

BASF Plant Science GmbH

AMENDED REPORT

**Structure and DNA sequence of Insert and Flanking
genomic region of
Potato Event EH92-527-1**

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The report was amended to add additional pertinent information.

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Structure and DNA sequence of Insert and Flanking genomic region of Potato Event EH92-527-1

Summary

The purpose of the investigation presented was to determine and disclose the structure and DNA sequence of the insert including flanking potato chromosomal DNA sequence in potato event EH92-527-1. Using chromosome walking and PCR it was shown that the insert had the structure of an inverted repeat in a tail-to-tail arrangement with two right border regions as junctions to the potato chromosomal DNA. At the tail-to-tail fusion a short DNA sequence is found, which is present on opposite strands in two regions of the *gbss* antisense fragment of transformation vector pHoxwG as two patches of microhomology. Upon integration a minor DNA segment (27 bp) at the right T-DNA border was deleted. The structural rearrangement at the left border region led to the deletion of a fragment containing the T-DNA left border repeat and the nopaline synthase polyadenylation sequence connected to the *gbss* antisense gene fragment. No DNA sequences other than T-DNA were found within the tail-to-tail fusion insert. The inverted repeat extends into potato chromosomal DNA, thus the flanking DNA sequence on both sides of the insert were the same. The complete DNA sequence of the insert together with 2156 bp of potato flanking sequence is presented. Southern blot analysis results were consistent with the inverted repeat region extending into potato chromosomal DNA.

The structure of the insert in potato line EH92-527-1 including the same potato chromosomal DNA being present on either side of the insert is consistent with being the result of a DNA repair process occurring upon integration of the T-DNA of transformation vector pHoxwG.

Genomic DNA isolated in 1998 and 2005 showed the same hybridization patterns upon Southern blot analysis for four different restriction enzyme combinations, providing evidence for the genetic stability of the insert structure over multiple generations of clonally propagated EH92-527-1.

Introduction

Potatoes have been modified for altered starch content so that the ratio of amylopectin to amylose produced in the potato has been altered to a level of > 98 % amylopectin. This amylopectin starch is desirable for its properties in industrial applications. Potato variety Prevalent, was transformed via *Agrobacterium* with an antisense *gbss* (granule bound starch synthase) gene that caused reduced expression of a granule bound starch synthase gene. The potato transformant that gave rise to the genetically modified (GM) clone analyzed here, designated EH92-527-1, was transformed with the plasmid pHoxwG containing, within the T-DNA borders the *gbss* antisense gene under the control of the potato *gbss* promoter and the *nptII* (neomycin

phosphotransferase II) gene under control of the *nos* (nopaline synthase) promoter. The purpose of this study was to determine the structure and DNA sequence of the insert and the DNA sequence of the flanking potato genomic region.

Materials and Methods

DNA isolation

Total DNA was isolated from potato leaves according to Nucleon PhytoPure (Amersham Biosciences, Piscataway, NJ USA). Total DNA noted as isolated in 1998 was isolated according to Haymes (1996).

Amplification of insert related DNA fragments

Internal structures of the insert in event EH92-527-1 were amplified and cloned using Advantage™ Genomic PCR Kit (Clontech, Palo Alto, CA USA) and Advantage™ PCR Cloning Kit (Clontech). Specific primers used for amplification of fragments containing insert sequence are listed.

Primer name	Primer sequence
Kom2.1	5'TCCCTTAGCAGAAGGCAACTG3'
Kom2.2	5'CAAAAATGCTCCACTGACGTTTC3'
Kom6.1	5'AGACCTCCAACCTTTGAAGCTC3'
Kom6.2	5'GTTAGCTCACTCATTAGGCACC3'
Kom15	5'GATGTTTCGCTTGGTGGTC3'
Kom16	5'GGAAGTACAGAACCGCAAC3'

Internal fragments of the insert were amplified in the reaction setup:

BD Advantage Biosciences, Clontech

1 µl gDNA 527-1 (250 ng)
5 µl BD Advantage 2 PCR Buffer
1 µl of each primer (25mM)
1 µl 50X dNTP Mix
1 µl BD Advantage 2 Polymerase Mix
ddH₂O to a total volume of 50 µl

Amplifications were performed in an Eppendorf Mastercycler:

Primers KOM2.1 and KOM2.2

1. 95°C 1 min
2. 95°C 30 s
3. 62°C 30 s
4. 68°C 3 min

Goto 2 repeat 30

5. 68°C 10 min

Hold at 4°C

Primers KOM6.1 and KOM6.2

1. 95°C 1 min
2. 95°C 30 s
3. 54°C 30 s
4. 68°C 3 min

Goto 2 repeat 30

5. 68°C 10 min

Hold at 4°C

Primers KOM15 and KOM16

1. 95°C 1 min
2. 95°C 30 s
3. 62°C 30 s
4. 68°C 3 min

Goto 2 repeat 30

5. 68°C 10 min

Hold at 4°C

Isolation of EH92-527-1 insert and determination of flanking sequence.

In order to clarify the structure of the insert and extend the analysis of DNA sequences into the potato genome, reactions using GenomeWalker™ were performed.

GenomeWalker™ libraries for the purpose of isolating DNA sequence associated with the insert of event EH-92-527-1 were produced by the digestion of genomic DNA with restriction enzymes yielding blunt ended DNA fragments and the subsequent ligation of adaptor fragments to the generated blunt ended genomic fragments. The structure of the produced libraries can be utilized to amplify fragments of partly unknown DNA sequence by PCR. In a first PCR reaction, one primer is specific for known DNA sequence while the second primer is targeting the adaptor fragment DNA sequence ligated to the genomic DNA. In a second PCR reaction, a nested specific primer targeting known sequence is used together with a nested adaptor primer targeting the adaptor DNA sequence. The second PCR step is performed in order to increase the probability of intended fragments being amplified. Several libraries, using different restriction enzymes, are produced to ensure that fragments can be produced by PCR at least from some library, which is dependent on organism and local genome specific restriction patterns.

Internal structures and junctions between the insert and potato chromosomal DNA were amplified and cloned using Universal GenomeWalker™ Kit (Clontech), Advantage™ Genomic PCR Kit (Clontech) and Advantage™ PCR Cloning Kit (Clontech). Libraries were made of total DNA from EH92-527-1 for the Universal GenomeWalker™ Kit using the restriction enzymes *DraI*, *EcoRV*, *HpaI*, *MscI*, *PvuII*, *Scal* and *StuI* (New England Biolabs, Beverly MA, USA). The approach used in the GenomeWalker™ kit provides the basis for walking upstream or downstream in a genomic DNA from a known DNA sequence (Siebert et al. 1995a; Siebert et al. 1995b).

Specific primers, primary as well as nested, used for amplification of fragments containing internal structures as well as junctions to chromosomal DNA are listed.

Primer name	Primer sequence
LB1	5'GATACTGGCGTTGCGGTTGAGGTACATC3'
LB2	5'GCTACTTGAAGTCAATGTACCAGTCCAG3'
Kom8	5'GCGGATAACAATTTACACAGGAAACAG3'
Kom9	5'TCCACAGTTGCCTTCTGCTAAGGGATAG3'
Kom12	5'GATAGTGACCTTAGGCGACTTTTGAAC3'
Kom13	5'TGTCAGTTCCAAACGTAACACGGCTTG3'
Kom23	5'AGTATGGGCTCACTGTAACCACCTATG3'
Kom28	5'GCTTCAAAAGTTGGAGGACTACCACCAGC3'
Kom29	5'TACAAAGATGCTTGGGATACTGGCGTTGC3'
Kom30	5'TTGCTTTCTGCATCCATAACATTGCCTAC3'
Kom31	5'GGGGTTCTTTTGATTTTCATTGATGGGTATG3'
Kom32:	5'CGTAATCATGGTCATAGCTGTTTCCTGTG3'
Kom33:	5'CCGCTCACAATCCACACAACATACGAG3'
Kom55R	5'TACTGGCGTTGCGGTTGAGGTACATCTTC3'
Kom55RN	5'GTTTTTGTGGACCACCCAATGTTCTTGAG3'
Kom56F	5'CAATGTTATGGATGCAGAAAGCAACCTGG3'
Kom56FN	5'CATTGACTTCAAGTAGCAAGGAATGAGAGC3'
Kom56R	5'AAGGGAGTTCAAGCAAGATTGACACACTC3'
Kom56RN	5'AGGTGTCATCACATAAGGTTACGGTAAG3'
L1.2F	5'CATCAGAGCAGCCGATTGTCTG3'
L.3R	5'AACCAGGATCAACATCCAGCG3'

Reactions were performed as described in the protocols for Universal GenomeWalker™ Kit (Clontech) and Advantage™ Genomic PCR Kit (Clontech).

DNA sequencing was performed on a service basis by MWG-Biotech, www.mwg-biotech.com

Individual sequences were assembled using ContigExpress of the Vector NTI suite, Informax, www.invitrogen.com.

Southern blot analysis

Southern blot analysis was used to verify the structure of inserted DNA in EH92-527-1 and to determine stability of the insert over time. Genomic DNA was isolated from leaf tissue of EH92-527-1 and parental variety Prevalent.

For investigation of the insert, 10 µg of isolated DNA was digested with *EcoRI*, *EcoRV*, *MscI*, *HindIII*, *BspHI*, *MfeI* and *HpaI*, in single reactions or in different combinations of the enzymes (New England Biolabs), and separated by gel electrophoresis for 2 to 3 hours. The DNA was transferred onto membranes (Hybond N+, Amersham Biosciences), and hybridized with different probes of the T-DNA of pHoxwG (*nptII*, *gbss* promoter, part of *gbss* antisense fragment or *nos* promoter, *Figure 4*) using DIG Easy Hyb and PCR DIG Probe Synthesis kit (Roche Applied Science). The following wash, block and detection steps were made with solutions and buffers from DIG Wash and Block buffer set and DIG DNA Labeling and Detection kit (Roche Applied Science) according to the manufacturer's instructions. The membranes were exposed to Hyperfilm-ECL (Amersham Biosciences). Molecular markers used were DNA Molecular Weight Marker II, DIG-labeled and DNA Molecular Weight Marker III, DIG-labeled (Roche Applied Science).

Results

Amplification of insert related DNA fragments

Internal insert DNA fragments were amplified using the T-DNA sequence of pHoxwG as a guide as shown in *Figure 1*. Primer combinations KOM2.1-KOM2.2, KOM6.1-KOM6.2 and KOM15-KOM16 all yielded fragments of the expected size upon amplification of genomic DNA isolated from potato event EH92-527-1. The DNA sequences of the isolated fragments were consistent with transformation vector pHoxwG in the regions amplified. Attempts to amplify fragments towards the left border region were unsuccessful (data not shown).

Seven genomic libraries were constructed in the Universal GenomeWalker™ format using DNA isolated from event EH92-527-1, which was restriction digested with *DraI*, *EcoRV*, *HpaI*, *MscI*, *PvuII*, *ScaI* and *StuI*. Primer KOM8 and nested primer KOM9 were used to amplify a fragment which contained one partial *gbss* antisense DNA segment and an inverted *gbss* DNA segment. At the site of inversion a short DNA sequence was found that is present on opposite strands in two regions of the *gbss* antisense fragment of transformation vector pHoxwG as two patches of microhomology that are shown in *Figure 2*. Further primers were designed for targeting and amplifying unknown DNA sequence distal to the *gbss* fragment found as an inversion. Primer KOM28 and nested primer KOM29 were used to generate a 1909 bp fragment from the *HpaI* library, which contained the previously known inversion but further extending until the start of the *gbss* antisense segment and 3' DNA sequence of the *gbss* promoter. This shows that in addition to the inversion there is inverted repeated DNA sequence contained in the insert, since the 5' end of the *gbss* antisense segment as well as the *gbss* promoter already had been determined as constituents of the insert upstream of the amplified fragment using the nested KOM29 primer.

Two further primer pairs were designed that targeted the inversion and could thus only amplify DNA sequence downstream of known T-DNA sequence. Primer LB1 and nested primer LB2 yielded two different fragments of 1391 bp and 2503 bp upon amplification of the *EcoRV* library, which showed that the inverted repeat structure extended beyond the start of the *gbss* promoter. Primer KOM30 and nested primer KOM31 were used to amplify one fragment each from the *EcoRV*, *MscI* and *PvuII* libraries, all containing DNA sequence that provided evidence for an inverted repeat structure of the insert. All fragments, amplified by three different specific primers and determined to contain DNA sequence originating from the insert, were consistent with that the insert contain an inverted repeat structure derived from DNA sequence of transformation vector pHoxwG.

Primer KOM32 and nested primer KOM33 as well as primer KOM12 with nested primer KOM13 can target both parts of the inverted repeats but, notably, amplifications using these primer combinations yielded the same sequence structures from five different libraries strongly indicating that the inverted repeat structure extends until the junction of the insert towards assumed potato chromosomal DNA. Furthermore, all fragments isolated contained the same DNA sequence flanking the insert. This established that two truncated T-DNA fragments of different lengths were

fused tail-to-tail thus forming an inverted repeat. Furthermore amplification of flanking sequence yielded the same DNA sequence of all fragments isolated from the GenomeWalker™ libraries indicating that the inverted repeat structure extended into potato chromosomal DNA. Only T-DNA sequence was found in the insert. The structure of the insert of potato event EH92-527-1 including flanking DNA sequence is shown in *Figure 3*. Primers used for the amplification of fragments from GenomeWalker™ libraries are also shown in *Figure 3*.

Southern Blot analysis

Southern blot analysis was also used to investigate the structure of the insert. Preliminary Southern blot experiments consistently yielded one extra band when analyzing potato line EH92-527-1 in comparison with its parental variety Prevalent independent of probe used (data not shown). However from the DNA sequence of the insert derived from amplified fragments an asymmetrically located *EcoRI* site was found (*Figure 3*) that when utilized in combination with other restriction enzymes distinguished between the two repeats of the inverted repeat structure. Results of Southern blot experiments as shown in *Figures 4A to D* are summarized in *Table 1*.

Genomic DNA of EH92-527-1 and its parental variety Prevalent was digested with a number of restriction enzymes, *EcoRI*, *EcoRV*, *HindIII*, *BspHI*, and *MfeI*, in single reactions or in different combinations of the enzymes. All enzymes except *MfeI* cut within the T-DNA (*Figure 4A*) and within the determined structure of the insert (*Figure 3*). The next distal cut site would then be located in the plant genome. The distance to the genomic restriction enzyme site depended on the integration site of the insert. *Figure 5 A to D* show results from Southern blots of different restriction enzyme digests of parental variety Prevalent and potato event EH92-527-1 probed with the different probes representing different portions of pHoxwG T-DNA shown in *Figure 4B*. *Figure 5A* shows results from probing *EcoRI* and *EcoRI-HindIII* digested genomic DNA with a fragment corresponding to the *gbss* promoter. In the *EcoRI* digest one extra band was visualized in EH92-527-1 in comparison to Prevalent.¹ The size of the migrating band was in a region where separation is difficult to obtain and to clearly distinguish whether there is one band or two or more bands with similar migration. In the *EcoRI-HindIII* digest two extra bands corresponding to approximately 3000 bp and 1700 bp could be visualized. This result is consistent with the determined structure of the insert as shown in *Figure 3*, where the predicted results of the Southern blot would yield two bands corresponding to 2801 bp and 1723 bp, respectively. Using the *gbss* promoter as a probe also yielded signals in parental variety Prevalent with corresponding signals detected in EH92-527-1 due to the potato origin of the *gbss* promoter. The two lower bands of approximately 1300 bp, visible in both EH92-527-1 and Prevalent of the *EcoRI-HindIII* digest, correspond to endogenous alleles of the *gbss* promoter, which can yield fragments from 1200 to 1350 bp depending on allelic variation.

Figure 5B shows results from probing *EcoRV* digested genomic DNA with a fragment corresponding to the *nptII* gene. In the *EcoRV* digestion one band corresponding to approximately 3500 bp could be detected in EH92-527-1, which was not detected in Prevalent. This result is consistent with the determined structure of the insert as

¹ Annex B as an amendment to this report clarifies an apparent discrepancy of the Southern blot analysis presented here as compared to previously submitted data in Notification C/SE/96/3501 according to Directive 90/220/EEC.

shown in *Figure 3*, where the predicted results of the Southern blot would yield two bands both corresponding to 3511 bp.

Figure 5C shows results from probing *EcoRI-BspHI* and *EcoRI-MfeI* digested genomic DNA with a fragment corresponding to the *nos* promoter. In the *EcoRI-BspHI* and *EcoRI-MfeI* digestions two bands in each digest could be detected in EH92-527-1, which were not detected in Prevalent. This result is consistent with the structure of the insert as shown in *Figure 3*, where the predicted results of the Southern blot of the *EcoRI-BspHI* digest would yield two bands corresponding to 4152 bp and 5140 bp and is furthermore consistent with the predicted results for the *EcoRI-MfeI* digest, which would yield two bands corresponding to 4306 bp and 5294 bp. *BspHI* would, according to *Figure 3*, digest the genomic DNA of EH92-527-1 at the distal ends of the insert while *MfeI* would digest the genomic DNA of EH92-527-1 in the flanking region outside the distal ends of the insert.

Figure 5D shows results from probing *EcoRI*, *EcoRI-MfeI*, *EcoRI-BspHI* and *EcoRV* digested genomic DNA with a fragment corresponding to the *nptII* gene. These results confirm the results shown in *Figure 5B* and *Figure 5C*. Furthermore, the band seen for the *EcoRV* digest in *Figure 5D* yielded a stronger signal than other bands obtained from the Southern blot which provides evidence that the two expected fragments in the *EcoRV* digest co-migrated. This result is consistent with the structure shown in *Figure 3* with the same flanking sequence being present on both sides of the insert in potato event EH92-527-1.

Results of Southern blot experiments as shown in *Figures 5A* to *D* are summarized in *Table 1*.

Determination of insert and flanking DNA sequence

DNA sequence was assembled from DNA sequence determinations of fragments amplified from GenomeWalker™ libraries using primers, as shown in *Figure 3* and amplicons from PCR reactions using insert locus specific primers as shown in *Figure 1*. Multiple DNA sequence reactions covering all regions were conducted to reduce any potential errors caused by the DNA polymerase during the amplification reactions.

The flanking region was amplified in three independent PCR reactions using primers L1.2F and L1.3R. Cloned fragments (2453 bp) of the three independent reactions were subjected to DNA sequencing. The resulting DNA sequence is shown in *Figure 7*.

The insert was amplified as two overlapping fragments in three independent PCR reactions for each fragment by using primers KOM56R-KOM55R and KOM56F-KOM56R in a first reaction and KOM56RN-KOM55RN and KOM56FN-KOM56RN in a nested reaction. Primer annealing targets are shown in *Figure 6*. The use of these primers produce overlapping PCR fragments where KOM56R anneal to both flanking regions and primers KOM55R and KOM56F anneal to a DNA sequence of the *gbss* antisense fragment in the center of the insert that is not contained in the inverted repeat. Thus each reaction was specific and uniquely targeted one half of the inverted repeat structure of the insert in EH92-527-1 which further verifies the structure as shown in *Figure 3* and *Figure 6*. Three independent KOM56RN-KOM55RN

fragments and three independent KOM56FN-KOM56RN fragments were fully sequenced to allow the determination of a consensus sequence for the insert of EH92-527-1, sequence alignments are shown in *Figure 8* and *Figure 9* respectively. The consensus sequences corresponding to the KOM56RN-KOM55RN fragment and the KOM56FN-KOM56RN fragment were assembled and aligned to a predicted DNA sequence derived from T-DNA sequence of transformation vector pHoxwG, which is shown in *Figure 10*. The determined insert DNA sequence was found to be completely consistent with DNA sequence derived from the T-DNA sequence of transformation vector pHoxwG with no DNA base deviations.

Consensus DNA sequences were used to assemble the complete DNA sequence of the insert structure that is shown in *Figure 11* including the flanking DNA sequence ending at the *EcoRV* site known to be present by Southern blotting analysis (see *Figure 5B* and *Figure 5D*) thus the presented flanking sequence is shorter in *Figure 11* (2156bp) as compared to *Figure 7* (2386 bp).

Stability of insert

Southern blot analysis was used to determine the stability of the insert structure over time where the asymmetrically located *EcoRI* site was utilized alone or in combination with other restriction sites to provide different degrees of resolution and fragment sizes for probe hybridization. Additionally the determined *EcoRV* site in the insert flanking region was utilized. Genomic DNA of EH92-527-1 isolated in 1998 and 2005 was digested with restriction enzyme *EcoRI*, *EcoRV* and combinations *EcoRI-BspHI*, *EcoRI-MfeI*. The results of genomic DNA restriction digested as above and probed with a fragment corresponding to the *nptII* gene are shown in *Figure 12*. The hybridization pattern and thereby restriction pattern is consistent between the DNA isolated in 1998 and 2005 which provides evidence that no structural rearrangements have occurred over this time in the region of investigation and thus the context of the insert is stable.

Conclusions

All presented data are consistent with an inverted repeat structure in the insert of amylopectin potato clone EH92-527-1 extending into potato chromosomal DNA. Southern blot analyses provided complementary evidence for the insert organization suggested by the PCR and the chromosome walking results up to an *EcoRV* restriction site distal to the insert. 2156 bp of insert flanking DNA sequence up to the *EcoRV* restriction site was determined and is presented. No DNA base deviations were found in the insert region as compared to DNA sequence derived from the T-DNA sequence of transformation vector pHoxwG. All inserted DNA sequence was found to be of T-DNA origin and no other DNA was found interspersed among the inserted DNA.

Genomic DNA isolated in 1998 and 2005 was restriction digested and subjected to Southern blot analysis resulting in the same hybridization pattern over four different restriction enzyme combinations providing evidence for genetic stability of the insert over multiple generations of clonally propagated EH92-527-1 in the intervening seven years.

The right borders of the tail-to-tail inverted repeat structure of the insert are truncated, with the complete right border repeat and two further bases deleted. This junction is consistent with right border junctions that are suggested as repair of double-strand breaks (DSB) (Kumar & Fladung 2002). Repair of DSB in plants is commonly achieved by non-homologous end joining that recognize and align microhomologies between different strands of DNA (Gorbunova & Levy 1999). The inverted repeat structure of the insert is starting exactly at such an observed microhomology. DNA repair synthesis utilizing the microhomology on the *gbss* antisense fragment would explain the inverted repeat structure of the insert. DSBs have furthermore recently been suggested to be a major pathway for T-DNA integration in plants (Tzfira et al. 2004).

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Table 1. Summary results of Southern blot analysis

Southern blot	Digest	Probe	Expected bands from Figure 2.	Confirms structure determined by ChromosomeWalker libraries
4A	<i>EcoRI</i>	<i>gbss</i> promoter	na	
	<i>EcoRI-HindIII</i>	<i>gbss</i> promoter	1723 bp, 2801 bp	Yes
4B	<i>EcoRV</i>	<i>nptII</i> fragment	3511 bp	Yes
4C	<i>BspHI-EcoRI</i>	<i>nos</i> promoter	4152 bp, 5140 bp	Yes
	<i>MfeI-EcoRI</i>	<i>nos</i> promoter	4306 bp, 5294 bp	Yes
4D	<i>EcoRI</i>	<i>nptII</i> fragment	na	
	<i>EcoRI-MfeI</i>	<i>nptII</i> fragment	4152 bp, 5140 bp	Yes
	<i>EcoRI-BspHI</i>	<i>nptII</i> fragment	4306 bp, 5294 bp	Yes
	<i>EcoRV</i>	<i>nptII</i> fragment	3511 bp	Yes

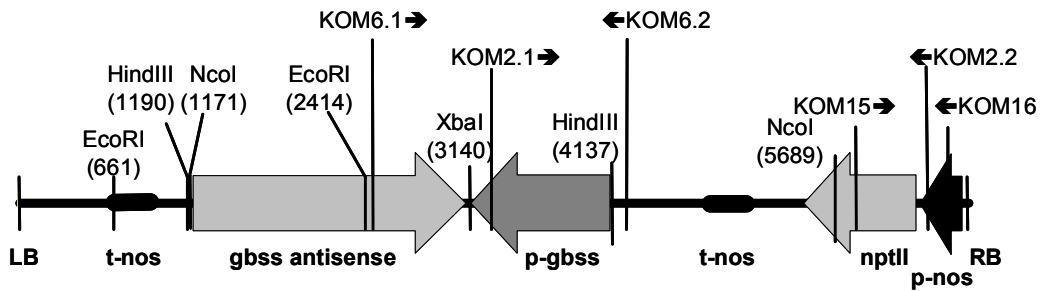


Figure 1. T-DNA of transformation vector pHoxwG (6637 bp). Primers used for the amplification of internal insert segments are indicated. Structural components noted, LB-left border repeat, t-nos-nopaline synthase polyadenylation sequence, gbss antisense fragment, gbss p-gbss-potato gbss promoter, t-nos-nopaline synthase polyadenylation sequence, nptII-coding sequence for aminoglycoside transferaseII, p-nos-nopaline synthase promoter, RB-right border repeat.

Micro IR 1. 5' AAAGTTGGAGGTCTGATT
 | | | | | | | |
Micro IR 2. 3' CAAGAACCACCTGATGGT

Figure 2. Patches of inverted repeat microhomology (Micro IR) available on the gbss antisense fragment of pHoxwG and which sequence is found at the site of inversion creating the inverted repeat structure of the insert in potato event EH92-527-1.

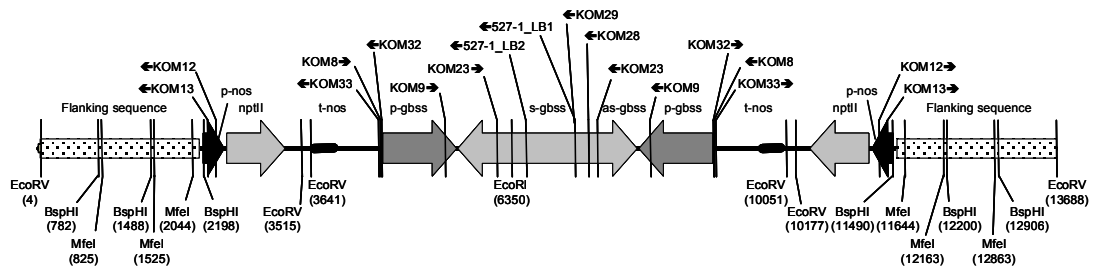
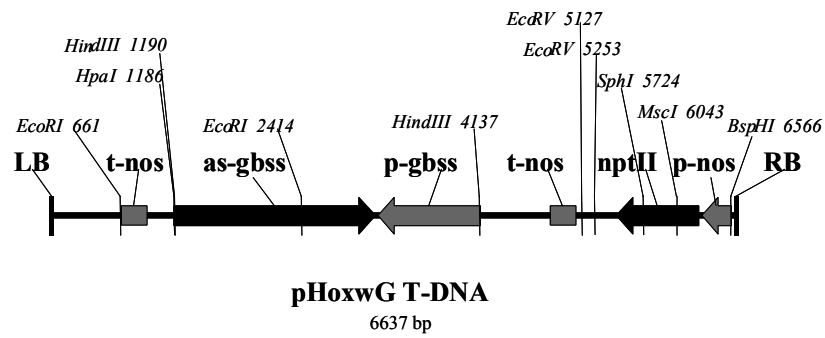


Figure 3. Determined structure of genetic insert (9378 bp) and flanking sequences of EH92-527-1. DNA segments outside the p-nos elements is 2156 bp potato chromosomal flanking DNA on each side of the insert. Primers used for amplification and their direction are indicated. Restriction sites utilized to digest genomic DNA for hybridization are indicated. Structural components noted, p-nos-nopaline synthase promoter, nptII -coding sequence for aminoglycoside phosphotransferase II, t-nos-nopaline synthase polyadenylation sequence, p-gbss-potato gbss promoter, s-gbss-truncated gbss antisense fragment, as-gbss-truncated gbss antisense fragment.

A



B

as-gbss probe

p-gbss probe

nptII probe

p-nos probe



Figure 4 A. T-DNA from pHoxwG used for *Agrobacterium* mediated potato transformation, for production of amylopectin lines. The T-DNA has a total size of 6637 bp. **B.** Probes used for Southern blot analyses for determination of T-DNA insert; *gbss* antisense fragment, *gbss* promoter, *nptII* gene, nos promoter. LB, Left border; t-nos, nos terminator; as-gbss, antisense fragment of granule bound starch synthase; p-gbss, granular bound starch synthase promoter; *nptII*, neomycin phosphotransferase II; p-nos, nos promoter; RB, right border.

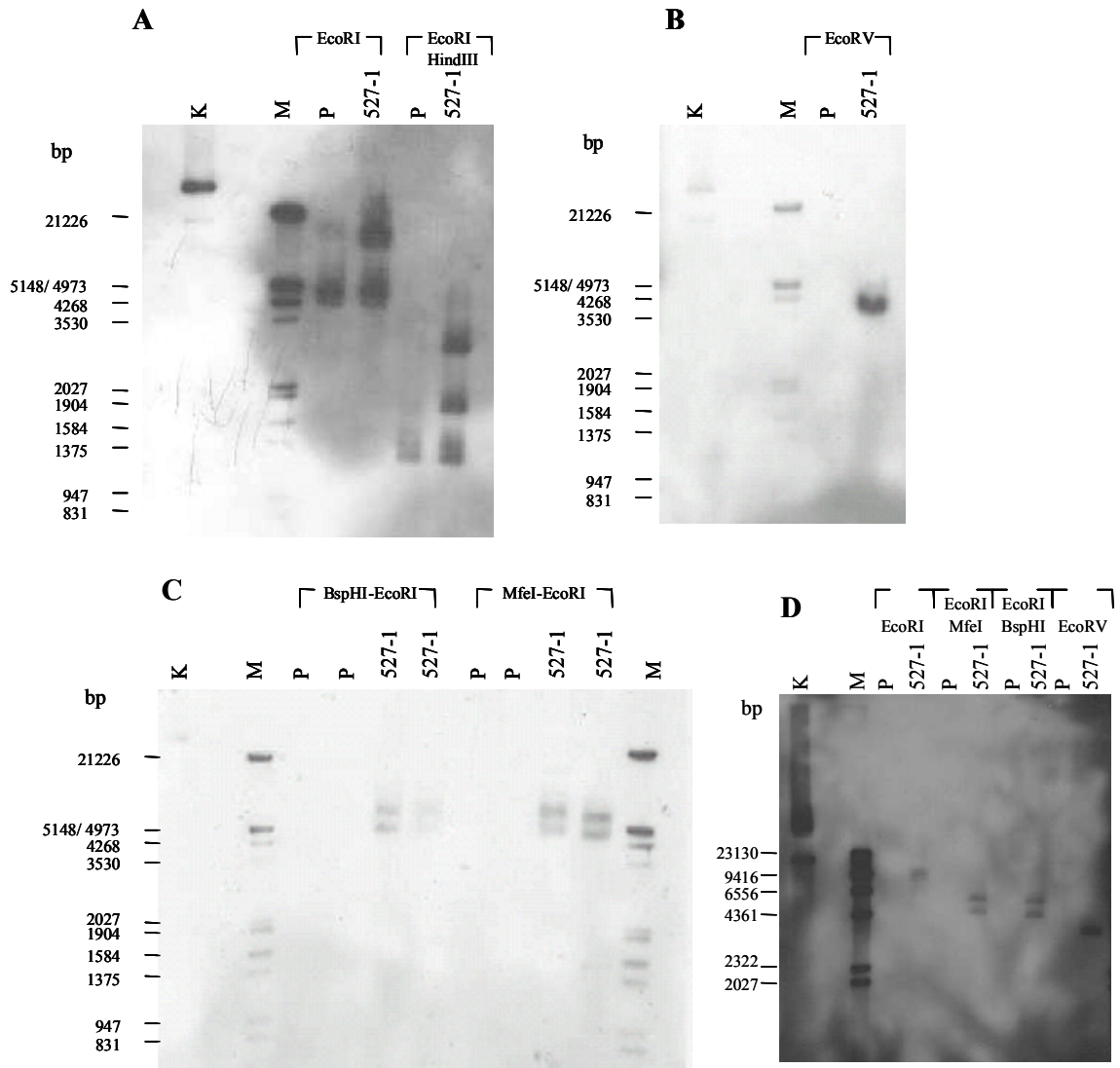


Figure 5. Southern blot analyses for determination of T-DNA insertions in EH92-527-1. 10 μ g total DNA from EH92-527-1 and the parental variety Prevalent was digested with various restriction enzymes and probed with fragments corresponding to pHoxwG T-DNA. A. *EcoRI* and *EcoRI-HindIII* digested total DNA of EH92-527-1 and Prevalent hybridized with a fragment corresponding to the *gbss* promoter. B. *EcoRV* digested total DNA of EH92-527-1 and Prevalent hybridized with a fragment corresponding to the *nptII* gene. C. *BspHI-EcoRI* and *MfeI-EcoRI* digested total DNA of EH92-527-1 and Prevalent hybridized with a fragment corresponding to the *nos* promoter. D. *EcoRI*, *EcoRI-MfeI*, *EcoRI-BspHI* and *EcoRV* and digested total DNA of EH92-527-1 and Prevalent hybridized with a fragment corresponding to the *nptII* gene. P, Prevalent; K, positive control; M, marker; bp, base pair.

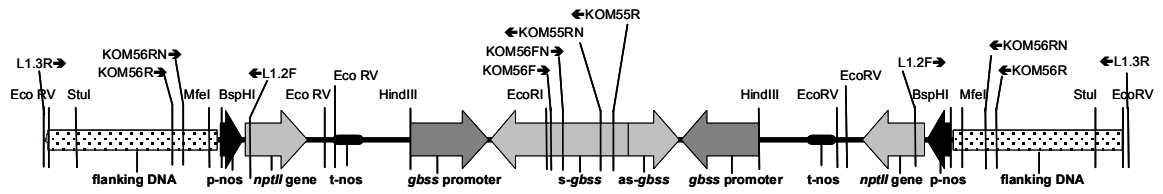


Figure 6. Structure of insert locus with primers used for amplification of specific fragments for verification of flanking DNA sequence, insert structure and complementary sequencing.

EcoRV

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1  CACGACAACC CAATACCCAT AGACCATCAA TCAAACACAT TAGTTCTAAA
51  ACCTCTCTCT CGAGCAAGCC AAGAACACAA AGGTAGAACT GTATTTGCAA
101 CTACAATTCT TAAATTA AAC CACAATTATT GATTGAACTC ACTTCTAAAT
151 AGCATTTAAT CTAACAATTA GCAATACCCA TAAACTAAAT CAGTCCATAA
201 TCACACCCCA AGAATTTGGA GTTTTAGCTA GATATCATAA AAAGATAAAA
251 GTCGTTACCA AATTGAGTTT CCATCAACTG GGTAAGATTG ATTTTGTCTT
301 TACAGTGGTC CAATTCAAAG AATCTCAAAG ACCCACTTCA AATTTCTCAA
351 AAGTGAAAAA CTTCAATTCT TCAAAAGCTAA AGGAAAACTA GAGAAAACTT
401 GTCTCATAGT TCAAAACTTA GTAAAAAATT GTTCTAAAAGA GTAATTGATA
451 CTAAACTAAA TGTTCAAAAA TGTATTTATA GTCACCAAAA ATGTGTTGCA
501 AAGTGTCACT CGGTGAAGCA AGTCGGGCTC GCCGAACCAC TCGGCGATCC
551 GCCCTTTGGT CATTTCTTTC GCCTCTCTGC CTAGGCCTTC AGCATCCTCA
601 AGTATGTAA CTTTGGGCGA TCCAACACTG CATCGCGGAA CCCTAGGCG
651 ATCCGCCGAC TTGGTTCTTT CCTTCAAGGC TTGGCACTCT AGAACTTGAG
701 GCGGTCAAGT AGCCATTCGG CAACTCGCCA AGTGGACTTG GCGATCACCA
751 TGCTTGCTTT TCTTCATTCT TTCAGCTTGC TTCGTTCTTT TTTGCAAATC
801 AGTGTCTTGT TTTTGTTCCT GAATCTCTAT ACCTAGAAAT CATCAGTTAT
851 TGGCACAATG AGGACACTAA TTCTATATAA ATAAAGCCCT AAATGAGTCC
901 AAATCTCGGA CTCATCAACA CCCCCA ACTT AAATTTTTCG TTGTCTCAA
951 GTAAA ACTCA AGTTCAGCAG TTCAAAAAAG ATGTCTCAA CAGTGCTACA
1001 CAAGACTCAA TCATGAATGC ACACAATAAG ACTCAAATTA CTCATGCAAG
1051 GATCAATTGT GCACTAAAAG ATTCAAGTTG TGACTCACCA TTATCAAAGA
1101 TTCTCAAATT CACAATACTT GCTTCAAATG CAAGTTCAAG CTCACAAAAG
1151 GTACTCCAAT GCCCTCACAC AAAGATGATT CCATATTCAC ACATAATTGT
1201 TCAACTTTT ATAGCTCCGG AATCACATAC AACTCTCACA CTCACAAAAGA
1251 TGAACACATG CATGACTTCA CCCATAGGTT TGCCCTTATT TTCCAATCAA
1301 CATTGCTTTC AGCTCACTCA AGGTCAAAAA GGCTTTTTCA AGGCTTGTAG
1351 CAGAGCTGAG TGCAAAGGCA TGGTCATTTA GGCTCGGTGG TTGCTATCCT
1401 CATAAAATGT GGTATGAACA TCACCTTCTT TCCTTTTCTT CAACATTCTC
1451 ATTCATGCTC AAATTCACCC CATTATTAC TTTTCATGGA ATACCGA ACT
1501 CCTTATTTCT TTTGCAACTT TCACA ACTTT ATTCCACAAC TTTTTCATTC
1551 TTTTCTTTT TCATTCTTCT TTTGTCTTTT TTTTGTATGG AGGGGTTCCA
1601 TATTTTTTCAA AACCATGGAT CAAATGGGGA CTTCTTTGCA TTTCTTGATT
1651 TACCTTCTTC TTTTACCACA CCCCCAACTT AGGCTTTTAG CCTAAGCTAT
1701 TCAAACAAAC CACACTTCAT GAGGAATATG GGTGAAAGGA TAAAGAGGGG
1751 TTACAATTGC ATCAAGTTTC TTCCAAGAAA AGGACAAGGC TCAAAAAGGG
1801 AGTTCAAGCA AGATTGACAC ACTCACAAGG TTGGCCACAA AAGAGGTATA
1851 TTGTCAAATT GTTTC ACTCT TAAAACCTGT TGCTAAGAT CATTC AAGAG
1901 CTTGCATCAC TTAGTCAACC GGACCAACGG GGTA AATTCT AGGTGTCATC
1951 ACATAAGGTT CACGGTAAGC TCATCACACA AGGCATTGGC ACCAATATCA
2001 AAC AAGACTC CACACTTTTCG CTAGTGTGCA ATGTT CATCA CAAAAGACTC
2051 ATTCAATAAC CGGCTAGTTA CAATGAGATG CAAAAAGTTC ACATATTATC
2101 TATGCAACTT TATTTAGCAT CATCATAGCC GTACATT CAT TTTTGTTCGA
2151 TTAAGAGCAC TATTCAAGTC ATCGGTATTG ATCATAACCG ATACTCAAAT
2201 TTGCAAAAAGA ACAACCACAA TCAAAACAAA TAAGAGGTGG CAAAAATTTT
2251 CAGAAGGGTC AAAAACCATT TACAATTGAA ACAAGGAGTC ATAAGCTCAA
2301 ACATCCACAA AACAGTGTC AAACACAATT TACAGCACAA AAACCAATA
2351 TATAAACAAA AATGATAATC ACAAGAGGTA GGTATGCACT GATAGTTTAA
2401 ACTGAAGGCG GGAAACGACA ATCTGATCAT GAGCGGAGAA TTAAGGGAGT
2451 CAC

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Figure 7. DNA sequence flanking the insert of potato event EH92-527-1. Flanking DNA sequence is shown in bold and insert DNA sequence is shown in italics.

		1	50
KOM5556R_1	(1)	AGGTGTCATCACATAAGGTTACGGTAAGCTCATCACACAAGGCATTGGC	
KOM5556R_2	(1)	AGGTGTCATCACATAAGGTTACGGTAAGCTCATCACACAAGGCATTGGC	
KOM5556R_3	(1)	AGGTGTCATCACATAAGGTTACGGTAAGCTCATCACACAAGGCATTGGC	
Consensus	(1)	AGGTGTCATCACATAAGGTTACGGTAAGCTCATCACACAAGGCATTGGC	
		51	100
KOM5556R_1	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
KOM5556R_2	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
KOM5556R_3	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
Consensus	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
		101	150
KOM5556R_1	(101)	CAAAAGACTCATTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
KOM5556R_2	(101)	CAAAAGACTCATTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
KOM5556R_3	(101)	CAAAAGACTCATTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
Consensus	(101)	CAAAAGACTCATTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
		151	200
KOM5556R_1	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTCAT	
KOM5556R_2	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTCAT	
KOM5556R_3	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTCAT	
Consensus	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTCAT	
		201	250
KOM5556R_1	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
KOM5556R_2	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
KOM5556R_3	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
Consensus	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
		251	300
KOM5556R_1	(251)	ATACTCAAATTTGCAAAAGAACCAACCACAATCAAACAAAATAAGAGGTGG	
KOM5556R_2	(251)	ATACTCAAATTTGCAAAAGAACCAACCACAATCAAACAAAATAAGAGGTGG	
KOM5556R_3	(251)	ATACTCAAATTTGCAAAAGAACCAACCACAATCAAACAAAATAAGAGGTGG	
Consensus	(251)	ATACTCAAATTTGCAAAAGAACCAACCACAATCAAACAAAATAAGAGGTGG	
		301	350
KOM5556R_1	(301)	CAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
KOM5556R_2	(301)	CAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
KOM5556R_3	(301)	CAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
Consensus	(301)	CAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
		351	400
KOM5556R_1	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAAAACAATTTACAGCACAA	
KOM5556R_2	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAAAACAATTTACAGCACAA	
KOM5556R_3	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAAAACAATTTACAGCACAA	
Consensus	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAAAACAATTTACAGCACAA	
		401	450
KOM5556R_1	(401)	AAACCCAATATATAAAACAAAATGATAATCACAAGAGGTAGGTATGCAC	
KOM5556R_2	(401)	AAACCCAATATATAAAACAAAATGATAATCACAAGAGGTAGGTATGCAC	
KOM5556R_3	(401)	AAACCCAATATATAAAACAAAATGATAATCACAAGAGGTAGGTATGCAC	
Consensus	(401)	AAACCCAATATATAAAACAAAATGATAATCACAAGAGGTAGGTATGCAC	
		451	500
KOM5556R_1	(451)	GATAGTTTAAACTGAAGGCGGGAAACGACAATCTGATCATGAGCGGAGAA	
KOM5556R_2	(451)	GATAGTTTAAACTGAAGGCGGGAAACGACAATCTGATCATGAGCGGAGAA	
KOM5556R_3	(451)	GATAGTTTAAACTGAAGGCGGGAAACGACAATCTGATCATGAGCGGAGAA	
Consensus	(451)	GATAGTTTAAACTGAAGGCGGGAAACGACAATCTGATCATGAGCGGAGAA	
		501	550
KOM5556R_1	(501)	TTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGACAAGCCGTTT	
KOM5556R_2	(501)	TTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGACAAGCCGTTT	
KOM5556R_3	(501)	TTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGACAAGCCGTTT	
Consensus	(501)	TTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGACAAGCCGTTT	
		551	600
KOM5556R_1	(551)	TACGTTTGGAAGTACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
KOM5556R_2	(551)	TACGTTTGGAAGTACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
KOM5556R_3	(551)	TACGTTTGGAAGTACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
Consensus	(551)	TACGTTTGGAAGTACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
		601	650
KOM5556R_1	(601)	GGTTTCTGGAGTTTAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	
KOM5556R_2	(601)	GGTTTCTGGAGTTTAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	
KOM5556R_3	(601)	GGTTTCTGGAGTTTAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	
Consensus	(601)	GGTTTCTGGAGTTTAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	

		651	700
KOM5556R_1	(651)	GCGTTCAAAGTCGCCTAAGGTC	ACTATCAGCTAGCAAATATTTCTTGTC
KOM5556R_2	(651)	GCGTTCAAAGTCGCCTAAGGTC	ACTATCAGCTAGCAAATATTTCTTGTC
KOM5556R_3	(651)	GCGTTCAAAGTCGCCTAAGGTC	ACTATCAGCTAGCAAATATTTCTTGTC
Consensus	(651)	GCGTTCAAAGTCGCCTAAGGTC	ACTATCAGCTAGCAAATATTTCTTGTC
		701	750
KOM5556R_1	(701)	AAAAATGCTCCACTGACGTTCCATAAAAT	TCCCCTCGGTATCCAATTAGAG
KOM5556R_2	(701)	AAAAATGCTCCACTGACGTTCCATAAAAT	TCCCCTCGGTATCCAATTAGAG
KOM5556R_3	(701)	AAAAATGCTCCACTGACGTTCCATAAAAT	TCCCCTCGGTATCCAATTAGAG
Consensus	(701)	AAAAATGCTCCACTGACGTTCCATAAAAT	TCCCCTCGGTATCCAATTAGAG
		751	800
KOM5556R_1	(751)	TTCATATTCACTCTCAATCCAATAATCTGCACCGGATCTGGATCGTTT	
KOM5556R_2	(751)	TTCATATTCACTCTCAATCCAATAATCTGCACCGGATCTGGATCGTTT	
KOM5556R_3	(751)	TTCATATTCACTCTCAATCCAATAATCTGCACCGGATCTGGATCGTTT	
Consensus	(751)	TTCATATTCACTCTCAATCCAATAATCTGCACCGGATCTGGATCGTTT	
		801	850
KOM5556R_1	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
KOM5556R_2	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
KOM5556R_3	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
Consensus	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
		851	900
KOM5556R_1	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
KOM5556R_2	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
KOM5556R_3	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
Consensus	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
		901	950
KOM5556R_1	(901)	ATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTGTC	
KOM5556R_2	(901)	ATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTGTC	
KOM5556R_3	(901)	ATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTGTC	
Consensus	(901)	ATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTGTC	
		951	1000
KOM5556R_1	(951)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
KOM5556R_2	(951)	AAGACCGACCTGTCCGATGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
KOM5556R_3	(951)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
Consensus	(951)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
		1001	1050
KOM5556R_1	(1001)	GCTATCGTGGCTGGCCACGACGGGCGTTCCCTGCGCAGCTGTGCTCGACG	
KOM5556R_2	(1001)	GCTATCGTGGCTGGCCACGACGGGCGTTCCCTGCGCAGCTGTGCTCGACG	
KOM5556R_3	(1001)	GCTATCGTGGCTGGCCACGACGGGCGTTCCCTGCGCAGCTGTGCTCGACG	
Consensus	(1001)	GCTATCGTGGCTGGCCACGACGGGCGTTCCCTGCGCAGCTGTGCTCGACG	
		1051	1100
KOM5556R_1	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG	
KOM5556R_2	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG	
KOM5556R_3	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG	
Consensus	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG	
		1101	1150
KOM5556R_1	(1101)	CAGGATCTCCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
KOM5556R_2	(1101)	CAGGATCTCCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
KOM5556R_3	(1101)	CAGGATCTCCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
Consensus	(1101)	CAGGATCTCCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
		1151	1200
KOM5556R_1	(1151)	GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
KOM5556R_2	(1151)	GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
KOM5556R_3	(1151)	GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
Consensus	(1151)	GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
		1201	1250
KOM5556R_1	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAA	
KOM5556R_2	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAA	
KOM5556R_3	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAA	
Consensus	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAA	
		1251	1300
KOM5556R_1	(1251)	GCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	
KOM5556R_2	(1251)	GCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	
KOM5556R_3	(1251)	GCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	
Consensus	(1251)	GCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	

		1301	1350
KOM5556R_1	(1301)	GCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
KOM5556R_2	(1301)	GCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
KOM5556R_3	(1301)	GCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
Consensus	(1301)	GCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
		1351	1400
KOM5556R_1	(1351)	ATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
KOM5556R_2	(1351)	ATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
KOM5556R_3	(1351)	ATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
Consensus	(1351)	ATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
		1401	1450
KOM5556R_1	(1401)	AATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
KOM5556R_2	(1401)	AATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
KOM5556R_3	(1401)	AATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
Consensus	(1401)	AATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
		1451	1500
KOM5556R_1	(1451)	CCGCTATCAGGACATAGCGTTGGCCACCCGTGATATTGCTGAAGAGCTTG	
KOM5556R_2	(1451)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
KOM5556R_3	(1451)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
Consensus	(1451)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
		1501	1550
KOM5556R_1	(1501)	GCGGCGAATGGGCTGACCGCTTCTCTCGTGCTTTACGGTATCGCCGCTCCC	
KOM5556R_2	(1501)	GCGGCGAATGGGCTGACCGCTTCTCTCGTGCTTTACGGTATCGCCGCTCCC	
KOM5556R_3	(1501)	GCGGCGAATGGGCTGACCGCTTCTCTCGTGCTTTACGGTATCGCCGCTCCC	
Consensus	(1501)	GCGGCGAATGGGCTGACCGCTTCTCTCGTGCTTTACGGTATCGCCGCTCCC	
		1551	1600
KOM5556R_1	(1551)	GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCCTCTGAGC	
KOM5556R_2	(1551)	GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCCTCTGAGC	
KOM5556R_3	(1551)	GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCCTCTGAGC	
Consensus	(1551)	GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCCTCTGAGC	
		1601	1650
KOM5556R_1	(1601)	GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
KOM5556R_2	(1601)	GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
KOM5556R_3	(1601)	GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
Consensus	(1601)	GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
		1651	1700
KOM5556R_1	(1651)	ACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAA	
KOM5556R_2	(1651)	ACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAA	
KOM5556R_3	(1651)	ACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAA	
Consensus	(1651)	ACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAA	
		1701	1750
KOM5556R_1	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
KOM5556R_2	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
KOM5556R_3	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
Consensus	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
		1751	1800
KOM5556R_1	(1751)	CTGGAGTTCCTTCGCCCACGGGATCTCTGCGGAACAGGCGGTCTGAAGGTGC	
KOM5556R_2	(1751)	CTGGAGTTCCTTCGCCCACGGGATCTCTGCGGAACAGGCGGTCTGAAGGTGC	
KOM5556R_3	(1751)	CTGGAGTTCCTTCGCCCACGGGATCTCTGCGGAACAGGCGGTCTGAAGGTGC	
Consensus	(1751)	CTGGAGTTCCTTCGCCCACGGGATCTCTGCGGAACAGGCGGTCTGAAGGTGC	
		1801	1850
KOM5556R_1	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
KOM5556R_2	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
KOM5556R_3	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
Consensus	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
		1851	1900
KOM5556R_1	(1851)	GCGACAATATGATCGGGCCCGCGTCCACATCAACGGCGTCGGCGGCGAC	
KOM5556R_2	(1851)	GCGACAATATGATCGGGCCCGCGTCCACATCAACGGCGTCGGCGGCGAC	
KOM5556R_3	(1851)	GCGACAATATGATCGGGCCCGCGTCCACATCAACGGCGTCGGCGGCGAC	
Consensus	(1851)	GCGACAATATGATCGGGCCCGCGTCCACATCAACGGCGTCGGCGGCGAC	
		1901	1950
KOM5556R_1	(1901)	TGCCCAGGCAAGACCGAGATGCACCGCGATATCTTGCTGCGTTCGGATAT	
KOM5556R_2	(1901)	TGCCCAGGCAAGACCGAGATGCACCGCGATATCTTGCTGCGTTCGGATAT	
KOM5556R_3	(1901)	TGCCCAGGCAAGACCGAGATGCACCGCGATATCTTGCTGCGTTCGGATAT	
Consensus	(1901)	TGCCCAGGCAAGACCGAGATGCACCGCGATATCTTGCTGCGTTCGGATAT	

		1951	2000
KOM5556R_1	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA	
KOM5556R_2	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA	
KOM5556R_3	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA	
Consensus	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA	
		2001	2050
KOM5556R_1	(2001)	TTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG	
KOM5556R_2	(2001)	TTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG	
KOM5556R_3	(2001)	TTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG	
Consensus	(2001)	TTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG	
		2051	2100
KOM5556R_1	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACAT	
KOM5556R_2	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACAT	
KOM5556R_3	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACAT	
Consensus	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACAT	
		2101	2150
KOM5556R_1	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCC GC	
KOM5556R_2	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCC GC	
KOM5556R_3	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCC GC	
Consensus	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCC GC	
		2151	2200
KOM5556R_1	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAA ACTAG	
KOM5556R_2	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAA ACTAG	
KOM5556R_3	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAA ACTAG	
Consensus	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAA ACTAG	
		2201	2250
KOM5556R_1	(2201)	GATAAAC TATCGCGCGCGGTGTCATCTATGTTACTAGATCGGGCCTCCTG	
KOM5556R_2	(2201)	GATAAAT TATCGCGCGCGGTGTCATCTATGTTACTAGATCGGGCCTCCTG	
KOM5556R_3	(2201)	GATAAAT TATCGCGCGCGGTGTCATCTATGTTACTAGATCGGGCCTCCTG	
Consensus	(2201)	GATAAAT TATCGCGCGCGGTGTCATCTATGTTACTAGATCGGGCCTCCTG	
		2251	2300
KOM5556R_1	(2251)	TCAATGCTGGCGGCGGCTCTGGTGGTGGTTCGGTGGCGGCTCTGAGGGT	
KOM5556R_2	(2251)	TCAATGCTGGCGGCGGCTCTGGTGGTGGTTCGGTGGCGGCTCTGAGGGT	
KOM5556R_3	(2251)	TCAATGCTGGCGGCGGCTCTGGTGGTGGTTCGGTGGCGGCTCTGAGGGT	
Consensus	(2251)	TCAATGCTGGCGGCGGCTCTGGTGGTGGTTCGGTGGCGGCTCTGAGGGT	
		2301	2350
KOM5556R_1	(2301)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG	
KOM5556R_2	(2301)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG	
KOM5556R_3	(2301)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG	
Consensus	(2301)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG	
		2351	2400
KOM5556R_1	(2351)	TTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCAA	
KOM5556R_2	(2351)	TTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCAA	
KOM5556R_3	(2351)	TTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCAA	
Consensus	(2351)	TTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCAA	
		2401	2450
KOM5556R_1	(2401)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGATAACGCGCTACAG	
KOM5556R_2	(2401)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGATAACGCGCTACAG	
KOM5556R_3	(2401)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGATAACGCGCTACAG	
Consensus	(2401)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGATAACGCGCTACAG	
		2451	2500
KOM5556R_1	(2451)	TCTGACGCTAAAGGCAAAC TTGATTCTGTCGCTACTGATTACGGTGCTGC	
KOM5556R_2	(2451)	TCTGACGCTAAAGGCAAAC TTGATTCTGTCGCTACTGATTACGGTGCTGC	
KOM5556R_3	(2451)	TCTGACGCTAAAGGCAAAC TTGATTCTGTCGCTACTGATTACGGTGCTGC	
Consensus	(2451)	TCTGACGCTAAAGGCAAAC TTGATTCTGTCGCTACTGATTACGGTGCTGC	
		2501	2550
KOM5556R_1	(2501)	TATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAGTGGTG	
KOM5556R_2	(2501)	TATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAGTGGTG	
KOM5556R_3	(2501)	TATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAGTGGTG	
Consensus	(2501)	TATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAGTGGTG	
		2551	2600
KOM5556R_1	(2551)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTCGGTGAC	
KOM5556R_2	(2551)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTCGGTGAC	
KOM5556R_3	(2551)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTCGGTGAC	
Consensus	(2551)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTCGGTGAC	

		2601	2650
KOM5556R_1	(2601)	GGTGATAATTCACCTTTAATGAATAAATTTCCGTCAATATTTACCTTCCCT	
KOM5556R_2	(2601)	GGTGATAATTCGCCTTTAATGAATAAATTTCCGTCAATATTTACCTTCCCT	
KOM5556R_3	(2601)	GGTGATAATTCACCTTTAATGAATAAATTTCCGTCAATATTTACCTTCCCT	
Consensus	(2601)	GGTGATAATTCACCTTTAATGAATAAATTTCCGTCAATATTTACCTTCCCT	
		2651	2700
KOM5556R_1	(2651)	CCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCCCAATACGCAAAC	
KOM5556R_2	(2651)	CCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCCCAATACGCAAAC	
KOM5556R_3	(2651)	CCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCCCAATACGCAAAC	
Consensus	(2651)	CCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCCCAATACGCAAAC	
		2701	2750
KOM5556R_1	(2701)	CGCCTCTCCCCGCGCTTGGCCGATTCAATTAATGCAGCTGGCAGCAGAGG	
KOM5556R_2	(2701)	CGCCTCTCCCCGCGCTTGGCCGATTCAATTAATGCAGCTGGCAGCAGAGG	
KOM5556R_3	(2701)	CGCCTCTCCCCGCGCTTGGCCGATTCAATTAATGCAGCTGGCAGCAGAGG	
Consensus	(2701)	CGCCTCTCCCCGCGCTTGGCCGATTCAATTAATGCAGCTGGCAGCAGAGG	
		2751	2800
KOM5556R_1	(2751)	TTTCCCAGCTGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTA	
KOM5556R_2	(2751)	TTTCCCAGCTGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTA	
KOM5556R_3	(2751)	TTTCCCAGCTGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTA	
Consensus	(2751)	TTTCCCAGCTGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTA	
		2801	2850
KOM5556R_1	(2801)	GCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTA	
KOM5556R_2	(2801)	GCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTA	
KOM5556R_3	(2801)	GCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTA	
Consensus	(2801)	GCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTA	
		2851	2900
KOM5556R_1	(2851)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT	
KOM5556R_2	(2851)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT	
KOM5556R_3	(2851)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT	
Consensus	(2851)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT	
		2901	2950
KOM5556R_1	(2901)	GACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT	
KOM5556R_2	(2901)	GACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT	
KOM5556R_3	(2901)	GACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT	
Consensus	(2901)	GACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT	
		2951	3000
KOM5556R_1	(2951)	TTTGTTTCATTACTTAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT	
KOM5556R_2	(2951)	TTTGTTTCATTACTTAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT	
KOM5556R_3	(2951)	TTTGTTTCATTACTTAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT	
Consensus	(2951)	TTTGTTTCATTACTTAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT	
		3001	3050
KOM5556R_1	(3001)	CTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA	
KOM5556R_2	(3001)	CTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA	
KOM5556R_3	(3001)	CTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA	
Consensus	(3001)	CTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA	
		3051	3100
KOM5556R_1	(3051)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTATGAATC	
KOM5556R_2	(3051)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTATGAATC	
KOM5556R_3	(3051)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTATGAATC	
Consensus	(3051)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTATGAATC	
		3101	3150
KOM5556R_1	(3101)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGATAGTA	
KOM5556R_2	(3101)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA	
KOM5556R_3	(3101)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA	
Consensus	(3101)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA	
		3151	3200
KOM5556R_1	(3151)	TCTTCTGTTTGGGTATTTTTTTTCTGCCAAGTGGAACGGAGACATGT	
KOM5556R_2	(3151)	TCTTCTGTTTGGGTATTTTTTTTCTGCCAAGTGGAACGGAGACATGT	
KOM5556R_3	(3151)	TCTTCTGTTTGGGTATTTTTTTTCTGCCAAGTGGAACGGAGACATGT	
Consensus	(3151)	TCTTCTGTTTGGGTATTTTTTTTCTGCCAAGTGGAACGGAGACATGT	
		3201	3250
KOM5556R_1	(3201)	TATGATGTATACGGGAAGCTCGTTAAAAAATAACAATAGGAAGAAAT	
KOM5556R_2	(3201)	TATGATGTATACGGGAAGCTCGTTAAAAAATAACAATAGGAAGAAAT	
KOM5556R_3	(3201)	TATGATGTATACGGGAAGCTCGTTAAAAAATAACAATAGGAAGAAAT	
Consensus	(3201)	TATGATGTATACGGGAAGCTCGTTAAAAAATAACAATAGGAAGAAAT	

		3251	3300
KOM5556R_1	(3251)	GTAACAAACATTGAATGTTGTTTTAACCATCCTTCCTTTAGCAGTGTAT	
KOM5556R_2	(3251)	GTAACAAACATTGAATGTTGTTTTAACCATCCTTCCTTTAGCAGTGTAT	
KOM5556R_3	(3250)	GTAACAAACATTGAATGTTGTTTTAACCATCCTTCCTTTAGCAGTGCAT	
Consensus	(3251)	GTAACAAACATTGAATGTTGTTTTAACCATCCTTCCTTTAGCAGTGTAT	
		3301	3350
KOM5556R_1	(3301)	CAATTTTGTAAATAGAACCATGCATCTCAATCTTAATACTAAAATGCAACT	
KOM5556R_2	(3301)	CAATTTTGTAAATAGAACCATGCATCCAATCTTAATACTAAAATGCAACT	
KOM5556R_3	(3300)	CAATTTTGTAAATAGAACCATGCATCTCGATCTTAATACTAAAATGCAACT	
Consensus	(3301)	CAATTTTGTAAATAGAACCATGCATCTCAATCTTAATACTAAAATGCAACT	
		3351	3400
KOM5556R_1	(3351)	TAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGTG	
KOM5556R_2	(3351)	TAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGTG	
KOM5556R_3	(3350)	TAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGTG	
Consensus	(3351)	TAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGTG	
		3401	3450
KOM5556R_1	(3401)	CATTCATAATTAGATCTTGTTTGTTCGTAAAAAATAGAAAATATATTTAC	
KOM5556R_2	(3401)	CATTCATAATTAGATCTTGTTTGTTCGTAAAAAATTTGAAAATATATTTAC	
KOM5556R_3	(3400)	CATTCATAATTAGATCTTGTTTGTTCGTAAAAAATAGAAAATATATTTAC	
Consensus	(3401)	CATTCATAATTAGATCTTGTTTGTTCGTAAAAAATAGAAAATATATTTAC	
		3451	3500
KOM5556R_1	(3451)	AGTAATTTGGAATACAAAGCTAAGGGGAAGTAACTAATATTCTAGTGGA	
KOM5556R_2	(3451)	AGTAATTTGGAATACAAAGCTAAGGGGAAGTAACTAATATTCTAGTGGA	
KOM5556R_3	(3450)	AGTAATTTGGAATACAAAGCTAAGGGGAAGTAACTAATATTCTAGTGGA	
Consensus	(3451)	AGTAATTTGGAATACAAAGCTAAGGGGAAGTAACTAATATTCTAGTGGA	
		3501	3550
KOM5556R_1	(3501)	GGGAGGGACCAGTACCAGTACCTAGATATTATTTTTAATTACTATAATAA	
KOM5556R_2	(3501)	GGGAGGGACCAGTACCAGTACCTAGATATTATTTTTAATTACTATAATAA	
KOM5556R_3	(3500)	GGGAGGGACCAGTACCAGTACCTAGATATTATTTTTAATTACTATAATAA	
Consensus	(3501)	GGGAGGGACCAGTACCAGTACCTAGATATTATTTTTAATTACTATAATAA	
		3551	3600
KOM5556R_1	(3551)	TAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAGG	
KOM5556R_2	(3551)	TAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAGG	
KOM5556R_3	(3550)	TAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAGG	
Consensus	(3551)	TAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAGG	
		3601	3650
KOM5556R_1	(3601)	GAGTTGGTTTAGTTTTTTAGATACTAGGAGACAGAACCGGACGGGCCCAT	
KOM5556R_2	(3601)	GAGTTGGTTTAGTTTTTTAGATACTAGGAGACAGAACCGGACGGGCCCAT	
KOM5556R_3	(3600)	GAGTTGGTTTAGTTTTTTAGATACTAGGAGACAGAACCGGACGGGCCCAT	
Consensus	(3601)	GAGTTGGTTTAGTTTTTTAGATACTAGGAGACAGAACCGGACGGGCCCAT	
		3651	3700
KOM5556R_1	(3651)	TGCAAGGCCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCCA	
KOM5556R_2	(3651)	TGCAAGGCCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCCA	
KOM5556R_3	(3650)	TGCAAGGCCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCCA	
Consensus	(3651)	TGCAAGGCCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCCA	
		3701	3750
KOM5556R_1	(3701)	TAATACTGTCGATGAGCATTTCCTTATAATACAGTGTCCACAGTTGCCTT	
KOM5556R_2	(3701)	TAATACTGTCGATGAGCATTTCCTTATAATACAGTGTCCACAGTTGCCTT	
KOM5556R_3	(3700)	TAATACTGTCGATGAGCATTTCCTTATAATACAGTGTCCACAGTTGCCTT	
Consensus	(3701)	TAATACTGTCGATGAGCATTTCCTTATAATACAGTGTCCACAGTTGCCTT	
		3751	3800
KOM5556R_1	(3751)	CTGCTAAGGGATAACCACCCGCTATTCTCTTGACACGTGTCACTGAAACC	
KOM5556R_2	(3751)	CTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAACC	
KOM5556R_3	(3750)	CTGCTGAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAACC	
Consensus	(3751)	CTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAACC	
		3801	3850
KOM5556R_1	(3801)	TGCTACAAATAAGGCAGGCACCTCCTCATTCTCACTCACTCACTCACACA	
KOM5556R_2	(3801)	TGCTACAAATAAGGCAGGCACCTCCTCATTCTCACTCACTCACTCACACA	
KOM5556R_3	(3800)	TGCTACAAATAAGGCAGGCACCTCCTCATTCTCACTCACTCACTCACACA	
Consensus	(3801)	TGCTACAAATAAGGCAGGCACCTCCTCATTCTCACTCACTCACTCACACA	
		3851	3900
KOM5556R_1	(3851)	GCTCAACAAGTGGTAAC'TTTACTCATCTCCTCCAATTATTTCTGATTTTC	
KOM5556R_2	(3851)	GCTCAACAAGTGGTAAC'TTTACTCATCTCCTCCAATTATTTCTGATTTTC	
KOM5556R_3	(3850)	GCTCAACAAGTGGTAAC'TTTACTCATCTCCTCCAATTATTTCTGATTTTC	
Consensus	(3851)	GCTCAACAAGTGGTAAC'TTTACTCATCTCCTCCAATTATTTCTGATTTTC	

		3901		3950
KOM5556R_1	(3901)	ATGCAGGTCGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCAG		
KOM5556R_2	(3901)	ATGCAGGTCGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCAG		
KOM5556R_3	(3900)	ATGCAGGTCGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCAG		
Consensus	(3901)	ATGCAGGTCGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCAG		
		3951		4000
KOM5556R_1	(3951)	GTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGAG		
KOM5556R_2	(3951)	GTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGAG		
KOM5556R_3	(3950)	GTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGAG		
Consensus	(3951)	GTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGAG		
		4001		4050
KOM5556R_1	(4001)	TCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAAC		
KOM5556R_2	(4001)	TCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAAC		
KOM5556R_3	(4000)	TCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAAC		
Consensus	(4001)	TCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAAC		
		4051		4100
KOM5556R_1	(4051)	TTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTCT		
KOM5556R_2	(4051)	TTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTCT		
KOM5556R_3	(4050)	TTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTCT		
Consensus	(4051)	TTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTCT		
		4101		4150
KOM5556R_1	(4101)	GCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGCAAGCCAAGT		
KOM5556R_2	(4101)	GCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGCAAGCCAAGT		
KOM5556R_3	(4100)	GCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGCAAGCCAAGT		
Consensus	(4101)	GCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGCAAGCCAAGT		
		4151		4200
KOM5556R_1	(4151)	CTGCTTGAAGAGCCTCCTTTAGTAGAGGTTTTGCGTCCATGACCTGTATA		
KOM5556R_2	(4151)	CTGCTTGAAGAGCCTCCTTTAGTAGAGGTTTTGCGTCCATGACCTGTATA		
KOM5556R_3	(4150)	CTGCTTGAAGAGCCTCCTTTAGTAGAGGTTTTGCGTCCATGACCTGTATA		
Consensus	(4151)	CTGCTTGAAGAGCCTCCTTTAGTAGAGGTTTTGCGTCCATGACCTGTATA		
		4201		4250
KOM5556R_1	(4201)	GAGATTTTGATTAGCAAGAAGTCTTTAATTTTATAAACATACAAAATAAT		
KOM5556R_2	(4201)	GAGATTTTGATTAGCAAGAAGTCTTTAATTTTATAAACATACAAAATAAT		
KOM5556R_3	(4200)	GAGATTTTGATTAGCAAGAAGTCTTTAATTTTATAAACATACAAAATAAT		
Consensus	(4201)	GAGATTTTGATTAGCAAGAAGTCTTTAATTTTATAAACATACAAAATAAT		
		4251		4300
KOM5556R_1	(4251)	TTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTGGTTATATCGT		
KOM5556R_2	(4251)	TTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTGGTTATATCGT		
KOM5556R_3	(4250)	TTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTGGTTATATCGT		
Consensus	(4251)	TTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTGGTTATATCGT		
		4301		4350
KOM5556R_1	(4301)	ATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTCTTGTGTATCC		
KOM5556R_2	(4301)	ATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTCTTGTGTATCC		
KOM5556R_3	(4300)	ATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTCTTGTGTATCC		
Consensus	(4301)	ATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTCTTGTGTATCC		
		4351		4400
KOM5556R_1	(4351)	ATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCAA		
KOM5556R_2	(4351)	ATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCAA		
KOM5556R_3	(4350)	ATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCAA		
Consensus	(4351)	ATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCAA		
		4401		4450
KOM5556R_1	(4401)	TTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGGC		
KOM5556R_2	(4401)	TTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGGC		
KOM5556R_3	(4400)	TTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGGC		
Consensus	(4401)	TTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGGC		
		4451		4500
KOM5556R_1	(4451)	TCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTTCATCCAGTTG		
KOM5556R_2	(4451)	TCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTTCATCCAGTTG		
KOM5556R_3	(4450)	TCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTTCATCCAGTTG		
Consensus	(4451)	TCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTTCATCCAGTTG		
		4501		4550
KOM5556R_1	(4501)	ATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTTAAAAACTC		
KOM5556R_2	(4501)	ATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTTAAAAACTC		
KOM5556R_3	(4500)	ATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTTAAAAACTC		
Consensus	(4501)	ATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTTAAAAACTC		

		4551	4600
KOM5556R_1	(4551)	AATTTACTAGCATCAAAGAGCTTCAAAGTTGGAGGTCTGATTTCAAGC	
KOM5556R_2	(4551)	AATTTACTAGCATCAAAGGAGCTTCAAAGTTGGAGGTCTGATTTCAAGC	
KOM5556R_3	(4550)	AATTTACTAGCATCAAAGAGCTTCAAAGTTGGAGGTCTGATTTCAAGC	
Consensus	(4551)	AATTTACTAGCATCAAAGAGCTTCAAAGTTGGAGGTCTGATTTCAAGC	
		4601	4650
KOM5556R_1	(4601)	GTAATACATACCCATCAATGAAATCAAAGAACCCTGAATTCATCAGG	
KOM5556R_2	(4601)	ATAAATACATACCCATCAATGAAATCAAAGAACCCTGAATTCATCAGG	
KOM5556R_3	(4600)	ATAAATACATACCCAGCAATGAAATCAAAGAACCCTGAATTCATCAGG	
Consensus	(4601)	ATAAATACATACCCATCAATGAAATCAAAGAACCCTGAATTCATCAGG	
		4651	4700
KOM5556R_1	(4651)	AAGATTGAGAAGAGGGAAGTCAGAGAAAGAAAATCGACCTTGGTAGGCAA	
KOM5556R_2	(4651)	AAGATTGAGAAGAGGGAAGTCAGAGAAAGAAAATCGACCTTGGTAGGCAA	
KOM5556R_3	(4650)	AAGATTGAGAAGAGGGAAGTCAGAGAAAGAAAATCGACCTTGGTAGGCAA	
Consensus	(4651)	AAGATTGAGAAGAGGGAAGTCAGAGAAAGAAAATCGACCTTGGTAGGCAA	
		4701	4750
KOM5556R_1	(4701)	TGTTATGGATGCAGAAAGCAACCTGGAGGCAATGTGAAATTTATCATATA	
KOM5556R_2	(4701)	TGTTATGGATGCAGAAAGCAACCTGGAGGCAATGTGAAATTTATCATATA	
KOM5556R_3	(4700)	TGTTATGGATGCAGAAAGCAACCTGGAGGCAATGTGAAATTTATCATATA	
Consensus	(4701)	TGTTATGGATGCAGAAAGCAACCTGGAGGCAATGTGAAATTTATCATATA	
		4751	4800
KOM5556R_1	(4751)	TTAATACAACCTTACTGATTTGCAGGGTAACGTGCAATCGAGTGAATACA	
KOM5556R_2	(4751)	TTAATACAACCTTACTGATTTGCAGGGTAACGTGCAATCGAGTGAATACA	
KOM5556R_3	(4750)	TTAATACAACCTTACTGATTTGCAGGGTAACGTGCAATCGAGTGAATACA	
Consensus	(4751)	TTAATACAACCTTACTGATTTGCAGGGTAACGTGCAATCGAGTGAATACA	
		4801	4850
KOM5556R_1	(4801)	AAGAAATTTTACCTTGGCATTCAAGTAGATTCCCTCTGGACTGGTACATTG	
KOM5556R_2	(4801)	AAGAAATTTTACCTTGGCATTCAAGTAGATTCCCTCTGGACTGGTACATTG	
KOM5556R_3	(4800)	AAGAAATTTTACCTTGGCATTCAAGTAGATTCCCTCTGGACTGGTACATTG	
Consensus	(4801)	AAGAAATTTTACCTTGGCATTCAAGTAGATTCCCTCTGGACTGGTACATTG	
		4851	4900
KOM5556R_1	(4851)	ACTTCAAGTAGCAAGGAATGAGAGCTGTGTGCCAATCATTGGCAATGAAG	
KOM5556R_2	(4851)	ACTTCAAGTAGCAAGGAATGAGAGCTGTGTGCCAATCATTGGCAATGAAG	
KOM5556R_3	(4850)	ACTTCAAGTAGCAAGGAATGAGAGCTGTGTGCCAATCATTGGCAATGAAG	
Consensus	(4851)	ACTTCAAGTAGCAAGGAATGAGAGCTGTGTGCCAATCATTGGCAATGAAG	
		4901	4950
KOM5556R_1	(4901)	AGAACATCCTCTCCTGCAGGAATAGGCAAAATAAAGATGATTACCTACAA	
KOM5556R_2	(4901)	AGAACATCCTCTCCTGCAGGATAGGCAAAATAAAGATGATTACCTACAA	
KOM5556R_3	(4900)	AGAACATCCTCTCCTGCAGGAATAGGCAAAATAAAGATGATTACCTACAA	
Consensus	(4901)	AGAACATCCTCTCCTGCAGGAATAGGCAAAATAAAGATGATTACCTACAA	
		4951	5000
KOM5556R_1	(4951)	TGATATAGTAAGGAGTTTTCTGAAACTAGGATGTGTTAATTACCATATGG	
KOM5556R_2	(4951)	TGATATAGTAAGGAGTTTTCTGAAACTAGGATGTGTTAATTACCATATGG	
KOM5556R_3	(4950)	TGATATAGTAAGGAGTTTTCTGAAACTAGGATGTGTTAATTACCATATGG	
Consensus	(4951)	TGATATAGTAAGGAGTTTTCTGAAACTAGGATGTGTTAATTACCATATGG	
		5001	5050
KOM5556R_1	(5001)	TCCTGAGAAGTAGTTGCTACTGTTCAAATTCAAAACCTTTAGGTGCCTCTA	
KOM5556R_2	(5001)	TCCTGAGAAGTAGTTGCTACTGTTCAAATTCAAAACCTTTAGGTGCCTCTA	
KOM5556R_3	(5000)	TCCTGAGAAGTAGTTGCTACTGTTCAAATTCAAAACCTTTAGGTGCCTCTA	
Consensus	(5001)	TCCTGAGAAGTAGTTGCTACTGTTCAAATTCAAAACCTTTAGGTGCCTCTA	
		5051	5100
KOM5556R_1	(5051)	GGGCTGCCTGAGAAAACAAGGTTAAAAAACGATTAAGACAAAAGAGTA	
KOM5556R_2	(5051)	GGGCTGCCTGAGAAAACAAGGTTAAAAAACGATTAAGACAAAAGAGTA	
KOM5556R_3	(5050)	GGGCTGCCTGAGAAAACAAGGTTAAAAAACGATTAAGACAAAAGAGTA	
Consensus	(5051)	GGGCTGCCTGAGAAAACAAGGTTAAAAAACGATTAAGACAAAAGAGTA	
		5101	5150
KOM5556R_1	(5101)	AAATGCCACATAAAAATCAAGAGTAACCTAACTTACTTGACACAACAAGCT	
KOM5556R_2	(5101)	AAATGCCACATAAAAATCAAGAGTAACCTAACTTACTTGACACAACAAGCT	
KOM5556R_3	(5100)	GAATGCCACATAAAAATCAAGAGTAACCTAACTTACTTGACACAACAAGCT	
Consensus	(5101)	AAATGCCACATAAAAATCAAGAGTAACCTAACTTACTTGACACAACAAGCT	
		5151	5200
KOM5556R_1	(5151)	GAACCTAAGTTCATTGTCCAGATAATCTAGTCCAGCTTTGGGGCCATAGA	
KOM5556R_2	(5151)	GAACCTAAGTTCATTGTCCAGATAATCTAGTCCAGCTTTGGGGCCATAGA	
KOM5556R_3	(5150)	GAACCTAAGTTCATTGTCCAGATAATCTAGTCCAGCTTTGGGGCCATAGA	
Consensus	(5151)	GAACCTAAGTTCATTGTCCAGATAATCTAGTCCAGCTTTGGGGCCATAGA	

		5201		5250
KOM5556R_1	(5201)	<u>TTTTTGAACCAGTTTTGCCCCAAACCTTAAAAGAGTAAAAGCACCAGTAG</u>		
KOM5556R_2	(5201)	<u>TTTTTGAACCAGTTTTGCCCCAAACCTTAAAAGAGTAAAAGCACCAGTAG</u>		
KOM5556R_3	(5200)	<u>TTTTTGAACCAGTTTTGCCCCAAACCTTAAAAGAGTAAAAGCACCAGTAG</u>		
Consensus	(5201)	<u>TTTTTGAACCAGTTTTGCCCCAAACCTTAAAAGAGTAAAAGCACCAGTAG</u>		
		5251		5300
KOM5556R_1	(5251)	<u>AGTTAAAAGATACTCAAAATGACCTGTTCTGCGTATCCCTCAGGACGGAT</u>		
KOM5556R_2	(5251)	<u>AGTTAAAAGATACTCAAAATGACCTGTTCTGCGTATCCCTCAGGACGGAT</u>		
KOM5556R_3	(5250)	<u>AGTTAAAAGATACTCAAAATGACCTGTTCTGCGTATCCCTCAGGACGGAT</u>		
Consensus	(5251)	<u>AGTTAAAAGATACTCAAAATGACCTGTTCTGCGTATCCCTCAGGACGGAT</u>		
		5301		5350
KOM5556R_1	(5301)	<u>TCATAATCATAATATGCTTACTTTCTCCAAGAACATTGGGTGGTCAACAA</u>		
KOM5556R_2	(5301)	<u>TCATAATCATAATATGCTTACTTTCTCCAAGAACATTGGGTGGTCAACAA</u>		
KOM5556R_3	(5300)	<u>TCATAATCATAATATGCTTACTTTCTCCAAGAACATTGGGTGGTCAACAA</u>		
Consensus	(5301)	<u>TCATAATCATAATATGCTTACTTTCTCCAAGAACATTGGGTGGTCAACAA</u>		
		5351		
KOM5556R_1	(5351)	<u>AAAC</u>		
KOM5556R_2	(5351)	<u>AAAC</u>		
KOM5556R_3	(5350)	<u>AAAC</u>		
Consensus	(5351)	<u>AAAC</u>		

Figure 8. DNA sequence alignment of three independently amplified fragments from reactions with primers KOM56RN and KOM55RN. A consensus sequence is derived from the alignment in view of errors introduced by the DNA polymerase.

		1	50
KOM56_1	(1)	AGGTGTCATCACATAAGGTTACGGTAAGCTCATCACACAAGGCATTGGC	
KOM56_2	(1)	AGGTGTCATCACATAAGGTTACGGTAAGCTCATCACACAAGGCATTGGC	
KOM56_3	(1)	AGGTGTCATCACATAAGGTTACGGTAAGCTCATCACACAAGGCATTGGC	
Consensus	(1)	AGGTGTCATCACATAAGGTTACGGTAAGCTCATCACACAAGGCATTGGC	
		51	100
KOM56_1	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
KOM56_2	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
KOM56_3	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
Consensus	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
		101	150
KOM56_1	(101)	CAAAAGACTCATTTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
KOM56_2	(101)	CAAAAGACTCATTTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
KOM56_3	(101)	CAAAAGACTCATTTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
Consensus	(101)	CAAAAGACTCATTTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
		151	200
KOM56_1	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTCAT	
KOM56_2	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTCAT	
KOM56_3	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTCAT	
Consensus	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTCAT	
		201	250
KOM56_1	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
KOM56_2	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
KOM56_3	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
Consensus	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
		251	300
KOM56_1	(251)	ATACTCAAATTTGCAAAAGAACAACCACAATCAAACAAAATAAGAGGTGG	
KOM56_2	(251)	ATACTCAAATTTGCAAAAGAACAACCACAATCAAACAAAATAAGAGGTGG	
KOM56_3	(251)	ATACTCAAATTTGCAAAAGAACAACCACAATCAAACAAAATAAGAGGTGG	
Consensus	(251)	ATACTCAAATTTGCAAAAGAACAACCACAATCAAACAAAATAAGAGGTGG	
		301	350
KOM56_1	(301)	CAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
KOM56_2	(301)	CAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
KOM56_3	(301)	CAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
Consensus	(301)	CAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
		351	400
KOM56_1	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAAACACAATTTACAGCACAA	
KOM56_2	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAAACACAATTTACAGCACAA	
KOM56_3	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAAACACAATTTACAGCACGA	
Consensus	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAAACACAATTTACAGCACAA	
		401	450
KOM56_1	(401)	AAACCCAATATATAAACAAAAATGATAATCACAAGAGGTAGGTATGCACT	
KOM56_2	(401)	AAACCCAATATATAAACAAAAATGATAATCACAAGAGGTAGGTATGCACT	
KOM56_3	(401)	AAACCCAATATATAAACAAAAATGATAATCACAAGAGGTAGGTATGCACT	
Consensus	(401)	AAACCCAATATATAAACAAAAATGATAATCACAAGAGGTAGGTATGCACT	
		451	500
KOM56_1	(451)	GATAGTTTAAACTGAAGGCGGAAACGACAATCTGATCATGAGCGGAGAA	
KOM56_2	(451)	GATAGTTTAAACTGAAGGCGGAAACGACAATCTGATCATGAGCGGAGAA	
KOM56_3	(451)	GATAGTTTAAACTGAAGGCGGAAACGACAATCTGATCATGAGCGGAGAA	
Consensus	(451)	GATAGTTTAAACTGAAGGCGGAAACGACAATCTGATCATGAGCGGAGAA	
		501	550
KOM56_1	(501)	TTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGACAAGCCGTTT	
KOM56_2	(501)	TTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGACAAGCCGTTT	
KOM56_3	(501)	TTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGACAAGCCGTTT	
Consensus	(501)	TTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGACAAGCCGTTT	
		551	600
KOM56_1	(551)	TACGTTTGGAACTGACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
KOM56_2	(551)	TACGTTTGGAACTGACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
KOM56_3	(551)	TACGTTTGGAACTGACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
Consensus	(551)	TACGTTTGGAACTGACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
		601	650
KOM56_1	(601)	GGTTTCTGGAGTTTAAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	
KOM56_2	(601)	GGTTTCTGGAGTTTAAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	
KOM56_3	(601)	GGTTTCTGGAGTTTAAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	
Consensus	(601)	GGTTTCTGGAGTTTAAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	

		651	700
KOM56_1	(651)	CGGTTCAAAAAGTCGCCTAAGGTCACCTATCAGCTAGCAAATATTTCTTGCC	
KOM56_2	(651)	CGGTTCAAAAAGTCGCCTAAGGTCACCTATCAGCTAGCAAATATTTCTTGTC	
KOM56_3	(651)	CGGTTCAAAAAGTCGCCTAAGGTCACCTATCAGCTAGCAAATATTTCTTGTC	
Consensus	(651)	CGGTTCAAAAAGTCGCCTAAGGTCACCTATCAGCTAGCAAATATTTCTTGTC	
		701	750
KOM56_1	(701)	AAAAATGCTCCACTGACGTTCCATAAATCCCCCTCGGTATCCAATTAGAG	
KOM56_2	(701)	AAAAATGCTCCACTGACGTTCCATAAATCCCCCTCGGTATCCAATTAGAG	
KOM56_3	(701)	AAAAATGCTCCACTGACGTTCCATAAATCCCCCTCGGTATCCAATTAGAG	
Consensus	(701)	AAAAATGCTCCACTGACGTTCCATAAATCCCCCTCGGTATCCAATTAGAG	
		751	800
KOM56_1	(751)	CCTCATATTCACCTCTCAATCCAAATAATCTGCACCGGATCTGGATCGTTT	
KOM56_2	(751)	TCTCATATTCACCTCTCAATCCAAATAATCTGCACCGGATCTGGATCGTTT	
KOM56_3	(751)	TCTCATATTCACCTCTCAATCCAAATAATCTGCACCGGATCTGGATCGTTT	
Consensus	(751)	TCTCATATTCACCTCTCAATCCAAATAATCTGCACCGGATCTGGATCGTTT	
		801	850
KOM56_1	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
KOM56_2	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
KOM56_3	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
Consensus	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
		851	900
KOM56_1	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
KOM56_2	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
KOM56_3	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
Consensus	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
		901	950
KOM56_1	(901)	ATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGTTCTTTTGTGTC	
KOM56_2	(901)	ATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGTTCTTTTGTGTC	
KOM56_3	(901)	ATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGTTCTTTTGTGTC	
Consensus	(901)	ATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGTTCTTTTGTGTC	
		951	1000
KOM56_1	(951)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
KOM56_2	(951)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
KOM56_3	(951)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
Consensus	(951)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
		1001	1050
KOM56_1	(1001)	GCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACG	
KOM56_2	(1001)	GCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACG	
KOM56_3	(1001)	GCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACG	
Consensus	(1001)	GCTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACG	
		1051	1100
KOM56_1	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTTGGGCGAAGTGCCGGGG	
KOM56_2	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTTGGGCGAAGTGCCGGGG	
KOM56_3	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTTGGGCGAAGTGCCGGGG	
Consensus	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTTGGGCGAAGTGCCGGGG	
		1101	1150
KOM56_1	(1101)	CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
KOM56_2	(1101)	CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
KOM56_3	(1101)	CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
Consensus	(1101)	CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
		1151	1200
KOM56_1	(1151)	GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
KOM56_2	(1151)	GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
KOM56_3	(1151)	GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
Consensus	(1151)	GGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
		1201	1250
KOM56_1	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAA	
KOM56_2	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAA	
KOM56_3	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAA	
Consensus	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAA	
		1251	1300
KOM56_1	(1251)	GCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	
KOM56_2	(1251)	GCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	
KOM56_3	(1251)	GCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	
Consensus	(1251)	GCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	

		1301	1350
KOM56_1	(1301)	GCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
KOM56_2	(1301)	GCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
KOM56_3	(1301)	GCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
Consensus	(1301)	GCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
		1351	1400
KOM56_1	(1351)	ATCTCGTCTGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
KOM56_2	(1351)	ATCTCGTCTGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
KOM56_3	(1351)	ATCTCGTCTGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
Consensus	(1351)	ATCTCGTCTGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
		1401	1450
KOM56_1	(1401)	AATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
KOM56_2	(1401)	AATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
KOM56_3	(1401)	AATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
Consensus	(1401)	AATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
		1451	1500
KOM56_1	(1451)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
KOM56_2	(1451)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
KOM56_3	(1451)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
Consensus	(1451)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
		1501	1550
KOM56_1	(1501)	GCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCC	
KOM56_2	(1501)	GCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCC	
KOM56_3	(1501)	GCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCC	
Consensus	(1501)	GCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCC	
		1551	1600
KOM56_1	(1551)	GATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGC	
KOM56_2	(1551)	GATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGC	
KOM56_3	(1551)	GATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGC	
Consensus	(1551)	GATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGC	
		1601	1650
KOM56_1	(1601)	GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
KOM56_2	(1601)	GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
KOM56_3	(1601)	GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
Consensus	(1601)	GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
		1651	1700
KOM56_1	(1651)	ACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAA	
KOM56_2	(1651)	ACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAA	
KOM56_3	(1651)	ACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAA	
Consensus	(1651)	ACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAA	
		1701	1750
KOM56_1	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
KOM56_2	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
KOM56_3	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
Consensus	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
		1751	1800
KOM56_1	(1751)	CTGGAGTTCTTCGCCCACGGGATCTCTGCGGAACAGGCGGTGCAAGGTGC	
KOM56_2	(1751)	CTGGAGTTCTTCGCCCACGGGATCTCTGCGGAACAGGCGGTGCAAGGTGC	
KOM56_3	(1751)	CTGGAGTTCTTCGCCCACGGGATCTCTGCGGAACAGGCGGTGCAAGGTGC	
Consensus	(1751)	CTGGAGTTCTTCGCCCACGGGATCTCTGCGGAACAGGCGGTGCAAGGTGC	
		1801	1850
KOM56_1	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
KOM56_2	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
KOM56_3	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
Consensus	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
		1851	1900
KOM56_1	(1851)	GCGACAATATGATCGGGCCCGCGTCCACATCAACGGCGTCGGCGGCGAC	
KOM56_2	(1851)	GCGACAATATGATCGGGCCCGCGTCCACATCAACGGCGTCGGCGGCGAC	
KOM56_3	(1851)	GCGACAATATGATCGGGCCCGCGTCCACATCAACGGCGTCGGCGGCGAC	
Consensus	(1851)	GCGACAATATGATCGGGCCCGCGTCCACATCAACGGCGTCGGCGGCGAC	
		1901	1950
KOM56_1	(1901)	TGCCAGGCAAGACCGAGATGCACCGGATATCTTGCTACGTTTCGGATAT	
KOM56_2	(1901)	TGCCAGGCAAGACCGAGATGCACCGGATATCTTGCTACGTTTCGGATAT	
KOM56_3	(1901)	TGCCAGGCAAGACCGAGATGCACCGGATATCTTGCTACGTTTCGGATAT	
Consensus	(1901)	TGCCAGGCAAGACCGAGATGCACCGGATATCTTGCTACGTTTCGGATAT	

		1951		2000
KOM56_1	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA		
KOM56_2	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA		
KOM56_3	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA		
Consensus	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA		
		2001		2050
KOM56_1	(2001)	TTTGGCAATAAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG		
KOM56_2	(2001)	TTTGGCAATAAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG		
KOM56_3	(2001)	TTTGGCAATAAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG		
Consensus	(2001)	TTTGGCAATAAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG		
		2051		2100
KOM56_1	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAAATTAACAT		
KOM56_2	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAAATTAACAT		
KOM56_3	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAAATTAACAT		
Consensus	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAAATTAACAT		
		2101		2150
KOM56_1	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGC		
KOM56_2	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGC		
KOM56_3	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGC		
Consensus	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGC		
		2151		2200
KOM56_1	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAAC TAG		
KOM56_2	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAAC TAG		
KOM56_3	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAAC TAG		
Consensus	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAAC TAG		
		2201		2250
KOM56_1	(2201)	GATAAATTATCGCGCGCGGTGCATCTATGTTACTAGATCGGGCCTCCTG		
KOM56_2	(2201)	GATAAATTATCGCGCGCGGTGCATCTATGTTACTAGATCGGGCCTCCTG		
KOM56_3	(2201)	GATAAATTATCGCGCGCGGTGCATCTATGTTACTAGATCGGGCCTCCTG		
Consensus	(2201)	GATAAATTATCGCGCGCGGTGCATCTATGTTACTAGATCGGGCCTCCTG		
		2251		2300
KOM56_1	(2251)	TCAATGCTGGCGCGCGCTCTGGTGGTG---CTGGCGGCGGCTCTGAGGGT		
KOM56_2	(2251)	TCAATGCTGGCGCGCGCTCTGGTGGTG---CTGGCGGCGGCTCTGAGGGT		
KOM56_3	(2251)	TCAATGCTGGCGCGCGCTCTGGTGGTG---CTGGCGGCGGCTCTGAGGGT		
Consensus	(2251)	TCAATGCTGGCGCGCGCTCTGGTGGTG---CTGGCGGCGGCTCTGAGGGT		
		2301		2350
KOM56_1	(2298)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG		
KOM56_2	(2301)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG		
KOM56_3	(2301)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG		
Consensus	(2301)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG		
		2351		2400
KOM56_1	(2348)	TTCCGGTGGTGGCTCTGGTCCGGTGATTTTGATTATGAAAAGATGGCAA		
KOM56_2	(2351)	TTCCGGTGGTGGCTCTGGTCCGGTGATTTTGATTATGAAAAGATGGCAA		
KOM56_3	(2351)	TTCCGGTGGTGGCTCTGGTCCGGTGATTTTGATTATGAAAAGATGGCAA		
Consensus	(2351)	TTCCGGTGGTGGCTCTGGTCCGGTGATTTTGATTATGAAAAGATGGCAA		
		2401		2450
KOM56_1	(2398)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAG		
KOM56_2	(2401)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAG		
KOM56_3	(2401)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAG		
Consensus	(2401)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAG		
		2451		2500
KOM56_1	(2448)	TCTGACGCTAAAGGCAAACCTTGATTCTGTGCTACTGATTACGGTGCTGC		
KOM56_2	(2451)	TCTGACGCTAAAGGCAAACCTTGATTCTGTGCTACTGATTACGGTGCTGC		
KOM56_3	(2451)	TCTGACGCTAAAGGCAAACCTTGATTCTGTGCTACTGATTACGGTGCTGC		
Consensus	(2451)	TCTGACGCTAAAGGCAAACCTTGATTCTGTGCTACTGATTACGGTGCTGC		
		2501		2550
KOM56_1	(2498)	TATCGATGATTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGGTG		
KOM56_2	(2501)	TATCGATGATTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGGTG		
KOM56_3	(2501)	TATCGATGATTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGGTG		
Consensus	(2501)	TATCGATGATTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGGTG		
		2551		2600
KOM56_1	(2548)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTCGGTGAC		
KOM56_2	(2551)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTCGGTGAC		
KOM56_3	(2551)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTCGGTGAC		
Consensus	(2551)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAAATGGCTCAAGTCGGTGAC		

		2601	2650
KOM56_1	(2598)	GGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCT	
KOM56_2	(2601)	GGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCT	
KOM56_3	(2600)	GGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCT	
Consensus	(2601)	GGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCT	
		2651	2700
KOM56_1	(2648)	CCCTCAATCGGTTGAATGTGCGCCCTTTTGTCTTTGGCCCAATACGCAAAC	
KOM56_2	(2651)	CCCTCAATCGGTTGAATGTGCGCCCTTTTGTCTTTGGCCCAATACGCAAAC	
KOM56_3	(2650)	CCCTCAATCGGTTGAATGTGCGCCCTTTTGTCTTTGGCCCAATACGCAAAC	
Consensus	(2651)	CCCTCAATCGGTTGAATGTGCGCCCTTTTGTCTTTGGCCCAATACGCAAAC	
		2701	2750
KOM56_1	(2698)	CGCCTCTCCCGCGCGTGGCCGATTCAATTAATGCAGCTGGCACGACAGG	
KOM56_2	(2701)	CGCCTCTCCCGCGCGTGGCCGATTCAATTAATGCAGCTGGCACGACAGG	
KOM56_3	(2700)	CGCCTCTCCCGCGCGTGGTTCGATTCAATTAATGCAGCTGGCACGACAGG	
Consensus	(2701)	CGCCTCTCCCGCGCGTGGCCGATTCAATTAATGCAGCTGGCACGACAGG	
		2751	2800
KOM56_1	(2748)	TTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGGGTTA	
KOM56_2	(2751)	TTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGGGTTA	
KOM56_3	(2750)	TTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGGGTTA	
Consensus	(2751)	TTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGGGTTA	
		2801	2850
KOM56_1	(2798)	GCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTA	
KOM56_2	(2801)	GCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTA	
KOM56_3	(2800)	GCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTA	
Consensus	(2801)	GCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTA	
		2851	2900
KOM56_1	(2848)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT	
KOM56_2	(2851)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT	
KOM56_3	(2850)	CGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT	
Consensus	(2851)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT	
		2901	2950
KOM56_1	(2898)	GACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT	
KOM56_2	(2901)	GACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT	
KOM56_3	(2900)	GACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT	
Consensus	(2901)	GACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT	
		2951	3000
KOM56_1	(2948)	TTTGTTTCATTACTTAAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT	
KOM56_2	(2951)	TTTGTTTCATTACTTAAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT	
KOM56_3	(2950)	TTTGTTTCATTACTTAAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT	
Consensus	(2951)	TTTGTTTCATTACTTAAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT	
		3001	3050
KOM56_1	(2998)	CTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA	
KOM56_2	(3001)	CTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA	
KOM56_3	(3000)	CTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA	
Consensus	(3001)	CTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA	
		3051	3100
KOM56_1	(3048)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTTATGAATC	
KOM56_2	(3051)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTTATGAATC	
KOM56_3	(3050)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTTATGAATC	
Consensus	(3051)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTTATGAATC	
		3101	3150
KOM56_1	(3098)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA	
KOM56_2	(3101)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA	
KOM56_3	(3100)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA	
Consensus	(3101)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA	
		3151	3200
KOM56_1	(3148)	TCTTCCTGTTTGGGTATTTTTTTTCTGCCAAGTGGAACGGAGACATGT	
KOM56_2	(3151)	TCTTCCTGTTTGGGTATTTTTTTTCTGCCAAGTGGAACGGAGACATGT	
KOM56_3	(3150)	TCTTCCTGTTTGGGTATTTTTTTTCTGCCAAGTGGAACGGAGACATGT	
Consensus	(3151)	TCTTCCTGTTTGGGTATTTTTTTTCTGCCAAGTGGAACGGAGACATGT	
		3201	3250
KOM56_1	(3198)	TATGATGTATACGGGAAGCTCGTTAAAAAAAAA-TACAATAGGAAGAAA	
KOM56_2	(3201)	TATGATGTATACGGGAAGCTCGTTAAAAAAAAA-TACAATAGGAAGAAA	
KOM56_3	(3200)	TATGATGTATACGGGAAGCTCGTTAAAAAAAAA-TACAATAGGAAGAAA	
Consensus	(3201)	TATGATGTATACGGGAAGCTCGTTAAAAAAAAA-TACAATAGGAAGAAA	

		3251	3300
KOM56_1	(3247)	TGTAACAAACATTGAATGTTGTTTTAACCATCCTTCCTTTAGCAGTGTA	
KOM56_2	(3251)	TGTAACAAACATTGAATGTTGTTTTAACCATCCTTCCTTTAGCAGTGTA	
KOM56_3	(3249)	TGTAACAAACATTGAATGTTGTTTTAACCATCCTTCCTTTAGCAGTGTA	
Consensus	(3251)	TGTAACAAACATTGAATGTTGTTTTAACCATCCTTCCTTTAGCAGTGTA	
		3301	3350
KOM56_1	(3297)	TCAATTTTGTAAATAGAACCATGCATCTCAATCTTAATACTAAAATGCAAC	
KOM56_2	(3301)	TCAATTTTGTAAATAGAACCATGCATCTCAATCTTAATACTAAAATGCAAC	
KOM56_3	(3299)	TCAATTTTGTAAATAGAACCATGCATCTCAATCTTAATACTAAAATGCAAC	
Consensus	(3301)	TCAATTTTGTAAATAGAACCATGCATCTCAATCTTAATACTAAAATGCAAC	
		3351	3400
KOM56_1	(3347)	TTAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGT	
KOM56_2	(3351)	TTAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGT	
KOM56_3	(3349)	TTAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGT	
Consensus	(3351)	TTAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGT	
		3401	3450
KOM56_1	(3397)	GCATTCATAATTAGATCTTGTGTTGTCGTAAAAAATAGAAAATATATTTA	
KOM56_2	(3401)	GCATTCATAATTAGATCTTGTGTTGTCGTAAAAAATAGAAAATATATTTA	
KOM56_3	(3399)	GCATTCATAATTAGATCTTGTGTTGTCGTAAAAAATAGAAAATATATTTA	
Consensus	(3401)	GCATTCATAATTAGATCTTGTGTTGTCGTAAAAAATAGAAAATATATTTA	
		3451	3500
KOM56_1	(3447)	CAGTAATTTGGAATACAAAGCTAAGGGGAAGTAACTAATATTCTAGTGG	
KOM56_2	(3451)	CAGTAATTTGGAATACAAAGCTAAGGGGAAGTAACTAATATTCTAGTGG	
KOM56_3	(3449)	CAGTAATTTGGAATACAAAGCTAAGGGGAAGTAACTAATATTCTAGTGG	
Consensus	(3451)	CAGTAATTTGGAATACAAAGCTAAGGGGAAGTAACTAATATTCTAGTGG	
		3501	3550
KOM56_1	(3497)	AGGGAGGGACCAGTACCAGTACCTAGATATTATTTTTAATTACTATAATA	
KOM56_2	(3501)	AGGGAGGGACCAGTACCAGTACCTAGATATTATTTTTAATTACTATAATA	
KOM56_3	(3499)	AGGGAGGGACCAGTACCAGTACCTAGATATTATTTTTAATTACTATAATA	
Consensus	(3501)	AGGGAGGGACCAGTACCAGTACCTAGATATTATTTTTAATTACTATAATA	
		3551	3600
KOM56_1	(3547)	ATAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAG	
KOM56_2	(3551)	ATAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAG	
KOM56_3	(3549)	ATAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAG	
Consensus	(3551)	ATAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAG	
		3601	3650
KOM56_1	(3597)	GGAGTTGGTTTAGTTTTTTAGATACTAGGAGACAGAACCGGACGGGCCCA	
KOM56_2	(3601)	GGAGTTGGTTTAGTTTTTTAGATACTAGGAGACAGAACCGGACGGGCCCA	
KOM56_3	(3599)	GGAGTTGGTTTAGTTTTTTAGATACTAGGAGACAGAACCGGACGGGCCCA	
Consensus	(3601)	GGAGTTGGTTTAGTTTTTTAGATACTAGGAGACAGAACCGGACGGGCCCA	
		3651	3700
KOM56_1	(3647)	TTGCAAGGCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCC	
KOM56_2	(3651)	TTGCAAGGCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCC	
KOM56_3	(3649)	TTGCAAGGCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCC	
Consensus	(3651)	TTGCAAGGCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCC	
		3701	3750
KOM56_1	(3697)	ATAATACTGTCGATGAGCATTTCCTTATAATACAGTGTCCACAGTTGCCT	
KOM56_2	(3701)	ATAATACTGTCGATGAGCATTTCCTTATAATACAGTGTCCACAGTTGCCT	
KOM56_3	(3699)	ATAATACTGTCGATGAGCATTTCCTTATAATACAGTGTCCACAGTTGCCT	
Consensus	(3701)	ATAATACTGTCGATGAGCATTTCCTTATAATACAGTGTCCACAGTTGCCT	
		3751	3800
KOM56_1	(3747)	TCTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAAC	
KOM56_2	(3751)	TCTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAAC	
KOM56_3	(3749)	TCTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAAC	
Consensus	(3751)	TCTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAAC	
		3801	3850
KOM56_1	(3797)	CTGCTACAAATAAGGCAGGCACCTCCTCATTCTCACTCACTCACTCACAC	
KOM56_2	(3801)	CTGCTACAAATAAGGCAGGCACCTCCTCATTCTCACTCACTCACTCACAC	
KOM56_3	(3799)	CTGCTACAAATAAGGCAGGCACCTCCTCATTCTCACTCACTCACTCACAC	
Consensus	(3801)	CTGCTACAAATAAGGCAGGCACCTCCTCATTCTCACTCACTCACTCACAC	
		3851	3900
KOM56_1	(3847)	AGCTCAACAAGTGGTAACTTTTACTCATCTCCTCCAATTATTTCTGATTT	
KOM56_2	(3851)	AGCTCAACAAGTGGTAACTTTTACTCATCTCCTCCAATTATTTCTGATTT	
KOM56_3	(3849)	AGCTCAACAAGTGGTAACTTTTACTCATCTCCTCCAATTATTTCTGATTT	
Consensus	(3851)	AGCTCAACAAGTGGTAACTTTTACTCATCTCCTCCAATTATTTCTGATTT	

		3901	3950
KOM56_1	(3897)	CATGCAGGTCGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCA	
KOM56_2	(3901)	CATGCAGGTCGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCA	
KOM56_3	(3899)	CATGCAGGTCGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCA	
Consensus	(3901)	CATGCAGGTCGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCA	
		3951	4000
KOM56_1	(3947)	GGTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGA	
KOM56_2	(3951)	GGTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGA	
KOM56_3	(3949)	GGTCAATTTTCAGTTTCGGCACAATAAAACTCAACAAGAGAGATACCATGA	
Consensus	(3951)	GGTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGA	
		4001	4050
KOM56_1	(3997)	GTCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAA	
KOM56_2	(4001)	GTCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAA	
KOM56_3	(3999)	GTCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAA	
Consensus	(4001)	GTCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAA	
		4051	4100
KOM56_1	(4047)	CTTGTGAATTGCAGCAACAAGAATATCCGAACCTTTCTGCTCCTCAAGTC	
KOM56_2	(4051)	CTTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTC	
KOM56_3	(4049)	CTTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTC	
Consensus	(4051)	CTTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTC	
		4101	4150
KOM56_1	(4097)	TGCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGCAAGCCAAC	
KOM56_2	(4101)	TGCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGCAAGCCAAC	
KOM56_3	(4099)	TGCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGCAAGCCAAC	
Consensus	(4101)	TGCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGCAAGCCAAC	
		4151	4200
KOM56_1	(4147)	GCTGCTTGAAGAGCCTCCTTTAGTAAAGGTTTTGCGTCCATGACCTGTAT	
KOM56_2	(4151)	GCTGCTTGAAGAGCCTCCTTTAGTAAAGGTTTTGCGTCCATGACCTGTAT	
KOM56_3	(4149)	GCTGCTTGAAGAGCCTCCTTTAGTAAAGGTTTTGCGTCCATGACCTGTAT	
Consensus	(4151)	GCTGCTTGAAGAGCCTCCTTTAGTAAAGGTTTTGCGTCCATGACCTGTAT	
		4201	4250
KOM56_1	(4197)	AGAGATTTTGATTAGCAAGAAGTCTTTAATTTTATAAACATACAAAATAA	
KOM56_2	(4201)	AGAGATTTTGATTAGCAAGAAGTCTTTAATTTTATAAACATACAAAATAA	
KOM56_3	(4199)	AGAGATTTTGATTAGCAAGAAGTCTTTAATTTTATAAACATACAAAATAA	
Consensus	(4201)	AGAGATTTTGATTAGCAAGAAGTCTTTAATTTTATAAACATACAAAATAA	
		4251	4300
KOM56_1	(4247)	TTTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTGGTTATATCG	
KOM56_2	(4251)	TTTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTGGTTATATCG	
KOM56_3	(4249)	TTTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTGGTTATATCG	
Consensus	(4251)	TTTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTGGTTATATCG	
		4301	4350
KOM56_1	(4297)	TATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTCTTGTGTATC	
KOM56_2	(4301)	TATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTCTTGTGTATC	
KOM56_3	(4299)	TATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTCTTGTGTATC	
Consensus	(4301)	TATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTCTTGTGTATC	
		4351	4400
KOM56_1	(4347)	CATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCA	
KOM56_2	(4351)	CATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCA	
KOM56_3	(4349)	CATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCA	
Consensus	(4351)	CATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCA	
		4401	4450
KOM56_1	(4397)	ATTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGG	
KOM56_2	(4401)	ATTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGG	
KOM56_3	(4399)	ATTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGG	
Consensus	(4401)	ATTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGG	
		4451	4500
KOM56_1	(4447)	CTCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTTCATCCAGTT	
KOM56_2	(4451)	CTCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTTCATCCAGTT	
KOM56_3	(4449)	CTCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTTCATCCAGTT	
Consensus	(4451)	CTCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTTCATCCAGTT	
		4501	4550
KOM56_1	(4497)	GATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTTAAAAACT	
KOM56_2	(4501)	GATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTTAAAAACT	
KOM56_3	(4499)	GATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTTAAAAACT	
Consensus	(4501)	GATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTTAAAAACT	

		4551	4600
KOM56_1	(4547)	CAATTTACTAGCATCAAAGAGCTTCAAAGTTGGAGGACTACCACCAGC	
KOM56_2	(4551)	CAATTTACTAGCATCAGAAGAGCTTCAAAGTTGGAGGACTACCACCAGC	
KOM56_3	(4549)	CAATTTACTAGCATCAAAGAGCTTCAAAGTTGGAGGACTACCACCAGC	
Consensus	(4551)	CAATTTACTAGCATCAAAGAGCTTCAAAGTTGGAGGACTACCACCAGC	
		4601	4650
KOM56_1	(4597)	CCTTGCAGTAAGTCTTTCTTTTCATTTGGTTACCTACTCATTCACTACTTA	
KOM56_2	(4601)	CCTTGCAGTAAGTCTTTCTTTTCATTTGGTTACCTACTCATTCACTACTTA	
KOM56_3	(4599)	CCTTGCAGTAAGTCTTTCTTTTCATTTGGTTACCTACTCATTCACTACTTA	
Consensus	(4601)	CCTTGCAGTAAGTCTTTCTTTTCATTTGGTTACCTACTCATTCACTACTTA	
		4651	4700
KOM56_1	(4647)	TTTTGTTTAGTTAGTTTCTACTGCATCAGTCTTTTTATCATTAGGCCCG	
KOM56_2	(4651)	TTTTGTTTAGTTAGTTTCTACTGCATCAGTCTTTTTATCATTAGGCCCG	
KOM56_3	(4649)	TTTTGTTTAGTTAGTTTCTACTGCATCAGTCTTTTTATCATTAGGCCCG	
Consensus	(4651)	TTTTGTTTAGTTAGTTTCTACTGCATCAGTCTTTTTATCATTAGGCCCG	
		4701	4750
KOM56_1	(4697)	CGGACATCGGGTAATGACAAATATCCCCCGTTATGACCAATACAAAGATG	
KOM56_2	(4701)	CGGACATCGGGTAATGACAAATATCCCCCGTTATGACCAATACAAAGATG	
KOM56_3	(4699)	CGGACATCGGGTAATGACAAATATCCCCCGTTATGACCAATACAAAGATG	
Consensus	(4701)	CGGACATCGGGTAATGACAAATATCCCCCGTTATGACCAATACAAAGATG	
		4751	4800
KOM56_1	(4747)	CTTGGGATACTGGCGTTGCGGTTGAGGTACATCTTCCTATATTGATACGG	
KOM56_2	(4751)	CTTGGGATACTGGCGTTGCGGTTGAGGTACATCTTCCTATATTGATACGG	
KOM56_3	(4749)	CTTGGGATACTGGCGTTGCGGTTGAGGTACATCTTCCTATATTGATACGG	
Consensus	(4751)	CTTGGGATACTGGCGTTGCGGTTGAGGTACATCTTCCTATATTGATACGG	
		4801	4850
KOM56_1	(4797)	TACAATATTGTTCTCTTACATTTCTGATTCAAGAATGTGATCATCTGCA	
KOM56_2	(4801)	TACAATATTGTTCTCTTACATTTCTGATTCAAGAATGTGATCATCTGCA	
KOM56_3	(4799)	TACAATATTGTTCTCTTACATTTCTGATTCAAGAATGTGATCATCTGCA	
Consensus	(4801)	TACAATATTGTTCTCTTACATTTCTGATTCAAGAATGTGATCATCTGCA	
		4851	4900
KOM56_1	(4847)	GGTCAAAGTTGGAGACAGCATTGAAATTGTTGTTTCTTTCACTGCTATA	
KOM56_2	(4851)	GGTCAAAGTTGGAGACAGCATTGAAATTGTTGTTTCTTTCACTGCTATA	
KOM56_3	(4849)	GGTCAAAGTTGGAGACAGCATTGAAATTGTTGTTTCTTTCACTGCTATA	
Consensus	(4851)	GGTCAAAGTTGGAGACAGCATTGAAATTGTTGTTTCTTTCACTGCTATA	
		4901	4950
KOM56_1	(4897)	AACGTGGGGTTGATCGTGTTTTGTTGACCACCCAATGTTCTTGGAGAAA	
KOM56_2	(4901)	AACGTGGGGTTGATCGTGTTTTGTTGACCACCCAATGTTCTTGGAGAAA	
KOM56_3	(4899)	AACGTGGGGTTGATCGTGTTTTGTTGACCACCCAATGTTCTTGGAGAAA	
Consensus	(4901)	AACGTGGGGTTGATCGTGTTTTGTTGACCACCCAATGTTCTTGGAGAAA	
		4951	5000
KOM56_1	(4947)	GTAAGCATATTATGATTATAAATCCGTCTGAGGGATACGCAGAACAGGT	
KOM56_2	(4951)	GTAAGCATATTATGATTATGAATCCGTCTGAGGGATACGCAGAACAGGT	
KOM56_3	(4949)	GTAAGCATATTATGATTATGAATCCGTCTGAGGGATACGCAGAACAGGT	
Consensus	(4951)	GTAAGCATATTATGATTATGAATCCGTCTGAGGGATACGCAGAACAGGT	
		5001	5050
KOM56_1	(4997)	CATTTTGAGTATCTTTTAACTCTACTGGTGCTTTTACTCTTTTAAAGGTTT	
KOM56_2	(5001)	CATTTTGAGTATCTTTTAACTCTACTGGTGCTTTTACTCTTTTAAAGGTTT	
KOM56_3	(4999)	CATTTTGAGTATCTTTTAACTCTACTGGTGCTTTTACTCTTTTAAAGGTTT	
Consensus	(5001)	CATTTTGAGTATCTTTTAACTCTACTGGTGCTTTTACTCTTTTAAAGGTTT	
		5051	5100
KOM56_1	(5047)	GGGGCAAAC TGTTCAA AAAATCTATGGCCCCAAAGCTGGACTAGATTAT	
KOM56_2	(5051)	GGGGCAAAC TGTTCAA AAAATCTATGGCCCCAAAGCTGGACTAGATTAT	
KOM56_3	(5049)	GGGGCAAAC TGTTCAA AAAATCTATGGCCCCAAAGCTGGACTAGATTAT	
Consensus	(5051)	GGGGCAAAC TGTTCAA AAAATCTATGGCCCCAAAGCTGGACTAGATTAT	
		5101	5150
KOM56_1	(5097)	CTGGACAATGAACTTAGGTT CAGCTTGTTGTGTCAAGTAAGTTAGTTACT	
KOM56_2	(5101)	CTGGACAATGAACTTAGGTT CAGCTTGTTGTGTCAAGTAAGTTAGTTACT	
KOM56_3	(5099)	CTGGACAATGAACTTAGGTT CAGCTTGTTGTGTCAAGTAAGTTAGTTACT	
Consensus	(5101)	CTGGACAATGAACTTAGGTT CAGCTTGTTGTGTCAAGTAAGTTAGTTACT	
		5151	5200
KOM56_1	(5147)	CTTGATTTTTATGTGGCATT TTA CTCTTTTGTCTTTAATCGTTTTTTTAA	
KOM56_2	(5151)	CTTGATTTTTATGTGGCATT TTA CTCTTTTGTCTTTAATCGTTTTTTTAA	
KOM56_3	(5149)	CTTGATTTTTATGTGGCATT TTA CTCTTTTGTCTTTAATCGTTTTTTTAA	
Consensus	(5151)	CTTGATTTTTATGTGGCATT TTA CTCTTTTGTCTTTAATCGTTTTTTTAA	

		5201		5250
KOM56_1	(5197)	CCTTGTTTTCTCAGGCAGCCCTAGAGGCACCTAAAGTTTTGAATTTGAAC		
KOM56_2	(5200)	CCTTGTTTTCTCAGGCAGCCCTAGAGGCACCTAAAGTTTTGAATTTGAAC		
KOM56_3	(5199)	CCTTGTTTTCTCAGGCAGCCCTAGAGGCACCTAAAGTTTTGAATTTGAAC		
Consensus	(5201)	CCTTGTTTTCTCAGGCAGCCCTAGAGGCACCTAAAGTTTTGAATTTGAAC		
		5251		5300
KOM56_1	(5247)	AGTAGCAACTACTTCTCAGGACCATATGGTAATTAACACATCCTAGTTTC		
KOM56_2	(5250)	AGTAGCAACTACTTCTCAGGACCATATGGTAATTAACACATCCTAGTTTC		
KOM56_3	(5249)	AGTAGCAACTACTTCTCAGGACCATATGGTAATTAACACATCCTAGTTTC		
Consensus	(5251)	AGTAGCAACTACTTCTCAGGACCATATGGTAATTAACACATCCTAGTTTC		
		5301		5350
KOM56_1	(5297)	AGAAAACCTCCTTACTATATCATTTGTAGGTAATCATCTTTATTTGCCTAT		
KOM56_2	(5300)	AGAAAACCTCCTTACTATATCATTTGTAGGTAATCATCTTTATTTGCCTAT		
KOM56_3	(5299)	AGAAAACCTCCTTACTATATCATTTGTAGGTAATCATCTTTATTTGCCTAT		
Consensus	(5301)	AGAAAACCTCCTTACTATATCATTTGTAGGTAATCATCTTTATTTGCCTAT		
		5351		5400
KOM56_1	(5347)	TCCTGCAGGAGAGGATGTTCTCTTCATTGCCAATGATTGGCACACAGCTC		
KOM56_2	(5350)	TCCTGCAGGAGAGGATGTTCTCTTCATTGCCAATGATTGGCACACAGCTC		
KOM56_3	(5349)	TCCTGCAGGAGAGGATGTTCTCTTCATTGCCAATGATTGGCACACAGCTC		
Consensus	(5351)	TCCTGCAGGAGAGGATGTTCTCTTCATTGCCAATGATTGGCACACAGCTC		
		5401		5426
KOM56_1	(5397)	TCATTCCCTTGCTACTTGAAGTCAATG		
KOM56_2	(5400)	TCATTCCCTTGCTACTTGAAGTCAATG		
KOM56_3	(5399)	TCATTCCCTTGCTACTTGAAGTCAATG		
Consensus	(5401)	TCATTCCCTTGCTACTTGAAGTCAATG		

Figure 9. DNA sequence alignment of three independently amplified fragments from reactions with primers KOM56FN and KOM56RN. A consensus sequence is derived from the alignment in view of errors introduced by the DNA polymerase.

		1	50
Insert consensus	(1)	AGGTGTCATCACATAAGGTTACCGGTAAGCTCATCACACAAGGCATTGGC	
T-DNA derived seq	(1)	-----	
		51	100
Insert consensus	(51)	ACCAATATCAAACAAGACTCCACACTTTCGCTAGTGTGCAATGTTTCATCA	
T-DNA derived seq	(1)	-----	
		101	150
Insert consensus	(101)	CAAAAGACTCATTCAATAACCGGCTAGTTACAATGAGATGCAAAAAGTTC	
T-DNA derived seq	(1)	-----	
		151	200
Insert consensus	(151)	ACATATTATCTATGCAACTTTATTTAGCATCATCATAGCCGTACATTTCAT	
T-DNA derived seq	(1)	-----	
		201	250
Insert consensus	(201)	TTTTGTTTCGATTAAGAGCACTATTCAAGTCATCGGTATTGATCATAACCG	
T-DNA derived seq	(1)	-----	
		251	300
Insert consensus	(251)	ATACTCAAATTTGCAAAAAGAACAACCACAATCAAACAAAATAAGAGGTGG	
T-DNA derived seq	(1)	-----	
		301	350
Insert consensus	(301)	CAAAAATTTTCAGAAGGTCAAAAACCATTTACAATTGAAACAAGGAGTC	
T-DNA derived seq	(1)	-----	
		351	400
Insert consensus	(351)	ATAAGCTCAAACATCCACAAAACAGTGTCAAACACAATTTACAGCACAA	
T-DNA derived seq	(1)	-----	
		401	450
Insert consensus	(401)	AAACCAATATATAAAACAAAAATGATAATCACAAAGAGGTAGGTATGCACT	
T-DNA derived seq	(1)	-----CACT	
		451	500
Insert consensus	(451)	GATAGTTTAAACTGAAGCGGGAAACGACAATCTGATCATGAGCGGAGAA	
T-DNA derived seq	(5)	GATAGTTTAAACTGAAGCGGGAAACGACAATCTGATCATGAGCGGAGAA	
		501	550
Insert consensus	(501)	TTAAGGGAGTCACGTTATGACCCCGCCGATGACGCGGGACAAGCCGTTT	
T-DNA derived seq	(55)	TTAAGGGAGTCACGTTATGACCCCGCCGATGACGCGGGACAAGCCGTTT	
		551	600
Insert consensus	(551)	TACGTTTGGAACTGACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
T-DNA derived seq	(105)	TACGTTTGGAACTGACAGAACCGCAACGTTGAAGGAGCCACTCAGCCGCG	
		601	650
Insert consensus	(601)	GGTTTCTGGAGTTTAAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	
T-DNA derived seq	(155)	GGTTTCTGGAGTTTAAATGAGCTAAGCACATACGTCAGAAACCATTTATTGC	
		651	700
Insert consensus	(651)	GCGTTCAAAGTTCGCCTAAGGTCACTATCAGCTAGCAAATATTTCTTGTG	
T-DNA derived seq	(205)	GCGTTCAAAGTTCGCCTAAGGTCACTATCAGCTAGCAAATATTTCTTGTG	
		701	750
Insert consensus	(701)	AAAAATGCTCCACTGACGTTCCATAAAATCCCCCTCGGTATCCAATTAGAG	
T-DNA derived seq	(255)	AAAAATGCTCCACTGACGTTCCATAAAATCCCCCTCGGTATCCAATTAGAG	
		751	800
Insert consensus	(751)	TCTCATATTCACCTCTCAATCCAAATAATCTGCACCGGATCTGGATCGTTT	
T-DNA derived seq	(305)	TCTCATATTCACCTCTCAATCCAAATAATCTGCACCGGATCTGGATCGTTT	
		801	850
Insert consensus	(801)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
T-DNA derived seq	(355)	CGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGT	
		851	900
Insert consensus	(851)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
T-DNA derived seq	(405)	GGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTG	
		901	950
Insert consensus	(901)	ATGCCCGCGTGTCCGGCTGTCAGCGCAGGGCGCCCGTTCCTTTTGTGTC	
T-DNA derived seq	(455)	ATGCCCGCGTGTCCGGCTGTCAGCGCAGGGCGCCCGTTCCTTTTGTGTC	
		951	1000
Insert consensus	(951)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
T-DNA derived seq	(505)	AAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCG	
		1001	1050
Insert consensus	(1001)	GCTATCGTGGCTGGCCACGACGGCGTTCCTTGCGCAGCTGTGCTCGACG	
T-DNA derived seq	(555)	GCTATCGTGGCTGGCCACGACGGCGTTCCTTGCGCAGCTGTGCTCGACG	
		1051	1100
Insert consensus	(1051)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG	
T-DNA derived seq	(605)	TTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG	
		1101	1150
Insert consensus	(1101)	CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
T-DNA derived seq	(655)	CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCAT	
		1151	1200
Insert consensus	(1151)	GGCTGATGCAATGCGGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
T-DNA derived seq	(705)	GGCTGATGCAATGCGGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCAT	
		1201	1250
Insert consensus	(1201)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTIONCGGATGGAA	
T-DNA derived seq	(755)	TCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTIONCGGATGGAA	

		1251	1300
Insert consensus	(1251)	GCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	
T-DNA derived seq	(805)	GCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC	
		1301	1350
Insert consensus	(1301)	GCCAGCCGAACGTGTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
T-DNA derived seq	(855)	GCCAGCCGAACGTGTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATG	
		1351	1400
Insert consensus	(1351)	ATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
T-DNA derived seq	(905)	ATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAA	
		1401	1450
Insert consensus	(1401)	AATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
T-DNA derived seq	(955)	AATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGA	
		1451	1500
Insert consensus	(1451)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
T-DNA derived seq	(1005)	CCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG	
		1501	1550
Insert consensus	(1501)	GCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCC	
T-DNA derived seq	(1055)	GCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCC	
		1551	1600
Insert consensus	(1551)	GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGC	
T-DNA derived seq	(1105)	GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGC	
		1601	1650
Insert consensus	(1601)	GGGACTCTGGGTTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
T-DNA derived seq	(1155)	GGGACTCTGGGTTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATC	
		1651	1700
Insert consensus	(1651)	ACGAGATTTTCGATTCACCCGCCCTTCTATGAAAGGTTGGGCTTCGGAA	
T-DNA derived seq	(1205)	ACGAGATTTTCGATTCACCCGCCCTTCTATGAAAGGTTGGGCTTCGGAA	
		1701	1750
Insert consensus	(1701)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
T-DNA derived seq	(1255)	TCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATG	
		1751	1800
Insert consensus	(1751)	CTGGAGTTCTTCGCCACGGGATCTCTCGGGAACAGGCGGTTCGAAGGTGC	
T-DNA derived seq	(1305)	CTGGAGTTCTTCGCCACGGGATCTCTCGGGAACAGGCGGTTCGAAGGTGC	
		1801	1850
Insert consensus	(1801)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
T-DNA derived seq	(1355)	CGATATCATTACGACAGCAACGGCCGACAAGCACAACGCCACGATCCTGA	
		1851	1900
Insert consensus	(1851)	GCGACAATATGATCGGGCCCGGCTCCACATCAACGGCGTCGGCGGGCAGC	
T-DNA derived seq	(1405)	GCGACAATATGATCGGGCCCGGCTCCACATCAACGGCGTCGGCGGGCAGC	
		1901	1950
Insert consensus	(1901)	TGCCAGGCAAGACCGAGATGCACCGGATATCTTGCTGCGTTCCGATAT	
T-DNA derived seq	(1455)	TGCCAGGCAAGACCGAGATGCACCGGATATCTTGCTGCGTTCCGATAT	
		1951	2000
Insert consensus	(1951)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA	
T-DNA derived seq	(1505)	TTTCGTGGAGTTCCCGCCACAGACCCGGATGATCCCCGATCGTTCAAACA	
		2001	2050
Insert consensus	(2001)	TTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG	
T-DNA derived seq	(1555)	TTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATG	
		2051	2100
Insert consensus	(2051)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACAT	
T-DNA derived seq	(1605)	ATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACAT	
		2101	2150
Insert consensus	(2101)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGC	
T-DNA derived seq	(1655)	GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGC	
		2151	2200
Insert consensus	(2151)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGAAAAC TAG	
T-DNA derived seq	(1705)	AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGAAAAC TAG	
		2201	2250
Insert consensus	(2201)	GATAAATTATCGCGCGCGGTGTATCTATGTTACTAGATCGGGCCTCCTG	
T-DNA derived seq	(1755)	GATAAATTATCGCGCGCGGTGTATCTATGTTACTAGATCGGGCCTCCTG	
		2251	2300
Insert consensus	(2251)	TCAATGCTGGCGCGGCTCTGGTGGTGGTTCTGGTGGCGGCTCTGAGGGT	
T-DNA derived seq	(1805)	TCAATGCTGGCGCGGCTCTGGTGGTGGTTCTGGTGGCGGCTCTGAGGGT	
		2301	2350
Insert consensus	(2301)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG	
T-DNA derived seq	(1855)	GGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGGCGG	
		2351	2400
Insert consensus	(2351)	TTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCAA	
T-DNA derived seq	(1905)	TTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCAA	
		2401	2450
Insert consensus	(2401)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAG	
T-DNA derived seq	(1955)	ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAG	
		2451	2500
Insert consensus	(2451)	TCTGACGCTAAAGGCAAACCTTGATTCTGTGCTACTGATTACGGTGCTGC	
T-DNA derived seq	(2005)	TCTGACGCTAAAGGCAAACCTTGATTCTGTGCTACTGATTACGGTGCTGC	

		2501		2550
Insert consensus	(2501)	TATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGGTG		
T-DNA derived seq	(2055)	TATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGGTG		
		2551		2600
Insert consensus	(2551)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAATATTTACCTTCCCT		
T-DNA derived seq	(2105)	CTACTGGTGATTTTGCTGGCTCTAATTCCTCAATATTTACCTTCCCT		
		2601		2650
Insert consensus	(2601)	GGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCT		
T-DNA derived seq	(2155)	GGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCT		
		2651		2700
Insert consensus	(2651)	CCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCCCAATACGCAAAC		
T-DNA derived seq	(2205)	CCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCCCAATACGCAAAC		
		2701		2750
Insert consensus	(2701)	CGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCAGCAGG		
T-DNA derived seq	(2255)	CGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCAGCAGG		
		2751		2800
Insert consensus	(2751)	TTTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTA		
T-DNA derived seq	(2305)	TTTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTA		
		2801		2850
Insert consensus	(2801)	GCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTA		
T-DNA derived seq	(2355)	GCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTA		
		2851		2900
Insert consensus	(2851)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT		
T-DNA derived seq	(2405)	TGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTAT		
		2901		2950
Insert consensus	(2901)	GACCATGATTACGCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT		
T-DNA derived seq	(2455)	GACCATGATTACGCAAGCTTTAACGAGATAGAAAATTATGTTACTCCGT		
		2951		3000
Insert consensus	(2951)	TTTGTTCATTACTTAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT		
T-DNA derived seq	(2505)	TTTGTTCATTACTTAACAAATGCAACAGTATCTTGTACCAAATCCTTTCT		
		3001		3050
Insert consensus	(3001)	CTCTTTTCAAACTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA		
T-DNA derived seq	(2555)	CTCTTTTCAAACTTTTCTATTTGGCTGTTGACGGAGTAATCAGGATACAA		
		3051		3100
Insert consensus	(3051)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTTATGAATC		
T-DNA derived seq	(2605)	ACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGATTTATGAATC		
		3101		3150
Insert consensus	(3101)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA		
T-DNA derived seq	(2655)	CTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATACTTGACAGTA		
		3151		3200
Insert consensus	(3151)	TCTTCTGTTTGGGTATTTTTTTTTCCTGCCAAGTGGAAACGGAGACATGT		
T-DNA derived seq	(2705)	TCTTCTGTTTGGGTATTTTTTTTTCCTGCCAAGTGGAAACGGAGACATGT		
		3201		3250
Insert consensus	(3201)	TATGATGTATACGGGAAGCTCGTTAAAAAATAACAATAGGAAGAAAT		
T-DNA derived seq	(2755)	TATGATGTATACGGGAAGCTCGTTAAAAAATAACAATAGGAAGAAAT		
		3251		3300
Insert consensus	(3251)	GTAACAAACATTGAATGTTGTTTTTAACCATCCTTCCCTTTAGCAGTGTAT		
T-DNA derived seq	(2805)	GTAACAAACATTGAATGTTGTTTTTAACCATCCTTCCCTTTAGCAGTGTAT		
		3301		3350
Insert consensus	(3301)	CAATTTTGTAAATAGAACCATGCATCTCAATCTTAATACTAAAATGCAACT		
T-DNA derived seq	(2855)	CAATTTTGTAAATAGAACCATGCATCTCAATCTTAATACTAAAATGCAACT		
		3351		3400
Insert consensus	(3351)	TAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGTG		
T-DNA derived seq	(2905)	TAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTTTAGAATTGTG		
		3401		3450
Insert consensus	(3401)	CATTCATAATTAGATCTTGTGTTGTCGTAAAAAATAGAAAATATATTTAC		
T-DNA derived seq	(2955)	CATTCATAATTAGATCTTGTGTTGTCGTAAAAAATAGAAAATATATTTAC		
		3451		3500
Insert consensus	(3451)	AGTAATTTGGAATACAAAGCTAAGGGGAAGTAATAATTTCTAGTGGTA		
T-DNA derived seq	(3005)	AGTAATTTGGAATACAAAGCTAAGGGGAAGTAATAATTTCTAGTGGTA		
		3501		3550
Insert consensus	(3501)	GGGAGGGACCAGTACCAGTACCTAGATATATTTTAAATTAATAATAA		
T-DNA derived seq	(3055)	GGGAGGGACCAGTACCAGTACCTAGATATATTTTAAATTAATAATAA		
		3551		3600
Insert consensus	(3551)	TAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAGG		
T-DNA derived seq	(3105)	TAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAGCGGTAGGAGG		
		3601		3650
Insert consensus	(3601)	GAGTTGGTTTAGTTTTTTTAGATACTAGGAGACAGAACCAGGACGGCCAT		
T-DNA derived seq	(3155)	GAGTTGGTTTAGTTTTTTTAGATACTAGGAGACAGAACCAGGACGGCCAT		
		3651		3700
Insert consensus	(3651)	TGCAAGGCCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCCA		
T-DNA derived seq	(3205)	TGCAAGGCCCAAGTTGAAGTCCAGCCGTGAATCAACAAAGAGAGGGCCCA		
		3701		3750
Insert consensus	(3701)	TAATACTGTCGATGAGCATTCCCTATAATACAGTGTCCACAGTTGCCTT		
T-DNA derived seq	(3255)	TAATACTGTCGATGAGCATTCCCTATAATACAGTGTCCACAGTTGCCTT		

		3751		3800
Insert consensus	(3751)	CTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAACC		
T-DNA derived seq	(3305)	CTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGTCACTGAAACC		
		3801		3850
Insert consensus	(3801)	TGCTACAAATAAGGCAGGCACCTCCTCATCTCACTCACTCACTCACACA		
T-DNA derived seq	(3355)	TGCTACAAATAAGGCAGGCACCTCCTCATCTCACTCACTCACTCACACA		
		3851		3900
Insert consensus	(3851)	GCTCAACAAGTGGTAACTTTTACTCATCTCCTCCAATTATTTCTGATTC		
T-DNA derived seq	(3405)	GCTCAACAAGTGGTAACTTTTACTCATCTCCTCCAATTATTTCTGATTC		
		3901		3950
Insert consensus	(3901)	ATGCAGGTGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCAG		
T-DNA derived seq	(3455)	ATGCAGGTGACTCTAGAGGATCTGATCATATGCATAGGATGAGTAGCAG		
		3951		4000
Insert consensus	(3951)	GTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGAG		
T-DNA derived seq	(3505)	GTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAGATACCATGAG		
		4001		4050
Insert consensus	(4001)	TCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAAC		
T-DNA derived seq	(3555)	TCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAATCCGATGAAC		
		4051		4100
Insert consensus	(4051)	TTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTCT		
T-DNA derived seq	(3605)	TTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCTCCTCAAGTCT		
		4101		4150
Insert consensus	(4101)	GCCGATGAAGCCAATCAAAGGGATCTTCTTGTC AACAGGCAAGCCAAC TG		
T-DNA derived seq	(3655)	GCCGATGAAGCCAATCAAAGGGATCTTCTTGTC AACAGGCAAGCCAAC TG		
		4151		4200
Insert consensus	(4151)	CTGCTTGAAGAGCTCCTTTAGTAAAGGTTTTGCGTCCATGACCTGTATA		
T-DNA derived seq	(3705)	CTGCTTGAAGAGCTCCTTTAGTAAAGGTTTTGCGTCCATGACCTGTATA		
		4201		4250
Insert consensus	(4201)	GAGATTTTGATTAGCAAGAACTCTTAAATTTTCATAAACATACAAAATAAT		
T-DNA derived seq	(3755)	GAGATTTTGATTAGCAAGAACTCTTAAATTTTCATAAACATACAAAATAAT		
		4251		4300
Insert consensus	(4251)	TTAGTATATACTGGAGTCGAAAAATCTTATCTTACAGTGGTTATATCGT		
T-DNA derived seq	(3805)	TTAGTATATACTGGAGTCGAAAAATCTTATCTTACAGTGGTTATATCGT		
		4301		4350
Insert consensus	(4301)	ATTTGACATCTGTGATTTGTTCAGTCGCTGGGTTCCACTCTTGTGTATCC		
T-DNA derived seq	(3855)	ATTTGACATCTGTGATTTGTTCAGTCGCTGGGTTCCACTCTTGTGTATCC		
		4351		4400
Insert consensus	(4351)	ATGCCATTACCAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCAA		
T-DNA derived seq	(3905)	ATGCCATTACCAATCCCAGTTATGCAAGTCTTACGAAGGACACTGTCCAA		
		4401		4450
Insert consensus	(4401)	TTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGGC		
T-DNA derived seq	(3955)	TTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCATAGTATGGGC		
		4451		4500
Insert consensus	(4451)	TCACTGTAACCACCTATGTGATTCTAATATCCAGCCTTCATCCAGTTG		
T-DNA derived seq	(4005)	TCACTGTAACCACCTATGTGATTCTAATATCCAGCCTTCATCCAGTTG		
		4501		4550
Insert consensus	(4501)	ATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTAAAAACTC		
T-DNA derived seq	(4055)	ATTTTCCTACCCTTAACAGGCTTCTCATATCTGCAAAAATTTAAAAACTC		
		4551		4600
Insert consensus	(4551)	AAATTTACTAGCATCAAAAAGAGCTTCAAAAAGTTGGAGGCTGATTTCAAGC		
T-DNA derived seq	(4105)	AAATTTACTAGCATCAAAAAGAGCTTCAAAAAGTTGGAGGCTGATTTCAAGC		
		4601		4650
Insert consensus	(4601)	ATAAATACATACCCATCAATGAAATCAAAAAGAAGCCCTGAATTCATCAGG		
T-DNA derived seq	(4155)	ATAAATACATACCCATCAATGAAATCAAAAAGAAGCCCTGAATTCATCAGG		
		4651		4700
Insert consensus	(4651)	AAGATTGAGAAGAGGGAAGTCAGAGAAAAGAAAATCGACCTTGGTAGGCAA		
T-DNA derived seq	(4205)	AAGATTGAGAAGAGGGAAGTCAGAGAAAAGAAAATCGACCTTGGTAGGCAA		
		4701		4750
Insert consensus	(4701)	TGTTATGGATGCAGAAAAGCAACCTGGAGGCAATGTGAAATTTATCATATA		
T-DNA derived seq	(4255)	TGTTATGGATGCAGAAAAGCAACCTGGAGGCAATGTGAAATTTATCATATA		
		4751		4800
Insert consensus	(4751)	TTAATACAACCTTACTGATTTGCAGGGTAACGTGCAATCGAGTGAATACA		
T-DNA derived seq	(4305)	TTAATACAACCTTACTGATTTGCAGGGTAACGTGCAATCGAGTGAATACA		
		4801		4850
Insert consensus	(4801)	AAGAAATTTTACCTTGGCATTCAAGTAGATTCTCTGGACTGGTACATTG		
T-DNA derived seq	(4355)	AAGAAATTTTACCTTGGCATTCAAGTAGATTCTCTGGACTGGTACATTG		
		4851		4900
Insert consensus	(4851)	ACTTCAAGTAGCAAGGAATGAGAGCTGTGTGCCAATCATTTGGCAATGAAG		
T-DNA derived seq	(4405)	ACTTCAAGTAGCAAGGAATGAGAGCTGTGTGCCAATCATTTGGCAATGAAG		
		4901		4950
Insert consensus	(4901)	AGAACATCCTCTCCTGCAGGAATAGGCAAAAATAAAGATGATTACCTACAA		
T-DNA derived seq	(4455)	AGAACATCCTCTCCTGCAGGAATAGGCAAAAATAAAGATGATTACCTACAA		
		4951		5000
Insert consensus	(4951)	TGATATAGTAAGGAGTTTTCTGAAACTAGGATGTGTTAATTACCATATGG		
T-DNA derived seq	(4505)	TGATATAGTAAGGAGTTTTCTGAAACTAGGATGTGTTAATTACCATATGG		

		5001		5050
Insert consensus	(5001)	TCCTGAGAAGTAGTTGCTACTGTTCAAATTCAAAACCTTAGGTGCCTCTA		
T-DNA derived seq	(4555)	TCCTGAGAAGTAGTTGCTACTGTTCAAATTCAAAACCTTAGGTGCCTCTA		
		5051		5100
Insert consensus	(5051)	GGGCTGCCTGAGAAAACAGGTTAAAAAACGATTAAGACAAAAGAGTA		
T-DNA derived seq	(4605)	GGGCTGCCTGAGAAAACAGGTTAAAAAACGATTAAGACAAAAGAGTA		
		5101		5150
Insert consensus	(5101)	AAATGCCACATAAAAATCAAGAGTAACCTACTTGACACAACAAGCT		
T-DNA derived seq	(4655)	AAATGCCACATAAAAATCAAGAGTAACCTACTTGACACAACAAGCT		
		5151		5200
Insert consensus	(5151)	GAACCTAAGTTCATTGTCCAGATAATCTAGTCCAGCTTTGGGGCCATAGA		
T-DNA derived seq	(4705)	GAACCTAAGTTCATTGTCCAGATAATCTAGTCCAGCTTTGGGGCCATAGA		
		5201		5250
Insert consensus	(5201)	TTTTTGAACCAGTTTGGCCCAAACCTTAAAAGAGTAAAAGCACCAGTAG		
T-DNA derived seq	(4755)	TTTTTGAACCAGTTTGGCCCAAACCTTAAAAGAGTAAAAGCACCAGTAG		
		5251		5300
Insert consensus	(5251)	AGTTAAAAGATACTCAAATGACCTGTTCTGCGTATCCCTCAGGACGGAT		
T-DNA derived seq	(4805)	AGTTAAAAGATACTCAAATGACCTGTTCTGCGTATCCCTCAGGACGGAT		
		5301		5350
Insert consensus	(5301)	TCATAATCATAATATGCTTACTTTCTCCAAGAACATTGGGTGGTCAACAA		
T-DNA derived seq	(4855)	TCATAATCATAATATGCTTACTTTCTCCAAGAACATTGGGTGGTCAACAA		
		5351		5400
Insert consensus	(5351)	AAACACGATCAACCCACGTTTATAGCAGTGAAAGAAACGAACAATTTCA		
T-DNA derived seq	(4905)	AAACACGATCAACCCACGTTTATAGCAGTGAAAGAAACGAACAATTTCA		
		5401		5450
Insert consensus	(5401)	ATGCTGTCTCCAACCTTTGACCTGCAGATGATCACATTCTTGAATCAGGAA		
T-DNA derived seq	(4955)	ATGCTGTCTCCAACCTTTGACCTGCAGATGATCACATTCTTGAATCAGGAA		
		5451		5500
Insert consensus	(5451)	ATGTAAGAGAACAATATGTACCGTATCAATATAGGAAGATGTACCTCAA		
T-DNA derived seq	(5005)	ATGTAAGAGAACAATATGTACCGTATCAATATAGGAAGATGTACCTCAA		
		5501		5550
Insert consensus	(5501)	CCGCAACGCCAGTATCCCAAGCATCTTTGTATTGGTCATAACGGGGGGAT		
T-DNA derived seq	(5055)	CCGCAACGCCAGTATCCCAAGCATCTTTGTATTGGTCATAACGGGGGGAT		
		5551		5600
Insert consensus	(5551)	ATTGTCATTACCCGATGTCCGCGGGCCTAAATGATAAAAAGACTGATGCA		
T-DNA derived seq	(5105)	ATTGTCATTACCCGATGTCCGCGGGCCTAAATGATAAAAAGACTGATGCA		
		5601		5650
Insert consensus	(5601)	GTAGAACTAACTAAACAAAATAAGTAATGAATGAGTAGGTAACCAAATG		
T-DNA derived seq	(5155)	GTAGAACTAACTAAACAAAATAAGTAATGAATGAGTAGGTAACCAAATG		
		5651		5700
Insert consensus	(5651)	AAAGAAAGACTTACTGCAAGGGCTGGTGGTAGTCCTCCAACCTTTGAAGC		
T-DNA derived seq	(5205)	AAAGAAAGACTTACTGCAAGGGCTGGTGGTAGTCCTCCAACCTTTGAAGC		
		5701		5750
Insert consensus	(5701)	TCTTTTGATGCTAGTAAATTGAGTTTTTAAAAATTTGCAGATATGAGAAG		
T-DNA derived seq	(5255)	TCTTTTGATGCTAGTAAATTGAGTTTTTAAAAATTTGCAGATATGAGAAG		
		5751		5800
Insert consensus	(5751)	CCTGTTAAGGGTAGGAAAATCAACTGGATGAAGGCTGGGATATTAGAATC		
T-DNA derived seq	(5305)	CCTGTTAAGGGTAGGAAAATCAACTGGATGAAGGCTGGGATATTAGAATC		
		5801		5850
Insert consensus	(5801)	ACATAGGGTGGTTACAGTGAGCCATACTATGCCAAGAACTTGTCTCTG		
T-DNA derived seq	(5355)	ACATAGGGTGGTTACAGTGAGCCATACTATGCCAAGAACTTGTCTCTG		
		5851		5900
Insert consensus	(5851)	CTGTTGACAAGGGAGTTGAATTGGACAGTGTCTTCGTAAGACTTGCATA		
T-DNA derived seq	(5405)	CTGTTGACAAGGGAGTTGAATTGGACAGTGTCTTCGTAAGACTTGCATA		
		5901		5950
Insert consensus	(5901)	ACTGGGATTGTGAATGGCATGGATACACAAGAGTGGAACCCAGCGACTGA		
T-DNA derived seq	(5455)	ACTGGGATTGTGAATGGCATGGATACACAAGAGTGGAACCCAGCGACTGA		
		5951		6000
Insert consensus	(5951)	CAAATACACAGATGTCAAATACGATATAACCCTGTAAGATAAGATTTTT		
T-DNA derived seq	(5505)	CAAATACACAGATGTCAAATACGATATAACCCTGTAAGATAAGATTTTT		
		6001		6050
Insert consensus	(6001)	CCGACTCCAGTATATACTAAATATTTTGTATGTTTATGAAATTAAGAG		
T-DNA derived seq	(5555)	CCGACTCCAGTATATACTAAATATTTTGTATGTTTATGAAATTAAGAG		
		6051		6100
Insert consensus	(6051)	TTCTTGCTAATCAAATCTCTATACAGGTCATGGACGCAAAACCTTTACT		
T-DNA derived seq	(5605)	TTCTTGCTAATCAAATCTCTATACAGGTCATGGACGCAAAACCTTTACT		
		6101		6150
Insert consensus	(6101)	AAAGGAGGCTCTTCAAGCAGCAGTTGGCTTGCCTGTTGACAAGAAGATCC		
T-DNA derived seq	(5655)	AAAGGAGGCTCTTCAAGCAGCAGTTGGCTTGCCTGTTGACAAGAAGATCC		
		6151		6200
Insert consensus	(6151)	CTTTGATTGGCTTCATCGGCAGACTTGAGGAGCAGAAAGGTTTCAAGATTT		
T-DNA derived seq	(5705)	CTTTGATTGGCTTCATCGGCAGACTTGAGGAGCAGAAAGGTTTCAAGATTT		
		6201		6250
Insert consensus	(6201)	CTTGTGCTGCAATTCACAAGTTCATCGGATTGGATGTTCAAATTTGTAGT		
T-DNA derived seq	(5755)	CTTGTGCTGCAATTCACAAGTTCATCGGATTGGATGTTCAAATTTGTAGT		

		6251		6300
Insert consensus	(6251)	CCTTGTAAGTACCAAATGGACTCATGGTATCTCTCTTGTGAGTTACTT		
T-DNA derived seq	(5805)	CCTTGTAAGTACCAAATGGACTCATGGTATCTCTCTTGTGAGTTACTT		
		6301		6350
Insert consensus	(6301)	GTGCCGAAACTGAAATTGACCTGCTACTCATCCTATGCATATGATCAGAT		
T-DNA derived seq	(5855)	GTGCCGAAACTGAAATTGACCTGCTACTCATCCTATGCATATGATCAGAT		
		6351		6400
Insert consensus	(6351)	CCTCTAGAGTCGACCTGCATGAAATCAGAAATAATTGGAGGAGATGAGTA		
T-DNA derived seq	(5905)	CCTCTAGAGTCGACCTGCATGAAATCAGAAATAATTGGAGGAGATGAGTA		
		6401		6450
Insert consensus	(6401)	AAAGTTACCACTTGTGAGCTGTGTGAGTGAGTGAGTGAGAATGAGGAGG		
T-DNA derived seq	(5955)	AAAGTTACCACTTGTGAGCTGTGTGAGTGAGTGAGTGAGAATGAGGAGG		
		6451		6500
Insert consensus	(6451)	TGCTGCCTTATTTGTAGCAGGTTTTCAGTGACACGTGTCAAGAGAATAGC		
T-DNA derived seq	(6005)	TGCTGCCTTATTTGTAGCAGGTTTTCAGTGACACGTGTCAAGAGAATAGC		
		6501		6550
Insert consensus	(6501)	GGGTGGCTATCCCTTAGCAGAAGGCAACTGTGGACACTGTATTATAGGGA		
T-DNA derived seq	(6055)	GGGTGGCTATCCCTTAGCAGAAGGCAACTGTGGACACTGTATTATAGGGA		
		6551		6600
Insert consensus	(6551)	AATGCTCATCGACAGTATTATGGGCCCTCTTTGTTGATTACGGCTGG		
T-DNA derived seq	(6105)	AATGCTCATCGACAGTATTATGGGCCCTCTTTGTTGATTACGGCTGG		
		6601		6650
Insert consensus	(6601)	ACTTCAACTTGGGCCTTGCAATGGGCCCTCCGTTCTGTCTCCTAGTAT		
T-DNA derived seq	(6155)	ACTTCAACTTGGGCCTTGCAATGGGCCCTCCGTTCTGTCTCCTAGTAT		
		6651		6700
Insert consensus	(6651)	CTAAAAAATAAACCAACTCCCTCCTACCCTACCCTTGACATTCCCTAT		
T-DNA derived seq	(6205)	CTAAAAAATAAACCAACTCCCTCCTACCCTACCCTTGACATTCCCTAT		
		6701		6750
Insert consensus	(6701)	GTCTCGTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT		
T-DNA derived seq	(6255)	GTCTCGTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT		
		6751		6800
Insert consensus	(6751)	TACTGGTACTGGTCCCTCCCTCCACTAGAATATTAGTTACTTCCCCCTTA		
T-DNA derived seq	(6305)	TACTGGTACTGGTCCCTCCCTCCACTAGAATATTAGTTACTTCCCCCTTA		
		6801		6850
Insert consensus	(6801)	GCTTTGTATTCCAAATTACTGTAAATATATTTTCTAATTTTTTACGACAA		
T-DNA derived seq	(6355)	GCTTTGTATTCCAAATTACTGTAAATATATTTTCTAATTTTTTACGACAA		
		6851		6900
Insert consensus	(6851)	ACAAGATCTAATTAATGAATGCACAATTTAAAGGTTGAATACATTACTTT		
T-DNA derived seq	(6405)	ACAAGATCTAATTAATGAATGCACAATTTAAAGGTTGAATACATTACTTT		
		6901		6950
Insert consensus	(6901)	ACTTGGTTTAGCCTATATTAAGTTGCATTTTAGTATTAAGATTGAGATGC		
T-DNA derived seq	(6455)	ACTTGGTTTAGCCTATATTAAGTTGCATTTTAGTATTAAGATTGAGATGC		
		6951		7000
Insert consensus	(6951)	ATGGTTCTATTACAAAATTGATACACTGCTAAAGGAAGGATGGTTAAAAA		
T-DNA derived seq	(6505)	ATGGTTCTATTACAAAATTGATACACTGCTAAAGGAAGGATGGTTAAAAA		
		7001		7050
Insert consensus	(7001)	CAACATTCAATGTTTGTACATTTCTTCTATTGTATTTTTTTTTTAACG		
T-DNA derived seq	(6555)	CAACATTCAATGTTTGTACATTTCTTCTATTGTATTTTTTTTTTAACG		
		7051		7100
Insert consensus	(7051)	AGCTTCCCGTATACATCATAACATGCTCCCGTTCCACTTGGCAGGAAAAA		
T-DNA derived seq	(6605)	AGCTTCCCGTATACATCATAACATGCTCCCGTTCCACTTGGCAGGAAAAA		
		7101		7150
Insert consensus	(7101)	AAAATACCCAAACAGGAAGATACTGTCAAGTATATCCATAGATGAGGACT		
T-DNA derived seq	(6655)	AAAATACCCAAACAGGAAGATACTGTCAAGTATATCCATAGATGAGGACT		
		7151		7200
Insert consensus	(7151)	TAATGGATAGGCTTTTCGAGGATTATAAATCATAAATCTGGCGGAGGA		
T-DNA derived seq	(6705)	TAATGGATAGGCTTTTCGAGGATTATAAATCATAAATCTGGCGGAGGA		
		7201		7250
Insert consensus	(7201)	GTCAATTAATACTTGTGGTTTGTATCCTGATTACTCCGTCAACAGCCAA		
T-DNA derived seq	(6755)	GTCAATTAATACTTGTGGTTTGTATCCTGATTACTCCGTCAACAGCCAA		
		7251		7300
Insert consensus	(7251)	ATAGAAAAGTTTGAAAAGAGAGAAAGGATTTGGTACAAGATACTGTTGCA		
T-DNA derived seq	(6805)	ATAGAAAAGTTTGAAAAGAGAGAAAGGATTTGGTACAAGATACTGTTGCA		
		7301		7350
Insert consensus	(7301)	TTTGTAAAGTAATGAACAAAACGGAGTAACATAATTTTCTATCTCGTTAA		
T-DNA derived seq	(6855)	TTTGTAAAGTAATGAACAAAACGGAGTAACATAATTTTCTATCTCGTTAA		
		7351		7400
Insert consensus	(7351)	AGCTTGGCGTAATCATGGTCATAGCTGTTTCCCTGTGTGAAAATTGTTATCC		
T-DNA derived seq	(6905)	AGCTTGGCGTAATCATGGTCATAGCTGTTTCCCTGTGTGAAAATTGTTATCC		
		7401		7450
Insert consensus	(7401)	GCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCT		
T-DNA derived seq	(6955)	GCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCT		
		7451		7500
Insert consensus	(7451)	GGGGTGCCTAATGAGTGAGCTAACTCACATTAATGCGTTGCGCTCACTG		
T-DNA derived seq	(7005)	GGGGTGCCTAATGAGTGAGCTAACTCACATTAATGCGTTGCGCTCACTG		

		7501		7550
Insert consensus	(7501)	CCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGG		
T-DNA derived seq	(7055)	CCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGG		
		7551		7600
Insert consensus	(7551)	CCAACGCGCGGGGAGAGCGGTTTGCCTATTGGGCCAAAGACAAAAGGGC		
T-DNA derived seq	(7105)	CCAACGCGCGGGGAGAGCGGTTTGCCTATTGGGCCAAAGACAAAAGGGC		
		7601		7650
Insert consensus	(7601)	GACATTCAACCGATTGAGGGAGGGAAGGTAAATATTGACGGAATTATTC		
T-DNA derived seq	(7155)	GACATTCAACCGATTGAGGGAGGGAAGGTAAATATTGACGGAATTATTC		
		7651		7700
Insert consensus	(7651)	ATTAAAGGTGAATTATCACCGTCACCGACTTGAGCCATTGGGAATTAGA		
T-DNA derived seq	(7205)	ATTAAAGGTGAATTATCACCGTCACCGACTTGAGCCATTGGGAATTAGA		
		7701		7750
Insert consensus	(7701)	GCCAGCAAAATCACCGTAGCACCATTACCATTAGCAAGGCCGGAACCGT		
T-DNA derived seq	(7255)	GCCAGCAAAATCACCGTAGCACCATTACCATTAGCAAGGCCGGAACCGT		
		7751		7800
Insert consensus	(7751)	CACCAATGAAACCATCGATAGCAGCACCGTAATCAGTAGCGACAGAATCA		
T-DNA derived seq	(7305)	CACCAATGAAACCATCGATAGCAGCACCGTAATCAGTAGCGACAGAATCA		
		7801		7850
Insert consensus	(7801)	AGTTTGCCTTTAGCGTCAGACTGTAGCGCGTTTTTCATCGGCATTTTCGGT		
T-DNA derived seq	(7355)	AGTTTGCCTTTAGCGTCAGACTGTAGCGCGTTTTTCATCGGCATTTTCGGT		
		7851		7900
Insert consensus	(7851)	CATAGCCCCCTTATTAGCGTTTGCCTCTTTTCATAATCAAATCACCGG		
T-DNA derived seq	(7405)	CATAGCCCCCTTATTAGCGTTTGCCTCTTTTCATAATCAAATCACCGG		
		7901		7950
Insert consensus	(7901)	AACCAGAGCCACCACCGAACCCTCCCTCAGAGCCGCCACCCTCAGAA		
T-DNA derived seq	(7455)	AACCAGAGCCACCACCGAACCCTCCCTCAGAGCCGCCACCCTCAGAA		
		7951		8000
Insert consensus	(7951)	CCGCCACCCTCAGAGCCACCACCCTCAGAGCCGCCACCAGAACCACCACC		
T-DNA derived seq	(7505)	CCGCCACCCTCAGAGCCACCACCCTCAGAGCCGCCACCAGAACCACCACC		
		8001		8050
Insert consensus	(8001)	AGAGCCGCGCCAGCATTGACAGGAGGCCGATCTAGTAACATAGATGAC		
T-DNA derived seq	(7555)	AGAGCCGCGCCAGCATTGACAGGAGGCCGATCTAGTAACATAGATGAC		
		8051		8100
Insert consensus	(8051)	ACCGCGCGGATAATTTATCCTAGTTTGCAGCTATATTTGTTTCTAT		
T-DNA derived seq	(7605)	ACCGCGCGGATAATTTATCCTAGTTTGCAGCTATATTTGTTTCTAT		
		8101		8150
Insert consensus	(8101)	CGCGTATTAATGTATAATTGCGGGACTCTAATCATAAAAACCATCTCA		
T-DNA derived seq	(7655)	CGCGTATTAATGTATAATTGCGGGACTCTAATCATAAAAACCATCTCA		
		8151		8200
Insert consensus	(8151)	TAAATAACGTATGCATTACATGTTAATTATTACATGCTTAACGTAATTC		
T-DNA derived seq	(7705)	TAAATAACGTATGCATTACATGTTAATTATTACATGCTTAACGTAATTC		
		8201		8250
Insert consensus	(8201)	AACAGAAATTATATGATAATCATCGCAAGACCGCAACAGGATTCAATCT		
T-DNA derived seq	(7755)	AACAGAAATTATATGATAATCATCGCAAGACCGCAACAGGATTCAATCT		
		8251		8300
Insert consensus	(8251)	TAAGAACTTTATTGCCAAATGTTTGAACGATCGGGGATCATCCGGGTCT		
T-DNA derived seq	(7805)	TAAGAACTTTATTGCCAAATGTTTGAACGATCGGGGATCATCCGGGTCT		
		8301		8350
Insert consensus	(8301)	GTGGCGGAACTCCACGAAAATATCCGAACGCAGCAAGATATCGCGGTGC		
T-DNA derived seq	(7855)	GTGGCGGAACTCCACGAAAATATCCGAACGCAGCAAGATATCGCGGTGC		
		8351		8400
Insert consensus	(8351)	ATCTCGGTCTTGCTGGGCAGTCGCCCGGACGCGGTTGATGTGGACGCC		
T-DNA derived seq	(7905)	ATCTCGGTCTTGCTGGGCAGTCGCCCGGACGCGGTTGATGTGGACGCC		
		8401		8450
Insert consensus	(8401)	GGGCCGATCATATTGTCGCTCAGGATCGTGGCGTTGTGCTTGTGCGCCG		
T-DNA derived seq	(7955)	GGGCCGATCATATTGTCGCTCAGGATCGTGGCGTTGTGCTTGTGCGCCG		
		8451		8500
Insert consensus	(8451)	TTGCTGTCGTAATGATATCGGCACCTTCGACCGCCTGTTCCGCAGAGATC		
T-DNA derived seq	(8005)	TTGCTGTCGTAATGATATCGGCACCTTCGACCGCCTGTTCCGCAGAGATC		
		8501		8550
Insert consensus	(8501)	CCGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCA		
T-DNA derived seq	(8055)	CCGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCA		
		8551		8600
Insert consensus	(8551)	GCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTTCATAGAAGGCGG		
T-DNA derived seq	(8105)	GCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTTCATAGAAGGCGG		
		8601		8650
Insert consensus	(8601)	CGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTC		
T-DNA derived seq	(8155)	CGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTC		
		8651		8700
Insert consensus	(8651)	ATTTCGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAG		
T-DNA derived seq	(8205)	ATTTCGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAG		
		8701		8750
Insert consensus	(8701)	AAGGCGATGCGTGCGAATCGGGAGCGGCGATACCGTAAAGCAGGAGAA		
T-DNA derived seq	(8255)	AAGGCGATGCGTGCGAATCGGGAGCGGCGATACCGTAAAGCAGGAGAA		

		8751		8800
Insert consensus	(8751)	GCGGTCAGCCCATTGCGCCGCAAGCTCTTCAGCAATATCACGGGTAGCCA		
T-DNA derived seq	(8305)	GCGGTCAGCCCATTGCGCCGCAAGCTCTTCAGCAATATCACGGGTAGCCA		
		8801		8850
Insert consensus	(8801)	ACGCTATGTCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATG		
T-DNA derived seq	(8355)	ACGCTATGTCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATG		
		8851		8900
Insert consensus	(8851)	AATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC		
T-DNA derived seq	(8405)	AATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATC		
		8901		8950
Insert consensus	(8901)	GCCATGGGTACGACGAGATCATCGCCGTCGGGCATGCGCGCCTTGAGCC		
T-DNA derived seq	(8455)	GCCATGGGTACGACGAGATCATCGCCGTCGGGCATGCGCGCCTTGAGCC		
		8951		9000
Insert consensus	(8951)	TGGCGAACAGTTCGGCTGGCGCGAGCCCTGATGCTCTTCGTCCAGATCA		
T-DNA derived seq	(8505)	TGGCGAACAGTTCGGCTGGCGCGAGCCCTGATGCTCTTCGTCCAGATCA		
		9001		9050
Insert consensus	(9001)	TCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCG		
T-DNA derived seq	(8555)	TCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCG		
		9051		9100
Insert consensus	(9051)	ATGTTTCGCTTGGTGGTGAATGGGCAGGTAGCCGGATCAAGCGTATGCA		
T-DNA derived seq	(8605)	ATGTTTCGCTTGGTGGTGAATGGGCAGGTAGCCGGATCAAGCGTATGCA		
		9101		9150
Insert consensus	(9101)	GCCGCCGATTGCATCAGCCATGATGGATACTTCTCGCAGGAGCAAGG		
T-DNA derived seq	(8655)	GCCGCCGATTGCATCAGCCATGATGGATACTTCTCGCAGGAGCAAGG		
		9151		9200
Insert consensus	(9151)	TGAGATGACAGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTC		
T-DNA derived seq	(8705)	TGAGATGACAGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTC		
		9201		9250
Insert consensus	(9201)	CCTTCCCGCTTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG		
T-DNA derived seq	(8755)	CCTTCCCGCTTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCG		
		9251		9300
Insert consensus	(9251)	TCGTGGCCAGCCACGATAGCCGCGTGCCTCGTCTGCGAGTTTATTGAGG		
T-DNA derived seq	(8805)	TCGTGGCCAGCCACGATAGCCGCGTGCCTCGTCTGCGAGTTTATTGAGG		
		9301		9350
Insert consensus	(9301)	GCACCGGACAGGTCCGCTTTCGACAAAAAGAACCGGGCGCCCTGCGCTGA		
T-DNA derived seq	(8855)	GCACCGGACAGGTCCGCTTTCGACAAAAAGAACCGGGCGCCCTGCGCTGA		
		9351		9400
Insert consensus	(9351)	CAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCAGT		
T-DNA derived seq	(8905)	CAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCAGT		
		9401		9450
Insert consensus	(9401)	CATAGCCGAATAGCCTCTCCACCAAGCGGCCGAGAACCTGCGTGCAAT		
T-DNA derived seq	(8955)	CATAGCCGAATAGCCTCTCCACCAAGCGGCCGAGAACCTGCGTGCAAT		
		9451		9500
Insert consensus	(9451)	CCATCTTGTTCATCATGCGAAACGATCCAGATCCGGTGCAGATTATTTG		
T-DNA derived seq	(9005)	CCATCTTGTTCATCATGCGAAACGATCCAGATCCGGTGCAGATTATTTG		
		9501		9550
Insert consensus	(9501)	GATTGAGAGTGAATATGAGACTCTAATTGGATACCGAGGGGAATTTATGG		
T-DNA derived seq	(9055)	GATTGAGAGTGAATATGAGACTCTAATTGGATACCGAGGGGAATTTATGG		
		9551		9600
Insert consensus	(9551)	AACGTCAGTGGAGCATTTTTGACAAGAAATATTTGCTAGCTGATAGTGAC		
T-DNA derived seq	(9105)	AACGTCAGTGGAGCATTTTTGACAAGAAATATTTGCTAGCTGATAGTGAC		
		9601		9650
Insert consensus	(9601)	CTTAGGCGACTTTTGAACGCGCAATAATGGTTTCTGACGATATGTGCTTAG		
T-DNA derived seq	(9155)	CTTAGGCGACTTTTGAACGCGCAATAATGGTTTCTGACGATATGTGCTTAG		
		9651		9700
Insert consensus	(9651)	CTCATTAAACTCCAGAAACCCGCGCTGAGTGGCTCCTTCAACGTTGCGG		
T-DNA derived seq	(9205)	CTCATTAAACTCCAGAAACCCGCGCTGAGTGGCTCCTTCAACGTTGCGG		
		9701		9750
Insert consensus	(9701)	TTCTGTGAGTTCCAAACGTAACCGGCTTGTCCCGCTCATCGGCGGGGG		
T-DNA derived seq	(9255)	TTCTGTGAGTTCCAAACGTAACCGGCTTGTCCCGCTCATCGGCGGGGG		
		9751		9800
Insert consensus	(9751)	TCATAACGTGACTCCCTTAATTCTCCGCTCATGATCAGATTGTGTTTTCC		
T-DNA derived seq	(9305)	TCATAACGTGACTCCCTTAATTCTCCGCTCATGATCAGATTGTGTTTTCC		
		9801		9850
Insert consensus	(9801)	CGCCTTCAGTTTAAACTATCAGTG-CATACTACCTCTTGTGATTATCATT		
T-DNA derived seq	(9355)	CGCCTTCAGTTTAAACTATCAGTG-----		
		9851		9900
Insert consensus	(9851)	TTTGTATATATTTGGGTTTTTGTGCTGTAATTTGTGTTTTGACACTGTT		
T-DNA derived seq	(9379)	-----		
		9901		9950
Insert consensus	(9901)	TTGTGGATGTTTGGACTTATGACTCCTTGTTTCAATTGTAAATGGTTTTT		
T-DNA derived seq	(9379)	-----		
		9951		10000
Insert consensus	(9951)	GACCCTTCTGAAAATTTTTGCCACCTCTATTTTGTGTTGATTGTGGTTGT		
T-DNA derived seq	(9379)	-----		

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          10001                                     10050
Insert consensus (10001) TCTTTTGCAAATTTGAGTATCGGTTATGATCAATACCGATGACTTGAATA
T-DNA derived seq (9379) -----
          10051                                     10100
Insert consensus (10051) GTGCTCTTAATCGAACAAAAATGAATGTACGGCTATGATGATGCTAAATA
T-DNA derived seq (9379) -----
          10101                                     10150
Insert consensus (10101) AAGTTGCATAGATAATATGTGAACTTTTTCATCTCATTGTAAGTAGCCG
T-DNA derived seq (9379) -----
          10151                                     10200
Insert consensus (10151) GTTATTGAATGAGTCTTTTGTGATGAACATTGCACACTAGCGAAAGTGTG
T-DNA derived seq (9379) -----
          10201                                     10250
Insert consensus (10201) GAGTCTTGTGTTGATATTGGTGCCAATGCCTTGTGTGATGAGCTTACCGTG
T-DNA derived seq (9379) -----
          10251                                     10270
Insert consensus (10251) AACCTTATGTGATGACACCT
T-DNA derived seq (9379) -----

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Figure 10. DNA sequence alignment of the insert consensus DNA sequence with DNA sequence assembled from T-DNA sequence of transformation vector pHoxwG. The insert consensus DNA sequence was assembled from consensus DNA sequence of fragments from reactions with primers KOM56RN-KOM56FN and KOM56FN- KOM56RN.

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1 GATATCATAAAAAGATAAAAAGTCGTTACCAAATTGAGTTTCCATCAACTG  
51 GGTAAGATTGATTTTGTCTTTACAGTGGTCCAATTCAAAAGTCTCAAAG  
101 ACCCACTTCAAATTTCTCAAAGTGAAAACTTCAATTTCAAAGCTAA  
151 AGGAAAAGTAGAGAAAAGTTGTCTCATAGTTCAAAGCTTAGTAAAAAATT  
201 GTTCTAAAGAGTAATTGATACTAAACTAAAATGTTCAAAGTGTATTTATA  
251 GTCACCAAAAATGTGTTGCAAAGTGTCACTCGGTGAAGCAAGTCGGGCTC  
301 GCCGAACCACTCGGCGATCCGCCCTTTGGTCATTTCTTCGCCTCTCTGC

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351 CTAGGCCTTCAAGCATCTCAAGGTATGTAACTTTGGGCGATCCAACACTG
401 CATCGCGGAACCACTAGGCGATCCGCCGACTTGGTTCTTTCCTTCAAGGC

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451 TTGGCACTCTAGAAGTTGAGGCGGTCAAGTAGCCATTCGGCAACTCGCCA  
501 AGTGGACTTGGCGATCACCATGCTTGCTTTTCTTCATTTCTCAGCTTGC  
551 TTCGTTCTTTTGGCAAATCAGTGTCTTGTGTTTGTTCCTGAATCTCTAT  
601 ACCTAGAAATCATCAGTTATTGGCACAATGAGGACACTAATTTCTATATAA  
651 ATAAAGCCCTAAATGAGTCCAATCTCGGACTCATCAACACCCCAACTT  
701 AAACTTTGTCTTGTCTCAAGTAAAAGTCAAGTTCAAGTTCAAAAAG

BspHI

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751 ATGTCTCAAACAGTGCTACACAAGACTCAATCATGAATGCACACAATAAG

MfeI

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801 ACTCAAATTAATCATGCAAGGATCAATTGTGCACTAAAAGATTCAAGTTG  
851 TGACTCACCATTATCAAAGATTCTCAAATTCACAATACTTGCTTCAAATG  
901 CAAGTTCAAGCTCAACAAAGTACTCCAATGCCCTCACACAAAGATGATT  
951 CCATATTCACACATAATTGTTCAACACTTTATAGCTCCGGAATCACATAC  
1001 AACTCTCACACTCACAAAGATGAACACATGCATGACTTCACCCATAGGTT  
1051 TGCCCTTATTTCCAATCAACATTCGCTTCAAGTCACTCAAGGTCAAAAA  
1101 GGTCTTTTCAAGGCTTGTAGCAGAGCTGAGTGCAAAGGCATGGTCATTTA  
1151 GGCTCGGTGGTTGCTATCTCATAAAAATGTGGTATGAACATCACTTTCTT  
1201 TCCTTTTCTTCAACATTTCTCATTATGCTCAAATTCACCCATTATTAC  
1251 TTTTCATGGAATACCGAACTCCCTATTTCTTTTCAACTTTTCAACTTTT  
1301 ATTCCACAACTTTTTCACTTTTCTTTTCTTTTCACTTTCTTTTGTCTTTT  
1351 TTTTGTATGGAGGGTTCCATATTTTTCAAACCATGGATCAAATGGGGA  
1401 CTTCTTTGCATTTCTTGATTTACCTTCTTCTTTTCAACACACCCCAACTT

BspHI

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1451 AGGCTTTTAGCCTAAGCTATTCAAACAAACCACACTTCATGAGGAATATG

MfeI

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1501 GGTGAAAGGATAAAGAGGGGTTACAATTGCATCAAGTTTCTTCCAAGAAA  
1551 AGGACAAGGCTCAAAAAGGGAGTTCAAGCAAGATTGACACACTCACAAGG

MscI

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1601 TTGGCCACAAAAGAGGTATATTGTCAAATTTGTTTCACTCTTAAAACCTGT
1651 TGCCTAAGATCATTCAAGAGCTTGCATCACTTAGTCAACCGGACCAACGG
1701 GGTAATTTCTAGGTGTATCATAAGGTTACGGTAAGCTCATCACACA
1751 AGGCATTGGCACCAATATCAAACAAGACTCCACACTTTTCGCTAGTGTGCA
1801 ATGTTTATCACAAAAGACTCATTCAATAACCGGCTAGTTACAATGAGATG
1851 CAAAAGTTTACATATTATCTATGCAACTTTATTTAGCATCATCATAGCC
1901 GTACATTCATTTTGTTCGATTAAGAGCACTATTCAAGTCATCGGTATTG
1951 ATCATAACCGATACTCAAATTTGCAAAAAGAACAACCACAATCAAACAAA

MfeI
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2001 **TAAGAGGTGGCAAAAATTTTCAGAAGGGTCAAAAACCATTTACAATTGAA**  
2051 **ACAAGGAGTCATAAGCTCAAACATCCACAAAACAGTGTCAAAACACAATT**  
2101 **TACAGCACAAAACCCAATATATAAACAAAATGATAATCACAAGAGGTA**

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2151 **GGTATG**CACTGATAGTTTAAACTGAAGGCGGGAAACGACAATCTGATCAT
BspHI
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2201 GAGCGGAGAATTAAGGGAGTCACGTTATGACCCCCGCCGATGACGCGGGA
2251 CAAGCCGTTTTACGTTTTGGAAC TGACAGAACCGCAACGTTGAAGGAGCCA
2301 CTCAGCCGCGGGTTTCTGGAGTTTAATGAGCTAAGCACATAACGTCAGAAA
2351 CCATTATTGCGCGTTCAAAAAGTCGCCTAAGGTCACTATCAGCTAGCAAAT
2401 ATTTCTTGTCAAAAATGCTCCACTGACGTTCCATAAAATCCCCCTCGGTAT
2451 CCAATTAGAGTCTCATATTCACTCTCAATCCAATAATCTGCACCGGATC
2501 TGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGG
2551 CCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATC
2601 GGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGT
2651 TCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACG

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2701 AGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCT  
2751 GTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGA  
2801 AGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAG  
2851 TATCCATCATGGCTGATGCAATGCGGGCGGCTGCATACGTTGATCCGGCT  
2901 ACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAC  
2951 TCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATC  
3001 AGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCC  
3051 GACGGCGATGATCTCGTCTGTGACCCATGGCGATGCCTGCTTGCCGAATAT  
3101 CATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGG  
3151 GTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCT  
3201 GAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTAT  
3251 CGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGT  
3301 TCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCA  
3351 ACCTGCCATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTG  
3401 GGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGG  
3451 GGATCTCATGCTGGAGTTCTTCGCCACGGGATCTCTGCGGAACAGGCGG

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3501 TCGAAGGTGCCGATATCATTACGACAGCAACGGCCGACAAGCACAACGCC
3551 ACGATCCTGAGCGACAATATGATCGGGCCCCGGCGTCCACATCAACGGCGT

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3601 CGGCGGCGACTGCCCAGGCAAGACCGAGATGCACCGCGATATCTTGCTGC  
3651 GTTCGGATATTTTCGTGGAGTTCGCCACAGACCCGGATGATCCCCGAT  
3701 CGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGG  
3751 TCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAA  
3801 TAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATT  
3851 AGAGTCCC GCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCG  
3901 CGCAAAC TAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATC  
3951 GGGCCTCCTGTCAATGCTGGCGGCGGCTCTGGTGGTGGTCTGGTGGCGG  
4001 CTCTGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTG  
4051 AGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCGGTGATTTTGATTATGAA  
4101 AAGATGGCAAACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAA  
4151 CGCGCTACAGTCTGACGCTAAAGGCCAACTTGATTCTGTGCTACTGATT

4201 ACGGTGCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAAT  
4251 GGTAATGGTGCTACTGGTGATTTTGCTGGCTCTAATTCCCAAATGGCTCA  
4301 AGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATT  
4351 TACCTTCCCTCCCTCAATCGGTTGAATGTCGCCCTTTTGTCTTTGGCCCA  
4401 ATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTG  
4451 GCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTA  
4501 ATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTT  
4551 CCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACACAGG

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4601 AACAGCTATGACCATGATTACGCCAAGCTTTAACGAGATAGAAAATTAT
4651 GTTACTCCGTTTGTTCATTACTTAACAAATGCAACAGTATCTTGTACCA
4701 AATCCTTTCTCTCTTTTCAAACCTTTTCTATTTGGCTGTTGACGGAGTAAT
4751 CAGGATACAAACCACAAGTATTTAATTGACTCCTCCGCCAGATATTATGA
4801 TTTATGAATCCTCGAAAAGCCTATCCATTAAGTCCTCATCTATGGATATA
4851 CTTGACAGTATCTTCCTGTTTGGGTATTTTTTTTTCTCGCCAAGTGGAAC
4901 GGAGACATGTTATGATGTATACGGGAAGCTCGTTAAAAAAAAAATACAAT
4951 AGGAAGAAATGTAACAAACATGAATGTTGTTTTTAACCATCCTTCCCTT
5001 AGCAGTGTATCAATTTTGTAATAGAACCATGCATCTCAATCTTAATACTA
5051 AAATGCAACTTAATATAGGCTAAACCAAGTAAAGTAATGTATTCAACCTT
5101 TAGAATTGTGCATTACATAATTAGATCTTGTGTTGTCGTAATAAATTAGAAA
5151 ATATATTTACAGTAATTTGGAATACAAAGCTAAGGGGGGAGTAACTAATA
5201 TTCTAGTGGAGGGAGGGACCAGTACCAGTACCCTAGATATTATTTTTAATT
5251 ACTATAATAATAATTTAATTAACACGAGACATAGGAATGTCAAGTGGTAG
5301 CGGTAGGAGGGAGTTGGTTTAGTTTTTTTAGATACTAGGAGACAGAACCGG
5351 ACGGGCCCATGCAAGGCCCAAGTTGAAGTCCAGCCGTGAATCAACAAAG
5401 AGAGGGCCCATATACTGTTCGATGAGCATTCCCTATAATACAGTGTCCA
5451 CAGTTGCCCTTCTGCTAAGGGATAGCCACCCGCTATTCTCTTGACACGTGT
5501 CACTGAAACCTGCTACAAATAAGGCAGGCACCTCCTCATCTCACTCACT
5551 CACTCACACAGCTCAACAAGTGGTAACTTTTACTCATCTCCTCCAATTAT

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5601 TTCTGATTTTCATGCAGGTGACTCTAGAGGATCTGATCATATGCATAGGA  
5651 TGAGTAGCAGGTCAATTTTCAGTTTCGGCACAAGTAAACTCAACAAGAGAG  
5701 ATACCATGAGTCCATTTGGTACTTACAAGGACTACAATTTGAACATCCAA  
5751 TCCGATGAACTTGTGAATTGCAGCAACAAGAATATCTGAACCTTTCTGCT  
5801 CCTCAAGTCTGCCGATGAAGCCAATCAAAGGGATCTTCTTGTCAACAGGC  
5851 AAGCCAACCTGCTGCTTGAAGAGCCTCCTTTAGTAAAGGTTTTGCGTCCAT  
5901 GACCTGTATAGAGATTTTGATTAGCAAGAACTCTTTAATTTCATAAACAT  
5951 ACAAATAAATTTAGTATATACTGGAGTCGGAAAAATCTTATCTTACAGTG  
6001 GTTATATCGTATTTGACATCTGTGTATTTGTCAGTCGCTGGGTTCCACTC  
6051 TTGTGTATCCATGCCATTCACAATCCCAGTTATGCAAGTCTTACGAAGGA  
6101 CACTGTCCAATTCAACTCCCTTGTCAACAGCAGAGACAAGTTCTTGGGCA  
6151 TAGTATGGGCTCACTGTAACCACCCTATGTGATTCTAATATCCCAGCCTT  
6201 CATCCAGTTGATTTTCCCTACCCTTAAACAGGCTTCTCATATCTGCAAAAT  
6251 TTAAAACTCAATTTACTAGCATCAAAGAGCTTCAAAGTTGGAGGTCT

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6301 GATTTCAAGCATAAATACATACCCATCAATGAAATCAAAGAACCCTGA  
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6351 ATTCATCAGGAAGATTGAGAAGAGGGAAGTCAGAGAAAGAAAATCGACCT
6401 TGGTAGGCAATGTTATGGATGCAGAAAGCAACCTGGAGGCAATGTGAAAT
6451 TTATCATATATTAATACAACCTTACTGATTTGCAGGGTAACGTGCAATCG
6501 AGTGAATACAAAGAAATTTTACCTTGGCATTCAAGTAGATTCTCTGGAC
6551 TGGTACATTGACTTCAAGTAGCAAGGAATGAGAGCTGTGTGCCAATCATT

6601 GGCAATGAAGAGAACATCCTCTCCTGCAGGAATAGGCAAAATAAAGATGA
6651 TTACCTACAATGATATAGTAAGGAGTTTTCTGAACTAGGATGTGTTAAT
6701 TACCATATGGTCCTGAGAAGTAGTTGCTACTGTTCAAATTCAAAACCTTA
6751 GGTGCCTCTAGGGCTGCCTGAGAAAACAAGGTTAAAAAACGATTAAGA
6801 CAAAAGAGTAAAATGCCACATAAAAATCAAGAGTAACTAACTTACTTGAC
6851 ACAACAAGCTGAACCTAAGTTCATTGTCCAGATAATCTAGTCCAGCTTTG
6901 GGGCCATAGATTTTTGAACCAAGTTTTGCCCCAAACCTTAAAAGAGTAAAA
6951 GCACCAGTAGAGTTAAAAGATACTCAAAATGACCTGTTCTGCGTATCCCT
7001 CAGGACGGATTCATAATCATAATATGCTTACTTTCTCCAAGAACATTGGG
7051 TGGTCAACAAAACACGATCAACCCACGTTTATAGCAGTGAAAGAAACG
7101 AACAAATTTCAATGCTGTCTCCAACCTTGACCTGCAGATGATCACATTCTT
7151 GAATCAGGAAATGTAAGAGAACAATATTGTACCGTATCAATATAGGAAGA
7201 TGTACCTCAACCGCAACGCCAGTATCCCAAGCATCTTTGTATTGGTCATA
7251 ACGGGGGGATATTGTCAATTACCCGATGTCCGCGGGCCTAAATGATAAAAA
7301 GACTGATGCAGTAGAACTAACTAAACAAAATAAGTAATGAATGAGTAGG
7351 TAACCAAATGAAAGAAAGACTTACTGCAAGGGCTGGTGGTAGTCTCCTCAA
7401 CTTTTGAAGCTCTTTTTGATGCTAGTAAATFGAGTTTTTAAAATTTTGCAG
7451 ATATGAGAAGCCTGTTAAGGGTAGGAAAATCAACTGGATGAAGGCTGGGA
7501 TATTAGAATCACATAGGGTGGTTACAGTGAGCCATACTATGCCCAAGAA
7551 CTTGTCTCTGCTGTTGACAAGGGAGTTGAATTGGACAGTGTCTTTCGTAA
7601 GACTTGCATAACTGGGATTGTGAATGGCATGGATACACAAGAGTGGAACC
7651 CAGCGACTGACAAATACACAGATGTCAAATACGATATAACCCTGTAAGA
7701 TAAGATTTTTCCGACTCCAGTATATACTAAATTTATTTTGTATGTTTATGA
7751 AATTAAGAGTTCTTGCTAATCAAAATCTCTATACAGGTCATGGACGCAA
7801 AACCTTTACTAAAGGAGGCTCTTCAAGCAGCAGTTGGCTTGCCTGTTGAC
7851 AAGAAGATCCCTTTGATTGGCTTCATCGGCAGACTTGAGGAGCAGAAAGG
7901 TTCAGATATTCTTGTGCTGCAATTCACAAGTTCATCGGATTGGATGTTT
7951 AAATTGTAGTCTTGTAAAGTACCAAATGGACTCATGGTATCTCTCTTGT
8001 GAGTTTACTTGTGCCGAAACTGAAATTGACCTGCTACTCATCCTATGCAT

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8051 ATGATCAGATCCTCTAGAGTCGACCTGCATGAAATCAGAAATAATTGGAG  
8101 GAGATGAGTAAAAGTTACCCTTGTGAGCTGTGTGAGTGAGTGAGTGAG  
8151 AATGAGGAGGTGCCCTGCCTTATTTGTAGCAGGTTTCAGTGACACGTGTCA  
8201 AGAGAATAGCGGGTGGCTATCCCTTAGCAGAAGGCAACTGTGGACACTGT  
8251 ATTATAGGGAAAATGCTCATCGACAGTATTATGGGCCCTCTTTTGTGAT  
8301 TCACGGCTGGACTTCAACTTGGGCCTTGCAATGGGCCCGTCCGGTTCTGT  
8351 CTCCTAGTATCTAAAAAATAAACCCTCCCTCCTACCGCTACCCTTG  
8401 ACATTCCTATGTCTCGTGTAAATTAATTAATTATTATAGTAATTAATAA  
8451 AATATCTAGGTACTGGTACTGGTCCCTCCCTCCACTAGAATATTAGTTAC  
8501 TTCCCCCTTAGCTTTGTATTCCAATTAAGTAAATATATTTTCTAATTT  
8551 TTTACGACAAACAAGATCTAATTATGAATGCACAATCTAAAGGTTGAAT  
8601 ACATTACTTTACTTGGTTTAGCCTATATTAAGTTGCATTTTAGTATTAAG  
8651 ATTGAGATGCATGGTTCTATTACAAAATTGATACACTGCTAAAGGAAGGA  
8701 TGGTTAAAAACAACATTCATGTTTGTACATTTCTTCTATTGTATTTT  
8751 TTTTTTAACGAGCTTCCCGTATACATCATAACATGTCTCCGTTCCACTTG  
8801 GCAGGAAAAAAAAAATACCCAAACAGGAAGATACTGTCAAGTATATCCATA  
8851 GATGAGGACTTAATGGATAGGCTTTTCGAGGATTCATAAATCATAATATC  
8901 TGGCGGAGGAGTCAATTAATACTTGTGGTTTGTATCCTGATTACTCCGT  
8951 CAACAGCCAAATAGAAAAGTTTAAAAGAGAGAAAGGATTTGGTACAAGA  
9001 TACTGTTGCATTTGTTAAGTAATGAACAAAACGGAGTAACATAATTTTCT

HindIII

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9051 ATCTCGTTAAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAA
9101 ATTGTTATCCGCTCACAATTCACACAACATACGAGCCGGAAGCATAAAG
9151 TGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
9201 GCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATT
9251 AATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTTCGTATTGGGCCAAAG
9301 ACAAAGGGCGACATTCAACCGATTGAGGGAGGGAAGGTAAATATTGACG
9351 GAAATTATTCATTAAGGTGAATTATCACCGTCACCGACTTGAGCCATTT
9401 GGAATTAGAGCCAGCAAATCACCAGTAGCACCATTACCATTAGCAAGG
9451 CCGGAAACGTCACCAATGAAACCATCGATAGCAGCACCGTAATCAGTAGC
9501 GACAGAATCAAGTTTGCCTTTAGCGTCAGACTGTAGCGCGTTTTTCATCGG
9551 CATTTTCGGTCATAGCCCCCTTATTAGCGTTTGCCATCTTTTCATAATCA
9601 AAATCACCGGAACCAGAGCCACCACCAGAACCGCCTCCCTCAGAGCCGCC
9651 ACCCTCAGAACCGCCACCCTCAGAGCCACCACCCTCAGAGCCGCCACCAG
9701 AACCACCACCAGAGCCGCCAGCATTGACAGGAGGCCGATCTAGTAA
9751 CATAGATGACACCGCGCGGATAATTTATCCTAGTTTTCGCGCTATATTT
9801 TGTTTTCTATCGCGTATTAATGTATAATTGCGGGACTCTAATCATAAAA
9851 ACCCATCTCATAAATAACGTCATGCATTACATGTTAATTATTACATGCTT
9901 AACGTAATTCAACAGAAATTATATGATAATCATCGCAAGACCGGCAACAG
9951 GATCAATCTTAAGAACTTTATTGCCAAATGTTTGAACGATCGGGGATC

EcoRV

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10001 ATCCGGGTCTGTGGCGGGAACCTCCACGAAAATATCCGAACGCAGCAAGAT  
EcoRV

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10051 ATCGCGGTGCATCTCGGTCTTGCCTGGGCAGTCGCCGCCGACGCCGTTGA
10101 TGTGGACGCCGGCCCGATCATATTGTCGCTCAGGATCGTGGCGTTGTGC

EcoRV

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10151 TTGTCGGCCGTTGCTGTGCGTAATGATATCGGCACCTTCGACCGCCTGTTC  
10201 CGCAGAGATCCCGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGA  
10251 GGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCA  
10301 TAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGC  
10351 TTGGTTCGGTCATTTTCGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAG  
10401 AAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAA  
10451 GCACGAGGAAGCGGTCAGCCCATTCGCCCAAGCTCTTCAGCAATATCA  
10501 CGGGTAGCCAACGCTATGTCTGATAGCGGTCCGCCACACCAGCCGCC  
10551 ACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTGCGCA  
10601 AGCAGGCATCGCCATGGGTCACGACGAGATCATCGCCGTCGGGCATGCGC  
10651 GCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCTGATGCTCTTC  
10701 GTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTC  
10751 GCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGCAGGTAGCCGGATCA  
10801 AGCGTATGCAGCCGCCGATTCATCAGCCATGATGGATACTTTCTCGGC  
10851 AGGAGCAAGGTGAGATGACAGGAGATCCTGCCCGGCACTTCGCCCAATA  
10901 GCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAA

MscI

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10951 GGAACGCCCGTTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAG
11001 TTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCC
11051 CCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGT
11101 TGTGCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGAGAACC
11151 TGCGTGCAATCCATCTTGTTCATCATGCGAAACGATCCAGATCCGGTGC
11201 AGATTATTTGGATTGAGAGTGAATATGAGACTCTAATTGGATACCGAGGG
11251 GAATTTATGGAACGTCAGTGGAGCATTTTTCGACAAGAAATATTTGCTAGC
11301 TGATAGTGACCTTAGGCGACTTTTGAACGCGCAATAATGTTTTCTGACGT


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StuI
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13301  TCGCCCAAAGTTACATACCTTGAGGATGCTGAAGGCCTAGGCAGAGAGGC
13351  GAAGGAAATGACCAAAGGGCGGATCGCCGAGTGGTTCGGCGAGCCCGACT
13401  TGCTTCACCGAGTGACACTTTGCAACACATTTTTGGTGA CTATAAATACA
13451  TTTTGAACATTTAGTTTAGTATCAATTACTCTTTAGAACAATTTTTTAC
13501  TAAGTTTTGAACTATGAGACAAGTTTTCTCTAGTTTTCTTTAGCTTTGA
13551  AGAATTGAAGTTTTTCACTTTTGAGAAATTTGAAGTGGGTCTTTGAGATT
13601  CTTTGAATTGGACCACTGTAAAGACAAAATCAATCTTACCCAGTTGATGG

EcoRV
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13651  AAACTCAATTTGGTAACGACTTTTATCTTTTATGATATC

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Figure 11. Determined DNA sequence of insert and flanking potato chromosomal DNA of potato line EH-92-527-1. Potato chromosomal DNA is shown in bold.

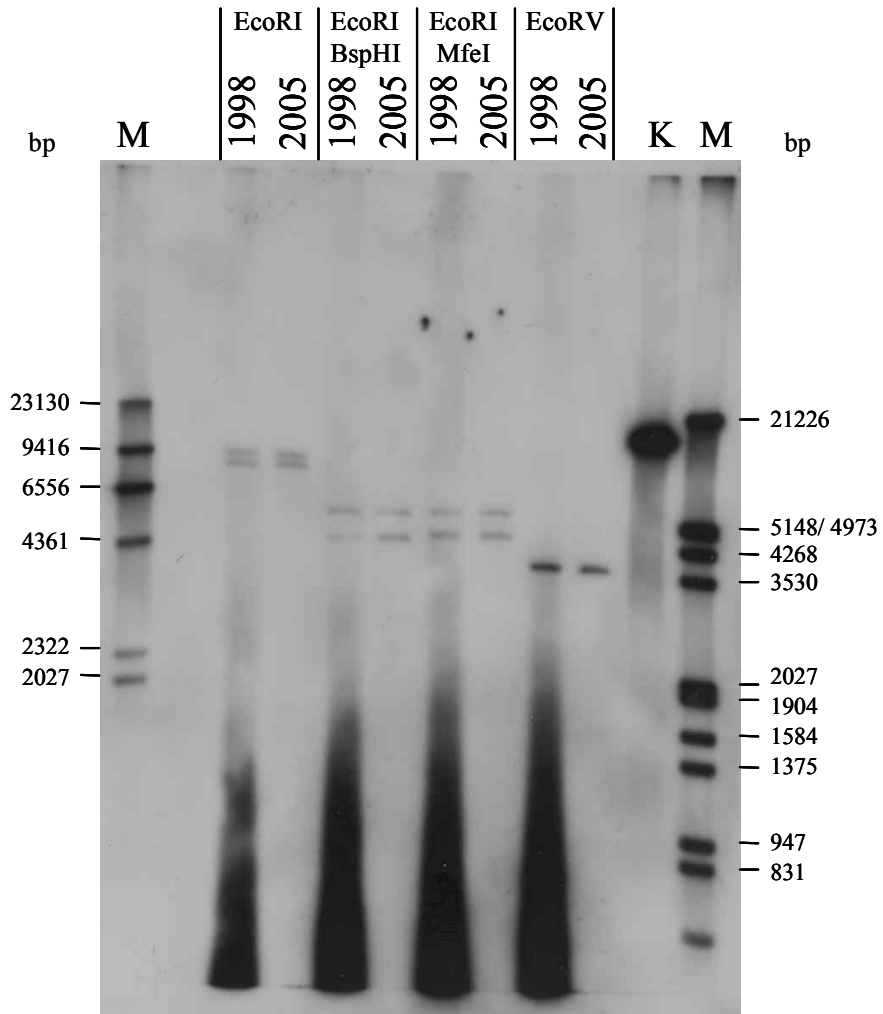


FIGURE 12. Southern blot analysis for determination of insert stability in EH92-527-1. 10µg total DNA from EH92-527-1 isolated in 1998 and 2005 was digested with various restriction enzymes and hybridized with a fragment corresponding to the *nptII* gene. K, positive control; M, marker; bp, base pair.

ANNEX A

Description of Amendments to the Report

The report was amended to add additional pertinent information including several figures containing sequence data, an additional Southern blot examining insert stability and corrections to the text.

Specific amendments to the report are as follows:

Page 2. Annexes A and B are new

Page 3. Figure 8. is now Figure 11. There is a new Figure 8. and Figures 9, 10 and 12 are new.

Page 4. Last paragraph of Summary is new.

Page 5. An additional DNA isolation method is included under DNA isolation.

Page 9. Under Southern Blot analysis, second paragraph the footnote is new.

Page 10. Under Determination of insert and flanking DNA sequence, third paragraph is amended.

Page 11. First paragraph is amended.

Page 11. Second paragraph is amended.

Page 11. Paragraph on Stability of insert is new.

Page 11. Under Conclusions, first paragraph is amended

Page 11. Under Conclusions, second paragraph is new.

Page 12. Haymes (1996) reference is new.

Figure 8 in the original report is now Figure 11.

Figure 8 is new.

Figure 9 is new.

Figure 10 is new.

Figure 12 is new.

ANNEX B

Amended Southern blot description

Notification C/SE/96/3501 submitted according to Directive 90/220/EEC included Annex 4 entitled “Southern blotting for determination of the number of gene copies incorporated in EH92-527-1” by Mariette Andersson. In this report a Southern blot analysis on an *EcoRI* digest of genomic DNA from both EH92-527-1 and the parental variety Prevalent was presented, hybridized with a probe targeting the *gbss* promoter. This blot was apparently inconsistent with a Southern blot analysis submitted as part of Notification C/SE/96/3501 Update according to Directive 2001/18/EC. Further investigation revealed that the autoradiogram used for original submission was inadvertently flipped and therefore a *HindIII* digest was mislabeled as an *EcoRI* digest. The Southern blot presented in the original submission is now labelled correctly and shown as *Figure 1* of this *Annex B*. The Southern blot analysis was performed in May of 1996 before the complete DNA sequence of the insert was known.

The complete DNA sequence, structure of the insert and flanking DNA sequence is now known permitting a comprehensive interpretation of the original Southern blot analysis. The probe targeting the *gbss* promoter will also hybridize with fragments separated in the digests of the parental variety Prevalent as the DNA segment used as probe is of potato origin. As can be seen from the known structure of the insert of EH92-527-1, *Figure 2*, a *HindIII* digest will yield one internal fragment from the insert region. This fragment represents 4434 bp of the insert and has two target sites for the *gbss* promoter probe. In *Figure 1*, hybridization to this fragment is indicated as A. In the original submission this band is indicated as representing a fragment size above 2027 bp and below 6557 bp, which is consistent with the determined structure of the insert in EH92-527-1. Hybridization to the *EcoRI* digest also results in one extra band as can be seen in *Figure 1* and which is indicated as B. As can be seen in *Figure 2*, the insert of EH92-527-1 contains one *EcoRI* restriction site and would upon digestion yield two separate fragments with one target site each for the probe used. In the main report an autoradiogram is shown that represents *EcoRI* digests of genomic DNA from EH92-527-1 isolated in 1998 and 2005. Both these hybridization patterns show two bands using a probe targeting the *nptII* gene. The bands seen in this Southern blot are represented by bands indicated as B and C in *Figure 1*, where C is superimposed on a band which is also present in the parental variety Prevalent.

Thus the Southern blot from the original submission is consistent with the known DNA sequence and structure of the insert in EH92-527-1 presented in the main report but was incorrectly labeled as an *EcoRI* digest in the original submission.

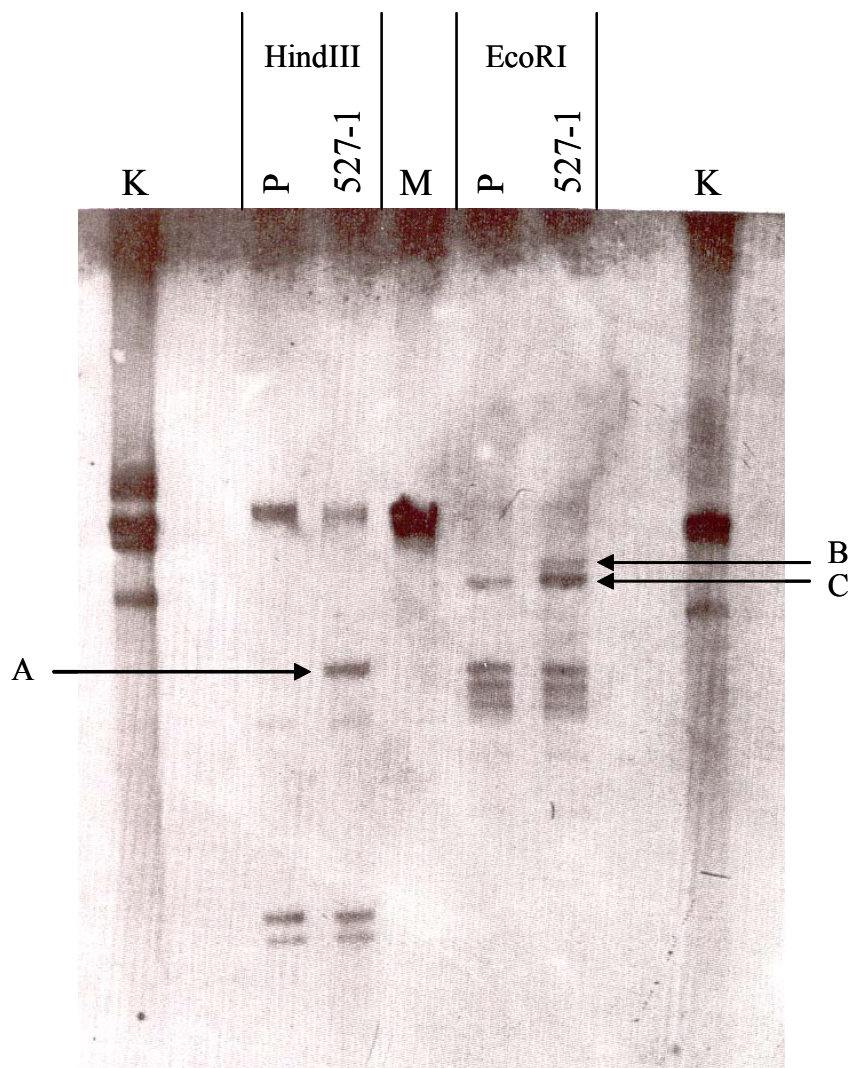


Figure 1. Southern blot analysis for determination of T-DNA insertions in EH92-527-1 produced in May of 1996. 10µg total DNA from EH92-527-1 and the parental variety Prevalent was digested with *HindIII* or *EcoRI* and hybridized with a fragment corresponding to the *gbss* promoter. A indicates a band of the *HindIII* digest, which is the result of an insert internal fragment with two probe target sites, B indicates a band of the *EcoRI* digest, C indicates a band of the *EcoRI* digest, which is superimposed on a fragment also detected in parental variety Prevalent. P, Prevalent; K, positive control; M, marker.

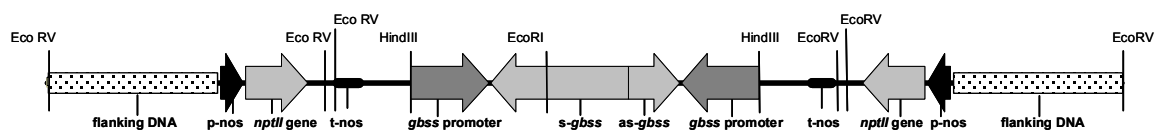


Figure 2. Determined structure of genetic insert (9378 bp) and flanking sequences of EH92-527-1. DNA segments outside the p-nos elements is 2156 bp potato chromosomal flanking DNA on each side of the insert. Structural components noted, p-nos-nopaline synthase promoter, nptII -coding sequence for aminoglycoside phosphotransferase II, t-nos-nopaline synthase polyadenylation sequence, p-gbss-potato gbss promoter, s-gbss-truncated gbss antisense fragment, as-gbss-truncated gbss antisense fragment.