty while achieving high reproducibility.

[0035] As described in the examples below, the inequations: $y > 3E + 08x^{-6.974}$ and $y < 8E + 08x^{-5.533}$, are developed to be able to represent the concentration of a random primer at which many DNA fragments comprising 100 to 500 bases can be obtained with high reproducibility as a result of thorough inspection of the correlation between random primer length and random primer concentration.

[0036] While the amount of genomic DNA serving as a template in a nucleic acid amplification reaction is not particularly limited, it is preferably 0.1 to 1000 ng, more preferably 1 to 500 ng, further preferably 5 to 200 ng, and most preferably 10 to 100 ng, when the amount of the reaction solution is 50 microliters. By designating the amount of genomic DNA as a template within such range, many amplified fragments can be obtained without inhibiting the amplification reaction from a random primer, while achieving high reproducibility.

[0037] Genomic DNA can be prepared in accordance with a conventional technique without particular limitation. With the use of a commercialized kit, also, genomic DNA can be easily prepared from a target organism species. Genomic DNA extracted from an organism in accordance with a conventional technique or with the use of a commercialized kit may be used without further processing, genomic DNA extracted from an organism and then purified may be used, or genomic DNA subjected to restriction enzyme treatment or ultrasonic treatment may be used.

[0038] DNA polymerase used in a nucleic acid amplification reaction is not particularly limited, and an enzyme having DNA polymerase activity under thermal cycling conditions for a nucleic acid amplification reaction can be used. Specifically, heatstable DNA polymerase used for a general nucleic acid amplification reaction can be used. Examples of DNA polymerases include thermophilic bacteria-derived DNA polymerase, such as Taq DNA polymerase, and hyperthermophilic archaea-derived DNA polymerase, such as KOD DNA polymerase and Pfu DNA polymerase. In a nucleic acid amplification reaction, it is particularly preferable that Pfu DNA polymerase be used as DNA polymerase in combination with the random primer

described above. With the use of such DNA polymerase, many amplified fragments can be obtained with more certainty while achieving high reproducibility.

[0039] In a nucleic acid amplification reaction, the concentration of deoxynucleoside triphosphate as a substrate (i.e., dNTP, which is a mixture of dATP, dCTP, dTTP, and dGTP) is not particularly limited, and it can be 5 microM to 0.6 mM, preferably 10 microM to 0.4 mM, and more preferably 20 microM to 0.2 mM. By designating the concentration of dNTP serving as a substrate within such range, errors caused by incorrect incorporation by DNA polymerase can be prevented, and many amplified fragments can be obtained while achieving high reproducibility.

[0040] A buffer used in a nucleic acid amplification reaction is not particularly limited. For example, a solution comprising MgCl_2 as described above, Tris-HCl (pH 8.3), and KCl can be used. The concentration of Mg^{2+} is not particularly limited. For example, it can be 0.1 to 4.0 mM, preferably 0.2 to 3.0 mM, more preferably 0.3 to 2.0 mM, and further preferably 0.5 to 1.5 mM. By designating the concentration of Mg^{2+} in the reaction solution within such range, many amplified fragments can be obtained while achieving high reproducibility.

[0041] Thermal cycling conditions of a nucleic acid amplification reaction are not particularly limited, and a common thermal cycle can be adopted. A specific example of a thermal cycle comprises a first step of thermal denaturation in which genomic DNA as a template is dissociated into single strands, a cycle comprising thermal denaturation, annealing, and extension repeated a plurality of times (e.g., 20 to 40 times), a step of extension for a given period of time according to need, and the final step of storage.

[0042] Thermal denaturation can be performed at, for example, 93 to 99 degrees C, preferably 95 to 98 degrees C, and more preferably 97 to 98 degrees C. Annealing can be performed at, for example, 30 to 70 degrees C, preferably 35 to 68 degrees C, and more preferably 37 to 65 degrees C, although it varies depending on a T_m value of the random primer. Extension can be performed at, for example, 70 to 76 degrees C, preferably 71 to 75 degrees C, and more preferably 72 to 74 degrees C. Storage can be performed at, for example, 4 degrees C.

[0043] The first step of thermal denaturation can be performed within the temperature range described above for a period of, for example, 5 seconds to 10 minutes, preferably 10 seconds to 5 minutes, and more preferably 30 seconds to 2 minutes. In the cycle comprising "thermal denaturation, annealing, and extension," thermal denaturation can be carried out within the temperature range described above for a period of, for example, 2 seconds to 5 minutes, preferably 5 seconds to 2 minutes, and more preferably 10 seconds to 1 minute. In the cycle comprising "thermal denaturation, annealing, and extension," annealing can be carried out within the temperature range described above for a period of, for example, 1 second to 3 minutes, preferably 3

seconds to 2 minutes, and more preferably 5 seconds to 1 minute. In the cycle comprising "thermal denaturation, annealing, and extension," extension can be carried out within the temperature range described above for a period of, for example, 1 second to 3 minutes, preferably 3 seconds to 2 minutes, and more preferably 5 seconds to 1 minute.

[0044] When producing a DNA library, amplified fragments may be obtained by a nucleic acid amplification reaction that employs a hot start method. The hot start method is intended to prevent mis-priming or non-specific amplification caused by primer-dimer formation prior the cycle comprising "thermal denaturation, annealing, and extension." The hot start method involves the use of an enzyme in which DNA polymerase activity has been suppressed by binding an anti-DNA polymerase antibody thereto or chemical modification thereof. Thus, DNA polymerase activity can be suppressed and a non-specific reaction prior to the thermal cycle can be prevented. According to the hot start method, a temperature is set high in the first thermal cycle, DNA polymerase activity is thus recovered, and the subsequent nucleic acid amplification reaction is then allowed to proceed.

[0045] As described above, many amplified fragments can be obtained with the use of genomic DNA as a template and a random primer by conducting a nucleic acid amplification reaction with the use of a random primer comprising 9 to 30 bases and prescribing the concentration thereof to 4 to 200 microM in a reaction solution. With the use of the random primer comprising 9 to 30 bases by prescribing the concentration thereof to 4 to 200 microM in a reaction solution, a nucleic acid amplification reaction can be performed with very high reproducibility. According to the nucleic acid amplification reaction, specifically, many amplified fragments can be obtained while achieving very high reproducibility. Accordingly, such many amplified fragments can be used for a DNA library in genetic analysis targeting genomic DNA.

[0046] By performing a nucleic acid amplification reaction with the use of the random primer comprising 9 to 30 bases and prescribing the concentration thereof in a reaction solution to 4 to 200 microM, in particular, many amplified fragments comprising about 100 to 500 bases can be obtained with the use of genomic DNA as a template. Such many amplified fragments comprising about 100 to 500 bases are suitable for mass analysis of nucleotide sequences with the use of, for example, a next-generation sequencer, and highly accurate sequence information can thus be obtained. According to the present invention, accordingly, a DNA library, including DNA fragments comprising about 100 to 500 bases, can be produced.

[0047] By performing a nucleic acid amplification reaction with the use of the random primer comprising 9 to 30 bases and prescribing the concentration thereof to 4 to 200 microM in a reaction solution, in particular, the entire genomic DNA can be uniformly

amplified. In other words, amplified DNA fragments are not obtained from a particular region of genomic DNA by the nucleic acid amplification reaction with the use of such random primer, but amplified fragments are obtained from the entire genome.

According to the present invention, specifically, a DNA library can be produced uniformly across the entire genome.

DNA probe

[0048] In the present invention, the term "DNA probe" refers to a DNA fragment that has a nucleotide sequence complementary to the target DNA fragment and is able to hybridize to such DNA fragment. A DNA probe that is applicable to a so-called oligonucleotide microarray is particularly preferable. An oligonucleotide microarray is a microarray in which oligonucleotides comprising nucleotide sequences of interest are synthesized on a support and the synthesized oligonucleotides are used as DNA probes. The synthesized oligonucleotides serving as DNA probes comprise, for example, 20 to 100 bases, preferably 30 to 90 bases, and more preferably 50 to 60 bases.

[0049] The DNA probes designed in accordance with the present invention may be applied to a microarray comprising the synthesized oligonucleotides with the base length described above immobilized on a support, as with the case of the so-called Stanford-type microarray. Specifically, the DNA probes designed in accordance with the present invention can be applied to any microarrays according to conventional techniques. Thus, the DNA probes designed in accordance with the present invention can be applied to a microarray comprising a flat substrate, such as a glass or silicone substrate, as a support and a bead array comprising a microbead support.

[0050] According to the method for producing a DNA probe of the present invention, a nucleotide sequence of a DNA probe is designed to detect a DNA fragment (a DNA library) on the basis of the nucleotide sequence of the DNA fragment. Specifically, the nucleotide sequence of the DNA fragment (the DNA library) produced in the manner described above is first determined, and a nucleotide sequence of a DNA probe is designed based on the determined nucleotide sequence. A method for determining a nucleotide sequence of a DNA fragment is not particularly limited. For example, a DNA sequencer in accordance with the Sanger method or a next-generation sequencer can be used. While a next-generation sequencer is not particularly limited, such sequencer is also referred to as a second-generation sequencer, and such sequencer is an apparatus for nucleotide sequencing that is capable of simultaneous determination of nucleotide sequences of several tens of millions of DNA fragments. A sequencing principle of the next-generation sequencer is not particularly limited. For example, sequencing can be carried out in accordance with the method in which target DNA is amplified on flow cells and sequencing is carried out while conducting synthesis with

the use of bridge PCR method and sequencing-by-synthesis method, or in accordance with emulsion PCR method and the method of Pyrosequencing in which sequencing is carried out by assaying the amount of pyrophosphoric acids released at the time of and DNA synthesis. More specific examples of next-generation sequencers include MiniSeq, MiSeq, NextSeq, HiSeq, and HiSeq X Series (Illumina) and Roche 454 GS FLX sequencers (Roche).

- [0051] Subsequently, a DNA probe is designed to comprise, for example, a nucleotide sequence complementary to the nucleotide sequence of the DNA fragment (the DNA library) described above. More specifically, a region or a plurality of regions of the base lengths shorter than those of the DNA fragment (the DNA library) and covering at least a part of the DNA fragment (the DNA library) is/are identified, and the identified one or more regions are designed as probes for detecting the DNA fragment (the DNA library).
- [0052] When a plurality of regions are designed for a particular DNA fragment, such DNA fragment is to be detected with the use of a plurality of DNA probes. A region may be designed for a particular DNA fragment, and two or more regions may be designed for another DNA fragment. Specifically, a different number of regions; that is, DNA probes, may be designed for each DNA fragment. When a plurality of DNA probes are to be designed for a DNA fragment, parts of such plurality of DNA probes may overlap with each other, or such plurality of DNA probes may be designed with intervals comprising several bases.
- [0053] The number of bases constituting a DNA probe to be designed in the manner described above is not particularly limited. Such DNA probe can comprise 20 to 100 bases, preferably 30 to 90 bases, more preferably 40 to 80 bases, and most preferably 50 to 60 bases.
- [0054] It is particularly preferable that a plurality of regions be designed, in such a manner that the entire region of a genomic DNA fragment, the nucleotide sequence of which had been determined, would be covered with a plurality of regions. In such a case, a plurality of probes can react with a genomic DNA fragment obtained from genomic DNA derived from a particular organism species via restriction enzyme treatment, and such genomic DNA fragment can be detected with the use of such plurality of probes.
- [0055] A T_m value of a DNA probe is not particularly limited, and it can be 60 to 95 degrees C, preferably 70 to 90 degrees C, more preferably 75 to 85 degrees C, and most preferably 78 to 82 degrees C.
- [0056] When preparing DNA fragments from genomic DNAs with the use of random primers as described above, DNA fragments are obtained from a plurality of different genomic DNAs, and nucleotide sequences of these DNA fragments with different origins can be determined independently from each other. By comparing the de-

terminated nucleotide sequences, regions having different nucleotide sequences among the genomic DNAs can be identified. According to the method for producing a DNA probe of the present invention, DNA probes can be designed to comprise regions having different nucleotide sequences among the genomic DNAs thus identified. Specifically, a DNA probe may be designed to comprise a region of a particular genomic DNA that is different from another genomic DNA, and another DNA probe may be designed to comprise a region of the other genomic DNA that is different from the aforementioned particular genomic DNA. With the use of a pair of DNA probes thus designed, a specific type of genomic DNA to be analyzed can be identified.

- [0057] The nucleotide sequence of the DNA fragment amplified from genomic DNA with the use of a random primer may be compared with a known nucleotide sequence, and a DNA probe may be designed to comprise a region different from such known nucleotide sequence. A known nucleotide sequence can be obtained from a variety of conventional databases. While any databases can be used without particular limitation, the DDBJ database provided by the DNA Data Bank of Japan, the EMBL database provided by the European Bioinformatics Institute, the Genbank database provided by the National Center for Biotechnology Information, the KEGG database provided by the Kyoto Encyclopedia of Genes and Genomes, or a combined database comprising such various databases can be adequately used.

Apparatus for DNA analysis

- [0058] The apparatus for DNA analysis according to the present invention comprises the DNA probes designed in the manner described above immobilized on a support. An apparatus for DNA analysis comprising DNA probes immobilized on a support is occasionally referred to as a "DNA microarray." Specifically, the apparatus for DNA analysis according to the present invention is not limited to a so-called DNA chip comprising DNA probes immobilized on a support (i.e., a DNA microarray in a narrow sense), and apparatuses composed to be capable of utilization of DNA probes designed in the manner described above on a support are within the scope of the present invention.
- [0059] For example, a DNA microarray comprising DNA probes designed in the manner described above can be produced in accordance with a conventional technique. A DNA microarray can be produced by, for example, synthesizing an oligonucleotide comprising a nucleotide sequence of the DNA probe designed in the manner described above on a support based on such nucleotide sequence. A method for oligonucleotide synthesis is not particularly limited, and any conventional technique can be employed. For example, oligonucleotide synthesis can be performed on a support by photolithography in combination with chemical synthesis via light application. Alternatively, an oligonucleotide comprising a linker molecule having a high affinity with a

support surface added to its terminus may be separately synthesized on the basis of the nucleotide sequence of the DNA probe designed in the manner described above, and the resulting oligonucleotide may then be immobilized on a support surface at a particular position. A DNA microarray can also be produced by spotting the DNA probe designed in the manner described above on a support with the use of a pin-type arrayer or a nozzle-type arrayer.

[0060] The DNA microarray thus produced (i.e., the apparatus for DNA analysis) comprises a DNA probe comprising a nucleotide sequence complementary to a DNA fragment amplified from genomic DNA derived from a particular type of organism with the use of a random primer at a high concentration. Specifically, the DNA microarray thus produced is intended to detect a DNA fragment amplified from genomic DNA with the use of a random primer at a high concentration with the use of a DNA probe.

[0061] A DNA microarray may be any of a microarray using a flat substrate made of glass or silicone as a support, a bead array comprising a microbead support, and a three-dimensional microarray comprising a probe immobilized on an inner wall of a hollow fiber.

Method of genomic DNA analysis

[0062] With the use of the DNA probe produced in the manner described above, analysis of genomic DNA, such as genotyping, can be performed. The DNA probe described above is equivalent to the DNA library produced with the use of a random primer at a high concentration. Such DNA library has very high reproducibility, the size of which is suitable for a next-generation sequencer, and it is uniform across the entire genome. Accordingly, the DNA library can be used as a DNA marker (it is also referred to as a genetic marker or a gene marker). The term "DNA marker" refers to a region in the genome serving as a marker associated with genetic traits. A DNA marker can be used for, for example, breeding comprising a step of selection with the use of genotype identification, linkage maps, gene mapping, or a marker, back crossing using a marker, quantitative trait locus mapping, bulked segregant analysis, variety identification, or discontinuous imbalance mapping.

[0063] Specifically, a DNA marker can be detected with the use of the DNA probe produced in the manner described above, and breeding comprising a step of selection with the use of genotype identification, linkage maps, gene mapping, and a marker, back crossing with the use of a marker, quantitative trait locus mapping, bulked segregant analysis, variety identification, or discontinuous imbalance mapping can be carried out.

[0064] More specifically, an example of a method for genomic DNA analysis involving the use of the DNA probe comprises bringing the DNA probe produced in the manner described above into contact with a DNA fragment derived from genomic DNA of the target of analysis. Such DNA fragment may be prepared with the use of the random

primer that was used for producing the DNA library. Alternatively, a pair of primers that specifically amplify the DNA marker of interest may be designed on the basis of the nucleotide sequence of interest, and a DNA fragment may be prepared via a nucleic acid amplification reaction with the use of the pair of designed primers.

[0065] Subsequently, hybridization occurring between the DNA probe and the DNA fragment is detected in accordance with a conventional technique. For example, a label is added to the amplified DNA fragment, and hybridization of interest can be thus detected on the basis of the label. Any conventional substance may be used as a label. Examples of labels that can be used include a fluorescent molecule, a pigment molecule, and a radioactive molecule. A labeled nucleotide may be used in the step of DNA fragment amplification.

[0066] When a DNA microarray comprising a DNA probe is used, for example, a labeled DNA fragment is brought into contact with the DNA microarray under given conditions, and a DNA probe immobilized on the DNA microarray is allowed to hybridize to a labeled genomic DNA fragment. In this case, a probe hybridizes to a part of the DNA fragment, and it is preferable that hybridization be carried out under highly stringent conditions, so that hybridization does not occur in the presence of mismatch of a base, but it occurs only when the bases completely match. Under such highly stringent conditions, a slight change in single nucleotide polymorphism can be detected.

[0067] The stringency conditions can be adjusted in terms of reaction temperatures and salt concentrations. At a higher temperature, specifically, higher stringency conditions can be achieved. At a lower salt concentration, higher stringency conditions can be achieved. When a probe comprising 50 to 75 bases is used, for example, higher stringency conditions can be achieved by conducting hybridization at 40 to 44 degrees C with 0.21 SDS and 6× SSC.

[0068] Hybridization occurring between a DNA probe and a labeled DNA fragment can be detected based on a label. After the hybridization reaction between the labeled DNA fragment and the DNA probe, specifically, an unreacted DNA fragment or the like is washed, and a label of the DNA fragment that had specifically hybridized to the DNA probe is then observed. When a label is a fluorescent substance, for example, the fluorescent wavelength is detected. When a label is a pigment molecule, the pigment wavelength is detected. More specifically, an apparatus used for general DNA microarray analysis, such as a fluorescence detector or image analyzer, can be used.

[0069] In particular, DNA fragments amplified using genomic DNA as a template and a random primer at a high concentration can be detected with the use of such DNA probe. When a DNA probe comprising regions that are different among a plurality of different genomic DNAs is used, the genomic DNA as the target of analysis can be

analyzed in accordance with the DNA probe to which a DNA fragment derived from the genomic DNA as the target of analysis had hybridized. For example, a DNA probe reacting with a DNA marker comprising differences in nucleotide sequences among genomic DNAs of relative species may be used, so that the species of the genomic DNA as the target of analysis can be identified.

Examples

[0070] Hereafter, the present invention is described in greater detail with reference to the following examples, although the technical scope of the present invention is not limited to these examples.

Example 1

[0071] 1. Flow chart

In this example, a DNA library was prepared via PCR using genomic DNAs extracted from various types of organism species as templates and various sets of random primers in accordance with the flow chart shown in Fig. 1. With the use of the prepared DNA library, also, sequence analysis was performed with the use of a so-called next-generation sequencer, and the genotype was analyzed based on the read data.

2. Materials

In this example, genomic DNAs were extracted from the sugarcane varieties NiF8 and Ni9, 22 hybrid progeny lines thereof, and the rice variety Nipponbare using the DNeasy Plant Mini kit (QIAGEN), and the extracted genomic DNAs were purified. The purified genomic DNAs were used as NiF8-derived genomic DNA, Ni9-derived genomic DNA, 22 hybrid sugarcane progeny-derived genomic DNAs, and Nipponbare-derived genomic DNA, respectively. In Example 1, human genomic DNA was purchased from TakaraBio and used as human-derived genomic DNA.

3. Method

3.1 Correlation between PCR condition and DNA fragment size

3.1.1 Random primer designing

In order to design random primers, GC content was set between 20% and 70%, and the number of continuous bases was adjusted to 5 or fewer. Sequence length was set at 16 levels (i.e., 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 26, 28, 29, 30, and 35). For each sequence length, 96 types of nucleotide sequences were designed, and 96 sets of random primers were prepared. Concerning 10-base primers, 6 sets of random primers each comprising 96 types of random primers were designed (these 6 sets are referred to as 10-base primer A to 10-base primer F, respectively). In this example, specifically, 21 different sets of random primers were prepared.

[0072] Tables 1 to 21 show nucleotide sequences of random primers contained in such 21

different sets of random primers.

[0073] [Table 1-1]

Table 1 List of random primers (10-base primers A)

No	Primer sequence	SEQ ID NO:	No	Primer sequence	SEQ ID NO:
1	AGACGTCGTT	1	33	GCCGAATAGT	33
2	GAGGCGATAT	2	34	GTACCTAGGC	34
3	GTGCGAACGT	3	35	GCTTACATGA	35
4	TTATACTGCC	4	36	TCCACGTAGT	36
5	CAAGTTCGCA	5	37	AGAGGCCATC	37
6	ACAAGGTAGT	6	38	CGGTGATGCT	38
7	ACACAGCGAC	7	39	CACTGTGCTT	39
8	TTACCGATGT	8	40	CATGATGGCT	40
9	CACAGAGTCG	9	41	GCCACACATG	41
10	TTCAGCGCGT	10	42	CACACACTGT	42
11	AGGACCGTGA	11	43	CAGAATCATA	43
12	GTCTGTTCGC	12	44	ATCGTCTACG	44
13	ACCTGTCCAC	13	45	CGAGCAATAC	45
14	CCGCAATGAC	14	46	ACAAGCGCAC	46
15	CTGCCGATCA	15	47	GCTTAGATGT	47
16	TACACGGAGC	16	48	TGCATTCTGG	48
17	CCGCATTCAT	17	49	TGTCGGACCA	49
18	GACTCTAGAC	18	50	AGGCACTCGT	50
19	GGAGAACTTA	19	51	CTGCATGTGA	51
20	TCCGGTATGC	20	52	ACCACGCCTA	52
21	GGTCAGGAGT	21	53	GAGGTCGTAC	53
22	ACATTGGCAG	22	54	AATACTCTGT	54
23	CGTAGACTGC	23	55	TGCCAACTGA	55
24	AGACTGTACT	24	56	CCTGTTCCGT	56
25	TAGACGCAGT	25	57	GTAGAGAGTT	57
26	CCGATAATCT	26	58	TACAGCGTAA	58
27	GAGAGCTAGT	27	59	TGACGTGATG	59
28	GTACCGCGTT	28	60	AGACGTCGGT	60
29	GACTTGCGCA	29	61	CGCTAGGTTC	61
30	CGTGATTGCG	30	62	GCCTTATAGC	62
31	ATCGTCTCTG	31	63	CCTTCGATCT	63
32	CGTAGCTACG	32	64	AGGCAACGTG	64

[Table 1-2]

No	Primer sequence	SEQ ID NO:
65	TGAGCGGTGT	65
66	GTGTCCAACG	66
67	CGATGTTGCG	67
68	AACAAGACAC	68
69	GATGCTGGTT	69
70	ACCGGTAGTC	70
71	GTGACTAGCA	71
72	AGCCTATATT	72
73	TCGTGAGCTT	73
74	ACACTATGGC	74
75	GACTCTGTCG	75
76	TCGATGATGC	76
77	CTTGGACACT	77
78	GGCTGATCGT	78
79	ACTCACAGGC	79
80	ATGTGCGTAC	80
81	CACCATCGAT	81
82	AGCCATTAAC	82
83	AATCGACTGT	83
84	AATACTAGCG	84
85	TCGTCACTGA	85
86	CAGGCTCTTA	86
87	GGTCGGTGAT	87
88	CATTAGGCGT	88
89	ACTCGCGAGT	89
90	TTCCGAATAA	90
91	TGAGCATCGT	91
92	GCCACGTAAC	92
93	GAACATACATG	93
94	TCGTGAGGAC	94
95	GCGGCCTTAA	95
96	GCTAAGGACC	96

[Table 2-1]

Table 2 List of random primers (10-base primers B)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	ATAGCCATTA	97	33	GGTATAGTAC	129
2	CAGTAATCAT	98	34	CTAATCCACA	130
3	ACTCCTTAAT	99	35	GCACCTTATT	131
4	TCGAACATTA	100	36	ATTGACGGTA	132
5	ATTATGAGGT	101	37	GACATATGGT	133
6	AATCTTAGAG	102	38	GATAGTCGTA	134
7	TTAGATGATG	103	39	CAATTATCGC	135
8	TACATATCTG	104	40	CTTAGGTGAT	136
9	TCCTTAATCA	105	41	CATACTACTG	137
10	GTTGAGATTA	106	42	TAACGCGAAT	138
11	TGTTAACGTA	107	43	CAAGTTACGA	139
12	CATACAGTAA	108	44	AATCTCAAGG	140
13	CTTATACGAA	109	45	GCAATCATCA	141
14	AGATCTATGT	110	46	TGTAACGTTTC	142
15	AAGACTTAGT	111	47	TATCGTTGGT	143
16	TGCGCAATAA	112	48	CGCTTAAGAT	144
17	TTGGCCATAT	113	49	TTAGAACTGG	145
18	TATTACGAGG	114	50	GTCATAACGT	146
19	TTATGATCGC	115	51	AGAGCAGTAT	147
20	AACTTAGGAG	116	52	CAACATCACT	148
21	TCACAATCGT	117	53	CAGAAGCTTA	149
22	GAGTATATGG	118	54	AACTAACGTG	150
23	ATCAGGACAA	119	55	TTATACCGCT	151
24	GTACTIONAG	120	56	GAATTCGAGA	152
25	CTTATACTCG	121	57	TTACGTAACC	153
26	TAACGGACTA	122	58	GCATGGTTAA	154
27	GCGTTGTATA	123	59	GCACCTAATT	155
28	CTTAAGTGCT	124	60	TGTAGGTTGT	156
29	ATACGACTGT	125	61	CCATCTGGAA	157
30	ACTGTTATCG	126	62	TTCGCGTTGA	158
31	AATCTTGACG	127	63	AACCGAGGTT	159
32	ACATCACCTT	128	64	GTACGCTGTT	160

[Table 2-2]

No	Primer sequence	SEQ ID NO
65	AGTATCCTGG	161
66	GGTTGTACAG	162
67	ACGTACACCA	163
68	TGTCGAGCAA	164
69	GTCGTGTTAC	165
70	GTGCAATAGG	166
71	ACTCGATGCT	167
72	GAATCGCGTA	168
73	CGGTCATTGT	169
74	ATCAGGCGAT	170
75	GTAAGATGCG	171
76	GGTCTCTGA	172
77	TCCTCGCTAA	173
78	CTGCGTGATA	174
79	CATACTCGTC	175
80	ATCTGAGCTC	176
81	ACGGATAGTG	177
82	ACTGCAATGC	178
83	TAACGACGTG	179
84	TAGACTGTCG	180
85	CAGCACTTCA	181
86	AACATTGCCC	182
87	ACTAGTGCGT	183
88	ACGCTGTTCT	184
89	CGTCGAATGC	185
90	CTCTGACGGT	186
91	GTCGCCATGT	187
92	GGTCCACGTT	188
93	CGAGCGACTT	189
94	TTGACGCGTG	190
95	CTGAGAGCCT	191
96	CGCGCTAACT	192

[Table 3-1]

Table 3 List of random primers (10-base primers C)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	GGTCGTCAAG	193	33	TGAGGCAACC	225
2	AGGTTGACCA	194	34	CAACTGCAGT	226
3	TAACGGCAAC	195	35	CGGAGATACG	227
4	GAGGCTGGAT	196	36	CTTCGCAAGT	228
5	GTGCACACCT	197	37	CTGGCATAACG	229
6	TGAGGACCAG	198	38	TAACGTTCCG	230
7	TACTTGCGAG	199	39	CCGGCGTTAA	231
8	AACTGTGAGA	200	40	ACAAGACGCC	232
9	CTCCATCAAC	201	41	CCATTAGACT	233
10	CGGACTGTTA	202	42	GTCTGTGACA	234
11	TAGGACAGTC	203	43	GGCATTGGAC	235
12	AGAGGACACA	204	44	TCTTCGCACG	236
13	ACATTCGCGG	205	45	TAGCCTGTGC	237
14	GCTTACTGCA	206	46	CACTGACCTA	238
15	CAATACGTAA	207	47	CCGCACGATT	239
16	AGACTTGCGC	208	48	ATAGCACACG	240
17	GAGCGGTGTT	209	49	GCACGTCATA	241
18	CGTGAGAGGT	210	50	AAGCCGTTGG	242
19	AATCCGTCAG	211	51	CGGACCGTTA	243
20	ATACGTACCG	212	52	TACACAGCGT	244
21	AACTGATTCC	213	53	CGGACTTCAG	245
22	CTGAGCGTAC	214	54	TAGAACGTCA	246
23	GTCGGATTCCG	215	55	GGCATTGGAG	247
24	GCCGACCATA	216	56	GGCACTCGTT	248
25	GCAGAACTAA	217	57	GTACCGTTAA	249
26	CTAACGACCG	218	58	AATACGTGTC	250
27	GCTGGACCAT	219	59	CCATTGACGT	251
28	GACGCGGTTA	220	60	CGTGAATCGC	252
29	AGTGGTGAGC	221	61	ATCAACGCGG	253
30	CAGGCAGTCA	222	62	CGCCAAGGTA	254
31	TCTGACGTCA	223	63	AGAAGACGCC	255
32	TACATGACGT	224	64	CCGCATAGTC	256

[Table 3-2]

No	Primer sequence	SEQ ID NO
65	CTTATATGTG	257
66	GGTCTCATCG	258
67	CCACCATGTC	259
68	ACGAATGTGT	260
69	GGTAGTAACA	261
70	GCCACTTAAT	262
71	ATATTGCGCC	263
72	GACCAATAGT	264
73	AACAACACGG	265
74	ATAGCCGATG	266
75	CGAGAGCATA	267
76	CGAGACATGA	268
77	CGCCAAGTTA	269
78	TTATAATCGC	270
79	TAGAAGTGCA	271
80	GGAGGCATGT	272
81	GCCACTTCGA	273
82	TCCACGGTAC	274
83	CAACTATGCA	275
84	CAAGGAGGAC	276
85	GAGGTACCTA	277
86	GAGCGCATAA	278
87	TCGTCACGTG	279
88	AACTGTGACA	280
89	TCCACGTGAG	281
90	ACACTGCTCT	282
91	TACGGTGAGC	283
92	CGGACTAAGT	284
93	AAGCCACGTT	285
94	CAATTACTCG	286
95	TCTGGCCATA	287
96	TCAGGCTAGT	288

[Table 4-1]

Table 4 List of random primers (10-base primers D)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	TTGACCCGGA	289	33	CAAGTCAGGA	321
2	TTTTTATGGT	290	34	GGGTCGCAAT	322
3	ATGTGGTGCG	291	35	CAGCAACCTA	323
4	AAGGCGCTAG	292	36	TTCCCGCCAC	324
5	TCCAACCTTG	293	37	TGTGCATTTT	325
6	CCATCCCATC	294	38	ATCAACGACG	326
7	CAATACGAGG	295	39	GTGACGTCCA	327
8	GAGTGTTACC	296	40	CGATCTAGTC	328
9	GCCTCCTGTA	297	41	TTACATCCTG	329
10	CGAAGGTGTC	298	42	AGCCTTCAAT	330
11	GAGGTGCTAT	299	43	TCCATCCGAT	331
12	TAGGATAATT	300	44	GACTGGGTCT	332
13	CGTTGTCTC	301	45	TTCGGTGGAG	333
14	TGAGACCAGC	302	46	GACCAGCACA	334
15	TGCCCAAGCT	303	47	CATTAACGGA	335
16	TACTGAATCG	304	48	TTTTTCTTGA	336
17	TTACATAGTC	305	49	CATTGCACTG	337
18	ACAAAGGAAA	306	50	TGCGGCGATC	338
19	CTCGCTTGGG	307	51	ATATTGCGGT	339
20	CCTTGCCTCA	308	52	GACGTCGCTC	340
21	TAATTCCGAA	309	53	TCGCTTATCG	341
22	GTGAGCTTGA	310	54	GCGCAGACAC	342
23	ATGCCGATTC	311	55	CATGTATTGT	343
24	GCTTGGGCTT	312	56	TCTATAACCT	344
25	ACAAAGCGCC	313	57	GTGGAGACAA	345
26	GAAAGCTCTA	314	58	CGAAGATTAT	346
27	TACCGACCGT	315	59	TAGCAACTGC	347
28	TCGAAGAGAC	316	60	ATAATCGGTA	348
29	GTCGCTTACG	317	61	CAGGATGGGT	349
30	GGGCTCTCCA	318	62	GACGATTCCC	350
31	GCGCCCTTGT	319	63	CACGCCCTAC	351
32	GGCAATAGGC	320	64	AGTTGGTTCC	352

[Table 4-2]

No	Primer sequence	SEQ ID NO
65	TCTTATCAGG	353
66	CGAGAAGTTC	354
67	GTGGTAGAAT	355
68	TAGGCTTGTG	356
69	ATGCGTTACG	357
70	ACTACCGAGG	358
71	CGAGTTGGTG	359
72	GGACGATCAA	360
73	AACAGTATGC	361
74	TTGGCTGATC	362
75	AGGATTGGAA	363
76	CATATGGAGA	364
77	CTGCAGGTTT	365
78	CTCTCTTTTT	366
79	AGTAGGGGTC	367
80	ACACCGCAAG	368
81	GAAGCGGGAG	369
82	GATACGGACT	370
83	TACGACGTGT	371
84	GTGCCTCCTT	372
85	GGTGACTGAT	373
86	ATATCTTACG	374
87	AATCATACGG	375
88	CTCTTGGGAC	376
89	GACGACAAAT	377
90	GTTGCGAGGT	378
91	AAACCGCACC	379
92	GCTAACACGT	380
93	ATCATGAGGG	381
94	GATTACGTA	382
95	TCTCGAAAAG	383
96	CTCGTAACCA	384

[Table 5-1]

Table 5 List of random primers (10-base primers E)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	GTTACACACG	385	33	TTCCGGTTAT	417
2	CGTGAAGGGT	386	34	GATAAACTGT	418
3	ACGAGCATCT	387	35	TACAGTTGCC	419
4	ACGAGGGATT	388	36	CGATGGCGAA	420
5	GCAACGTCGG	389	37	CCGACGTCAG	421
6	CACGGCTAGG	390	38	TATGGTGCAA	422
7	CGTGACTCTC	391	39	GACGACAGTC	423
8	TCTAGACGCA	392	40	GTCACCGTCC	424
9	CTGCGCACAT	393	41	GGTTTTAACA	425
10	ATGCTTGACA	394	42	GAGGACAGTA	426
11	TTTGTCGACA	395	43	GTTACCTAAG	427
12	ACGTGTCAGC	396	44	ATCACGTGTT	428
13	GAAAACATTA	397	45	TAAGGCCTGG	429
14	ACATTAACGG	398	46	TGTTTCGTAGC	430
15	GTACAGGTCC	399	47	TGAGGACGTG	431
16	CTATGTGTAC	400	48	GTGCTGTGTA	432
17	GCGTACATTA	401	49	GAGGGTACGC	433
18	GATTTGTGGC	402	50	CCGTGATTGT	434
19	TCGCGCGCTA	403	51	AAAATCGCCT	435
20	ACAAGGGCGA	404	52	CGATCGCAGT	436
21	AACGCGCGAT	405	53	ACGCAATAAG	437
22	CGTAAATGCG	406	54	AAGGTGCATC	438
23	TAGGCACTAC	407	55	CGCGTAGATA	439
24	GCGAGGATCG	408	56	CGAGCAGTGC	440
25	CACGTTTACT	409	57	ATACGTGACG	441
26	TACCACCACG	410	58	AGATTCCGCG	442
27	TTAACAGGAC	411	59	ACGTGATGCC	443
28	GCTGTATAAC	412	60	GTACGCATCG	444
29	GTTGCTGGCA	413	61	TCCCGACTTA	445
30	AGTGTGGCCA	414	62	GTTTTTACAC	446
31	CTGCGGTTGT	415	63	CCTGAGCGTG	447
32	TAGATCAGCG	416	64	CGGCATTGTA	448

[Table 5-2]

No	Primer sequence	SEQ ID NO
65	TAGAGTGGCT	449
66	ATGGCCAGAC	450
67	CTTAGCATGC	451
68	ACAACACCTG	452
69	AGTGACTATC	453
70	CATGCTACAC	454
71	AAAGCGGGCG	455
72	AGATCGCCGT	456
73	CGTAGATATT	457
74	AATGGCAGAC	458
75	GTATAACGTG	459
76	ATGTGCGTCA	460
77	CCTGCCAACT	461
78	TTTATAACTC	462
79	ACGGTTACGC	463
80	TAGCCTCTTG	464
81	TCGCGAAGTT	465
82	GTCTACAACC	466
83	GTCTACTGCG	467
84	GTTGCGTCTC	468
85	GGGCCGCTAA	469
86	GTACGTCGGA	470
87	AGCGAGAGAC	471
88	TGGCTACGGT	472
89	AGGCATCACG	473
90	TAGCTCCTCG	474
91	GGCTAGTCAG	475
92	CTCACTTTAT	476
93	ACGGCCACGT	477
94	AGCGTATATC	478
95	GACACGTCTA	479
96	GCCAGCGTAC	480

[Table 6-1]

Table 6 List of random primers (10-base primers F)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	AACATTAGCG	481	33	CAACCGACGT	513
2	AGTGTGCTAT	482	34	TGGTAACGCG	514
3	CACGAGCGTT	483	35	GTGCAGACAT	515
4	GTAACGCCTA	484	36	GTCTAGTTGC	516
5	CACATAGTAC	485	37	CAATTCGACG	517
6	CGCGATATCG	486	38	CTTAGCACCT	518
7	CGTTCTGTGC	487	39	TAATGTCGCA	519
8	CTGATCGCAT	488	40	CAATCGGTAC	520
9	TGGCGTGAGA	489	41	AGCACGCATT	521
10	TTGCCAGGCT	490	42	AGGTCCTCGT	522
11	GTTATACACA	491	43	TTGTGCCTGC	523
12	AGTGCCAACT	492	44	ACCGCCTGTA	524
13	TCACGTAGCA	493	45	GTACGTCAGG	525
14	TAATTCAGCG	494	46	GCACACAACT	526
15	AAGTATCGTC	495	47	TGAGCACTTA	527
16	CACAGTTACT	496	48	GTGCCGCATA	528
17	CCTTACCGTG	497	49	ATGTTTTCGC	529
18	ACGGTGTCGT	498	50	ACACTTAGGT	530
19	CGCGTAAGAC	499	51	CGTGCCGTGA	531
20	TTCGCACCAG	500	52	TTACTAATCA	532
21	CACGAACAGA	501	53	GTGGCAGGTA	533
22	GTTGGACATT	502	54	GCGCGATATG	534
23	GGTGCTTAAG	503	55	GAACGACGTT	535
24	TCGGTCTCGT	504	56	ATCAGGAGTG	536
25	TCTAGTACGC	505	57	GCCAGTAAGT	537
26	TTAGGCCGAG	506	58	GCAAGAAGCA	538
27	CGTCAAGAGC	507	59	AACTCCGCCA	539
28	ACATGTCTAC	508	60	ACTTGAGCCT	540
29	ATCGTTACGT	509	61	CGTGATCGTG	541
30	ACGGATCGTT	510	62	AATTAGCGAA	542
31	AATCTTGCGG	511	63	ACTTCCTTAG	543
32	AGTATCTGGT	512	64	TGTGCTGATA	544

[Table 6-2]

No	Primer sequence	SEQ ID NO
65	AGGCGGCTGA	545
66	CGTTTAGAGC	546
67	ACGCGTCTAA	547
68	GCGAATGTAC	548
69	CGTGATCCAA	549
70	CAACCAGATG	550
71	ACCATTAACC	551
72	CGATTCACGT	552
73	CTAGAACCTG	553
74	CCTAACGACA	554
75	GACGTGCATG	555
76	ATGTAACCTT	556
77	GATACAGTCG	557
78	CGTATGTCTC	558
79	AGATTATCGA	559
80	ATACTGGTAA	560
81	GTTGAGTAGC	561
82	ACCATTATCA	562
83	CACACTTCAG	563
84	GACTAGCGGT	564
85	AATTGTCGAG	565
86	CTAAGGACGT	566
87	ATTACGATGA	567
88	ATTGAAGACT	568
89	GCTTGTACGT	569
90	CCTACGTCAC	570
91	CACAACTTAG	571
92	GCGGTTTCATC	572
93	GTACTCATCT	573
94	GTGCATCACT	574
95	TCACATCCTA	575
96	CACGCGCTAT	576

[Table 7-1]

Table 7 List of random primers (8-base primers)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	CTATCTTG	577	33	CGTCAAGT	609
2	AAGTGCGT	578	34	AAGTAGAC	610
3	ACATGCGA	579	35	TCAGACAA	611
4	ACCAATGG	580	36	TCCTTGAC	612
5	TGCGTTGA	581	37	GTAGCTGT	613
6	GACATGTC	582	38	CGTCGTAA	614
7	TTGTGCGT	583	39	CCAATGGA	615
8	ACATCGCA	584	40	TTGAGAGA	616
9	GAAGACGA	585	41	ACAACACC	617
10	TCGATAGA	586	42	TCTAGTAC	618
11	TCTTGCAA	587	43	GAGGAAGT	619
12	AGCAAGTT	588	44	GCGTATTG	620
13	TTCATGGA	589	45	AAGTAGCT	621
14	TCAATTCG	590	46	TGAACCTT	622
15	CGGTATGT	591	47	TGTGTTAC	623
16	ACCACTAC	592	48	TAACCTGA	624
17	TCGCTTAT	593	49	GCTATTCC	625
18	TCTCGACT	594	50	GTTAGATG	626
19	GAATCGGT	595	51	CAGGATAA	627
20	GTTACAAG	596	52	ACCGTAGT	628
21	CTGTGTAG	597	53	CCGTGTAT	629
22	TGGTAGAA	598	54	TCCACTCT	630
23	ATACTGCG	599	55	TAGCTCAT	631
24	AACTCGTC	600	56	CGCTAATA	632
25	ATATGTGC	601	57	TACCTCTG	633
26	AAGTTGCG	602	58	TGCACTAC	634
27	GATCATGT	603	59	CTTGGAAG	635
28	TTGTTGCT	604	60	AATGCACG	636
29	CCTCTTAG	605	61	CACTGTTA	637
30	TCACAGCT	606	62	TCGACTAG	638
31	AGATTGAC	607	63	CTAGGTTA	639
32	AGCCTGAT	608	64	GCAGATGT	640

[Table 7-2]

No	Primer sequence	SEQ ID NO
65	AGTTCAGA	641
66	CTCCATCA	642
67	TGGTTACG	643
68	ACGTAGCA	644
69	CTCTTCCA	645
70	CGTCAGAT	646
71	TGGATCAT	647
72	ATATCGAC	648
73	TTGTGGAG	649
74	TTAGAGCA	650
75	TAACTACC	651
76	CTATGAGG	652
77	CTTCTCAC	653
78	CGTCTCT	654
79	GTCACTAT	655
80	TCGTTAGC	656
81	ATCGTGTA	657
82	GAGAGCAA	658
83	AGACGCAA	659
84	TCCAGTTA	660
85	AATGCCAC	661
86	ATCACGTG	662
87	ACTGTGCA	663
88	TCACTGCA	664
89	GCATCCAA	665
90	AGCACTAT	666
91	CGAAGGAT	667
92	CCTTGTGT	668
93	TGCGGATA	669
94	AGGAATGG	670
95	ATCGTAAC	671
96	GAATGTCT	672

[Table 8-1]

Table 8 List of random primers (9-base primers)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	TTGCTACAT	673	33	TGCGACTTA	705
2	TAACGTATG	674	34	TGTCCGTAA	706
3	CAGTATGTA	675	35	GTAATCGAG	707
4	TCAATAACG	676	36	GTACCTTAG	708
5	CACACTTAT	677	37	ATCACGTGT	709
6	GACTGTAAT	678	38	ACTTAGCGT	710
7	TATACACTG	679	39	GTAATCGTG	711
8	ACTGCATTA	680	40	ATGCCGTTA	712
9	ACATTAAGC	681	41	ATAACGTGC	713
10	CATATTACG	682	42	CTACGTTGT	714
11	ATATCTACG	683	43	TATGACGCA	715
12	AGTAACTGT	684	44	CCGATAACA	716
13	ATGACGTTA	685	45	ATGCGCATA	717
14	ATTATGCCA	686	46	GATAAGCGT	718
15	AGTATACAC	687	47	ATATCTGCG	719
16	TTAGCGTTA	688	48	ACTTAGACG	720
17	TATGACACT	689	49	ATCACCGTA	721
18	ATTAACGCT	690	50	TAAGACACG	722
19	TAGGACAAT	691	51	AATGCCGTA	723
20	AAGACGTTA	692	52	AATCACGTG	724
21	TATAAGCGT	693	53	TCGTTAGTC	725
22	ATACCTGGC	694	54	CATCATGTC	726
23	CTCGAGATC	695	55	TAAGACGGT	727
24	ATGGTGAGG	696	56	TGCATAGTG	728
25	ATGTCGACG	697	57	GAGCGTTAT	729
26	GACGTCTGA	698	58	TGCCTTACA	730
27	TACACTGCG	699	59	TTCGCGTTA	731
28	ATCGTCAGG	700	60	GTGTTAACG	732
29	TGCACGTAC	701	61	GACACTGAA	733
30	GTCGTGCAT	702	62	CTGTTATCG	734
31	GAGTGTTAC	703	63	GGTCGTTAT	735
32	AGACTGTAC	704	64	CGAGAGTAT	736

[Table 8-2]

No	Primer sequence	SEQ ID NO
65	ATACAGTCC	737
66	AATTCACGC	738
67	TATGTGCAC	739
68	GATGACGTA	740
69	GATGCGATA	741
70	GAGCGATTA	742
71	TGTCACAGA	743
72	TACTAACCG	744
73	CATAACGAG	745
74	CGTATACCT	746
75	TATCACGTG	747
76	GAACGTTAC	748
77	GTCGTATAC	749
78	ATGTCGACA	750
79	ATACAGCAC	751
80	TACTTACGC	752
81	AACTACGGT	753
82	TAGAACGGT	754
83	GAATGTCAC	755
84	TGTACGTCT	756
85	AACATTGCG	757
86	TTGAACGCT	758
87	AATCAGGAC	759
88	ATTGCGACA	760
89	CCATGTACT	761
90	TGTCCTGTT	762
91	TAATTGCGC	763
92	GATAGTGTG	764
93	ATAGACGCA	765
94	TGTACCGTT	766
95	ATTGTCGCA	767
96	GTCACGTAA	768

[Table 9-1]

Table 9 List of random primers (11-base primers)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	TTACACTATGC	769	33	CAGTCACGACA	801
2	GCGATAGTCGT	770	34	TTACTCGACGT	802
3	CTATTCACAGT	771	35	GCAATGTTGAA	803
4	AGAGTCACTGT	772	36	GACACGAGCAA	804
5	AGAGTCGAAGC	773	37	CGAGATTACAA	805
6	CTGAATATGTG	774	38	TACCGACTACA	806
7	ACTCCACAGGA	775	39	ACCGTTGCCAT	807
8	ATCCTCGTAAG	776	40	ATGTAATCGCC	808
9	TACCATCGCCT	777	41	AAGCCTGATGT	809
10	AACGCCTATAA	778	42	AAGTAACGTGG	810
11	CTGTGCAACTT	779	43	GTAGAGGTTGG	811
12	TCAGATGTCCG	780	44	CTCTGCCTCA	812
13	CTGCTTATCGT	781	45	ATCGTGAAGTG	813
14	ACATTGCGACA	782	46	ACCAGCACTAT	814
15	CCTTAATGCAT	783	47	CACCAGAATGT	815
16	GGCTAGCTACT	784	48	GAGTGAACAAC	816
17	TTCCAGTTGGC	785	49	TAACGTTACGC	817
18	GAGTCACAAGG	786	50	CTTGGATCTTG	818
19	CAGAAGGTTCA	787	51	GTTCCAACGTT	819
20	TCAACGTGCAG	788	52	CAAGGACCGTA	820
21	CAAGCTTACTA	789	53	GACTTCACGCA	821
22	AGAACTCGTTG	790	54	CACACTACTGG	822
23	CCGATACAGAG	791	55	TCAGATGAATC	823
24	GTACGCTGATC	792	56	TATGGATCTGG	824
25	TCCTCAGTGAA	793	57	TCTTAGGTGTG	825
26	GAGCCAACATT	794	58	TGTCAGCGTCA	826
27	GAGATCGATGG	795	59	GTCTAGGACAG	827
28	ATCGTCAGCTG	796	60	GCCTCTTCATA	828
29	GAAGCACACGT	797	61	AGAAGTGTTAC	829
30	ATCACGCAACC	798	62	CATGAGGCTTG	830
31	TCGAATAGTCG	799	63	TGGATTGCTCA	831
32	TATTACCGTCT	800	64	ATCTACCTAAG	832

[Table 9-2]

No	Primer sequence	SEQ ID NO
65	ATGAGCAGTGA	833
66	CCAGGAGATAC	834
67	CCGTTATACTT	835
68	CTCAGTACAAG	836
69	GGTGATCGTAG	837
70	CGAACGAGACA	838
71	ACTACGAGCTT	839
72	TTGCCACAGCA	840
73	GTCAACTCTAC	841
74	TGGACTGTGTC	842
75	GGAATGGACTT	843
76	CGAGAACATAA	844
77	ACCTGGTCAGT	845
78	CGAACGACACA	846
79	AGTCTAGCCAT	847
80	AGGCCTAGATG	848
81	GGTGCGTTAGT	849
82	ATTGTGTCCGA	850
83	GCAGACATTAA	851
84	ATTGGCTCATG	852
85	GAGGTTACATG	853
86	CCTATAGGACC	854
87	TTAGACGGTCT	855
88	GATTGACGCAC	856
89	AAGACACCTCG	857
90	TCGAATAATCG	858
91	TCTATGTCGGA	859
92	TCGCATGAACC	860
93	TGTTATGTCTC	861
94	TGGATCCTACA	862
95	ATCGTTCAGCC	863
96	TACCGCAAGCA	864

[Table 10-1]

Table 10 List of random primers (12-base primers)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	GCTGTTGAACCG	865	33	ACTGAGGCGTTC	897
2	ATACTCCGAGAT	866	34	TAAGGCTGACAT	898
3	CTTAAGGAGCGC	867	35	AGTTCGCATACA	899
4	TATACTACAAGC	868	36	GCAGAATTGCGA	900
5	TAGTGGTCGTCA	869	37	GGTTATGAAGAA	901
6	GTGCTTCAGGAG	870	38	AGAAGTCGCCTC	902
7	GACGCATACCTC	871	39	TTCGCGTTATTG	903
8	CCTACCTGTGGA	872	40	TACCTGGTCGGT	904
9	GCGGTCACATAT	873	41	GGTTACCGAGGA	905
10	CTGCATTACGA	874	42	ACACACTTCTAG	906
11	TGGATCCTTCAT	875	43	GGAAGTGATTAA	907
12	TTGTGCTGGACT	876	44	TCCATCAGATAA	908
13	ATTGAGAGCTAT	877	45	TGTCTGTATCAT	909
14	TCGCTAATGTAG	878	46	AATTGGCTATAG	910
15	CTACTGGCACAA	879	47	ACGTCGGAAGGT	911
16	AGAGCCAGTCGT	880	48	AGGCATCCGTTG	912
17	AATACTGGCTAA	881	49	ACCGTCGCTTGA	913
18	CTGCATGCATAA	882	50	TACCGTCAAGTG	914
19	TTGTCACAACCTC	883	51	CTCGATATAGTT	915
20	TGCTAACTCTCC	884	52	CGTCAACGTGGT	916
21	TCTCTAGTTCGG	885	53	TAGTCAACGTAG	917
22	TTACGTCGCAA	886	54	TGAGTAGGTCAG	918
23	GTGTTGCTACCA	887	55	CTTGGCATGTAC	919
24	CGCATGTATGCC	888	56	TGCCGAGACTTC	920
25	CCTGTTCTGATT	889	57	CTAAGACTTAAG	921
26	TAAGATGCTTGA	890	58	TTCTCGTGTGCG	922
27	ATATATCTCAGC	891	59	CACCTGCACGAT	923
28	TTCCTCGTGGTT	892	60	ATTAAGCCTAAG	924
29	ATGTCGATCTAG	893	61	GGTGAACCATG	925
30	CATCCACTAATC	894	62	ACTAACGCGACT	926
31	GCCTCTGCTAAC	895	63	CAGTTGTGCTAT	927
32	AGTCAAGAGATT	896	64	ACGCTGTTAGCA	928

[Table 10-2]

No	Primer sequence	SEQ ID NO
65	GTCAACGCTAAG	929
66	AGCTTAGGTATG	930
67	CGCAGGACGATT	931
68	AACCGGCTGTCT	932
69	GTTGCTCACGTG	933
70	GAATCTTCCGCG	934
71	AGAGCGTACACG	935
72	AAGGCTAATGTC	936
73	TCTATGTAGACG	937
74	AGACGGTCTAGT	938
75	TTGGTCACACGC	939
76	GTCGATATATGG	940
77	AACATGGATACG	941
78	TTGCGAGTTCCT	942
79	CGCATGTTGTGC	943
80	TGTTAAGTTGGA	944
81	CAAGTGTGATGA	945
82	CTGGTACCACGT	946
83	CGCTAGGATCAC	947
84	TGCTCATTACGG	948
85	TGCTCAGTAACA	949
86	ACGATCATAGCC	950
87	ACGATACGTGGA	951
88	GTTCGATGATGG	952
89	AAGAGCTGTGCC	953
90	GGTTGGATCAAC	954
91	GCGCGCTTATGA	955
92	CGTCGATCATCA	956
93	GAGACTGCACTC	957
94	GATAGATCGCAT	958
95	GGCCATCATCAG	959
96	GGTGTTCCTG	960

[Table 11-1]

Table 11 List of random primers (14-base primers)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	AGCTATACAGAGGT	961	33	GGTTGGAATCTTGC	993
2	AGGCCGTTCTGTCT	962	34	CATCGGTGCACTCA	994
3	CATTGGTCTGCTAT	963	35	AATGCACTAGACGT	995
4	CTACATACGCGCCA	964	36	TACAGTCAGGCTCG	996
5	GCTTAACGGCGCTT	965	37	AGAGAAGCTTAGCC	997
6	TACGATACTCCACC	966	38	CCATAGGATCGTAT	998
7	ACCGGCATAAGAAG	967	39	TTGTGCTACACCTG	999
8	GGATGCTTCGATAA	968	40	CTCCAGTAATACTA	1000
9	GTGTACCTGAATGT	969	41	TGATGCCGATGTGG	1001
10	CGCGGATACACAGA	970	42	GTCATACCGCTTAA	1002
11	TTCCACGGCACTGT	971	43	ACGTTCTCTTGAGA	1003
12	TAGCCAGGCAACAA	972	44	CAGCCATATCGTGT	1004
13	AGCGTCAACACGTA	973	45	TTGAACGTAGCAAT	1005
14	TAACGCTACTCGCG	974	46	ACAATCGCGGTAAT	1006
15	TAGATAGACGATCT	975	47	GTTCTGTAGATCC	1007
16	ACTCTTGCAATGCT	976	48	AGAGCCTTACGGCA	1008
17	ACTCGGTTAGGTCG	977	49	AATATGGCGCCACC	1009
18	CATTATCTACGCAT	978	50	ACCATATAGGTTCC	1010
19	CACACCGGCGATTA	979	51	ATGCACCACAGCTG	1011
20	TACGCAGTACTGTG	980	52	CTACTATTGAACAG	1012
21	CAAGCGCGTGAATG	981	53	TGCCATCACTCTAG	1013
22	GAATGGACTGACGA	982	54	GCGAACGAGAATCG	1014
23	CTAGCGCTGAAGTT	983	55	GAATCAAGGAGACC	1015
24	TGCGGCAGACCAAT	984	56	CAACATCTATGCAG	1016
25	AAGGCATAGAGATT	985	57	CAATCCGTCATGGA	1017
26	TTCTCCTCGCCATG	986	58	AGCTCTTAGCCATA	1018
27	TCATTGGTCGTGAA	987	59	AACAAGGCAACTGG	1019
28	ATTACGCTATACGA	988	60	GTCGTCGCTCCTAT	1020
29	ATGATCCTCCACGG	989	61	GTCATCATTAGATG	1021
30	CGTCGTTAGTAATC	990	62	GCACTAAGTAGCAG	1022
31	TGCACATAGTCTCA	991	63	ACCTTACCGGACCT	1023
32	GTCAAGGAGTCACG	992	64	GCTCAGGTATGTCA	1024

[Table 11-2]

No	Primer sequence	SEQ ID NO
65	TGTCACGAGTTAGT	1025
66	CAGATGACTTACGT	1026
67	GAAGTAGCGATTGA	1027
68	GCAGGCAATCTGTA	1028
69	CCTTATACAACAAG	1029
70	CCTTAGATTGATTG	1030
71	AGCCACGAGTGATA	1031
72	GGATGACTCGTGAC	1032
73	CTTCGTTGCCATT	1033
74	TCTTGCGTATTGAT	1034
75	CTTAACGTGGTGGC	1035
76	TGCTGTTACGGAAG	1036
77	CTGAATTAGTTCTC	1037
78	CCTCCAAGTACAGA	1038
79	CTGGTAATTCGCGG	1039
80	CGACTGCAATCTGG	1040
81	TGGATCGCGATTGG	1041
82	CGACTATTCCTGCG	1042
83	CAAGTAGGTCCGTC	1043
84	AGTAATCAGTG TTC	1044
85	TTATTCTCACTACG	1045
86	CATGTCTTCTTCGT	1046
87	AGGCACATACCATC	1047
88	AGGTTAGAGGATGT	1048
89	CAACTGGCAAGTGC	1049
90	CGCTCACATAGAGG	1050
91	GCAATGTCGAGATC	1051
92	GTTCTGTGGTGCTC	1052
93	AAGTGATCAGACTA	1053
94	ATTGAAGGATTCCA	1054
95	ACGCCATGCTACTA	1055
96	CTGAAGATGTCTGC	1056

[Table 12-1]

Table 12 List of random primers (16-base primers)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	GACAATCTCTGCCGAT	1057	33	AATGACGTTGAAGCCT	1089
2	GGTCCGCCTAATGTAA	1058	34	TCGATTCTATAGGAGT	1090
3	AGCCACAGGCAATTCC	1059	35	CGATAGGTTGAGCTAT	1091
4	ATCTCAAGTTCTCAAC	1060	36	CCATGTTGATAGAATA	1092
5	TGTAACGCATACGACG	1061	37	GAGCCACTTCTACAGG	1093
6	TATCTCGAATACCAGC	1062	38	GCGAACTCTCGGTAAT	1094
7	ACCGCAACACAGGCAA	1063	39	GACCTGAGTAGCTGGT	1095
8	GGCCAGTAACATGACT	1064	40	CGAGTCTATTAGCCTG	1096
9	GTGAACAGTTAAGGTG	1065	41	GTAGTGCCATACACCT	1097
10	CCAGGATCCGTATTGC	1066	42	CCAGTGGTCTATAGCA	1098
11	GACCTAGCACTAGACC	1067	43	GTCAGTGCCTTATTGC	1099
12	CGCCATCCTATTACG	1068	44	AGTGTGCGAGTGACGA	1100
13	AAGTGCAGTAATGGAA	1069	45	AATCTCCGCTATAGTT	1101
14	TCAACGCGTTCGTCTA	1070	46	CGAGTAGGTCTGACTT	1102
15	AGCGGCCACTATCTAA	1071	47	CTGTCGCTCTAATAAC	1103
16	CTCGGCGCCATATAGA	1072	48	GCTGTCAATATAACTG	1104
17	CGATAACTTAGAAGAA	1073	49	AGCTCAAGTTGAATCC	1105
18	CATAGGATGTGACGCC	1074	50	AATTCATGCTCCTAAC	1106
19	GGCTTGTCGTCTATC	1075	51	CCAAGGTCTGGTGATA	1107
20	CTTGTCTGAATATTAG	1076	52	CTCCACGTATCTTGAA	1108
21	ACAGTTCGAGTGTGCG	1077	53	TAGCCGAACAACACTT	1109
22	CTCTAACCTGTGACGT	1078	54	AGTACACGACATATGC	1110
23	CGCGCTAATTCAACAA	1079	55	ACGTTCTAGACTCCTG	1111
24	ACTCACGAATGCGGCA	1080	56	CGACTCAAGCACTGCT	1112
25	AATCTTCGGCATTTCAT	1081	57	TGAAGCTCAGGATTAA	1113
26	AAGTATCAGGATCGCG	1082	58	TATCTAACGTATGGTA	1114
27	AGTAACTCTGCAGACA	1083	59	TATACCATGTTCTTGG	1115
28	GGATTGAACATTGTGC	1084	60	TTCTACGATGACTTC	1116
29	GTGATGCTCACGCATC	1085	61	CTCTCCAATATGTGCC	1117
30	CGTAGCGTAACGGATA	1086	62	GAGTAGAGTCTTGCCA	1118
31	TGCGATGCACCGTTAG	1087	63	GCGAGATGTGGTCTTA	1119
32	CCAGTATGCTCTCAGG	1088	64	AAGCTACACGGACCAC	1120

[Table 12-2]

No	Primer sequence	SEQ ID NO
65	ATACAACTGGCAACCG	1121
66	CGGTAGATGCTATGCT	1122
67	TCTTGACCGGTCATCA	1123
68	AGATCGTGCGATGCGAT	1124
69	TCCTCGAGACAGCCTT	1125
70	TAGCCGGTACCACTTA	1126
71	GTAAGGCAGCGTGCAA	1127
72	TAGTCTGCTCCTGGTC	1128
73	TGGATTATAGCAGCAG	1129
74	AAGAATGATCAGACAT	1130
75	CAGCGCTATATACCTC	1131
76	GAGTAGTACCTCCACC	1132
77	GACGTGATCCTCTAGA	1133
78	GTTCCGTTCACTACGA	1134
79	TGCAAGCACCAGGATG	1135
80	TTAGTTGGCGGCTGAG	1136
81	CAGATGCAGACATACG	1137
82	GACGCTTGATGATTAT	1138
83	TGGATCAGGACTAGGA	1139
84	CTCGTCGGTATAACGC	1140
85	AAGCACGGATGCGATT	1141
86	AGATCTTCCGGTGAAC	1142
87	GGACAATAGCAACCTG	1143
88	GATAATCGGTTCCAAT	1144
89	CTCAAGCTACAGTTGT	1145
90	GTTGGCATGATGTAGA	1146
91	CAGCATGAGGTAAGTG	1147
92	GCCTCATCACACGTCA	1148
93	TCGATACTACACATCG	1149
94	TACACGAGGCTTGATC	1150
95	TTCTCGTGTCGCATT	1151
96	GGTGAAGCAACAGCAT	1152

[Table 13-1]

Table 13 List of random primers (18-base primers)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	CGAACCGACTGTACAGTT	1153	33	ATGTTCAAGTCACAAGCGA	1185
2	CCGACTGCCGATAAGTTA	1154	34	TAGGAAGTGTGTAATAGC	1186
3	CGACAGGTAGGTAAGCAG	1155	35	AATCCATGTAGCTGTACG	1187
4	TGATACGTTGGTATACAG	1156	36	CCAGATTCAGTGGCATAG	1188
5	CTACTATAGAATACGTAG	1157	37	TTGTCTCTACGTAATATC	1189
6	AGACTGTGGCAATGGCAT	1158	38	GTGGTGCTTGTGACAATT	1190
7	GGAAGACTGATACAACGA	1159	39	CAGCCTACTTGGCTGAGA	1191
8	TATGCACATATAGCGCTT	1160	40	TACTCAATGCATCTGTGT	1192
9	CATGGTAATCGACCGAGG	1161	41	TGTAGAGAGACGAATATA	1193
10	GTCATTGCCGTCAATTGCC	1162	42	GCCTACAACCATCCTACT	1194
11	CCTAAGAACTCCGAAGCT	1163	43	GCGTGGCATTGAGATTCA	1195
12	TCGCTCACCGTACTAGGA	1164	44	GCAATGCCAGCTAACTGAG	1196
13	TATTACTGTACAGCAGG	1165	45	GCGAGTAATCCGGTTGGA	1197
14	TGAGACAGGCTACGAGTC	1166	46	GCCTCTACCAGAACGTCA	1198
15	AAGCTATGCGAACACGTT	1167	47	GTCAGCAGAAGACTGACC	1199
16	AACGGAGGAGTGAGCCAA	1168	48	GATAACAGACGTAGCAGG	1200
17	CCACTATGGACATCATGG	1169	49	CAGGAGATCGCATGTCGT	1201
18	ATGGTGGTGGATAGCTCG	1170	50	CTGGAAGGAATGGAGCCA	1202
19	TCACCGGTTACACATCGC	1171	51	ATTGGTCTCTACCACAA	1203
20	AAGATACTGAGATATGGA	1172	52	CTCATTGTTGACGGCTCA	1204
21	GACCTGTTCTTGAAGTAG	1173	53	TTCAGGACTGTAGTTCAT	1205
22	AAGTAGAGCTCTCGGTTA	1174	54	AGACCGCACTAACTCAAG	1206
23	CTATGTTCTTACTCTCTT	1175	55	GGAATATTGTGCAGACCG	1207
24	CAAGGCTATAAGCGGTTA	1176	56	CCTATTACTAATAGCTCA	1208
25	GAAGCTAATTAACCGATA	1177	57	ATGGCATGAGTACTTCGG	1209
26	TTCACGTCTGCCAAGCAC	1178	58	GACACGTATGCGTCTAGC	1210
27	ATCGTATAGATCGAGACA	1179	59	GAAGGTACGGAATCTGTT	1211
28	GTCACAGATTACATCAT	1180	60	TATAACGTCCGACACTGT	1212
29	GTGCCTGTGAACTATCAG	1181	61	GCTAATACATTACCGCCG	1213
30	CAGCGTACAAGATAGTCG	1182	62	GAAGCCAACACTCCTGAC	1214
31	GCATGGCATGGTAGACCT	1183	63	CGAATAACGAGCTGTGAT	1215
32	GGTATGCTACTCTTCGCA	1184	64	GCCTACCGATCGCACTTA	1216

[Table 13-2]

No	Primer sequence	SEQ ID NO
65	CTGAGGAGAATAGCCTGC	1217
66	CAGCATGGACAGTACTTC	1218
67	GGTATAGAGCCTTCCTTA	1219
68	CGCTCTGCATATATAGCA	1220
69	CGGCTCTACTATGCTCGT	1221
70	CCTAATGCGAAGCTCACC	1222
71	ACAACCGGTGAGGCAGTA	1223
72	TTGGTTCGAACCAACCGC	1224
73	ATACTAGGTTGAACTAAG	1225
74	GCGTTGAGAGTAACATAT	1226
75	AGTTGTATAATAAGCGTC	1227
76	GTATGATGCCGTCCAATT	1228
77	GGACTCTCTGAAGAGTCT	1229
78	GGACTCTCTTGACTTGAA	1230
79	GATAACAGTGCTTCGTCC	1231
80	GGCCATTATAGATGAACT	1232
81	ATAGAGAGCACAGAGCAG	1233
82	GTGTGAGTGTATCATAAC	1234
83	ATAACCTTAGTGCGCGTC	1235
84	CCGACTGATATGCATGGA	1236
85	GGATATCTGATCGCATCA	1237
86	CAGCATTAAAGAGGCGAA	1238
87	GCGAGGCCTACATATTCG	1239
88	CGATAAGTGGTAAGGTCT	1240
89	AGATCCTGAGTCGAGCAA	1241
90	AAGATATAACGAGACCGA	1242
91	CCGACTGATTGAGAACGT	1243
92	TCGGCTTATATGACACGT	1244
93	AATAACGTACGCCGAGG	1245
94	AACACAGCATTGCCGACG	1246
95	GTAGTCTGACAGCAACAA	1247
96	AGAATGACTTGAGCTGCT	1248

[Table 14-1]

Table 14 List of random primers (20-base primers)

No	Primer sequence	SEQ ID NO	No	Primer sequence	SEQ ID NO
1	ACTGGTAGTAACGTCCACCT	1249	33	CACTTAAGTGTGATATAGAT	1281
2	AGACTGGTTGTTATTCGCCT	1250	34	ATCGGTATGCTGACCTAGAC	1282
3	TATCATTGACAGCGAGCTCA	1251	35	TACAATCTCGAATGCAGGAT	1283
4	TGGAGTCTGAAGAAGGACTC	1252	36	CCATATGAAGCGCAGCCGTC	1284
5	CATCTGGACTACGGCAACGA	1253	37	CGTCTCGTGGACATTTCGAGG	1285
6	AACTGTCATAAGACAGACAA	1254	38	CCGAGTACAGAAGCGTGGAA	1286
7	CCTCAACATGACATACACCG	1255	39	TTACGTGGTCGACAGGCAGT	1287
8	CAATACCGTTCGCGATTCTA	1256	40	AGCTGCAATCTGCATGATTA	1288
9	GCGTCTACGTTGATTGGGCC	1257	41	ACCTGCCGAAGCAGCCTACA	1289
10	TGAACAGAGGCACTTGCAGG	1258	42	AACATGATAACCACATGGTT	1290
11	CGACTAGAACCTACTACTGC	1259	43	ATCCGACTGATTGAATTACC	1291
12	GCACCGCACGTGGAGAGATA	1260	44	TCACGCTGACTCTTATCAGG	1292
13	CTGAGAGACCGACTGATGCG	1261	45	GCGCGCTCGAAGTACAACAT	1293
14	TCGTCCCTTCTACTTAATGAT	1262	46	ACAGCCAGATGCGTTGTTC	1294
15	CAAGCTATACCATCCGAATT	1263	47	GGAGCTCTGACCTGCAAGAA	1295
16	CAATACGTATAGTCTTAGAT	1264	48	AACATTAGCCTCAAGTAAGA	1296
17	CCATCCACAGTGACCTATGT	1265	49	TGTGATTATGCCGAATGAGG	1297
18	TATCCGTTGGAGAAGGTTCA	1266	50	GAGTAATAATCCAATCAGTA	1298
19	CGCCTAGGTACCTGAGTACG	1267	51	CTCCTTGCGCAGCTGAAC	1299
20	CAGAGTGCTCGTGTTCGCGA	1268	52	TTACGCACACATACACAGAC	1300
21	CGCTTGACATCCTTAAGAA	1269	53	ACGCCGTATGGCGACTTAGG	1301
22	GACCGCATGATTAGTCTTAC	1270	54	AGAACGACAATTACGATGGC	1302
23	CTTGCCGTAGTCACTCAGT	1271	55	TGCTAACGTACCACTGCCAC	1303
24	GATAGCGATATTCAGTTCGC	1272	56	CATCCAGAATGTCTATCATA	1304
25	ATCCAACACTAAGACAACCA	1273	57	GGAGAACGCCTATAGCACTC	1305
26	CCATTCTGTGCGTGTCTC	1274	58	ACCTCTTGTGACGGCCAGTC	1306
27	ACATTCTGTACGCTTGCAGC	1275	59	TGCCATAACTTGGCATAAGA	1307
28	TGCTGAACGCCAATCGCTTA	1276	60	ACAATTGTCTGACCACGCTC	1308
29	TCCTCTACAAGAATATTGCG	1277	61	TCGTACCTTCACAGAACGA	1309
30	CGACCAACGCAGCCTGATTC	1278	62	AGCAGCAGATGATGATCCAA	1310
31	ATTGCGAGCTTGAGTAGCGC	1279	63	TCGTGCCTTGGATTCCAGGA	1311
32	AAGGTGCGAGCATAGGAATC	1280	64	TGTTATAGCCACGATACTAT	1312

[Table 14-2]

No	Primer sequence	SEQ ID NO
65	AATCTCACCTGTACCTTCCG	1313
66	GAGTAGCGGAAGCGTTAGCG	1314
67	AATACTCCGGCGAGGTATAC	1315
68	TTCGCATCCTTGACGAACA	1316
69	AACCGGCTAATACTACTGGC	1317
70	CTAGCATCTTAGACACCAGA	1318
71	TAGTTGCGTGATACAAGATA	1319
72	TCGTCTCGACACAGTTGGTC	1320
73	TCCGTTCCGGTGCGAACTGA	1321
74	TCTGACTCTGGTGACAGTC	1322
75	ACAGCGCAATTATATCCTGT	1323
76	AGATCCGTACGTGAGACTAG	1324
77	TACATTGAAGCATCCGAACA	1325
78	CTCCTGAGAGATCAACGCCA	1326
79	TCACCTCGAATGAGTTCGTT	1327
80	TAGCGACTTAAGGTCCAAGC	1328
81	AGTACGTATTGCCGTGCAAG	1329
82	AGCCACGAACCGACGTCATA	1330
83	TGATGTGTACGCTACTACTA	1331
84	CCACTGTGTGCAGCAGACGA	1332
85	CTATTGTACAGCGAACGCTG	1333
86	CTCCGATATCGCACGGATCG	1334
87	AACTTATCGTCGGACGCATG	1335
88	TATCCTAATTCGTGCCGGTC	1336
89	ACAGCCTTCCTGTGTGGACT	1337
90	CCTCCGTGAGGATCGTACCA	1338
91	GCTCTAAGTAACAGAACTAA	1339
92	GACTTACCGCGCGTTCTGGT	1340
93	TCTGAGGATACACATGTGGA	1341
94	TGTAATCACACTGGTGTCGG	1342
95	CACTAGGCGGCAGACATACA	1343
96	CTAGAGCACAGTACCACGTT	1344

[Table 15-1]

Table 15 List of random primers (22-base primers)

No	Primer sequence	SEQ ID NO
1	TTCAGAGGTCTACGCTCCGGT	1345
2	AACACAGACTGCGTTATGCCAA	1346
3	TGCTGAGTTCTATACAGCAGTG	1347
4	ACCTATTATATGATAGCGTCAT	1348
5	ATCGTGAGCTACAGTGAATGCA	1349
6	CGTGATGTATCCGGCCTTGCA	1350
7	TCTTCTGGTCCTAGAGTTGTGC	1351
8	TGATGTCGGCGGCGGATCAGAT	1352
9	TCGGCCTTAGCGTTCAGCATCC	1353
10	TTAAGTAGGTCAGCCACTGCAC	1354
11	CCAGGTGAGTTGATCTGACACC	1355
12	TATACTATTACTGTGTTCCGATC	1356
13	CCGCAGTATGTCTAGTGTGTC	1357
14	GTCTACCGGTACGAAGCTCTC	1358
15	ATGCGAGTCCGTGGTCGATCCT	1359
16	TGGTAGATTGGTGTGAGAACTA	1360
17	AGGTTTCGTCGATCAACTGCTAA	1361
18	ACGACAAGCATCCTGCGATATC	1362
19	TTGAATCACAGAGAGCGTGATT	1363
20	GTACTTAGTGCTTACGTCAGCT	1364
21	GATTATTAAGGCCAAGCTCATA	1365
22	GCATGCAGAGACGTAATCATCG	1366
23	TAGCGGATGGTGTCTGCGCACT	1367
24	TACGGCTGCCAACTTAATAACT	1368
25	CTCATATGACAACTTCTATAGT	1369
26	CAAGCAATAGTTGTGCGGCCACC	1370
27	TTCAGCAATCCGTACTGCTAGA	1371
28	TGAGACGTTGCTGACATTCTCC	1372
29	GTTCCGATGAGTTAGATGTATA	1373
30	TTGACGCTTGGAGGAGTACAAG	1374
31	TTCATGTTACCTCCACATTGTG	1375
32	GAGCACGTGCCAGATTGCAACC	1376

[Table 15-2]

No	Primer sequence	SEQ ID NO
33	GGTCGACAAGCACAAGCCTTCT	1377
34	TAGGCAGGTAAGATGACCGACT	1378
35	CGAGGCATGCCAAGTCGCCAAT	1379
36	AGTGTGATAGGCGGATGAGAG	1380
37	TTCGGTCTAGACCTCTCACAAT	1381
38	GTGACGCTCATATCTTGCCACC	1382
39	GATGTAATTCTACGCGCGGACT	1383
40	GATGGCGATGTTGCATTACATG	1384
41	TATGCTCTGAATTAACGTAGAA	1385
42	AGGCAATATGGTGATCCGTAGC	1386
43	TGACAGCGATGCATACAGTAGT	1387
44	TTCTGCTAACGGTATCCAATAC	1388
45	GAGTCGTCCATACGATCTAGGA	1389
46	AGACGGACTCAACGCCAATTCC	1390
47	GTAGTGTGAGCGGACCGAGCT	1391
48	AATATAACTAGATCATAGCCAG	1392
49	TCAATCGGAGAATACAGAACGT	1393
50	ATCTCCGTCGTCCGAACCAACA	1394
51	TAGGCGTTCAGCGGTATGCTTA	1395
52	TGCGTGCTATACAACCTATACG	1396
53	ATGGCCGGCATACTGTGTATG	1397
54	TGATGCTGACATAAACTGAAT	1398
55	ATCCAAGGTACCTGAACATCCT	1399
56	TAGTGACGACCAGGTGAGCCTC	1400
57	AGGAGGATCCGTCAAGTCGACC	1401
58	AGAGTATGCCAGATCGTGAGGC	1402
59	CCACTCACTAGGATGGCTGCGT	1403
60	TATCCAACCTGTTATAGCGATT	1404
61	TCTTGCAGTGAGTTGAGTCTGC	1405
62	CCACTGTTGTACATACACCTGG	1406
63	ATGCGCGTAGGCCACTAAGTCC	1407
64	ACAGCGGTCTACAACCGACTGC	1408

[Table 15-3]

No	Primer sequence	SEQ ID NO
65	TCGCGCTCCAGACAATTGCAGC	1409
66	CCGGTAGACCAGGAGTGGTCAT	1410
67	ATCTCCTAACCTAGAGCCATCT	1411
68	CCACATCGAATCTAACAACCTAC	1412
69	TAGTCTTATTGAATACGTCCTA	1413
70	TCCTTAAGCCTTGGAAGTGGCG	1414
71	CCGTGATGGATTGACGTAGAGG	1415
72	GCCTGGATAACAGATGTCTTAG	1416
73	CTCGACCTATAATCTTCTGCCA	1417
74	AGCTACTTCTCCTTCCTAATCA	1418
75	ACACGCTATTGCCTTCCAGTTA	1419
76	AAGCCTGTGCATGCAATGAGAA	1420
77	TCGTTGGTTATAGCACAACTTC	1421
78	GCGATGCCTTCCAACATACCAA	1422
79	CCACCGTTAGCACGTGCTACGT	1423
80	GTTACCACAATGCCGCCATCAA	1424
81	GGTGCAATTAAGAACGAACTACC	1425
82	TCCTTCCGGATAATGCCGATTTC	1426
83	AACCGCAACTTCTAGCGGAAGA	1427
84	TCCTTAAGCAGTTGAACCTAGG	1428
85	TACTAAGTCAGATAAGATCAGA	1429
86	TTCGCCATAACTAGATGAATGC	1430
87	AAGAAGTTAGACGCGGTGGCTG	1431
88	GTATCTGATCGAAGAGCGGTGG	1432
89	TCAAGAGCTACGAAGTAAGTCC	1433
90	CGAGTACACAGCAGCATACCTA	1434
91	CTCGATAAGTTACTCTGCTAGA	1435
92	ATGGTGCTGGTTCTCCGTCTGT	1436
93	TCAAGCGGTCCAAGGCTGAGAC	1437
94	TGTCCTGCTCTGTTGCTACCGT	1438
95	AGTCATATCGCGTCACACGTTG	1439
96	GGTGAATAAGGACATGAGAAGC	1440

[Table 16-1]

Table 16 List of random primers (24-base primers)

No	Primer sequence	SEQ ID NO
1	CCTGATCTTATCTAGTAGAGACTC	1441
2	TTCTGTGTAGGTGTGCCAATCACC	1442
3	GACTTCCAGATGCTTAAGACGACA	1443
4	GTCTTCGACGGAGAACATCCGAG	1444
5	CTTGTTAGTGTACCGTCAACGTC	1445
6	AAGCGGCATGTGCCTAATCGACGT	1446
7	CGACCGTCGTTACACGGAATCCGA	1447
8	TCGCAAGTGTGCCGTTCTGTTTCAT	1448
9	CGTACTGAAGTTCGGAGTCGCCGT	1449
10	CCACTACAGAATGGTAGCAGATCA	1450
11	AGTAGGAGAGAGGCCTACACAACA	1451
12	AGCCAAGATACTCGTTCGGTATGG	1452
13	GTTCCGAGTACATTGAATCCTGGC	1453
14	AGGCGTACGAGTTATTGCCAGAGG	1454
15	GTGGCATCACACATATCTCAGCAT	1455
16	GAGACCGATATGTTGATGCCAGAA	1456
17	CAACTGTAGCCAGTCGATTGCTAT	1457
18	TATCAATGCAATGAGAGGATGCAG	1458
19	GTATGCTCGGCTCCAAGTACTGTT	1459
20	AGAGACTCTTATAGGCTTGACGGA	1460
21	ACTTAACAGATATGGATCATCGCC	1461
22	AATCAGAGCGAGTCTCGCTTCAGG	1462
23	ACCACCGAGGAACAGGTGCGACAA	1463
24	TGGTACATGTCAACCGTAAGCCTG	1464
25	CGTGCCGCGGTGTTCTTGTATATG	1465
26	GACAAGCGCGGTGAGACATATCA	1466
27	AGTGCACTCCGAACAAGAGTTAGT	1467
28	CCTCATTACCGGTTAGGAGTCCG	1468
29	TGCTTATTGCTTAGTTGCTATCTC	1469
30	GCGTGATCCTGTTCTATTCGTTAG	1470
31	GGCCAGAACTATGACGAGTATAAG	1471
32	GATGGCGACTATCTAATTGCAATG	1472

[Table 16-2]

No	Primer sequence	SEQ ID NO
33	TAGTAACCATAGCTCTGTACAACT	1473
34	CGTGATCGCCAATACACATGTCCG	1474
35	TAATAACGGATCGATATGCACGCG	1475
36	ATCATCGCGCTAATACTATCTGAA	1476
37	CACGTCCGTGCAGGTCAGTAT	1477
38	AGGTCCAATGCCGAGCGATCAGAA	1478
39	CAGCATAACAACGAGCCAGGTCAG	1479
40	ATGGCGTCCAATACTCCGACCTAT	1480
41	AGGAACATCGTGAATAATGAAGAC	1481
42	TCTCGACGTTTCATGTAATTAAGGA	1482
43	TCGCGGTAAACCTTACTTAGACGA	1483
44	ATCATATCTACGGCTCTGGCGCCG	1484
45	GCAGATGGAGACCAGAGGTACAGG	1485
46	AGACAGAAGATTACCACGTGCTAT	1486
47	CCACGGACAACATGCCGCTTAAC	1487
48	CTTGAAGTCTCAAGCTATGAGAGA	1488
49	ACAGCAGTCGTGCTTAGGTCAGT	1489
50	AGGTGTTAATGAACGTAGGTGAGA	1490
51	AGCCACTATGTTCAAGGCTGAGCC	1491
52	GCAGGCGGTGTCGTGTGACAATGA	1492
53	AGCCATTGCTACAGAGGTTACTTA	1493
54	ACAATCGAACCTACACTGAGTCCG	1494
55	CCGATCTCAATAGGTACCACGAAC	1495
56	GATACGTGGCGCTATGCTAATTAA	1496
57	AGAGAGATGGCACACATTGACGTC	1497
58	CTCAACTCATCCTTGTAGCCGATG	1498
59	GTGGAATAACGCGATACGACTCTT	1499
60	ATCTACCATGCGAATGCTCTCTAG	1500
61	ATACGCACGCCTGACACAAGGACC	1501
62	GTCCACTCTCAGTGTGTAGAGTCC	1502
63	AATATATCCAGATTCTCTGTGCAG	1503
64	CCTTCGCCACATGTTGACAAGG	1504

[Table 16-3]

No	Primer sequence	SEQ ID NO
65	ACTGTGCCATCATCCGAGGAGCCA	1505
66	TCTATGCCGCTATGGCGTCGTGTA	1506
67	CGTAACCTAAGGTAATATGTCTGC	1507
68	TACTGACCGTATCAAGATTACTAA	1508
69	TCATCGGAGCGCCATACGGTACGT	1509
70	GCAAGAGGAATGAACGAAGTGATT	1510
71	GGCTGATTGACATCCTGACTTAGT	1511
72	AAGGCGCTAGATTGGATTAACGTA	1512
73	GCTAGCTAGAAGAATAGGATTCGT	1513
74	CAGGTGACGGCCTCTATAACTCAT	1514
75	CAGGTTACACATACCACTATCTTC	1515
76	TTGCTACGTACCGTCTTAATCCGT	1516
77	CTCAACATGTCTTGCAAGCTTCGA	1517
78	GGTGCGGTACGTAGAACCAGATCA	1518
79	AATGCTCTCCAAGATCCTGACCTA	1519
80	GCTTCGCAGGTCTGGATGATGGAG	1520
81	ACATTGACCAGACAGCACCTTGCG	1521
82	AGGTATCAATGTGCTTAATAGGCG	1522
83	TCCGGACACAGATTAGTAACGGA	1523
84	TACGAAGTACTACAGATCGGTCAG	1524
85	AATTGTCAGACGAATACTGCTGGA	1525
86	TGAATCATGAGCCAGAGGTTATGC	1526
87	CACAAGACACGTCATTAACATCAA	1527
88	GAATGACTACATTACTCCGCCAGG	1528
89	AGCCAGAGATACTGGAACCTGACT	1529
90	TATCAGACACATCACAATGGATAC	1530
91	CTAGGACACCGCTAGTCGGTTGAA	1531
92	GTATAACTGCGTGTCTGGTGTAT	1532
93	ATGCAATACTAAGGTGGACCTCCG	1533
94	ATGCAGACGCTTGGGATAAGTCAT	1534
95	TTGCTCGATACAGTAGACCAGTG	1535
96	TACTGGAGGACGATTGTCTATCAT	1536

[Table 17-1]

Table 17 List of random primers (26-base primers)

No	Primer sequence	SEQ ID NO
1	ACTAAGGCACGCTGATTCGAGCATT	1537
2	CGGATTCTGGCACGTACAAGTAGCAG	1538
3	TTATGGCTCCAGATCTAGTCACCAGC	1539
4	CATACACTCCAGGCATGTATGATAGG	1540
5	AGTTGTAAGCCAACGAGTGTAGCGTA	1541
6	GTATCAGCTCCTTCCTCTGATTCCGG	1542
7	AACATACAGAATGTCTATGGTCAGCT	1543
8	GACTCATATTCATGTTTCACTATAGAG	1544
9	AGAGTGAACGAACGTGACCGACGCTC	1545
10	AATTGGCGTCCTTGCCACAACATCTT	1546
11	TCGTAGACGCCTCGTACATCCGAGAT	1547
12	CCGGCTCGTGAGGCGATAATCATATA	1548
13	AGTCCTGATCACGACCAGACTCACG	1549
14	GGCACTCAATCCTCCATGGAGAAGCT	1550
15	TCATCATTCCTCACGTTACCGGTGA	1551
16	TCAACTCTGTGCTAACCGGTCTGACA	1552
17	TGTTCTTATGCATTAATGCCAGGCTT	1553
18	GATTCACGACCTCAACAGCATCACTC	1554
19	GGCGAGTTCGACCAGAATGCTGGACA	1555
20	TTCCGTATACAATGCGATTAAGATCT	1556
21	GAGTAATCCGTAACCGGCCAACGTTG	1557
22	CGCTTCCATCATGGTACGGTACGTAT	1558
23	CCGTCGTGGTGTGTTGACTGGTCAAC	1559
24	TATTCGCATCTCCGTATTAGTTGTAG	1560
25	TATTATTGTATTCTAGGCGGTGCAAC	1561
26	AGGCTGCCTACTTCCTCGTCATCTCG	1562
27	GTAACATACGGCTCATCGAATGCATC	1563
28	TTATGGCACGGATATTACCGTACGCC	1564
29	ATAGCACTTCCTCTAATGCTCTGCTG	1565
30	TCACAGGCAATAGCCTAATATTATAT	1566
31	GGCGGATGTTTCGTTAATATTATAAGG	1567
32	TGCAATAGCCGTTGTCTCTGCCAGCG	1568

[Table 17-2]

No	Primer sequence	SEQ ID NO
33	TACAGCGCGTTGGCGAGTACTGATAG	1569
34	TGCAGTTAGTACCTTCTCACGCCAAC	1570
35	CCATTGGCTACCTAGCAGACTCTACC	1571
36	AACAGTAGCTCGCGTCTTGCTCTCGT	1572
37	GCAGTCCATCAGCTCTCGCTTATAGA	1573
38	TATCTCTCTGTGCCAGCTTGACCAA	1574
39	CAGACTGTTCAAGCTTGCTGTAGGAG	1575
40	TAACCGGAACCTCGTTCAGCAACATTC	1576
41	TCAATTATGCATGTCGTCCGATCTCT	1577
42	TTGTCTAAGTCAACCTGTGGATAATC	1578
43	TCTAAGAGTGGTATGACCAGGAGTCC	1579
44	TCGTAGTACTACTGGAACAGGTAATC	1580
45	ATGTCAACATTCTAATCATCTCTCGG	1581
46	AGCGCGCAACTGTTACGGTGATCCGA	1582
47	GCGATAGAATAATGGTGTCACACACG	1583
48	AAGGCTCGCATGAGAGGCGTACATCG	1584
49	GGTTCATGGTCTCAGTCGTGATCGCG	1585
50	TAGTGACTCTATGTCACCTCGGAGCC	1586
51	ATGTGATAGCAATGGCACCTCTAGTC	1587
52	TCGCGAAGTGTAATGCATCATCCGCT	1588
53	ATGTGGCGACGATCCAAGTTCAACGC	1589
54	ACCTTGTATGAGTCGGAGTGCCGGC	1590
55	ACCTCAAGAGAGTAGACAGTTGAGTT	1591
56	GGTGTAATCCTGTGTGCGAAGCTGGT	1592
57	ATAGCGGAACGTACGACGCTCCAGT	1593
58	AAGCACGAGTCGACCATTAGCCTGGA	1594
59	ATTCCGGTAACATCAGAAGGTACAAT	1595
60	GTGCAACGGCAGTCCAGTATCCTGGT	1596
61	CCATCTTATACACGGTGACCGAAGAT	1597
62	GCACTTAATCAAGCTTGAGTGATGCT	1598
63	AGTATTACGTGAGTACGAAGATAGCA	1599
64	TTCTTAGGTTAAGTTCCTTCTGGACC	1600

[Table 17-3]

No	Primer sequence	SEQ ID NO
65	GTCCTTGCTAGACACTGACCGTTGCT	1601
66	GCCGCTATGTGTGCTGCATCCTAAGC	1602
67	CCATCAATAACAGACTTATGTTGTGA	1603
68	CGCGTGTGCTTACAAGTGCTAACAAG	1604
69	CGATATGTGTTTCGCAATAAGAGAGCC	1605
70	CGCGGATGTGAGCGGCTCAATTAGCA	1606
71	GCTGCATGACTATCGGATGGAGGCAT	1607
72	CTATGCCGTGTATGGTACGAGTGGCG	1608
73	CCGGCTGGAGTTCATTACGTAGGCTG	1609
74	TGTAGGCCTACTGAGCTAGTATTAGA	1610
75	CCGTCAAGTGACTATTCTTCTAATCT	1611
76	GGTCTTACGCCAGAGACTGCGCTTCT	1612
77	CGAAGTGTGATTATTAAGTGAATCT	1613
78	GCACGCGTGGCCGTAAGCATCGATTA	1614
79	ATCCTGCGTCGGAACGTACTATAGCT	1615
80	AGTATCATCATATCCATTTCGAGTAC	1616
81	AGTCTGACGTTTCATATATAGACTCC	1617
82	CTTGCAATAATCTGAATCTGAAGGTT	1618
83	ATAACTTGGTTCCAGTAACGCATAGT	1619
84	GATAAGGATATGGCTGTAGCGAAGTG	1620
85	GTGGAGCGTTACAGACATGTGAACA	1621
86	CGCTTCCGGCAGGCGTCATATAAGTC	1622
87	ATAACATTCTAACCTCTATAAGCCGA	1623
88	ACGATCTATGATCCATATGGACTTCC	1624
89	TGAAGCTCAGATATCATGCCTCGAGC	1625
90	AGACTTCACCGCAATAACTCGTAGAT	1626
91	AGACTAAGACATACGCCATCACCGCT	1627
92	TGTAGCGTGATGTATCGTAATTCTGT	1628
93	TGTGCTATTGGCACCTCACGCTGACC	1629
94	TGTAGATAAGTATCCAGCGACTCTCT	1630
95	AATTCGCCAATTGTGTGTAGGCGCAA	1631
96	CGATTATGAGTACTTGTAGACCAGCT	1632

[Table 18-1]

Table 18 List of random primers (28-base primers)

No	Primer sequence	SEQ ID NO
1	TTGCAAGAACAACGTATCTCATATGAAC	1633
2	CACCGTGCTGTTATTACTTGGTATTCGG	1634
3	CACGTGTATTGTTGCACCAGAACGACAA	1635
4	ATGCACGTAATTACTTCCGGAGAAGACG	1636
5	TATGTTGTCTGATATGGTTCATGTGGCA	1637
6	AGCGGACTAGTTGATGCCAACATTGTA	1638
7	ATAGGCAGGTCCAGGCTCGGAACAAGTC	1639
8	GCGGTAGTCGGTCAAGAACTAGAACCGT	1640
9	ACTATACACTCTAGCTATTAGGAAGCAT	1641
10	GATCATCTTGCTTCTCCTGTGGAGATAA	1642
11	CTACTACGAGTCCATAACTGATAGCCTC	1643
12	GCACAGACACCTGTCCTATCTAGCAGGA	1644
13	AAGCGAGGCGCGAAGGAGATGGAAGGAT	1645
14	CTGAAGACGCCAGTCTGGATAGGTGCCT	1646
15	GTAAGCTCTGTCTTCGAGATTGATAAG	1647
16	GGTTAGAGAGATTATTGTGCGCATCCAT	1648
17	CCAGGAGGACCTATGATCTTGCCGCCAT	1649
18	ACTATTCGAGCTACTGTATGTGTATCCG	1650
19	GACATCGCGATACGTAACCTCCGAGTGT	1651
20	CCGCAATTCGTCTATATATTCTAGCATA	1652
21	CTACACTTGAGGTTGATGCTCAAGATCA	1653
22	CGATCAGTTCTAGTTCACCGCGGACAAT	1654
23	AAGAATGATGATTGGCCGCGAACCAAGC	1655
24	CACGACCGGAACTAGACTCCTACCAATT	1656
25	AGTTGCCTGTGAGTGAGGCTACTATCTC	1657
26	GATTCTTCCGATGATCATGCCACTACAA	1658
27	CGCTGAAGTGAACATGCAAGCACCGCA	1659
28	ATTATCGTGATGGTGAGACTGAGCTCGT	1660
29	CGAGGCCACTCTGAGCCAGGTAAGTATC	1661
30	TGCCGAGGACAGCCGATCACATCTTCGT	1662
31	GTTGACATGAAGGTTATCGTCGATATTC	1663
32	GTGGTCCAGGTCAAGCTCTGATCGAATG	1664

[Table 18-2]

No	Primer sequence	SEQ ID NO
33	CCAGTCCGGTGTACTCAGACCTAATAAC	1665
34	CGAGACACTGCATGAGCGTAGTCTTATT	1666
35	GACGGCTTGTATACTTCTCTACGGTCTG	1667
36	TTAGCTGGATGGAAGCCATATTCCGTAG	1668
37	CAGCCTACACTTGATTACTCAACAACCTC	1669
38	GTACGTAGTGTACGCGCCTACGTTTCGT	1670
39	CTACAACCTCTCAATCATGCCTCTGTTG	1671
40	CGAGGACAGAATTCGACATAAGGAGAGA	1672
41	GCCGAACGACACAGTGAGTTGATAGGTA	1673
42	GAACACTATATGCTGTCGCTGTCTGAGG	1674
43	GTTAAGTTCTTCGGCGGTCATGCTCATT	1675
44	TTGCTTACAGATCGCGTATCCATAGTAT	1676
45	GAGGACCACCTCTGCGAAGTTCACTGTG	1677
46	AATCCTAGCATATCGAGAACGACACTGA	1678
47	TGAATACTATAGCCATAGTCGACTCCG	1679
48	GACATCCACGAAGCTGGAATCGGAACC	1680
49	TTAGCCGTCTTAGAAGTGCTGACCGGC	1681
50	CTATTCTGCCGTAATTGATTCTTCGTT	1682
51	ACGCCTCTGGTCGAAGGTAGATTAGCTC	1683
52	CAGCCTATTGATCGTAAGTAGATGGTCC	1684
53	TTAAGTGAGGTGGACAACCATCAACTTC	1685
54	AAGGCCTTGCGGCTAAGTAGTATTCATC	1686
55	TTGTGATACTAATTCTTCTCAAGAGTCA	1687
56	GCATTAGGTGACGACCTTAGTCCATCAC	1688
57	GCGGATGGACGTATACAGTGAGTCGTGC	1689
58	GAACATGCCAGCCTCAACTAGGCTAAGA	1690
59	TCCGTCATTAGAGTATGAGTGACTACTA	1691
60	AACACTTAGTAACCAAGTTCGGACTGGAC	1692
61	CGCTAACTATTGCGTATATTGCGGCTT	1693
62	GCCATCTACGATCTTCGGCTTATCCTAG	1694
63	CCTGAGAATGTTGACTAAGATCTTGTGA	1695
64	TCGGTTAGTCTAATCATCACGCAACGGA	1696

[Table 18-3]

No	Primer sequence	SEQ ID NO
65	ATTATCTATTGAAGCAGTGACAGCGATC	1697
66	GAGGAGAATCACGGAACACGGTCACATG	1698
67	GCTGCAAGCATTATGACCATGGCATCTG	1699
68	GAACAACCTATAACGACGTTGTGGACAA	1700
69	TTAATCATCGATAGACGACATGGAATCA	1701
70	TCGAGTGTAAGCACACTACGATCTGGAA	1702
71	GCTACGCACAGTCTCTGCACAGCTACAC	1703
72	CCTGTATGTACGTTCTGGCTAATACCTT	1704
73	TGAAGCACCGGTACATGGTGTATCCGA	1705
74	TGCTGGAACCTAACTCGGTGATGACGAT	1706
75	CGCTATCTTACTGCCAAGTTCICATATA	1707
76	AACGCGCGGTATCGGCAATAATCTCAA	1708
77	CCATTAGGATGACCATCGACTATTAGAG	1709
78	TACTGCTAGACTGCGTGCATTTCATGGCG	1710
79	CATTGCGCGCTCCACGAACCTATTGTC	1711
80	GACGCGCCTAGAACTGTATAGCTCTACG	1712
81	CATTGCAACTTGTCGGTGATGGCAATCC	1713
82	TTAATGCACATGCAGTACGGCACCACAG	1714
83	AGCGGTACGTGGACGAGTGGTAATTAAT	1715
84	GACGTATTGCTATGCATTGGAAGATGCT	1716
85	AACACTTCGACCATTGCGCCTCAATGGT	1717
86	CGGTACGCTCTAGCGGTCATAAGATGCA	1718
87	CCTGAATAACAGCCGCGCCTAATTAGAT	1719
88	AAGCGTCTAATGTGCCTTAAGTCACATG	1720
89	GCTCTCCAAGAACCAGAAGTAAGCATCG	1721
90	GAGGAGAGTTGTCCGAGTGGTGTGATGT	1722
91	TAACGAGTGGTGGTCTAAGCAATTGAG	1723
92	CCAACAGTATGCTGACATAACTATGATA	1724
93	GATCCTTGCCACGCCTATGAGATATCGC	1725
94	AACGCGCTACCGTCCTTGTGCATAGAGG	1726
95	CTACATGTGCCTTATAGTACAGAGGAAC	1727
96	CAGCCTCGTAGTTAGCGTGATTCATGCG	1728

[Table 19-1]

Table 19 List of random primers (29-base primers)

No	Primer sequence	SEQ ID NO
1	CTCCTCGCCGATTGAAGTGCGTAGAACTA	1729
2	CAGCAGGCCTCAATAGGATAAGCCAACTA	1730
3	GACCATCAATCTCGAAGACTACGCTCTGT	1731
4	GGTTGCTCCGTCTGTTTCAGCACACTGTTA	1732
5	AATGTGCGACTGGCCATTATCGCCAAGTGT	1733
6	GATAGCTTGCCATGCGAATGGATCTCCAG	1734
7	CCAGACCGGAGCCAATTGGCTGCCAATAT	1735
8	AACGTCGCTCCATACGTTACCTAATGCAG	1736
9	GAATATGACGCGAACAGTCTATTCCGATC	1737
10	GACGAGAATGTATTAAGGATAAGCAAGGT	1738
11	AAGTCGTATGAATCGCTATCACATGAGTC	1739
12	GTCGTGGAGACTACAATTCTCCTCACGTT	1740
13	GTTGCCACCGTTACACGACTATCGACAGT	1741
14	AGGATAGGCTACGCCTTACTCTCCTAAGC	1742
15	TAATCATCCTGTTTCGCCTCGAGGTTGTTA	1743
16	GACAAGCAGTAATAATTACTGAGTGGACG	1744
17	TACAGCGTTACGCAGGTATATCAAGGTAG	1745
18	CTAACATCACTTACTATTAGCGGTCTCGT	1746
19	CCGCGCTTCTTGACACGTTCTCCACTAGG	1747
20	CAAGTAACATGAGATGCTATCGGTACATT	1748
21	CGACCACTAGGCTGTGACCACGATACGCT	1749
22	CAGGTCATGTGACGCAGTCGGCAGTCAAC	1750
23	ACTCCATCGTTAGTTCTTCCGCCGTGCTG	1751
24	CTCACCACGTATGCGTCACTCGGTTACGT	1752
25	TGCCTATGCTATGGACCTTGC GCGACTCT	1753
26	AATGAAGGTCAACGCTCTGTAGTTACGCG	1754
27	CACCATTGATTCATGGCTTCCATCACTGC	1755
28	GACACGCAAGGTAATTCGAGATTGCAGCA	1756
29	CACCGAGAGGAAGGTTGATCGCTTCTCG	1757
30	CAGTTATCGGATTGTGATATTCACCTCTG	1758
31	ATACTGTAACGCCTCAACCTATGCTGACT	1759
32	ATCTGTCTTATTCTGGCACACTCAGACTT	1760

[Table 19-2]

No	Primer sequence	SEQ ID NO
33	TCCAACCGGTGACGTGCTCTTGATCCAAC	1761
34	CACACTCAGTTCGGCTATCTCTGCGATAG	1762
35	AGCTGTAAGTCAGGTCTACGACTCGTACT	1763
36	GTCGGCGGCACGCACAGCTAACATTCGTA	1764
37	ATATGGTAGCCAGCCACGTATACTGAACA	1765
38	TGGACAATCCGACTCTAACACAGAGGTAG	1766
39	TCCGCGCTGACAGTTCAATCTATCAATT	1767
40	GGTTCCTTAGAATATGCACCTATCAGCGA	1768
41	CGGCTGTACGACATGGATCATAAGAGTGT	1769
42	TGCAGATGTACGCTGTGGCCAGTGGAGAG	1770
43	CCTACTCACTTAACAATAATCGGTTCGGT	1771
44	CGCTTCCTACTGCCTGTGCCGCGACATAA	1772
45	CTAGACCGACCGGTTATGCGCTATTGTTC	1773
46	TTGTGAGCACGTCTGCGGCAAGCCTATGG	1774
47	TCATCGGCCGGCGCTGTTGTTGTTACCAT	1775
48	GCGGTTAGGTGCAGTTAGGAAGACTATCA	1776
49	TATGCGGTCTGAGGCGTAGCATTCTAGA	1777
50	CCATCTATTTCGTCGAACTCTCAGCTCGTA	1778
51	ATCAGATCTACTGATCGCGGTAGAGTATC	1779
52	TACACATAGGCGGCGCAGCCTTCTAATTA	1780
53	TTAACCGTAGTTCTTAGCTTACGCCGCTC	1781
54	ACTATAGAGGACATGGCACTCCTCTTCTA	1782
55	CAGTTCGTATTAAGATTGAATGTAGCGGT	1783
56	AGTTATCGGTATCCGCTTATCCGTACGTA	1784
57	AGCTTATTCATACACTGCACCACAGCAAG	1785
58	CCGTCGGCTAGTCTATCCTCTAATTAGAA	1786
59	GTCCGCTTCCATGCCTGCTGTACGAACAC	1787
60	TCTCTTCCTCCTTCATTGTTGCTAGCTC	1788
61	TCTCTTGAGCGGTCCTCATACAGGTCTGC	1789
62	GACCAAGGTAGGTGATATCACCGGTACT	1790
63	AAGATTGTGATAGGTTGGTAGTTACCACA	1791
64	TCGCCTCCGAAGAGTATAGCATCGGCAGA	1792

[Table 19-3]

No	Primer sequence	SEQ ID NO
65	GAGGTAGTTATGAGCATCGAGGTCCTGTT	1793
66	GGACGCAAGATCGCAGGTAAGCT	1794
67	ACTCGTACACGTCATCGTCAGGCTCAG	1795
68	TAATCCGTCAGGAGTGAGATGGCTCGACA	1796
69	AAGATGGTTCCGCGCATTGACTAGCAAGT	1797
70	TCCGCGATCTGCGGATCTGAATGCTCAC	1798
71	TTCACGAGAGTCAACTGCTAGTATCCTAG	1799
72	TTCCAAGTGGATTCTTCCAAGTCTCGAA	1800
73	CACTACTACTCAAGTTATACGGTGTGAC	1801
74	CAACTGGATTCTCAGGATGCGTCTCTAGC	1802
75	TGGACTAGAGTGGAGCGATTACGTAATAT	1803
76	GAGGTCATTCAACTGGACTCGCCACGGAC	1804
77	CAGGTGTGTAACGCTGCAATCACATGAAT	1805
78	TATGCTGAGGTATTAGTTCTAACTATGCG	1806
79	CGTCTGAGTCGGATAAGGAAGGTTACCGC	1807
80	GTACTATCGTCGCAGGCACTATCTCTGCC	1808
81	GCTTCCTCCTTGCAACTTCATTGCTTCGA	1809
82	TGTCTACGAAGTAGAAGACACGAATAATG	1810
83	CCGTCATCTAAGGCAGAGTACATCCGCGA	1811
84	CCGGAGGCGTACTAACTGACCACAACACC	1812
85	AACTCGTCGCTGCCTGAATAGGTCAGAGT	1813
86	TTATAAGATTAATGTCGGTCAGTGTCCGA	1814
87	CGTCTCGATGGATCCACACGAACCTGTTG	1815
88	ATGCCATCATGGTCGTCCTATCTTAAGGC	1816
89	GCGCTTCAGCGATTTCGTCATGCAAGGCAC	1817
90	CCAAGCGATACCGAGGTACGGTTAACGAG	1818
91	ATATGACAGACAGGTGGACCTAAGCAAGC	1819
92	CACTACATCGTCAGGCCTGGAAGCCTCAG	1820
93	GCCGTGTAGACGAGGACATTATGTCGTAT	1821
94	CAACGTATATACACACCTTGTGAAGAGAA	1822
95	TCCAACGTAATTCGCGCTCTGTCGAGAC	1823
96	AATTCGTGCTTCGATCACCGTAGACTCAG	1824

[Table 20-1]

Table 20 List of random primers (30-base primers)

No	Primer sequence	SEQ ID NO
1	ACTATATTGTATTACGTCGACGACTCGC	1825
2	GACGAGCTTGTGGTACACTATACCTATGAG	1826
3	TGATTCAAGCACCAGGCATGCTTAAGCTAG	1827
4	CGGTCTCCTATAGGAAGGCTCATTCTGACG	1828
5	AGTCAGTGTGAATCAATCAAGGCGTCCTT	1829
6	CGAACGTAATGGCCATCACGCGCTGGCCTA	1830
7	CGAACCTGGACCACCTGGCATTACCATTAC	1831
8	ACATTAGGTTCTGTAAATGTCTTATCAACG	1832
9	CGTCTAATGCACCGTATCGTCTTCGCGCAT	1833
10	TCTATGACTTACAACGGAATCTTACTTCGT	1834
11	GTAACCGATCGGTACCGTCTGCTATTGTTC	1835
12	GGTGATTGATAAGCAACACATATTAGGAGG	1836
13	AATTATCGACGCTAATAGGCGAGCTGTTCA	1837
14	GGAGGTACATGACGAGTGGACAGACAGACC	1838
15	CTCTAATCCGTTATGCGGTGATGTAATCCG	1839
16	GCAAGCACGCGGCTTGGCGAACTTCTATGC	1840
17	TAGATGTAGGCCTGGTAGGCAGAGGAGTAA	1841
18	CCGAGTGGCGACCACACAGGTACGCATTAA	1842
19	GTCCTGGCTCAGATTAGTGCACTTAGTTAT	1843
20	GCGGTACCTACATGTTATGACTCAGACGAC	1844
21	TCTCTGCCAATGCTGGTCTCATCGAATCCA	1845
22	TCTCTACACAGCTACATACTATACTGTAAC	1846
23	TACGACGGACGCTGGTGGTGAAGAGAAGG	1847
24	GCCTCGATATATCTACGTATAGTTCAAGTT	1848
25	GGCTCCTGCATTCAATTGAAGGTCGGCCTTG	1849
26	CAGTTCGGTGATTCAAGAGAACAATGGTGG	1850
27	TATAACGAAGCCGGCTGGAACGGTAACTCA	1851
28	CTGTATCAATTCAAGTGACAGTGGCACGTC	1852
29	AGCAATTGCGGTTTATAGGCGTAATTATAT	1853
30	CATATGGACCTGGAGATCACCGTTCAGTCC	1854
31	GAAGGCCGTTGGTCTATCTTACTGGAGC	1855
32	GTGCGTTTATCTAGCCTAAGACGCTGACCT	1856

[Table 20-2]

No	Primer sequence	SEQ ID NO
33	GAGTAACTTATATCCTCTCTACGACATCGA	1857
34	ATTCTACGCTGATGTCTCCGCTGAACAGGA	1858
35	TCATCAACGTTACTCACTAGTACCACGGCT	1859
36	AACCATTCTTGAACGTTGAGAACCTGGTGG	1860
37	ACGACACCTCCGCGGAACATACCTGATTAG	1861
38	GCGCACTTATTGAAGTAATCTCATGGCCAA	1862
39	GCGCCAATTCAGCCAGTTAGCGTCTCCGTG	1863
40	AGCAACAAGTCGCTGTATATCGACTGGCCG	1864
41	CCTTACAATAGACCTCGCGGCGTTCATGCC	1865
42	GGATCCAACCTTCAGCGAAGCACCAACGTCG	1866
43	GCGCCAGTTCTCGTACTCTCGAGAAGCGAC	1867
44	GAGTGGGCGCAATCTGGAACCTCATGACGTT	1868
45	CCTGAGAGTGATTTCGTGTCTGCGAAGATGC	1869
46	GTGACTGGTTAAGGCAATATTGGTCGACCG	1870
47	CTATCAAGCCTTACAAGGTCACGTCCACTA	1871
48	ACTGCGTCCTTGCGTCGGAACCTCCTTGTGT	1872
49	TGCAACTCAGTGGCGGCGACACCAAGAGCT	1873
50	TTCGGTTCTACTAGGATCTCTATCTGAGCT	1874
51	AGCTAATCTATTAAGACAGATTAGACAGGA	1875
52	GGACCGCTCTTAGGTTATGCACCTGCGTAT	1876
53	CTCTAATACTAGTCCACAGGTTAGTACGAA	1877
54	ATCCATATATGCTCGTCGTCAGCCAGTGTT	1878
55	GCTATTACTGTGTTGATGTCCACAGGAGAA	1879
56	GCTACGGCGCAGATCTAGACAACCTGGAAGT	1880
57	GCCTCTTGTGTTAGCCGAATACCAATGACC	1881
58	TGAGGACGATAACATTACCTCTCGAGTCGC	1882
59	CGATTACCAATCCGACGACTTCGCAGCAGC	1883
60	ATGACACGAGTCCAGTACATATGCGAAGAC	1884
61	GCGCTCGCATGCACTAGTGTAGACTGACGA	1885
62	GCACATCTCAGAATTGATGGTCTATGTGCG	1886
63	TTCTTCGACGCCGCTACTAATAGGTCAAT	1887
64	GGAAGCGCCTCTAACAACCGATGCTTGTGG	1888

[Table 20-3]

No	Primer sequence	SEQ ID NO
65	CTCTAGACGCGTCGTGACTCCAATCTGTTG	1889
66	GTAGTTCGTCCGACTGACCTCGTACTCACT	1890
67	ATGCTGTCGAGTGTCGGCATAGAGCACAC	1891
68	GCGCATCTTGCAGCGTCCTGTAGTTCTGAA	1892
69	GCGATTGTTGAGGAACCACAGCGGCACCTA	1893
70	CACGCGTACTCTGCTTGCTGTGTGGTCGGT	1894
71	CATCCAACGCAGGACCTAGTAGTCATGCTT	1895
72	TTCTAGTTGTGATGAGAATCGCTAGCGTGC	1896
73	CATTCTGAATCTGGTCTCTCTCGATCATCC	1897
74	ATTAATGTAGAGGATAGTTCGGTTCTCTCC	1898
75	GTATCGCGCTTACGAATGAGGTGTGGCTTC	1899
76	GCTGGTGAGAGAGCCAGATTATCGGTGGAG	1900
77	GGCAGGAGCAGGTAGAACTAGAACCTAGAT	1901
78	TGTATTATCTCGAAGCGGTGCGTTAGAGTC	1902
79	CACGTGTTCTAGCTACTAATGGCGTCAATT	1903
80	CGCGCTACATTACTTCCTACACCATGCGTA	1904
81	TGAGGCAACTAGTGTTCCGAAGATGACGGA	1905
82	TTATTATTGTCTGTGGAACGCACGCCAGTC	1906
83	GCTATAGTATTATCCATGAATTCCGTCGGC	1907
84	GTATCAATAGCTCAATTCGTCAGAGTTGTG	1908
85	TAGTCCATGCGTGGATATATTGAGAGCTGA	1909
86	GCACAGTACGACTTATAACAGGTCTAGATC	1910
87	ACTCAATGGTGGCAGCTCGGCGCAGCATA	1911
88	GTAGTACCACTCCGCCTTAGGCAGCTTAAG	1912
89	CGTCAACTGATGCGTGCAACCAATGTTAT	1913
90	GCAGCTTGACTGCCTAGACAGCAGTTACAG	1914
91	GCAACTTCTTAGTACGAATTCATCGTCCAA	1915
92	ATCCGTATGCTGCGGCAGTGGAGGTGGCTT	1916
93	TGCGGATCAATCCAGTTCTGTGTACTGTGA	1917
94	TTATGATTATCACCGCGTAACATTCCGAA	1918
95	GCTACCTAGATTCTTCAACTCATCGCTACC	1919
96	CAGTGTTAGAATGGCGGTGTGTAGCCGCTA	1920

[Table 21-1]

Table 21 List of random primers (35-base primers)

No	Primer sequence	SEQ ID NO
1	GCTTATAGACTACAGCTGCGAGGTATAAGGTCAC	1921
2	CGCTCAGCAGGATGCTATCCTAAGTTAATGTGGTG	1922
3	GAACTGAGCGGACATCAGCTAGGCCTACAATACAT	1923
4	TCGTGAACTTCTGCGTTGGTCTCTACCAAGGCGGT	1924
5	TAAGTCAGGTATCTTATCAGTGGTACACGGTACGA	1925
6	TAATAATGTTGCGCGTGACCGAGGAGGAATCCACT	1926
7	CTAGGAGTTCTCGTAAGCTGGAGTACCGTAACGTG	1927
8	GGACTCTCCTCAGAGGATCCTTCTTGCGCAGGCAT	1928
9	GCTAGAGGCCTGAGTACACCTTCTCGCATCAGGAT	1929
10	ATATCGCGAGCACTAACGTCGTTGTCGTTCTAGGA	1930
11	AGCGGTTACTATACCTGGCGGCTGACGTTGTTAGT	1931
12	GAGCTAGGTAGATCTCCAAGTGTAGCTAAGAAGAG	1932
13	GGAGTCGCTGGTGACGTATGCCGAGGATGAGCTTC	1933
14	CGCCGACCTCCTGTTACGAAGCCGCTGATGTAA	1934
15	AGTAGGCACTTAGTTATCGATTACGTTAGTTAGTC	1935
16	GGATGACGTCTCAGTCTACCTCGCAGTGTGCTCTA	1936
17	CTGGTTCGCGTTAGCAATACTAAGGCAGTCAGGAG	1937
18	ATATGGTCATATTGGCCTCTTCGAACACAGACTGT	1938
19	TATCAGAGGATAGCAGGTCTGAGTTGCAAGGCTAA	1939
20	GGTGGTCTGACCATAGCTGTTCTTCTCACAGAGAC	1940
21	GCAATACCAACGAGATGAGTATTCGTTGAAGCTCT	1941
22	CCAAGTCGACGCTGCATGAATGAGCGCTATTCACT	1942
23	CCATTAGATCGCTTCGAGACAATTAGGAGACATGA	1943
24	GATGACTGTACCTCCTATCATTGAGTGTGGACCAA	1944
25	ATATCTGGATGAATAGTGGTTAGGTAAGCAAGTAA	1945
26	ACCGACTATGTTAATTCGTGTCTGGATGGCAGAAT	1946
27	GTGGCAGTCTTGCTAGTATCTTAGACCATCACCAA	1947
28	CGCTATCTTAGTCGAGCACAATGTCTTCGTATAGG	1948
29	ATTAGTACGGCACGAACCGGCCATTCATGGCAGCT	1949
30	AGTACGACTATCAAGACTCCAGCGCTCTCCTTGGA	1950
31	ATGAGCCTCGGAGCGAACGTTATCGATCAGGCTGT	1951
32	TTGCGTGCAGTAGCACCGATACACAGCGCTTGAT	1952

[Table 21-2]

No	Primer sequence	SEQ ID NO
33	AACGGCTGCATCACCTACACTATACTCAACATCTA	1953
34	GTCGCTATGCCAGAAGTGGCGTGAATGCTATGGT	1954
35	CATGGATACCTACTGACTTGACTTCTAGAGGACCG	1955
36	GAGTGACGCAGACACCGTAACGTCGAATCTTCTAG	1956
37	AGTACCGTCTGTGTGAATATTGTTCTACGTTACA	1957
38	GGCTAATCGATAGTGACGAGTTCTGCACGCCTGAA	1958
39	GGCGAGCGCTCGTGGTTCTGAGTCGCTGTTAGATG	1959
40	TATCTCCAGCGTTATAAGCTACTGGAGCCGCTCGG	1960
41	CCTTCTGCGCAAGTCAAGGATTCGCTTAGATGGAC	1961
42	GTTGCTGACAGCCGTTGCGTACTTGCCTTAAGAAC	1962
43	GTGGCCTAATCACTCGCGCTTCATAGGCCGATAGG	1963
44	TGCATCTAGCCTACATCGGACCTTGTTATGGTAAT	1964
45	GGACAGCTACTGGACACCACCGAACTGGTAGTGTC	1965
46	AACTGGCGATGGACGGCCGCTCTCCGCTACATAG	1966
47	GGAGCAGTTAGCTATGGAGCAGGCCGATAACCTGA	1967
48	ACTCTACGGTGACCTCAGCCTTCATGCAATAGGC	1968
49	CTTGTAGCACAATACATTACTCTCCACGTGATAGC	1969
50	GGACGCTATCGATACCGTTATTCCTACTCTGTCCG	1970
51	GGATGATCGTCAACGATCAACTGACAGTTAGTCGA	1971
52	TGACAGTAGCAATGTCTCACGTCTGCACAACGGAA	1972
53	GTCGCAGGACCTCACGGATAGTAGTGCAGGTCTA	1973
54	ATATCGGCGGACGCAATGACAGTTGTTGGCTGATG	1974
55	AAGCACCAAGGAGGTATGTTCCATCGAGGCGCTCG	1975
56	GACCGCACCTTATAGCTATATCCTGGTCTAGTACT	1976
57	TCTCAGAGGAAGGTTGAGCGTCTGACCAGGTTGGC	1977
58	TGGACCTAGAGACCTAGCTCGTCTCTTCGCGATCG	1978
59	CGGAGTGGTTCCACGCGACCTCGCAACTAATCCTT	1979
60	GGAGCCGCGCGCAGACTGACCTTGCTTGATCTACT	1980
61	ACTCTAAGTATATGCGCAGTTAGTATACTGAACCA	1981
62	GAGCATTGCTTCGCTTCGATGTCTATTCTGATCAG	1982
63	GCTTGATTGCCACTCGAGTAGGTCGTGGCAGTAG	1983
64	ATCTGGACATTGCATTCCGTGTGTATACAGAAGGC	1984

[Table 21-3]

No	Primer sequence	SEQ ID NO
65	GGTTGCGATCAGCTTGATAGCAGGTCATATCCTCA	1985
66	GCAGGTACTAACCTGAGATGCGTAGCTAACACAGG	1986
67	ATCTGCAAGGACGTAACGTCCTCGGAAGGTGAGGT	1987
68	ATAATCTTACGAGCCTCCAGTGAATAATGCAAGCA	1988
69	CAATCTCCGCACAGTCTTGTTTCAGGTACAGACTTA	1989
70	ATGTGCGCAATTCAGCGTAAGTGCCTATTCATAAT	1990
71	TCGGACGCACACATCCTGTTGTCGAGAAGAGGAAG	1991
72	TCGGAAGCATCACATGAGCATCAGGAGTTCATTGC	1992
73	ATCTGGTTGTGGACTTCTATACAGTACCAGAGTGG	1993
74	CGTCTGAATATAGTTAGCTAGTAGTGAATCCAGG	1994
75	TAATATCTGATCCGACCTATTATCTAGGACTACTC	1995
76	TATGCCGCCGTCCGTACCTCGTCTGCTTCAGTTGG	1996
77	TGGCTCAAGTTCATATTGCCAAGACGACCTGGAG	1997
78	GCAGTTCGCTAGGCGGTCCGAGGCAATTGAAGAG	1998
79	CATGGCACAGACGAAGTATGCACCACGCTCATTA	1999
80	GGAGCGTACTACGACCATTCAACCGAATATGTTAC	2000
81	GCGTAGATCTCGCAGACAGAGACAAGGTGCGAATGG	2001
82	TGGACTGAGGTTCTCCGGTCTATACTCCTGTAGGA	2002
83	TGGCTATAGCAACGGCTTCTTGATCGCATTGCA	2003
84	GGCGAAGAATCATGCGAGACGGAGTAGACGGACGT	2004
85	GAGCATTGCGAGTTGCACACGTGATATCAGACTGT	2005
86	CTGTTGACCTATGCCAGAATCAATACCTCAGATTA	2006
87	GTTAACAAGTAGATGCCAAGATACAACGAGAGACC	2007
88	GAGCAAGATTATAGTTAGGAAGATAGTTAACTCGC	2008
89	TCCGGAGTCGAGCATATGTGACCAACTCTCAACGC	2009
90	GGAGCTGCGATGCCGTTACCGACGTCATCTTCAAG	2010
91	GCTCTATCTTACACATTGGCGTACTGGACTCGCGA	2011
92	TTCTACATATTCATCGCCTACCGAGTTGCGCGAAG	2012
93	TGGACGTCTGACCTGTGTCTACATCGGTGGTGCTA	2013
94	GGCAGGACAGCTCCGTGTTCTACTCGAACCGCACT	2014
95	TGACAACTCATGTCTCCGACCGCAGGCATACAAT	2015
96	GCAGGCCAACAAGTGGTCACGAGGAGTCCTTATT	2016

3.1.2 Standard PCR

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers (final concentration: 0.6 microM; 10-base primer A), a 0.2mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA)

were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. In this example, numerous nucleic acid fragments obtained via PCR using random primers, including the standard PCR described above, are referred to as DNA libraries.

3.1.3 Purification of DNA library and electrophoresis

The DNA library obtained in 3.1.2 above was purified with the use of the MinElute PCR Purification Kit (QIAGEN) and subjected to electrophoresis with the use of the Agilent 2100 bioanalyzer (Agilent Technologies) to obtain a fluorescence unit (FU).

3.1.4 Examination of annealing temperature

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers (final concentration: 0.6 microM; 10-base primer A), a 0.2mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, various annealing temperatures for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. In this example, annealing temperature of 37 degrees C, 40 degrees, and 45 degrees C were examined. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3.

3.1.5 Examination of enzyme amount

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers (final concentration: 0.6 microM; 10-base primer A), a 0.2mM dNTP mixture, 1.0 mM MgCl₂, and 2.5 units or 125 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3.

3.1.6 Examination of MgCl₂ concentration

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers (final concentration: 0.6 microM; 10-base primer A), a 0.2mM dNTP mixture, MgCl₂ at a given concentration, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while

adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. In this example, MgCl₂ concentrations, which are 2 times (2.0 mM), 3 times (3.0 mM), and 4 times (4.0 mM) greater than a common level, respectively, were examined. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3.

3.1.7 Examination of base length of random primer

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers (final concentration: 0.6 microM), a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. In this example, the random primers comprising 8 bases (Table 7), 9 bases (Table 8), 11 bases (Table 9), 12 bases (Table 10), 14 bases (Table 11), 16 bases (Table 12), 18 bases (Table 13), and 20 bases (Table 14) were examined. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3.

3.1.8 Examination of random primer concentration

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers at a given concentration (10-base primer A), a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. In this example, random primer concentrations of 2, 4, 6, 8, 10, 20, 40, 60, 100, 200, 300, 400, 500, 600, 700, 800, 900, and 1000 microM were examined. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3. In this experiment, the reproducibility of the repeated data was evaluated on the basis of the Spearman's rank correlation ($\rho > 0.9$).

3.2 Verification of reproducibility via MiSeq

3.2.1 Preparation of DNA library

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers (final concentration: 60 microM, 10-base primer A), a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA)

were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3.

3.2.2 Preparation of sequence library

From the DNA library obtained in 3.2.1, a sequence library for MiSeq analysis was prepared using the KAPA Library Preparation Kit (Roche).

3.2.3 MiSeq analysis

With the use of the MiSeq Reagent Kit V2 500 Cycle (Illumina), the sequence library for MiSeq analysis obtained in 3.2.2 was analyzed via 100 base paired-end sequencing.

3.2.4 Read data analysis

Random primer sequence information was deleted from the read data obtained in 3.2.3, and the read patterns were identified. The number of reads was counted for each read pattern, the number of reads of the repeated analyses, and the reproducibility was evaluated using the correlational coefficient.

3.3 Analysis of rice variety Nipponbare

3.3.1 Preparation of DNA library

To the genomic DNA described in 2. above (15 ng, Nipponbare-derived genomic DNA), a random primer (final concentration: 60 microM, (10-base primer A), a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3.

3.3.2 Preparation of sequence library, MiSeq analysis, and read data analysis

Preparation of a sequence library using the DNA library prepared from Nipponbare-derived genomic DNA, MiSeq analysis, and analysis of the read data were performed in accordance with the methods described in 3.2.2, 3.2.3, and 3.2.4, respectively.

3.3.3 Evaluation of genomic homogeneity

The read patterns obtained in 3.3.2 were mapped to the genomic information of Nipponbare (NC_008394 to NC_008405) using bowde2, and the genomic positions of the read patterns were identified.

3.3.4 Non-specific amplification

On the basis of the positional information of the read patterns identified in 3.3.3, the

sequences of random primers were compared with the genome sequences to which such random primers would anneal, and the number of mismatches was determined.

3.4 Detection of polymorphism and identification of genotype

3.4.1 Preparation of DNA library

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA, Ni9-derived genomic DNA, hybrid progeny-derived genomic DNA, or Nipponbare-derived genomic DNA), random primers (final concentration: 60 microM, 10-base primer A), a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3.

3.4.2 HiSeq analysis

Analysis of the DNA libraries prepared in 3.4.1 was consigned to TakaraBio under conditions in which the number of samples was 16 per lane via 100 base paired-end sequencing, and the read data were obtained.

3.4.3 Read data analysis

Random primer sequence information was deleted from the read data obtained in 3.4.2, and the read patterns were identified. The number of reads was counted for each read pattern.

3.4.4 Detection of polymorphism and identification of genotype

On the basis of the read patterns and the number of reads obtained as a results of analysis conducted in 3.4.3, polymorphisms peculiar to NiF8 and Ni9 were detected, and the read patterns thereof were designated as markers. On the basis of the number of reads, the genotypes of the 22 hybrid progeny lines were identified. The accuracy for genotype identification was evaluated on the basis of the reproducibility attained by the repeated data concerning the 22 hybrid progeny lines.

3.5 Experiment for confirmation with PCR marker

3.5.1 Primer designing

Primers were designed for a total of 6 markers (i.e., 3 NiF8 markers and 3 Ni9 markers) among the markers identified in 3.4.4 based on the marker sequence information obtained via paired-end sequencing (Table 22).

[Table 22]

Table 22. Marker sequence information and PCR marker primer information

Genotype	Marker name	Marker sequence 1*	Marker sequence 2*	Primer 1	Primer 2
NiF8 type	N80521152	CCCATACACACACCATGAAGCTTGAACCTAATT AACATTCTCAAACTAATTAAACAGCATGCAAG CATGTTTTTACACAATGACAATATAT (SEQ ID NO:2017)	ATGGTGAGGGCGCAGAGGCAAGACATGGAG GTCCGCAAGGTAGAGCTCACATCAAGTCGA GTATGTTGAATGCCAATCCCATATATA (SEQ ID NO:2018)	CCCATACACACACCA TGAAGCTTG (SEQ ID NO:2019)	GGTAGAGCTCACAT CAAGTCGAG (SEQ ID NO:2020)
		AATCAGACAACGAGCTCTGGACGAGAACAGAG CTGGACATCTACACGACCGCATGCTAGTAGA GCATGTACTGCAAAAGCTTGAAGGC (SEQ ID NO:2021)	GATGCTGAGGGCGAAGTTGTACGCCAAGTCCT CAATGTCTATAGCGGAGATCGCAGTAGTTCTGT AACCATTCCTGCTAAACTGTGCCAT (SEQ ID NO:2022)	ACGAGAACAGAGCTG GACATCTAC (SEQ ID NO:2023)	TCAATGTCATAGCGG AGATCGGAG (SEQ ID NO:2024)
		AGACCAACAAGCAGCAAGTAGTCAGAGAAGTA CAAGAGAAGGAGAGCAAGAGGATAGTAGTT GCAAGCTTACCGTTACAAAGATGATA (SEQ ID NO:2025)	GGAGGAGCACAACCTAGGCGTTTATCAAGATGG GTCATCGAGCTCTTGGTGTCTTCAACCTTCTT GACATCAACTTCTCCAACTCTTGTCT (SEQ ID NO:2026)	GGAGGCAAGAAGGA TAGTAAGTTGC (SEQ ID NO:2027)	CGAGCTCTTGTGTC TTCAACCTTC (SEQ ID NO:2028)
Ni9 type	N91552391	TGGGGTAGTCTTGAAGCTCTAGGTATGCTCT TCATCTCCCTCCACCTCTGGTGTAGCACCTC CTGCTCTCGGGCACCTCTACCGGG (SEQ ID NO:2029)	GGATACTGATGTAGCTTTCACCGGGAGTATT CCAAAGGTATCGATTTTCCACGGGGAACGGAA GTGCACTAGTTGAGGTTTAGATTGCC (SEQ ID NO:2030)	GAAGCTCTAGGTATG CCTCTTCATC (SEQ ID NO:2031)	GTGCACTAGTTGAGG TTTAGATTGC (SEQ ID NO:2032)
		TCGGGAACCGAACGGGCGAAGCTACAGATGTC AGTACGAAGTAGTCTATGGCAGGAATAGTA GTCCATACGTGTGTCGACCGCAAGCC (SEQ ID NO:2033)	AGCAGGAGGAGAAAGGAACCTGGCATTCTAT CGGCTGTCTGCCATTGCCATGTGAGACAAGGA AATCTACTTCACCGCCCATCTATCGAG (SEQ ID NO:2034)	GGCGAAGCTACAGAT GTCAGTAGC (SEQ ID NO:2035)	CTGTCTGCCATTGCC ATGTGAGAC (SEQ ID NO:2036)
		AGACATAAGATTAACTATGAACAAATTACAGG GTCCGATTCTTTGGGATTTGCAGCTTCCAAG AACCTTCMAATACTCATATATCTTC (SEQ ID NO:2037)	TTAAGTTGCAGAAATTTGATACGAAGAACTTGA AGCATGGTGAGGTTGCCGAGCTCATTTGGGGAT GGTTCCAGAAAGGCTATTGTAGCTTA (SEQ ID NO:2038)	GAACAAATTCACGGG TCCGATTCC (SEQ ID NO:2039)	CGAAGAACTTGAAGC ATCGTGAGG (SEQ ID NO:2040)

* Marker sequence information by paired-end sequencing

3.5.2 PCR and electrophoresis

With the use of the TaKaRa Multiplex PCR Assay Kit Ver.2 (TAKARA) and the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA, Ni9-derived genomic DNA, or hybrid progeny-derived genomic DNA) as a template, 1.25 microliters of Multiplex PCR enzyme mix, 12.5 microliters of 2x Multiplex PCR buffer, and the 0.4 microM primer designed in 3.5.1 were added, and a reaction solution was prepared while adjusting the final reaction level to 25 microliters. PCR was carried out under thermal cycling conditions comprising 94 degrees C for 1 minute, 30 cycles of 94 degrees C for 30 seconds, 60 degrees C for 30 seconds, and 72 degrees C for 30 seconds, and retention at 72 degrees C for 10 minutes, followed by storage at 4 degrees C. The amplified DNA fragment was subjected to electrophoresis with the use of TapeStation (Agilent Technologies).

3.5.3 Comparison of genotype data

On the basis of the results of electrophoresis obtained in 3.5.2, the genotype of the marker was identified on the basis of the presence or absence of a band, and the results were compared with the number of reads of the marker.

3.6 Correlation between random primer density and length

3.6.1 Influence of random primer length at high concentration

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers of a given length (final concentration: 10 microM), a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. In this experiment, the random primer lengths of 9 bases (Table 8), 10 bases (Table 1, 10-base primer A), 11 bases (Table 9), 12 bases (Table 10), 14 bases (Table 11), 16 bases (Table 12), 18 bases (Table 13), and 20 bases (Table 14) were examined. In the reaction system using a random primer of 9 bases, PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 37 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. In the reaction system using a random primer of 10 or more bases, PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3.

3.6.2 Correlation between random primer density and length

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), random primers of a given length were added to a given concentration therein, a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR,

TAKARA) were added thereto, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. In this experiment, random primers comprising 8 to 35 bases shown in Tables 1 to 21 were examined, and the random primer concentration from 0.6 to 300 microM was examined.

[0075] In the reaction system using random primers each comprising 8 bases and 9 bases, PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 37 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. In the reaction system using a random primer of 10 or more bases, PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3. Also, the reproducibility of the repeated data was evaluated on the basis of the Spearman's rank correlation ($\rho > 0.9$).

3.7 Number of random primers

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), 1, 2, 3, 12, 24, or 48 types of random primers selected from the 96 types of random primers comprising 10 bases (10-base primer A) shown in Table 1 were added to the final concentration of 60 microM therein, a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added thereto, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. In this experiment, as the 1, 2, 3, 12, 24, or 48 types of random primers, random primers were selected successively from No. 1 shown in Table 1, and the selected primers were then examined. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3. Also, the reproducibility of the repeated data was evaluated on the basis of the Spearman's rank correlation ($\rho > 0.9$).

3.8 Random primer sequence

To the genomic DNA described in 2. above (15 ng, NiF8-derived genomic DNA), a set of primers selected from the 5 sets of random primers shown in Tables 2 to 6 was added to the final concentration of 60 microM therein, a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added thereto, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98

degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3. Also, the reproducibility of the repeated data was evaluated on the basis of the Spearman's rank correlation ($\rho > 0.9$).

3.9 DNA library using human-derived genomic DNA

To the genomic DNA described in 2. above (15 ng, human-derived genomic DNA), a random primer (final concentration: 60 microM; 10-base primer A), a 0.2 mM dNTP mixture, 1.0 mM MgCl₂, and 1.25 units of DNA polymerase (PrimeSTAR, TAKARA) were added, and a reaction solution was prepared while adjusting the final reaction level to 50 microliters. PCR was carried out under thermal cycling conditions comprising 98 degrees C for 2 minutes and 30 cycles of 98 degrees C for 10 seconds, 50 degrees C for 15 seconds, and 72 degrees C for 20 seconds, followed by storage at 4 degrees C. The DNA library obtained in this experiment was subjected to purification and electrophoresis in the same manner as in 3.1.3. Also, the reproducibility of the repeated data was evaluated on the basis of the Spearman's rank correlation ($\rho > 0.9$).

4. Results and examination

4.1 Correlation between PCR conditions and DNA library size

When PCR was conducted with the use of random primers in accordance with conventional PCR conditions (3.1.2 described above), the amplified DNA library size was as large as 2 kbp or more, but amplification of the DNA library of a target size (i.e., 100-bp to 500-bp) was not observed (Fig. 2). A DNA library of 100 bp to 500 bp could not be obtained because it was highly unlikely that a random primer would function as a primer in a region of 500 bp or smaller. In order to prepare a DNA library of the target size (i.e., 100 bp to 500 bp), it was considered necessary to induce non-specific amplification with high reproducibility.

[0076] The correlation between the annealing temperature (3.1.4 above), the enzyme amount (3.1.5 above), the MgCl₂ concentration (3.1.6 above), the primer length (3.1.7 above), and the primer concentration (3.1.8 above), which are considered to affect PCR specificity, and the DNA library size were examined.

[0077] Fig. 3 shows the results of the experiment described in 3.1.4 attained at an annealing temperature of 45 degrees C, Fig. 4 shows the results attained at an annealing temperature of 40 degrees C, and Fig. 5 shows the results attained at an annealing temperature of 37 degrees C. By reducing the annealing temperature from 45 degrees C, 40 degrees C, to 37 degrees C, as shown in Figs. 3 to 5, the amounts of high-molecular-weight DNA library amplified increased, although amplification of low-molecular-weight DNA library was not observed.

[0078] Fig. 6 shows the results of the experiment described in 3.1.5 attained when the enzyme amount is increased by 2 times, and Fig. 7 shows the results attained when the enzyme amount is increased by 10 times the original amount. By increasing the enzyme amount by 2 times or 10 times a common amount, as shown in Figs. 6 and 7, the amounts of high-molecular-weight DNA library amplified increased, although amplification of low-molecular-weight DNA library was not observed.

[0079] Fig. 8 shows the results of the experiment described in 3.1.6 attained when the MgCl_2 concentration is increased by 2 times a common amount, Fig. 9 shows the results attained when the MgCl_2 concentration is increased by 3 times, and Fig. 10 shows the results attained when the MgCl_2 concentration is increased by 4 times. By increasing the MgCl_2 concentration by 2 times, 3 times, and 4 times the common amount, as shown in Figs. 8 to 10, the amounts of high-molecular-weight DNA library amplified varied, although amplification of a low-molecular-weight DNA library was not observed.

[0080] Figs. 11 to 18 show the results of the experiment described in 3.1.7 attained at the random primer lengths of 8 bases, 9 bases, 11 bases, 12 bases, 14 bases, 16 bases, 18 bases, and 20 bases, respectively. Regardless of the length of a random primer, as shown in Figs. 11 to 18, no significant change was observed in comparison with the results shown in Fig. 2 (a random primer comprising 10 bases).

The results of experiment described in 3.1.8 are summarized in Table 23.

[0081]

[Table 23]

Concentration (μ M)	Repeat	Fig. No.	Correlational coefficient (ρ)
2	—	Fig. 19	—
4	—	Fig. 20	—
6	First	Fig. 21	0.889
	Second	Fig. 22	
8	First	Fig. 23	0.961
	Second	Fig. 24	
10	First	Fig. 25	0.979
	Second	Fig. 26	
20	First	Fig. 27	0.950
	Second	Fig. 28	
40	First	Fig. 29	0.975
	Second	Fig. 30	
60	First	Fig. 31	0.959
	Second	Fig. 32	
100	First	Fig. 33	0.983
	Second	Fig. 34	
200	First	Fig. 35	0.991
	Second	Fig. 36	
300	First	Fig. 37	0.995
	Second	Fig. 38	
400	First	Fig. 39	0.988
	Second	Fig. 40	
500	First	Fig. 41	0.971
	Second	Fig. 42	
600	—	Fig. 43	—
700	—	Fig. 44	—
800	—	Fig. 45	—
900	—	Fig. 46	—
1000	—	Fig. 47	—

With the use of random primers comprising 10 bases, as shown in Figs. 19 to 47, amplification was observed in a 1-kbp DNA fragment at the random primer concentration of 6 microM. As the concentration increased, the molecular weight of a DNA fragment decreased. Reproducibility at the random primer concentration of 6 to 500 microM was examined. As a result, a relatively low rho value of 0.889 was attained at the concentration of 6 microM, which is 10 times higher than the usual level. At the concentration of 8 microM, which is equivalent to 13.3 times higher than the usual level, and at 500 microM, which is 833.3 times higher than the usual level, a high rho value of 0.9 or more was attained. The results demonstrate that a DNA fragment of 1 kbp or

smaller can be amplified while achieving high reproducibility by elevating the random primer concentration to a level significantly higher than the concentration employed under general PCR conditions. When the random primer concentration is excessively higher than 500 microliter, amplification of a DNA fragment of a desired size cannot be observed. In order to amplify a low-molecular-weight DNA fragment with excellent reproducibility, accordingly, it was found that the random primer concentration should fall within an optimal range, which is higher than the concentration employed in a general PCR procedure and equivalent to or lower than a given level.

4.2 Confirmation of reproducibility via MiSeq

In order to confirm the reproducibility for DNA library production, as described in 3.2 above, the DNA library amplified with the use of the genomic DNA extracted from NiF8 as a template and random primers was analyzed with the use of a next-generation sequencer (MiSeq), and the results are shown in Fig. 48. As a result of 3.2.4 above, 47,484 read patterns were obtained. As a result of comparison of the number of reads obtained through repeated measurements, a high correlation (i.e., a correlational coefficient "r" of 0.991) was obtained, as with the results of electrophoresis. Accordingly, it was considered that a DNA library could be produced with satisfactory reproducibility with the use of random primers.

4.3 Analysis of rice variety Nipponbare

As described in 3.3 above, a DNA library was prepared with the use of genomic DNA extracted from the rice variety Nipponbare, the genomic information of which has been disclosed, as a template, and random primers and subjected to electrophoresis, and the results are shown in Figs. 49 and 50. On the basis of the results shown in Figs. 49 and 50, the rho value was found to be as high as 0.979. Also, Fig. 51 shows the results of analysis of the read data with the use of MiSeq. On the basis of the results shown in Fig. 51, the correlational coefficient "r" was found to be as high as 0.992. These results demonstrate that a DNA library of rice could be produced with very high reproducibility with the use of random primers.

[0082] As described in 3.3.3, the obtained read pattern was mapped to the genomic information of Nipponbare. As a result, DNA fragments were found to be evenly amplified throughout the genome at intervals of 6.2 kbp (Fig. 52). As a result of comparison of the sequence and genome information of random primers, 3.6 mismatches were found on average, and one or more mismatches were observed in 99.0% of primer pairs (Fig. 53). The results demonstrate that a DNA library involving the use of random primers is produced with satisfactory reproducibility via non-specific amplification evenly throughout the genome.

4.4 Detection of polymorphism and genotype identification of sugarcane

As described in 3.4, DNA libraries of the sugarcane varieties NiF8 and Ni9 and 22

hybrid progeny lines were produced with the use of random primers, the resulting DNA libraries were analyzed with the next-generation sequencer (HiSeq), the polymorphisms of the parent varieties were detected, and the genotypes of the hybrid progenies were identified on the basis of the read data. Table 24 shows the results.

[0083]

[Table 24]

Number of markers		F1_01		F1_02		Total	
		Consistency	Reproducibility	Consistency	Reproducibility	Consistency	Reproducibility
NiF8 type	8,683	8,680	99.97%	8,682	99.99%	17,362	99.98%
Ni9 type	11,655	11,650	99.96%	11,651	99.97%	23,301	99.96%
Total	20,338	20,330	99.96%	20,333	99.98%	40,663	99.97%

As shown in Table 24, 8,683 NiF8 markers and 11,655 Ni9 markers; that is, a total of

20,338 markers, were produced. In addition, reproducibility for genotype identification of hybrid progeny lines was as high as 99.97%. This indicates that the accuracy for genotype identification is very high. In particular, sugarcane is polyploid ($8x+n$), the number of chromosomes is as large as 100 to 130, and the genome size is as large as 10 Gbp, which is at least 3 times greater than that of humans. Accordingly, it is very difficult to identify the genotype throughout the genomic DNA. As described above, numerous markers can be produced with the use of random primers, and the sugarcane genotype can thus be identified with high accuracy.

4.5 Experiment for confirmation with PCR marker

As described in 3.5 above, the sugarcane varieties NiF8 and Ni9 and 22 hybrid progeny lines were subjected to PCR with the use of the primers shown in Table 22, genotypes were identified via electrophoresis, and the results were compared with the number of reads. Figs. 54 and 55 show the number of reads and the electrophoretic pattern of the NiF8 marker N80521152, respectively. Figs. 56 and 57 show the number of reads and the electrophoretic pattern of the NiF8 marker N80997192, respectively. Figs. 58 and 59 show the number of reads and the electrophoretic pattern of the NiF8 marker N80533142, respectively. Figs. 60 and 61 show the number of reads and the electrophoretic pattern of the Ni9 marker N91552391, respectively. Figs. 62 and 63 show the number of reads and the electrophoretic pattern of the Ni9 marker N91653962, respectively. Figs. 64 and 65 show the number of reads and the electrophoretic pattern of the Ni9 marker N91124801, respectively.

[0084] As shown in Figs. 54 to 65, the results for all the PCR markers designed in 3.5 above were consistent with the results of analysis with the use of a next-generation sequencer. It was thus considered that genotype identification with the use of a next-generation sequencer would be applicable as a marker technique.

4.6 Correlation between random primer density and length

As described in 3.6.1, the results of DNA library production with the use of random primers comprising 9 bases (Table 8), 10 bases (Table 1, 10-base primer A), 11 bases (Table 9), 12 bases (Table 10), 14 bases (Table 11), 16 bases (Table 12), 18 bases (Table 13), and 20 bases (Table 14) are shown in Figs. 66 to 81. The results are summarized in Table 25.

[0085]

[Table 25]

Random primer length	Repeat	Fig. No.	Correlational coefficient (ρ)
9	First	Fig. 66	0.981
	Second	Fig. 67	
10	First	Fig. 68	0.979
	Second	Fig. 69	
11	First	Fig. 70	0.914
	Second	Fig. 71	
12	First	Fig. 72	0.957
	Second	Fig. 73	
14	First	Fig. 74	0.984
	Second	Fig. 75	
16	First	Fig. 76	0.989
	Second	Fig. 77	
18	First	Fig. 78	0.995
	Second	Fig. 79	
20	First	Fig. 80	0.999
	Second	Fig. 81	

When random primers were used at a high concentration of 10.0 microM, which is 13.3 times greater than the usual level, as shown in Figs. 66 to 81, it was found that a low-molecular-weight DNA fragment could be amplified with the use of random primers comprising 9 to 20 bases while achieving very high reproducibility. As the base length of a random primer increased (12 bases or more, in particular), the molecular weight of the amplified fragment was likely to be decreased. When random primers comprising 9 bases were used, the amount of the DNA fragment amplified was increased by setting the annealing temperature at 37 degrees C.

[0086] In order to elucidate the correlation between the density and the length of random primers, as described in 3.6.2 above, PCR was carried out with the use of random primers comprising 8 to 35 bases at the concentration of 0.6 to 300 microM, so as to produce a DNA library. The results are shown in Table 26.

[0087]

[Table 26]

Correlation between concentration and length of random primer relative to DNA library																	
Primer μM	Concentration relative to standard	Primer length															
		8	9	10	11	12	14	16	18	20	22	24	26	28	29	30	35
0.6	standard	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
2	3.3 x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
4	6.7 x	x	x	x	x	x	o	o	o	o	o	o	o	o	x	x	x
6	10.0 x	x	x	x	x	x	o	o	o	o	o	o	o	o	o	o	x
8	13.3 x	x	x	x	x	o	o	o	o	o	o	o	o	o	o	x	x
10	16.7 x	x	x	x	x	o	o	o	o	o	o	o	o	o	o	x	x
20	33.3 x	x	x	x	o	o	o	o	o	o	o	x	x	x	x	x	x
40	66.7 x	x	o	o	o	o	o	o	o	x	x	x	x	x	x	x	x
60	100.0 x	x	o	o	o	o	o	o	o	x	x	x	x	x	x	x	x
100	166.7 x	-	x	o	o	o	o	o	x	-	-	-	-	-	-	-	-
200	333.3 x	-	x	o	o	x	x	x	x	-	-	-	-	-	-	-	-
300	500.0 x	-	x	x	x	x	x	x	x	-	-	-	-	-	-	-	-

○: DNA library covering 100 to 500 bases is amplified with good reproducibility ($\rho > 0.9$)

×: DNA library not covering 100 to 500 bases or reproducibility is poor ($\rho \leq 0.9$)

-: Unperformed

As shown in Table 26, it was found that a low-molecular-weight (100 to 500 bases) DNA fragment could be amplified with high reproducibility with the use of random primers comprising 9 to 30 bases at 4.0 to 200 microM. In particular, it was confirmed that low-molecular-weight (100 to 500 bases) DNA fragments could be amplified assuredly with high reproducibility with the use of random primers comprising 9 to 30 bases at 4.0 to 100 microM.

[0088] The results shown in Table 26 are examined in greater detail. As a result, the correlation

between the length and the concentration of random primers is found to be preferably within a range surrounded by a frame as shown in Fig. 82. More specifically, the random primer concentration is preferably 40 to 60 microM when the random primers comprise 9 to 10 bases. It is preferable that a random primer concentration satisfy the condition represented by an inequation: $y > 3E + 08x^{-6.974}$, provided that the nucleotide length of the random primer is represented by x and the random primer concentration is represented by y, and 100 microM or lower, when the random primer comprises 10 to 14 bases. The random primer concentration is preferably 4 to 100 mM when the random primer comprises 14 to 18 bases. When a random primer comprises 18 to 28 bases, the random primer concentration is preferably 4 microM or higher, and it satisfies the condition represented by an inequation: $y < 8E + 08x^{-5.533}$. When a random primer comprises 28 to 29 bases, the random primer concentration is preferably 4 to 10 microM. The inequations $y > 3E + 08x^{-6.974}$ and $y < 8E + 08x^{-5.533}$ are

determined on the basis of the Microsoft Excel power approximation.

[0089] By prescribing the number of bases and the concentration of random primers within given ranges as described above, it was found that low-molecular-weight (100 to 500 bases) DNA fragments could be amplified with high reproducibility. For example, the accuracy of the data obtained via analysis of high-molecular-weight DNA fragments with the use of a next-generation sequencer is known to deteriorate to a significant extent. As described in this example, the number of bases and the concentration of random primers may be prescribed within given ranges, so that a DNA library with a molecular size suitable for analysis with a next-generation sequencer can be produced with satisfactory reproducibility, and such DNA library can be suitable for marker analysis with the use of a next-generation sequencer.

4.7 Number of random primers

As described in 3.7 above, 1, 2, 3, 12, 24, or 48 types of random primers (concentration: 60 microM) were used to produce a DNA library, and the results are shown in Figs. 83 to 94. The results are summarized in Table 27.

[0090] [Table 27]

Number of random primers	Repeat	Fig. No.	Correlational coefficient (ρ)
1	First	Fig. 83	0.984
	Second	Fig. 84	
2	First	Fig. 85	0.968
	Second	Fig. 86	
3	First	Fig. 87	0.974
	Second	Fig. 88	
12	First	Fig. 89	0.993
	Second	Fig. 90	
24	First	Fig. 91	0.986
	Second	Fig. 92	
48	First	Fig. 93	0.978
	Second	Fig. 94	

As shown in Figs. 83 to 94, it was found that low-molecular-weight DNA fragments could be amplified with the use of any of 1, 2, 3, 12, 24, or 48 types of random primers while achieving very high reproducibility. As the number of types of random primers increases, in particular, a peak in the electrophoretic pattern lowers, and a deviation is likely to disappear.

4.8 Random primer sequence

As described in 3.8 above, DNA libraries were produced with the use of sets of random primers shown in Tables 2 to 6 (i.e., 10-base primer B, 10-base primer C, 10-base primer D, 10-base primer E, and 10-base primer F), and the results are shown

in Figs. 95 to 104. The results are summarized in Table 28.

[0091] [Table 28]

Set of random primers	Repeat	Fig. No.	Correlational coefficient (ρ)
10-base primers B	First	Fig. 95	0.916
	Second	Fig. 96	
10-base primers C	First	Fig. 97	0.965
	Second	Fig. 98	
10-base primers D	First	Fig. 99	0.986
	Second	Fig. 100	
10-base primers E	First	Fig. 101	0.983
	Second	Fig. 102	
10-base primers F	First	Fig. 103	0.988
	Second	Fig. 104	

As shown in Figs. 95 to 104, it was found that low-molecular-weight DNA fragments could be amplified with the use of any sets of 10-base primer B, 10-base primer C, 10-base primer D, 10-base primer E, or 10-base primer F while achieving very high reproducibility.

4.9 Production of human DNA library

As described in 3.9 above, a DNA library was produced with the use of human-derived genomic DNA and random primers at a final concentration of 60 microM (10-base primer A), and the results are shown in Figs. 105 and 106. Fig. 105 shows the results of the first repeated experiment, and Fig. 106 shows the results of the second repeated experiment. As shown in Figs. 105 and 106, it was found that low-molecular-weight DNA fragments could be amplified while achieving very high reproducibility even if human-derived genomic DNA was used.

Example 2

[0092] In Example 2, a DNA probe was designed in accordance with the step schematically shown in Fig. 107, and a DNA microarray comprising the designed DNA probe was produced. In this example, whether or not a DNA marker could be detected with the use of such DNA microarray was examined.

[0093] In this example, a DNA library was produced in the same manner as described in 3.2.1 of Example 1, except that the random primers comprising 10 bases shown in Table 1 and 30 ng of genomic DNAs of the sugarcane varieties NiF8 and Ni9 were used. In this example, also, a sequence library was produced in the same manner as described in 3.2.2 of Example 1 and the sequence library was subjected to MiSeq analysis in the same manner as described in 3.2.3.

[0094] In this example, 306,176 types of DNA probes comprising 50 to 60 bases were

designed on the basis of the sequence information of the DNA libraries of NiF8 and Ni9 obtained as a result of MiSeq analysis, so as to adjust a TM at around 80 degrees C. The sequences of the designed DNA probes were compared with the sequence information of NiF8 and Ni9, and 9,587 types of probes peculiar to NiF8, which are not found in the Ni9 DNA library, and 9,422 types of probes peculiar to Ni9, which are not found in the NiF8 DNA library, were selected. On the bases of a total of 19,002 types of the selected DNA probes, production of G3 CGH 8×60K Microarrays was consigned to Agilent Technologies, Inc.

- [0095] With the use of the DNA microarrays thus produced, DNA libraries produced from NiF8, Ni9, and 22 hybrid progeny lines were subjected to detection.
- [0096] DNA libraries of NiF8, Ni9, and 22 hybrid progeny lines were produced in the same manner as described in 3.2.1 of Example 1. Two DNA libraries were produced for Ni9 and for 2 hybrid progeny lines (i.e., Fl_01 and Fl_02), so as to obtain the repeated data. The DNA libraries were fluorescently labeled with the use of Cy3-Random Nonamers of the NimbleGen One-Color DNA Labeling Kit in accordance with the NimbleGen Arrays User's Guide.
- [0097] With the use of the DNA microarrays and the fluorescently-labeled DNA libraries, subsequently, hybridization was carried out in accordance with the array-comparative genomic hybridization (array-CGH) method using the Agilent in-situ oligo-DNA microarray kit. Subsequently, signals on the DNA microarrays when a relevant DNA library was used were detected with the use of the SureScan scanner.
- [0098] On the basis of the signals detected for NiF8, Ni9, and 22 hybrid progeny lines, 7,140 types of DNA probes exhibiting clear signal intensities were identified. DNA fragments corresponding to such DNA probes can be used as NiF8 markers and Ni9 markers. In this example, genotype data were obtained on the basis of signals obtained from DNA probes corresponding to the NiF8 markers and the Ni9 markers, genotype data obtained through repeated measurements of two hybrid progeny lines (Fl_01 and Fl_02) were compared, and the accuracy for genotype identification was evaluated on the basis of the data reproducibility.
- [0099] In this example, genotype data were obtained with the use of PCR markers in order to compare such data with the results of the DNA microarray experiment described above. Specifically, the primers described in 3.5 of Example 1 (Table 22) were used for the 3 NiF8 markers and the 3 Ni9 markers described in 3.5 of Example 1 (i.e., a total of 6 markers). PCR and electrophoresis were performed in the manner as described in 3.5.2 of Example 1, and the results were compared with the signals obtained from the DNA microarray.
- [0100] In this example, the DNA probes shown below were designed for the 6 markers shown in Table 22 (Table 29).

[0101] [Table 29]

Marker name	DNA probe sequence
N80521152	CACACACCATGAAGCTTGAACATAATTAACATTCTCAAACATAATTAACAAGCATGCAAGCA (SEQ ID NO:2041)
N80997192	CAAGTCCTCAATGTCATAGGCGAGATCGCAGTAGTTCTGTAACCATTCCTGCTAAACTG (SEQ ID NO:2042)
N80533142	GTTTATCAAGATGGGTCATCGAGCTCTGGTGTCTTCAACCTTCTTGACATCAACTTCTC (SEQ ID NO:2043)
N91552391	CTGAAGCTCTAGGTATGCCTCTTCATCTCCCTGCACCTCTGGTGCTAGCA (SEQ ID NO:2044)
N91653962	CTGTCTGCCATTGCCATGTGAGACAAGGAAATCTACTTCACCCCATCTATCGA (SEQ ID NO:2045)
N91124801	TAAGATTAACTATGAACAAATTCACGGGTCCGATTCCTTTGGGATTTCAGCTTGCAAGA (SEQ ID NO:2046)

Results and Examination

[0102]

DNA microarray analysis

[0103] The sugarcane varieties NiF8 and Ni9 and 22 hybrid progeny lines were analyzed with the use of the DNA microarray produced in the manner described above. As a result, 3,570 markers exhibiting apparently different signals between parent varieties were identified as shown in Table 30 (Fig. 108).

[0104]

[Table 30]

	Number of markers	F1_01		F1_02		Total	
		Consistency	Reproducibility	Consistency	Reproducibility	Consistency	Reproducibility
NiF8 type	1,695	1,695	100.00%	1,695	100.00%	3,390	100.00%
Ni9 type	1,875	1,874	99.95%	1,875	100.00%	3,749	99.97%
Total	3,570	3,569	99.97%	3,570	100.00%	7,139	99.99%

Concerning Ni9, signals obtained through repeated procedures were compared, and a

high correlation was found therebetween as a consequence (Fig. 109: $r = 0.9989$). On the basis of the results, the use of random primers at a high concentration was predicted to enable the production of a DNA library with excellent reproducibility and the use of a DNA probe was predicted to enable the detection of a DNA fragment contained in a DNA library (i.e., a marker).

- [0105] As a result of DNA microarray analysis using the 22 hybrid progeny lines, a total of 78,540 genotype data were obtained, and no missing values were observed for any markers. In order to evaluate the accuracy for genotype identification, the data obtained through repeated analyses of Fl_01 and those of Fl_02 were compared. As a result, all the data concerning the NiF8 markers were consistent. Concerning the Ni9 marker, a result concerning Fl_01 was different, although all the results concerning Fl_02 were consistent. With respect to all the markers, 7,139 data out of 7,140 genotype data were consistent; that is, a very high degree of reproducibility was observed (i.e., the degree of consistency: 99.99%).

Experiment for confirmation with the use of PCR marker

- [0106] Concerning a total of 6 markers (i.e., 3 NiF8 markers and 3 Ni9 markers), primers designed on the basis of the paired-end marker sequence information were used to subject NiF8, Ni9, and 22 hybrid progeny lines to PCR, the genotypes thereof were identified via electrophoresis, and the results were compared with the signals obtained from the DNA microarray. Fig. 110 shows the results of measurement of signal levels obtained from the DNA probes corresponding to the marker (N80521152), Fig. 111 shows the results of measurement of signal levels obtained from the DNA probes reacting with the marker (N80997192), Fig. 112 shows the results of measurement of signal levels obtained from the DNA probes reacting with the marker (N80533142), Fig. 113 shows the results of measurement of signal levels obtained from the DNA probes reacting with the marker (N91552391), Fig. 114 shows the results of measurement of signal levels obtained from the DNA probes reacting with the marker (N91653962), and Fig. 115 shows the results of measurement of signal levels obtained from the DNA probes reacting with the marker (N91124801). Fig. 55 shows the electrophoretic pattern for the marker (N80521152), Fig. 57 shows the electrophoretic pattern for the marker (N80997192), Fig. 59 shows the electrophoretic pattern for the marker (N80533142), Fig. 61 shows the electrophoretic pattern for the marker (N91552391), Fig. 63 shows the electrophoretic pattern for the marker (N91653962), and Fig. 65 shows the electrophoretic pattern for the marker (N91124801). As a result of comparison of the results of electrophoretic patterns and the results of measurement of signal values obtained from DNA probes, the results for all markers are found to be consistent among all the markers. The results demonstrate that a DNA probe may be designed on the basis of the nucleotide sequence of the DNA fragment contained in the

DNA library resulting from the use of a random primer at a high concentration, so that the DNA fragment can be detected with high accuracy.

{CLAIMS}

{Claim 1}

A method for producing a DNA probe comprising steps of:

conducting a nucleic acid amplification reaction in a reaction solution containing genomic DNA and a random primer having 9-30 bases using genomic DNA as a template to obtain DNA fragments, wherein when the random primer comprises 9 to 10 bases, the concentration of the random primer is 40 to 60 microM; when the random primer comprises 10 to 14 bases, the concentration of the random primer satisfy the conditions defined by an inequation: $y > 3E + 08x^{-6.974}$ and be 100 microM or less, provided that the nucleotide length of the random primer is represented by "x" and the concentration of the random primer is represented by "y"; when the random primer comprises 14 to 18 bases, the concentration of the random primer is 4 to 100 microM; when the random primer comprises 18 to 28 bases, the concentration of such random primer be 4 microM or more and satisfy the conditions defined by an inequation: $y < 8E + 08x^{-5.533}$; when the random primer comprises 28 to 29 bases, the concentration of the random primer is 6 to 10 microM; when the random primer comprises 30 bases, the concentration of the random primer is 6 microM;

determining the nucleotide sequence of the obtained DNA fragments; and

designing a DNA probe used for detecting a DNA fragment obtained in the above step on the basis of the nucleotide sequence of the DNA fragments, the DNA probe comprising a nucleotide sequence complementary to the nucleotide sequence the DNA fragment.

{Claim 2}

The method for producing a DNA probe according to claim 1, wherein DNA fragments are obtained from a plurality of different genomic DNAs with the use of the random primers and, on the basis of the nucleotide sequence of the DNA fragments, the DNA probe containing regions different between the genomic DNAs is designed.

{Claim 3}

The method for producing a DNA probe according to claim 1, wherein the nucleotide sequence of the DNA fragment is compared with a known nucleotide sequence and the DNA probe containing a region different from that of the known nucleotide sequence is

designed.

{Claim 4}

The method for producing a DNA probe according to claim 1, wherein the DNA fragment contains 100 to 500 nucleotides.

{Claim 5}

A method for analyzing genomic DNA comprising steps of: conducting a nucleic acid amplification reaction with the use of the genomic DNA subjected to analysis and the random primer of claim 1 to obtain a DNA fragment; bringing the DNA probe produced by the method for producing a DNA probe according to any one of claims 1 to 4 into contact with the DNA fragment derived from the genomic DNA subjected to analysis; and detecting hybridization occurring between the DNA probe and the DNA fragment.

{Claim 6}

The method for analyzing genomic DNA according to claim 5, wherein the DNA fragment derived from genomic DNA is a DNA marker and the presence or absence of the DNA marker is detected with the use of the DNA probe.