

(19) **DANMARK**



Patent- og
Varemærkestyrelsen

(10) **DK/EP 2970864 T3**

(12) **Oversættelse af
europæisk patentskrift**

-
- (51) Int.Cl.: **C 12 N 1/18 (2006.01)** **C 12 P 7/08 (2006.01)**
- (45) Oversættelsen bekendtgjort den: **2021-02-01**
- (80) Dato for Den Europæiske Patentmyndigheds bekendtgørelse om meddelelse af patentet: **2020-10-28**
- (86) Europæisk ansøgning nr.: **14725932.9**
- (86) Europæisk indleveringsdag: **2014-03-13**
- (87) Den europæiske ansøgnings publiceringsdag: **2016-01-20**
- (86) International ansøgning nr.: **US2014025460**
- (87) Internationalt publikationsnr.: **WO2014151318**
- (30) Prioritet: **2013-03-15 US 201361800323 P**
- (84) Designerede stater: **AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR**
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- (54) Benævnelse: **FREMGANGSMÅDER TIL AT REGULERE NITROGENMETABOLISME UNDER PRODUKTIONEN AF ETHANOL FRA MAJS MED METABOLISK MANIPULEREDE GÆRSTAMMER**
- (56) Fremdragne publikationer:
EP-A1- 2 277 989
WO-A1-2005/093041
WO-A2-2011/140386
NISSSEN T L ET AL: "Optimization of ethanol production in Saccharomyces cerevisiae by metabolic engineering of the ammonium assimilation", METABOLIC ENGINEERING, ACADEMIC PRESS, US, vol. 2, no. 1, 1 January 2000 (2000-01-01) , pages 69-77, XP002236030, ISSN: 1096-7176, DOI: 10.1006/MBEN.1999.0140
QING-XUE KONG ET AL: "Overexpressing GLT1 in gpd1[Delta] mutant to improve the production of ethanol of Saccharomyces cerevisiae", APPLIED MICROBIOLOGY AND BIOTECHNOLOGY, vol. 73, no. 6, 9 January 2007 (2007-01-09), pages 1382-1386, XP055005262, ISSN: 0175-7598, DOI: 10.1007/s00253-006-0610-4
C. ROCA ET AL: "Metabolic Engineering of Ammonium Assimilation in Xylose-Fermenting Saccharomyces cerevisiae Improves Ethanol Production", APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 69, no. 8, 1 August 2003 (2003-08-01) , pages 4732-4736, XP055138495, ISSN: 0099-2240, DOI: 10.1128/AEM.69.8.4732-4736.2003
COULON JOANA ET AL: "Metabolic engineering of Saccharomyces cerevisiae to minimize the production of ethyl carbamate in wine", AMERICAN JOURNAL OF ENOLOGY AND VITICULTURE, AMERICAN SOCIETY FOR ENOLOGY AND VITICULTURE, US, vol. 57, no. 2, 1 January 2006 (2006-01-01), pages 113-124, XP009108170,

Fortsættes ...

ISSN: 0002-9254 cited in the application

SALMON JEAN-MICHEL ET AL: "Improvement of nitrogen assimilation and fermentation kinetics under enological conditions by depression of alternative nitrogen-assimilatory pathways in an industrial *Saccharomyces cerevisiae* strain", APPLIED AND ENVIRONMENTAL MICROBIOLOGY, AMERICAN SOCIETY FOR MICROBIOLOGY, US, vol. 64, no. 10, 1 October 1998 (1998-10-01), pages 3831-3837, XP002428301, ISSN: 0099-2240 cited in the application

GUO Z-P ET AL: "Minimization of glycerol synthesis in industrial ethanol yeast without influencing its fermentation performance", METABOLIC ENGINEERING, ACADEMIC PRESS, US, vol. 13, no. 1, 1 January 2011 (2011-01-01), pages 49-59, XP027575826, ISSN: 1096-7176 [retrieved on 2010-12-24]

V. G. MEDINA ET AL: "Elimination of Glycerol Production in Anaerobic Cultures of a *Saccharomyces cerevisiae* Strain Engineered To Use Acetic Acid as an Electron Acceptor", APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 76, no. 1, 13 November 2009 (2009-11-13), pages 190-195, XP055029601, ISSN: 0099-2240, DOI: 10.1128/AEM.01772-09

ANTONIUS J A VAN MARIS ET AL: "Alcoholic fermentation of carbon sources in biomass hydrolysates by *Saccharomyces cerevisiae*: current status", ANTONIE VAN LEEUWENHOEK, KLUWER ACADEMIC PUBLISHERS, DO, vol. 90, no. 4, 11 October 2006 (2006-10-11), pages 391-418, XP019446684, ISSN: 1572-9699, DOI: 10.1007/S10482-006-9085-7

P. O. Ljungdahl ET AL: "Regulation of Amino Acid, Nucleotide, and Phosphate Metabolism in *Saccharomyces cerevisiae*", Genetics, vol. 190, no. 3, 1 March 2012 (2012-03-01) , pages 885-929, XP055138445, ISSN: 0016-6731, DOI: 10.1534/genetics.111.133306

Description

BACKGROUND OF THE INVENTION

[0001] Energy conversion, unitization and access underlie many of the great challenges of our time, including those associated with sustainability, environmental quality, security, and poverty. New applications of emerging technologies are required to respond to these challenges. Biotechnology, one of the most powerful of the emerging technologies, can give rise to important new energy conversion processes. Plant biomass and derivatives thereof are a resource for the biological conversion of energy to forms useful to humanity.

[0002] Among forms of plant biomass, both grain-based biomass and lignocellulosic biomass (collectively "biomass") are well-suited for energy applications. Each feedstock has advantages and disadvantages. For example, because of its large-scale availability, low cost, and environmentally benign production lignocellulosic biomass has gained attention as a viable feed source for biofuel production. In particular, many energy production and utilization cycles based on cellulosic biomass have near-zero greenhouse gas emissions on a life-cycle basis.

[0003] However, grain-based feed stocks are more readily converted to fuels by existing microorganisms, although grain-based feed stock is more expensive than lignocellulosic feed stock and conversion to fuel competes with alternative uses for the grain.

[0004] Biomass processing schemes involving enzymatic or microbial hydrolysis commonly involve four biologically mediated transformations: (1) the production of saccharolytic enzymes (cellulases and hemicellulases); (2) the hydrolysis of carbohydrate components present in pretreated biomass to sugars; (3) the fermentation of hexose sugars (e.g., glucose, mannose, and galactose); and (4) the fermentation of pentose sugars (e.g., xylose and arabinose). These four transformations can occur in a single step in a process configuration called consolidated bioprocessing ("CBP"), which is distinguished from other less highly integrated configurations in that it does not involve a dedicated process step for cellulase and/or hemicellulase production.

[0005] CBP offers the potential for lower cost and higher efficiency than processes featuring dedicated cellulase production. The benefits result in part from avoided capital costs, substrate and other raw materials, and utilities associated with cellulase production. In addition, several factors support the realization of higher rates of hydrolysis, and hence reduced reactor volume and capital investment using CBP, including enzyme-microbe synergy and the use of thermophilic organisms and/or complexed cellulase systems. Moreover, cellulose-adherent cellulolytic microorganisms are likely to compete successfully for products of cellulose hydrolysis with non-adhered microbes, e.g., contaminants. Successful competition of desirable microbes increases the stability of industrial processes based on microbial cellulose utilization. Progress in developing CBP-enabling microorganisms is being made through two strategies: engineering naturally occurring cellulolytic microorganisms to improve product-related properties, such as yield and titer; and engineering non-cellulolytic organisms that exhibit high product yields and titers to express a heterologous cellulase and hemicellulase system enabling cellulose and hemicellulose utilization.

[0006] One way to meet the demand for ethanol production is to convert sugars found in biomass, i.e., materials such as agricultural wastes, corn hulls, corncobs, cellulosic materials, and the like to produce ethanol. Efficient biomass conversion in large-scale industrial applications requires a microorganism that is able to tolerate high concentrations of sugar and ethanol, and which is able to ferment more than one sugar simultaneously.

[0007] Bakers' yeast (*Saccharomyces cerevisiae*) is the preferred microorganism for the production of ethanol (Hahn-Hägerdal, B., et al., Adv. Biochem. Eng. Biotechnol. 73, 53-84 (2001)). Attributes in favor of this microbe are (i) high productivity at close to theoretical yields (0.51 g ethanol produced/g glucose used), (ii) high osmo- and ethanol tolerance, (iii) natural robustness in industrial processes, also (iv) being generally regarded as safe (GRAS) due to its long association with wine and bread making, and beer brewing. Furthermore, *S. cerevisiae* exhibits tolerance to inhibitors commonly found in hydrolysates resulting from biomass pretreatment. Exemplary metabolic pathways for the production of ethanol are depicted in Figure 1. However, *S. cerevisiae* does not naturally break down components of cellulose, nor does it efficiently use pentose sugars.

[0008] Glycerol is a metabolic end-product of native yeast ethanolic fermentation (Figure 1). During anaerobic growth on carbohydrates, production of ethanol and carbon dioxide is redox neutral, while the reactions that create cell biomass and associated carbon dioxide are more oxidized relative to carbohydrates. The production of glycerol, which is more reduced relative to carbohydrates, functions as an electron sink to off-set cell biomass formation, so that overall redox neutrality is conserved. This is essential from a theoretical consideration of conservation of mass, and in practice strains unable to produce glycerol are unable (or only very poorly able) to grow under anaerobic conditions.

[0009] There is a strong commercial incentive not to produce glycerol as a byproduct because it represents lost ethanol yield. In industrial corn ethanol fermentations, this yield loss can be up to 6% of theoretical, for a market of ~14 billion gallons/yr. At selling price of \$2.50/gal, this is a total market value of \$2 B/yr.

[0010] Strategies from the literature to address this problem include decreasing glycerol formation by engineering ammonia fixation to function with NADH instead of NADPH via up-regulation of GLN1, encoding glutamine synthetase,

or GLT1, encoding glutamate synthase with deletion of GDH1, encoding the NADPH-dependent glutamate dehydrogenase. (Nissen, T.L., et al., *Metabolic Engineering* 2: 69-77 (2000)). Another strategy engineering cells to produce excess NADPH during glycolysis via expression of a NADPH linked glyceraldehyde-3-phosphate dehydrogenase. (Bro, C., et al., *Metabolic Engineering* 8: 102-111 (2006)). A nother strategy contained a deletion of GDH1, and over-expression of glutamate synthase (GLT1) and glutamine synthase (GLN1), which also resulted in reduced glycerol formation. However, growth rates and biomass formation were well below the control strain and improvements on the initial performance have not been demonstrated. Additionally, industrially relevant yields, titers and fermentation rates were never demonstrated. (U.S. Patent No. 7,018,82.9)., A nother strategy describes deletion of only GDH1 without everexpression of GDH2 or GLT1/GLN1. However, the strategy was dependent on the use of an industrial polyploid yeast strain capable of tolerating high ethanol concentrations. It is noted in the patent that GDH1 was the only deletion, and that there are no heterologous DNA sequences in the genome. Additionally, the maximum reduction in glycerol production seen was 12.04%, and the technology was not demonstrated on an industrially relevant substrate (U.S. Patent No. 7,935,514). Most glycerol reduction strategies either only partially reduce the requirement for glycerol formation, or create a by-product other than ethanol. The present invention overcomes the shortcomings of these other strategies.

[0011] Corn mash contains free amino nitrogen. However the amount is too low to enable yeast biomass formation sufficient to meet the needs of the process. Nitrogen is added to industrial com ethanol fermentations to promote yeast growth, most commonly in the form of urea and ammonia. Excess nitrogen can improve the fermentation kinetics of conventional yeasts; however ethanol yields are often lower due to excess biomass and glycerol formation. Typically, urea is added to industrial com fermentations in concentrations that range from 500ppm to 1000ppm.

[0012] Yeast take up and assimilate ammonium as its preferred nitrogen source, followed by amino acids, and finally urea (Figures 2-4) (extensively reviewed by Lungdhal et al., *Genetics* 190: 885-929 (2012)). The mechanism of nitrogen catabolite repression (NCR) control is established by transcription factors which control the expression of ammonium, amino acid and urea transporters. These transcription factors also control expression of proteins responsible for degradation and assimilation of nitrogen containing molecules. It has been shown that de-repression of non-preferred nitrogen source assimilation pathways can improve fermentation kinetics (Salmon, J. M., and Barre, P., *Appl. Environ. Microbiol.* 64:3831-3837 (1998)); however, effects on ethanol productivity were not measured.

[0013] *S. cerevisiae* contains three known ammonium transporters, MEP1, MEP2 and MEP3. MEP1 and MEP2 are high affinity transporters while MEP3 is a low affinity transporter. *S. cerevisiae* breaks down urea through the enzymatic action of a urea-amido lyase (EC 6.3.4.6). This activity is encoded by the enzyme DUR1/2 in *S. cerevisiae* (Figures 2-4). Overexpression of DUR1/2 in wine yeasts has been shown to enhance urea degradation rates during fermentation of grape must (Coulon, J., et al., *Am. J. Enol. Vitic.* 57:2 (2006)). There are two known urea transporters in *S. cerevisiae*, DUR3 and DUR4 (Figures 2-4). It has been shown that overexpression of DUR3 resulted in improved urea degradation rates during wine fermentation (Dababieh, M.S., et al., *Am. J. Enol. Vitic.* 60:4 (2009)). U.S. Patent Publ. No. 2011/0129566 describes the expression of DUR1/2 and DUR3 in wine yeasts.

[0014] Industrial com mash substrates contain as much as 3% protein (w/v); however, much of the amino acid content contained in these proteins is unavailable to *S. cerevisiae*. Expression of one or more proteases would release amino acids that could serve as a nitrogen source for yeast. Additionally, the use of amino acids as a nitrogen source for *S. cerevisiae* in corn ethanol fermentations would improve yield through a reduction in the surplus NADH generated from *in vivo* amino acid synthesis during anaerobic growth.

[0015] Guo *et al.* engineered *S. cerevisiae* to express a heterologous protease for the purpose of improving ethanol yield (Guo, Z-p, et al., *Enzyme and Microbial Technology* 48: 148-154 (2011)). However, the work was conducted in a wild type yeast background that had not been previously engineered for reduced glycerol formation, and the activity of the expressed endoprotease primarily breaks protein into short polypeptides which are not transported by *S. cerevisiae*.

[0016] One aspect of the present invention relates to improved fermentation performance through co-expression of an exoprotease to release single amino acids. Additionally, com kernel protein is primarily a class of storage proteins known as zeins. Zeins have been shown to be recalcitrant to hydrolysis by many proteases and it is possible that expression of zein specific proteases would result in improved proteolysis. Thus, another aspect of the present invention relates to expressing zein-specific proteases to improve corn protein hydrolysis and amino acid utilization by the yeast.

[0017] Amino acids are transported by a large family of amino acid permeases. One aspect of this invention relates to deregulation or over-expression of a specific or general amino acid permease to complement protease expression or metabolic engineering by improving the uptake rate of free amino acids released during proteolysis. For example, expression of the general amino acid permease GAP1 is negatively regulated by AUA1. One aspect of this invention relates to the deletion of ADA1 or over expression of GAP1 that could result in improved amino acid uptake rates.

[0018] PCT/US2012/032443 teaches a method of eliminating glycerol formation through the production of formate. The formate production pathway can also be combined with strains engineered for reduced activity of the native glycerol production pathway. These combinations can be designed such that strains are built with different degrees of glycerol reduction as shown in Figure 5. Several embodiments of the current invention relate to a combination of those or related genetic modifications described in PCT/US2012/032443, with additional genetic modifications that are designed to alter

nitrogen transport and assimilation.

[0019] One aspect of this invention relates to strains of *S. cerevisiae* with reduced glycerol production that get a kinetic benefit from higher nitrogen concentration without sacrificing ethanol yield. A second aspect of the invention relates to metabolic modifications resulting in altered transport and/or intracellular metabolism of nitrogen sources present in corn mash.

[0020] WO2011/140386 provides a genetically modified thermophilic or mesophilic microorganism, wherein a first native gene is partially, substantially, or completely deleted, silenced, inactivated, or down-regulated, which first native gene encodes a first native enzyme involved in the metabolic production of an organic acid or a salt thereof, thereby increasing the native ability of said thermophilic or mesophilic microorganism to produce lactate or acetate as a fermentation product.

[0021] EP2277989 provides a recombinant yeast cell lacking or having reduced enzymatic activity needed for the NADH-dependent glycerol synthesis compared with the corresponding wild-type yeast cell, the yeast cell having one or more sequences encoding an NAD⁺ dependent acetylating acetaldehyde dehydrogenase [EC 1.2.1.10] activity.

BRIEF SUMMARY OF THE INVENTION

[0022] According to one aspect the invention provides a recombinant yeast comprising: at least one engineered genetic modification that leads to the up-regulation of one or more heterologous enzymes that function in one or more ethanol production pathways; at least one engineered genetic modification that leads to the down-regulation of an enzyme in a glycerol-production pathway; and at least one engineered genetic modification that leads to the upregulation or down-regulation of an enzyme in a nitrogen-assimilation pathway, wherein wherein the up-regulated enzyme that acts in an ethanol production pathway is pyruvate formate lyase (EC 2.3.1.54), pyruvate formate lyase activating enzyme (EC 1.91.1.4), and/or bifunctional acetaldehyde-alcohol dehydrogenase selected from a group of enzymes having both of the following Enzyme Commission Numbers: EC 1.2.1.10 and 1.1.1.1;

wherein the down-regulated enzyme that acts in the glycerol production pathway is at least one enzyme selected from the group consisting of: a glycerol-3-phosphate dehydrogenase 1 polynucleotide (GPD1) (EC 1.1.1.8), a glycerol-3-phosphate dehydrogenase 1 polypeptide (Gpd1) (EC 1.1.1.8), a glycerol-3-phosphate dehydrogenase 2 polynucleotide (GPD2) (EC 1.1.1.8), a glycerol-3-phosphate dehydrogenase 2 polypeptide (Gpd2) (EC 1.1.1.8), a glycerol-3-phosphate phosphatase 1 polynucleotide (GPP1) (EC 3.1.3.21), a glycerol-3-phosphate phosphatase polypeptide 1 (Gpp1) (EC 3.1.3.21), a glycerol-3-phosphate phosphatase 2 polynucleotide (GPP2) (EC 3.1.3.21), and a glycerol-3-phosphate phosphatase polypeptide 2 (Gpp2) (EC 3.1.3.21); and

wherein the down-regulated enzyme that acts in the nitrogen-assimilation pathway is glutamate dehydrogenase (Gdh) (EC 1.4.1.4) and wherein the up-regulated enzyme in the nitrogen-assimilation pathway is at least one enzyme selected from the group consisting of glutamate dehydrogenase (Gdh) (EC 1.4.1.2), glutamate synthase (Glt) (EC 1.4.1.14), and glutamine synthase (Gln) (EC 6.3.1.2), an ammonium transporter, a urea amidolyase (EC 6.3.4.6), and a urea transporter.

[0023] In some embodiments of the invention, the up-regulated enzyme that acts in the ethanol production pathway is an NADPH-dependent bifunctional acetaldehyde-alcohol dehydrogenase selected from a group of enzymes having both of the following Enzyme Commission Numbers: EC 1.2.1.10 and 1.1.1.2.

[0024] In some embodiments, the microorganism further comprises a down-regulation in one or more native enzymes encoded by formate dehydrogenase enzyme selected from the group consisting of: EC 1.2.1.43 and EC 1.2.1.2.

[0025] In some embodiments of the invention, the recombinant microorganism further comprises a heterologous GPD1 polynucleotide operably linked to a native GPD2 promoter. In some embodiments of the invention, the recombinant microorganism further comprises a heterologous GPD2 polynucleotide operably linked to a native GPD1 promoter.

[0026] In some embodiments of the invention, the microorganism further comprises an up-regulation or down-regulation of a regulatory element. In some embodiments the regulatory element is selected from the group consisting of Ure2 and Aua1.

[0027] In some embodiments of the invention, the microorganism further comprises at least one additional up-regulated enzyme. In some embodiments of the invention, the additional up-regulated enzyme is a glucoamylase enzyme with EC number 3.2.1.3. In some embodiments of the invention, the additional up-regulated enzyme is a permease. In some embodiments of the invention, the additional up-regulated enzyme is a protease with EC number: 3.4.23.41.

[0028] In some embodiments of the invention, the up-regulated or down-regulated enzymes are under the control of a heterologous promoter, in some embodiments of the invention, the heterologous promoter is selected from a group consisting of: *TEF2* (SEQ ID NO: 58), *HXT7* (SEQ ID NO: 59), *ADH1* (SEQ ID NO: 60), and *TPI* (SEQ ID NO: 61).

[0029] In some embodiments, the microorganism is a yeast. In some embodiments, the yeast is from the genus *Saccharomyces*. In some embodiments, the yeast is *Saccharomyces cerevisiae*. In some embodiments, the microorganism produces ethanol at higher yield than an otherwise identical microorganism lacking the generic modifications. In some embodiments, the microorganism produces an ethanol titer about 1% to about 10% more than an otherwise identical microorganism lacking the genetic modifications. In some embodiments, the microorganism produces an ethanol

titer of at least about 125 g/L.

[0030] In some embodiments, the microorganism produces glycerol at a lower yield than an otherwise identical microorganism lacking the genetic modifications. In some embodiments, the microorganism produces a glycerol titer of about 10 to about 100% less than an otherwise identical microorganism lacking the genetic modifications.

[0031] According to a second aspect, the invention relates to a composition comprising a recombinant yeast, and a carbon-containing feedstock.

[0032] According to a third aspect the invention provides a method of producing a fermentation product comprising: providing the composition of the second aspect; contacting the composition with carbon containing feedstock, wherein the recombinant yeast, is capable of fermenting the carbon containing feedstock to yield the fermentation product; and, optionally recovering the fermentation production.

[0033] According to a fourth aspect the invention provides -a method of producing ethanol comprising; providing the recombinant yeast of the first aspect; culturing the recombinant yeast in the presence of carbon containing feedstock for sufficient time to produce ethanol; and, optionally, extracting the ethanol.

[0034] According to a fifth aspect the invention provides a co-culture comprising at least two host cells, wherein one of the host cells comprises a recombinant yeast according to the first aspect; and another host cell that is genetically distinct from the recombinant yeast.

[0035] Some embodiments of the invention are directed to a recombinant microorganism comprising: down-regulated Gpd1, down-regulated Gpd2, down-regulated Fdh1, down-regulated Fdh2, down-regulated Gdh1, up-regulated AdhE, up-regulated pyruvate formate lyase, an up-regulated pyruvate formate lyase-activating enzyme, *GPD1* under the control of the *GPD2* promoter, *GPD2* under the control of the *GPD1* promoter, and up-regulated Gdh2.

[0036] Some embodiments of the invention are directed to a recombinant microorganism comprising; down-regulated Gpd1, down-regulated Gpd2, down-regulated Fdh1, down-regulated Fdh2, down-regulated Gdh1, up-regulated AdhE, up-regulated pyruvate formate lyase, an up-regulated pyruvate formate lyase-activating enzyme, *GPD1* under the control of the *GPD1* promoter, *GPD2* under the control of the *GPD1* promoter, up-regulated Glt1 and up-regulated Gln1.

[0037] Some embodiments of the invention are directed to a recombinant microorganism comprising: down-regulated Gpd1, down-regulated Fdh1, down-regulated Fdh2, down-regulated Gdh1, up-regulated AdhE, up-regulated pyruvate formate lyase, an up-regulated pyruvate formate lyase-activated enzyme, *GPD1* under the control of the *GPB2* promoter, *GPD2* under the control of the *GPD1* promoter, up-regulated Glt1 and up-regulated Gln1.

[0038] Some embodiments of the invention are directed to a recombinant microorganism comprising: down-regulated Gpd2, down-regulated Fdh1, down-regulated Fdh2, down-regulated Gdh1, up-regulated AdhE, up-regulated pyruvate formate lyase, and an up-regulated pyruvate formate lyase-activating enzyme.

[0039] Some embodiments of the invention are directed to a recombinant microorganism comprising; down-regulated Gpd1, down-regulated Fdh1 down-regulated Fdh2, down-regulated Gdh1, up-regulated AdhE, up-regulated pyruvate formate lyase, an up-regulated pyruvate formate lyase-activating enzyme, and *GPD2* under the control of the *GPD1* promoter.

[0040] Some embodiments of the invention are directed to a recombinant microorganism comprising: down-regulated Gpd1, down-regulated Fdh1, down-regulated Fdh2, down-regulated Gdh1, up-regulated AdhE, up-regulated pyruvate formate lyase, and an up-regulated pyruvate formate lyase-activating enzyme.

[0041] Some embodiments of the invention are directed to a recombinant microorganism comprising: down-regulated Gpd1, down-regulated Fdh1, down-regulated Fdh2, up-regulated AdhE, up-regulated pyruvate formate lyase, an up-regulated pyruvate formate lyase-activating enzyme, up-regulated-DUR/12, and *GPD2* under the control of the *GPD1* promoter.

[0042] Some embodiments of the invention are directed to a recombinant microorganism comprising: down-regulated Gpd1, down-regulated Fdh1, down-regulated Fdh2, up-regulated AdhE, up-regulated pyruvate formate lyase, an up-regulated pyruvate formate lyase-activating enzyme, and up-regulated-DUR/12.

[0043] Some embodiments of the invention are directed to a recombinant microorganism comprising: down-regulated Gpd1, down-regulated Gpd2, down-regulated Fdh1, down-regulated Fdh2, down-regulated Ure2, up-regulated AdhE, up-regulated pyruvate formate lyase, an up-regulated pyruvate formate lyase-activating enzyme, *GPD1* under the control of the *GPD2* promoter, and *GPD2* under the control of the *GPD1* promoter.

[0044] Some embodiments of the invention are directed to a recombinant microorganism comprising: down-regulated Gpd1, down-regulated Gpd2, down-regulated Fdh1, down-regulated Fdh2, up-regulated AdhE, up-regulated pyruvate formate lyase, an up-regulated pyruvate formate lyase-activating enzyme, up-regulated GDH2, *GPD1* under the control of the *GPD2* promoter, and *GPD2* under the control of the *GPD1* promoter.

BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

[0045]

Figure 1 depicts simplified carbon and redox pathways utilized by wildtype *S. cerevisiae* during anaerobic growth. Ethanol formation is redox neutral while cell biomass formation generates net NADH, which is balanced by glycerol formation.

Figure 2 depicts urea transport and intracellular catabolism. The enzymes Dur3 and Dur4 are known transporters of urea. Once inside the cell, urea is broken down into 2 ammonia molecules and 2 carbon dioxide molecules in a reaction catalyzed by Dur 1,2.

Figure 3 depicts the process by which an unmodified *S. cerevisiae* assimilates urea.

Figure 4 depicts process by which a genetically modified glycerol reduction strain which contains a deletion of Gdh1 assimilates urea.

Figure 5 depicts the glycerol titers of the wild type and glycerol reduction strains containing the formate pathway (M2390 (wildtype), M3465, M3467, M3469, and M3624 are depicted). This data shows total glycerol present in corn mash which contained 7 g/l glycerol prior to fermentation.

Figure 6 depicts a schematic diagram of the MA0631 insertion cassette.

Figure 7 depicts a schematic diagram of the MA0425 insertion cassette.

Figure 8 depicts a schematic diagram of the MA0426 insertion cassette.

Figure 9 depicts a schematic diagram of the MA0888 insertion cassette.

Figure 10 depicts a schematic diagram of the MA0837 insertion cassette.

Figure 11 depicts a schematic diagram of the MA0616 insertion cassette.

Figure 12 depicts a schematic diagram of the MA0616.1 insertion cassette.

Figure 13 depicts a schematic diagram of the MA0615 insertion cassette.

Figure 14 depicts a schematic diagram of the MA0615.1 insertion cassette.

Figure 15 depicts a schematic diagram of the MA0622 insertion cassette.

Figure 16 depicts a schematic diagram of the MA0622.1 insertion cassette.

Figure 17 depicts a schematic diagram of the MA0580 insertion cassette,

Figure 18 depicts a schematic diagram of the MA0581 insertion cassette.

Figure 19 depicts a schematic diagram of the MA0582 insertion cassette

Figure 20 depicts a schematic diagram of the MA0583 insertion cassette.

Figure 21 depicts a schematic diagram of the MA0584 insertion cassette.

Figure 22 depicts a schematic diagram of the MA0585 insertion cassette.

Figure 23 depicts a schematic diagram of the MA0617 insertion cassette.

Figure 24 depicts a schematic diagram of the MA0617.1 insertion cassette.

Figure 25 depicts a schematic diagram of the MA0434 insertion cassette.

Figure 26 depicts a schematic diagram of the MA0434.2 insertion cassette.

Figure 27 depicts a schematic diagram of the MA0434.3 insertion cassette.

Figure 28 depicts a schematic diagram of the MA0434.4 insertion cassette.

Figure 29 depicts a schematic diagram of the MA0434.5 insertion cassette.

Figure 30 depicts a schematic diagram of the MA0454.14 insertion cassette.

Figure 31 depicts a schematic diagram of the MA0464 insertion cassette.

Figure 32 depicts a schematic diagram of the MA0464.1 insertion cassette.

Figure 33 depicts a schematic diagram of the MA0464.2 insertion cassette.

Figure 34 depicts a schematic diagram of the MA0464.3 insertion cassette.

Figure 35 depicts a schematic diagram of the MA0464.4 insertion cassette.

Figure 36 depicts a schematic diagram of the MA0464.5 insertion cassette.

Figure 37 depicts a schematic diagram of the MA0465.1 insertion cassette.

Figure 38 depicts a schematic diagram of the MA0467 insertion cassette.

Figure 39 depicts a schematic diagram of the MA0467.1 insertion cassette.

Figure 40 depicts a schematic diagram of the MA0467.2 insertion cassette,

Figure 41 depicts a schematic diagram of the MA0467.3 insertion cassette.

Figure 42 depicts a schematic diagram of the MA0467.4 insertion cassette.

Figure 43 depicts a schematic diagram of the MA0881 insertion cassette.

Figure 44 depicts a schematic diagram of the MA0881.1 insertion cassette.

Figure 45 depicts a plasmid map for pMU2373.

Figure 46 depicts a plasmid map for pMU2879.

Figure 47 depicts a plasmid map for pMU2908.

Figure 48 depicts a plasmid map for pMU2909.

Figure 49 depicts a plasmid map for pMU2911.

Figure 50 depicts a plasmid map for pMU2913.

Figure 51 depicts a plasmid map for pMU3409.

Figure 52 depicts a plasmid map for pMU3410.

Figure 53 depicts a plasmid map for pMU3411.

Figure 54 depicts a plasmid map for pMU3459.

Figure 55 depicts a plasmid map for pMU3460.

5 Figure 56 depicts a plasmid map for pMU3461.

Figure 57 depicts a plasmid map for pMU3463.

Figure 58 depicts a plasmid map for pMU3464.

Figure 59 depicts a plasmid map for pMU3465.

Figure 60 depicts a plasmid map for pMU3466.

10 Figure 61 depicts a plasmid map for pMU3468.

Figure 62 depicts a plasmid map for pMU3471.

Figure 63 depicts a plasmid map for pMU3472.

Figure 64 depicts a plasmid map for pMU3473.

Figure 65 depicts a plasmid map for pMU3475.

15 Figure 66 depicts a plasmid map for pMU3605.

Figure 67 depicts a plasmid map for pMU3606.

Figure 68 depicts a plasmid map for pMU3607.

Figure 69 depicts the final ethanol titers measured following fermentation of 31% solids corn mash in wildtype cells (M2390), a glycerol reduction strain containing the formate pathway (M3624), and 2 strains with modification of the ammonium assimilation pathway (M4117, which contains a deletion of *gdh1* and an over-expression of *Gdh2*, and M4118, which contains a deletion of *gdh1* and an over-expression of *Glt1* and *Gln1*).

Figure 70 depicts the ethanol titers measured following fermentation of 31% solids corn mash for glycerol reduction strains containing the formate pathway (M3465, M3467, M3469) that additionally have a deletion of *gdh1* (M4400, M4401, M4402), M2390 was a parental control. Figure 71 depicts the ethanol titers measured following fermentation

25 of 31% solids corn mash for M2390, M3467, M3469, M4427 (M3467 parent strain: expression of DUR1/2 driven by the TEF2 promoter), M4428 (M3467 parent strain: expression of DUR1/2 driven by the HXT7 promoter), M4429 (M3467 parent strain: expression of DUR1/2 driven by the ADH1 promoter), M4430 (M3467 parent strain: expression of DUR1/2 driven by the HXT7/TEF2 promoters), M4431 (M3469 parent strain: expression of DUR 1/2 driven by the TEF2 promoter), M4432 (M3469 parent strain: expression of DUR1/2 driven by the HXT7 promoter), M4433 (M3469 parent strain: expression of DUR1/2 driven by the ADH1 promoter), and M4434 (M3469 parent strain: expression of DUR1/2 driven by the HXT7/TEF2 promoters)

30 Figure 72 depicts the ethanol titers measured following fermentation of 31% solids corn mash for M2390, M3624, M4406, and M4407.

35 Figure 73 depicts the ethanol titers produced after 68hrs fermentation in mini-vials for strains M2390, M3624, M4117, M5841, M5842, M5843, and M5844.

Figure 74 depicts the glycerol titers produced after 68hrs fermentation in mini-vials for strains M2390, M3624, M4117, M5841, M5842, M5843, and M5844.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

45 **[0046]** Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art of microbial metabolic engineering. Although methods and materials similar or equivalent to those described herein can be used in the practice of the disclosed methods and compositions, exemplary methods, devices and materials are described herein.

50 The embodiments described, and references in the specification to "one embodiment", "an embodiment", "an example embodiment", etc., indicate that the embodiments described can include a particular feature, structure, or characteristic, but every embodiment does not necessarily include the particular feature, structure, or characteristic. Moreover, such phrases are not necessarily referring to the same embodiment. Further, when a particular feature, structure, or characteristic is described in connection with an embodiment, it is understood that it is within the knowledge of one skilled in the art to effect such feature, structure, or characteristic in connection with other embodiments whether or not explicitly described.

55 The description of "a" or "an" item herein may refer to a single item or multiple items. It is understood that wherever embodiments are described herein with the language "comprising," otherwise analogous embodiments described in terms of "consisting of and/or "consisting essentially of" are also provided. Thus, for example, reference to "a polynucleotide" includes a plurality of such polynucleotides and reference to "the microorganism" includes reference

to one or more microorganisms, and so forth.

The term "heterologous" is used in reference to a polynucleotide or a gene not normally found in the host organism. "Heterologous" includes up-regulated or downregulated endogenous genes. "Heterologous" also includes a native coding region, or portion thereof, that is reintroduced into the source organism in a form that is different from the corresponding native gene, *e.g.*, not in its natural location in the organism's genome. "Heterologous" also includes any gene that has been modified and placed into an organism. A heterologous gene may include a native coding region that is a portion of a chimeric gene including a non-native regulatory region that is reintroduced into the native host or modifications to the native regulatory sequences that affect the expression level of the gene. Foreign genes can comprise native genes inserted into a non-native organism, or chimeric genes. A heterologous polynucleotide, gene, polypeptide, or an enzyme may be derived or isolated from any source, *e.g.*, eukaryotes, prokaryotes, viruses, or synthetic polynucleotide fragments, and includes up-regulated endogenous genes.

The terms "gene(s)" or "polynucleotide" or "nucleic acid" or "polynucleotide sequence(s)" are intended to include nucleic acid molecules, *e.g.*, polynucleotides which include an open reading frame encoding a polypeptide, and can further include non-coding regulatory sequences, and introns. In addition, the terms are intended to include one or more genes that map to a functional locus. Also, the terms are intended to include a specific gene for a selected purpose. The gene may be endogenous to the host cell or may be recombinantly introduced into the host cell, *e.g.*, as a plasmid maintained episomally or a plasmid (or fragment thereof) that is stably integrated into the genome. In addition to the plasmid form, a gene may, for example, be in the form of linear DNA or RNA. The term "gene" is also intended to cover multiple copies of a particular gene, *e.g.*, all of the DNA sequences in a cell encoding a particular gene product. A "gene" refers to an assembly of nucleotides that encode a polypeptide, and includes cDNA and genomic DNA nucleic acids. "Gene" also refers to a nucleic acid fragment that expresses a specific protein, including intervening sequences (introns) between individual coding segments (exons), as well as regulatory sequences preceding (5' non-coding sequences) and following (3' non-coding sequences) the coding sequence. "Native" or "endogenous" refers to a gene as found in nature with its own regulatory sequences.

A "nucleic acid," "polynucleotide," or "nucleic acid molecule" is a polymeric compound comprised of covalently linked subunits called nucleotides. Nucleic acid includes polyribonucleic acid (RNA) and polydeoxyribonucleic acid (DNA), both of which may be single-stranded or double-stranded. DNA includes cDNA, genomic DNA, synthetic DNA, and semi-synthetic DNA.

An "isolated nucleic acid molecule" or "isolated nucleic acid fragment" refers to the phosphate ester polymeric form of ribonucleosides (adenosine, guanosine, uridine or cytidine; "RNA molecules") or deoxyribonucleosides (deoxyadenosine, deoxyguanosine, deoxythymidine, or deoxycytidine; "DNA molecules"), or any phosphoester analogs thereof, such as phosphorothioates and thioesters, in either single stranded form, or a double-stranded helix. Double stranded DNA-DNA, DNA-RNA and RNA-RNA helices are possible. The term nucleic acid molecule, and in particular DNA or RNA molecule, refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear or circular DNA molecules (*e.g.*, restriction fragments), plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the non-transcribed strand of DNA (*i.e.*, the strand having a sequence homologous to the mRNA).

The term "expression" is intended to include the expression of a gene at least at the level of mRNA production, generally subsequently translated into a protein product. The term "expression," refers to the transcription and stable accumulation of sense (mRNA) or antisense RNA derived from the nucleic acid fragment of the invention. Expression may also refer to translation of mRNA into a polypeptide.

As used herein, an "expression vector" is a vector capable of directing the expression of genes to which it is operably linked.

A "vector," *e.g.*, a "plasmid" or "YAC" (yeast artificial chromosome) refers to an extrachromosomal element often carrying one or more genes that are not part of the central metabolism of the cell, and is usually in the form of a circular double-stranded DNA molecule. Such elements may be autonomously replicating sequences, genome integrating sequences" phage or nucleotide sequencer linear, circular, or supercoiled, of a single- or double-stranded DNA or RNA, derived from any source, in which a number of nucleotide sequences have been joined or recombined into a unique construction which is capable of introducing a promoter fragment and DNA sequence for a selected gene product along with appropriate 3' untranslated sequence into a cell. Preferably, the plasmids or vectors of the present invention are stable and self-replicating.

The term "integrated" as used herein refers to genetic elements that are placed, through molecular biology techniques, into a chromosome of a host cell. For example, genetic elements can be placed into the chromosomes of the host cell as opposed to in a vector such as a plasmid carried by the host cell. Methods for integrating genetic elements into the genome of a host cell are well known in the art and include homologous recombination.

The term "domain" as used herein refers to a part of a molecule or structure that shares common physical or chemical

features, for example hydrophobic, polar, globular, helical domains or properties, e.g., a DNA binding domain or an ATP binding domain. Domains can be identified by their homology to conserved structural or functional motifs. Examples of cellobiohydrolase (CBH) domains include the catalytic domain (CD) and the cellulose binding domain (CBD).

A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a eDNA, genomic DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and solution ionic strength. Hybridization and washing conditions are well known and exemplified, e.g., in Sambrook, J., Fritsch, E. F. and Maniatis, T. MOLECULAR CLONING: A LABORATORY MANUAL, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor (1989), particularly Chapter 11 and Table 11.1 therein (hereinafter "Maniatis"). The conditions of temperature and ionic strength determine the "stringency" of the hybridization. Stringency conditions can be adjusted to screen for moderately similar fragments, such as homologous sequences from distantly related organisms, to highly similar fragments, such as genes that duplicate functional enzymes from closely related organisms. Post-hybridization washes determine stringency conditions. One set of conditions uses a series of washes starting with 6X SSC, 0.5% SDS at room temperature, for 15 min, then repeated with 2X SSC, 0.5% SDS at 45°C for 30 min, and then repeated twice with 0.2X SSC, 0.5% SDS at 50°C for 30 min. For more stringent conditions, washes are performed at higher temperatures in which the washes are identical to those above except for the temperature of the final two 30 min washes in 0.2X SSC, 0.5% SDS are increased to 60°C. Another set of highly stringent conditions uses two final washes in 0.1X SSC, 0.1% SDS at 65°C. An additional set of highly stringent conditions are defined by hybridization at 0.1X SSC, 0.1% SDS, 65°C and washed with 2X SSC, 0.1% SDS followed by 0.1X SSC, 0.1% SDS.

Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating T_m have been derived (see, e.g., Maniatis at 9.50-9.51). For hybridizations with shorter nucleic acids, i.e., oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (see, e.g., Maniatis, at 11.7-11.8). In one embodiment the length for a hybridizable nucleic acid is at least about 10 nucleotides. Preferably a minimum length for a hybridizable nucleic acid is at least about 15 nucleotides; more preferably at least about 20 nucleotides; and most preferably the length is at least 30 nucleotides. Furthermore, the skilled artisan will recognize that the temperature and wash solution salt concentration may be adjusted as necessary according to factors such as length of the probe.

The term "percent identity", as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and conserved amino acid substitutes thereto of the polypeptide to the sequence of a second polypeptide.

"Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in: Computational Molecular Biology (Lesk, A. M., ed.) Oxford University Press, NY (1998); Biocomputing: Informatics and Genome Projects (Smith, D. W., ed.) Academic Press, NY (1993); Computer Analysis of Sequence Data, Part I (Griffin, A. M., and Griffin, H. G., eds.) Humana Press, NJ (1994); Sequence Analysis in Molecular Biology (von Heinje, G., ed.) Academic Press (1987); and Sequence Analysis Primer (Gibbskov, M. and Devereux, J., eds.) Stockton Press, NY (1991). Preferred methods to determine identity are designed to give the best match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Sequence alignments and percent identity calculations may be performed using the Megalign program of the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, Wis.). Multiple alignments of the sequences disclosed herein were performed using the Clustal method of alignment (Higgins and Sharp (1989) CABIOS. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10), Default parameters for pairwise alignments using the Clustal method were KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5.

Suitable nucleic acid sequences or fragments thereof (isolated polynucleotides of the present invention) encode polypeptides that are at least about 70% to about 75% identical to the amino acid sequences reported herein, at least about 80%, about 85%, or about 90% identical to the amino acid sequences reported herein, or at least about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequences reported herein. Suitable nucleic acid fragments are at least about 70%, about 75%, or about 80% identical to the nucleic

acid sequences reported herein, at least about 80%, about 85%, or about 90% identical to the nucleic acid sequences reported herein, or at least about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the nucleic acid sequences reported herein. Suitable nucleic acid fragments not only have the above identities/similarities but typically encode a polypeptide having at least 50 amino acids, at least 100 amino acids, at least 150 amino acids, at least 200 amino acids, or at least 250 amino acids.

A DNA or RNA "coding region" is a DNA or RNA molecule which is transcribed and/or translated into a polypeptide in a cell *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. "Suitable regulatory regions" refer to nucleic acid regions located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding region, and which influence the transcription, RNA processing or stability, or translation of the associated coding region. Regulatory regions may include promoters, translation leader sequences, RNA processing site, effector binding site and stem-loop structure. The boundaries of the coding region are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding region can include, but is not limited to, prokaryotic regions, cDNA from mRNA, genomic DNA molecules, synthetic DNA molecules, or RNA molecules. If the coding region is intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding region.

An "isoform" is a protein that has the same function as another protein but which is encoded by a different gene and may have small differences in its sequence.

A "paralogue" is a protein encoded by a gene related by duplication within a genome.

An "orthologue" is gene from a different species that has evolved from a common ancestral gene by speciation. Normally, orthologues retain the same function in the course of evolution as the ancestral gene.

"Open reading frame" is abbreviated ORF and means a length of nucleic acid, either DNA, cDNA or RNA, that comprises a translation start signal or initiation codon, such as an ATG or AUG, and a termination codon and can be potentially translated into a polypeptide sequence.

"Promoter" refers to a DNA fragment capable of controlling the expression of a coding sequence or functional RNA.

In general, a coding region is located 3' to a promoter. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic DNA segments. It is understood by those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of cellular development, or in response to different environmental or physiological conditions. Promoters which cause a gene to be expressed in most cell types at most times are commonly referred to as "constitutive promoters". It is further recognized that since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity. A promoter is generally bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter will be found a transcription initiation site (conveniently defined for example, by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

A coding region is "under the control" of transcriptional and translational control elements in a cell when RNA polymerase transcribes the coding region into mRNA, which is then trans-RNA spliced (if the coding region contains introns) and translated into the protein encoded by the coding region.

"Transcriptional and translational control regions" are DNA regulatory regions, such as promoters, enhancers, terminators, and the like, that provide for the expression of a coding region in a host cell. In eukaryotic cells, polyadenylation signals are control regions.

The term "operably associated" refers to the association of nucleic acid sequences on a single nucleic acid fragment so that the function of one is affected by the other. For example, a promoter is operably associated with a coding region when it is capable of affecting the expression of that coding region (*i.e.*, that the coding region is under the transcriptional control of the promoter). Coding regions can be operably associated to regulatory regions in sense or antisense orientation.

As used herein, the term "anaerobic" refers to an organism, biochemical reaction or process that is active or occurs under conditions of an absence of gaseous O₂.

"Anaerobic conditions" are defined as conditions under which the oxygen concentration in the fermentation medium is too low for the microorganism to use as a terminal electron acceptor. Anaerobic conditions may be achieved by sparging a fermentation medium with an inert gas such as nitrogen until oxygen is no longer available to the microorganism as a terminal electron acceptor. Alternatively, anaerobic conditions may be achieved by the microorganism consuming the available oxygen of fermentation until oxygen is unavailable to the microorganism as a terminal electron acceptor.

"Aerobic metabolism" refers to a biochemical process in which oxygen is used as a terminal electron acceptor to convert energy, typically in the form of ATP, from carbohydrates. Aerobic metabolism typically occurs, for example, via the electron transport chain in mitochondria in eukaryotes, wherein a single glucose molecule is metabolized

completely into carbon dioxide in the presence of oxygen.

In contrast, "anaerobic metabolism" refers to a biochemical process in which oxygen is not the final acceptor of electrons generated. Anaerobic metabolism can be divided into anaerobic respiration, in which compounds other than oxygen serve as the terminal electron acceptor, and substrate level phosphorylation, in which no exogenous

electron acceptor is used and products of an intermediate oxidation state are generated via a "fermentative pathway." In "fermentative pathways", the amount of NAD(P)H generated by glycolysis is balanced by the consumption of the same amount of NAD(P)H in subsequent steps. For example, in one of the fermentative pathways of certain yeast strains, NAD(P)H generated through glycolysis donates its electrons to acetaldehyde, yielding ethanol. Fermentative pathways are usually active under anaerobic conditions but may also occur under aerobic conditions, under conditions where NADH is not fully oxidized via the respiratory chain.

As used herein, the term "end-product" refers to a chemical compound that is not or cannot be used by a cell, and so is excreted or allowed to diffuse into the extracellular environment. Common examples of end-products from anaerobic fermentation include, but are not limited to, ethanol, acetic acid, formic acid, lactic acid, hydrogen and carbon dioxide.

As used herein, "cofactors" are compounds involved in biochemical reactions that are recycled within the cells and remain at approximately steady state levels. Common examples of cofactors involved in anaerobic fermentation include, but are not limited to, NAD⁺ and NADP⁺. In metabolism, a cofactor can act in oxidation-reduction reactions to accept or donate electrons. When organic compounds are broken down by oxidation in metabolism, their energy can be transferred to NAD⁺ by its reduction to NADH, to NADP⁺ by its reduction to NADPH, or to another cofactor, FAD⁺, by its reduction to FADH₂. The reduced cofactors can then be used as a substrate for a reductase.

As used herein, a "pathway" is a group of biochemical reactions that together can convert one compound into another compound in a step-wise process. A product of the first step in a pathway may be a substrate for the second step, and a product of the second step may be a substrate for the third, and so on. Pathways of the present invention include, but are not limited to, the pyruvate metabolism pathway the lactate production pathway, the ethanol production pathway, the glycerol-production pathway, the nitrogen assimilation pathway, and the ammonium assimilation pathway.

The term "recombination" or "recombinant" refers to the physical exchange of DNA between two identical (homologous), or nearly identical, DNA molecules. Recombination can be used for targeted gene deletion or to modify the sequence of a gene. The term "recombinant microorganism" and "recombinant host cell" are used interchangeably herein and refer to microorganisms that have been genetically modified to express or over-express endogenous polynucleotides, or to express heterologous polynucleotides, such as those included in a vector, or which have a modification in expression of an endogenous gene.

By "expression modification" it is meant that the expression of the gene, or level of a RNA molecule or equivalent RNA molecules encoding one or more polypeptides or polypeptide subunits, or activity of one or more polypeptides or polypeptide subunits is up regulated or down-regulated, such that expression, level, or activity, is greater than or less than that observed in the absence of the modification,

In one aspect of the invention genes or particular polynucleotide sequences are partially, substantially, or completely deleted, silenced, inactivated, or down-regulated in order to inactivate the enzymatic activity they encode. Complete deletions provide maximum stability because there is no opportunity for a reverse mutation to restore function. Alternatively, genes can be partially, substantially, or completely deleted, silenced, inactivated, or down-regulated by insertion, deletion, removal or substitution of nucleic acid sequences that disrupt the function and/or expression of the gene.

As used herein, the term "down-regulate" includes the deletion or mutation of a genetic sequence, or insertion of a disrupting genetic element, coding or non-coding, such that the production of a gene product is lessened by the deletion, mutation, or insertion. It includes a decrease in the expression level (*i.e.*, molecular quantity) of an mRNA or protein. "Delete" or "deletion" as used herein refers to a removal of a genetic element such that a corresponding gene is completely prevented from being expressed. In some embodiments, deletion refers to a complete gene deletion. Down-regulation can also occur by engineering the repression of genetic elements by chemical or other environmental means, for example by engineering a chemically-responsive promoter element (or other type of conditional promoter) to control the expression of a desired gene product. Down-regulation can also occur through use of a weak promoter.

As used herein, the term "up-regulate" includes the insertion, reintroduction, mutation, or increased expression of a genetic sequence, such that the production of a gene product is increased by the insertion, reintroduction, or mutation. It includes an increase in the expression level (*i.e.*, molecular quantity) of an mRNA or protein. "Insert" or "insertion" as used herein refers to an introduction of a genetic element such that a corresponding gene is expressed. Up-regulation can also occur by causing the increased expression of genetic elements through an alteration of the associated regulatory sequence. Up-regulation can occur by engineering the expression of genetic elements by chemical or other environmental means, for example by engineering a chemically-responsive promoter element (or

other type of conditional promoter) to control the expression of a desired gene product. Up-regulation can also occur through use of a strong promoter.

As used herein, the term "glycerol-production pathway" refers to the collection of biochemical pathways that produce glycerol from DHAP. Components of the pathway consist of all substrates, cofactors, byproducts, intermediates, end-products, and enzymes in the pathway.

As used herein, the term "ethanol production pathway" refers the collection of biochemical pathways that produce ethanol from a carbohydrate source. Components of the pathway consist of all substrata cofactors, byproducts, intermediates, end-products, and enzymes in the pathway.

As used herein, the term "nitrogen assimilation pathway" refers to the collection of biochemical pathways that result in the formation of organic nitrogen containing compounds from inorganic nitrogen compounds. Components of the pathway consist of all substrates, cofactors, byproducts, intermediates, end-products, and enzymes in the pathway.

As used herein, the term "ammonium assimilation pathway" refers to the collection of biochemical pathways that assimilate ammonia or ammonium (NH_4^+) into glutamate and/or glutamine. The ammonium assimilation pathway is part of the larger nitrogen assimilation pathway. Components of the pathway consist of all substrates, cofactors, byproducts, intermediates, end-products, and enzymes in the pathway.

As used herein, the term "glycolysis" or "glycolytic pathway" refers to the canonical pathway of basic metabolism in which a sugar such as glucose is broken down into more oxidized products, converting energy and compounds required for cell growth. Components of the pathway consist of all substrates, cofactors, byproducts, intermediates end-products, and enzymes in the pathway.

As used herein, the term "alcohol dehydrogenase" or "ADM" is intended to include the enzymes that catalyze the conversion of ethanol into acetaldehyde. Very commonly, the same enzyme catalyzes the reverse reaction from acetaldehyde to ethanol, which is the direction more relevant to fermentation. Alcohol dehydrogenase includes those enzymes that correspond to EC 1.1.1.1 and 1.1.1.2 and exemplified by the enzymes disclosed in GenBank Accession No. U49975.

As used herein, the term "aldehyde dehydrogenase", "ALD" or "ALDH" is intended to include the enzymes that catalyze the oxidation of aldehydes. Aldehyde dehydrogenase enzymes include "acetaldehyde dehydrogenase", which catalyzes the conversion of acetaldehyde into acetyl-CoA. Very commonly, the same enzyme catalyzes the reverse reaction from acetyl-CoA to acetaldehyde, which is the direction more relevant to fermentation. Aldehyde dehydrogenase includes those enzymes that correspond to EC 1.2.1.3, 1.2.1.4 and 1.2.1.10.

As used herein, the term "glycerol-3-phosphate dehydrogenase" or "GPD" is intended to include those enzymes capable of converting dihydroxyacetone phosphate to glycerol-3-phosphate. GPD includes those enzymes that correspond to EC 1.1.1.8. In some embodiments, the GPD is GPD1 and/or GPD2 from *S. cerevisiae* (GDP1: SEQ ID NO: 4 and 5, GDP2: SEQ ID NO: 6 and 7),

As used herein, the term "glycerol-3-phosphate phosphatase" or "GPP" is intended to include those enzymes capable of converting glycerol-1-phosphate to glycerol. Glycerol-3-phosphate is intended to include those enzymes that correspond to EC 3.1.3.21. (GPP1:SEQ ID NO:158 and 159, GPP2: SEQ ID NO 160 and 161)

As used herein, the term "formate dehydrogenase" or "FDH" is intended to include those enzymes capable of converting formate to bicarbonate (carbon dioxide). Formate dehydrogenase includes those enzymes that correspond to EC 1.2.1.43 and EC 1.2.1.2. In some embodiments, the FDH is from *S. cerevisiae* (FDH1: SEQ ID NO: 1 and 2, FDH2: SEQ ID NO: 3).

As used herein, the term "bifunctional" is intended to include enzymes that catalyze more than one biochemical reaction step. A specific example of a bifunctional enzyme used herein is an enzyme (adhE) that catalyzes both the alcohol dehydrogenase and acetaldehyde dehydrogenase reactions, and includes those enzymes that correspond to EC 1.2.1.10 and 1.1.1.1. In some embodiments, the bifunctional acetaldehyde-alcohol dehydrogenase is from *B. adolescentis* (adhE: SEQ ID NO: 12 and 13). In some embodiments, the bifunctional enzyme is a NADPH specific bifunctional acetaldehyde-alcohol dehydrogenase, and includes those enzymes that correspond to EC 1.2.1.10 and 1.1.1.2. In some embodiments, the NADPH specific bifunctional acetaldehyde-alcohol dehydrogenase is from *L. mesenteroides* (SEQ ID NO: 14 and 15) or *O. oenii* (SEQ ID NO: 16 and 17).

As used herein, the term "pyruvate formate lyase" or "PFL" is intended to include the enzymes capable of converting pyruvate to formate and acetyl-CoA. PFL includes those enzymes that correspond to EC 2-3.1.54 and exemplified by SEQ ID NO: 8 and 9.

As used herein, the term "PFL-activating enzymes" is intended to include those enzymes capable of aiding in the activation of PFL. PFL-activating enzymes include those enzymes that correspond to EC 1.97.1.4 and are exemplified by SEQ ID NO: 10 and 11.

As used herein, the term "glutamate dehydrogenase", "GDH", or "GLDH" is intended to include those enzymes that convert glutamate to α -ketoglutarate, as well as those enzymes that catalyze the reverse reaction. The glutamate dehydrogenase can be NADPH-dependent (e.g. GDH1 or GDH3 in *S. cerevisiae*). The glutamate dehydrogenase can be NADH-dependent (e.g. GDH2 in *S. cerevisiae*). Glutamate dehydrogenases include those enzymes that

correspond to EC 1.4.1.2 and EC 1.4.1.4. Glutamate dehydrogenases include those enzymes that correspond to accession numbers: M10590, S66436, S 66039.1, U12980, NP_015020, NP_010066, S66039.1 and AAC04972. In some embodiments, the glutamate dehydrogenase is from *S. cerevisiae* (GDH1; SEQ ID NOs: 25 and 25; GDH2. SEQ ID NOs: 26 and 27; GDH3: SEQ ID NOs: 30 and 31.) or *N. crassa* (GDH2: SEQ ID NOs: 28 29).

As used herein, the term "glutamate synthase" or "GLT" is intended to include those enzymes that convert L-glutamine and 2-oxoglutarate to L-glutamate, as well as those enzymes that catalyze the reverse reaction. Glutamate synthases include those enzymes that correspond to EC 1.4.1.14 and EC 1.4.1.13. In some embodiments, the glutamate synthase is GLT1 from *S. cerevisiae* (SEQ ID NOs: 32 and 33; accession numbers: X89221 and NP_010110.1).

As used herein, the term "glutamine synthase", "glutamine synthetase", or "GLN" is intended to include those enzymes that convert glutamate to glutamine. Glutamine synthases include those enzymes that correspond to EC 6.3.1.2. In some embodiments, the glutamine synthase is GLN1 from *S. cerevisiae* (SEQ ID NOs: 34 and 35; accession numbers: M65157 and NP_015360.2).

As used herein, the term "urea-amido lyase" is intended to include those enzymes that convert urea to ure-1-carboxylate. Urea-amido lyases include those enzymes that correspond to EC 6.3.4.6. In some embodiments, the urea-amido lyase is DUP1/2 (DUR1,2) from *S. cerevisiae* (SEQ ID NOs: 36 and 37; accession numbers: M64926 and NP_009767.1)

As used herein, the term "urea transporter" is a membrane protein that transports urea across a cellular membrane. In some embodiments, the urea transporter is Dur3 or Dur4 from *S. cerevisiae* (DUR3: SEQ ID NOs: 38 and 39; accession numbers: AY693170 and NP_011847.1).

As used herein, the term "protease" is any enzyme that hydrolyzes the peptide bonds between amino acids together in a protein. An exoprotease is a protease that breaks the peptide bonds of terminal amino acids in a protein. An endoprotease is a protease that breaks the peptide bonds of non-terminal amino acids in a protein. Proteases include those enzymes that correspond to EC 3.4.23.41. Proteases include those enzymes that correspond to accession numbers: NP_001151278, NP_001150196, NP_001148706, NCU00338, XP_001908191, XP_369812, EU970094.1, NM_001156724, NM_001155234.1, XP_957809.2, XM_001908156.1, and XM_003717209.1. In some embodiments, the protease is from *Z. mays* (SEQ ID NOs: 40-45), *N. crassa* (SEQ ID NOs: 46-47), *P. anserine* (SEQ ID NOs: 48-49), or *M. oryzae* (SEQ ID NOs: 50-51).

As used herein, the term "glucoamylase" or " γ -amylase" refers to an amylase that acts on α -1,6-glycosidic bonds. Glucoamylases include those enzymes that correspond to EC 3.2.1.3. In some embodiments, the glucoamylase is *S. fibuligera* glucoamylase (glu-0111-CO) (SEQ ID NO: 162 and 163).

As used herein, the term "permease" refers to a membrane transport protein that facilitates the diffusion of a molecule through the use of passive transport in or out of a cell. In some embodiments, the permease is the amino acid permease GAP1 from *S. cerevisiae*. (SEQ ID NO: 52 and 53).

As used herein, the term "ammonium transporter" refers to permeases, and is intended to include the enzymes that are involved in the transport of ammonium and ammonia, and are exemplified by the *S. cerevisiae* MEP1, MEP2 and MEP3 enzymes (MEP 1: SEQ ID NOs: 18 and 19; MEP2: SEQ ID NOs: 20 and 21; MEP3: SEQ ID NOs: 22 and 23). Ammonium transporters include those enzymes that correspond to accession numbers: X77608, X83608, AY692775, NP_011636.3, NP_014257.1, and NP_015464.1.

As used herein, the term "URE2" refers to transcription factor known in the art by that name that represses the nitrogen catabolism of glutamate by controlling the transcription factor. URE2 is a regulator of GLN3. In some embodiments, the URE2 is from *S. cerevisiae* (SEQ ID NOs: 54 and 55).

As used herein, "AUA1" refers to a transcription factor known in the art by that name which is required for the negative regulation of Gap1. In some embodiments, the AUA1 is from *S. cerevisiae* (SEQ ID NOs: 56 and 57).

As used herein, "GLN3" refers to a transcription factor known in the art by that name that activates genes that are regulated by nitrogen catabolite metabolism. In some embodiments, the GLN3 is from *S. cerevisiae* (SEQ ID NOs: 156 and 157). The term "feedstock" is defined as a raw material or mixture of raw materials supplied to a microorganism or fermentation process from which other products can be made. For example, a carbon source, such as biomass or the carbon compounds derived from biomass are a feedstock for a microorganism that produces a product in a fermentation process. A feedstock can contain nutrients other than a carbon source.

Biomass can include any type of biomass known in the art or described herein. The terms "lignocellulosic material," "lignocellulosic substrate" and "cellulosic biomass" mean any type of carbon containing feed stock including woody biomass, such as recycled wood pulp fiber, sawdust, hardwood, softwood, grasses, sugar-processing residues, agricultural wastes, such as, but not limited to, rice straw, rice hulls, barley straw, corn cobs, cereal straw, wheat straw, canola straw, oat straw, oat hulls, corn fiber, stover, succulents, agave, or any combination thereof.

The term "yield" is defined as the amount of product obtained per unit weight of raw material and may be expressed as gram product per gram substrate (g/g). Yield may be expressed as a percentage of the theoretical yield. "Theoretical yield" is defined as the maximum amount of product that can be generated per a given amount of substrate

as dictated by the stoichiometry of the metabolic pathway used to make the product. For example, the theoretical yield for one typical conversion of glucose to ethanol is 0.51g EtOH per 1g glucose. As such, a yield of 4.8g ethanol from 10g of glucose would be expressed as 94% of theoretical or 94% theoretical yield.

The term "titer" is defined as the strength of a solution or the concentration of a substance in solution. For example, the titer of a product in a fermentation broth is described as gram of product in solution per liter of fermentation broth (g/L) or as g/kg broth.

As used herein, the term "flux" is the rate of flow of molecules through a metabolic pathway, akin to the flow of material in a process.

"Bacteria", or "eubacteria", refers to a domain of prokaryotic organisms. Bacteria include gram-positive (gram+) bacteria and gram-negative (gram-) bacteria.

"Yeast" refers to a domain of eukaryotic organisms that are unicellular fungi.

The terms "derivative" and "analog" refer to a polypeptide differing from the enzymes of the invention, but retaining essential properties thereof. Generally, derivatives and analogs are overall closely similar, and, in many regions, identical to the enzymes of the invention. The terms "derived from", "derivative" and "analog" when referring to enzymes of the invention include any polypeptides which retain at least some of the activity of the corresponding native polypeptide or the activity of its catalytic domain.

Derivatives of enzymes disclosed herein are polypeptides which may have been altered so as to exhibit features not found on the native polypeptide. Derivatives can be covalently modified by substitution, (e.g. amino acid substitution), chemical, enzymatic, or other appropriate means with a moiety other than a naturally occurring amino acid (e.g., a detectable moiety such as an enzyme or radioisotope). Examples of derivatives include fusion proteins, or proteins which are based on a naturally occurring protein sequence, but which have been altered. For example, proteins can be designed by knowledge of a particular amino acid sequence, and/or a particular secondary, tertiary, and quaternary structure. Derivatives include proteins that are modified based on the knowledge of a previous sequence, natural or synthetic, which is then optionally modified, often, but not necessarily to confer some improved function. These sequences, or proteins, are then said to be derived from a particular protein or amino acid sequence. In some embodiments of the invention, a derivative must retain at least about 50% identity, at least about 60% identity, at least about 70% identity, at least about 80% identity, at least about 90% identity, at least about 95% identity, at least about 97% identity, or at least about 99% identity to the sequence the derivative is "derived from." In some embodiments of the invention, an enzyme is said to be derived from an enzyme naturally found in a particular species if, using molecular genetic techniques, the DNA sequence for part or all of the enzyme is amplified and placed into a new host cell.

"Isolated" from, as used herein, refers to a process whereby, using molecular biology techniques, genetic material is harvested from a particular organism often with the end goal of putting the genetic material into a non-native environment.

The term "percent identity", as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and conserved amino acid substitutes thereto of the polypeptide to the sequence of a second polypeptide.

"Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in: Computational Molecular Biology (Lesk, A. M., ed.) Oxford University Press, NY (1988); Biocomputing: Informatics and Genome Projects (Smith, D. W., ed.) Academic Press, NY (1993); Computer Analysis of Sequence Data, Part I (Griffin, A. M., and Griffin, H. G., eds.) Humana Press, NJ (1994); Sequence Analysis in Molecular Biology (von Heinje, G., ed.) Academic Press (1987); and Sequence Analysis Primer (Gribskov, M. and Devereux, J., eds.) Stockton Press, NY (1991). Preferred methods to determine identity are designed to give the best match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Sequence alignments and percent identity calculations may be performed using the Megalign program of the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, Wis.). Multiple alignments of the sequences disclosed herein were performed using the Clustal method of alignment (Higgins and Sharp (1989) CABIOS. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the Clustal method were KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5.

[0047] Suitable nucleic acid sequences or fragments thereof (isolated polynucleotides of the present invention) encode polypeptides that are at least about 70% to 75% identical to the amino acid sequences disclosed herein, at least about 80%, at least about 85%, or at least about 90% identical to the amino acid sequences disclosed herein, or at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 100% identical

to the amino acid sequences disclosed herein. Suitable nucleic acid fragments are at least about 70%, at least about 75%, or at least about 80% identical to the nucleic acid sequences disclosed herein, at least about 80%, at least about 85%, or at least about 90% identical to the nucleic acid sequences disclosed herein, or at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 100% identical to the nucleic acid sequences disclosed herein. Suitable nucleic acid fragments not only have the above identities/similarities but typically encode a polypeptide having at least about 50 amino acids, at least about 100 amino acids, at least about 150 amino acids, at least about 200 amino acids, or at least about 250 amino acids.

Codon Optimization

[0048] In some embodiments of the present invention, exogenous genes may be codon-optimized in order to express the polypeptide they encode most efficiently in the host cell. Methods of codon optimization are well known in the art. (See, e.g. Welch et al. "Designing genes for successful protein expression." Methods Enzymol. 2011. 498:43-66.)

[0049] In general, highly expressed genes in an organism are biased towards codons that are recognized by the most abundant tRNA species in that organism. One measure of this bias is the "codon adaptation index" or "CAI," which measures the extent to which the codons used to encode each amino acid in a particular gene are those which occur most frequently in a reference set of highly expressed genes from an organism. The Codon Adaptation Index is described in more detail in Sharp et al., "The Codon Adaptation Index; a Measure of Directional Synonymous Codon Usage Bias, and Its Potential Applications." Nucleic Acids Research (1987) 15: 1281-1295.

[0050] A codon optimized sequence may be further modified for expression in a particular organism, depending on that organism's biological constraints. For example, large runs of "As" or "Ts" (e.g., runs greater than 3, 4, 5, 6, 7, 8, 9, or 10 consecutive bases) can effect transcription negatively. Therefore, it can be useful to remove a run by, for example, replacing at least one nucleotide in the run with another nucleotide. Furthermore, specific restriction enzyme sites may be removed for molecular cloning purposes by replacing at least one nucleotide in the restriction site with another nucleotide. Examples of such restriction enzyme sites include PaeI, AscI, BamHI, BglII, EcoRI and XhoI. Additionally, the DNA sequence can be checked for direct repeats, inverted repeats and mirror repeats with lengths of about 5, 6, 7, 8, 9 or 10 bases or longer, Runs of "As" or "Ts", restriction sites and/or repeats can be modified by replacing at least one codon within the sequence with the "second best" codons, i.e., the codon that occurs at the second highest frequency for a particular amino acid within the particular organism for which the sequence is being optimized.

[0051] Deviations in the nucleotide sequence that comprise the codons encoding the amino acids of any polypeptide chain allow for variations in the sequence coding for the gene. Since each codon consists of three nucleotides, and the nucleotides comprising DNA are restricted to four specific bases, there are 64 possible combinations of nucleotides, 61 of which encode amino acids (the remaining three codons encode signals ending translation). The "genetic code" which shows which codons encode which amino acids is reproduced herein as Table 1. As a result, many amino acids are designated by more than one codon. For example, the amino acids alanine and proline are coded for by four triplets, serine and arginine by six triplets each, whereas tryptophan and methionine are coded for by just one triplet. This degeneracy allows for DNA base composition to vary over a wide range without altering the amino acid sequence of the proteins encoded by the DNA.

TABLE 1: The Standard Genetic Code

	T	C	A	G
T	TTT phe (F) TTC " TTA Leu (L) TTG "	TCT Ser (S) TCC " TCA " TCG "	TAT Tyr (Y) TAC " TAA Ter TAG Ter	TGT Cys (C) TGC TGA Ter TGG Trp (W)
C	CTT Leu (L) CTC " CTA " CTG "	CCT Pro (P) CCC " CCA " CCG "	CAT His (H) CAC " CAA Gln (Q) CAG "	CGT Arg (R) CGC " CGA " CGG "
A	ATT Ile (I) ATC " ATA " ATG Met (M)	ACT Thr (T) ACC " ACA " ACG "	Asn (N) AAT AAC " AAA Lys (K) AAG "	AGT Ser (S) AGC " AGA Arg (R) AGG "

(continued)

	T	C	A	G
G	GTT Val (V) GTC " GTA " GTG "	GCT Ala (A) GCC " GCA " GCG "	Asp (D) GAC " GAT GAA Gln (E) GAG "	GGT Gly (G) GGC " GGA " GGG "

[0052] Many organisms display a bias for use of particular codons to code for insertion of a particular amino acid in a growing peptide chain. Codon preference or codon bias, differences in codon usage between organisms, is afforded by degeneracy of the genetic code, and is well documented among many organisms. Codon bias often correlates with the efficiency of translation of messenger RNA (mRNA), which is in turn believed to be dependent on, inter alia, the properties of the codons being translated and the availability of particular transfer RNA (tRNA) molecules. The predominance of selected tRNAs in a cell is generally a reflection of the codons used most frequently in peptide synthesis. Accordingly, genes can be tailored for optimal gene expression in a given organism based on codon optimization.

Host cells

[0053] In some embodiments of the invention, the host cell is a eukaryotic microorganism. In some embodiments, the host cell is a yeast. In some embodiments, the host cell is able to digest and ferment cellulose. In some embodiments, the host cell is from the genus *Saccharomyces*. In some embodiments, the host cell is *Saccharomyces cerevisiae*.

[0054] In some embodiments, the host cells of the invention are cultured at a temperature above about 20°C, above about 25°C, above about 27°C, above about 30°C, above about 33°C, above about 35°C, above about 37°C, above about 40°C, above about 43°C, above about 45°C, or above about 47°C. In some embodiments, the host cells of the invention contain genetic constructs that lead to the down-regulation of one or more genes encoding a polypeptide at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to one or more of the polypeptides encoded SEQ ID NOs: 2, 5, 7, 25, 31, 55, 57, 159 and 161, and the polynucleotide sequence encoded by SEQ ID NO: 3. In some embodiments, the host cells of the invention contain genetic constructs that lead to the expression or up-regulation of a polypeptide encoding the activity associated with EC Nos.: 1.1.1.8, 3.1.3.21, 1.2.1.43, 1.2.1.2, 1.4.1.2, and 1.4.1.4,

[0055] In some embodiments, the host cells of the invention contain genetic constructs that lead to the expression or up-regulation of one or more genes encoding a polypeptide at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or about 100% identical to one or more of the polypeptides encoded by SEQ ID NOs: 9, 11, 13, 15, 17, 19, 21, 23, 27, 33, 35, 37, 39, 41, 41, 45, 47, 49, 51, 53, 157, and 163. In some embodiments, the host cells of the invention contain genetic constructs that lead to the expression or up-regulation of a polypeptide encoding the activity associated with EC Nos.: 1.1.1.1, 1.1.1.2, 1.2.1.3, 1.2.1.4, 1.2.1.10, 2.3.1.54, 1.97.1.4, 1.4.1.2, 1.4.1.4, 1.1.1.14, 1.4.1.13, 6.3.1.2, 6.3.4.6, and 3.2.1.3.

[0056] In some embodiments, bifunctional acetaldehyde-alcohol dehydrogenase is up-regulated. In some embodiments, the up-regulated bifunctional acetaldehyde-alcohol dehydrogenase is from an enzyme that corresponds to an EC number selected from the group consisting of: EC 1.2.1.0 and 1.1.1.1. In some embodiments, the bifunctional acetaldehyde-alcohol dehydrogenase is a NADPH dependent bifunctional acetaldehyde-alcohol dehydrogenase selected from a group of enzymes having the following Enzyme Commission Numbers: EC 1.2.1.10 and 1.1.1.2. In some embodiments, the bifunctional acetaldehyde-alcohol dehydrogenase corresponds to a polypeptide selected from the group consisting of SEQ ID NOs: 13, 15, and 17. In some embodiments, the bifunctional acetaldehyde-alcohol dehydrogenase is adhE.

[0057] In some embodiments, pyruvate formate lyase is up-regulated. In some embodiments, the up-regulated pyruvate formate lyase is from an enzyme that corresponds to EC 2.3.1.54. In some embodiments, the pyruvate formate lyase corresponds to a polypeptide encoded by SEQ ID NO: 2. In some embodiments, pyruvate formate lyase activating enzyme is up-regulated. In some embodiments, the up-regulated pyruvate formate lyase activating enzyme is from an enzyme that corresponds to EC 1.97.1.4. In some embodiments, the pyruvate formate lyase activating enzyme corresponds to a polynucleotide encoded by SEQ ID NO: 3.

[0058] In some embodiments, glutamate dehydrogenase is up-regulated. In some embodiments, the glutamate dehydrogenase that is up-regulated is NADH-dependent. In some embodiments, the up-regulated glutamate dehydrogenase corresponds to EC 1.4.1.2. In some embodiments, glutamate dehydrogenase from *S. cerevisiae* is up-regulated. In some embodiments, the glutamate dehydrogenase that is up-regulated is from *S. cerevisiae* is GDH2 and corresponds to a polypeptide corresponding to SEQ ID NO: 29. In some embodiments, glutamate synthase is up-regulated. In some embodiments, the up-regulated glutamate synthase corresponds to EC 1.4.1.14. In some embodiments, glutamate

synthase from *S. cerevisiae* is up-regulated. In some embodiments, the glutamate dehydrogenase that is up-regulated is from *S. cerevisiae* is GLT1 and corresponds to a polypeptide corresponding to SEQ ID NO: 33. In some embodiments, glutamine synthase is up-regulated. In some embodiments, the up-regulated glutamine synthase corresponds to EC 6.3.1.2. In some embodiments, glutamine synthase from *S. cerevisiae* is up-regulated. In some embodiments, the glutamine dehydrogenase that is up-regulated is from *S. cerevisiae* is GLN1 and corresponds to a polypeptide corresponding to SEQ ID NO: 35.

[0059] In some embodiments, a urea-amido lyase is up-regulated. In some embodiments, the up-regulated urea-amido lyase corresponds to EC 6.3.4.6. In some embodiments, urea-amido lyase from *S. cerevisiae* is up-regulated. In some embodiments, the urea-amido lyase that is up-regulated is from *S. cerevisiae* is DUR1/2 and corresponds to a polypeptide corresponding to SEQ ID NO: 37.

[0060] In some embodiments, a protease is up-regulated. In some embodiments, the up-regulated protease corresponds to EC 3.4.23.41. In some embodiments, the protease is an endoprotease. In some embodiments, the protease is an exoprotease. In some embodiments, a protease from *Z. mays*, *N. crassa*, *P. anserine*, or *M. oryzae* is up-regulated. In some embodiments, the protease that is up-regulated corresponds to a polypeptide corresponding to SEQ ID NOs: 41, 43, 45, 47, 49 or 51. In some embodiments, a permease is up-regulated. In some embodiments, a permease from *S. cerevisiae* is up-regulated. In some embodiments, the permease that is up-regulated is GAP1 and corresponds to a polypeptide corresponding to SEQ ID NO: 53.

[0061] In some embodiments, a glucoamylase is up-regulated. In some embodiments, the up-regulated glucoamylase corresponds to EC 3.2.1.3. In some embodiments, a glucoamylase from *S. fibuligera* is up-regulated. In some embodiments, the glucoamylase from *S. fibuligera* that is up-regulated corresponds to a polypeptide corresponding to SEQ ID NO: 163.

[0062] In some embodiments, an ammonium transporter is up-regulated. In some embodiments, an ammonium transporter from *S. cerevisiae* is up-regulated. In some embodiments, the ammonium transporter that is up-regulated is MEP1, MEP2, or MEP3 from *S. cerevisiae* and corresponds to a polypeptide corresponding to SEQ ID NOs: 19, 21, and 23. In some embodiments, a urea transporter is up-regulated. In some embodiments, a urea transporter from is from *S. cerevisiae*. In some embodiments, the urea transporter that is up-regulated is DUR3 or DUR4 from *S. cerevisiae* and corresponds to a polypeptide corresponding to SEQ ID NOs: 39.

[0063] In some embodiments, glycerol-3-phosphate dehydrogenase is down-regulated. In some embodiments, the down-regulated Gpd is from an enzyme that corresponds to EC 1.1.1.8. In some embodiments, the glycerol-3-phosphate dehydrogenase is selected from the group consisting of glycerol-3-phosphate dehydrogenase 1 ("Gpd1"), glycerol-3-phosphate dehydrogenase 2 ("Gpd2"), and combinations thereof. In some embodiments, the Gpd1 is from *S. cerevisiae* and corresponds to a polypeptide encoded by SEQ ID NO: 5. In some embodiments, the Gpd2 is from *S. cerevisiae* and corresponds to a polypeptide encoded by SEQ ID NO: 7. In some embodiments, formate dehydrogenase is down-regulated. In some embodiments, the down-regulated formate dehydrogenase corresponds to an EC number selected from the group consisting of EC 1.2.1.43 and EC 1.2.1.2. In some embodiments, formate dehydrogenase from *S. cerevisiae* is down-regulated. In some embodiments, the formate dehydrogenase from *S. cerevisiae* corresponds to a polypeptide corresponding to SEQ ID NO: 2 or a polynucleotide corresponding to SEQ ID NO: 3. In some embodiments, glycerol-3-phosphate phosphatase is down-regulated. In some embodiments, the down-regulated glycerol-3-phosphate phosphatase corresponds to EC 3.1.3.21. In some embodiments, the down-regulated glycerol-3-phosphate phosphatase corresponds to a polynucleotide corresponding to SEQ ID NOs 158 or 160 or a polypeptide corresponding to SEQ ID NOs 159 or 161.

[0064] In some embodiments, glutamate dehydrogenase is down-regulated. In some embodiments, the glutamate dehydrogenase that is down-regulated is NADPH-dependent. In some embodiments, the down-regulated glutamate dehydrogenase corresponds to EC 1.4.1.4. In some embodiments, glutamate dehydrogenase that is down-regulated is from *S. cerevisiae*. In some embodiments, the glutamate dehydrogenase is from *S. cerevisiae* is GDH1 and corresponds to a polypeptide corresponding to SEQ ID NO: 25.

[0065] In some embodiments, a regulatory element is down-regulated. In some embodiments, the regulatory element that is down-regulated is from *S. cerevisiae*. In some embodiments, the regulatory element from *S. cerevisiae* is Ure2 and corresponds to a polypeptide corresponding to SEQ ID NO: 55. In some embodiments, the regulatory element from *S. cerevisiae* is Aua1 and corresponds to a polypeptide corresponding to SEQ ID NO: 57.

[0066] In some embodiments, bifunctional acetaldehyde-alcohol dehydrogenase (AdhE), *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme are up-regulated, and Gpd1 and Gpd2 are down-regulated. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme are up-regulated, and Gpd1, Gpd2, Fdh1 and Fdh2 are down-regulated. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme are up-regulated, Gpd1, Gpd2, Fdh1 and Fdh2 are down-regulated, *GPD1* is expressed under the control of the *GPD2* promoter, and *GPD2* is expressed under the control of the *GPD1* promoter. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme are up-regulated,

Gpd1, Gpd2, Fdh1, Fdh2, Gdh1 are down-regulated, *GPD1* is expressed under the control of the *GPD2* promoter, and *GPD2* is expressed under the control of the *GPD1* promoter. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme, and Glt1 are up-regulated, Gpd1, Gpd2, Fdh1, Fdh2, Gdh1 are down-regulated, *GPD1* is expressed under the control of the *GPD2* promoter, and *GPD2* is expressed under the control of the *GPD1* promoter. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme, and Gln1 are up-regulated, Gpd1, Gpd2, Fdh1, Fdb2, Gdh1 are down-regulated, *GPD1* is expressed under the control of the *GPD2* promoter, and *GPD2* is expressed under the control of the *GPD1* promoter. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme, Gln1 and Glt1 are up-regulated. Gpd1, Gpd2, Fdh1, Fdh2, Gdh1 are down-regulated, *GPD1* is expressed under the control of the *GPD2* promoter, and *GPD2* is expressed under the control of the *GPD1* promoter. In some embodiments, the regulatory element Ure2 is down-regulated. In some embodiments, the regulatory element Aua1 is down-regulated. In some embodiments, Gln3 is up-regulated.

[0067] In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme are up-regulated, and Gpd2, Fdh1, and Fdh2 are down-regulated. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme are up-regulated, and Gpd2, Fdh1, Fdh2, and Gdh1 are down-regulated. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme are up-regulated, and Gpd1, Fdh1, and Fdh2 are down-regulated. In some embodiments, AdhE, *B. adolescentis* pyruvate formate lyase, and *B. adolescentis* pyruvate formate lyase activating enzyme are up-regulated, and Gpd1, Fdh1, Fdh2, and Gdh1 are down-regulated. In some embodiments, Dur1/2 is additionally expressed. In some embodiments, Dur1/2 is expressed from the *TEF2* promoter. In some embodiments, Dur1/2 is expressed from the *HXT7* promoter. In some embodiments, Dur1/2 is expressed from the *GPM1* promoter. In some embodiments, Dur1/2 is expressed from the *ADH1* promoter. In some embodiments, Dur1/2 is expressed from the *HXT7/TEF2* promoters. In some embodiments, Gln3 is up-regulated. In some embodiments, *GPD1* is expressed from the *GPD2* promoter. In some embodiments, *GPD2* is expressed from a *GPD1* promoter. Ethanol Production

[0068] For a microorganism to produce ethanol most economically, it is desired to produce a high yield. In one embodiment, the only product produced is ethanol. Extra products lead to a reduction in product yield and an increase in capital and operating costs, particularly if the extra products have little or no value. Extra products also require additional capital and operating costs to separate these products from ethanol.

[0069] Ethanol production can be measured using any method known in the art. For example, the quantity of ethanol in fermentation samples can be assessed using HPLC analysis. Additionally, many ethanol assay kits are commercially available, for example, alcohol oxidase enzyme based assays. Methods of determining ethanol production are within the scope of those skilled in the art from the teachings herein.

[0070] In some embodiments of the invention where redirected carbon flux generates increased ethanol production, the ethanol output can be improved by growth-coupled selection. For example, continuous culture or serial dilution cultures can be performed to select for cells that grow faster and/or produce ethanol (or any desired product) more efficiently on a desired feedstock.

[0071] One embodiment of the present invention relates to a method of producing ethanol using a microorganism described herein wherein the microorganism is cultured in the presence of a carbon containing feedstock for sufficient time to produce ethanol and, optionally, extracting the ethanol. In some embodiments, nitrogen is added to the culture containing the recombinant microorganism and the feedstock.

[0072] Ethanol may be extracted by methods known in the art. (See, e.g., U.S. Appl. Pub. No. 2011/0171709)

[0073] Another embodiment of the present invention relates to a method of producing ethanol using a co-culture composed of at least two microorganisms in which at least one of the organisms is an organism described herein, and at least one of the organisms is a genetically distinct microorganism. In some embodiments, the genetically distinct microorganism is a yeast or bacterium. In some embodiments the genetically distinct microorganism is any organism from the genus *Issatchenkia*, *Pichia*, *Clavispora*, *Candida*, *Hansenula*, *Kluyveromyces*, *Saccharomyces*, *Trichoderma*, *Thermoascus*, *Escherichia*, *Clostridium*, *Caldicellulosiruptor*, *Thermoanaerobacter* and *Thermoanaerobacterium*.

[0074] In some embodiments, the recombinant microorganism produces about 2% to about 3% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 2% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 5% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 7% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 10% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 15% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 20% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 30% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 50% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 75% higher ethanol titer than a wildtype, non-recombinant organism; at least about 1% to at least about 100% higher ethanol titer than a wildtype, non-recombinant

organism. In some embodiments, the recombinant microorganism produces at least about 0.5g/L ethanol to at least about 2 g/L ethanol, at least about 0.5g/L ethanol to at least about 3 g/L ethanol, at least about 0.5g/L ethanol to at least about 5 g/L ethanol, at least about 0.5g/L ethanol to at least about 7 g/L ethanol, at least about 0.5g/L ethanol to at least about 10 g/L ethanol, at least about 0.5g/L ethanol to at least about 15 g/L ethanol, at least about 0.5g/L ethanol to at least about 20 g/L ethanol, at least about 0.5g/L ethanol to at least about 30 g/L ethanol, at least about 0.5g/L ethanol to at least about 40 g/L ethanol, at least about 0.5g/L ethanol to at least about 50 g/L ethanol, at least about 0.5g/L ethanol to at least about 75 g/L ethanol, at least about 0.5g/L ethanol to at least about 99 g/L ethanol, at least about 0.5 g/L ethanol to at least about 125 g/L ethanol, or at least about 0.5 g/L to at least about 150 g/L ethanol per at least about 24 hour, at least about 48 hour, or at least about 72 hour incubation on a carbon-containing feed stock, such as corn mash.

[0075] In some embodiments, the recombinant microorganism produces ethanol at least about 55% to at least about 75% of theoretical yield, at least about 50% to at least about 80% of theoretical yield, at least about 45% to at least about 85% of theoretical yield, at least about 40% to at least about 90% of theoretical yield, at least about 35% to at least about 95% of theoretical yield, at least about 30% to at least about 99% of theoretical yield, or at least about 25% to at least about 99% of theoretical yield. In some embodiments, methods of producing ethanol can comprise contacting a biomass feedstock with a host cell or co-culture of the invention and additionally contacting the biomass feedstock with externally produced saccharolytic enzymes. In some embodiments, the host cells are genetically engineered (e.g., transduced, transformed, or transfected) with the polynucleotides encoding saccharolytic enzymes.

[0076] An "amylolytic enzyme" can be any enzyme involved in amylase digestion, metabolism and/or hydrolysis. The term "amylase" refers to an enzyme that breaks starch down into sugar. Amylase is present in human saliva, where it begins the chemical process of digestion. Foods that contain much starch but little sugar, such as rice and potato, taste slightly sweet as they are chewed because amylase turns some of their starch into sugar in the mouth. The pancreas also makes amylase (α -amylase) to hydrolyse dietary starch into disaccharides and trisaccharides which are converted by other enzymes to glucose to supply the body with energy. Plants and some bacteria also produce amylase. All amylases are glycoside hydrolases and act on α -1,4-glycosidic bonds. Some amylases, such as γ -amylase (glucoamylase), also act on α -1,6-glycosidic bonds. Amylase enzymes include α -amylase (EC 3.2.1.1), β -amylase (EC 3.2.1.2), and γ -amylase (EC 3.2.1.3). The α -amylases are calcium metalloenzymes, unable to function in the absence of calcium. By acting at random locations along the starch chain, α -amylase breaks down long-chain carbohydrates, ultimately yielding maltotriose and maltose from amylose, or maltose, glucose and "limit dextrin" from amylopectin. Because it can act anywhere on the substrate, α -amylase tends to be faster-acting than β -amylase. In animals, it is a major digestive enzyme and its optimum pH is about 6.7-7.0. Another form of amylase, β -amylase is also synthesized by bacteria, fungi, and plants. Working from the non-reducing end, β -amylase catalyzes the hydrolysis of the second α -1,4 glycosidic bond, cleaving off two glucose units (maltose) at a time. Many microbes produce amylase to degrade extracellular starches. In addition to cleaving the last α (1-4) glycosidic linkages at the nonreducing end of amylose and amylopectin, yielding glucose, γ -amylase will cleave α (1-6) glycosidic linkages. Another amylolytic enzyme is alpha-glucosidase that acts on maltose and other short malto-oligosaccharides produced by alpha-, beta-, and gamma-amylases, converting them to glucose. Another amylolytic enzyme is pullulanase. Pullulanase is a specific kind of glucanase, an amylolytic exoenzyme, that degrades pullulan. Pullulan is regarded as a chain of maltotriose units linked by alpha-1,6-glycosidic bonds. Pullulanase (EC 3.2.1.41) is also known as pullulan-6-glucanohydrolase (debranching enzyme). Another amylolytic enzyme, isopullulanase, hydrolyses pullulan to isopanose (6-alpha-maltosylglucose). Isopullulanase (EC 3.2.1.57) is also known as pullulan 4-glucanohydrolase. An "amylase" can be any enzyme involved in amylase digestion metabolism and/or hydrolysis, including α -amylase, β -amylase, glucoamylase, pullulanase, isopullulanase, and alpha-glucosidase.

[0077] In some embodiments, the recombinant microorganisms of the invention further comprise one or more native and/or heterologous enzymes which encodes a saccharolytic enzyme, including amylases, cellulases, hemicellulases, cellulolytic and amylolytic accessory enzymes, inulinases, levanases, and pentose sugar utilizing enzymes. In one aspect, the saccharolytic enzyme is an amylase, where the amylase is selected from *H. grisea*, *T. aurantiacus*, *T. emersonii*, *T. reesei*, *C. lacteus*, *C. formosanus*, *N. takasagoensis*, *C. acinaciformis*, *M. darwinensis*, *N. walkeri*, *S. fibuligera*, *C. luckowense*, *R. speratus*, *Thermobifida fusca*, *Clostridium thermocellum*, *Clostridium cellulolyticum*, *Clostridium josui*, *Bacillus pumilis*, *Cellulomonas fimi*, *Saccharophagus degradans*, *Piromyces equii*, *Neocallimastix patricarum* or *Arabidopsis thaliana*. In another aspect, the saccharolytic enzyme is a glucoamylase (glu-0111-CO) from *S. fibuligera*.

[0078] The term "xylanolytic activity" is intended to include the ability to hydrolyze glycosidic linkages in oligopentoses and polypentoses. The term "xylanase" is the name given to a class of enzymes which degrade the linear polysaccharide beta-1,4-xylan into xylose, thus breaking down hemicellulose, one of the major components of plant cell walls. As such, it plays a major role in micro-organisms thriving on plant sources (mammals, conversely, do not produce xylanase). Additionally, xylanases are present in fungi for the degradation of plant matter into usable nutrients. Xylanases include those enzymes that correspond to E.C. Number 3.2.1.8. A "xylose metabolizing enzyme" can be any enzyme involved in xylose digestion, metabolism and/or hydrolysis, including a xylose isomerase, xylulokinase, xylose reductase, xylose dehydrogenase, xylitol dehydrogenase, xylonate dehydratase, xylose transketolase, and a xylose transaldolase protein.

[0079] The term "pectinase" is a general term for enzymes, such as pectolyase, pectozyme and polygalacturonase,

commonly referred to in brewing as pectic enzymes. These enzymes break down pectin, a polysaccharide substrate that is found in the cell walls of plants. One of the most studied and widely used commercial pectinases is polygalacturonase. Pectinases are commonly used in processes involving the degradation of plant materials, such as speeding up the extraction of fruit juice from fruit, including apples and sapota. Pectinases have also been used in wine production since the 1960s.

[0080] A "saccharolytic enzyme" can be any enzyme involved in carbohydrate digestion, metabolism and/or hydrolysis, including amylases, cellulases, hemicellulases, cellulolytic and amylolytic accessory enzymes, inulinases, levanases, and pentose sugar utilizing enzymes.

[0081] A "pentose sugar utilizing enzyme" can be any enzyme involved in pentose sugar digestion, metabolism and/or hydrolysis, including xylanase, arabinase, arabinoxylanase, arabinosidase, arabinofuranosidase, arabinoxylanase, arabinosidase, and arabinofuranosidase, arabinose isomerase, ribulose-5-phosphate 4-epimerase, xylose isomerase, xylokinase, xylose reductase, xylose dehydrogenase, xylitol dehydrogenase, xylonate dehydratase, xylose transketolase, and/or xylose transaldolase.

Glycerol production

[0082] In some embodiments of the invention where redirected carbon flux generates increased ethanol production, the glycerol output can be decreased by growth-coupled selection. For example, continuous culture or serial dilution cultures can be performed to select for cells that produce less glycerol on a desired feedstock. Glycerol can be measured, for example, by HPLC analysis of metabolite concentrations.

[0083] In some embodiments, the recombinant microorganism produces at least about 20% to at least about 30% less glycerol than a wildtype, non-recombinant organism; at least about 30% to at least about 50% less glycerol than a wildtype, non-recombinant organism; at least about 40% to at least about 60% less glycerol than a wildtype, non-recombinant organism; at least about 50% to at least about 70% less glycerol than a wildtype, non-recombinant organism; at least about 60% to at least about 80% less glycerol than a wildtype, non-recombinant organism; at least about 70% to at least about 90% less glycerol than a wildtype, non-recombinant organism; at least about 75% to at least about 95% less glycerol than a wildtype, non-recombinant organism; at least about 70% to at least about 99% less glycerol than a wildtype, non-recombinant organism; at least about 15% to at least about 30% less glycerol than a wildtype, non-recombinant organism; at least about 10% to at least about 40% less glycerol than a wildtype, non-recombinant organism; at least about 10% to at least about 50% less glycerol than a wildtype, non-recombinant organism; at least about 10% to at least about 60% less glycerol than a wildtype, non-recombinant organism; at least about 10% to at least about 70% less glycerol than a wildtype, non-recombinant organism; at least about 10% to at least about 80% less glycerol than a wildtype, non-recombinant organism; at least about 10% to at least about 90% less glycerol than a wildtype, non-recombinant organism; at least about 10% to at least about 99% less glycerol than a wildtype, non-recombinant organism; at least about 10% to at least about 100% less glycerol than a wildtype, non-recombinant organism; at least about 5% to at least about 100% less glycerol than a wildtype, non-recombinant organism; at least about 1% to at least about 100% less glycerol than a wildtype, non-recombinant organism. In some embodiments, the recombinant microorganism produces no glycerol. In some embodiments, the recombinant microorganism has a growth rate at least about 1/2 to at least about equal to the growth rate of a wildtype, non-recombinant organism, at least about 1/4 to at least about equal to the growth rate of a wildtype, non-recombinant organism, at least about 1/8 to at least about equal to the growth rate of a wildtype, non-recombinant organism, at least about 1/10 to at least about equal to the growth rate of a wildtype, non-recombinant organism, at least about 1/25 to at least about equal to the growth rate of a wildtype, non-recombinant organism, at least about 1/50 to at least about equal to the growth rate of a wildtype, non-recombinant organism or at least about 1/100th to at least about equal to the growth rate of a wildtype, non-recombinant organism.

[0084] A wildtype-non-recombinant organism produces glycerol at a rate of at least about 8-11 mM glycerol per gram dry cell weight (DCW) during anaerobic growth. In some embodiments, glycerol production is reduced to a rate of between 1-10 mM glycerol per gram dry cell weight during anaerobic growth.

EXAMPLES

[0085] Strains used in the following examples were created using Mascoma Assemblies ("MAs"). Schematic diagrams of the MAs can be seen in Figures 6-44. Plasmids used to make the MAs can be seen in Figures 45-68 and Table 2. Primers used to create the MAs can be seen in Table 3 below and in SEQ ID NOs: 66-155. Strains used in the invention can be seen in Table 4 below. For a general description of molecular methods that could be used to create the strains, see U.S. Application No 61/728,450, which is incorporated herein by reference.

Table 2. Plasmids used to make the MAs.

Plasmid ID	Description
pMU2873	AGTEF pro-KAN-AGTEF ter/HXT2 pro-TDK-ACT1 ter
pMU2879	AGTEF pro-cloNAT-AGTEF ter/HXT2 pro-TDK-ACT1 ter
PMU2908	PGK1 pro- <i>S. cerevisiae</i> GDH2-ENO1 ter
pMU2909	ADH1 pro- <i>S. cerevisiae</i> GDH2-PDC1 ter
pMU2911	ADH1 pro-GLN1-PDC1 ter
pMU2913	PGK1 pro-GLT1-ENO1 ter
pMU3409	TEF2 pro-DUR1,2-ADH3 ter
pMU3410	HXT7 pro-DUR1,2-PMA1t
pMU3411	ADH1 pro-DUR1,2-PDC1 ter
pMU3459	ADH1 pro-DUR3-PDC1 ter
pMU3460	ADH1 pro-MEP1-PDC1 ter
pMU3461	ADH1 pro-MEP2-PDC1 ter
pMU3463	ADH1 pro-GAP1-PDC1 ter
pMU3464	TEF2 pro-DUR3-ADH3 ter
pMU3465	TEF2 pro-MEP1-ADH3 ter
pMU3466	TEF2 pro-MEP2-ADH3 ter
pMU3468	TEF2 pro-GAP1-ADH3 ter
pMU3471	TPI pro-DUR3-FBA1 ter
pMU3472	TPI pro-MEP1-FBA1 ter
pMU3473	TPI pro-MEP2-FBA1 ter
pMU3475	TPI pro-GAP1-FBA1 ter
pMU3597	ADH1 pro- <i>N. crassa</i> GDH2-PDC1 ter
pMU3605	ADH1 pro-MEP3-PDC1 ter
pMU3606	TEF2 pro-MEP3-ADH3ter
pMU3607	TPI1 pro-MEP3-FBA1 ter

Table 3. Primers used to create MAs.

SEQ ID	Primer	Sequence 5' to 3'	Description
66	X14961	gcagttaccttttagcacccaac	5' GDH1 5' flank
67	X14966	gggtaggtgaagcagaatgaggag	3' GDH1 3' flank
68	X15464	GTCCATGTAAAAATGATTGCTCCAATGATTGAAA-GAGGTTTAGACATTGGCTCTTCATTG	ENOt+PDC1t
69	X15465	ctaagctcaatgaagagagccaatgtctaaacctcttccaatcattggag-caatcatttta	PDC1t+ENOt
70	X18846	gtccatgtaaaatgattgcitccaatgatgaaaaagcacgcag-cacgctgtattacgtat	FCY3'+PDC1t
71	X18847	AATTAAATACGTAAATACAGCGTGTGCGT-GCTTTTCAATCATTTGGAGCAATCATTTTA	PDC1t+FCY3'
72	X18858	agccagctaaagtattaaaaaatttcatagtactactattcccttc-gagttatatct	pTPI+FCY5'
73	X18859	GTTCTAGATATAATCTCGAAGGGAATAAG-TAGTAGCTATGAAATTTTAACTCTTTAA	FCY5'+pTPI
74	X18860	acatcatctttaactgaatttattctctagcagcacgcagcgcgtg-tattacgtat	FCY3'+FBA1t
75	X18861	AATTAAATACGTAAATACAGCGTGTGCGT-GCTGCTAGAGAAATAATTCAAGTTAAAAAG	FBA1t+FCY3'
76	X18869	AGATCCTGTGGTAGTGTGCTGTCTGAACAGAA	FCY3' for 2kb
77	X18955	ataaaattaaatacgtaaatacacagcgtgctgcgtcgcgattttt-tctaaaccgtgga	pADH1+FCY3' rev
78	X19513	acttggcggtccatgtaaaatgattgctccaatgattgaaaatgag-gaagaaatccaa	ADH3t+PDC1t
79	X19514	TGAAGGTCATTAGGATTTGGATTTCTTCCT-CATTTTCAATCATTTGGAGCAATCATTTTAC	PDC1t+ADH3t
80	X19551	agccagcttaaagagttaaatttcatagtagggcgccataac-caaggtatctatag	pTEF2+FCY5'
81	X19552	TGGCGGTCTATAGATAACCTTGTTATGCGGCCCTAGCTATGAAATTTTAACTCTTTAAG	FCY5'+pTEF2
82	X19721	aaagaaatgtcagagccagaatttcaacaagctaagctttctaact-gatctatccaaaa	pPGK+GDH15'
83	X19722	TTTTTCAGTTTTTGGTAGATCAGTTAGAAAGCT-TAGCTTGTGAAATTCTGGCTGGCAT	GDH15'+pPGK

(continued)

SEQ ID	Primer	Sequence 5' to 3'	Description
84	X19726	atccgaaatattccacggttttagaaaaaatcggtatgctatgtttgac- caagggtgatga	GDH13'+pADH1
85	X19727	TTAAAAATACATCACACCTTGGTCAAACATAGCATC- CGATTTTTTTCTAAACCGTGGAATATT	pADH1+GDH13'
86	X19948	aaagaaatgtcagagccagaatttcaacaagctgatgctatgttt- gaccaaggtgatga	GDH13'+GPH15' for deletion
87	X19949	TTAAAAATACATCACACTTGGTCAAACATAGCAT- CAGCTTGTTGAAATTCTGGCTGACAT	CDH15'+GDH13' for deletion
88	X19950	atccgaaatattccacggttttagaaaaaatcgagcacgcag- cacgcgtatttacgtat	FCY3'+pADH1
89	X19967	tgaaggctattaggatttggatttcttcctcataaattagtggtgcat- tatatatat	PMA1t+ADH3t
90	X19968	TTTTTAATATATATAATGCACACACACTAATT- TATGAGGAAGAAATCCAAATCCTAATGA	ADH3t+PMA1t
91	X19969	AATTAATAACGTAAATACAGCGTGTGCGT- GCTCCACGAAAGGCAACGCAAAATTTTTTT	pHXT7+FCY3'
92	X19970	ccctgaaaaaaaattgcgttccttccttgagcacgcacgcct- gtatttacgtat	FCY3'+pHXT7
93	X20022	aggtagacgctacagtcacaggtgtcacaaact	URE2 5' flank
94	X20023	GGACGAGGCAAGCTAAACAGATCTCTAGAC- CTATTGGGTGTACAACTTAATTTGCAGCTTA	URE2 5' flank
95	X20024	cgtttctttcttggactatcatgtatcctcaggctgttataaaaca- gaaagaaaag	URE2 3' flank
96	X20025	GAGTGGGATGCGCATATAGTGCATGAACCAT- AT	URE2 3' flank
97	X20026	ttgtttaagctgcaaatgaattgtacaccaaaggctgctt- taaaaacaagaagaaaag	URE2 3' + 5' for deletion
98	X20027	CTTCCTTCCTTCTTCTTGTGTTTTTAAAGCAGCCTT	URE2 5' + 3' for deletion
99	X20028	TGGTGTACAACTTAATTTGCAGCTTA	pAGTEF+URE2 5'
100	X20029	CTTCCTTCCTTCTTCTTGTGTTTTTAAAGCAGCCT- GAGACTACATGATAGTCCAAAGAAAAG	pHXT2rc+URE2 3'
101.	X20043	ATAAAATTAAATACGTAAATACAGCGTGCT- GCGCTGCTATGAGGAAGAAATCCAAATCCT	ADH3 t tails for FCY1 3' flank

(continued)

SEQ ID	Primer	Sequence 5' to 3'	Description
102	X20044	tgaaggtcattaggatttggatttctctcatagcacgcagcagctg-tatttacgta	FCY 3' flank tails for ADH3t
103	X20282	agccagctaaagagttaaaaaatttcatagctaccagaaaag-gcaacgcaaaaatttttt	pHXT7+FCY5'
104	X20283	CCCTGGAAAAAATTTTGGCGTTGCCTTTCT-GGTAGCTATGAAATTTTAACTCTTTAAG	FCY5'+pHXT7
105	X20284	ttttaatatataatgcacacacactaatttagcacgcagcagctg-tatttacgtat	FCY3'+PMA1t
106	X20285	AATTAATAACGTAAATACAGCGTGCTGCGT-GCTAAATTAGTGTGTGCGATTATATATAT	PMA1t+FCY3'
107	X20286	agccagctaaagagttaaaaaatttcatagctatgttgtagaat-tcaaaagactatgtga	pGPM1+FCY5'
108	X20287	ATGGCATCACATAGTCTTTTGAATTCTACCA-CATAGCTATGAAATTTTAACTCTTTAAG	FCY5'+pGPM1
109	X20288	ttttaattgcttttcaattactgttattaaaaagcacgcagcagctg-tatttacgtat	FCY3'+TPIIt
110	X20289	AATTAATAACGTAAATACAGCGTGCTGCGT-GCTTTTAAATACAGTAATTGAAAAAGCAATA	TPIIt+FCY3'
111	X20620	ggtgattggaatggttatggttcggaatcgc	AUA1 5' Flank
112	X20621	GGACGAGGCAAGCTAAACAGATCTCTAGAC-CTATATACTACATAGAAAGCAATTAAAGA	AUA15'+pAGTEF
113	X20622	cggttcttttggactatcatgtactctccacctaacaaccccg-caccaac	AUA13'+pHXT2re
114	X20623	GTCATATGGCCTCTTAACGTGTCCTTTGTGG	AUA1 3'Flank
115	X20630	ttttatctttaattgctttctatgtagtatataggctagagatcgtt-tagcttgcc	pAGTEF+AUA1 5'
116	X20631	TACTTGGTGTGGTGCGGGTTTGTTAGGT-GGAGGAGACTACATGATAGTCCAAAGAAAAAG	pHXT2re+AUA13'
117	X20632	ttttatctttaattgctttctatgtagtatactccacctaacaacccg-caccaacac	AUA13'+AUA15'
118	X20633	TACTTGGTGTGGTGCGGGTTTGTTAGGT-GGAGTATACTACATAGAAAGCAATTAAAGA	AUA15'+AUA13'
119	X21123	gcgacatgtgatgagattgcacctccacagaa	GDH2 5' Flank

(continued)

SEQ ID	Primer	Sequence 5' to 3'	Description
120	X21124	GGACGAGGCAAGCTAAACAGATCTCTAGAC-CTATCTTTATTCCTTTTATTGTTGTGAATT	GDH2 5' Flank+pAGTEF
121	X21125	ccgtctttctttggactatctctagctcgccttcaataaaattgtutg-tataaat	GDH2 3' Flank+pHXT2rc
122	X21126	GGCAGCTATCTCTACTATCCCGTTTAGTAC-TATCC	GDH2 3' Flank
123	X21127	atattaaattcacaacaataaaaaagaataaagataggctctaga-gatctgttagcttgcc	pAGTEF+GDH2 5'
124	X21128	GAACTAATTTATACAAACAAATTTTATTGAAGCGAGACTACATGATAGTCCAAAGAAAAAG	pHXT2rc+GDH2 3'
125	X21133	atattaaattcacaacaataaaaaagaataaagagct-tcaataaaattgtttgtataaa	CDH2 3'+GDH2 5' for deletion
126	X21135	gcattgattgtctatcagagcatatcaagtggt	GDH3 5' Flank
127	X21136	GGACGAOGCAAGCTAAACAGATCTCTAGAC-CTAOGGTCACGTGTGCFACCTCCCTATATA	GDH3 5' Flank+pAGTEF
128	X21137	ccgttcttttcggactatcagtagtctcccgtaagcgctstttcttttgt-tcg	GDH3 3' Flank+pHXT2rc
129	X21138	GGCTAGGACCCCGTAAGGAGGAGAAAGAAATAG-GCAAG	GDH3 3' Flank
130	X21139	tatatatataggggaagtatcaacagtcaccgtaggtctagagatct-gtttagcttgcc	pAGTEF+GDH3 5'
131	X21140	TAGTTACGAACAAAAAGAAAAATAGCGCTTACG-GGAGACTACATGATAGTCCAAAAAG	pHXT2rc+GDH3 3'
132	X21147	tatatatataggggaagttagcaacagtcacgcgcgcg-taagcgctatttcttttgitcg	GDH3 3'+GDH3 5'
133	X21148	TAGTTACGAACAAAAAGAAAAATAGCGCTTACG-GCGGTGACTGTTGCTACTTCCCTATATA	GDH3 5'+GDH3 3'
134	X21179	tgttttaagctgcaaaattagttgtacaccaaggcgccataac-caaggtatctataga	pTEF2+URE2 5'
135	X21180	TGGCGGCTCTATAGTATACCTTGTTATFFCFC-CCTTGGGTGTACAACTTAATTTGCAGCTTA	URE2 5'+pTEF2
136	X21181	CTTCCTTCCTTCCTTCCTGTTTTTAAAGCAGCCTCGATTCTTTCTAATTTTCTAAACCGTGGAATATTTTCTCTT-TCTTTCTTGTTTTTAAAGCAGCCTCGATTTTTT-TCTAAACCGTGGAATATT	pADH1rc+URE2 3'

(continued)

SEQ ID	Primer	Sequence 5' to 3'	Description
137	X21182	atccgaatatccacggttttagaaaaaatcagaggctgctt- taaaaacaaagaaaaaag	URE2 3'+pADH1rc
138	X21289	aagaaatgtcagagccagaatttcaacaagctaggtctagagatct- gttagcttgccct	pAGTEF+GDH1 5'
139	X21290	TAAATACATCACCTTGGTCAAAACATAGCATC- GAGACTACATGATAGTCCAAAGAAAAG	pHXT2rc+GDH1 3'
140	X21291	GGACGAGGCAAGCTAAACAGATCTCTAGAC- CTAGCTTGTGAAATTCTGGCTCTGACAT	GDH1 5'+pAGTEF
141	X21292	ccgttcttttctggactatcatgtagctcgaatgctatgtttgaccaag- gtgatgt	GDH1 3'+pHXT2rc
142	X21319	tgtttaagcgtcaaatgaagttgtacaccaacgaatttttctaaaccgt- ggaatatt	pADH1+URE2 5'
143	X21320	ATCCGAAATACCTTCCACGGTTTAGAAAAAAATC GTTGGTGACAACTTAATTTGCTT	URE2 5'+pADH1
144	X21321	tttcgttttggataggatagatcagttagaagccttaggcgtcgtt- taaaaacaagaagaag	URE2 3'+PGKprc
145	X21322	CTTCTTCTTTCTTTCTTTGTTTAAAGCAGCCTA AGCTTCTTAACCTGATCTATCCAAAAC	PGKprc+URE2 3'
146	X21507	GAACATAATTTATACAAAAACAATTTTATTGAAGCT CTTTATTCTTTTATTGTTGTGAATT	GDH25'+GDH23' for deletion
147	X21735	agccagctaaagagtaa aaatttcatagtacgatttttctaaac- cgtggaatatt	pADH1+FCY5'
148	X21736	ATCCGAAATATTCCACGGTTTAGAAAAAAATCG- TAGCTATGAAATTTTAACTCTTTAAG	FCY5'+pADH1
149	X21754	gccaaagtggaattctctactcaagcttgc aaagaaatgtcagagccagaatttcaacaagctcgattttt- tctaaaccgtggaatatt	FCY5'Flank
150	X23319	ATCCGAAATATTCCACGGTTTAGAAAAAAATC- GAGCTTGTGAAATTCTGGCTCTGACAT	pADH1+GDH15'
151	X23320	gtccatgtaa aatgattgctccaatgattgaaagatgctatgtttgac- caagggtgatga	GDHL15'+pADH1
152	X23321	TTAAAAATACATCACCTTGGTCAAAACATAG- CATCTTTCAATCATTTGGAGCAATCATTTTAC	GDH1 3'+PDC1t
153	X23322		PDC1t+GDH13'

SEQ ID	Primer	Sequence 5' to 3'	Description
154	X23408	TTTTCAGTTTTGGATAGATCAGTTTGAAAGCTT- TAGCTATGAAATTTTTAACTCTTTAAG	FCY5'+pPGK
155	X23409	agccagcttaagaggttaaaaaattcatagctaaagctttctaact- gatctatccaaaac	pPGK+FCY5'

Table 4. Strain genotypes. Strains shown in examples are highlighted grey.

	Strain	Description	Genotype	Associated MA Cassette(s)
5	M2390	Type Strain	WT	
	M3465	Glycerol Reduction Strain	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd2::MA0289$	MA0280, MA0289, MA0608
	M3467	Glycerol Reduction Strain	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290$	MA0280, MA0290, MA0608
	M3469	Glycerol Reduction Strain	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293$	MA0280, MA0608, MA0293
10	M3624	Strain	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286$	MA0286, MA0280, MA0290, MA0608
	M4076	GDH1 marked deletion	$h1::MA0631$	MA0286, MA0280, MA0290, MA0608, MA0631
	M4117	<i>S. cerevisiae</i> GDH2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0425$	MA0286, MA0280, MA0290, MA0608, MA0425
15	M4118	<i>S. cerevisiae</i> GLN1/GLT1 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0426$	MA0286, MA0280, MA0290, MA0608, MA0426
	M4312	URE2 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta ure2::MA0622$	MA0286, MA0280, MA0290, MA0608, MA0622
	M4373	GDH1 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd2::MA0289\Delta gdh1::MA0631$	MA0280, MA0289, MA0608, MA0631
	M4375	GDH1 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gdh1::MA0631$	MA0280, MA0290, MA0608, MA0631
20	M4377	GDH1 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta gdh1::MA0631$	MA0280, MA0608, MA0293, MA0631
	M4400	GDH1 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd2::MA0289\Delta gdh1::MA0888$	MA0280, MA0289, MA0608, MA0888
	M4401	GDH1 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gdh1::MA0888$	MA0280, MA0290, MA0608, MA0888
	M4402	GDH1 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta gdh1::MA0888$	MA0280, MA0608, MA0293, MA0888
	M4406	URE2 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta ure2::MA0622.1$	MA0286, MA0280, MA0290, MA0608, MA0622.1
25	M4427	DUR1,2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta fcy1::MA0464.1$	MA0280, MA0290, MA0608, MA0464.1
	M4428	DUR1,2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta fcy1::MA0465.1$	MA0280, MA0290, MA0608, MA0465.1
30	M4429	DUR1,2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta fcy1::MA0467.1$	MA0280, MA0290, MA0608, MA0467.1
	M4430	DUR1,2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta fcy1::MA0454.14$	MA0280, MA0290, MA0608, MA0454.14
	M4431	DUR1,2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta fcy1::MA0464.1$	MA0280, MA0293, MA0608, MA0464.1
	M4432	DUR1,2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta fcy1::MA0465.1$	MA0280, MA0293, MA0608, MA0465.1
35	M4433	DUR1,2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta fcy1::MA0467.1$	MA0280, MA0290, MA0608, MA0467.1
	M4434	DUR1,2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta fcy1::MA0454.14$	MA0280, MA0290, MA0608, MA0454.14
40	M4469	<i>S. cerevisiae</i> GDH2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd2::MA0289\Delta gdh1::MA0425$	MA0280, MA0289, MA0608, MA0425
	M4471	<i>S. cerevisiae</i> GDH2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta gdh1::MA0425$	MA0280, MA0608, MA0293, MA0425
	M4507	AUA1 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta au\alpha 1::MA0617$	MA0286, MA0280, MA0290, MA0608, MA0617
	M4538	GDH1 marked deletion	$\Delta gdh1::MA0631$	MA0631
45	M4540	AUA1 marked deletion	$\Delta au\alpha 1::MA0617$	MA0617
	M4542	URE2 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta ure2::MA0622$	MA0280, MA0608, MA0293, MA0622
	M4571	AUA1 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta au\alpha 1::MA0617.1$	MA0286, MA0280, MA0290, MA0608, MA0617.1
	M4573	GDH1 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0888$	MA0286, MA0280, MA0290, MA0608, MA0888
	M4590	GDH1 clean deletion	$\Delta gdh1::MA0888$	MA0888
50	M4591	AUA1 clean deletion	$\Delta au\alpha 1::MA0617.1$	MA0617.1
	M4592	URE2 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta ure2::MA0622.1$	MA0280, MA0608, MA0293, MA0622.1
55	M4614	URE2 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0425\Delta ure2::MA0622$	MA0286, MA0280, MA0290, MA0608, MA0425, MA0622
	M4615	URE2 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0426\Delta ure2::MA0622$	MA0286, MA0280, MA0290, MA0608, MA0426, MA0622
	M4616	URE2 marked deletion	$\Delta ure2::MA0622$	MA0622

5	M4622	<i>S. cerevisiae</i> GDH2 over expression	$\Delta gdh1::MA0425$	MA0425
	M4623	<i>S. cerevisiae</i> GLN1/GLT1 over expression	$\Delta gdh1::MA0426$	MA0426
	M4624	<i>S. cerevisiae</i> GLN1/GLT1 over expression	$\Delta gdh1::MA0426$	MA0426
10	M4625	<i>S. cerevisiae</i> GLN1/GLT1 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd2::MA0289\Delta gdh1::MA0426$	MA0280, MA0289, MA0608, MA0426
	M4625	<i>S. cerevisiae</i> GLN1/GLT1 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta gdh1::MA0426$	MA0280, MA0608, MA0293, MA0426
15	M4626	<i>S. cerevisiae</i> GLN1/GLT1 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0293\Delta gdh1::MA0426$	MA0280, MA0608, MA0293, MA0426
	M4654	GDH3 marked deletion	$\Delta gdh3::MA0615$	MA0615
	M4655	GDH2 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0426\Delta gdh2::MA0616$	MA0286, MA0280, MA0290, MA0608, MA0426, MA0616
20	M4656	GDH3 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0426\Delta gdh3::MA0615$	MA0286, MA0280, MA0290, MA0608, MA0426, MA0615
	M4657	GDH3 marked deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0425\Delta gdh3::MA0615$	MA0286, MA0280, MA0290, MA0608, MA0425, MA0615
	M4674	URE2 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0425\Delta ure2::MA0622.1$	MA0286, MA0280, MA0290, MA0608, MA0425, MA0622.1
25	M4675	URE2 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0426\Delta ure2::MA0622.1$	MA0286, MA0280, MA0290, MA0608, MA0426, MA0622.1
	M4676	URE2 clean deletion	$\Delta ure2::MA0622.1$	MA0622.1
	M4677	GDH2 marked deletion	$\Delta gdh2::MA0616$	MA0616
30	M4690	GDH3 clean deletion	$\Delta gdh3::MA0615.1$	MA0615.1
	M4691	GDH2 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0426\Delta gdh2::MA0616.1$	MA0286, MA0280, MA0290, MA0608, MA0426, MA0616.1
	M4692	GDH3 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0426\Delta gdh3::MA0615.1$	MA0286, MA0280, MA0290, MA0608, MA0426, MA0615.1
35	M4693	GDH3 clean deletion	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0425\Delta gdh3::MA0615.1$	MA0286, MA0280, MA0290, MA0608, MA0425, MA0615.1
	M4694	GDH2 clean deletion	$\Delta gdh2::MA0616.1$	MA0616.1
	M4748	DUR3 over expression	$\Delta fcy1::MA0464$	MA0464
40	M4749	GAP1 over expression	$\Delta fcy1::MA0464.4$	MA0464.4
	M4750	MEP1 over expression	$\Delta fcy1::MA0464.2$	MA0464.2
	M4751	DUR1,2 over expression	$\Delta fcy1::MA0465.1$	MA0465.1
45	M4752	MEP1 over expression	$\Delta fcy1::MA0434.2$	MA0434.2
	M4753	MEP2 over expression	$\Delta fcy1::MA0434.3$	MA0434.3
	M4754	DUR3 over expression	$\Delta fcy1::MA0434$	MA0434
50	M4755	GAP1 over expression	$\Delta fcy1::MA0434.4$	MA0434.4
	M4756	MEP2 over expression	$\Delta fcy1::MA0464.2$	MA0464.2
	M4810	DUR3 over expression	$\Delta fcy1::MA0467$	MA0467
55	M4811	DUR3 over expression	$\Delta fcy1::MA0467$	MA0467
	M4812	MEP1 over expression	$\Delta fcy1::MA0467.2$	MA0467.2
	M4813	MEP1 over expression	$\Delta fcy1::MA0467.2$	MA0467.2
55	M4814	GAP1 over expression	$\Delta fcy1::MA0467.4$	MA0467.4
	M4815	GAP1 over expression	$\Delta fcy1::MA0467.4$	MA0467.4
	M5841	<i>N. crassa</i> GDH2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0837$	MA0280, MA0608, MA0286, MA0290, MA0837
55	M5842	<i>N. crassa</i> GDH2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0837$	MA0280, MA0608, MA0286, MA0290, MA0837
	M5843	<i>N. crassa</i> GDH2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0837$	MA0280, MA0608, MA0286, MA0290, MA0837
	M5844	<i>N. crassa</i> GDH2 over expression	$\Delta fdh1::MA0608\Delta fdh2::MA0280\Delta gpd1::MA0290\Delta gpd2::MA0286\Delta gdh1::MA0837$	MA0280, MA0608, MA0286, MA0290, MA0837

Example 1:

Deletion of GDH1 and overexpression of GDH2 or GLT1/GLN1

5 **[0086]** M3624 ($\Delta gpd1::GPD2$ -*B.adolescentis*pflA/pfIB/adhE $\Delta gpd2::GPD1$ -*B.adolescentis*pflA/pfIB/adhE $\Delta fdh1\Delta fdh2::B.adolescentispflA/pfIB/adhE) has an approximately 85% reduction in glycerol formation when grown on > 30% solids corn mash. However, the strain is unable to complete the fermentation even after extended incubation periods. Two modifications of the ammonium assimilation pathway were constructed in M3624 and evaluated for fermentation performance. The modifications were a deletion of *GDH1* and over-expression of *Gdh2*, resulting in strain M4117 (M3634 *Gdh2*; $\Delta gdh1$). The second modification was a deletion of *GDH1* and overexpression of *GLT1* and *GLN1*, resulting in strain M4118 (M3634 *Glt1*; *Gln1*; $\Delta gdh1$). These strains were compared to M3624 and the conventional yeast control (M2390 (a wild type unmodified strain isolated from industrial sources)) following fermentation of 31% solids corn mash.$

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15 **[0087]** An industrial corn mash was prepared to a final solids concentration of 31% supplemented with penicillin (0.006mg/mL) and urea (0.5 g/l). Glucoamylase was added at a concentration of 0.6 AGU/gTS. Fermentation was stopped by addition of each strain to an final starting concentration of 0.1 g/l. Vials were capped with a rubber stopper and sealed. A 23-gauge needle was inserted through the stopper to vent and for the safety of the experiment. Vials were incubated at 35°C with shaking at 125rpm. At the termination of the experiment samples were prepared for HPLC analysis of ethanol and residual sugars.

20 **[0088]** The results in Figure 69 illustrate that both M4117 and M4118 reach a much higher final ethanol titer than M3624, which was unable to complete the fermentation. Relative to M2390 both M4117 and M4118 had ethanol titers that were 4.2% and 5.2% higher respectively.

Example 2:

25

Deletion of *GDH1*

[0089] As shown in Figure 5, M3465 ($\Delta gpd2::B.adolescentis$ pflA/pfIB/adhE $\Delta fdh1\Delta fdh2::B.adolescentis$ pflA/pfIB/adhE), M3467 ($\Delta fdh1\Delta fdh2::PFK$ -pro-adhE-HXT-ter *ENO1*-pro-pfIB-*ENO1*-ter *ADH1*-pro-adhE-PDC10-ter *TPI*-pro-pfIA-FBA-ter $\Delta gpd1::GPD2::PFK$ -pro-adhE-HXT-ter *ENO1*-pro-pfIB-*ENO1*-ter *ADH1*-pro-adhE-PDC10-ter *TPI*-pro-pfIA-FBA-ter) and M3469 ($\Delta gpd1::B.adolescentis$ pflA/pfIB/adhE $\Delta fdh1\Delta fdh2::B.adolescentis$ pflA/pfIB/adhE) have degrees of glycerol reduction ranging from 20% to -45% relative to the control strain M2390. A clean deletion of *GDH1* was constructed in each of these backgrounds resulting in M4400 (M3465 $\Delta gdh1$). M4401 (M3467 $\Delta gdh1$) and M4402 (M3469 $\Delta gdh1$) and compared to the conventional yeast control (M2390) following fermentation of 31% solids corn mash (The fermentation was performed as described in Example 1). As shown in Figure 70, all three glycerol reduction strains engineered with a deletion of *GDH1* reached a higher ethanol titer than their respective parent strain.

Example 3:

40 Overexpression of *DUR1/2*

[0090] Four different *DUR1/2* expression cassettes were constructed in both M3467 $\Delta fdh1\Delta fdh2::PFK$ -pro-adhE-HXT-ter *ENO1*-pro-pfIB-*ENO1*-ter *ADH1*-pro-adhE-PDC10-ter *TPI*-pro-pfIA-FBA-ter $\Delta fdh1::GPD2::PFK$ -pro-adhE-HXT-ter *ENO1*-pro-pfIB-*ENO1*-ter *ADH1*-pro-adhE-PDC10-ter *TPI*-pro-pfIA-FBA-ter) and M3469 ($\Delta gpd1::B.adolescentis$ pflA/pfIB/adhE $\Delta fdh1\Delta fdh2::B.adolescentis$ pflA/pfIB/adhE) resulting in strains M4427-M3343 (Table 5). These strains were compared to their parent strain and the conventional yeast control (M2390) following fermentation of 31% solids corn mash (The fermentation was performed as described in Example 1). As shown in Figure 71, all strains containing an overexpression of *DUR1/2* reached the same or higher ethanol titers than their respective parent strain but the *TEF2* and *ADH1* promoter appeared particularly affective. Promoters and terminators used and that could be used include:

50 *S. cerevisiae* *TEF2* promoter: SEQ ID NO: 58, *S. cerevisiae* *HXT7* promoter: SEQ ID NO: 59, *S. cerevisiae*, *S. cerevisiae* *ADH1* promoter: SEQ ID NO: 60, *S. cerevisiae* *TP1* promoter: SEQ ID NO: 61, *S. cerevisiae* *FBA1* terminator: SEQ ID NO: 62, *S. cerevisiae* *PDC1* terminator: SEQ ID NO: 63, *S. cerevisiae* *PMA1* terminator: SEQ IS NO: 64, and *S. cerevisiae* *ADH3* terminator: SEQ ID NO: 65.

55 **Table 5.** Description of constructions and strain designations containing over-expression of *DUR1/2*

Parent strain	Strain designation	Genetic modification
M3467	M4427	MA0464. 1 : expression of <i>DUR1,2</i> from the <i>TEF2</i> promoter

(continued)

Parent strain	Strain designation	Genetic modification
M3467	M4428	MA0465.1 : expression of DUR1,2 from the HXT7 promoter
M3467	M4429	MA467.1 : expression of DUR1,2 from the ADH1 promoter
M3467	M4430	MA454.14 : expression of DUR1,2 from the HXT7/TEF2 promoters
M3469	M4431	MA0464.1 : expression of DUR1,2 from the TEF2 promoter
M3469	M4432	MA0465.1 : expression of DUR1,2 from the HXT7 promoter
M3469	M4433	MA467.1 : expression of DUR1,2 from the ADH1 promoter
M3469	M4434	MA454.14 : expression of DUR1,2 from the HXT7/TEF2 promoters

Example 4

Deletion of URE2

[0091] To evaluate an alteration in the *S. cerevisiae* nitrogen catabolite repression system in glycerol reduction back-grounds, a deletion of *URE2* was constructed in M3624 (Example 1), creating strain M4406 (M3624 Δ ure2). This strain was compared to M3624 and the conventional yeast control (M2390) following fermentation of 31% solids corn mash (The fermentation was performed as described in Example 1). As shown in Figure 72, M4406 reached a higher titer than M3624 however a yield increase over the conventional strain was not observed and there was ~15 g/l residual glucose. This is an indication that additional modifications to the NCR system may give improved performance or that an adaptation of M4406 may be required to obtain the potential yield increase.

Example 5

Regulation of nitrogen utilization

[0092] Preferred nitrogen sources generally repress transcription of genes required to utilize non-preferred nitrogen sources. Urea is added as a supplemental nitrogen source in corn mash fermentation; however, there are significant quantities of amino acids and ammonia, both of which are preferred nitrogen sources over urea. Expression of the urea transporter (Dur3) and the urea:amido lyase responsible for intracellular degradation (Dur1/2) may be repressed in the presence amino acids and ammonia as part of a phenomenon referred to as Nitrogen Catabolite Repression (NCR). This repression could slow the rate of urea uptake or require larger quantities to be added. It would be an economic benefit to a corn ethanol producer if constitutive expression of Dur3 and Dur1,2 allowed them to either reduce the amount of urea needed or accelerate fermentation rate.

[0093] The NCR is controlled by Ure2 and four transcription factors known as Gln3, Gat1, Dal80, and Gzf3. Ure2 participates in repressing gene expression in the presence of non-preferred nitrogen source. It has been observed that deletion of *URE2* activates the expression of genes involved in the uptake of non-preferred nitrogen sources. Inactivation of Ure2 results in dephosphorylation and nuclear localization of the transcription factor Gln3.

Example 5A

Deletion of URE2 deletion of URE2 results in nuclear localization of GLN3 and activation of NCR sensitive genes.

[0094] To evaluate an alteration in the *S. cerevisiae* nitrogen catabolite repression system in glycerol reduction back-grounds, a deletion of Ure2 is constructed as in Example 4. A deletion of *URE2* will be constructed in M3624 (Example 1). Strains in which *URE2* is deleted show a nuclear localization of Gln3, and an activation of NCR sensitive genes, including Dur3 and Dur1/2.

Example 5B

Overexpression GLN3 results in activation of NCR sensitive genes.

[0095] To evaluate an alteration in the *S. cerevisiae* nitrogen catabolite repression system in glycerol redaction back-grounds, Gln3 (SEQ ID NOs: 156 and 157) is overexpressed. Strains in which Gln3 is overexpressed show an activation of NCR sensitive genes, including Dur3 and Dur1/2.

Example 6

Deletion of GDH1 and expression of *S. cerevisiae* GDH2

[0096] The results show that strain M3624 (Example 1) was able to reach a slightly higher titer than strain M2390 (WT), producing 1.5 g/l more ethanol (Figure 73). To create strain M4117 (M3634 Gdh2; Δ gdh1), the *GDH1* gene was deleted and replaced with 4 copies of the *S. cerevisiae* GDH2 gene expression cassette. The results in figure 73 below demonstrate that when compared to M3624, M4117 had a clear improvement of 3.7 g/l more ethanol. The data shown in Figure 74 shows that M3624 makes 1.3 g/l glycerol which is 87% less than the wild type strain M2390, which made 10 g/l. The deletion of GDH1 and addition of the *S. cerevisiae* GDH2 expression cassette decreased the glycerol titers to around 1 g/l. These results illustrate that the combination of glycerol reduction through formate production is synergistic with modifications to the ammonium assimilation pathway.

Example 7

Deletion of GDH1 and expression of *N. crassa* GDH2

[0097] To create strains M5841-M5844, the GDH1 gene was deleted and replaced with 4 copies of the *N. crassa* GDH2 gene expression cassette in Figure 10. Each strain resulted from independent colonies and have the same genotype (Table 6). The results shown in Figure 73 demonstrate that the addition of the *N. crassa* GDH2 to M3624 resulted in titers that were between 3.6g/l and 4.3 g/l higher than M3624. The data shown in Figure 74 shows that M3624 makes 1.3 g/l glycerol which is 87% less than the wild type strain M2390, which made 10 g/l. The deletion of GDH1 and addition of the *N. crassa* GDH2 expression cassette decreased the glycerol titers to around 1 g/l. These results support the conclusion that a combination of glycerol reduction through formate production is synergistic with modifications to the ammonium assimilation pathway, even when using a heterologous expression of GDH2.

Table 6. Glycerol deletion strains which further comprise a deletion of gdh1 and an expression of Gdh2.

Strain	Genotype
M2390	WT
M3624	Δ fdh1 Δ fdh2::4a2p Δ gpd1::gpd24a2p Δ gpd2::gpd14a2p
M4117	Δ fdh1 Δ fdh2::4a2p Δ gpd1::gpd24a2p Δ gpd2::gpd14a2p Δ Scgdh1::4gdh2
M5841	Δ fdh1 Δ fdh2::4a2p Δ gpd1::gpd24a2p Δ gpd2::gpd14a2p Δ Ncrassagdh1::4gdh2
M5842	Δ fdh1 Δ fdh2::4a2p Δ gpd1::gpd24a2p Δ gpd2::gpd14a2p Δ Ncrassagdh1::4gdh2
MS843	Δ fdh1 Δ fdh2::4a2p Δ gpd1::gpd24a2p Δ gpd2::gpd14a2p Δ Ncrassagdh1::4gdh2
M5844	Δ fdh1 Δ fdh2::4a2p Δ gpd1::gpd24a2p Δ gpd2::gpd14a2p Δ Ncrassagdh1::4gdh2

[0098] The strains in Table 6 were inoculated in vials containing 4ml industrial com mash (mini-vials). The fermentation was allowed to proceed for 68hrs and samples were run on an HPLC to obtain ethanol and glycerol values.

SEQUENCE LISTING

[0099]

<110> MASCOMA CORPORATION
ARGYROS, AARON
BARRETT, TRISHA

5 <120> METHODS FOR REGULATING NITROGEN METABOLISM DURING THE PRODUCTION OF ETHANOL
FROM CORN BY METABOLICALLY ENGINEERED YEAST STRAINS

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 <151> 2013-03-15

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35	Ser	Glu	Ala	Gly	Val	Tyr	Ala	Glu	Phe	Met	Ile	Thr	Leu	Thr	Lys	Val	
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	385					390					395					400
10	Glu	Asn	Asn	Glu	Ile	Ser	Leu	Ala	Ala	Thr	Arg	Phe	Asn	Ser	Thr	Gly
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15	Thr	Arg	Val	Glu	Glu	Ile	Gly	Lys	Gly	Glu	Gly	Gly	Val	Pro	Gly	Ala
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20	Thr	Lys	Val	Glu	Asn	Pro	Thr	Lys	Ala	Thr	Glu	Gly	Leu	Asp	Gly	Pro
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<212> DNA
<213> Magnaporthe oryzae

<400> 50

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	ccaccgcaga agctacgtct tcaccttgac accggcagca gtgacctgtg ggtcaacacg	300
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	ggctcaggcg ccaatggcga ctatgtctcc gatatgggtca cgggtgggcaa caccaagatc	480
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20	ccctcgcgca tggtcgagga gggcctgatc gcttccaacg cctacagcct ttacctcaat	660
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	ggaacgctgc agaccgtccc gatccagccc aacggtggcc gcatggccga gtttctcatc	780
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30	tacagcgccg tgggcgccca gtacgacagc aacgagggcg ccgcatacgt cccctgctcc	960
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	cccatgaacg agctcgtctt ggacctggta acttccaacg gccgccggcc ctcgttccgc	1080
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40	ctcgctcaga ccagcttcaa cgctaccaag agcaacgtca aggagatcgg caagggcagc	1260
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- <211> 474
- <212> PRT
- 50<213> Magnaporthe oryzae
- <400> 51

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				20					25					30		
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		50					55					60				
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55

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10	Ile Leu Gly Val Gly Tyr Glu Ala Asn Glu Val Gln Val Gly Arg Ala	
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15	Gln Leu Lys Pro Tyr Arg Asn Leu Pro Ser Arg Met Val Glu Glu Gly	
		195 200 205
20	Leu Ile Ala Ser Asn Ala Tyr Ser Leu Tyr Leu Asn Asp Leu Gln Ser	
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25	Asn Lys Gly Ser Ile Leu Phe Gly Gly Ile Asp Thr Glu Gln Tyr Thr	
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30	Gly Thr Leu Gln Thr Val Pro Ile Gln Pro Asn Gly Gly Arg Met Ala	
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35	Glu Phe Leu Ile Thr Leu Thr Ser Val Ser Leu Thr Ser Ala Ser Ile	
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40	Gly Gly Asp Lys Leu Ala Leu Ala Val Leu Leu Asp Ser Gly Ser Ser	
		275 280 285
45	Leu Thr Tyr Leu Pro Asp Asp Ile Val Lys Asn Met Tyr Ser Ala Val	
		290 295 300
50	Gly Ala Gln Tyr Asp Ser Asn Glu Gly Ala Ala Tyr Val Pro Cys Ser	
		305 310 315 320
55	Leu Ala Arg Asp Gln Ala Asn Ser Leu Thr Phe Ser Phe Ser Gly Ile	
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60	Pro Ile Val Val Pro Met Asn Glu Leu Val Leu Asp Leu Val Thr Ser	
		340 345 350
65	Asn Gly Arg Arg Pro Ser Phe Arg Asn Gly Val Pro Ala Cys Leu Phe	
		355 360 365
70	Gly Val Ala Pro Ala Gly Lys Gly Thr Asn Val Leu Gly Asp Thr Phe	
		370 375 380
75	Leu Arg Ser Ala Tyr Val Val Tyr Asp Leu Glu Asn Asn Ala Ile Ser	
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5	Gly	Lys	Gly	Ser	Asn	Pro	Val	Pro	Gly	Ala	Val	Ala	Val	Ser	Gln	Pro	
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10	Val	Ala	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Asn	Gly	Gly	Asn	Arg	Ser	Gly	
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<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 53

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50	Gly 50	Ser	Lys	Trp	Gln	Asp	Phe 55	Lys	Asp	Ser	Phe	Lys 60	Arg	Val	Lys	Pro
55	Ile 65	Glu	Val	Asp	Pro	Asn 70	Leu	Ser	Glu	Ala	Glu 75	Lys	Val	Ala	Ile 80	Ile
	Thr	Ala	Gln	Thr	Pro 85	Leu	Lys	His	His	Leu 90	Lys	Asn	Arg	His	Leu 95	Gln
	Met	Ile	Ala	Ile 100	Gly	Gly	Ala	Ile	Gly 105	Thr	Gly	Leu	Leu	Val 110	Gly	Ser

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15	Leu	Gln	Trp	Leu	Val	Val	Leu	Pro	Leu	Glu	Ile	Val	Ser	Ala	Ser	Ile	
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<211> 1062

<212> DNA
<213> Saccharomyces cerevisiae

<400> 54

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10	acaggtgtaa ataataataa taataacaat agcagtagta ataacaataa tgttcaaaac	180
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	ttagaacaac atcgacaaca acaacaggca ttttcggata tgagtcacgt ggagtattcc	300
15	agaattacaa aatttttttca agaacaacca ctggagggat ataccctttt ctctcacagg	360
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<212> PRT
<213> Saccharomyces cerevisiae

<400> 55

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REFERENCES CITED IN THE DESCRIPTION

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Patent documents cited in the description

- US 701882 A [0010]
- US 7935514 B [0010]
- US 20110129566 A [0013]
- US 2012032443 W [0018]
- WO 2011140386 A [0020]
- EP 2277989 A [0021]
- US 20110171709 [0072]
- US 61728450 B [0085]
- US 61800323 B [0099]

Non-patent literature cited in the description

- HAHN-HÄGERDAL, B. et al. *Adv. Biochem. Eng. Biotechnol.*, 2001, vol. 73, 53-84 [0007]
- NISSEN, T.L. et al. *Metabolic Engineering*, 2000, vol. 2, 69-77 [0010]
- BRO, C. et al. *Metabolic Engineering*, 2006, vol. 8, 102-111 [0010]
- LUNGDHAL et al. *Genetics*, 2012, vol. 190, 885-929 [0012]
- SALMON, J. M. ; BARRE, P. *Appl. Environ. Microbiol.*, 1998, vol. 64, 3831-3837 [0012]
- COULON, J. et al. *Am. J. Enol. Vitic.*, 2006, vol. 57, 2 [0013]
- DABABIEH, M.S. et al. *Am. J. Enol. Vitic.*, 2009, vol. 60, 4 [0013]
- GUO, Z-P et al. *Enzyme and Microbial Technology*, 2011, vol. 48, 148-154 [0015]
- SAMBROOK, J. ; FRITSCH, E. F. ; MANIATIS, T. MOLECULAR CLONING: A LABORATORY MANUAL. Cold Spring Harbor Laboratory Press, 1989 [0046]
- Computational Molecular Biology. Oxford University Press, 1998 [0046]
- Biocomputing: Informatics and Genome Projects. Academic Press, 1993 [0046]
- Computer Analysis of Sequence Data. Humana Press, 1994 [0046]
- Sequence Analysis in Molecular Biology. Academic Press, 1987 [0046]
- Sequence Analysis Primer. Stockton Press, 1991 [0046]
- HIGGINS ; SHARP. *CABIOS*, 1989, vol. 5, 151-153 [0046]
- Computational Molecular Biology. Oxford University Press, 1988 [0046]
- Biocomputing: Informatics and Genome Projects. Academic Press, 1993 [0046]
- WELCH et al. Designing genes for successful protein expression. *Methods Enzymol.*, 2011, vol. 498, 43-66 [0048]
- SHARP et al. The Codon Adaptation Index; a Measure of Directional Synonymous Codon Usage Bias, and Its Potential Applications. *Nucleic Acids Research*, 1987, vol. 15, 1281-1295 [0049]

Patentkrav**1.** Rekombinant gær omfattende:

- 5 a. mindst en modificeret genetisk modifikation, som fører til opreguleringen af et eller flere heterologe enzymer, som fungerer i en eller flere ethanolproduktionsveje;
- b. mindst en modificeret genetisk modifikation, som fører til nedreguleringen af et enzym i en glycerolproduktionsvej; og,
- 10 c. mindst en modificeret genetisk modifikation, som fører til opreguleringen eller nedreguleringen af et enzym i en nitrogen-assimileringsvej, hvor det opregulerede enzym, som virker i en ethanolproduktionsvej, er pyruvat-format-lyase (EC 2.3.1.54), pyruvat-format-lyase-aktiverende enzym (EC 1.91.1.4), og/eller bifunktionel acetaldehyd-alkoholdehydrogenase valgt fra en gruppe af enzymer, som har begge af de følgende enzymkommissionsnumre: EC
- 15 1.2.1.10 og 1.1.1.1;
- hvor det nedregulerede enzym, der virker i glycerolproduktionsvejen, er mindst et enzym valgt fra gruppen bestående af: et glycerol-3-phosphatdehydrogenase-1-polynukleotid (GPD1) (EC 1.1.1.8), et glycerol-3-phosphatdehydrogenase-1-polypeptid (Gpd1) (EC 1.1.1.8), et glycerol-3-phosphatdehydrogenase-2-
- 20 polynukleotid (GPD2) (EC 1.1.1.8), et glycerol-3-phosphatdehydrogenase-2-polypeptid (Gpd2) (EC 1.1.1.8), et glycerol-3-phosphatphosphatase-I-polynukleotid (GPP1) (EC 3.1.3.21), et glycerol-3-phosphatphosphatase-polypeptid-I (Gpp1) (EC 3.1.3.21), et glycerol-3-phosphatphosphatase-2-polynukleotid (GPP2) (EC 3.1.3.21), og et glycerol-3-phosphatphosphatase-
- 25 polypeptid-2 (Gpp2) (EC 3.1.3.21); og
- hvor det nedregulerede enzym, som virker i nitrogen-assimileringsvejen, er glutamatdehydrogenase (Gdh) (EC 1.4.1.4) og hvor det opregulerede enzym i nitrogen-assimileringsvejen er mindst et enzym valgt fra gruppen bestående af glutamatdehydrogenase (Gdh) (EC 1.4.1.2), glutamatsyntase (Glt) (EC 1.4.1.14),
- 30 og glutaminsyntase (Gln) (EC 6.3.1.2), en ammonium-transporter, en urinstofamido-lyase (EC 6.3.4.6) og en urinstoftransporter.

- 2.** Rekombinant gær ifølge krav 1, hvor det opregulerede enzym i nitrogen-assimileringsvejen er en Gdh2 isoleret fra en organisme fra en art valgt fra
- 35 gruppen bestående af *Saccharomyces* og *Neurospora* (Gdh2); en Glt1 isoleret fra

en organisme fra arten *Saccharomyces* (GltI); en GIn1 isoleret fra en organisme fra arten *Saccharomyces* (GIn1'); et MEP-protein valgt fra gruppen bestående af; Mep1, Mep2, og Mep3 og isoleret fra en organisme fra en art valgt fra arten *Saccharomyces*; en urinstofamido-lyase isoleret fra en organisme fra

5 *Saccharomyces*; en Dur3 eller en Dur4 isoleret fra en organisme fra arten *Saccharomyces*; eller en G1n 3 isoleret fra arten *Saccharomyces*.

3. Rekombinant gær ifølge krav 1, hvor det nedregulerede enzym i nitrogen-assimileringsvejen er en polypeptidsekvens, der er mindst omkring 80%, 90%,

10 95 eller 100% identisk med en polypeptidsekvens valgt fra gruppen bestående af: SEQ ID NOs: 25 og 31 (*S. cerevisiae* Gdh1 og Gdh3).

4. Rekombinant gær ifølge et hvilket som helst af kravene 1-2, hvor det opregulerede enzym i nitrogen-assimileringsvejen er en polypeptidsekvens, der

15 er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens valgt fra gruppen bestående af: SEQ ID NOs: 27 og 29 (Gdh2); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens SEQ ID NO: 33 (GltI); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en

20 polypeptidsekvens SEQ ID NO: 35 (GInI); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens SEQ ID NO: 19 (Mep1); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens SEQ ID NO: 21 (Mep2); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk

25 med en polypeptidsekvens SEQ ID NO: 23 (Mep3); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens SEQ ID NO: 37 (Dur1/2).; en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens: SEQ ID NO: 39 (Dur3); eller en polypeptidsekvens mindst omkring 80%, 90%, 95% eller 100%

30 identisk med en polypeptidsekvens SEQ ID NO: 156 (GIn3).

5. Rekombinant gær ifølge krav 1, hvor enzymet i glycerolproduktionsvejen er en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med polypeptidsekvensen: SEQ ID NO: 5 (Gpd1); en polypeptidsekvens, der er

35 mindst omkring 80%, 90%, 95% eller 100% identisk med polypeptidsekvensen:

SEQ ID NO: 7 (Gpd2); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med polypeptidsekvensen: SEQ ID NO: 159 (Gpp1); eller en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med polypeptidsekvensen: SEQ ID NO: 161 (Gpp2).

5

6. Rekombinant gær ifølge et hvilket som helst af kravene 1-5, hvor det opregulerede enzym, som virker i en ethanolproduktionsvej, er en NADPH-afhængig bifunktionel acetaldehyd-alkoholdehydrogenase valgt fra en gruppe af enzymer, som har begge af de følgende enzymkommissionsnumre; EC 1.2.1.10
10 og 1.1.1.2 fortrinsvist isoleret fra en art valgt fra gruppen bestående af *Leuconostoc* og *Oenococcus*.

7. Rekombinant gær ifølge et hvilket som helst af kravene 1-6, hvor enzymet, som virker i ethanolproduktionsvejen, er en polypeptidsekvens, der er mindst
15 omkring 80%, 90%, 95% eller 100% identisk med polypeptidsekvensen SEQ ID NO: 9 (*B. adolescentis* Pfl); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med polypeptidsekvensen SEQ ID NO: 11. (*B. adolescentis* Pfl-aktiverende enzym); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med polypeptidsekvensen SEQ ID
20 NO: 13 (*B. adolescentis* AdhE); eller en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens valgt fra gruppen bestående af SEQ ID NOs: 15 og 17.

8. Rekombinant gær ifølge et hvilket som helst af kravene 1-7, hvor gæren
25 yderligere omfatter en nedregulering i et eller flere native formiat-dehydrogenase-enzymmer valgt fra gruppen bestående af: EC 1.2.1.43 og EC 1.2.1.2 og/eller et heterologt GPD1-polynukleotid, der er virksomt forbundet til en nativ GPD2-promoter og/eller et heterologt GPD2-polynukleotid, der er virksomt forbundet til en nativ GPD1-promoter og/eller en opregulering eller nedregulering af et
30 regulatorisk element.

9. Rekombinant gær ifølge krav 8, hvor det nedregulerede enzym er en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens SEQ ID NO: 2 (Fdh1); eller en polypeptidsekvens, der
35 er mindst 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens kodet

af polynukleotidsekvensen ifølge SEQ ID NO: 3 (Fdh2).

10. Rekombinant gær ifølge krav 8, hvor det regulatoriske element er valgt fra gruppen bestående af Ure2 og Aual, mere fortrinsvist er det regulatoriske element en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens ifølge SEQ ID NO: 55 (Ure2), mere fortrinsvist er det regulatoriske element en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens ifølge SEQ ID NO: 57 (Aual).

10

11. Rekombinant gær ifølge et hvilket som helst af kravene 1-10, hvor gæret yderligere omfatter mindst et yderligere opreguleret enzym, fortrinsvist et glucoamylaseenzym med et EC-nummer 3.2.1.3 fortrinsvist isoleret fra arten *Saccharomycopsis*; en permease fortrinsvist isoleret fra arten *Saccharomyces* (permease); eller en protease med EC-nummer: 3.4.23.41 fortrinsvist isoleret fra en art valgt fra gruppen bestående af: *Zea*, *Neurospora*, *Podospora*• og *Magnaporthe* (protease).

12. Rekombinant gær ifølge krav 11, hvor det opregulerede enzym er en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens ifølge SEQ ID NO: 163 (glucoamylase); en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens ifølge SEQ ID NO: 53 (Gap); eller en polypeptidsekvens, der er mindst omkring 80%, 90%, 95% eller 100% identisk med en polypeptidsekvens valgt fra gruppen bestående af SEQ ID NOs: 41, 43, 45, 47, 49, og 51 (protease).

13. Rekombinant gær ifølge et hvilket som helst af kravene 1-12, hvor de opregulerede eller nedregulerede enzymer er under kontrol af en heterolog promoter, fortrinsvist er den heterologe promoter valgt fra gruppen bestående af: TEF2 (SEQ ID NO: 58), HXT7 (SEQ ID NO: 59), ADH1 (SEQ ID NO: 60), og TP1 (SEQ ID NO: 61).

14. Rekombinant gær ifølge et hvilket som helst af kravene 1-13, hvor gæren producerer ethanol ved et højere udbytte end en ellers identisk gær, der mangler

35

de genetiske modifikationer, fortrinsvist fremstiller den rekombinante gær en ethanol titer fra omkring 1% til omkring 10% mere end en ellers identisk gær, der mangler de genetiske modifikationer, mere fortrinsvist producerer den rekombinante gær en ethanol titer på mindst omkring 125 g/L, fortrinsvist producerer gæren glycerol ved et lavere udbytte end en ellers identisk gær, der mangler de genetiske modifikationer, mest fortrinsvist producerer gæren en glycerol titer på fra omkring 10 til omkring 100% mindre end en anden ellers identisk gær, der mangler de genetiske modifikationer.

- 10 **15.** Rekombinant gær ifølge et hvilket som helst af kravene 1 til 14, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Gpd2, nedreguleret Fdh1, nedreguleret Fdh2, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, og et opreguleret pyruvat-formiat-lyase-aktiverende enzym, fortrinsvist er GdhI nedreguleret, fortrinsvist er Glt1 opreguleret, fortrinsvist er GIn1 opreguleret, 15 fortrinsvist er AuaI nedreguleret eller fortrinsvist er Ure1 nedreguleret, mest fortrinsvist omfatter den rekombinante gær yderligere Dur1/2 og/eller et opreguleret enzym valgt fra gruppen bestående af: Dur3 og Dur4 og/eller et opreguleret enzym valgt fra gruppen bestående af: Mep1, Mep2, og Mep3 og/eller en opreguleret Gln3 og/eller en GPD1 udtrykt fra en GPD2-promoter og/eller en 20 GPD2 udtrykt fra en GPD1-promoter.

- 16.** Rekombinant gær ifølge et hvilket som helst af kravene 1 til 15, hvor enzymerne er nedreguleret Gpd1, nedreguleret Fdh1, nedreguleret Fdh2, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, og et opreguleret pyruvat- 25 formiat-lyase-aktiverende enzym, fortrinsvist er GdhI nedreguleret, fortrinsvist er Glt1 opreguleret, fortrinsvist er GIn1 opreguleret, fortrinsvist er AuaI nedreguleret eller fortrinsvist er Ure1 nedreguleret, mest fortrinsvist omfatter den rekombinante gær yderligere et eller flere native og/eller heterologe enzymer, hvor enzymerne er Dur1/2 og/eller et opreguleret enzym valgt fra gruppen 30 bestående af: Dur3 og Dur4 og/eller et opreguleret enzym valgt fra gruppen bestående af: Mep1, Mep2, og Mep3 og/eller en opreguleret Gln3 og/eller en GPD1 udtrykt fra en GPD2-promoter og/eller en GPD2 udtrykt fra en GPD1-promoter.

17. Rekombinant gær ifølge et hvilket som helst af kravene 1 til 16, hvor enzymerne er: nedreguleret Gpd2, nedreguleret Fdh1, nedreguleret Fdh2, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, og et opreguleret pyruvat-formiat-lyase-aktiverende enzym, fortrinsvist er Gdh1 nedreguleret, fortrinsvist er GtI1 opreguleret, fortrinsvist er GIn1 opreguleret, fortrinsvist er Aua1 nedreguleret eller fortrinsvist er Ure1 nedreguleret, mest fortrinsvist omfatter den rekombinante gær yderligere et eller flere native og/eller heterologe enzymer, hvor enzymerne er Dur1/2 og/eller et opreguleret enzym valgt fra gruppen bestående af: Dur3 og Dur4 og/eller et opreguleret enzym valgt fra gruppen bestående af: Mep1, Mep2, og Mep3 og/eller en opreguleret Gln3 og/eller en GPD1 udtrykt fra en GPD2-promoter og/eller en GPD2 udtrykt fra en GPD1-promoter.

18. Rekombinant gær ifølge et hvilket som helst af kravene 1 til 17, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Gpd2, nedreguleret Fdh1, nedreguleret Fdh2, nedreguleret Gdh1, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, et opreguleret pyruvat-format-lyase-aktiverende enzym, GPD1 under kontrollen af GPD2-promoteren, GPD2 under kontrollen af GPD1-promoteren, og opreguleret Gdh2; eller en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Gpd2, nedreguleret Fdh1, nedreguleret Fdh2, nedreguleret Gdh1, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, et opreguleret pyruvat-format-lyase-aktiverende enzym, GPD1 under kontrollen af GPD2-promoteren, GPD2 under kontrollen af GPD1-promoteren, opreguleret Glt1 og opreguleret GIn1; eller en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Fdh1, nedreguleret Fdh2, nedreguleret Gdh1, opreguleret AdhE, opreguleret pyruvat-format-lyase, et opreguleret pyruvat-format-lyase-aktiverende enzym, GPD1 under kontrollen af GPD2-promoteren, GPD2 under kontrollen af GPD1-promoteren, opreguleret Glt1 og opreguleret Gln1; eller en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd2, nedreguleret Fdh1, nedreguleret Fdh2, nedreguleret Gdh1, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, og et opreguleret pyruvat-formiat-lyase-aktiverende enzym; eller en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd1,

nedreguleret Fdh1, nedreguleret Fdh2, nedreguleret Gdh1, opreguleret AdhE, opreguleret pyruvate-formiat-lyase, et opreguleret pyruvate-formiat-lyase-aktiverende enzym, og GPD2 under kontrollen af GPD1-promoteren; en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Fdh1, nedreguleret Fdh2, nedreguleret Gdh1, opreguleret AdhE, opreguleret pyruvate-formiat-lyase, og et opreguleret pyruvate-formiat-lyase-aktiverende enzym; eller en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Fdh1, nedreguleret Fdh2, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, et opreguleret pyruvat-formiat-lyase-aktiverende enzym, opreguleret DUR1/2, og GPD2 under kontrollen af GPD1-promoteren; eller en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Fdh1, nedreguleret Fdh2, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, et opreguleret pyruvat-formiat-lyase-aktiverende enzym, og opreguleret DUR1/2, fortrinsvist er DUR1/2 drevet af en TEF2-promoter, en HXT7-promoter, en ADH1-promoter eller en HXT7/TEF2-promoter; eller en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Gpd2, nedreguleret Fdh1, nedreguleret Fdh2, nedreguleret Ure2, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, et opreguleret pyruvat-formiat-lyase-aktiverende enzym, GPD1 under kontrollen af GPD2-promoteren, og GPD2 under kontrollen af GPD1-promoteren, fortrinsvist omfatter den rekombinante gær yderligere en opreguleret DUR3 og/eller DUR1/2 og/eller GIn3; eller en rekombinant gær omfattende et eller flere native og/eller heterologe enzymer, hvor enzymerne er: nedreguleret Gpd1, nedreguleret Gpd2, nedreguleret Fdh1, nedreguleret Fdh2, opreguleret AdhE, opreguleret pyruvat-formiat-lyase, et opreguleret pyruvat-formiat-lyase-aktiverende enzym, opreguleret GDH2, GPD1 under kontrollen af GPD2-promoteren, og GPD2 under kontrollen af GPD1-promoteren.

30

19. Sammensætning omfattende en rekombinant gær ifølge et hvilket som helst af kravene 1-18 og et kulstof-indeholdende råmateriale, fortrinsvist er råmaterialet valgt fra gruppen bestående af træagtig biomasse, græsser, sukkerforarbejdningsrester, kommunalt affald, landbrugsaffald eller en hvilken som helst kombination deraf, mere fortrinsvist omfatter råmaterialet genbrugt

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træmassefiber, savsmuld, hårdt træ, blødt træ, risstrå, risskaller, bygghalm, majskolber, kornhalm, hvedehalm, rapsstrå, oafhalm, havreskaller, majsfiber, blade og stilke, sukkulenter, agave, sukkerrør bagasse, præriegræs, miscanthus, papirslam, kommunalt affald eller enhver kombination deraf.

5

20. Fremgangsmåde til fremstilling af et fermenteringsprodukt omfattende: a) at tilvejebringe sammensætningen ifølge krav 19; b) at bringe sammensætningen i kontakt med et kulstof-indeholdende råmateriale, hvor den rekombinante gær er i stand til at fermentere det kulstof-indeholdende råmateriale til at opnå fermenteringsproduktet; og, c) eventuelt at genvinde fermenteringproduktionen, fortrinsvist reduceres glycerolproduktionen sammenlignet med en ellers identisk gær, der mangler de genetiske modifikationer, og hvor ethanoltiteren steg med mindst omkring 1 til omkring 10%, når den rekombinante gær dyrkes under tilstedeværelsen af et kulstof-indeholdende råmateriale i tilstrækkelig tid til at producere ethanol, mere fortrinsvist tilsættes nitrogen til kulturen, der indeholder den rekombinante gær og råmaterialet.

21. Fremgangsmåde til fremstilling af ethanol omfattende: a) at tilvejebringe den rekombinante gær, ifølge et hvilket som helst af kravene 1-18; b) at dyrke den rekombinante gær under tilstedeværelsen af et kulstof-indeholdende råmateriale i tilstrækkelig tid til at producere ethanol; og, eventuelt, c) at ekstrahere ethanolet, fortrinsvist reduceres glycerolproduktionen sammenlignet med en ellers identisk gær, der mangler de genetiske modifikationer, og hvor ethanoltiteren steg med mindst omkring 1 til omkring 10%, når den rekombinante gær dyrkes under tilstedeværelsen af et kulstof-indeholdende råmateriale i tilstrækkelig tid til at producere ethanol, mere fortrinsvist tilsættes nitrogen til kulturen, der indeholder den rekombinante gær og råmaterialet.

22. Fremgangsmåde til at reducere glycerolproduktion omfattende at tilvejebringe en rekombinant gær ifølge et hvilket som helst af kravene 1-18, hvor glyceroltiteren er fra omkring 10 til omkring 100% mindre end hastigheden sammenlignet med en ellers identisk gær, der mangler de genetiske modifikationer, fortrinsvist reduceres glycerolproduktionen sammenlignet med en ellers identisk gær, der mangler de genetiske modifikationer, og hvor ethanoltiteren steg med mindst omkring 1 til omkring 10%, når den rekombinante

gær dyrkes under tilstedeværelsen af et kulstof-indeholdende råmateriale i tilstrækkelig tid til at producere ethanol, mere fortrinsvist tilsættes nitrogen til kulturen, der indeholder den rekombinante gær og råmaterialet.

- 5 **23.** Samkultur omfattende mindst to værtsceller, hvor a) en af værtscellerne omfatter en rekombinant gær fra et hvilket som helst af kravene 1-18; og, b) en anden værtscelle, som er genetisk adskilt fra (a), fortrinsvist er den genetisk adskilte værtscelle en gær eller bakterie, mest fortrinsvist er den genetisk adskilte værtscelle en hvilken som helst organisme fra arten *Saccharomyces*, *Issatchenkia*,
10 *Pichia* , *Clavispora*, *Candida* , *Hansenula*, *Kluyveromyces*, *Trichoderma*, *Thermoascus*, *Escherichia*, *Clostridium*, *Caldicellulosiruptor*, *Zymomonas*, *Thermoanaerobacter* eller *Thermoanaerobacterum*.

DRAWINGS

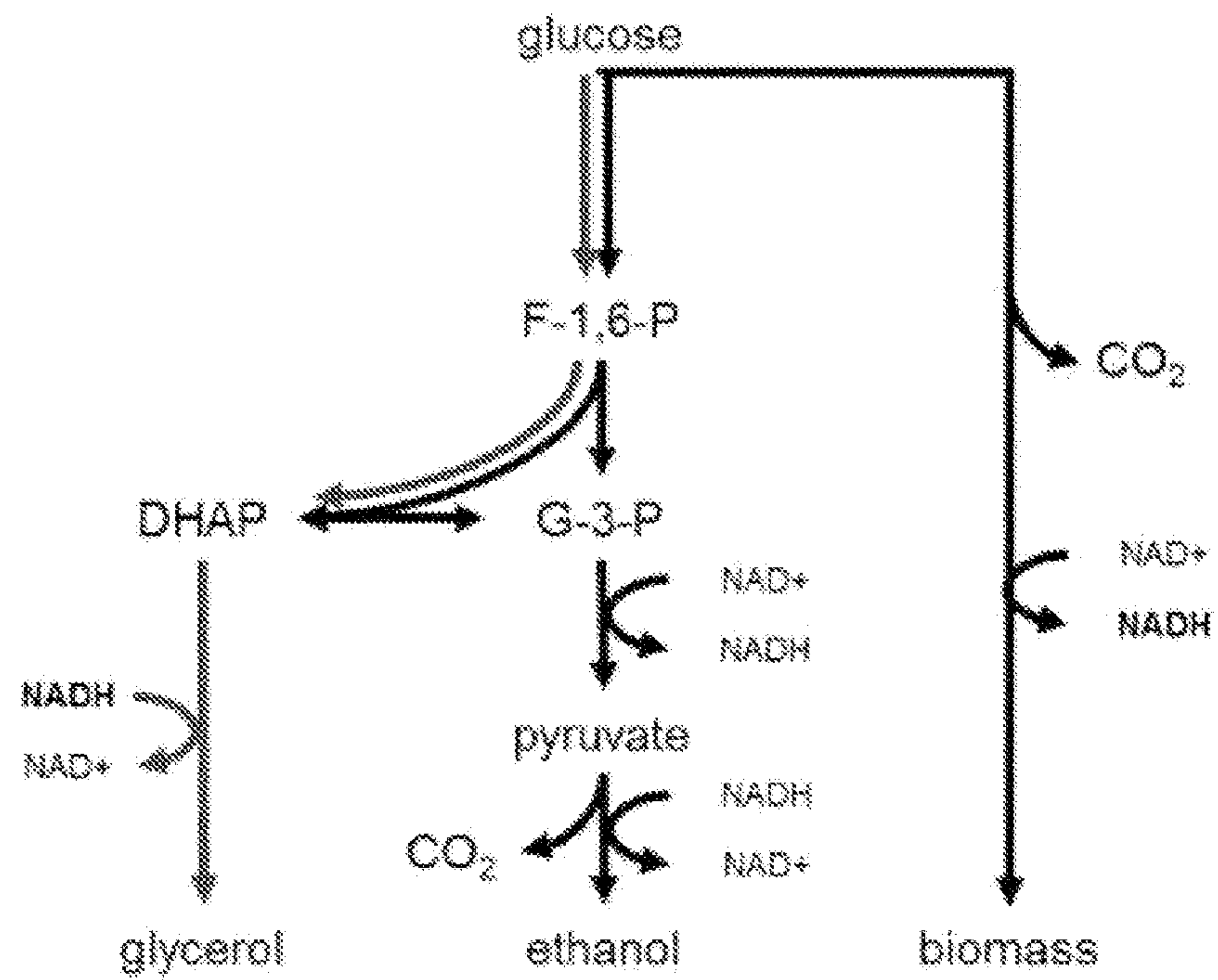


FIGURE 1

Active (Sodium Symport)
Sc enz: DUR3
Km 14 μ m (0.1 ppm)

Passive diffusion
Sc enz : DUR4
Km 0.5mM (600ppm)

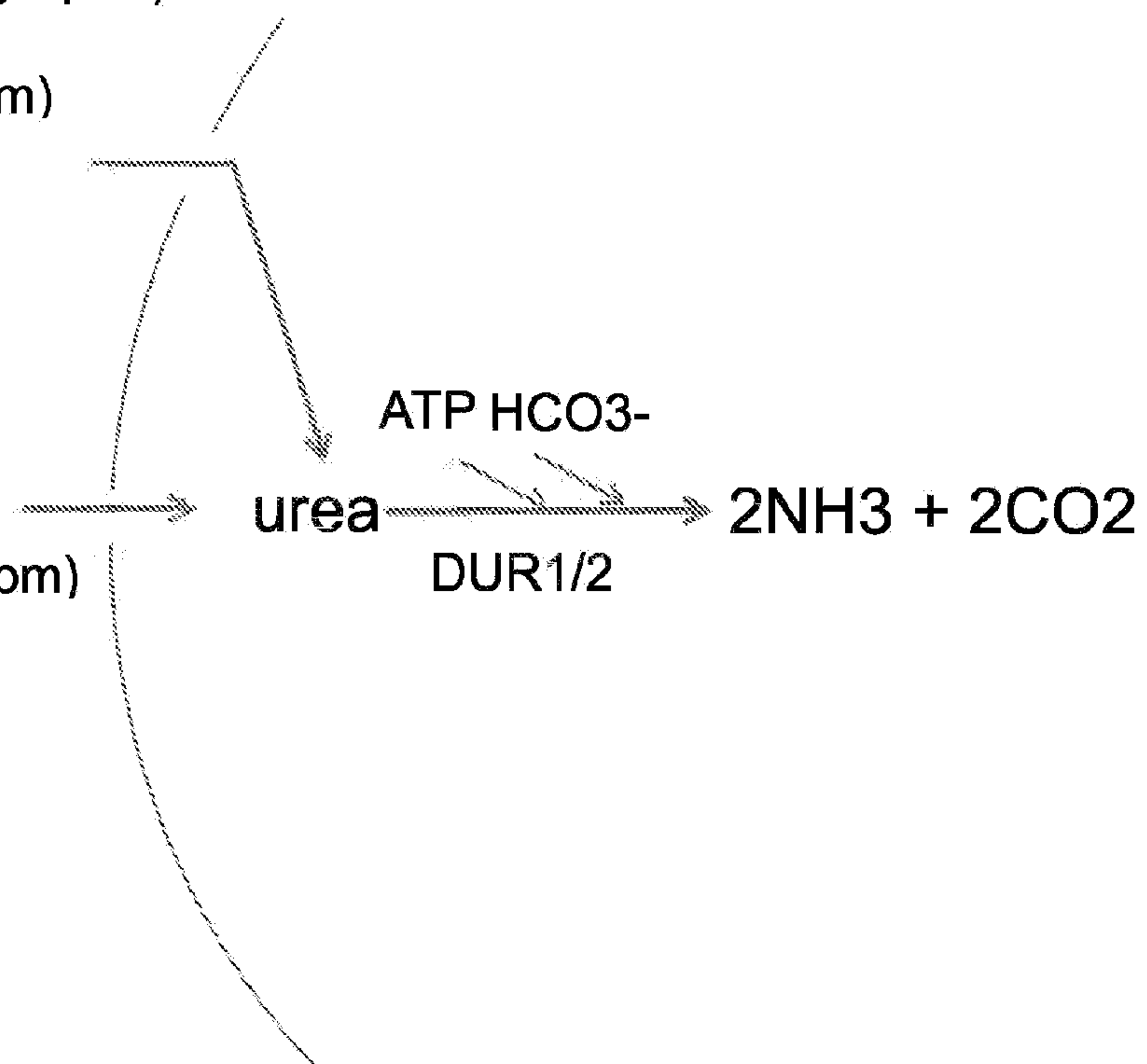


FIGURE 2

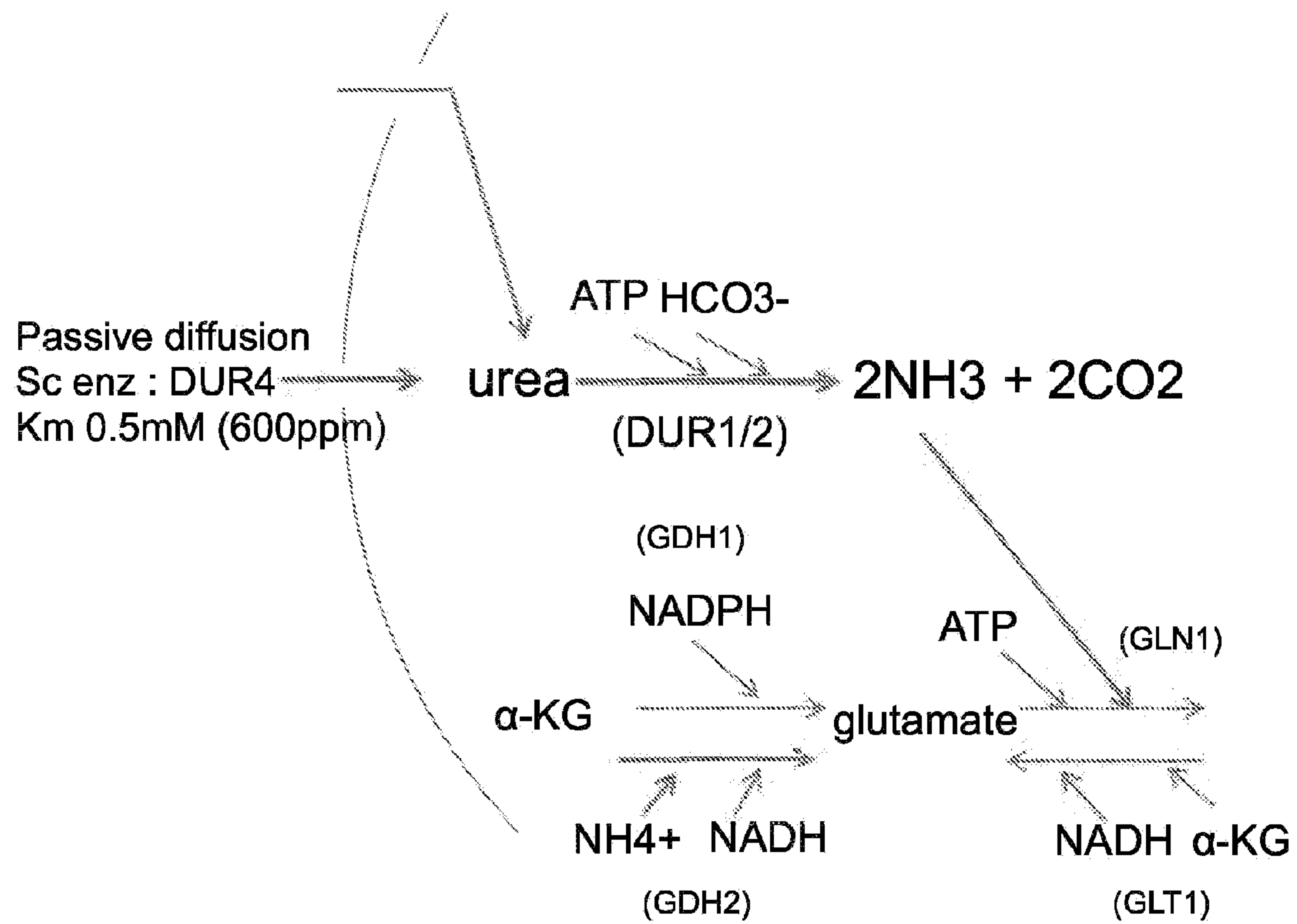


FIGURE 3

Active (Sodium Symport)

Sc enz: DUR3

Km 14um (0.1 ppm)

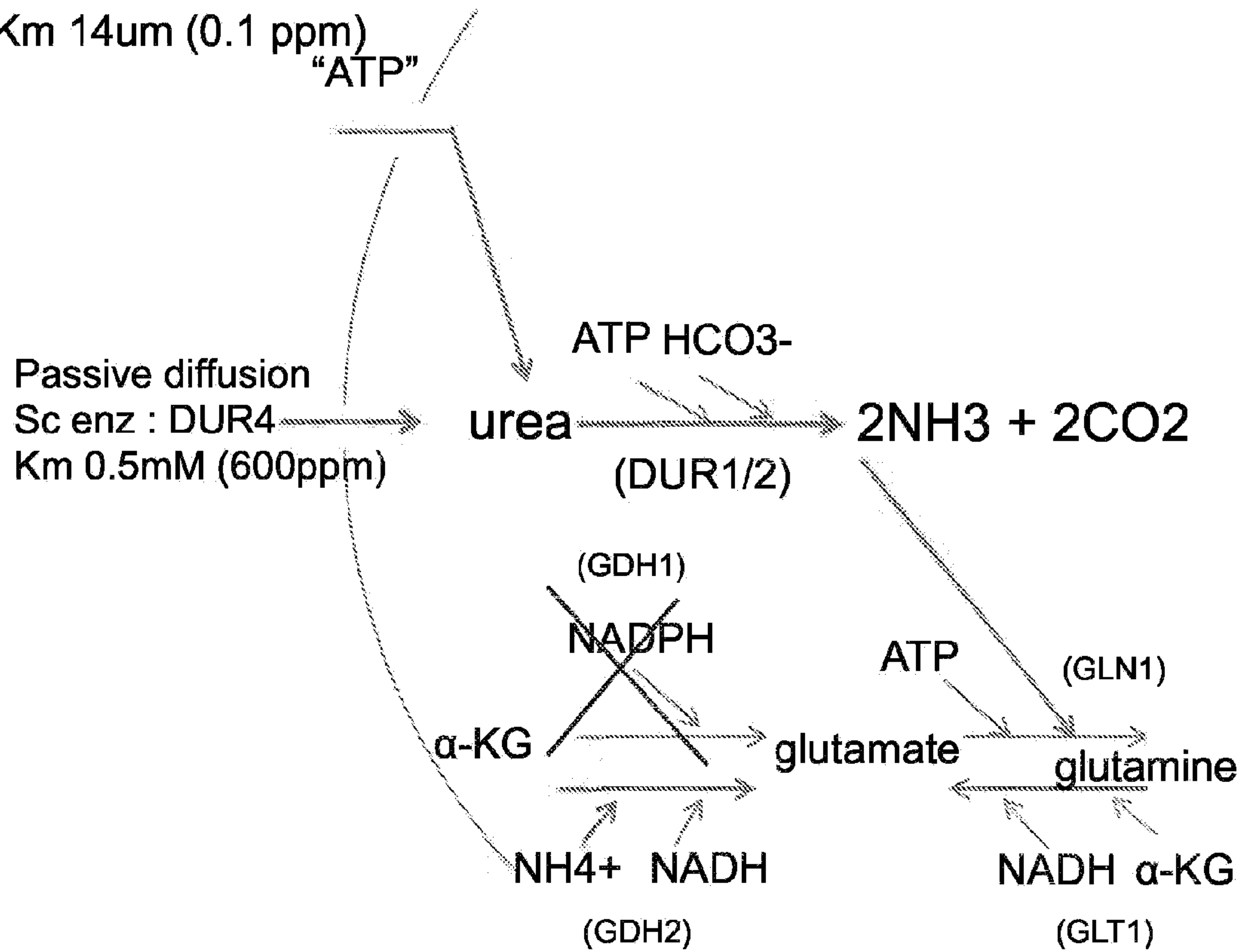


FIGURE 4

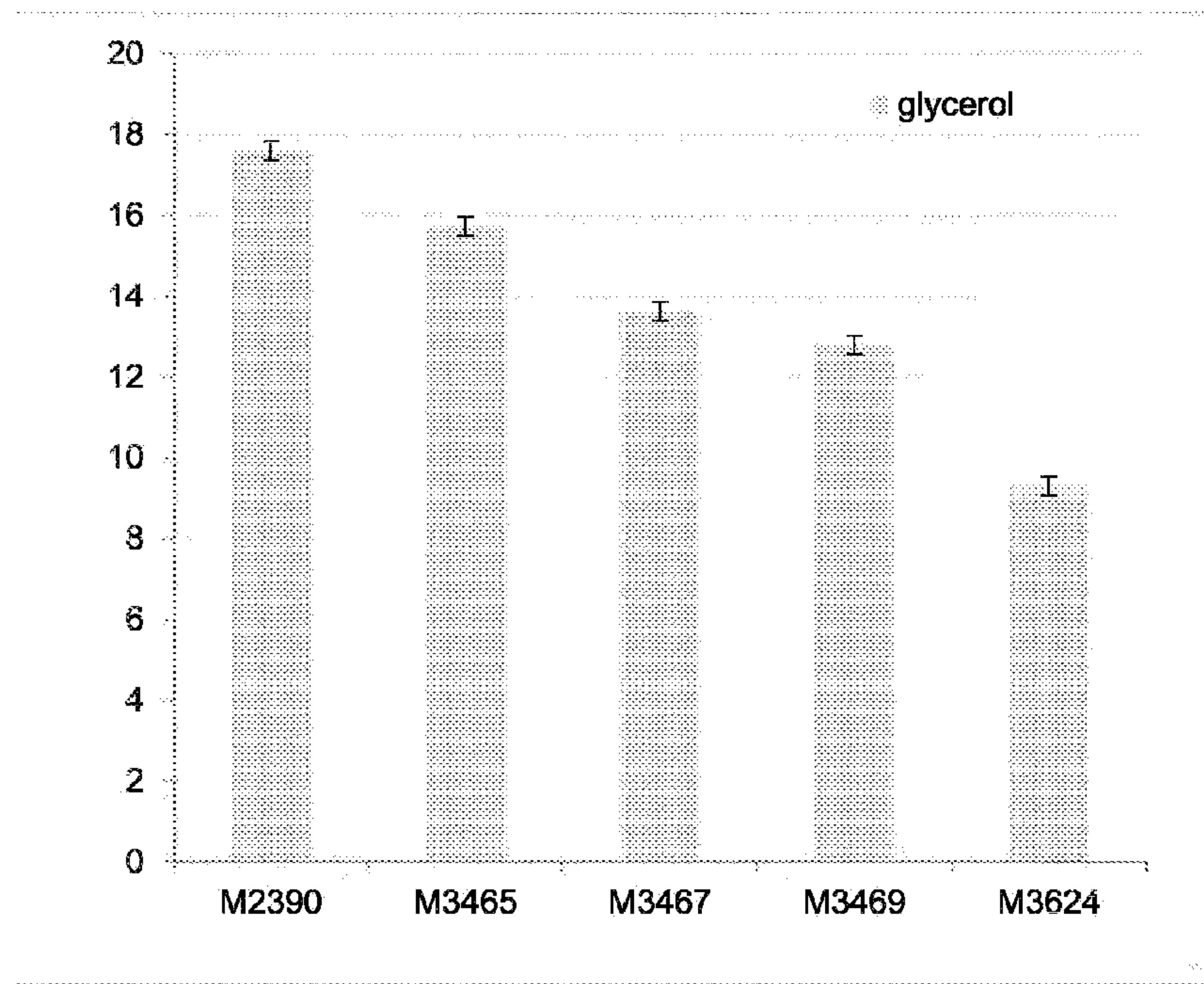


FIGURE 5

MA0631

Marked Deletion of GDH1 (just kan showed here – nat construct the same)

MA0631			
Fragment	Primers	Template	Expected Size
GDH1 5' Flank	X14961/X21291	gDNA	2065bp
AGTEF pro-kan/nat/tdk-HXT2 pro	X21289/X21290	pMU2873/pMU2879	3820bp and 3583bp
GDH1 3' Flank	X21292/X14966	gDNA	2056bp

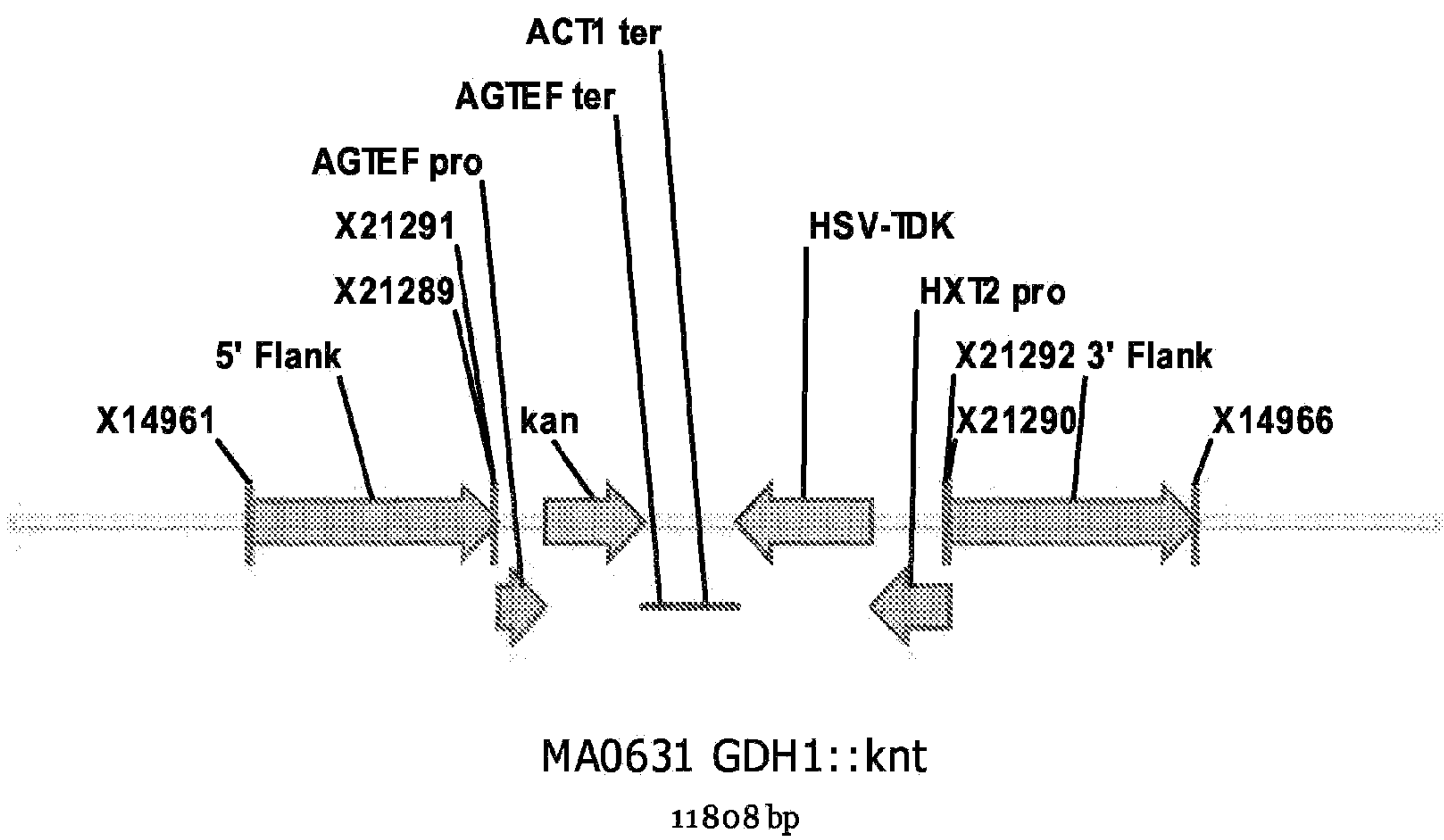
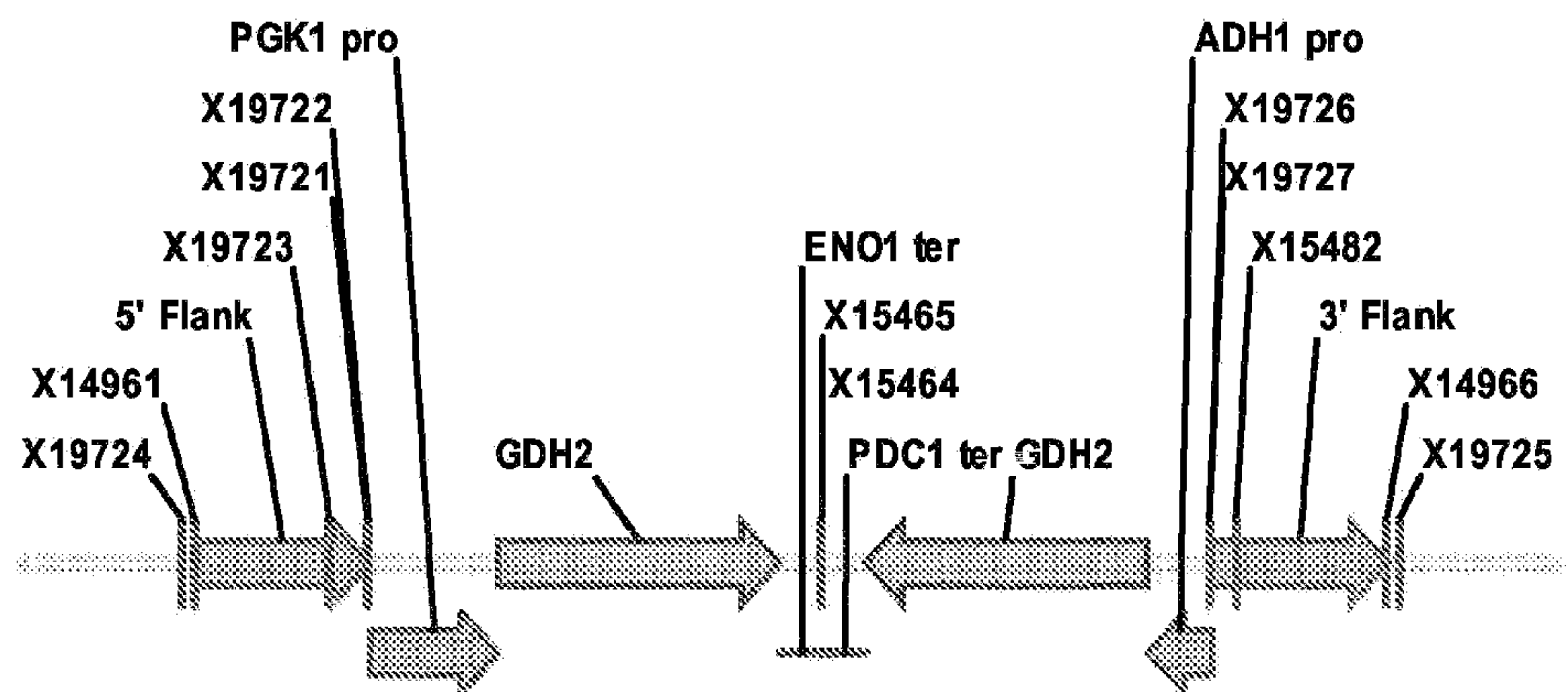


FIGURE 6

MA0425

4 copy *S. cerevisiae* GDH2 integrated at GDH1 locus

MA0425			
Fragment	Primers	Template	Expected Size
GDH1 5' Flank	X14961/X19722	gDNA	2065bp
PGKpro-GDH2-ENO1ter	X19721/X15464	pMU2908	5283bp
ADH1pro-GDH2-PDC1ter	X15465/X19727	pMU2909	4546bp
GDH1 3' Flank	X19726/X14966	gDNA	2056bp



MA0425
17884bp

FIGURE 7

MA0426

2 copy *S. cerevisiae* GLT1/GLN1 integrated at GDH1 locus
MA0426

Fragment	Primers	Template	Expected Size
GDH1 5' Flank	X14961/X19722	M2390 gDNA	2065bp
PGKpro-GLT1-ENOter	X19721/X15464	pMU2913	8442bp
ADH1pro-GLN1-PDC1ter	X15465/X19727	pMU2911	2363bp
GDH1 3' Flank	X19726/X14966	M2390 gDNA	2056bp

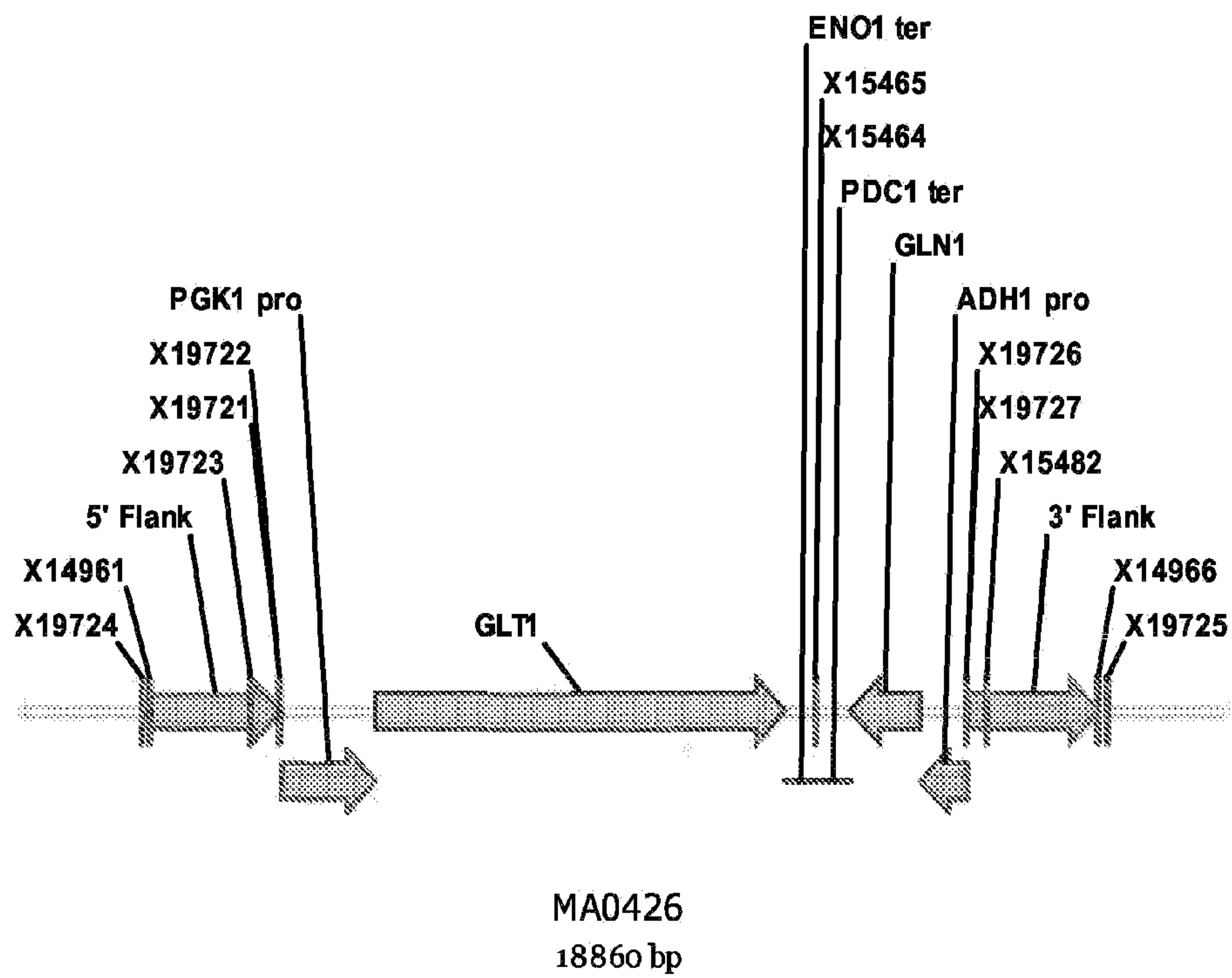
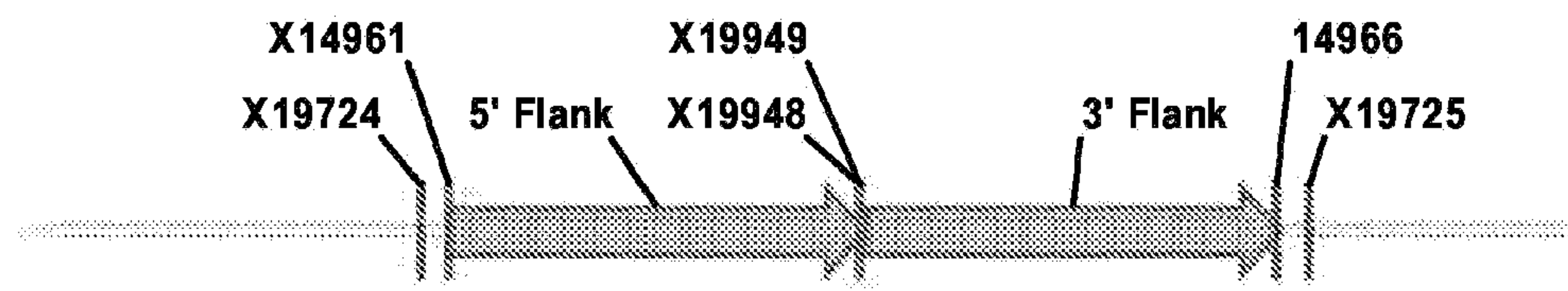


FIGURE 8

MA0888

Clean deletion of GDH1

MA0888			
Fragment	Primers	Template	Expected Size
5' Flank	X14961/X19949	M2390 gDNA	2065bp
3' Flank	X19948/X14966	M2390 gDNA	2056bp



MA0888 GDH1::deletion
8055bp

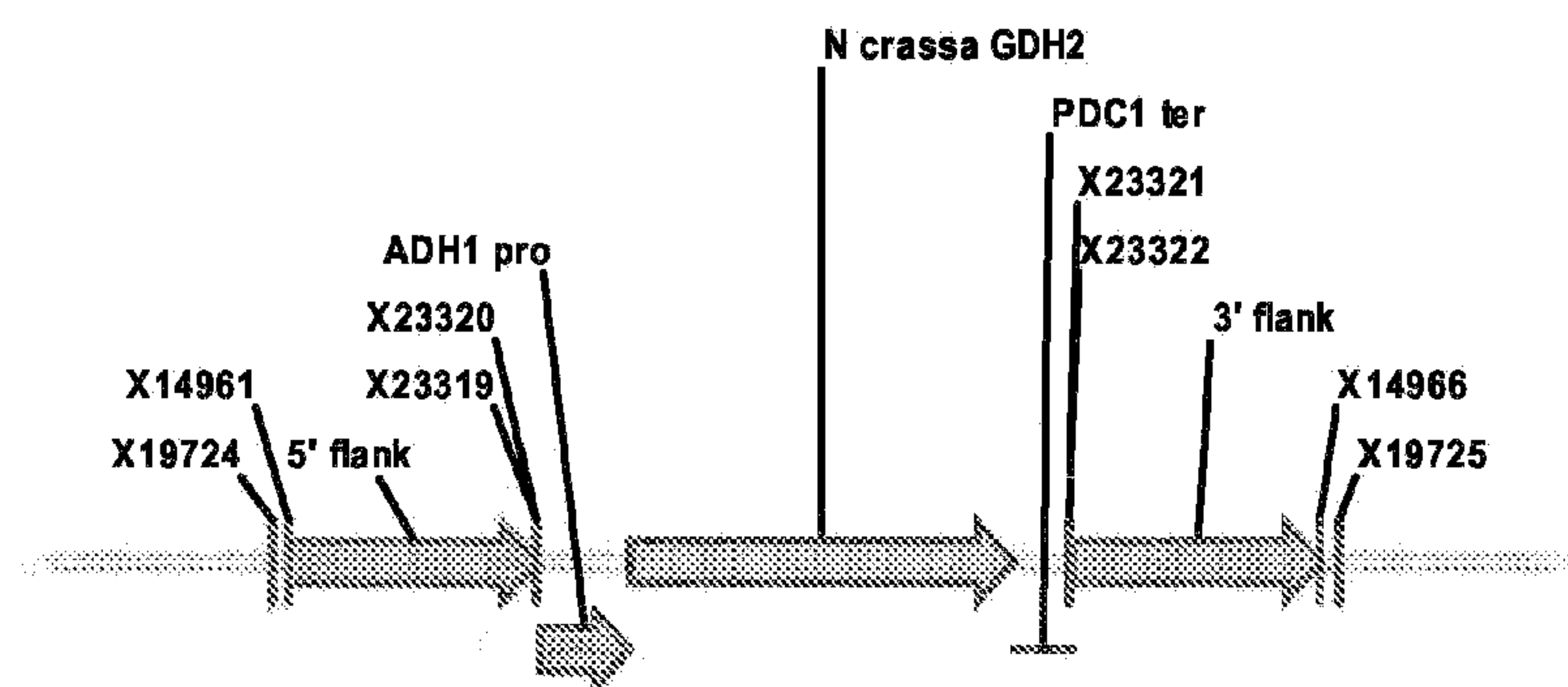
FIGURE 9

MA0837

2 copy *N. crassa* GDH2 integrated at GDH1 locus

MA0837

Fragment	Primers	Template	Expected Size
GDH1 5' Flank	X14961/X23320	gDNA	2065bp
ADH1pro-GDH2-PDC1 ter	X23319/X23322	pMU3597	4403bp
GDH1 3' Flank	X23321/X14966	gDNA	2056bp



MA0837
12458 bp
FIGURE 10

MA0616

GDH2 marked deletion

MA0616			
Fragment	Primers	Template	Expected Size
GDH2 5' Flank	X21123/X21124	M2390 gDNA	2024bp
AGTEFpro-kan/nat/tdk-HXT2pro	X21127/X21128	pMU2873/pMU2879	3820bp and 3583bp
GDH2 3' Flank	X21125/X21126	M2390 gDNA	1990bp

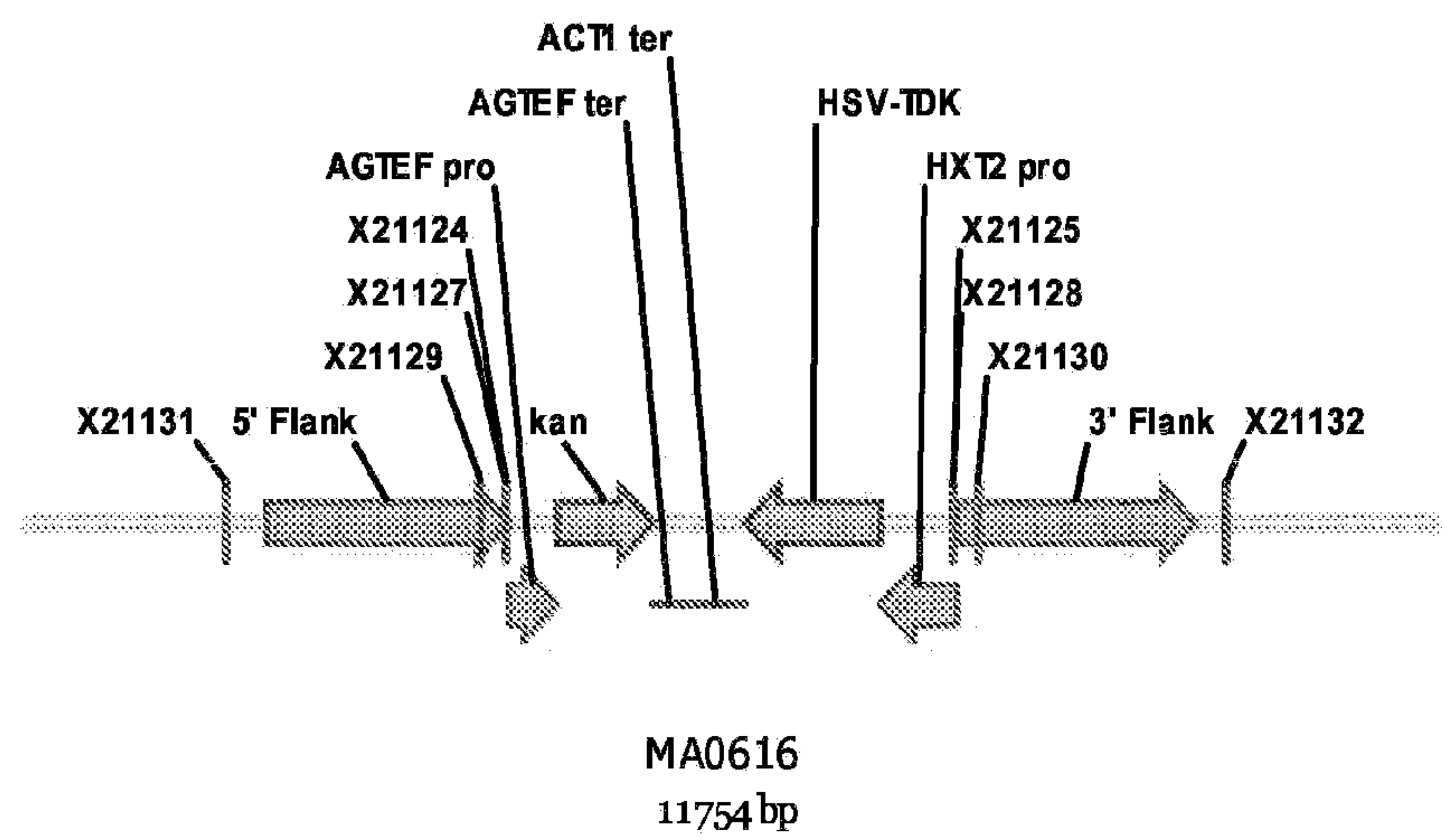


FIGURE 11

MA0616.1

GDH2 clean deletion

MA0616.1			
Fragment	Primers	Template	Expected Size
GDH2 5' Flank	X21123/X21507	M2390 gDNA	2024bp
GDH2 3' Flank	X21133/X21126	M2390 gDNA	1990bp

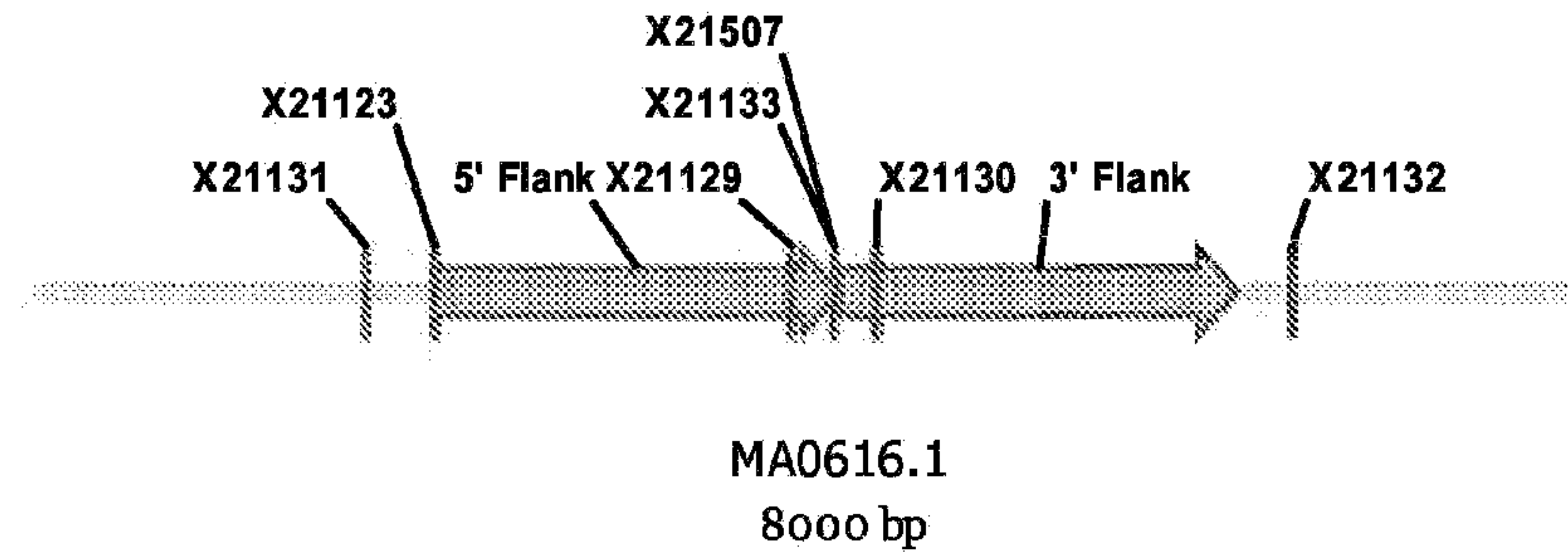


FIGURE 12

MA0615

GDH3 marked deletion

MA0615			
Fragment	Primers	Template	Expected Size
GDH3 5' Flank	X21135/X21136	M2390 gDNA	1976bp
AGTEFpro-kan/nat/tdk-HXT2pro	X21139/X21140	pMU2873/pMU2879	3820bp and 3583bp
GDH3 3' Flank	X21137/X21138	M2390 gDNA	2015bp

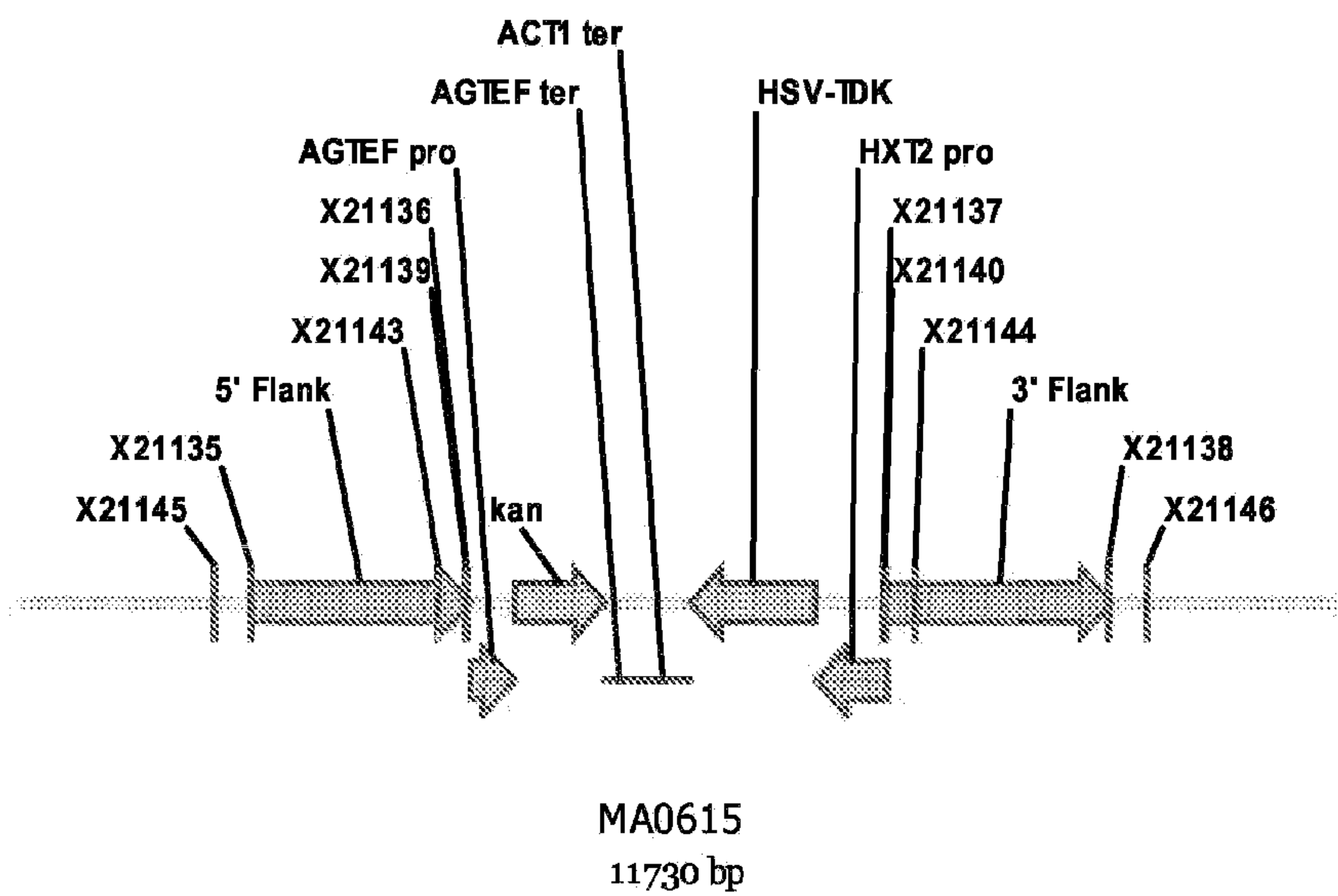


FIGURE 13

MA0615.1

GDH3 clean deletion

MA0615.1			
Fragment	Primers	Template	Expected Size
GDH3 5' Flank	X21135/X21148	M2390 gDNA	1976bp
GDH3 3' Flank	X21147/X21138	M2390 gDNA	2015bp

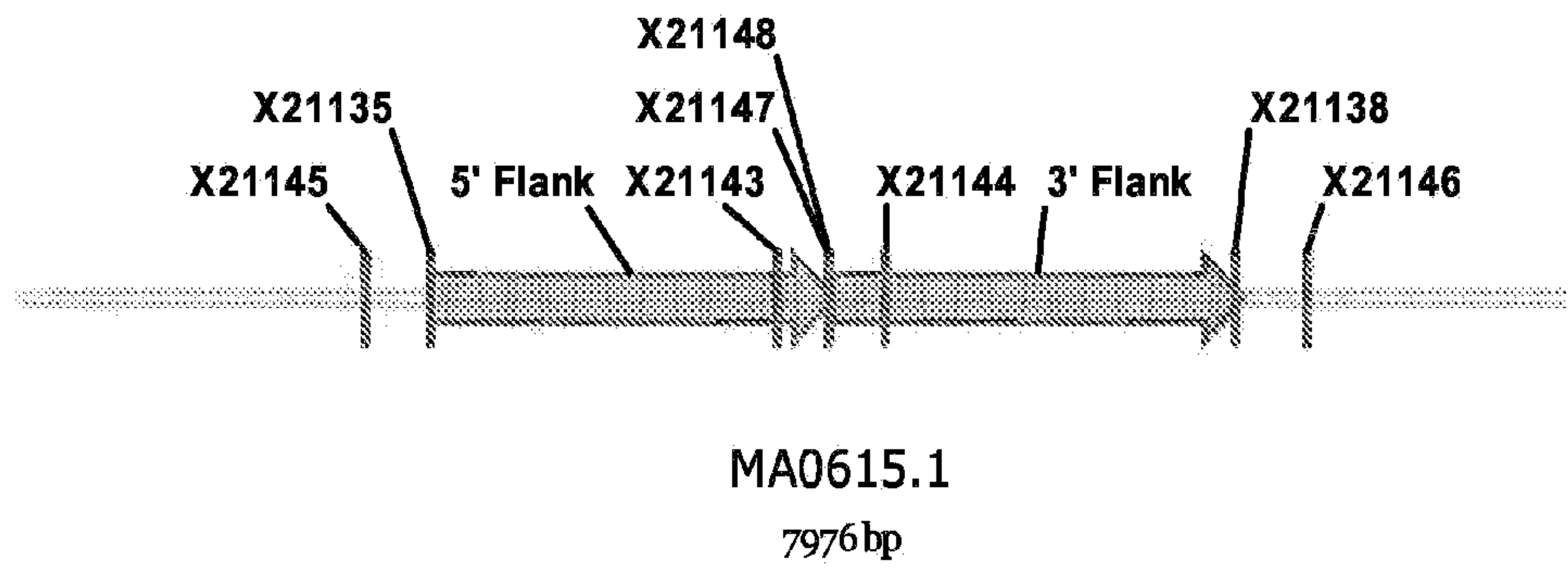


FIGURE 14

MA0622

URE2 marked deletion

MA0622			
Fragment	Primers	Template	Expected Size
URE2 5' Flank	X20022/X20023	M2390 gDNA	1968bp
AGTEF pro-kan/nat/tdk-HXT2 pro	X20028/X20029	pMU2873, pMU2879	3820bp and 3583bp
URE2 3' Flank	X20024/X20025	M2390 gDNA	1885bp

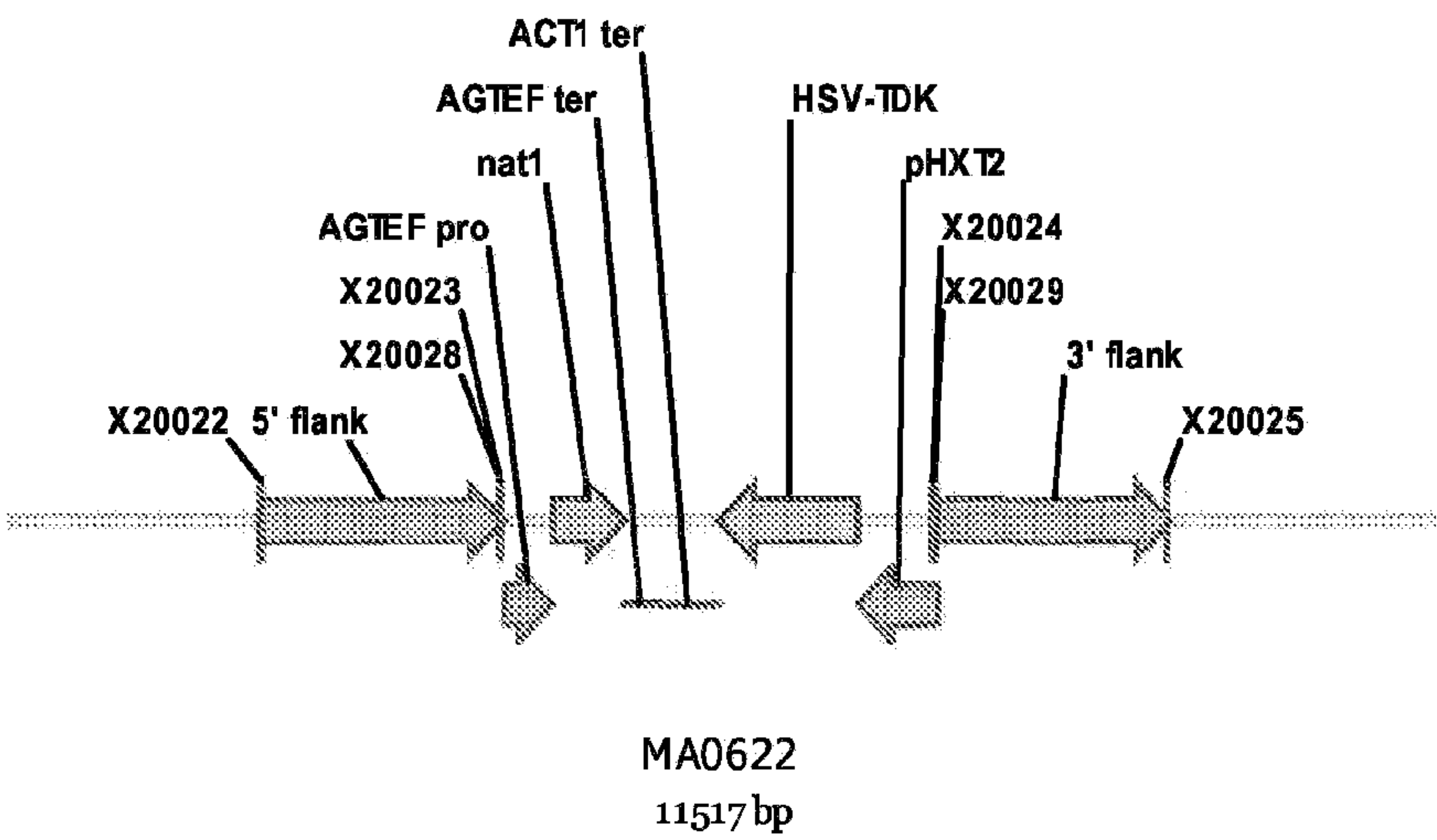


FIGURE 15

MA0622.1

URE2 clean deletion

MA0622.1			
Fragment	Primers	Template	Expected Size
URE2 5' Flank	X20022/X20027	M2390 gDNA	1968bp
URE2 3' Flank	X20026/X20025	M2390 gDNA	1885bp

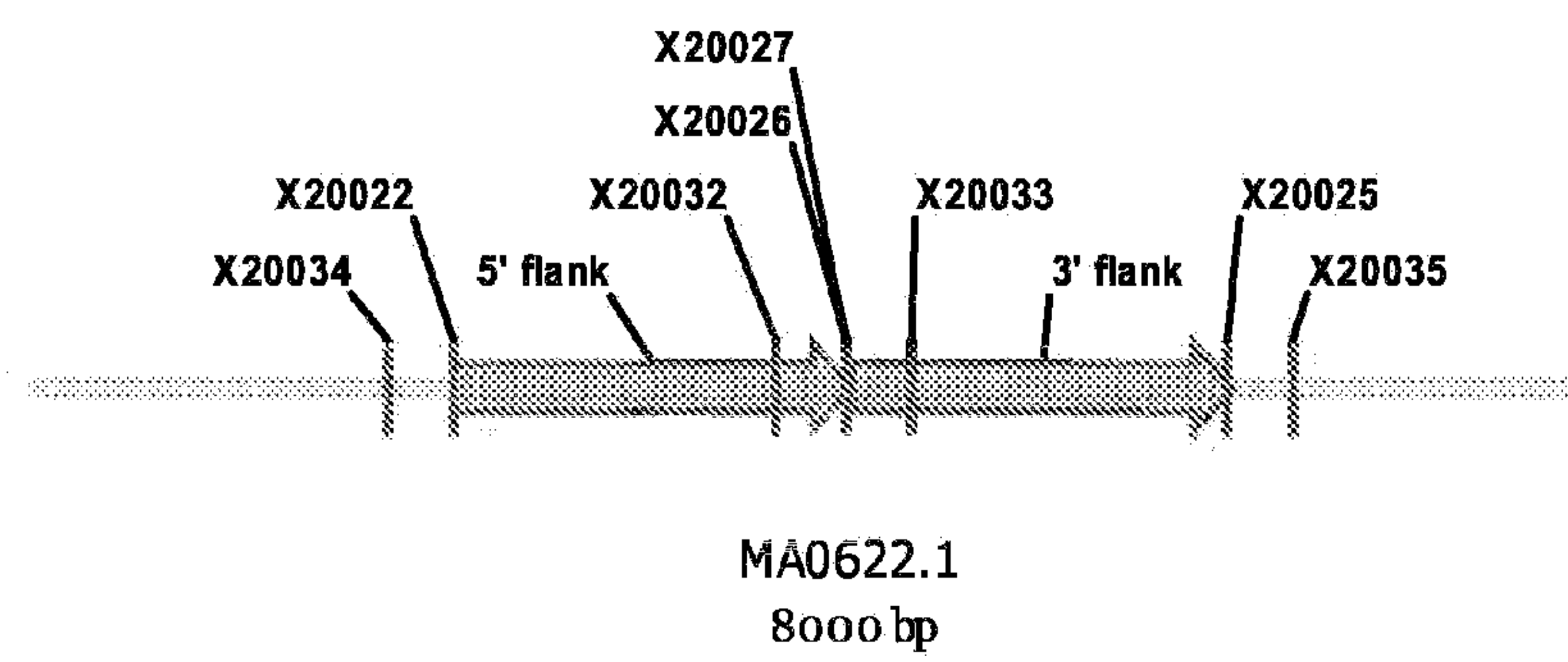


FIGURE 16

MA0580

DUR1,2,3 over expression at URE2 locus

MA0580			
Fragment	Primers	Template	Exp size
URE2 5' Flank	X20022/X21180	M2390 gDNA	1968bp
TEF2pro-DUR3-ADH3ter	X21179/X19513	pMU3464	3208bp
ADH1pro-DUR1,2-PDC1ter	X19514/X21181	pMU3411	6758bp
URE2 3' Flank	X21182/X20025	M2390 gDNA	1885bp

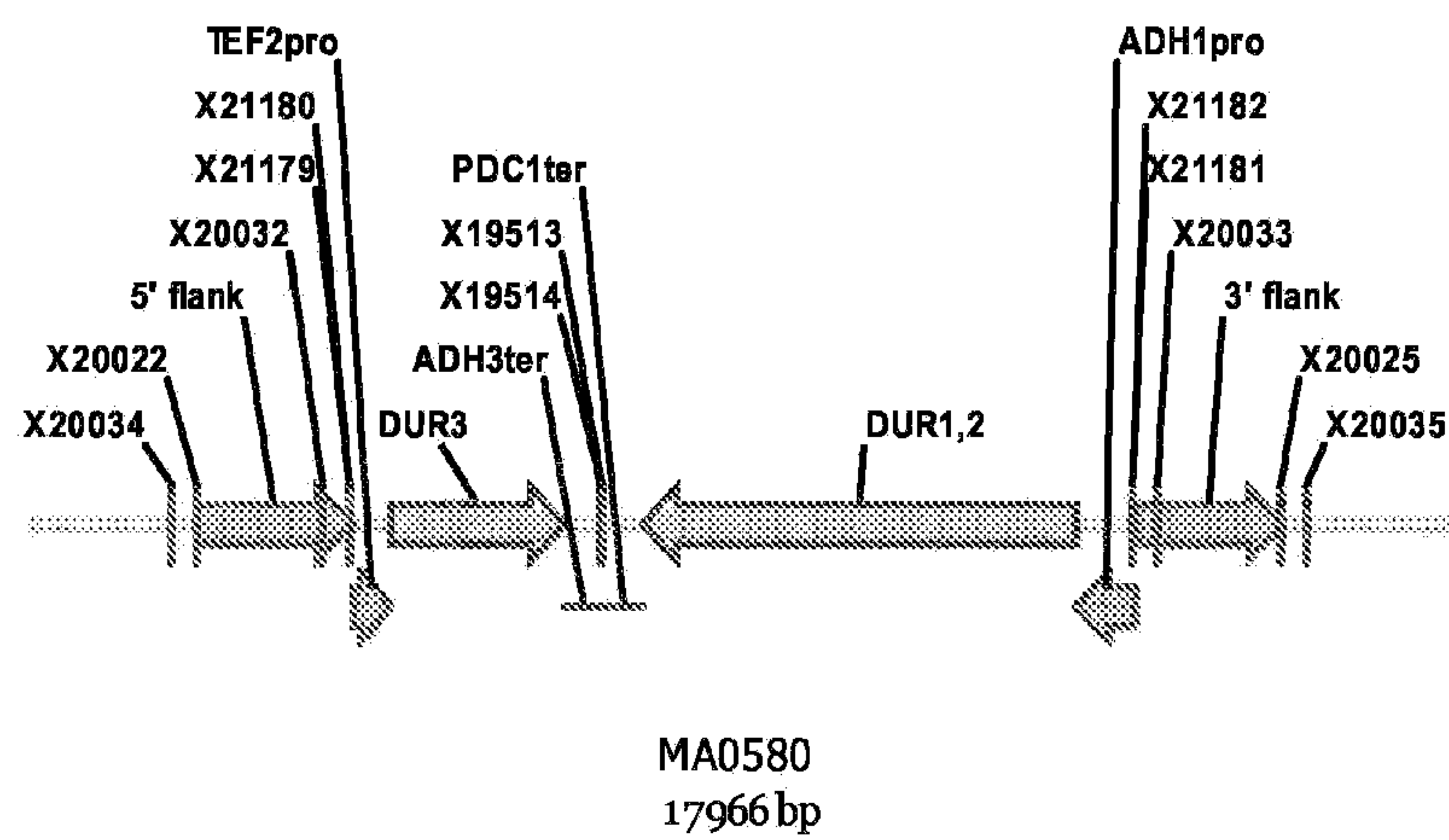


FIGURE 17

MA0581

MEP1 over expression at URE2 locus

MA0581			
Fragment	Primers	Template	Exp size
URE2 5' Flank	X20022/X21180	M2390 gDNA	1968bp
TEF2pro-MEP1-ADH3ter	X21179/X19513	pMU3465	2479bp
ADH1pro-MEP1-PDC1ter	X19514/X21181	pMU3460	2729bp
URE2 3' Flank	X21182/X20025	M2390 gDNA	1885bp

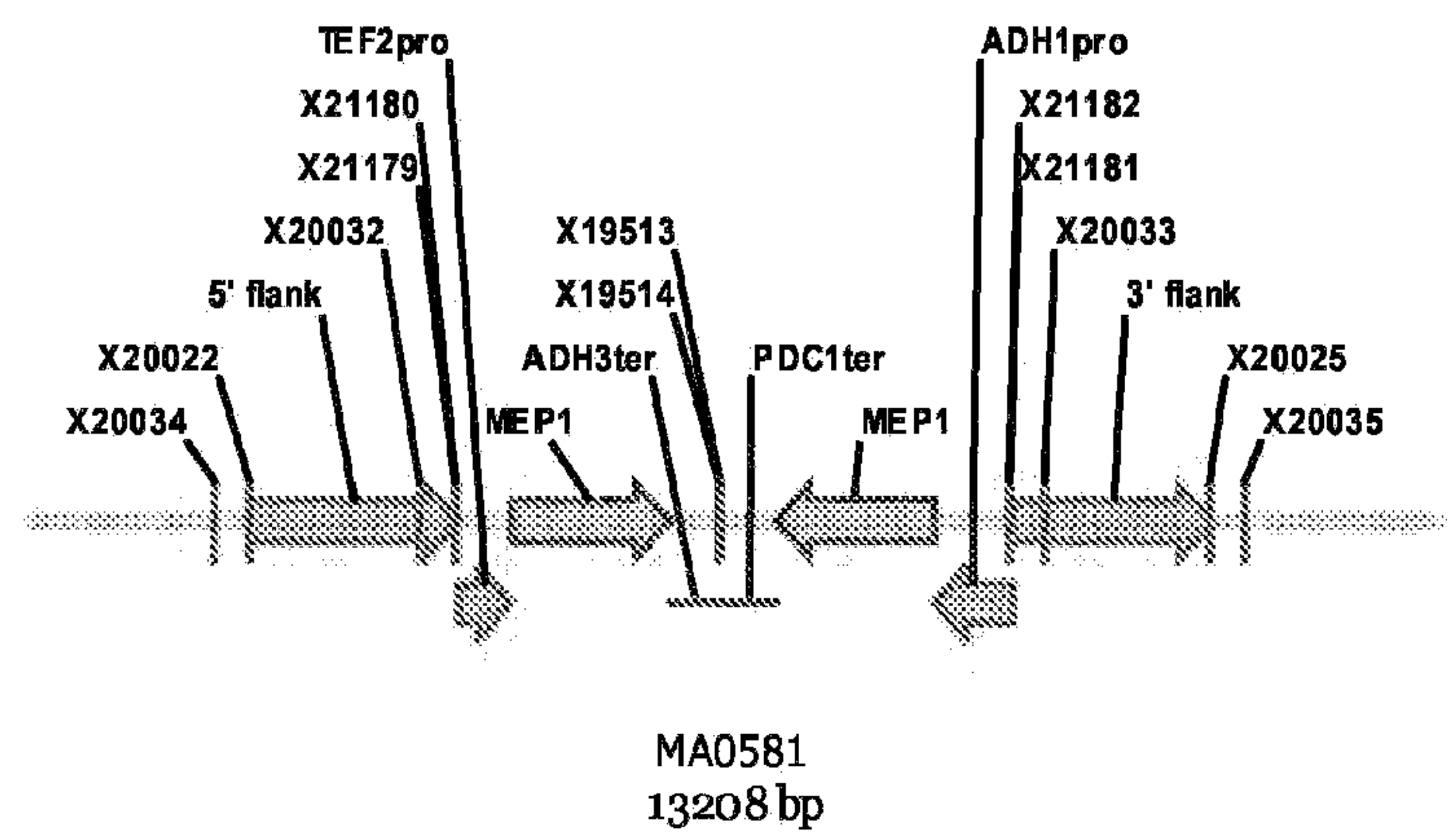


FIGURE 18

MA0582

MEP2 over expression at URE2 locus

MA0582			
Fragment	Primers	Template	Exp size
URE2 5' Flank	X20022/X21180	M2390 gDNA	1968bp
TEF2pro-MEP2-ADH3ter	X21179/X19513	pMU3465	2479bp
ADH1pro-MEP2-PDC1ter	X19514/X21181	pMU3461	2750bp
URE2 3' Flank	X21182/X20025	M2390 gDNA	1885bp

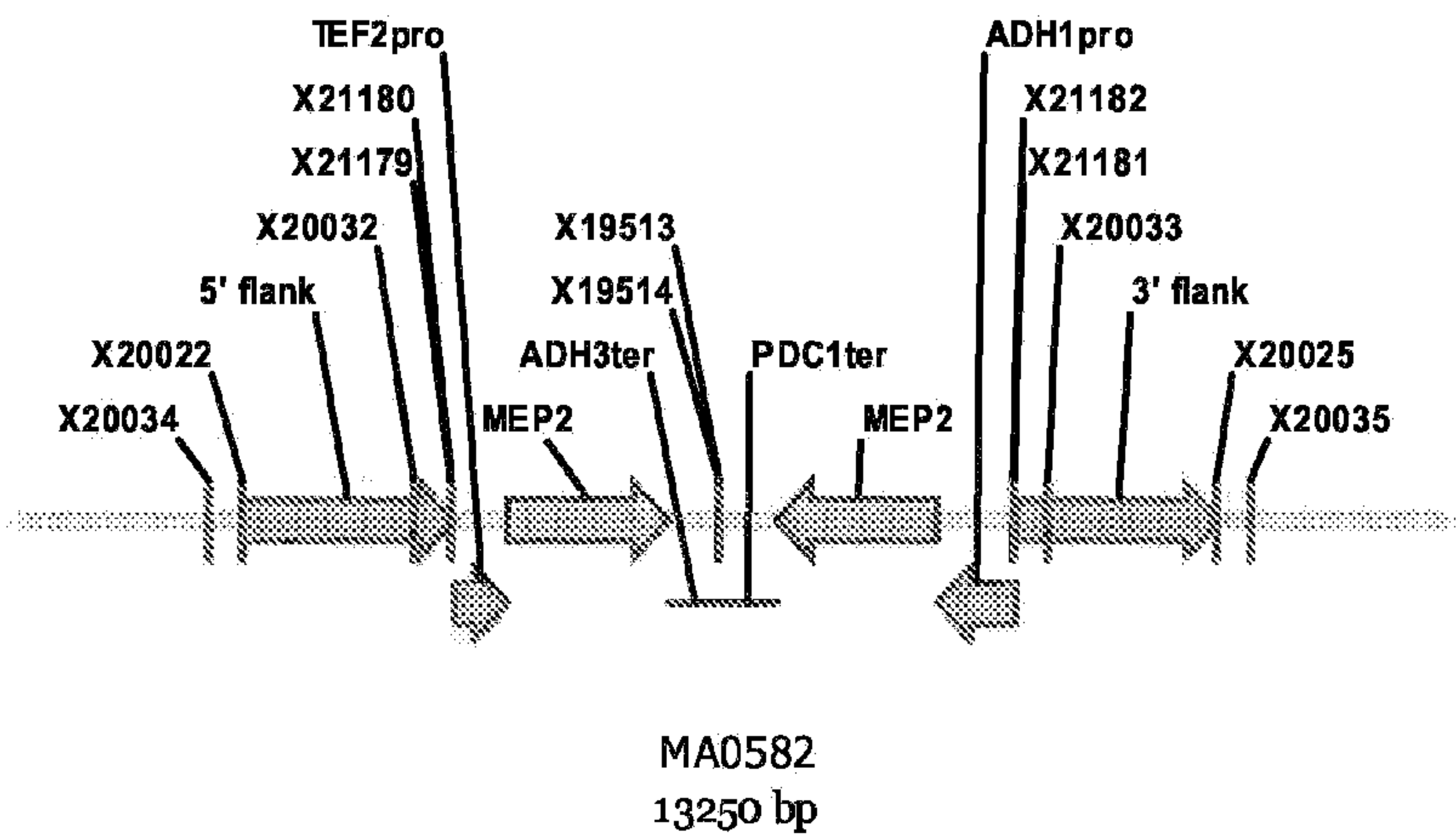


FIGURE 19

MA0583

GAP1 over expression at URE2 locus

MA0583

Fragment	Primers	Template	Exp size
URE2 5' Flank	X20022/X21180	M2390 gDNA	1968bp
TEF2pro-GAP1-ADH3ter	X21179/X19513	pMU3468	2809bp
ADH1pro-GAP1-PDC1ter	X19514/X21181	pMU3463	3059bp
URE2 3' Flank	X21182/X20025	M2390 gDNA	1885bp

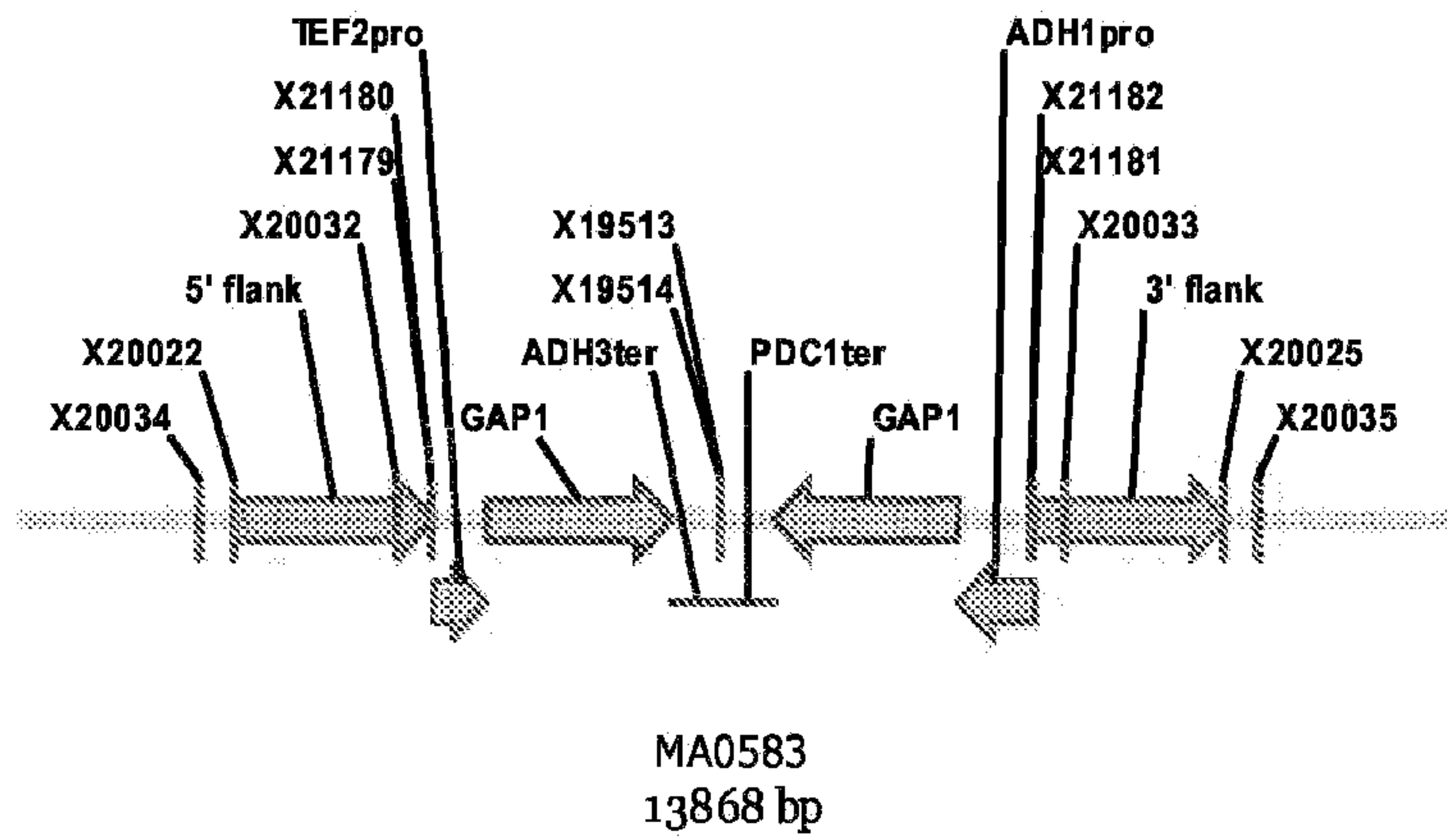


FIGURE 20

MA0584

S. cerevisiae GDH2 over expression at URE2 locus

MA0584			
Fragment	Primers	Template	Exp size
URE2 5' Flank	X20022/X21320	M2390 gDNA	1968bp
ADH1pro-GDH2-PDC1ter	X21319/X15465	pMU2909	4546bp
PGKpro-GDH2-ENO1ter	X15464/X21322	pMU2908	5283bp
URE2 3' Flank	X21321/X20025	M2390 gDNA	1885bp

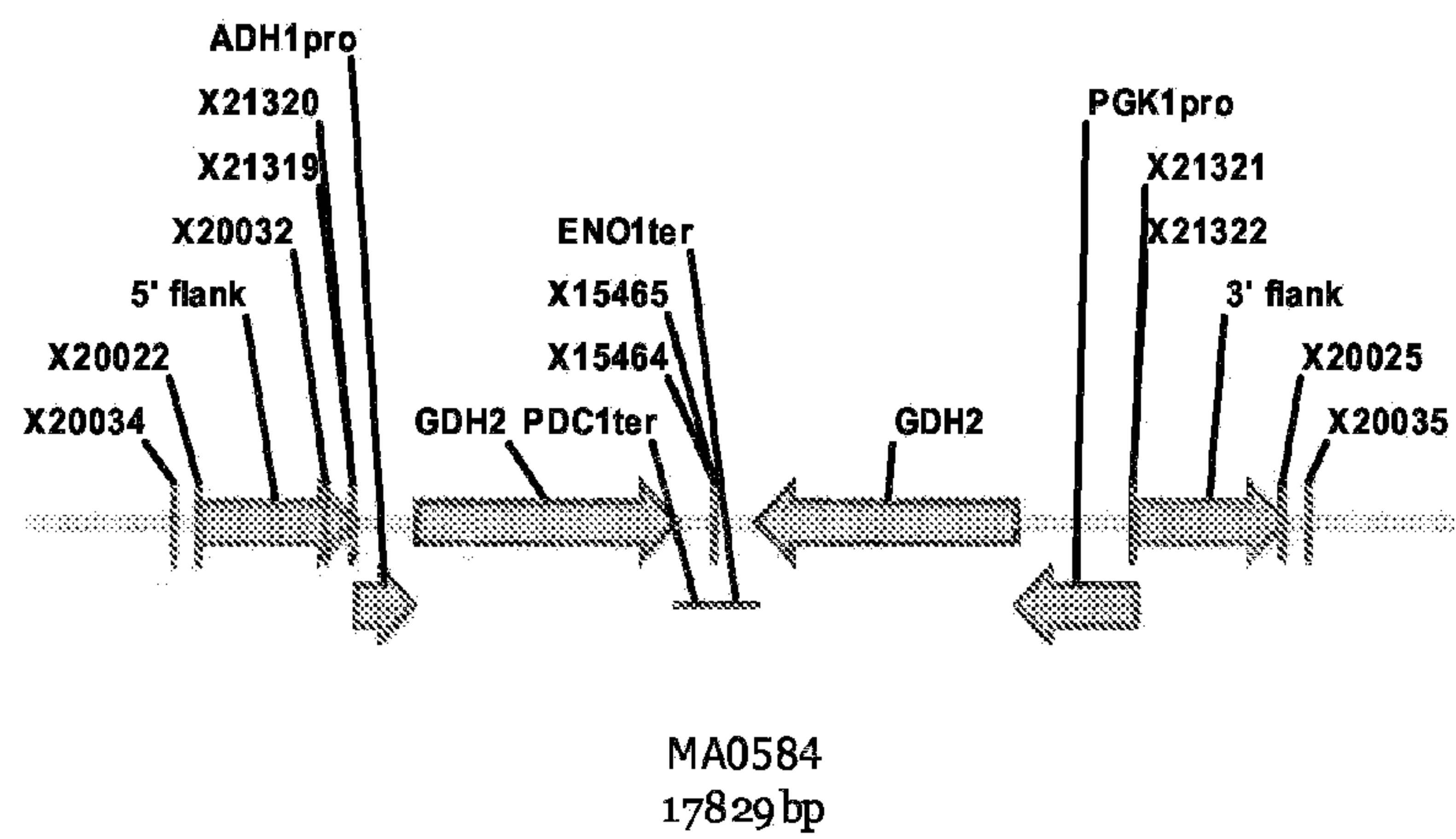


FIGURE 21

MA0585

GLT1/GLN1 over expression at the URE2 locus

MA0585			
Fragment	Primers	Template	Exp size
URE2 5' Flank	X20022/X21320	M2390 gDNA	1968bp
ADH1pro-GLTI-PDC1ter	X21319/X15465	pMU2911	2363bp
PGKpro-GLN1-ENO1ter	X15464/X21322	pMU2913	8442bp
URE2 3' Flank	X21321/X20025	M2390 gDNA	1885bp

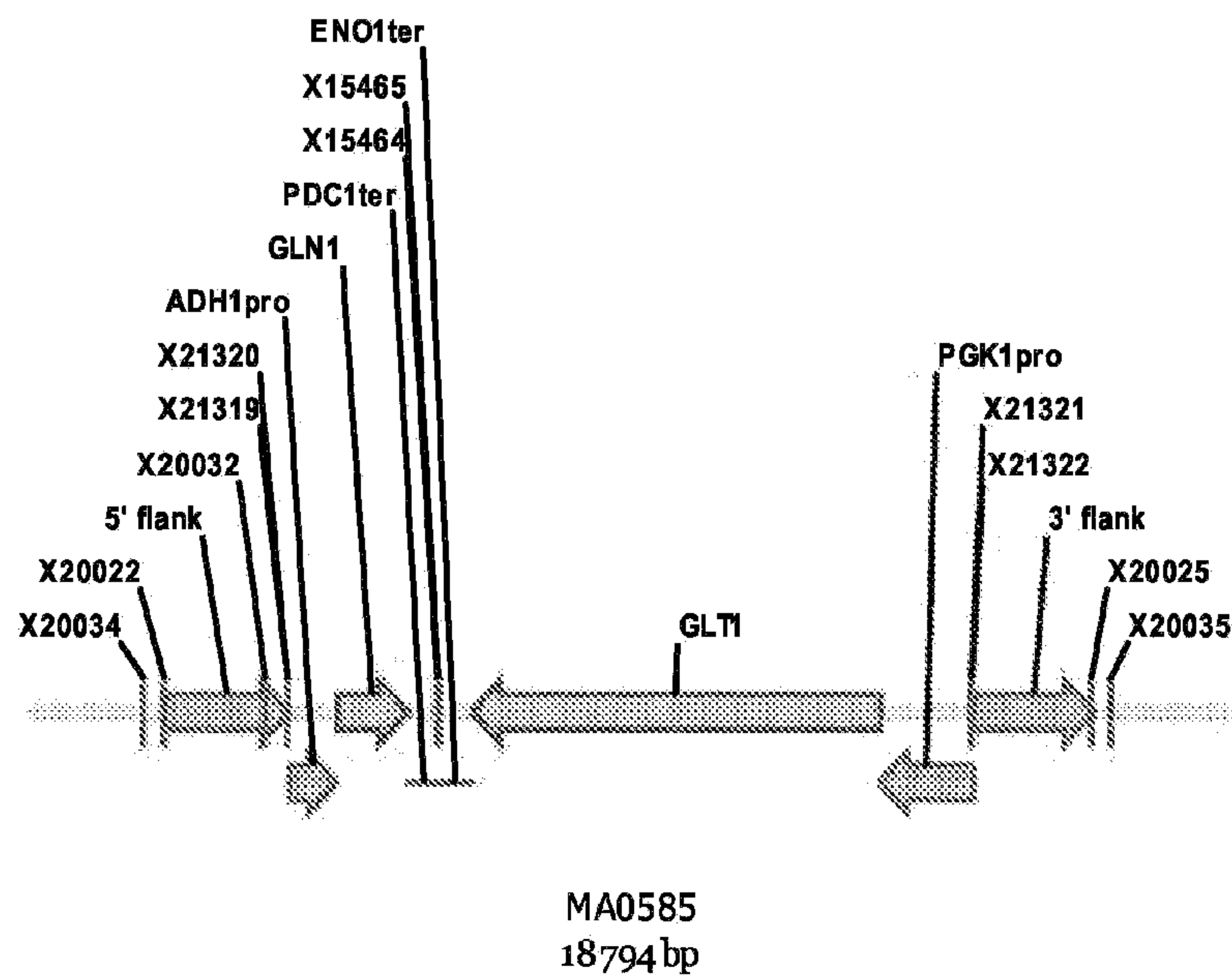


FIGURE 22

MA0617

AUA1 marked deletion

MA0617			
Fragment	Primers	Template	Expected Size
AUA1 5' Flank	X20620/X20621	M2390 gDNA	1947bp
AGTEFpro-kan/nat/tdk-HXT2pro	X20630/X20631	pMU2873,pMU2879	3820bp and 3583bp
AUA1 3' Flank	X20622/X20623	M2390 gDNA	2015bp

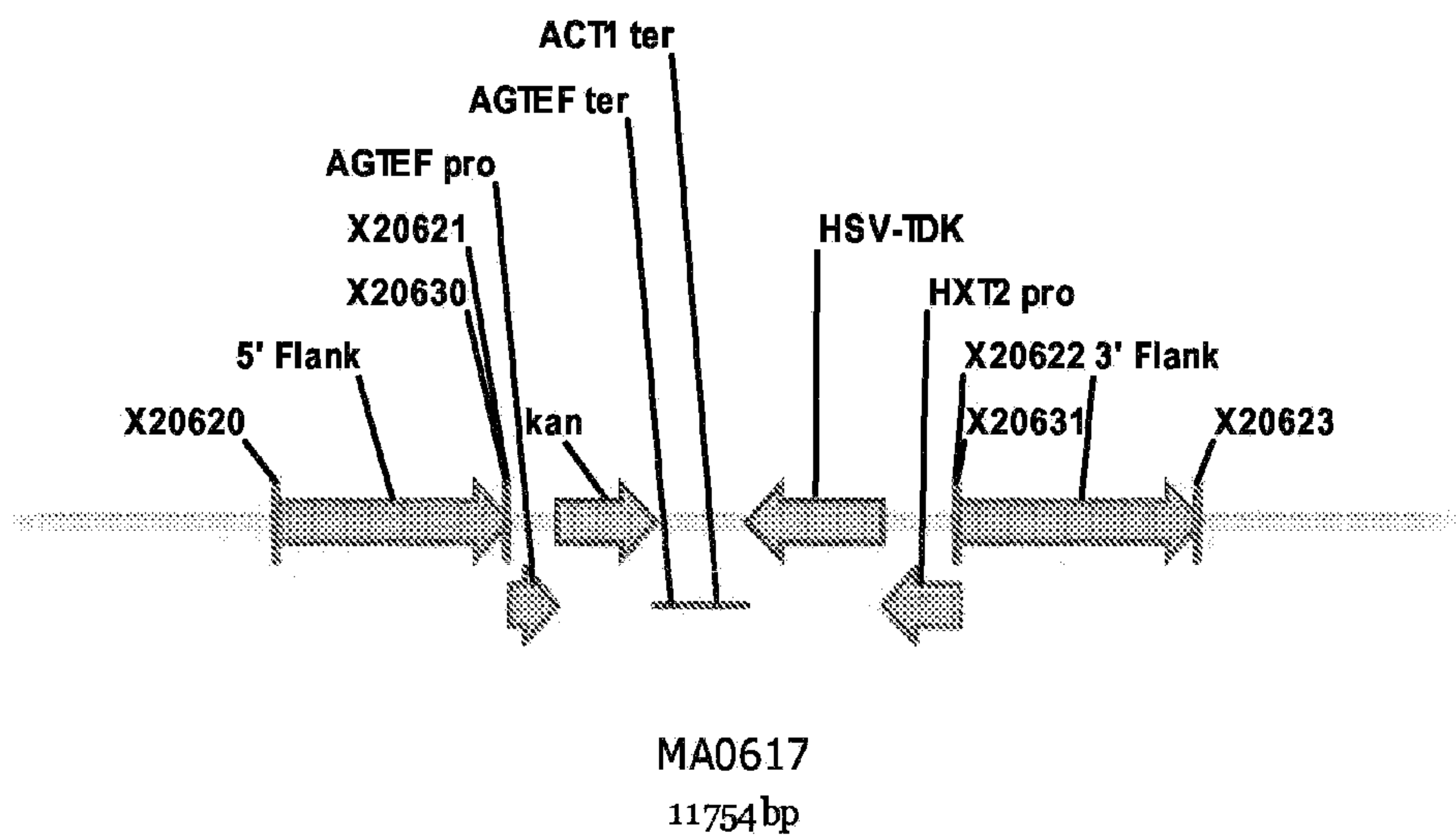


FIGURE 23

MA0617.1

AUA1 clean deletion

MA0617.1			
Fragment	Primers	Template	Expected Size
AUA1 5' Flank	X20620/X20633	M2390 gDNA	1947bp
AUA1 3' Flank	X20632/X20623	M2390 gDNA	2015bp

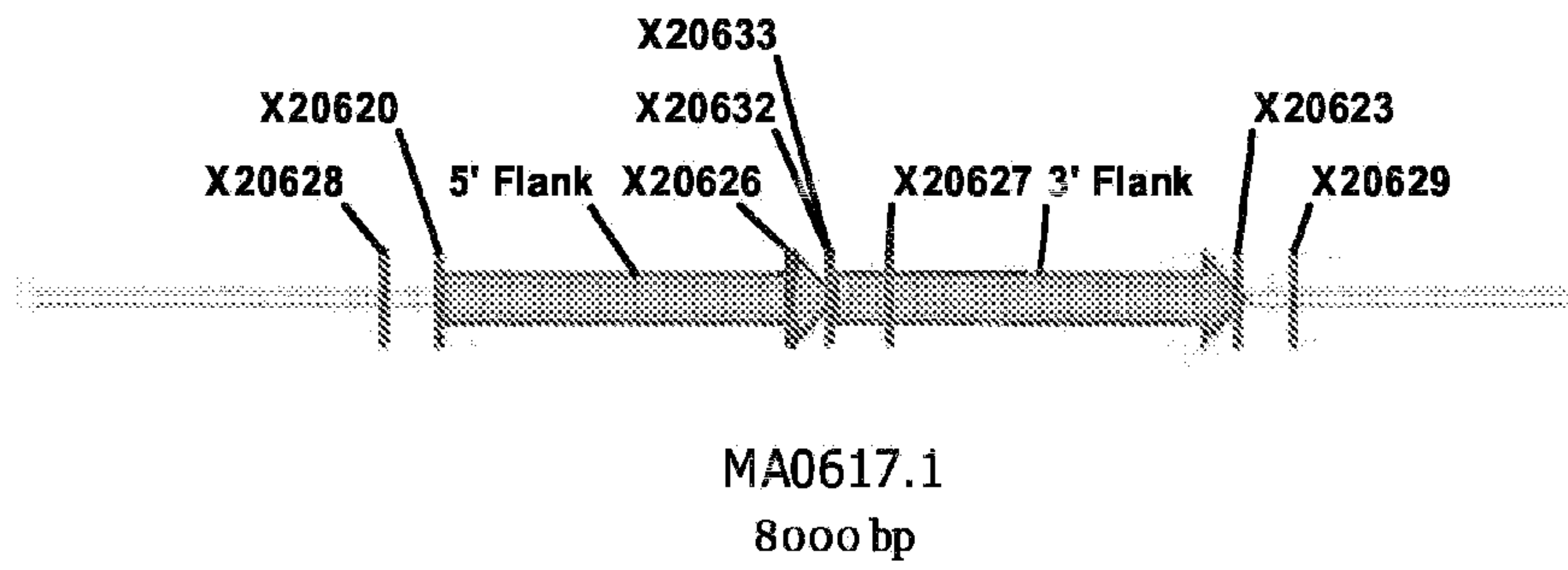
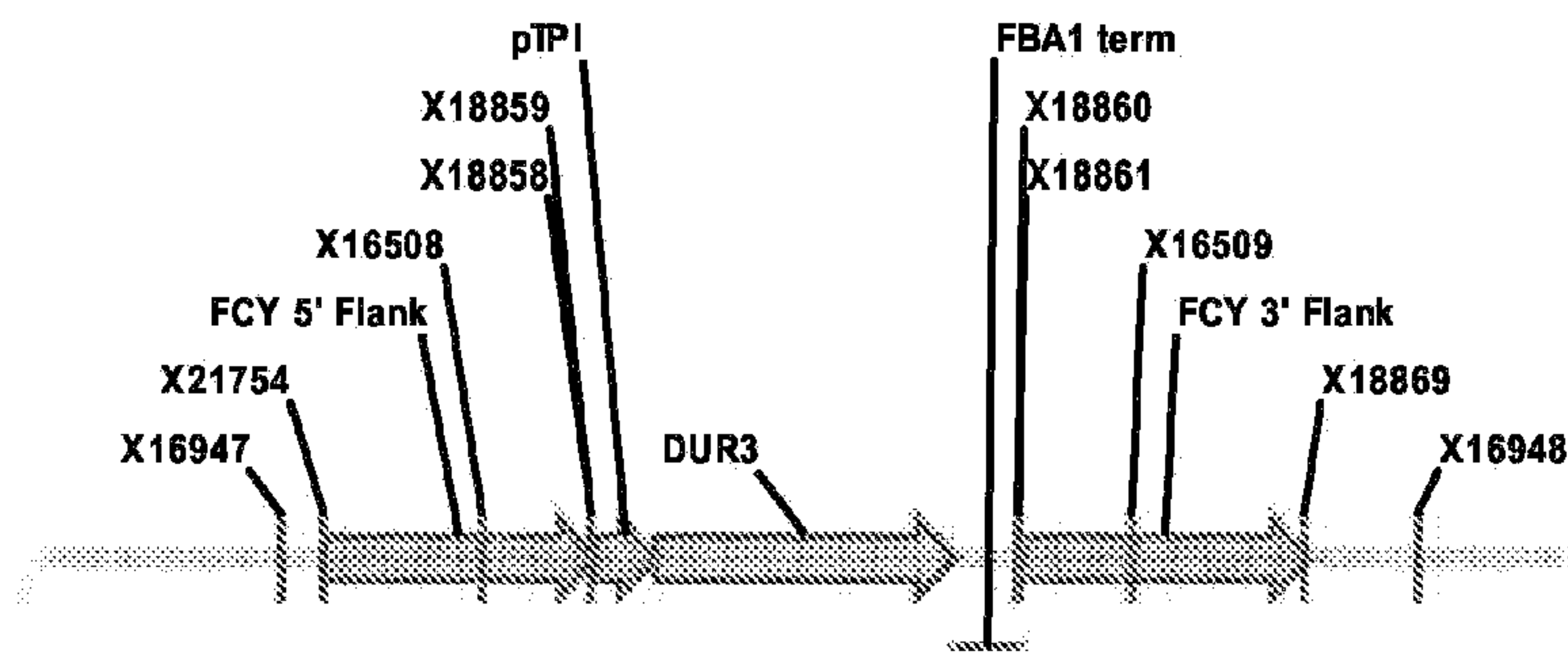


FIGURE 24

MA0434

DUR3 over expression at FCY1 locus

MA0434	DUR3		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X18859	gDNA	2049bp
TP1pro-DUR3-FBA1ter	X18858/X18861	pMU3471	3157bp
FCY 3' Flank	X18860/X18869	gDNA	2166bp



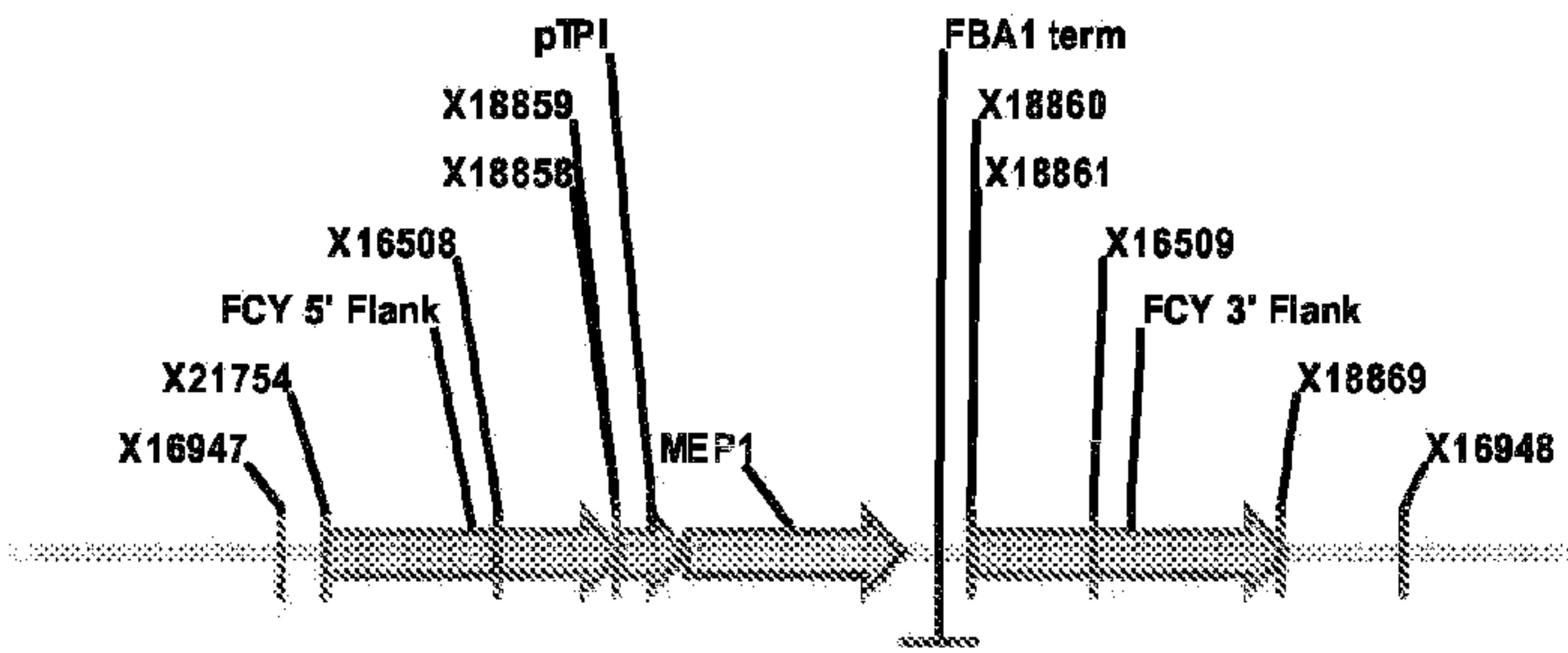
MA0434 with DUR3
11157bp

FIGURE 25

MA0434.2

MEP1 over expression at FCY1 locus

MA0434.2	MEP1		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X18859	gDNA	2049bp
TP1pro-MEP1-FBA1ter	X18858/X18861	pMU3472	2428bp
FCY 3' Flank	X18860/X18869	gDNA	2166bp



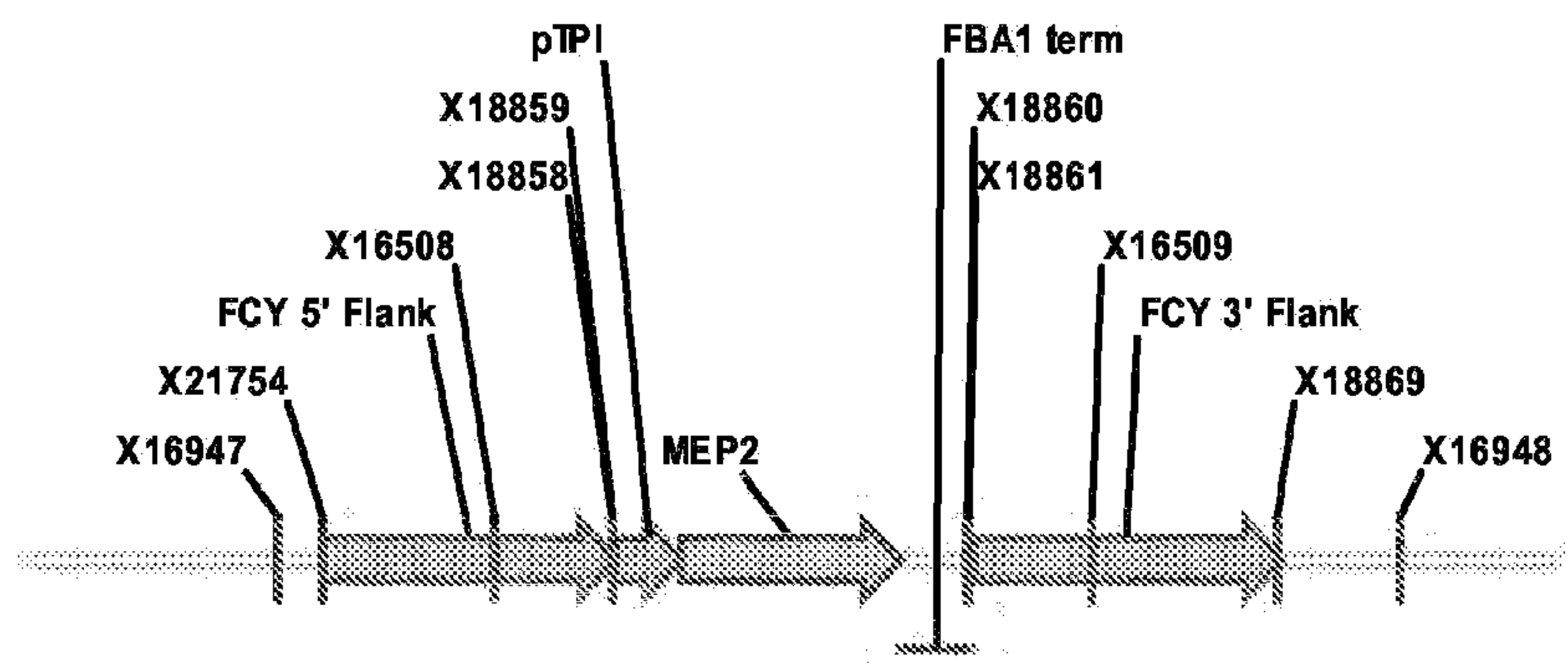
MA0434.2 with MEP1
10428 bp

FIGURE 26

MA0434.3

MEP2 over expression at FCY1 locus

MA0434.3	MEP2		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X18859	gDNA	2049bp
TP1pro-MEP2-FBA1ter	X18858/X18861	pMU3473	2449bp
FCY 3' Flank	X18860/X18869	gDNA	2166bp



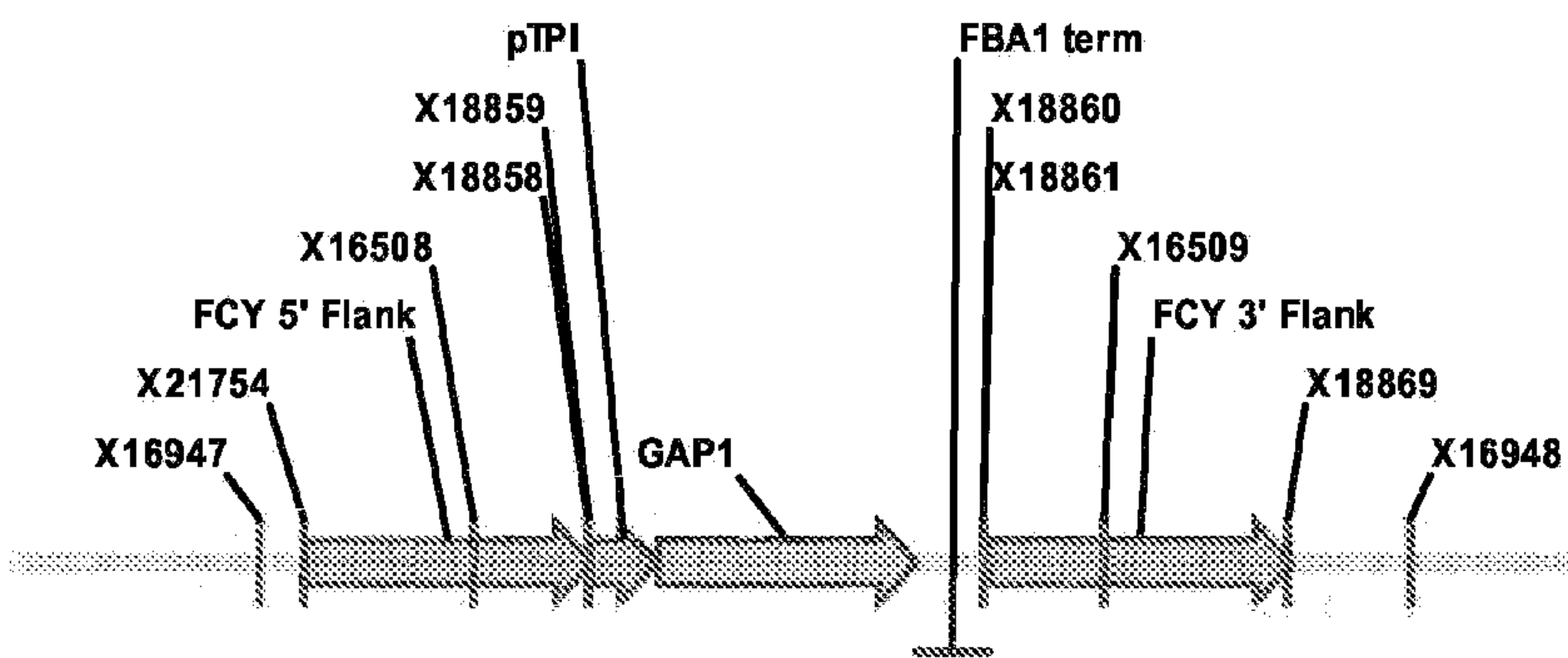
MA0434.3 with MEP2
10449 bp

FIGURE 27

MA0434.4

GAP1 over expression at FCY1 locus

MA0434.4	GAP1		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X18859	gDNA	2049bp
TP1pro-GAP1-FBA1ter	X18858/X18861	pMU3475	2758bp
FCY 3' Flank	X18860/X18869	gDNA	2166bp



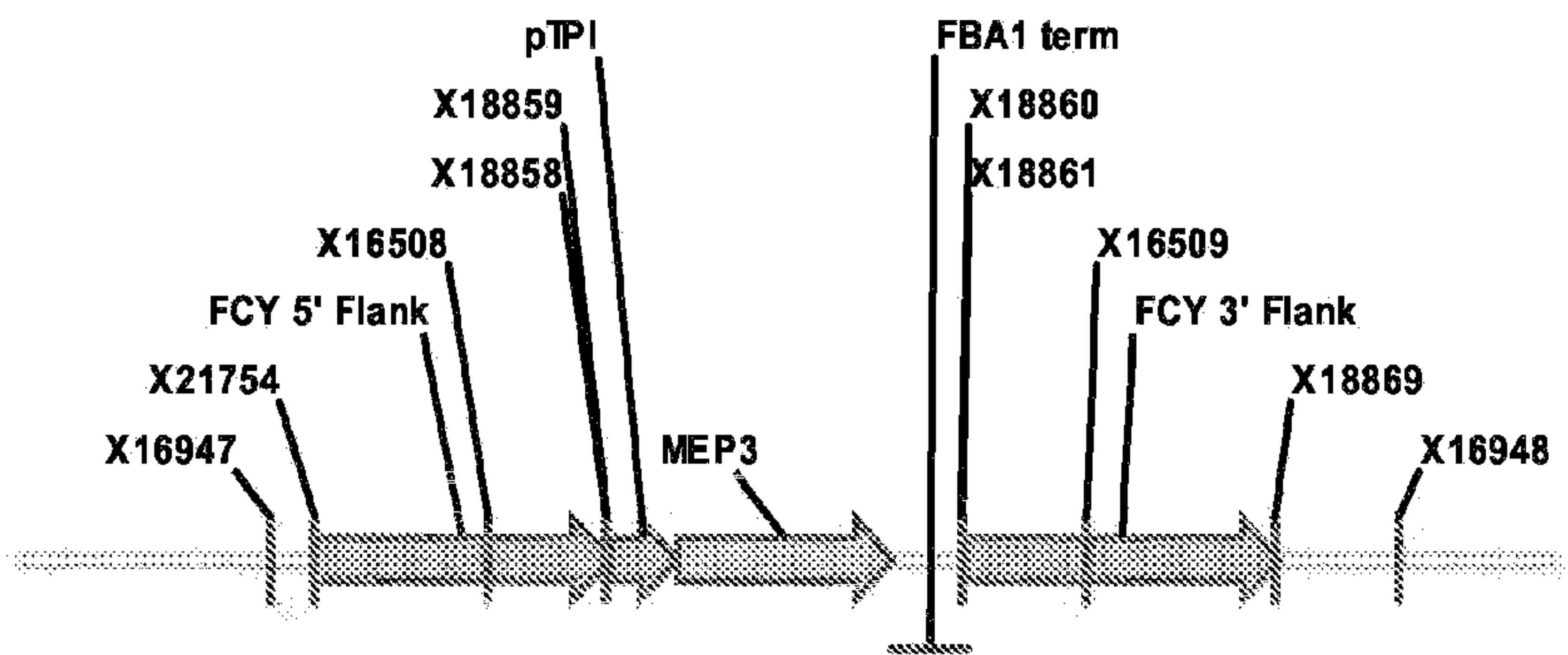
MA0434.4 with GAP1
10758 bp

FIGURE 28

MA0434.5

MEP3 over expression at FCY1 locus

MA0434.5	MEP3		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X18859	gDNA	2049bp
TP1pro-MEP3-FBA1ter	X18858/X18861	pMU3607	2420bp
FCY 3' Flank	X18860/X18869	gDNA	2166bp



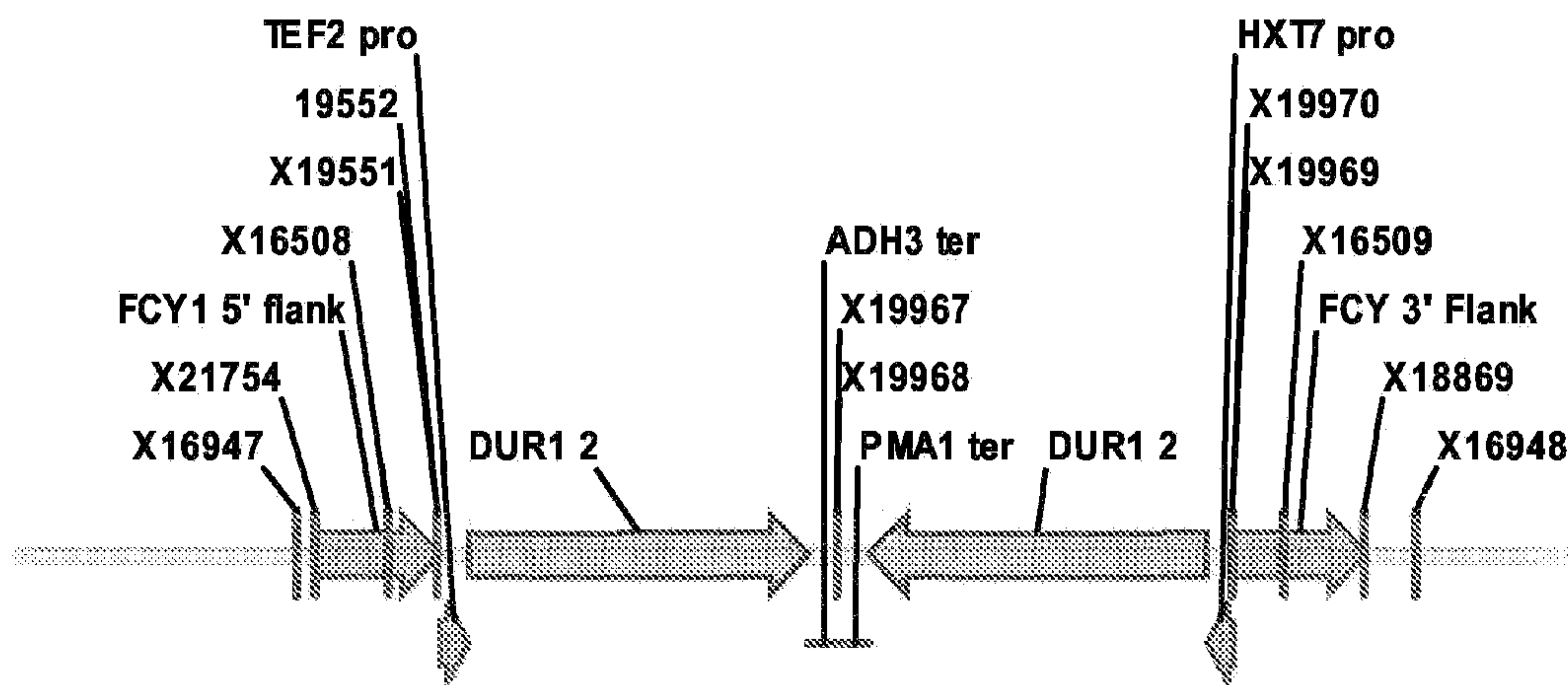
MA0434.5 with MEP3
10419 bp

FIGURE 29

MA0454.14

DUR1,2 over expression at FCY1 locus

MA0454.14			
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X19552	gDNA	2018bp
pTEF2/ADH3t	X19551/X19968	pMU3409	6508bp
pHXT7/PMA1trc	X19967/X19969	pMU3410	6458bp
FCY3' Flank	X19970/X18869	gDNA	2159bp



MA0454.14 with DUR1,2
24889bp

FIGURE 30

MA0464

DUR3 over expression at FCY1 locus

MA0464	DUR3		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X19552	M2390 gDNA	2018bp
TEF2pro-DUR3-ADH3ter	X19551/X20043	pMU3464	3208bp
FCY 3' Flank	X20044/X18869	M2390 gDNA	2133bp

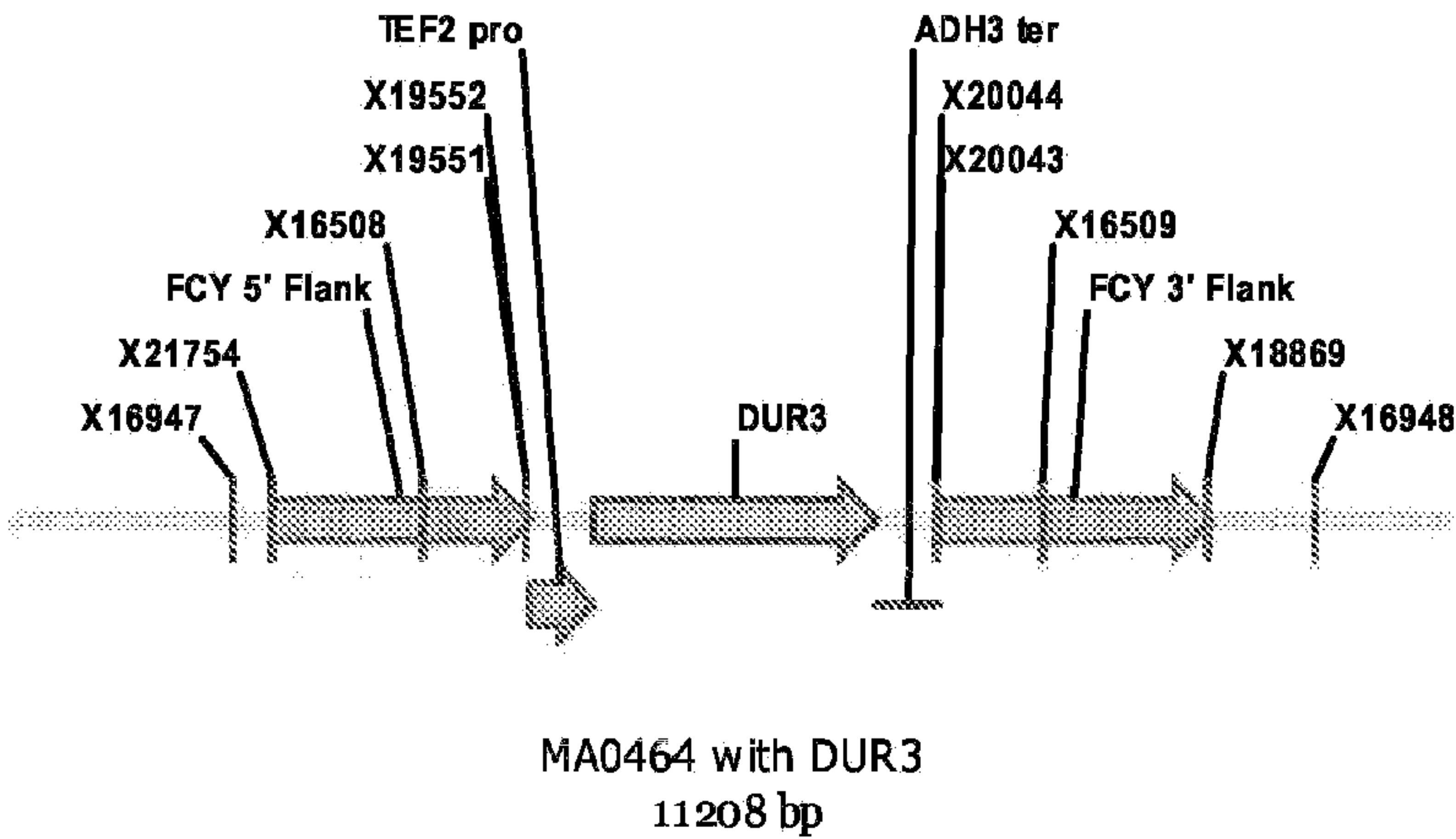


FIGURE 31

MA0464.1

DUR1,2 over expression at FCY1 locus

MA0464.1	DUR1,2		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X19552	M2390 gDNA	2049bp
TEF2pro-DUR1,2-ADH3ter	X19551/X20043	pMU3409	6508bp
FCY 3' Flank	X20044/X18869	M2390 gDNA	2166bp

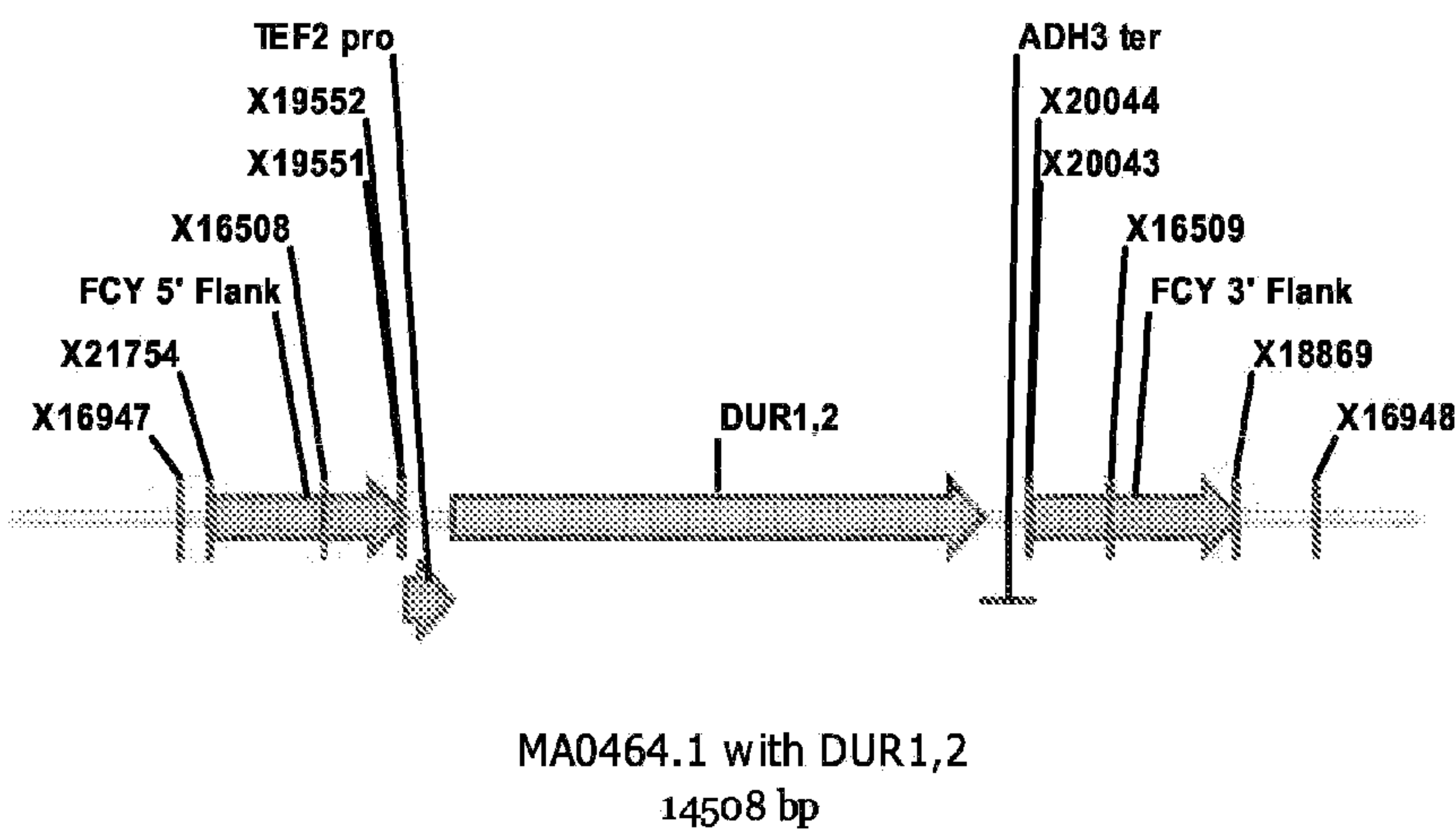


FIGURE 32

MA0464.2

MEP1 over expression at FCY1 locus

MA0464.2	MEP1		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X19552	M2390 gDNA	2049bp
TEF2pro-MEP1-ADH3ter	X19551/X20043	pMU3465	2479bp
FCY 3' Flank	X20044/X18869	M2390 gDNA	2166bp

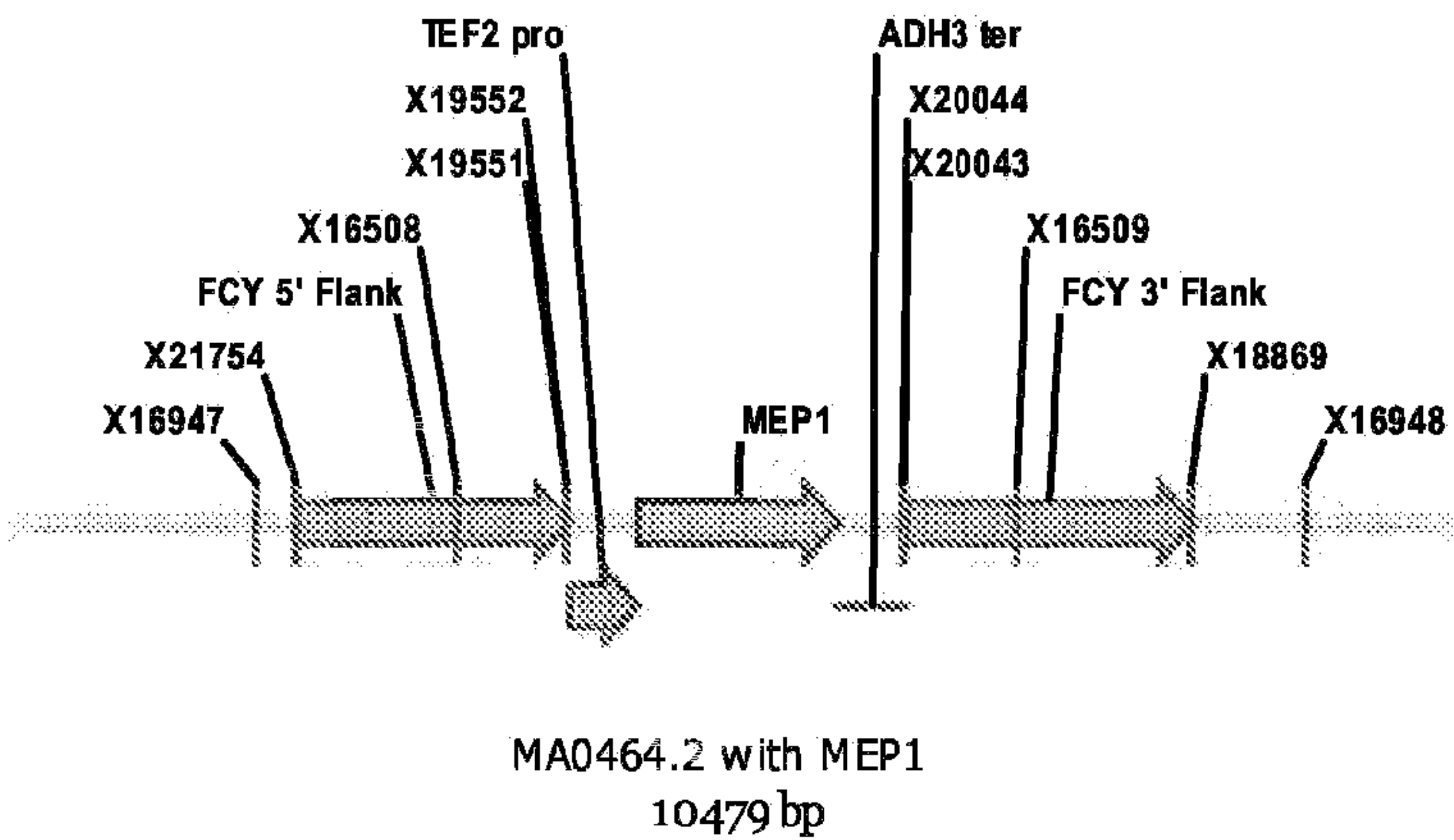


FIGURE 33

MA0464.3

MEP2 over expression at FCY1 locus

MA0464.3	MEP2		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X19552	M2390 gDNA	2049bp
TEF2pro-MEP2-ADH3ter	X19551/X20043	pMU3466	2500bp
FCY 3' Flank	X20044/X18869	M2390 gDNA	2166bp

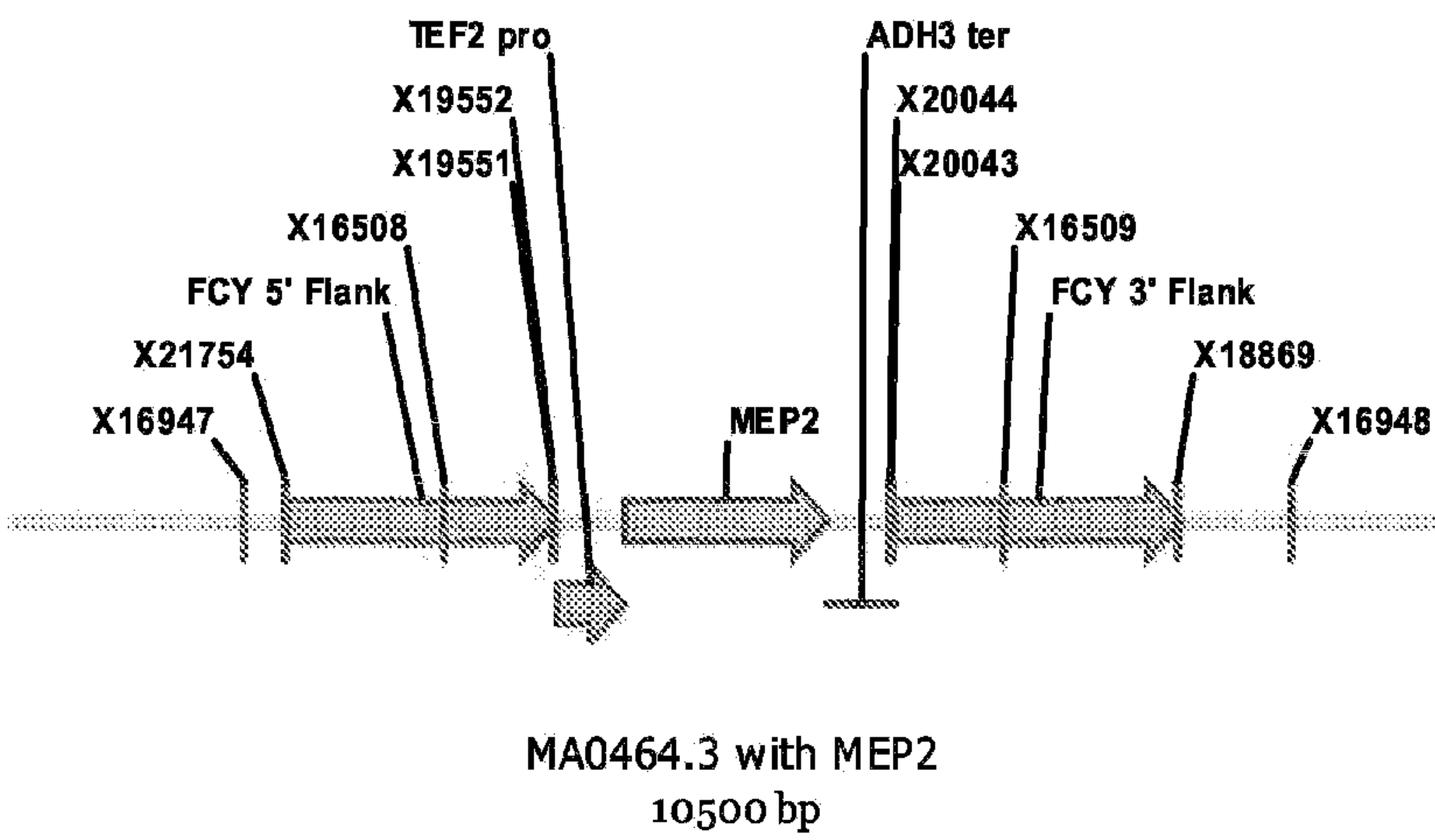


FIGURE 34

MA0464.4

GAP1 over expression at FCY1 locus

MA0464.4	GAP1		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X19552	M2390 gDNA	2049bp
TEF2pro-GAP1-ADH3ter	X19551/X20043	pMU3468	2809bp
FCY 3' Flank	X20044/X18869	M2390 gDNA	2166bp

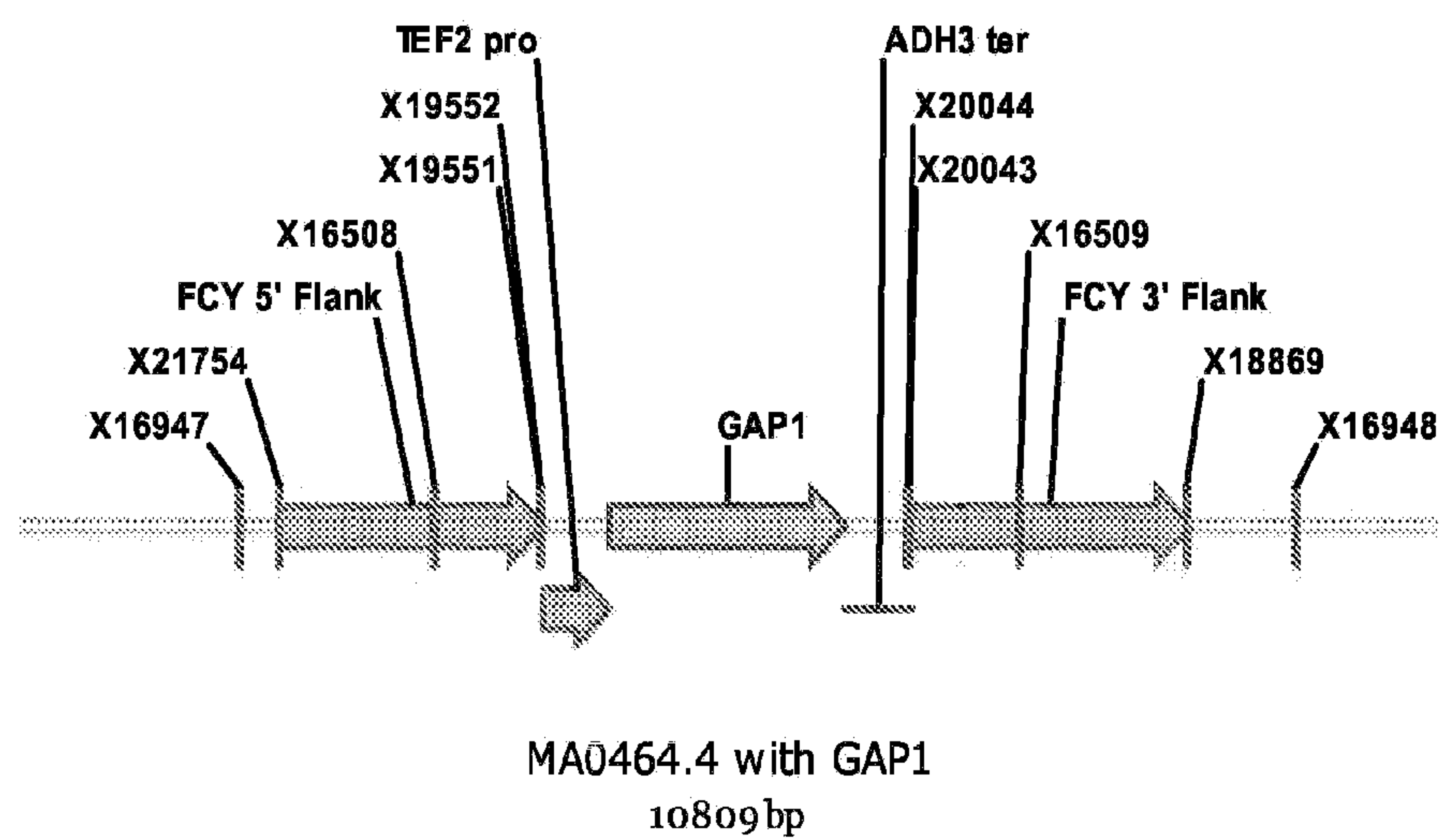


FIGURE 35

MA0464.5

MEP3 over expression at FCY1 locus

MA0464.5	MEP3		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X19552	M2390 gDNA	2049bp
TEF2pro-DUR1,2-ADH3ter	X19551/X20043	pMU3606	6508bp
FCY 3' Flank	X20044/X18869	M2390 gDNA	2166bp

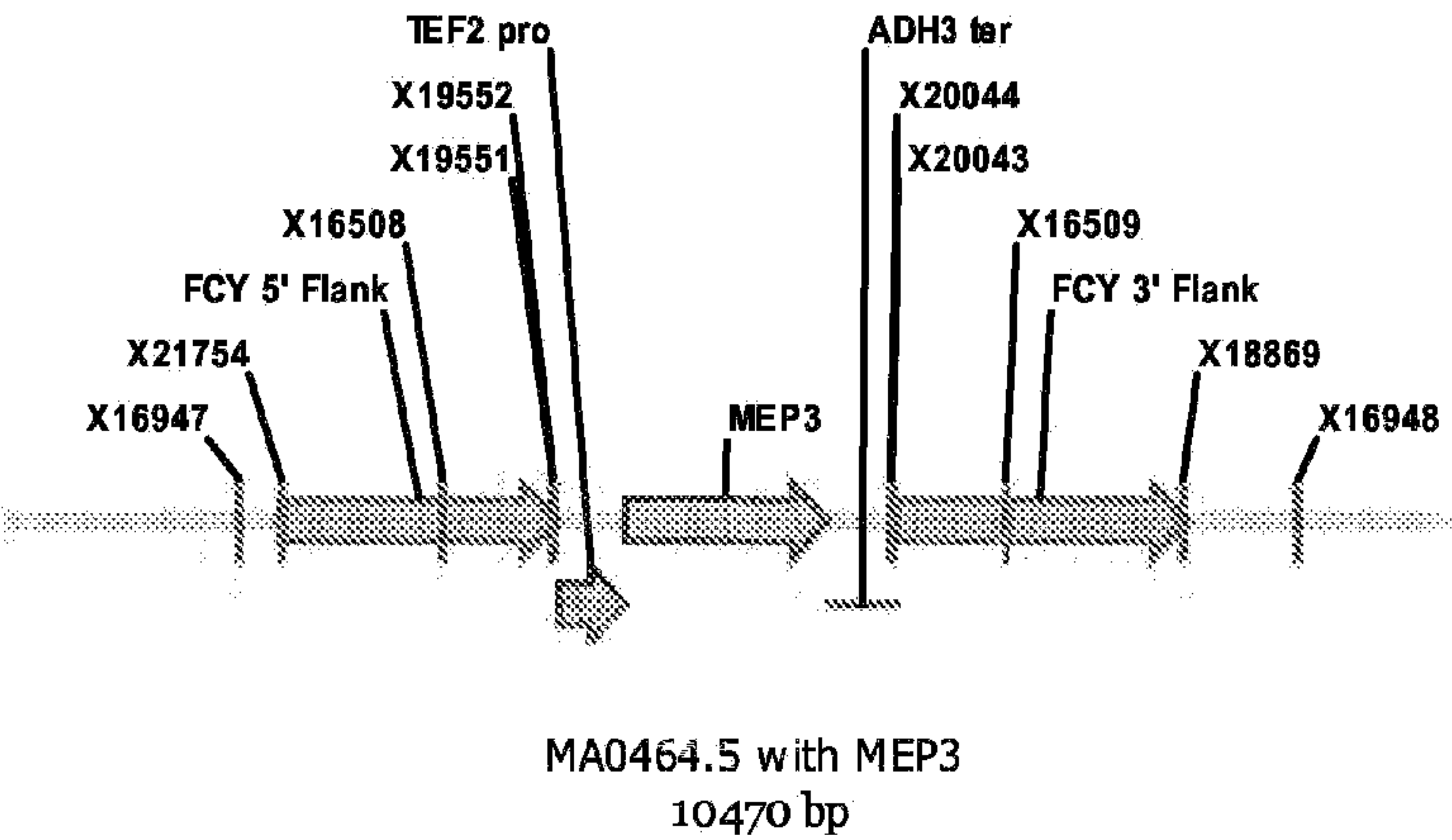


FIGURE 36

MA0465.1

DUR1,2 over expression at FCY1

MA0465.1	DUR1,2		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X20283	M2390 gDNA	2049bp
HXT7pro-DUR1,2-PMA1ter	X20282/X20285	pMU3410	6458bp
FCY 3' Flank	X20284/X18869	M2390 gDNA	2166bp

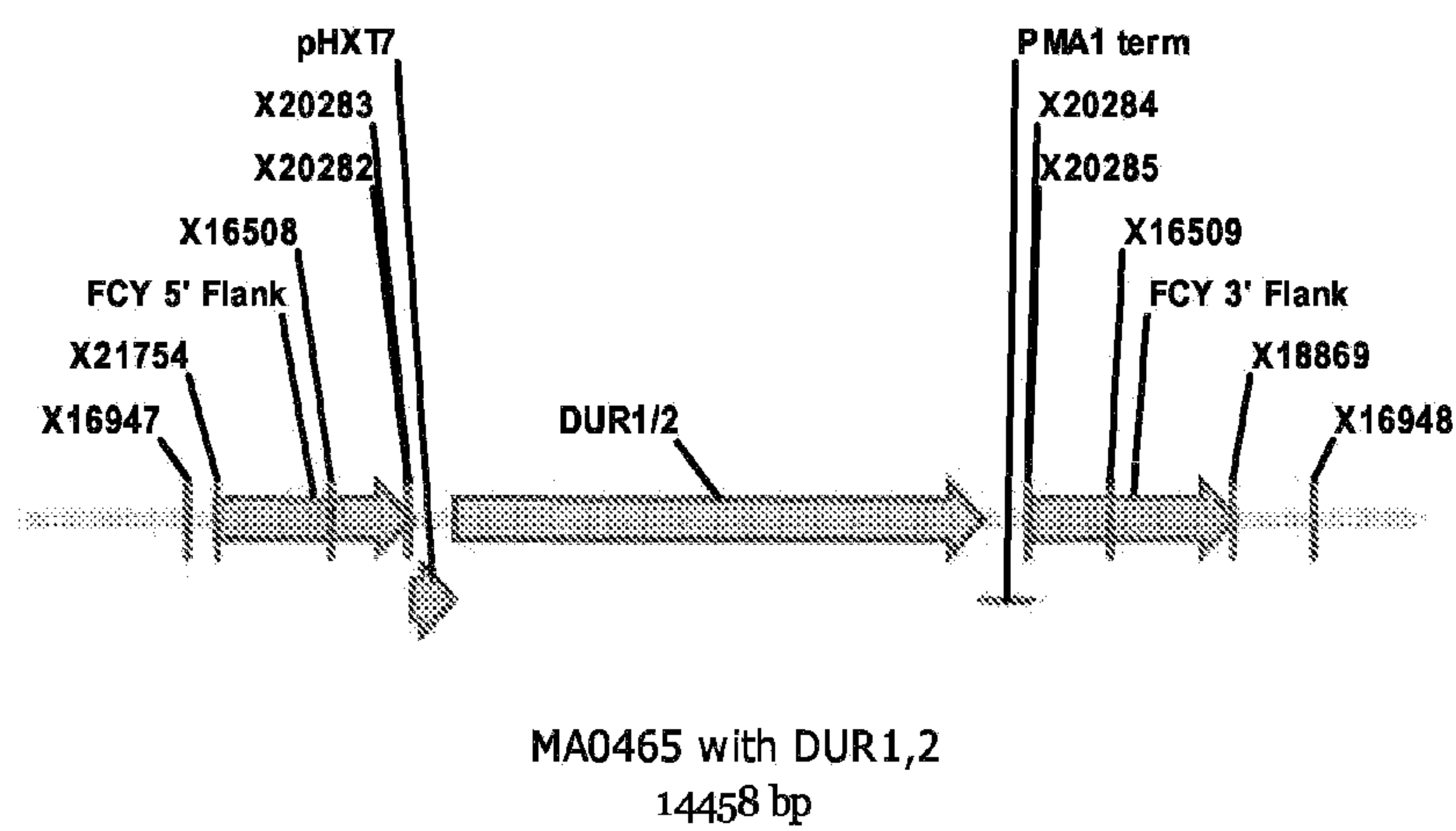


FIGURE 37

MA0467

DUR3 over expression at FCY1 locus

MA0467	DUR3		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X21736	M2390 gDNA	2049bp
ADH1pro-DUR3-PDC1ter	X21735/X18847	pMU3459	3458bp
FCY 3' Flank	X18846/X18869	M2390 gDNA	2166bp

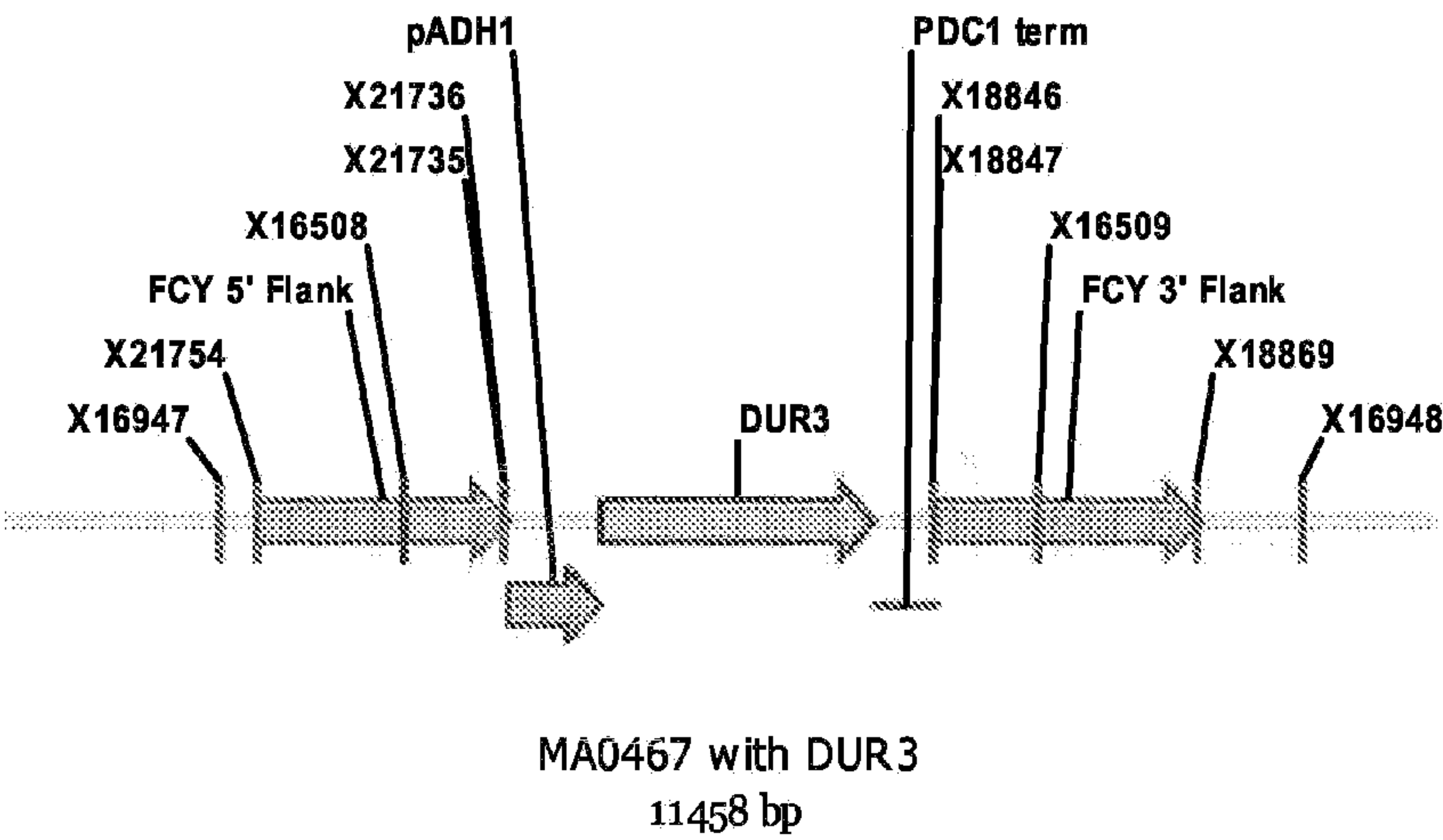


FIGURE 38

MA0467.1

DUR1,2 over expression at FCY1 locus

MA0467.1	DUR1,2		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X21736	M2390 gDNA	2049bp
ADH1pro-DUR1,2-PDC1ter	X21735/X18847	pMU3411	6758bp
FCY 3' Flank	X18846/X18869	M2390 gDNA	2166bp

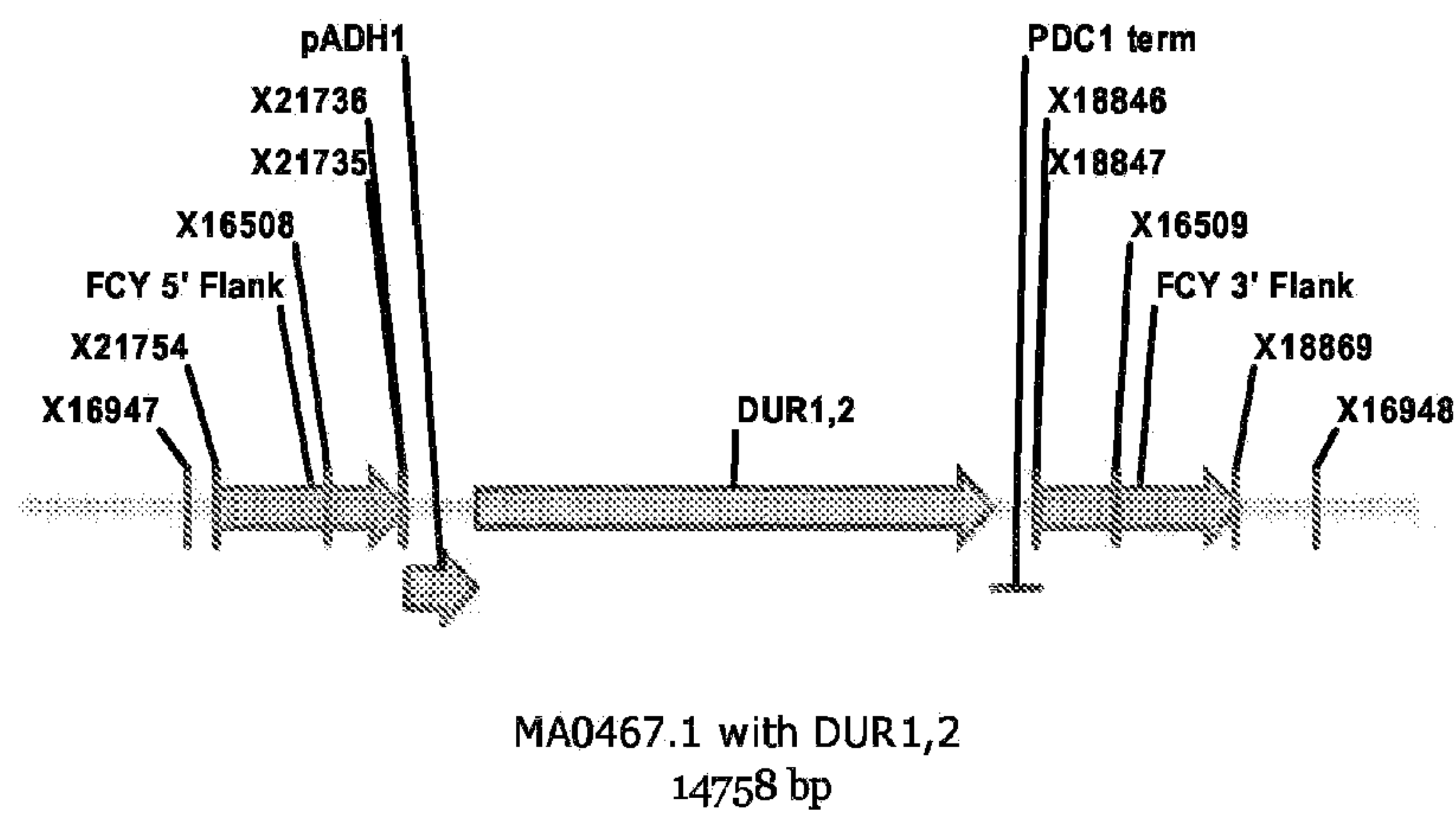


FIGURE 39

MA0467.2

MEP1 over expression at FCY1 locus

MA0467.2	MEP1		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X21736	M2390 gDNA	2049bp
ADH1pro-MEP1-PDC1ter	X21735/X18847	pMU3460	2729bp
FCY 3' Flank	X18846/X18869	M2390 gDNA	2166bp

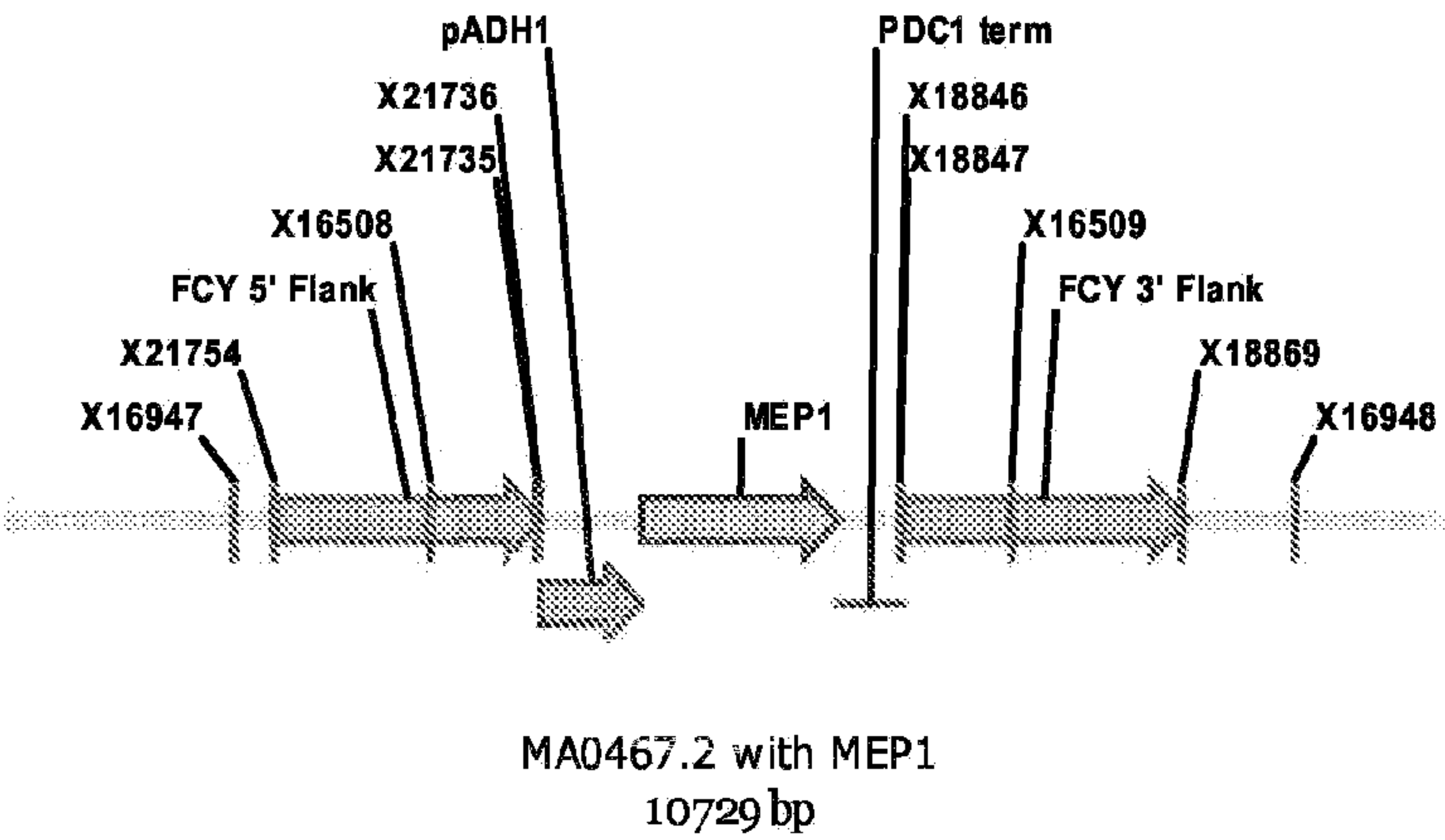


FIGURE 40

MA0467.3

MEP2 over expression at FCY1 locus

MA0467.3	MEP2		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X21736	M2390 gDNA	2049bp
ADH1pro-MEP2-PDC1ter	X21735/X18847	pMU3461	2750bp
FCY 3' Flank	X18846/X18869	M2390 gDNA	2166bp

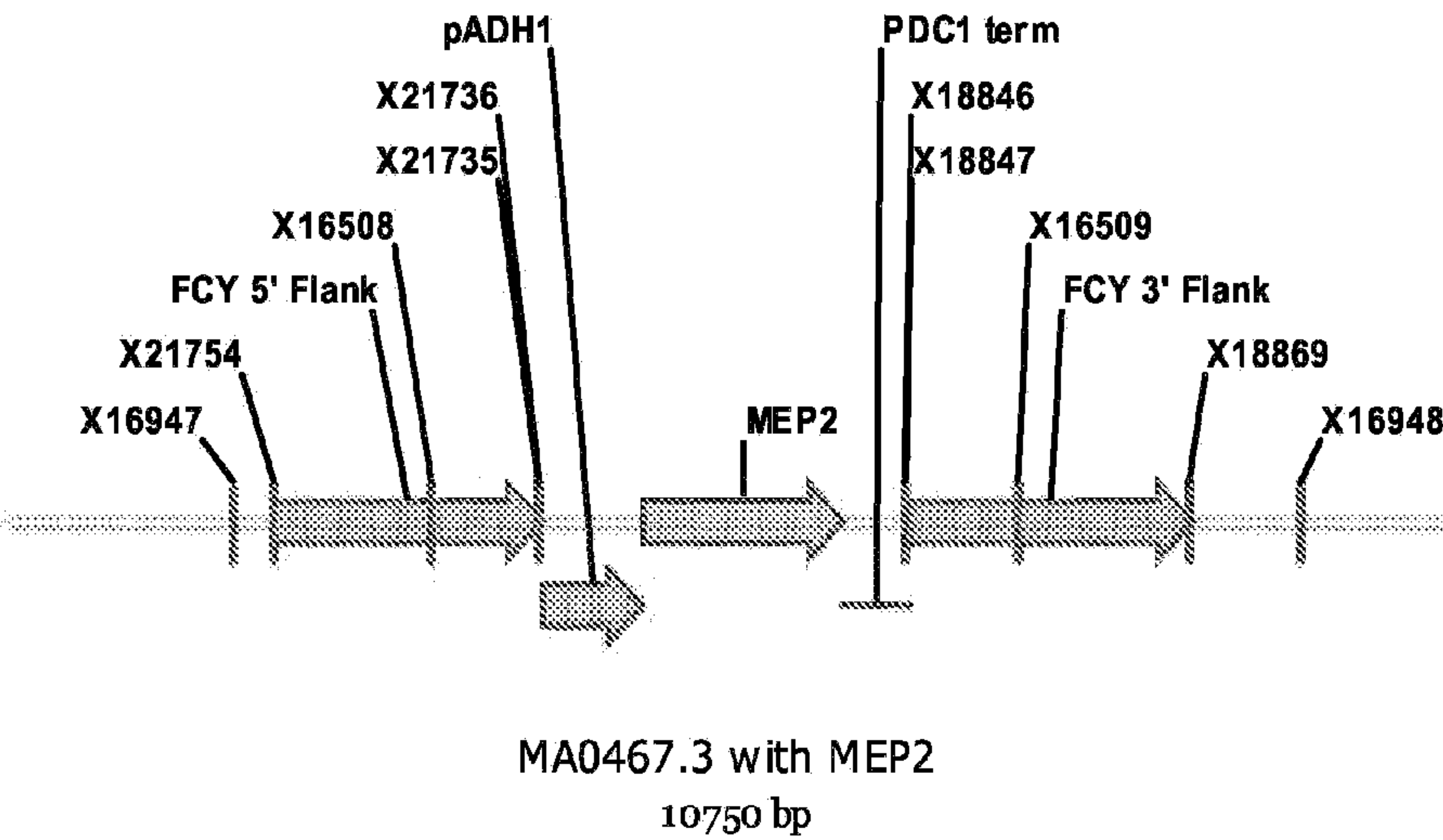


FIGURE 41

MA0467.4

GAP1 over expression at FCY1 locus

MA0467.4	GAP1		
Fragment	Primers	Template	Exp Size
FCY 5' Flank	X21754/X21736	M2390 gDNA	2049bp
ADH1pro-GAP1-PDC1ter	X21735/X18847	pMU3463	3059bp
FCY 3' Flank	X18846/X18869	M2390 gDNA	2166bp

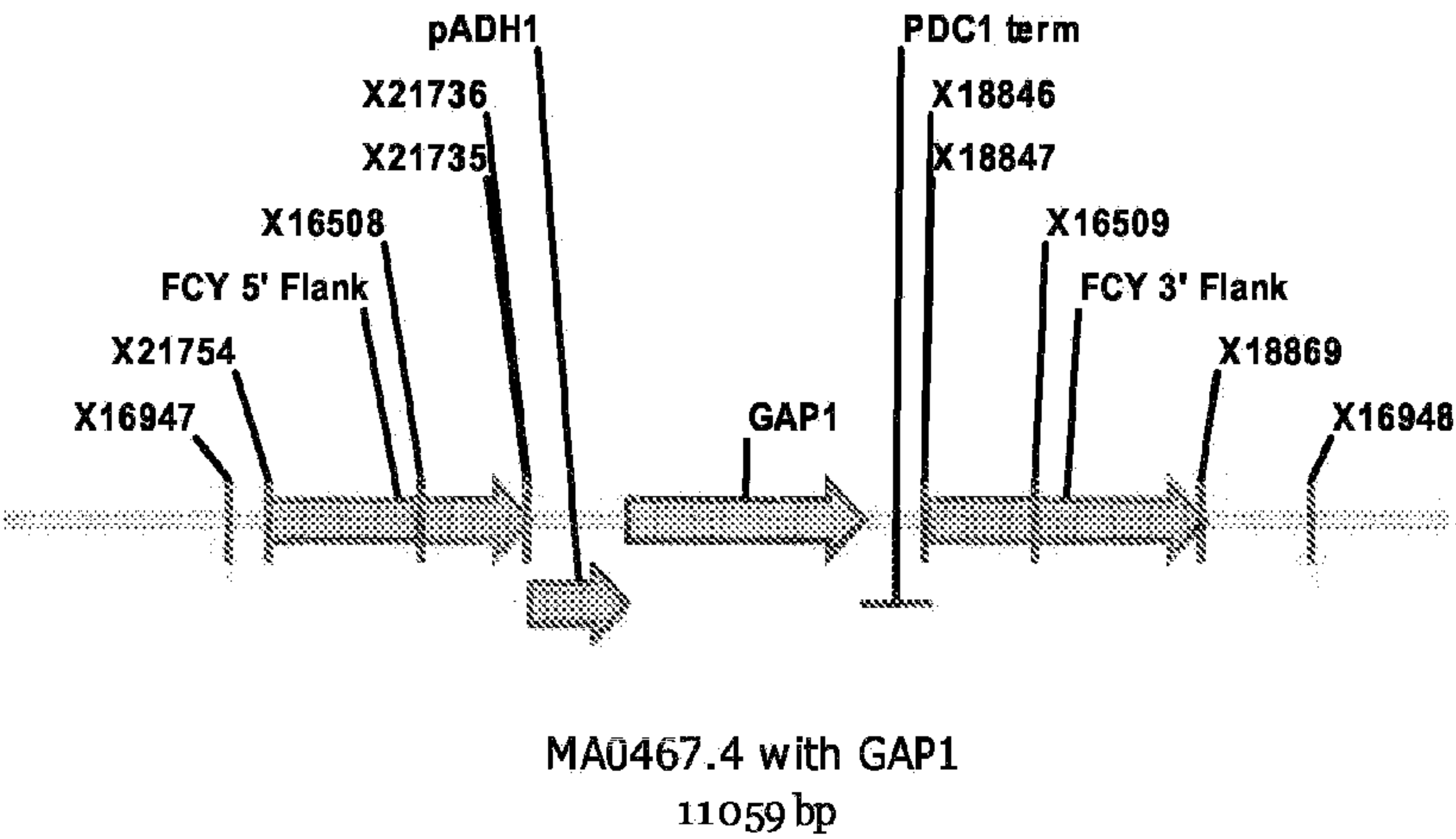


FIGURE 42

MA0881

S. cerevisiae GDH2 over expression at FCY1 locus

MA0881			
Fragment	Primers	Template	Expected Size
5' Flank	X21754/X23408	M2390 gDNA	2049bp
pPGK-GDH2-ENO1t	X23409/X15464	pMU2908	5283bp
pADH-GDH2-PDC1trc	X15465/X18955	pMU2909	4546bp
3' Flank	X19950/X18869	M2390 gDNA	2166bp

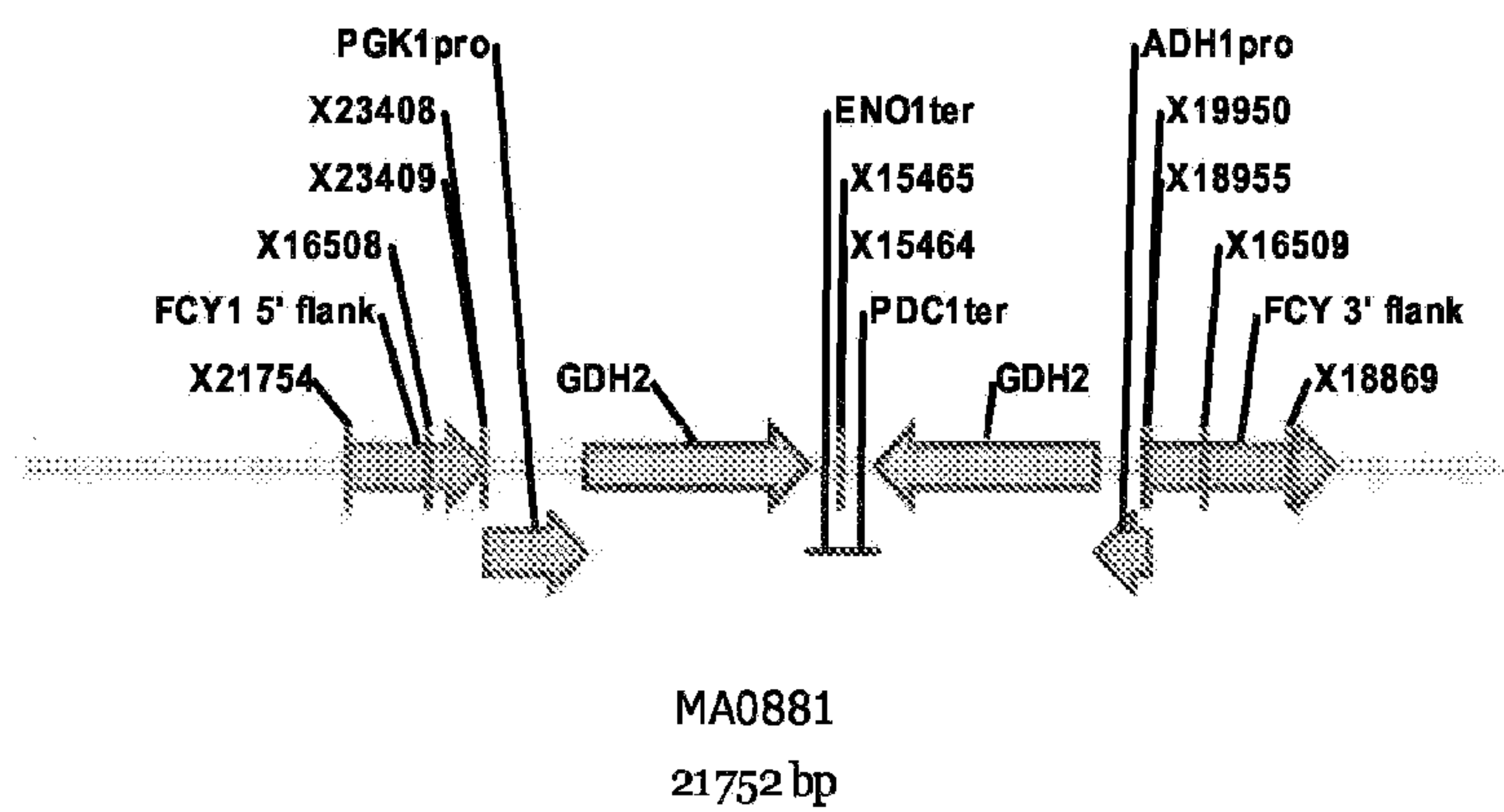
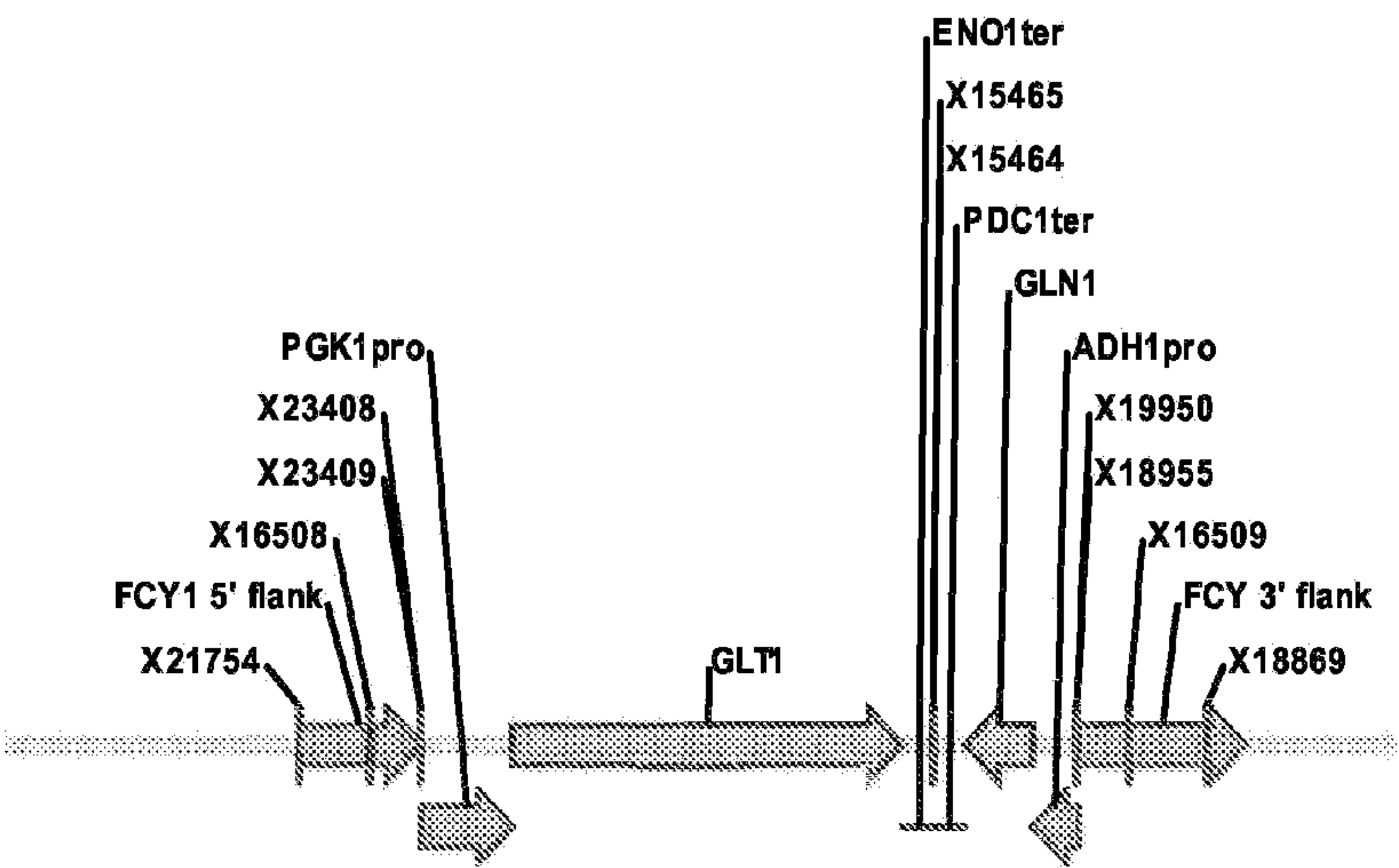


FIGURE 43

MA0881.1

GLT1/GLN1 over expression at FCY1 locus

MA0881.1			
Fragment	Primers	Template	Expected Size
5' Flank	X21754/X23408	M2390 gDNA	2049bp
pPGK-GLT1-ENO1t	X23409/X15464	pMU2913	8442bp
pADH-GLN1-PDC1trc	X15465/X18955	pMU2911	2363bp
3' Flank	X19950/X18869	M2390 gDNA	2166bp



MA0881.1
22745 bp

FIGURE 44

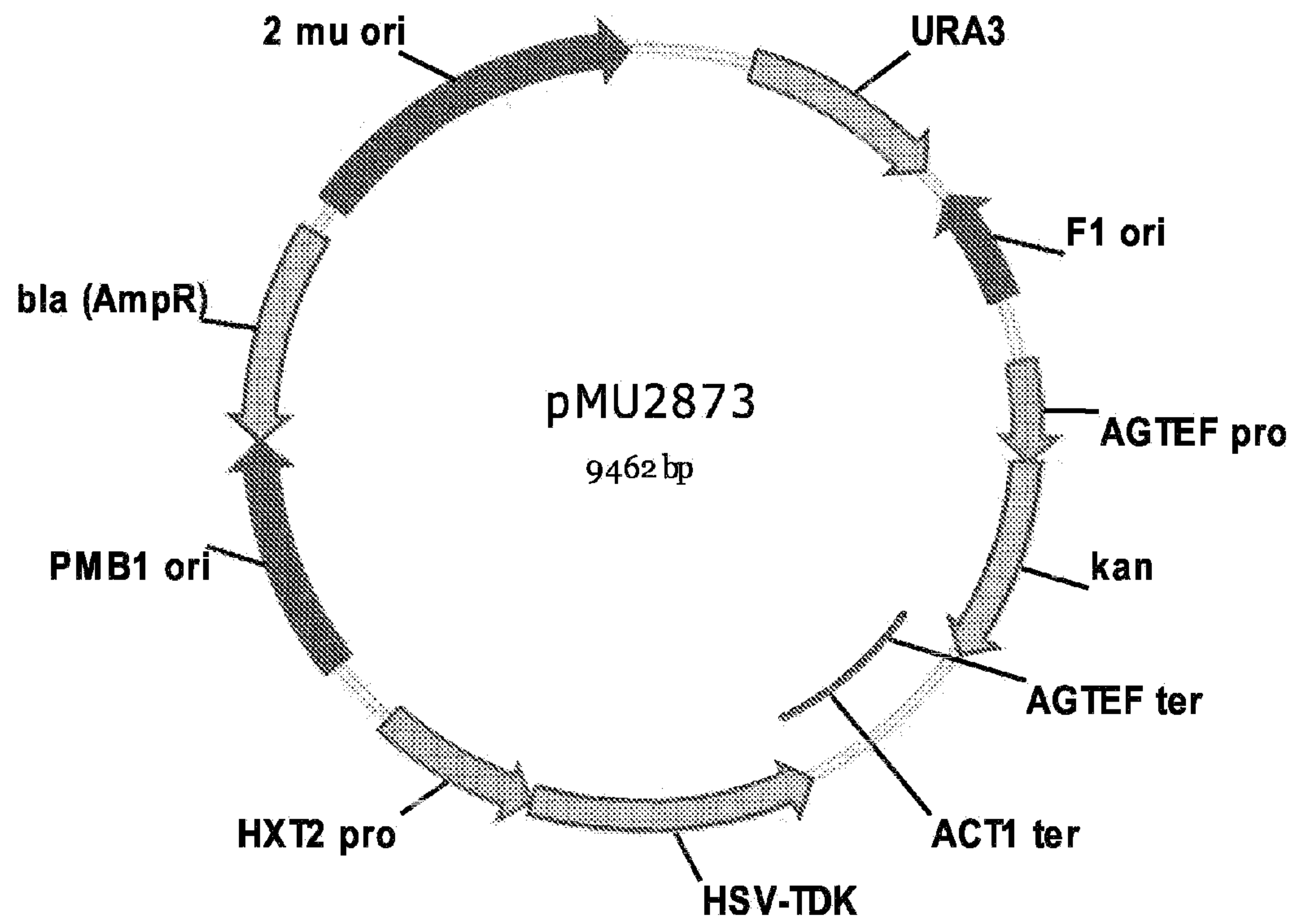


FIGURE 45

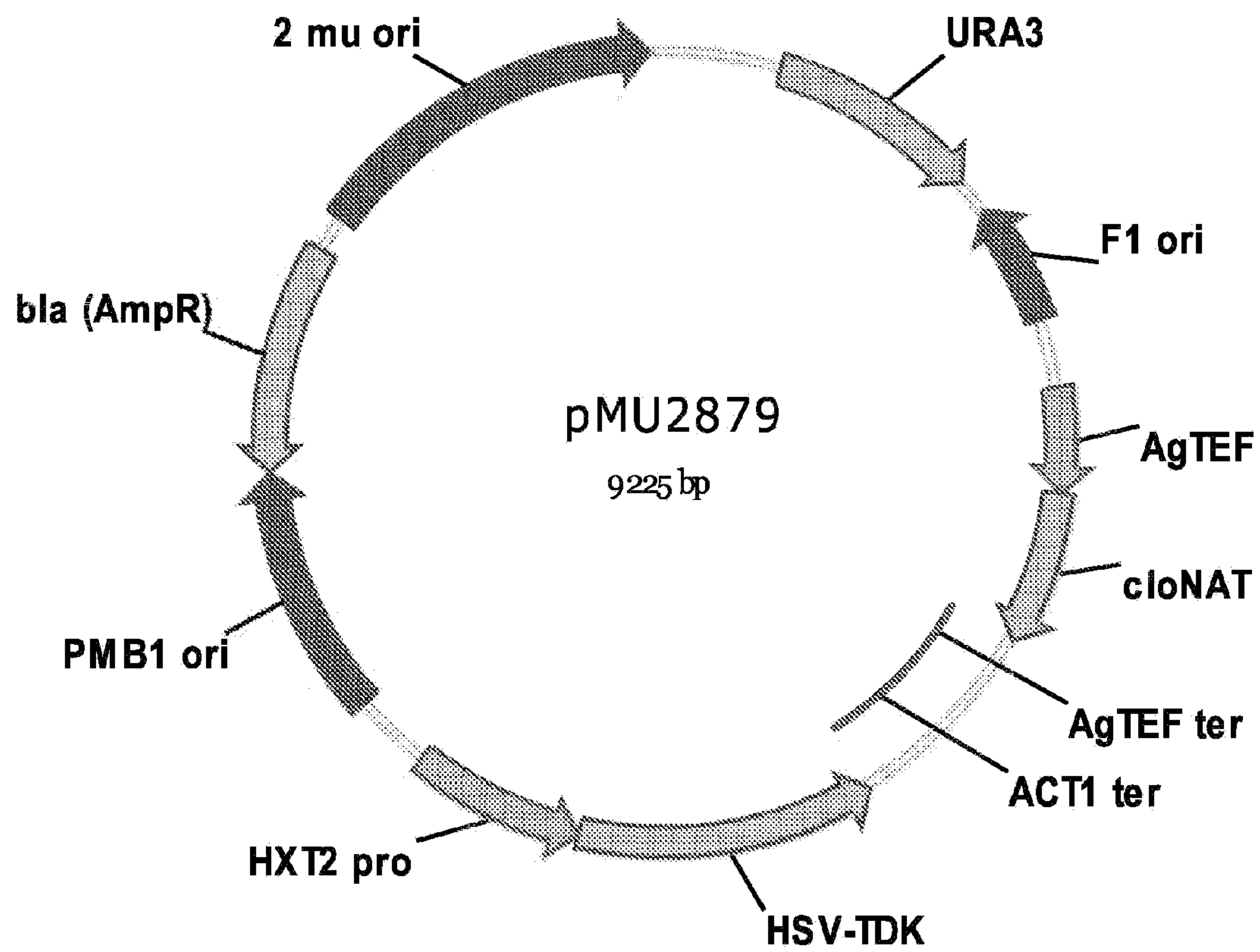


FIGURE 46

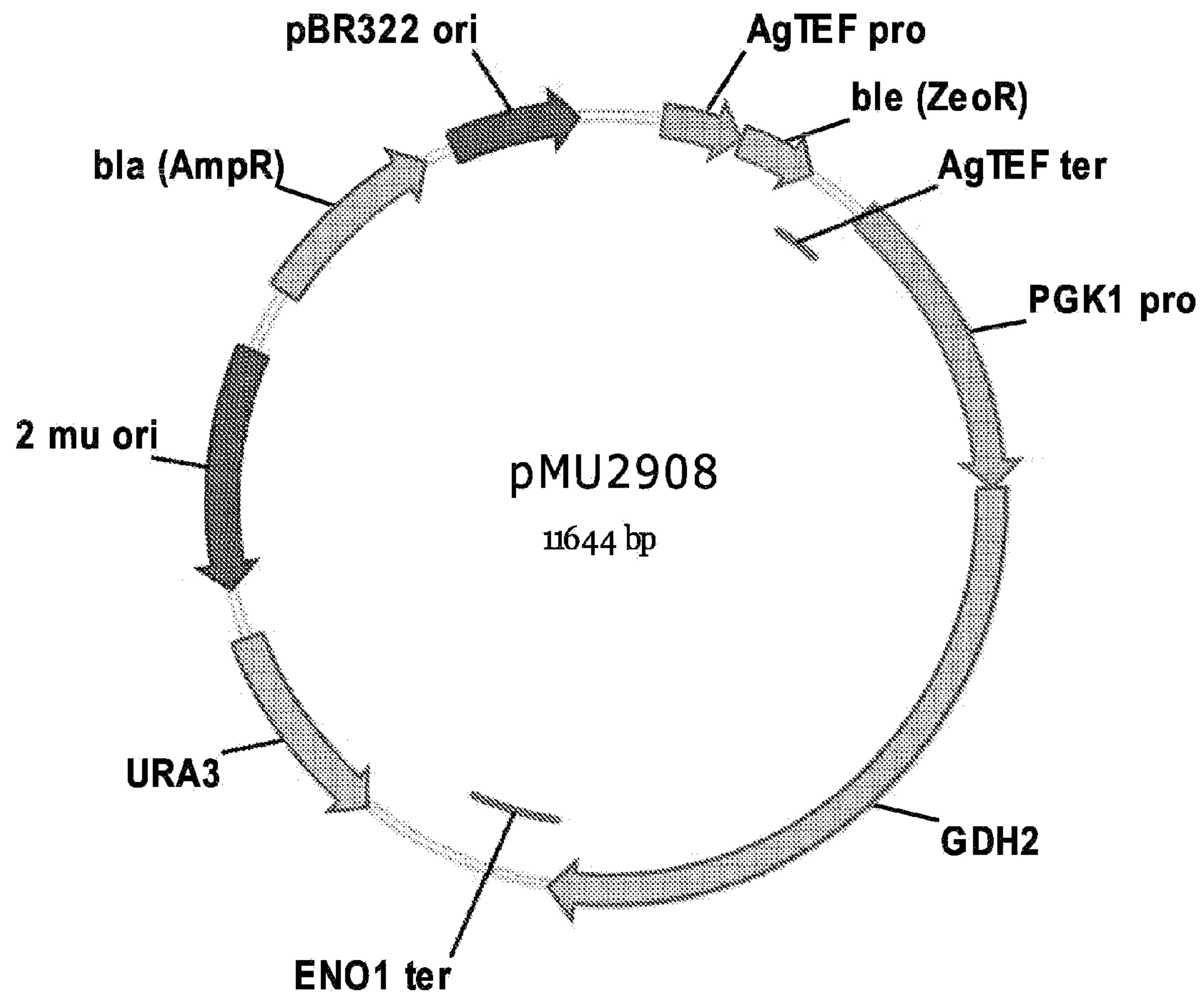


FIGURE 47

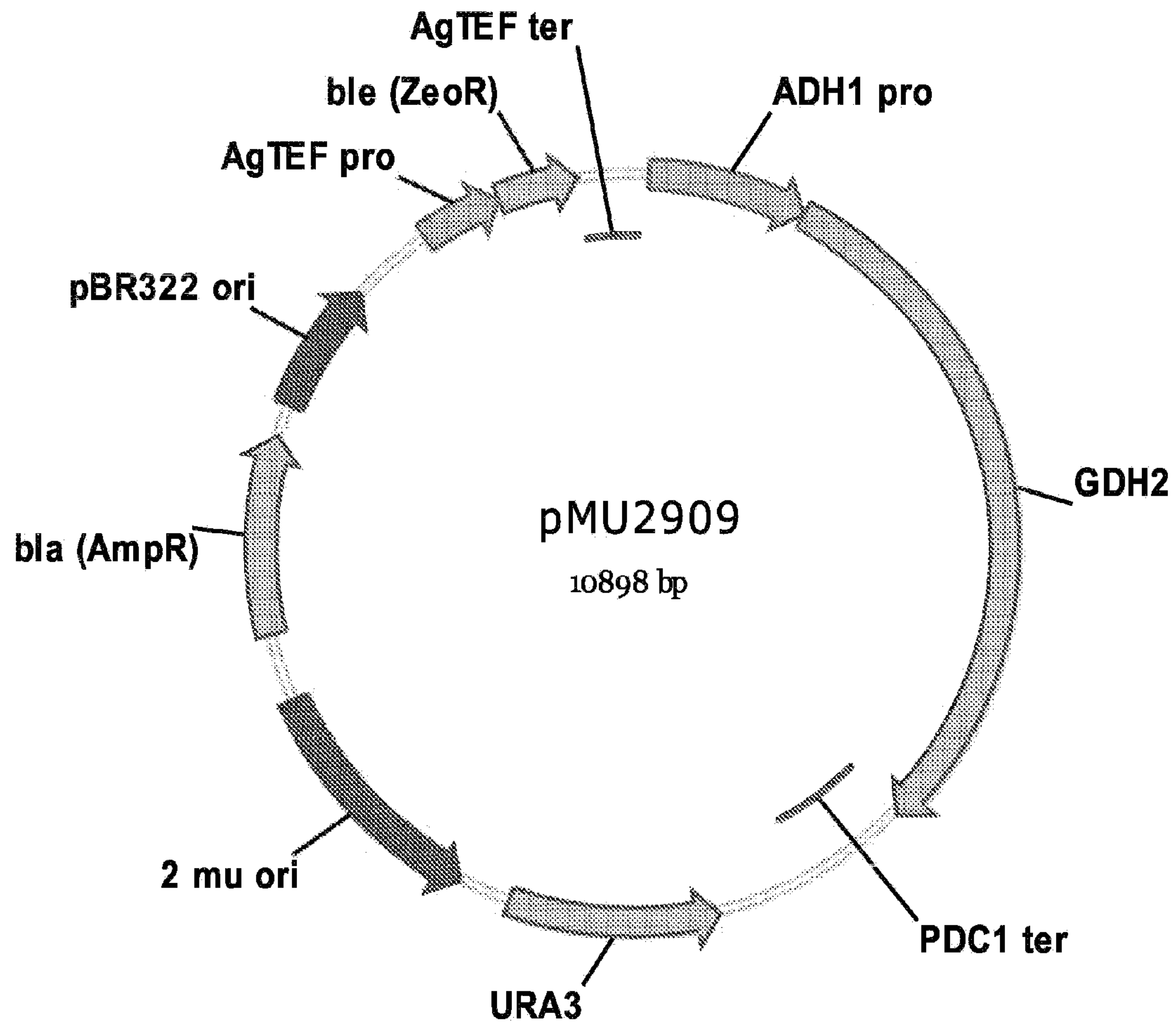


FIGURE 48

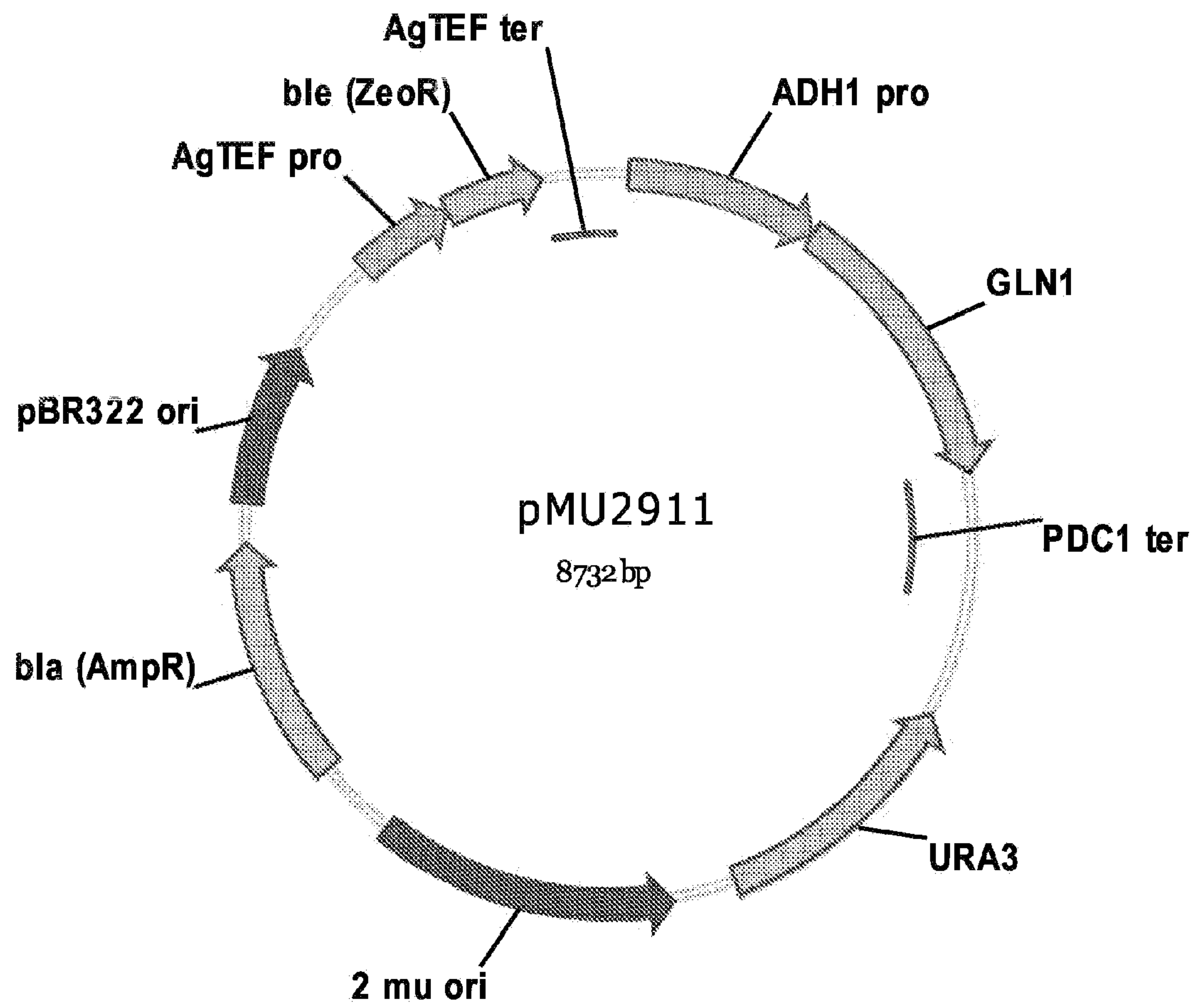


FIGURE 49

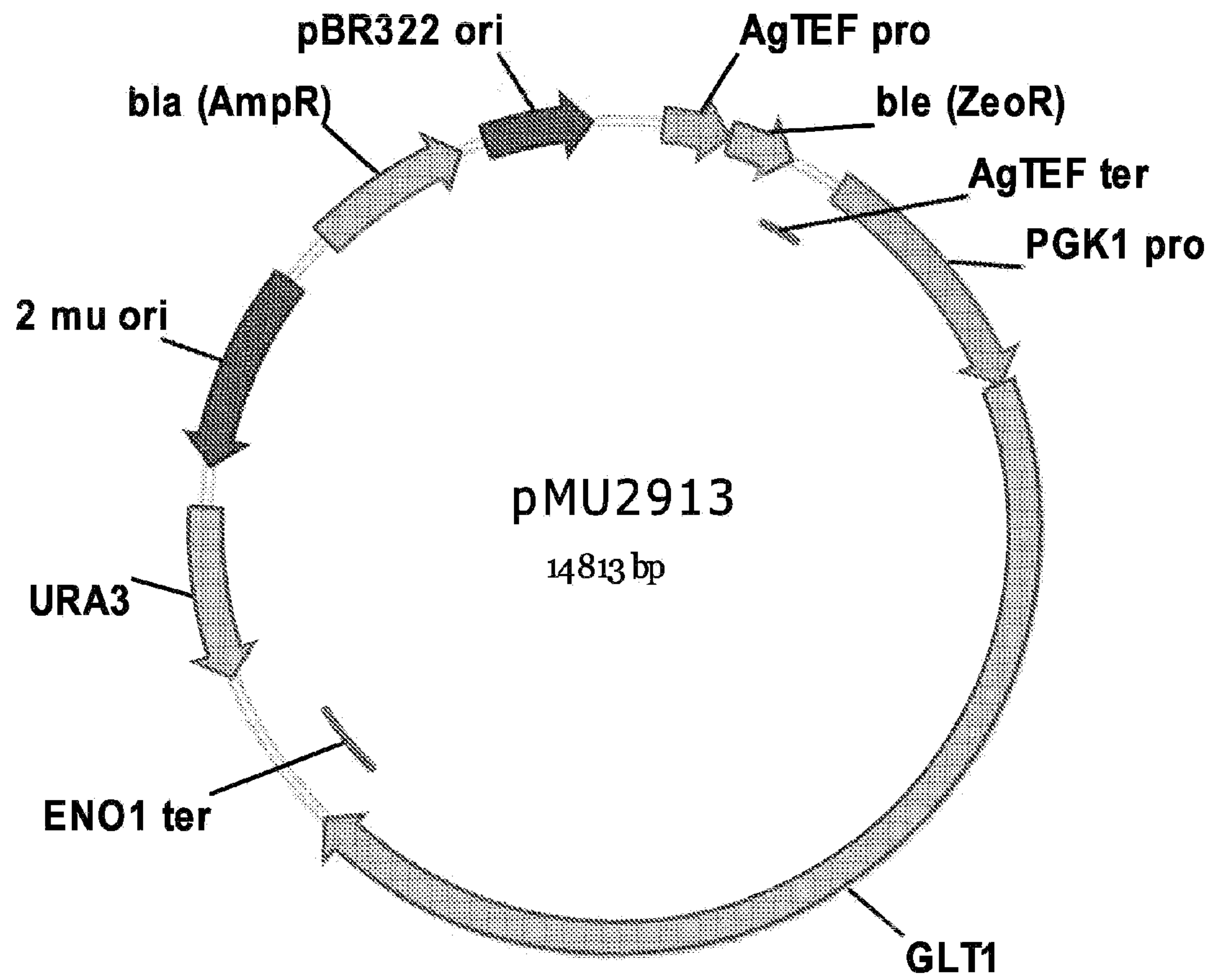


FIGURE 50

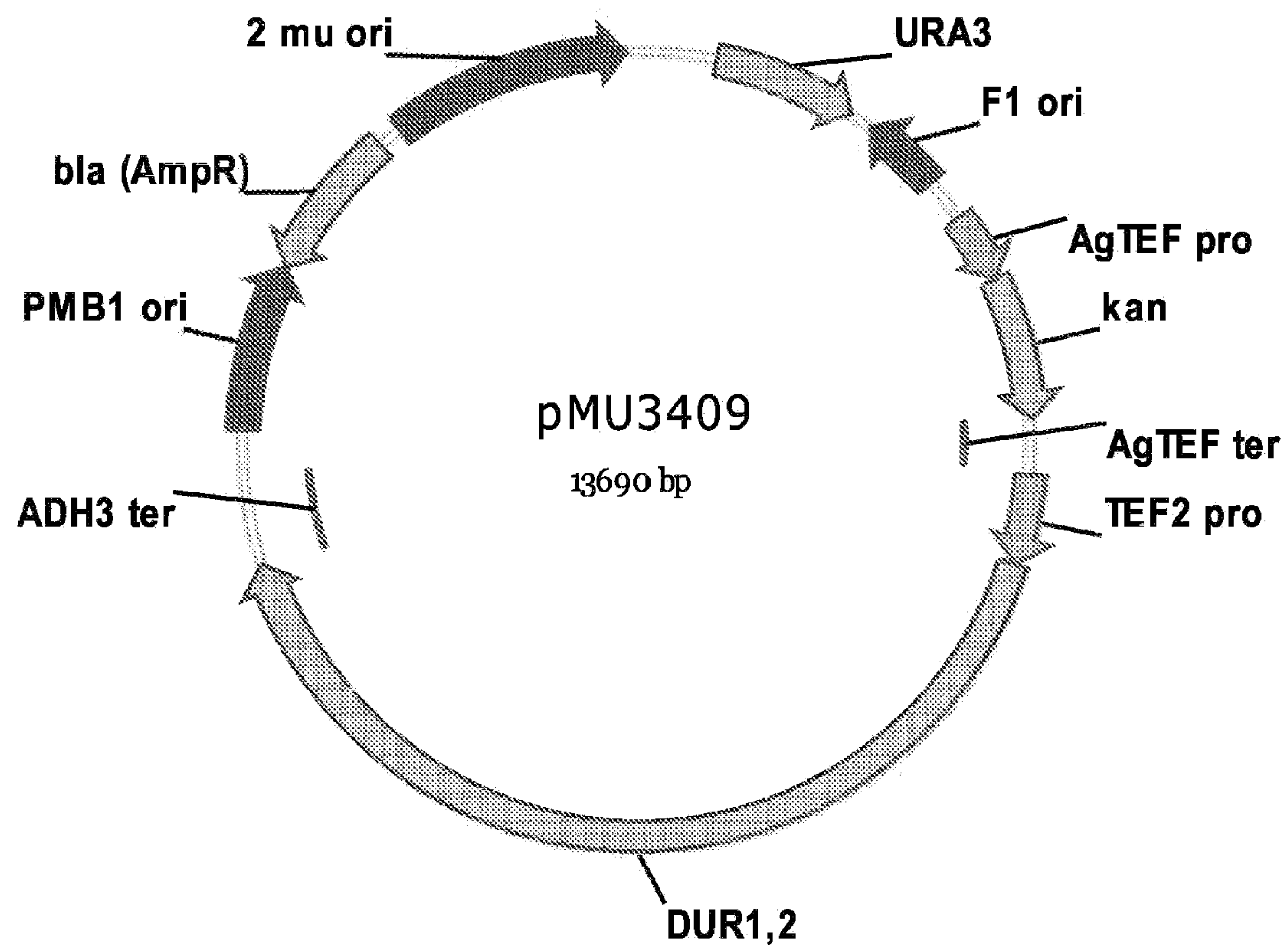


FIGURE 51

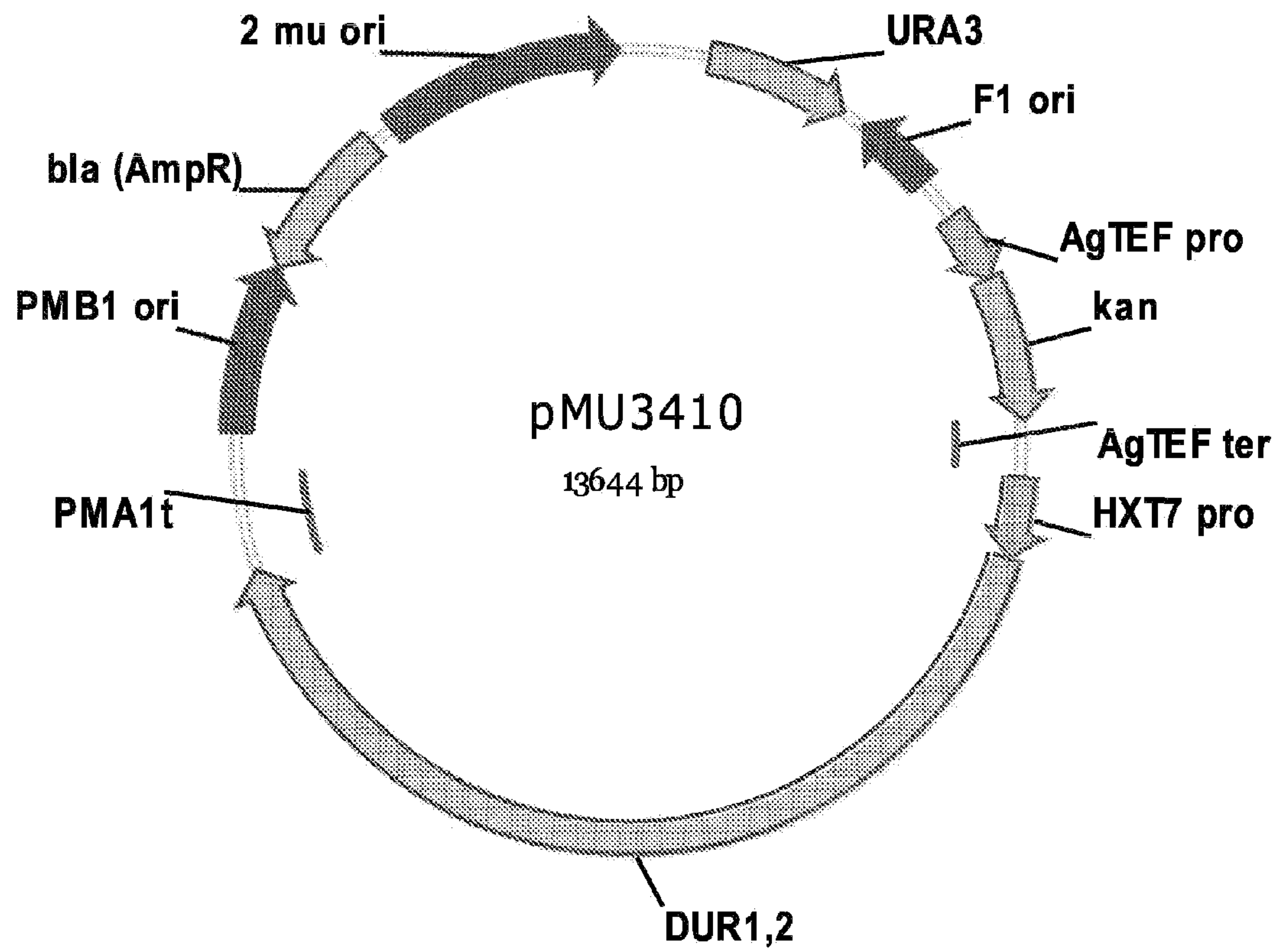


FIGURE 52

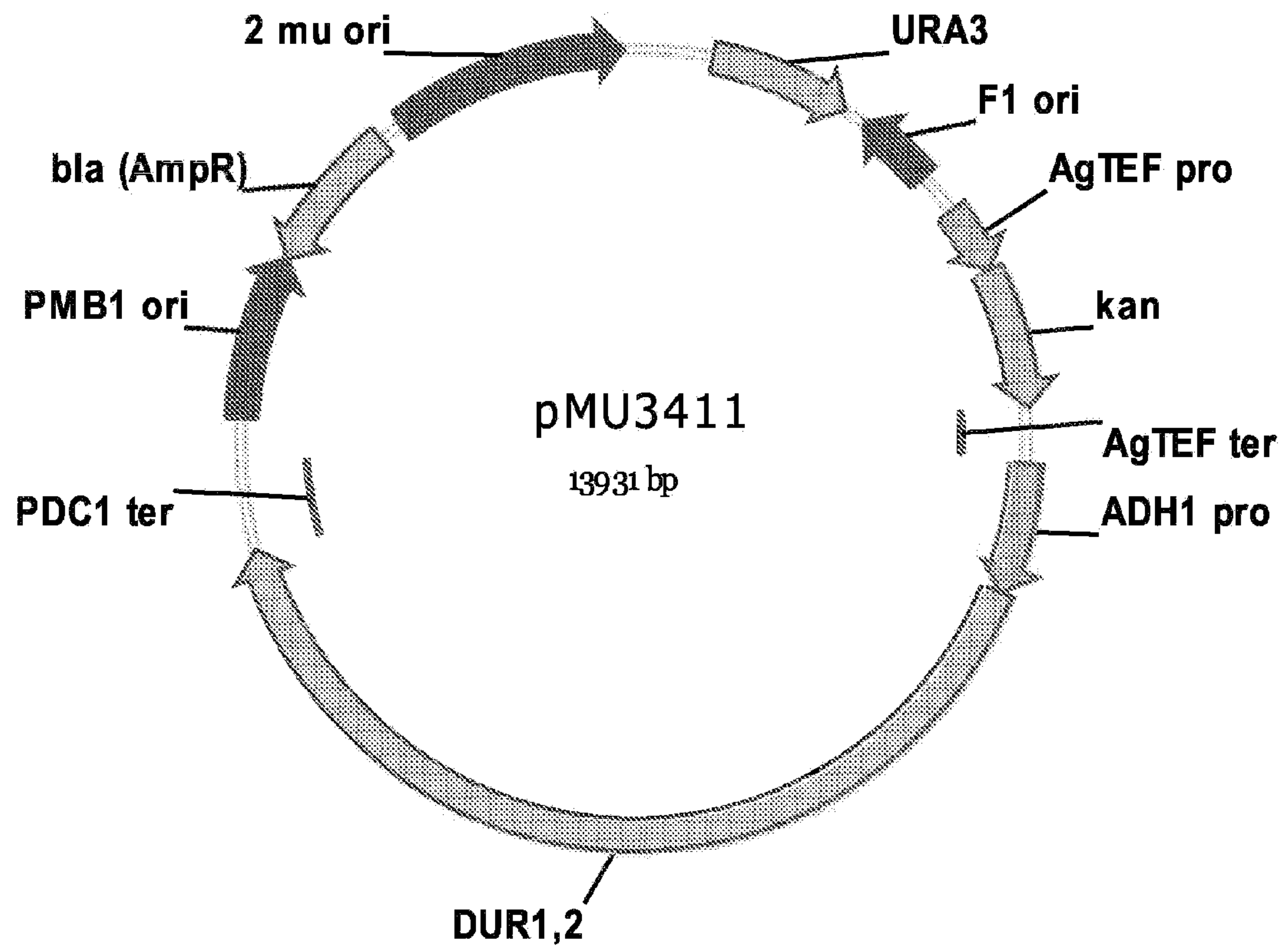


FIGURE 53

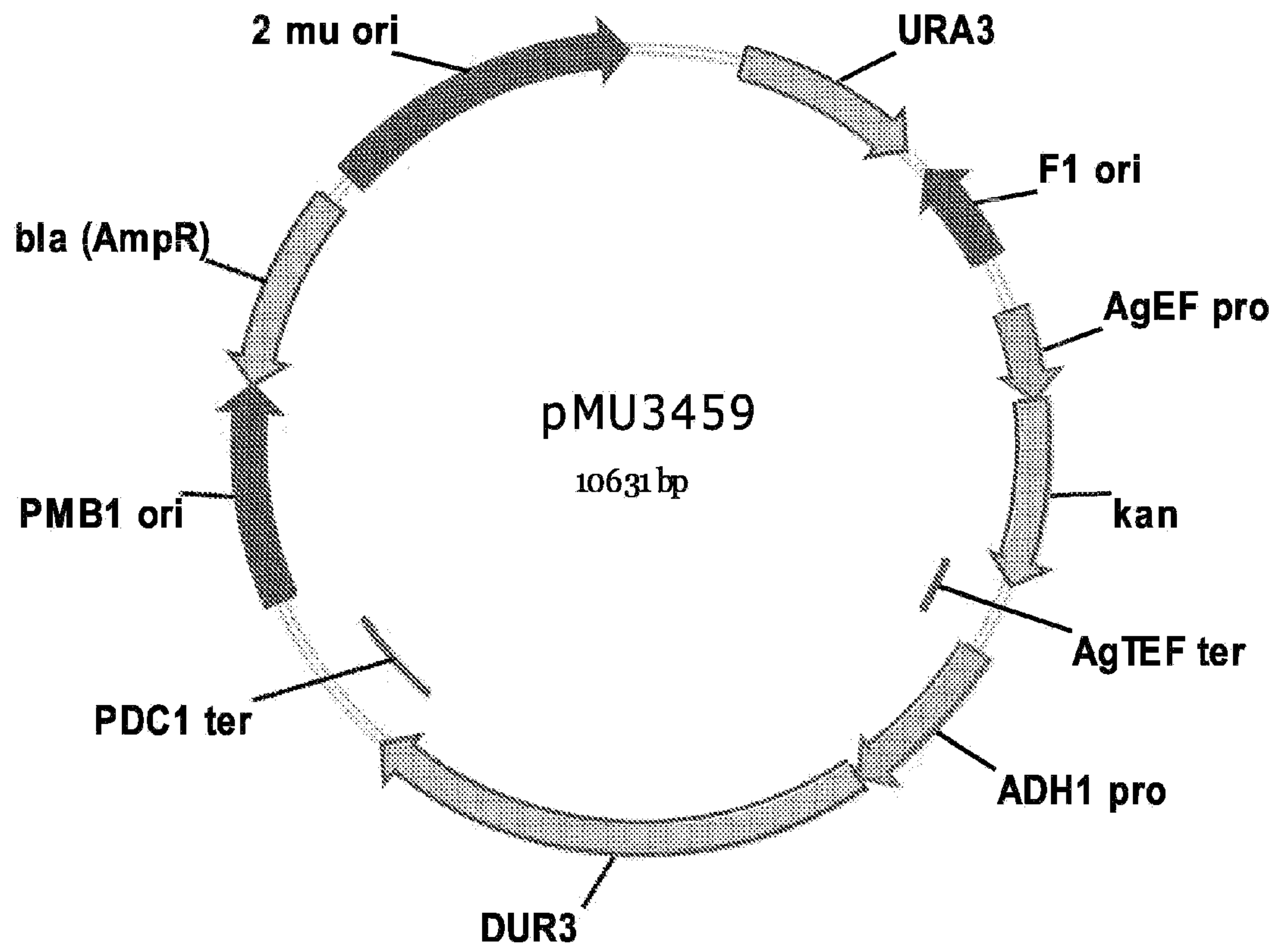


FIGURE 54

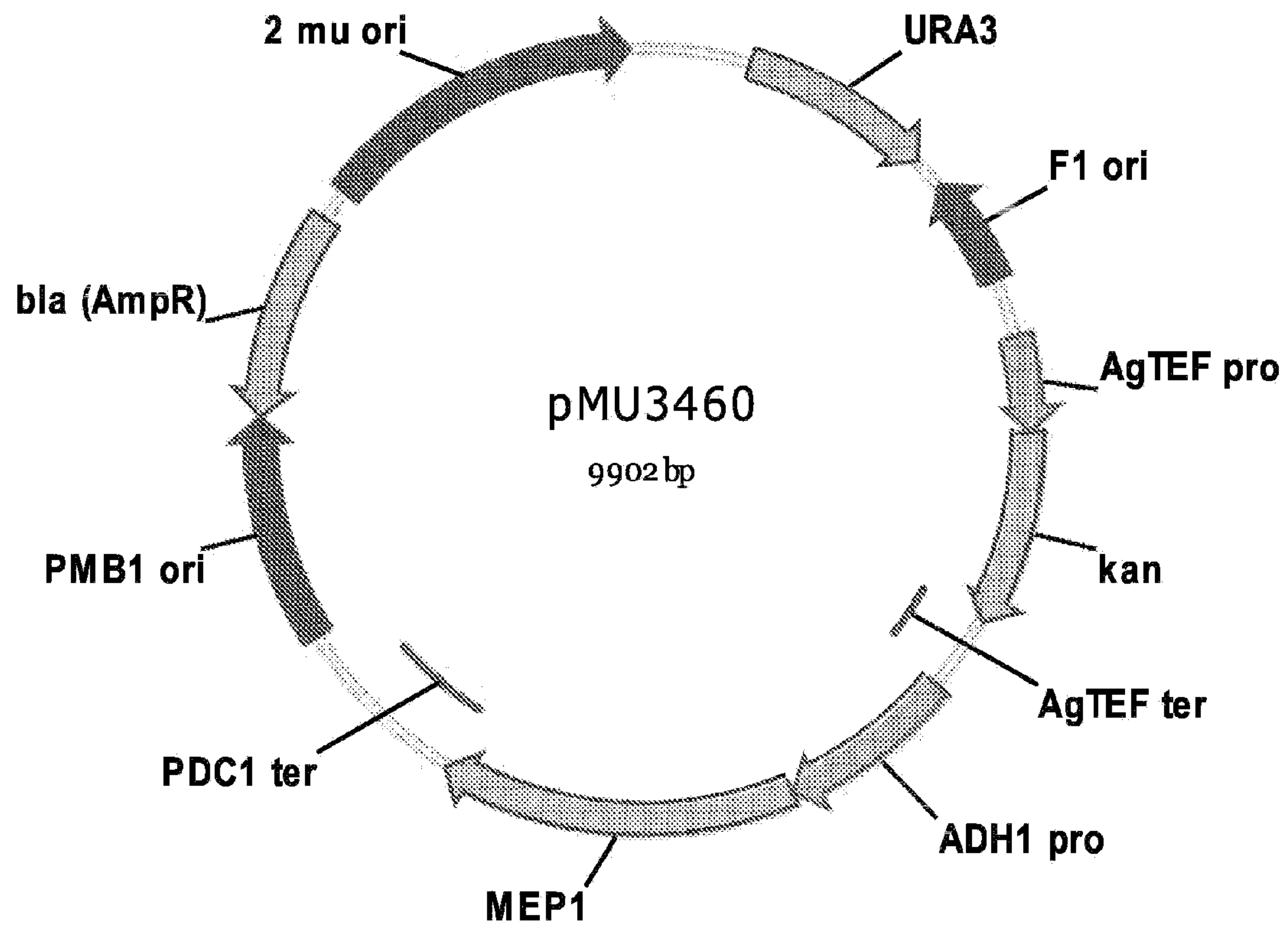


FIGURE 55

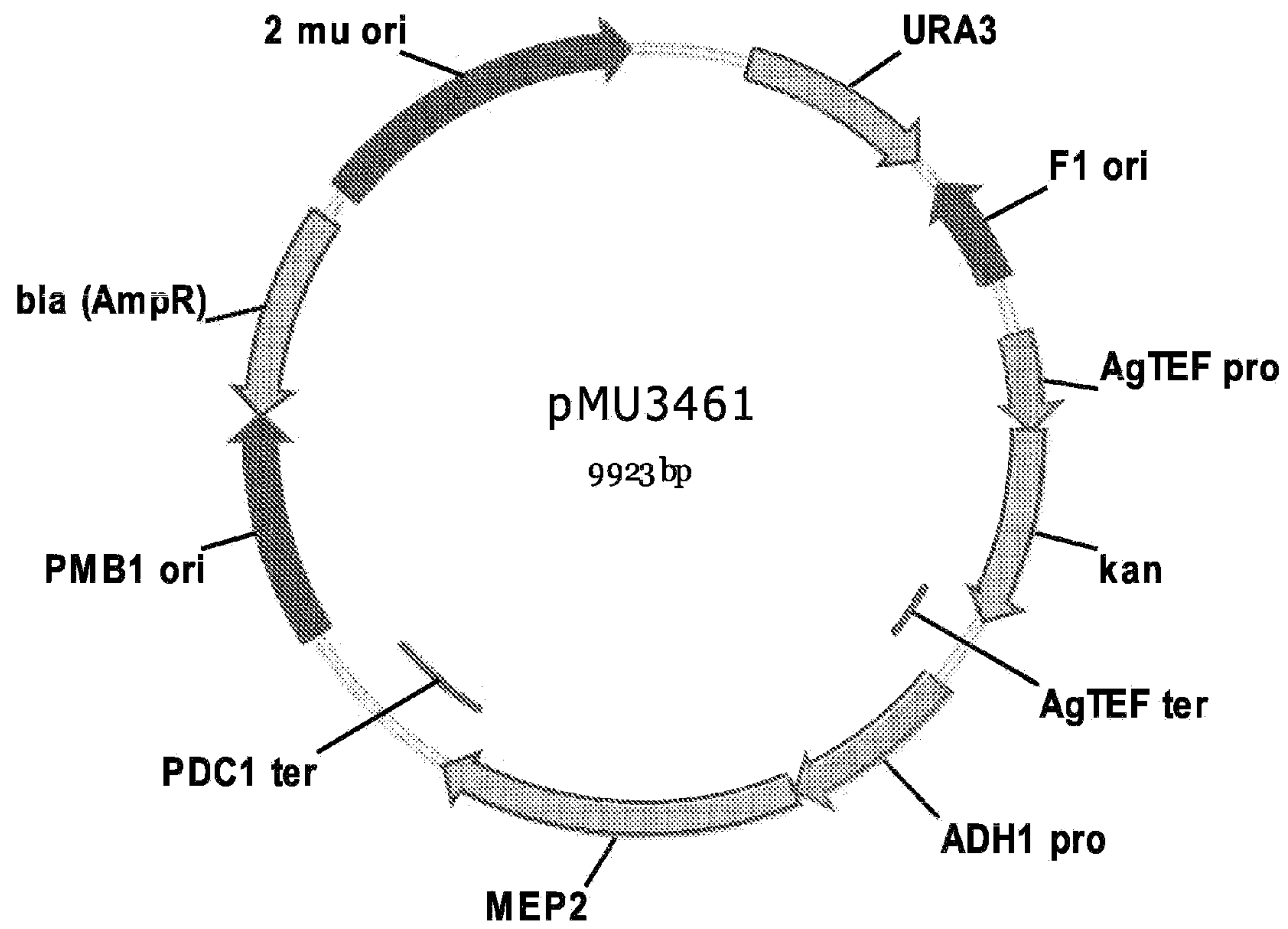


FIGURE 56

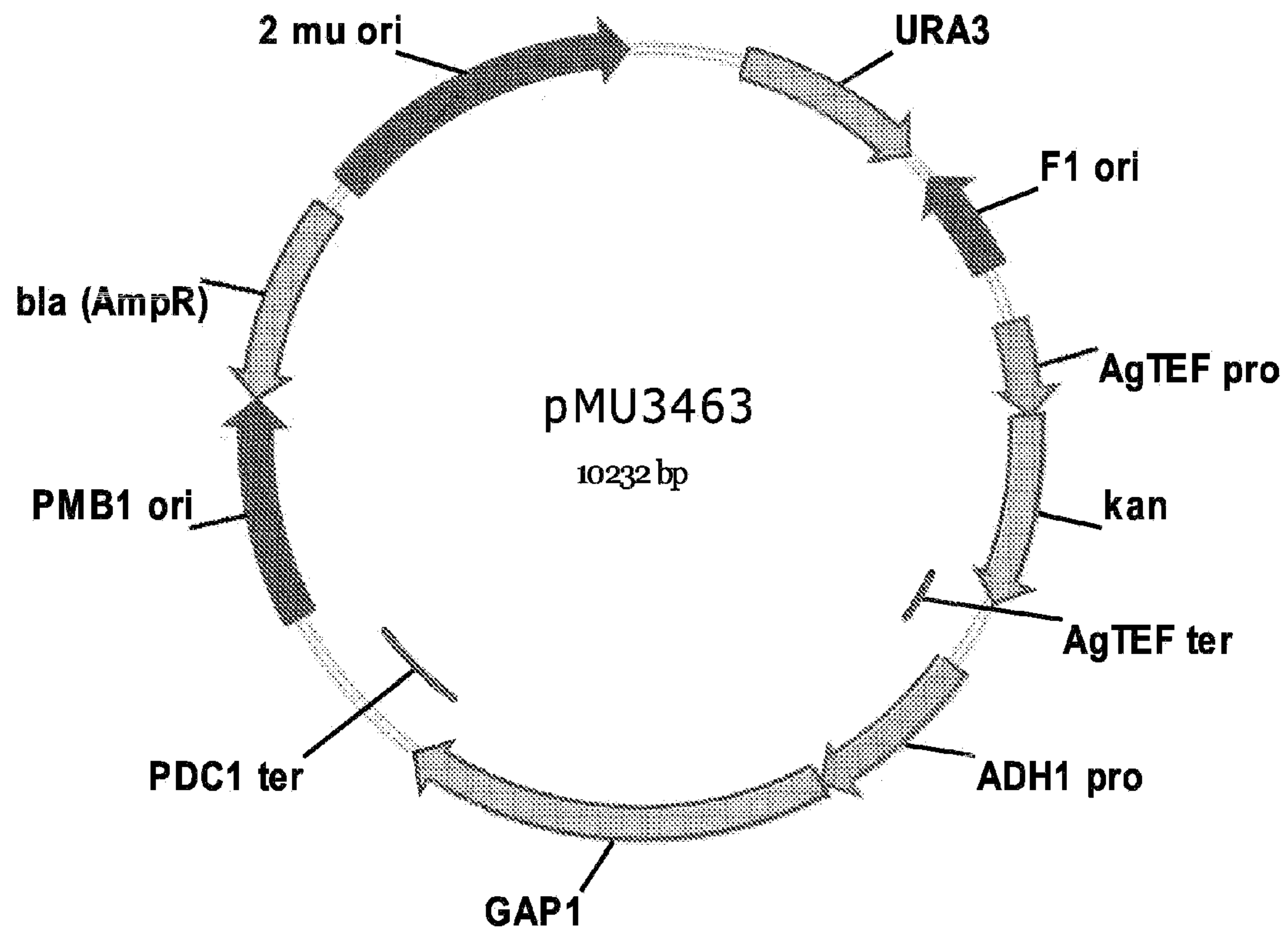


FIGURE 57

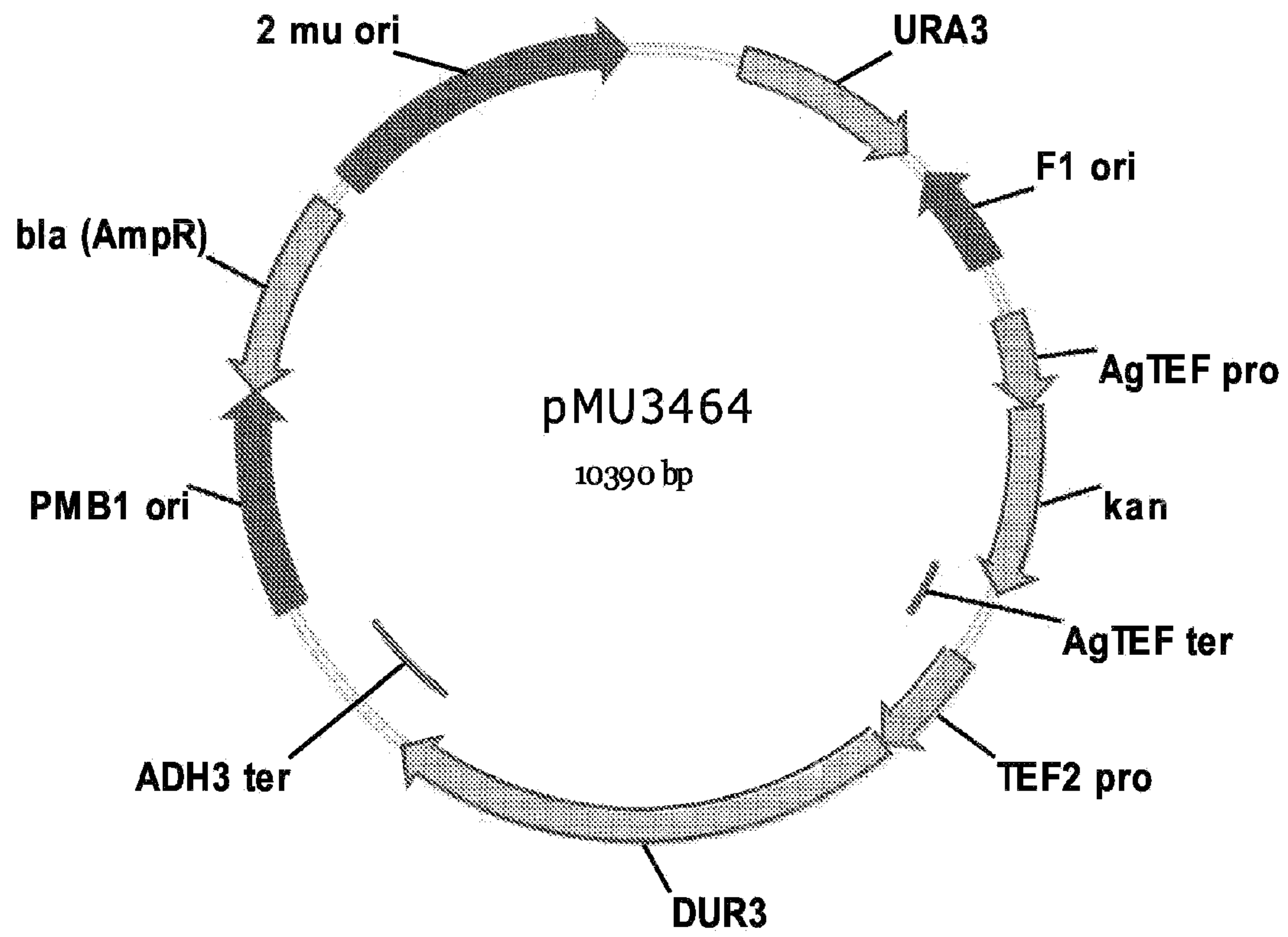


FIGURE 58

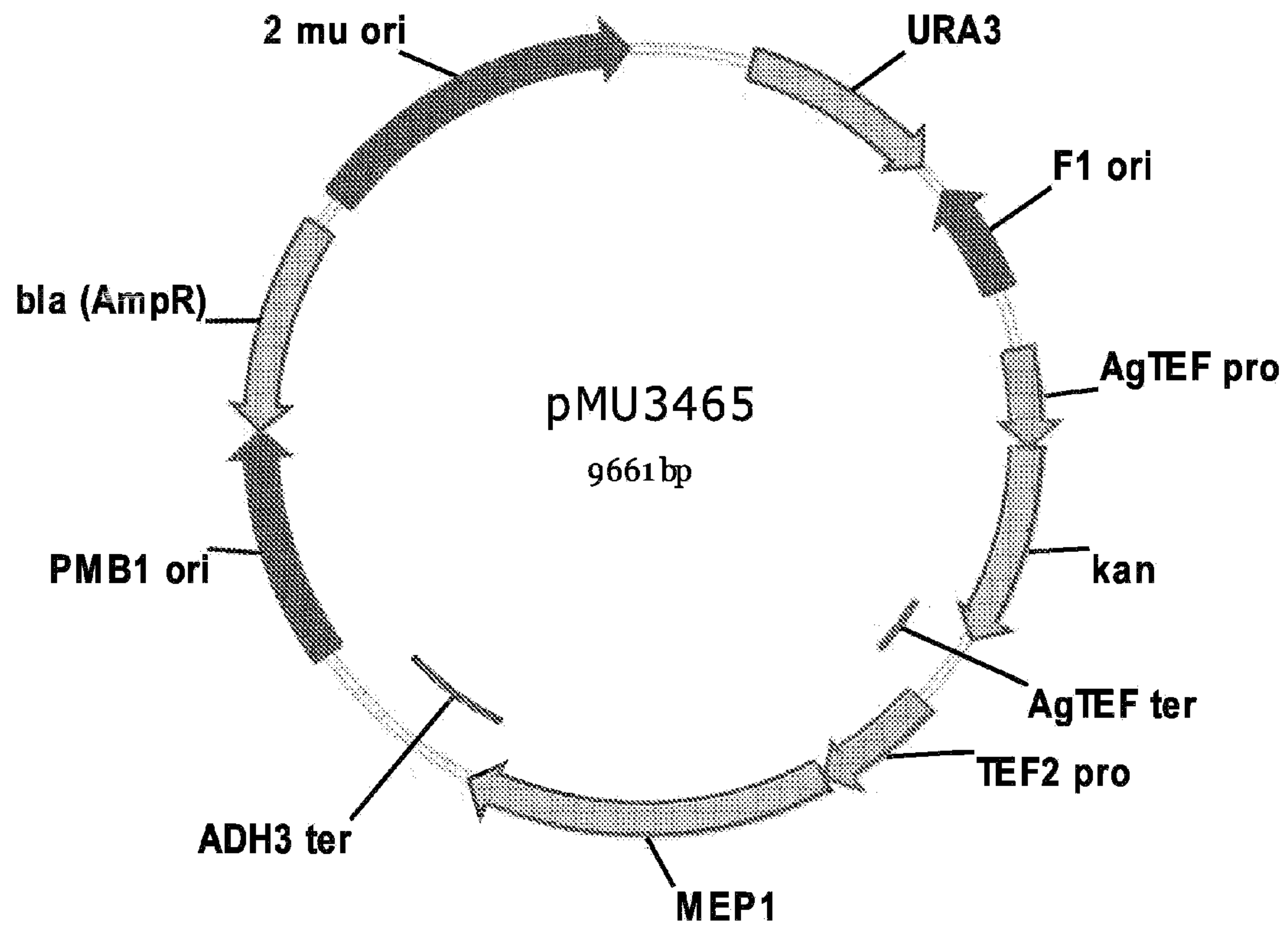


FIGURE 59

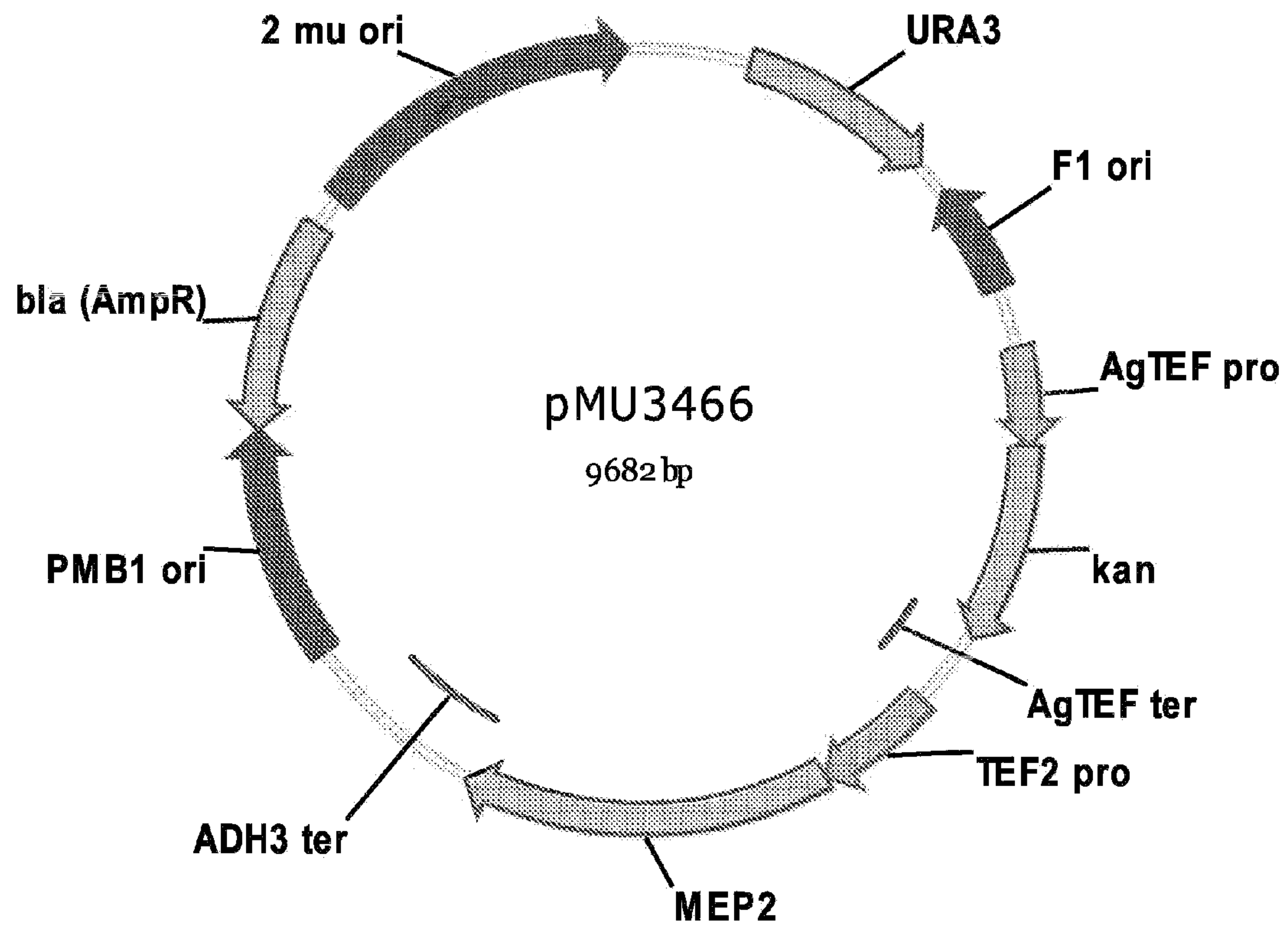


FIGURE 60

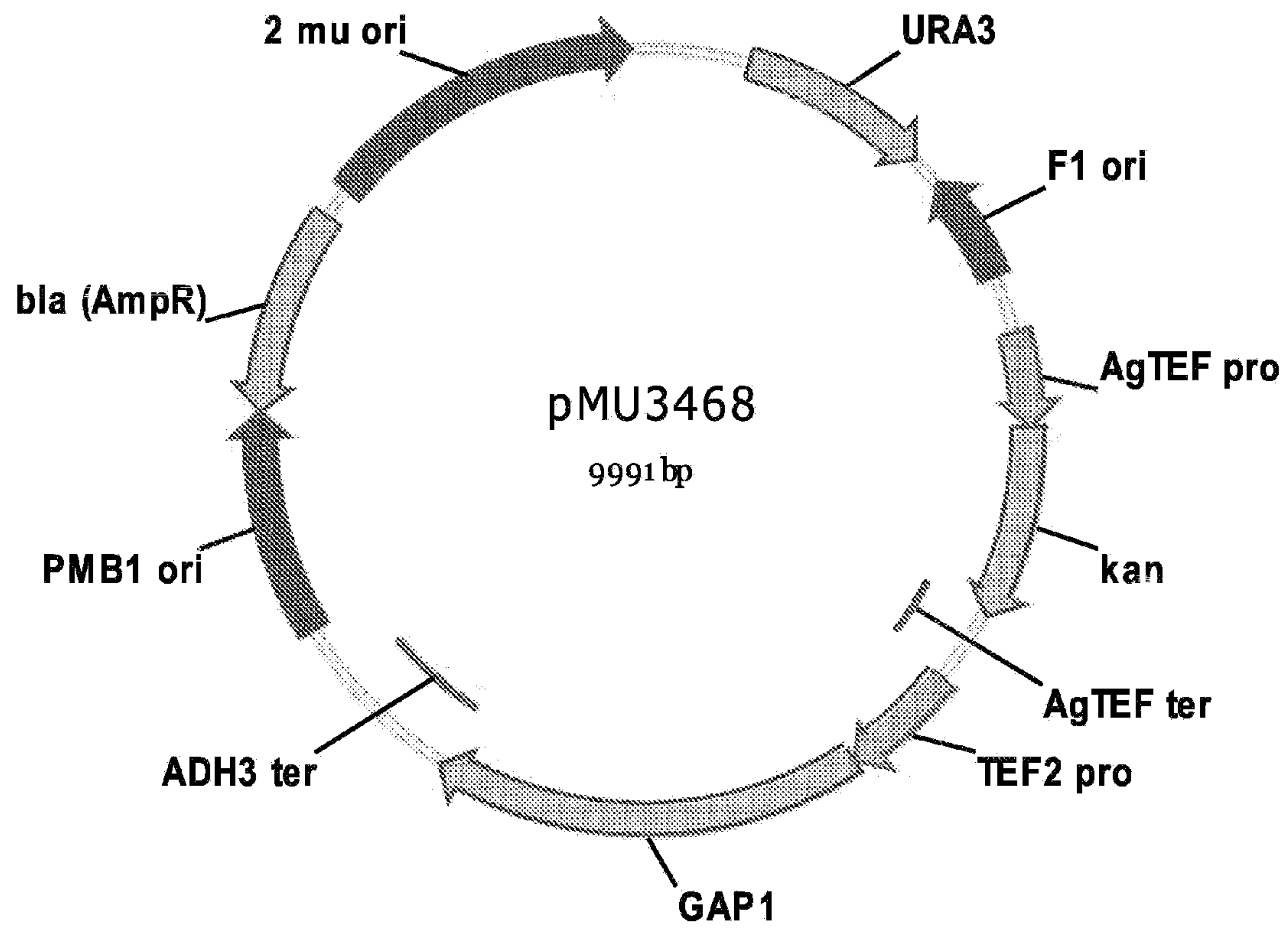


FIGURE 61

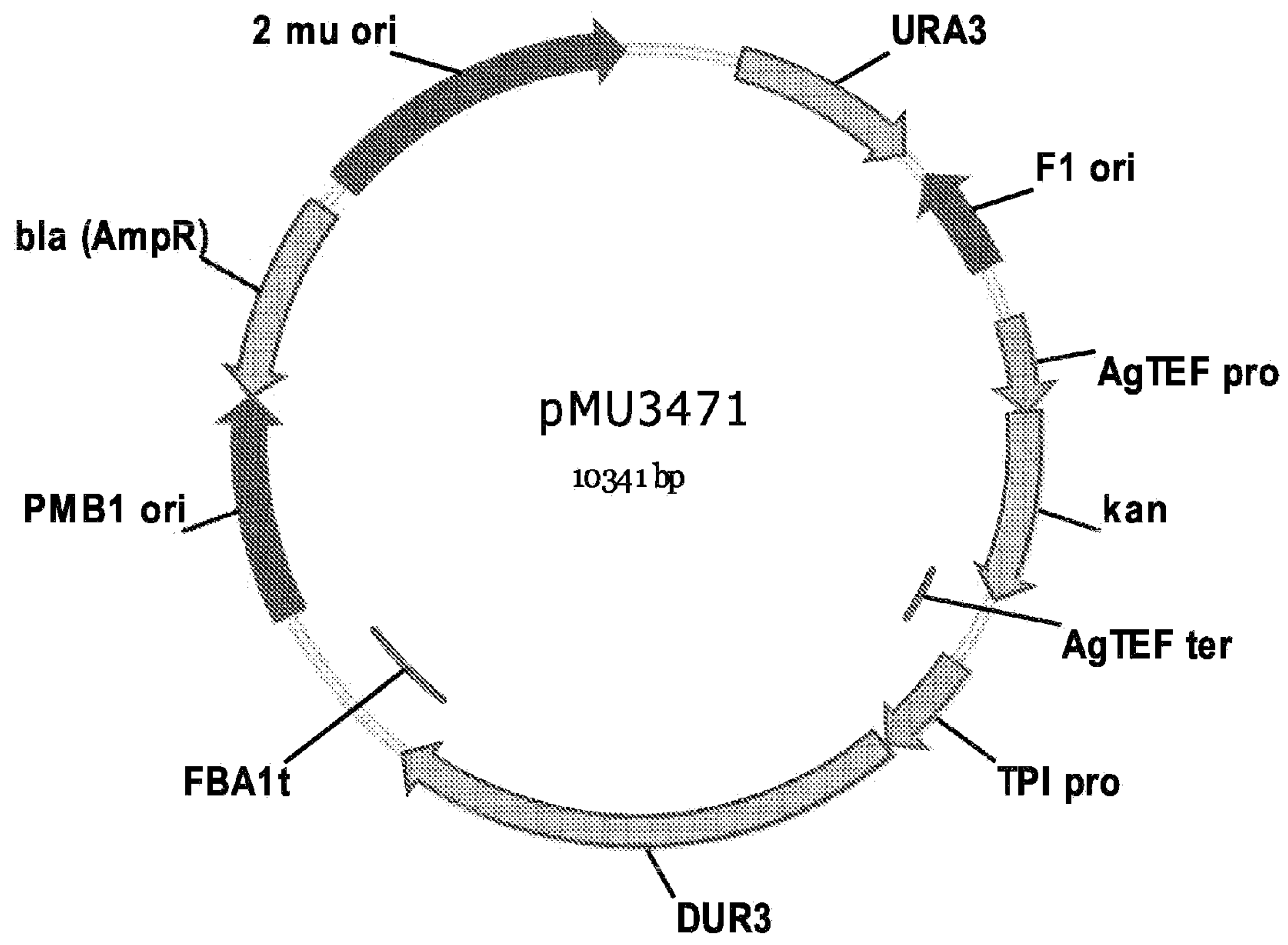


FIGURE 62

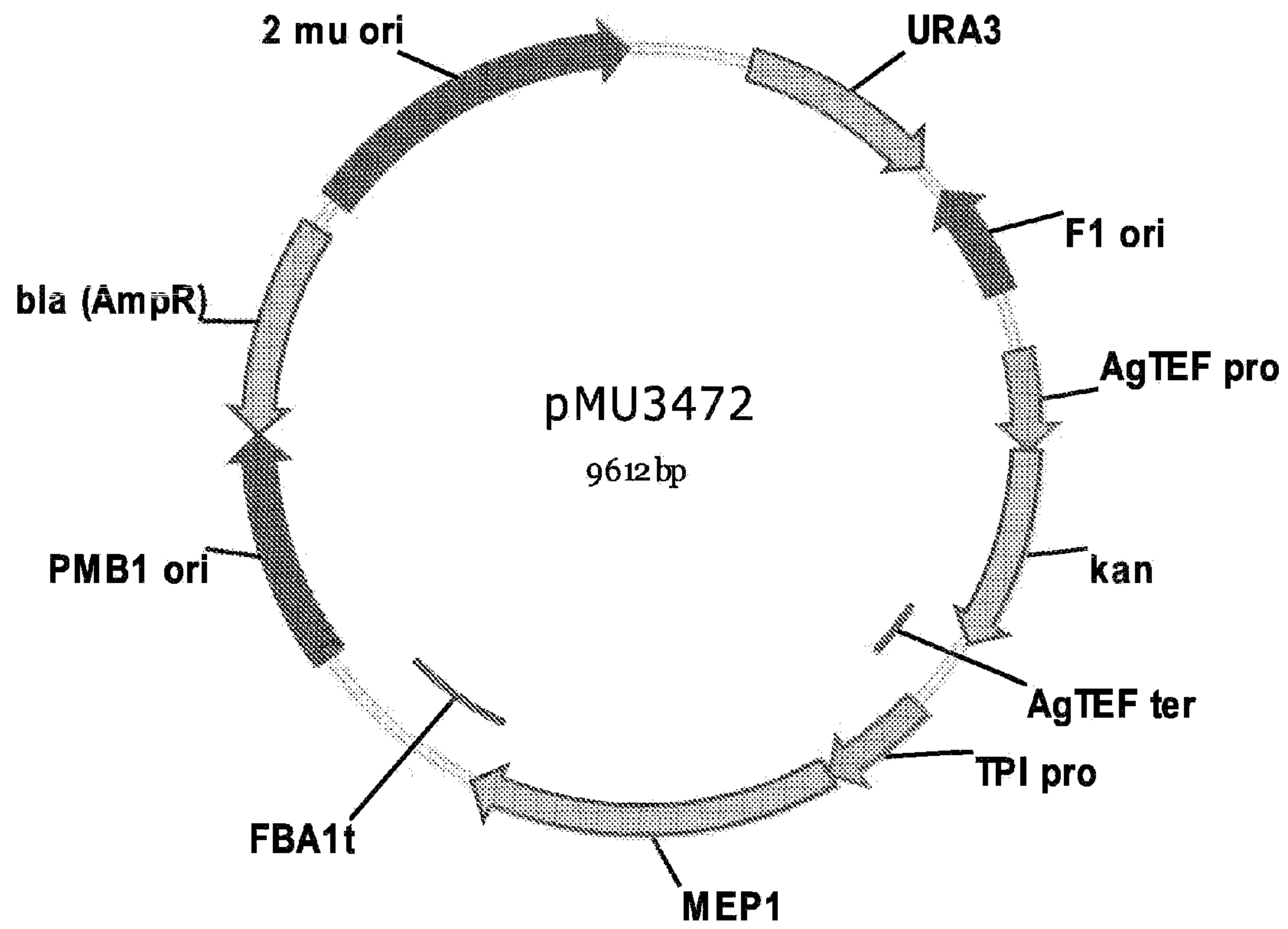


FIGURE 63

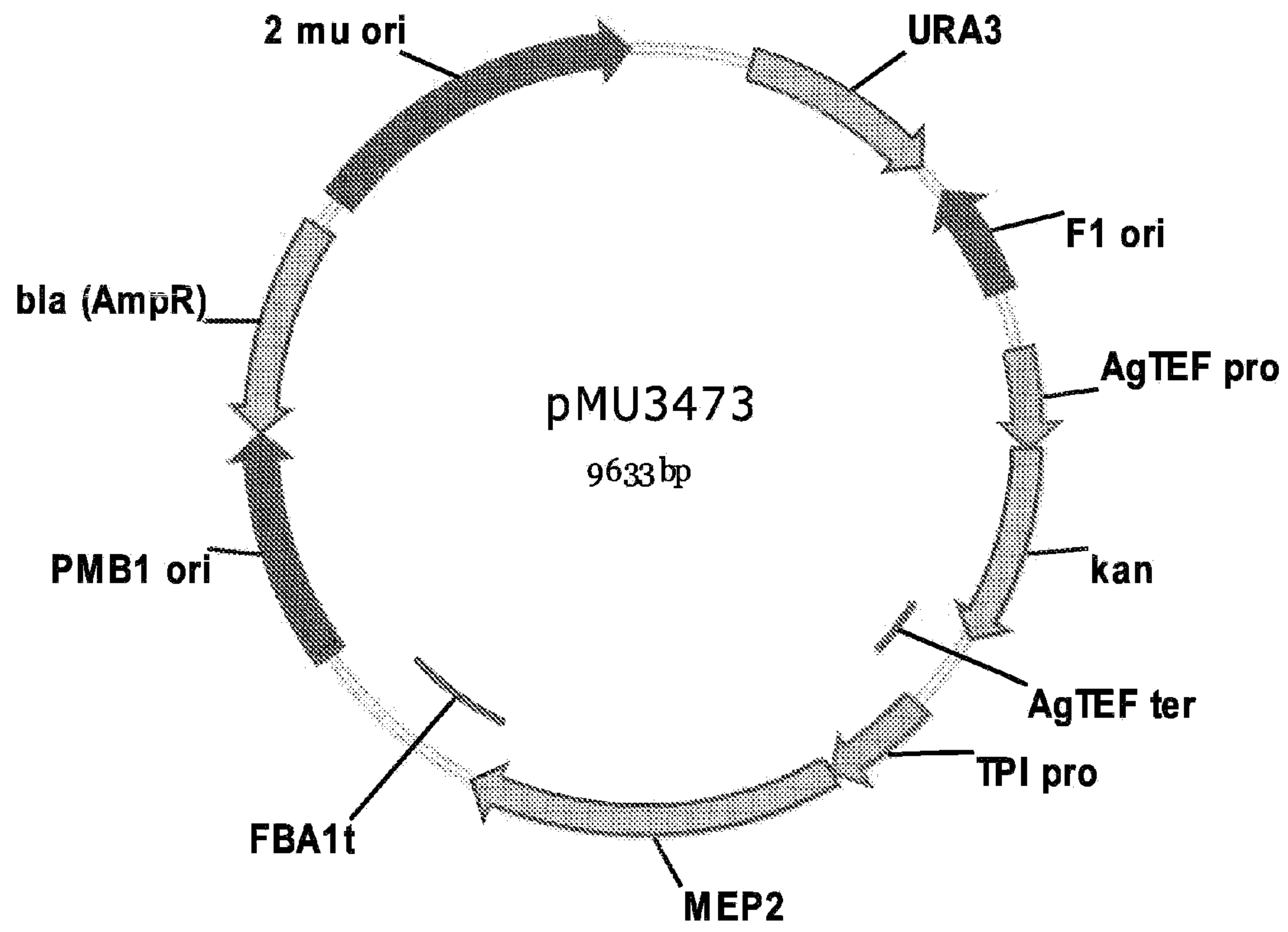


FIGURE 64

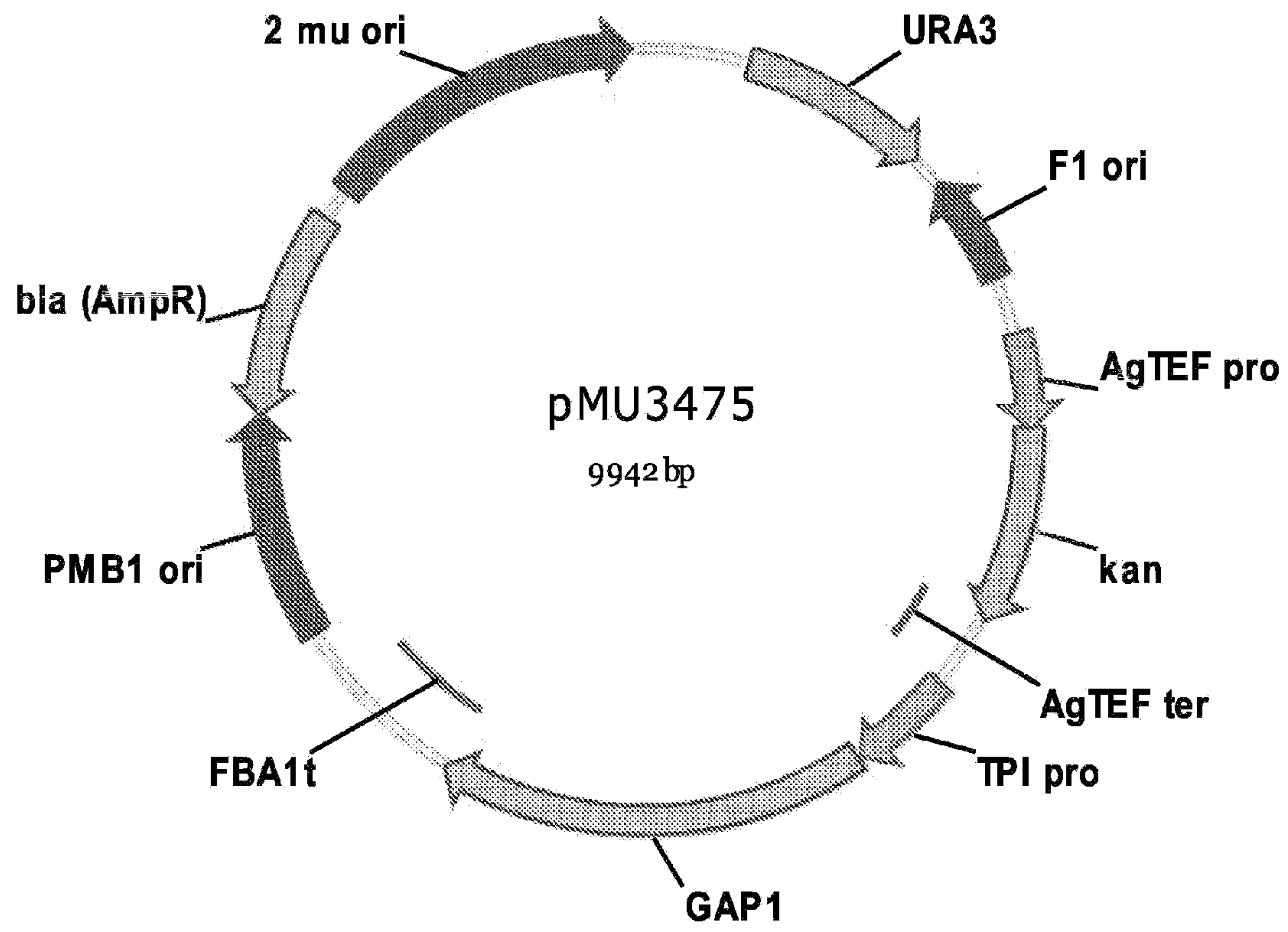


FIGURE 65

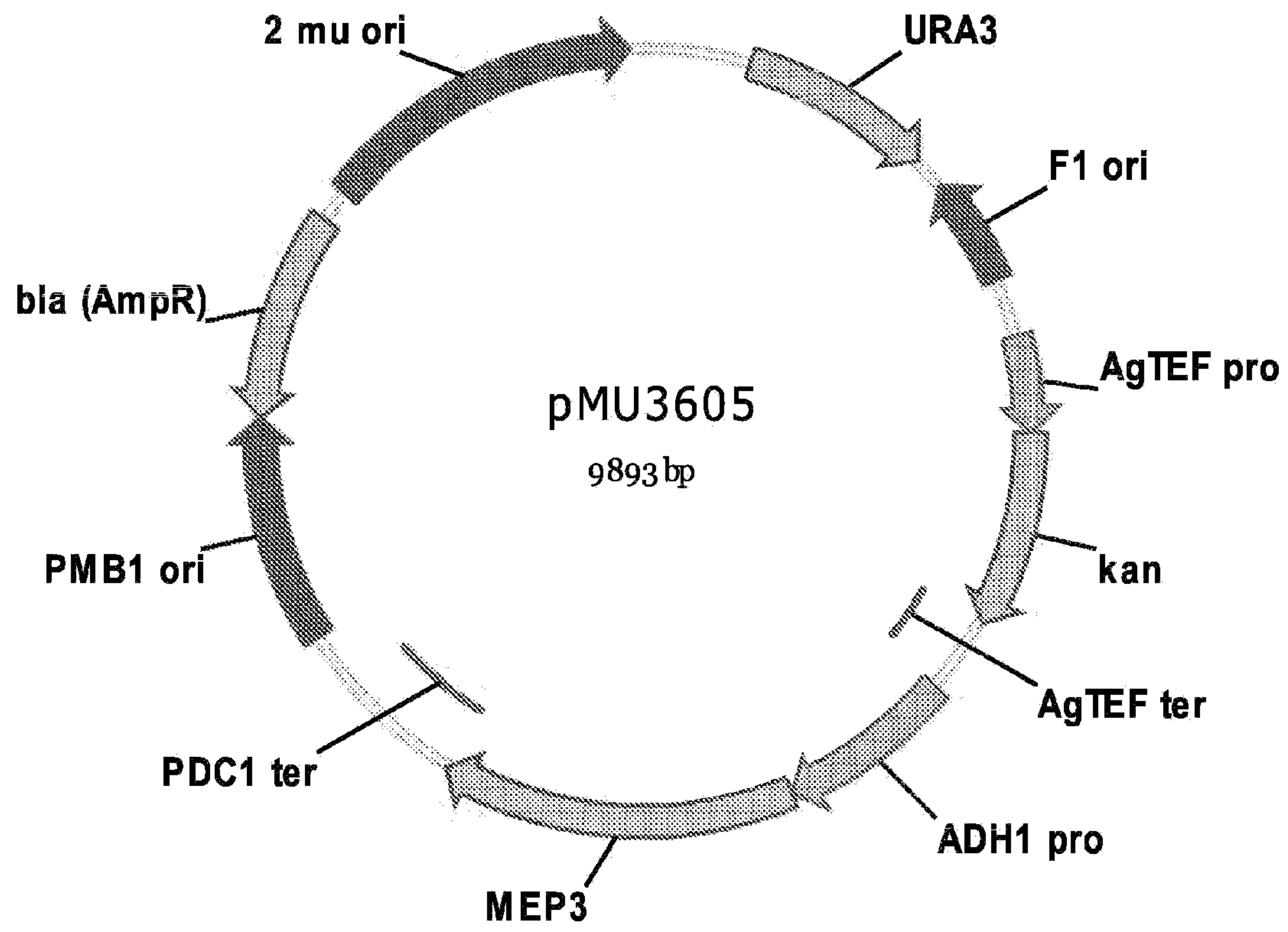


FIGURE 66

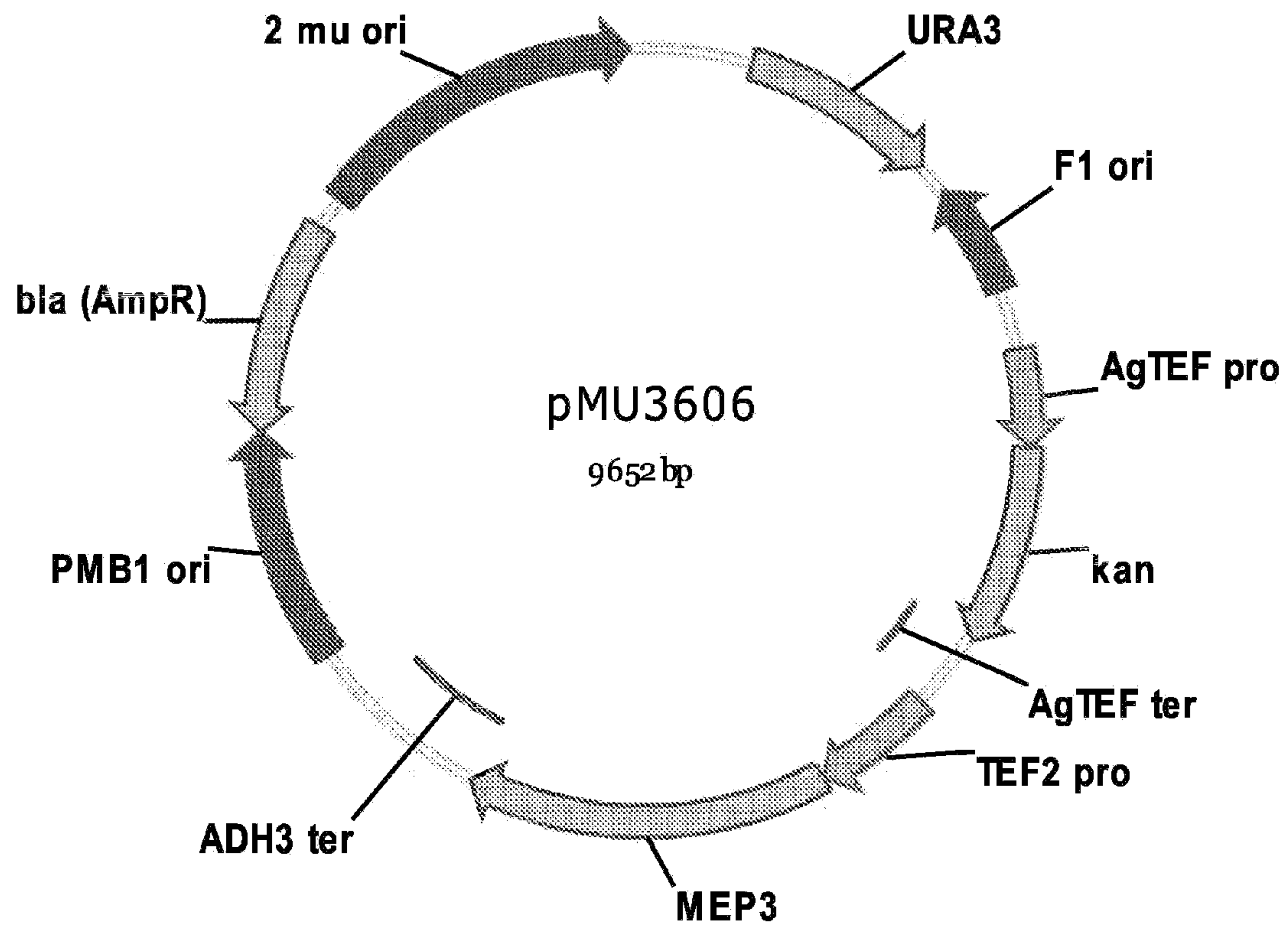


FIGURE 67

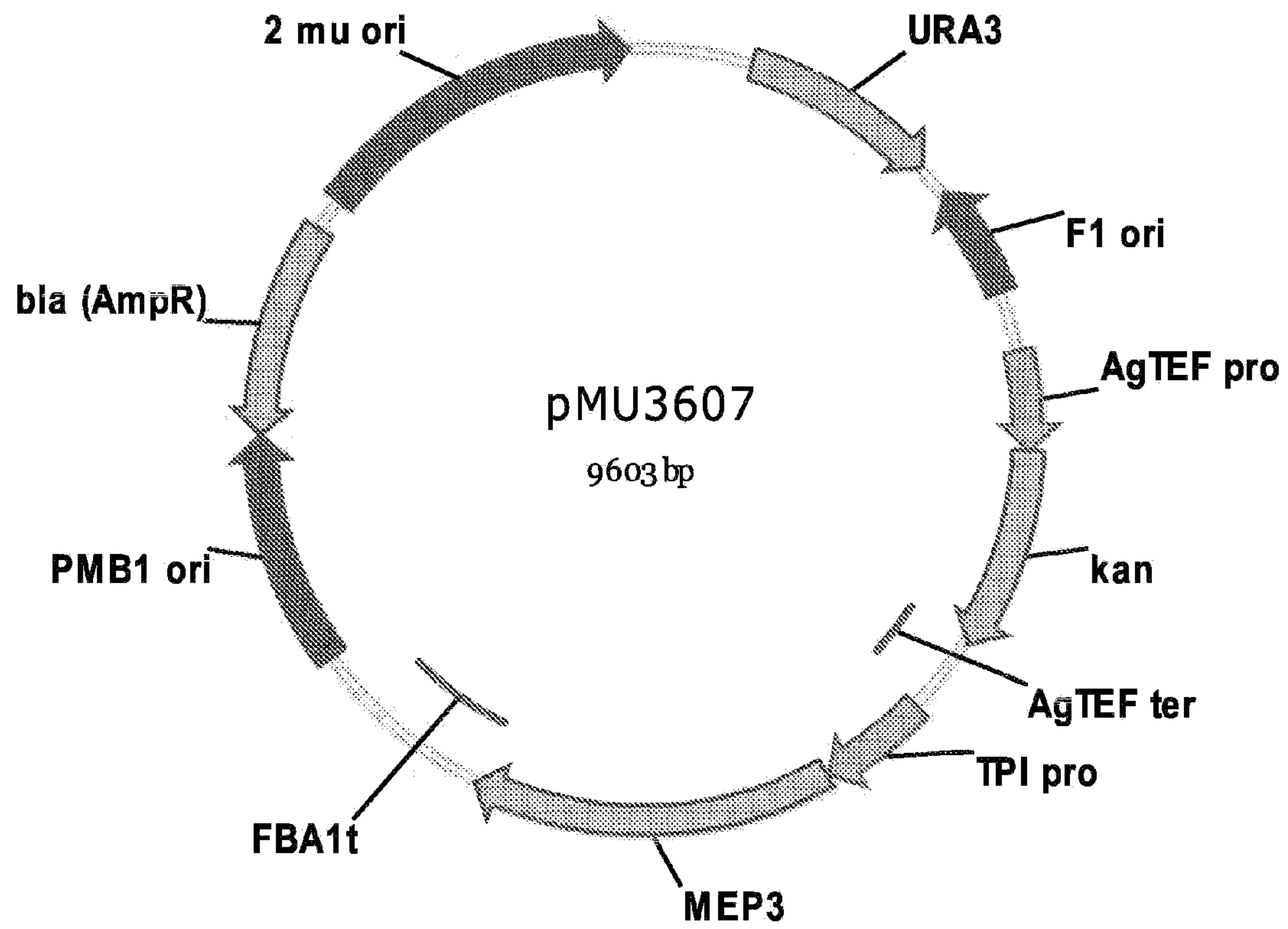


FIGURE 68

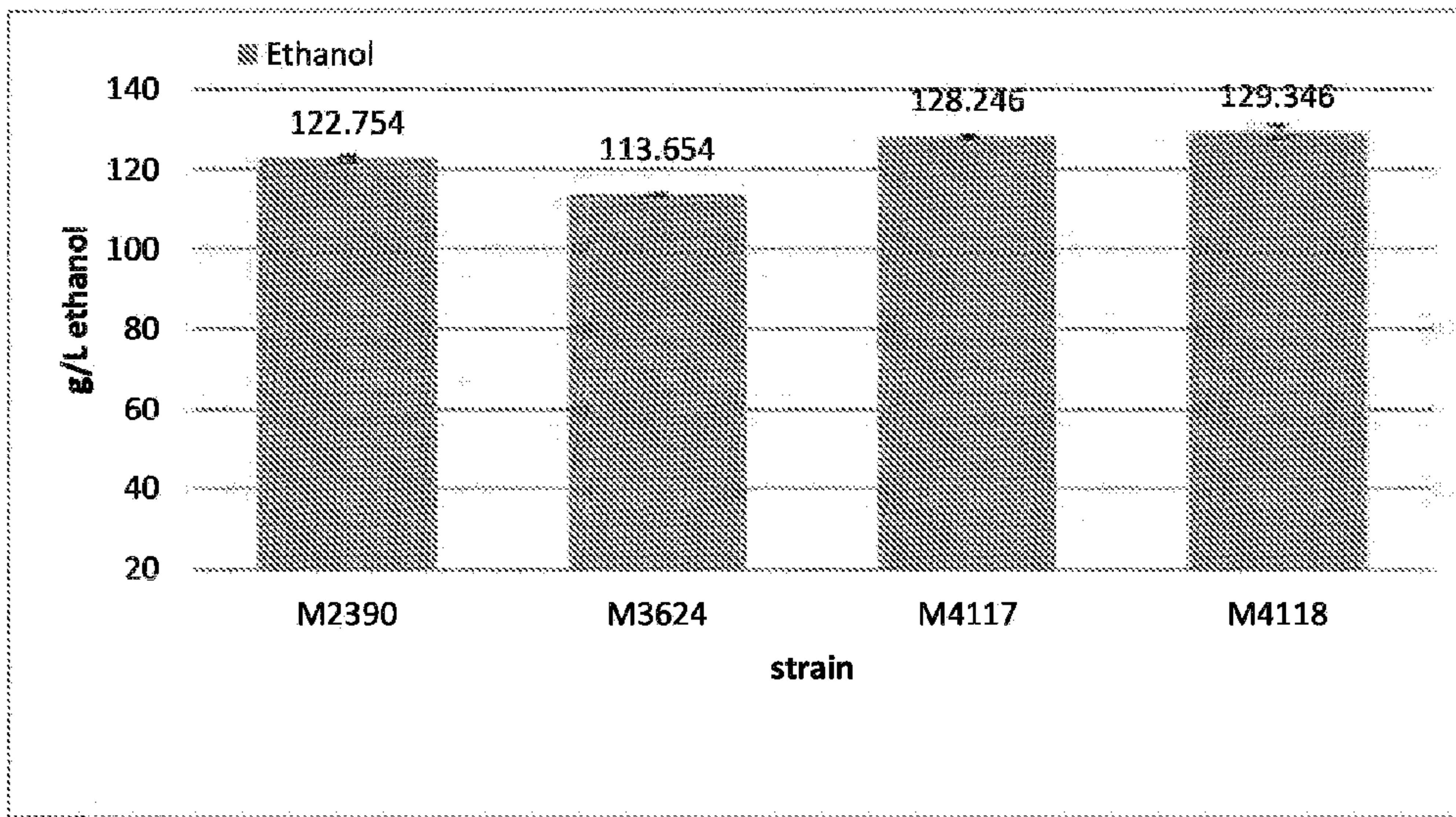


FIGURE 69

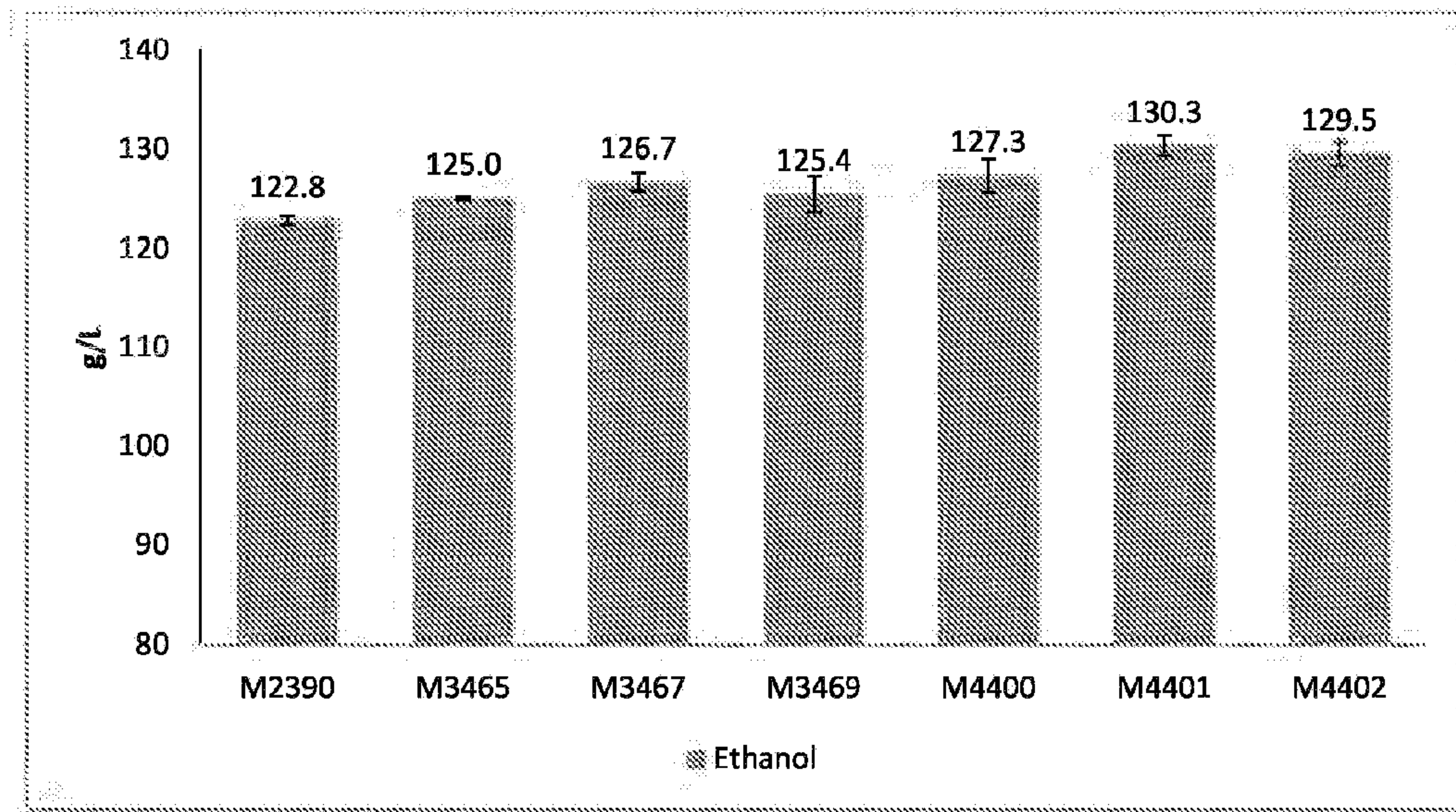


FIGURE 70

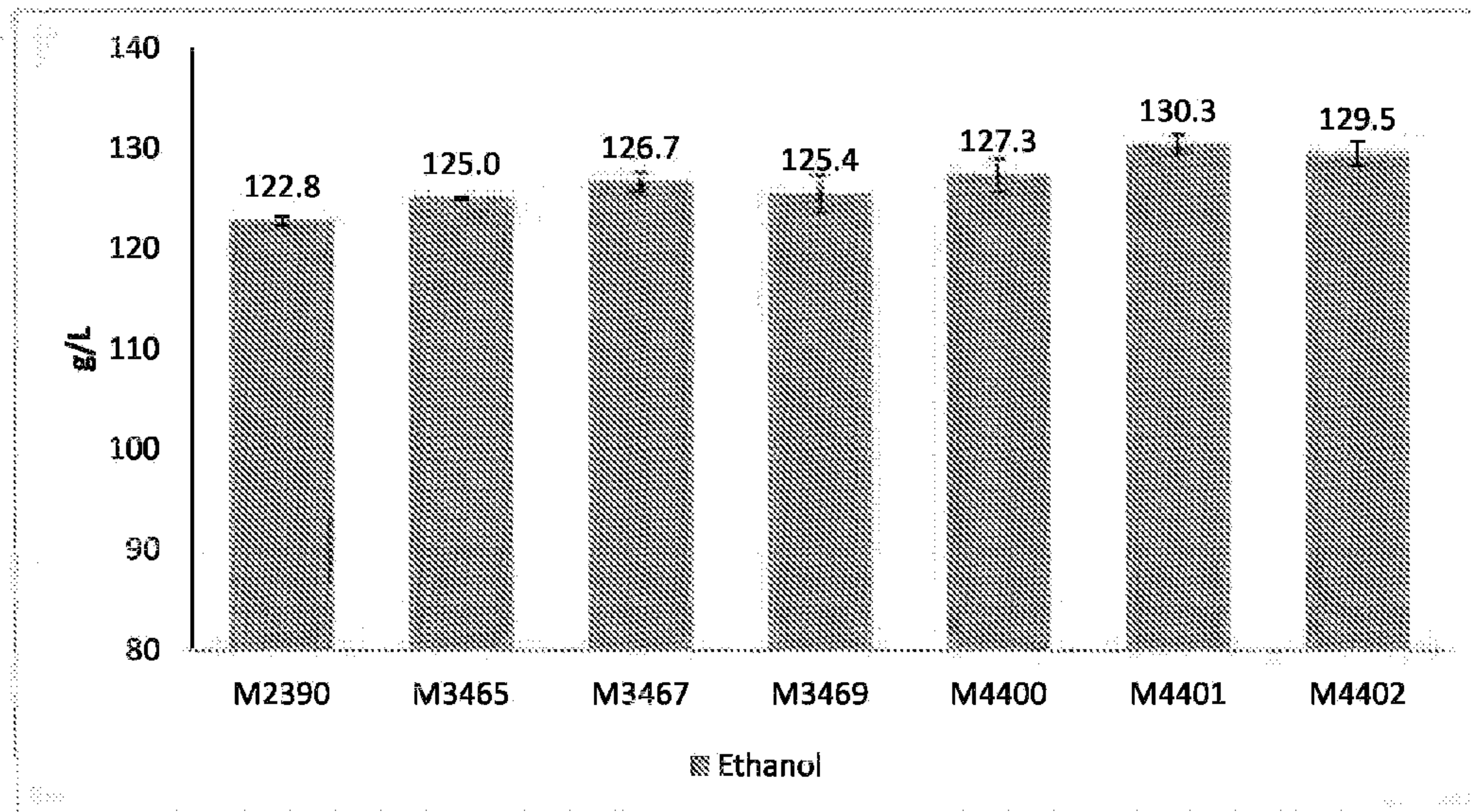


FIGURE 71

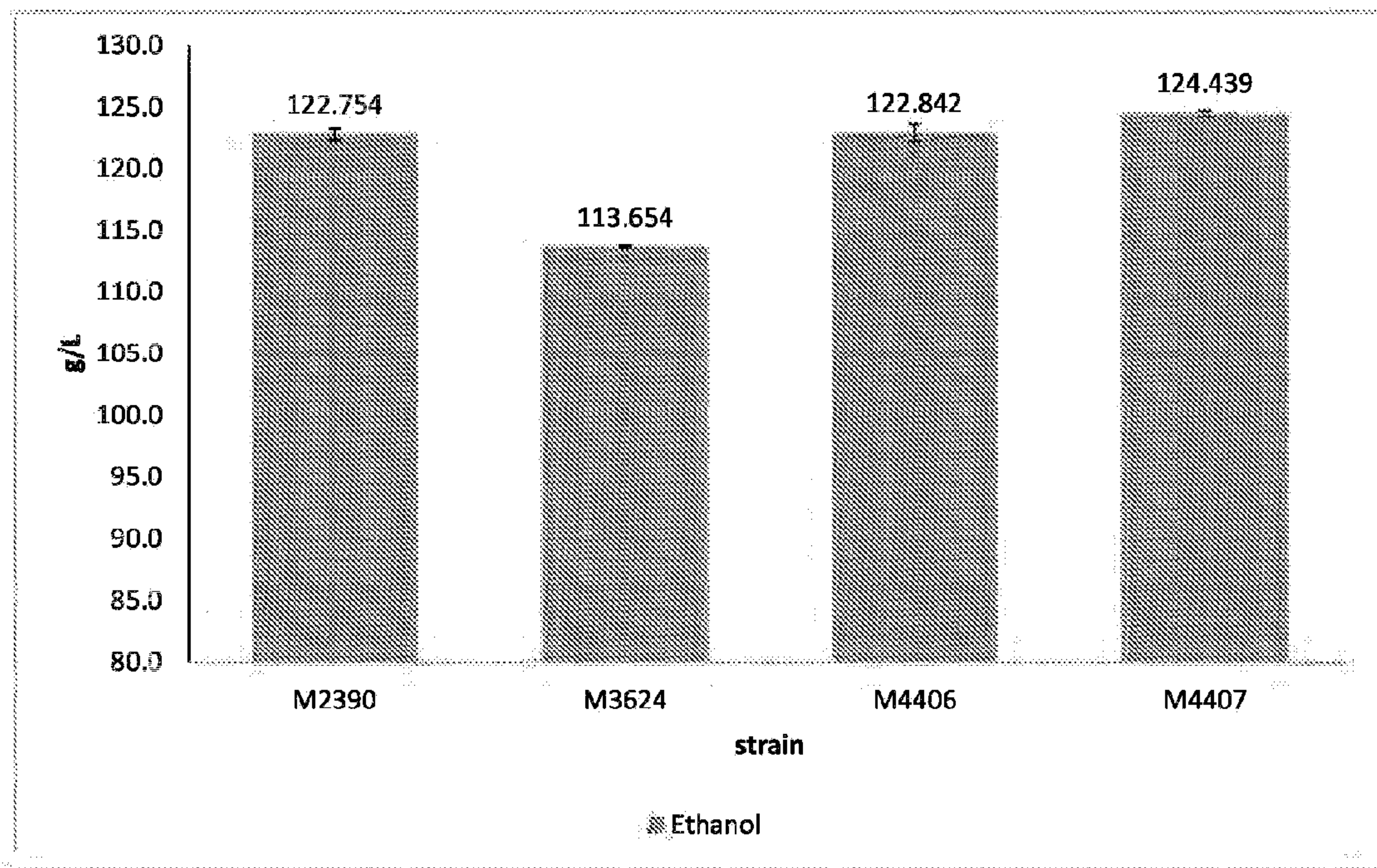


FIGURE 72

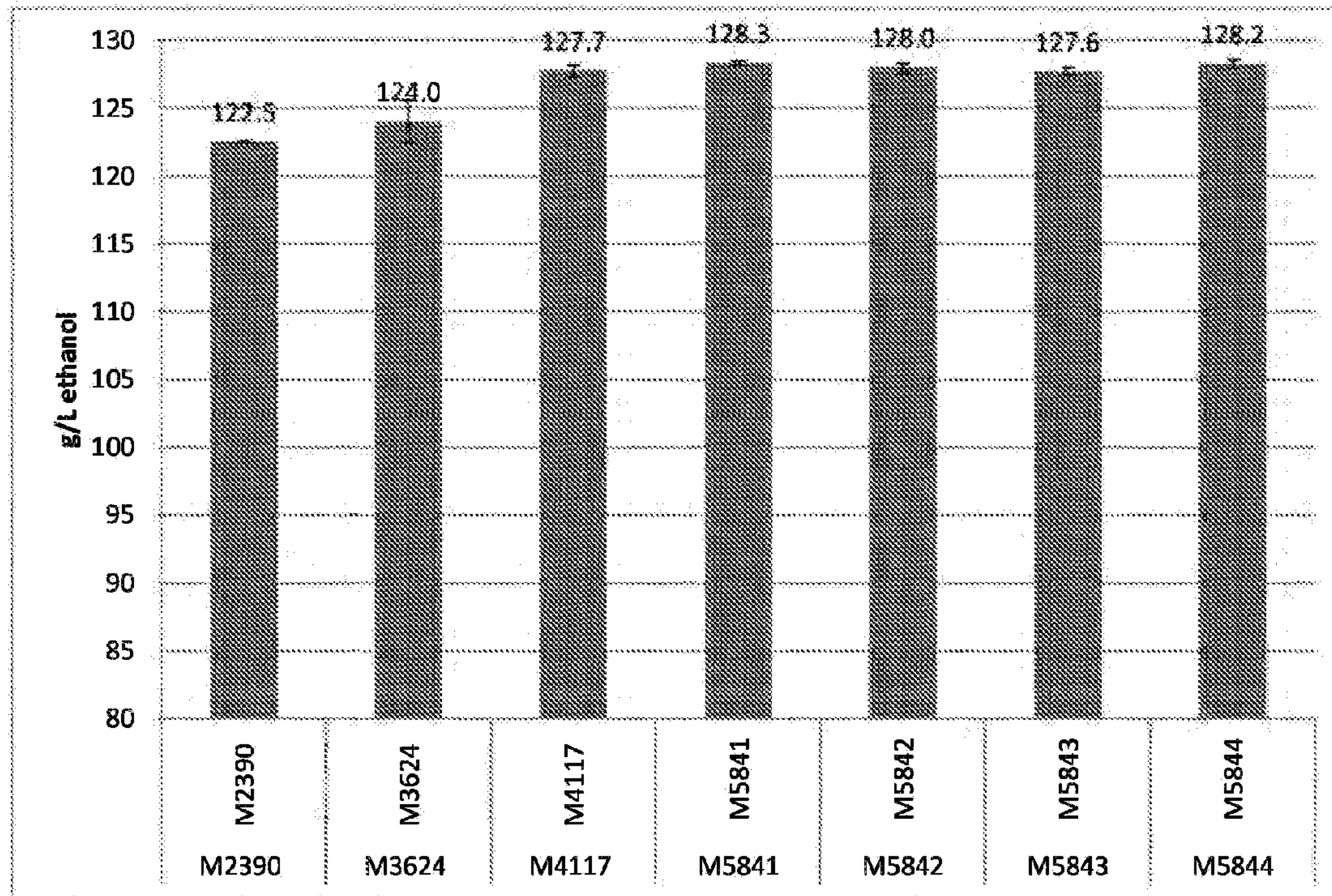


FIGURE 73

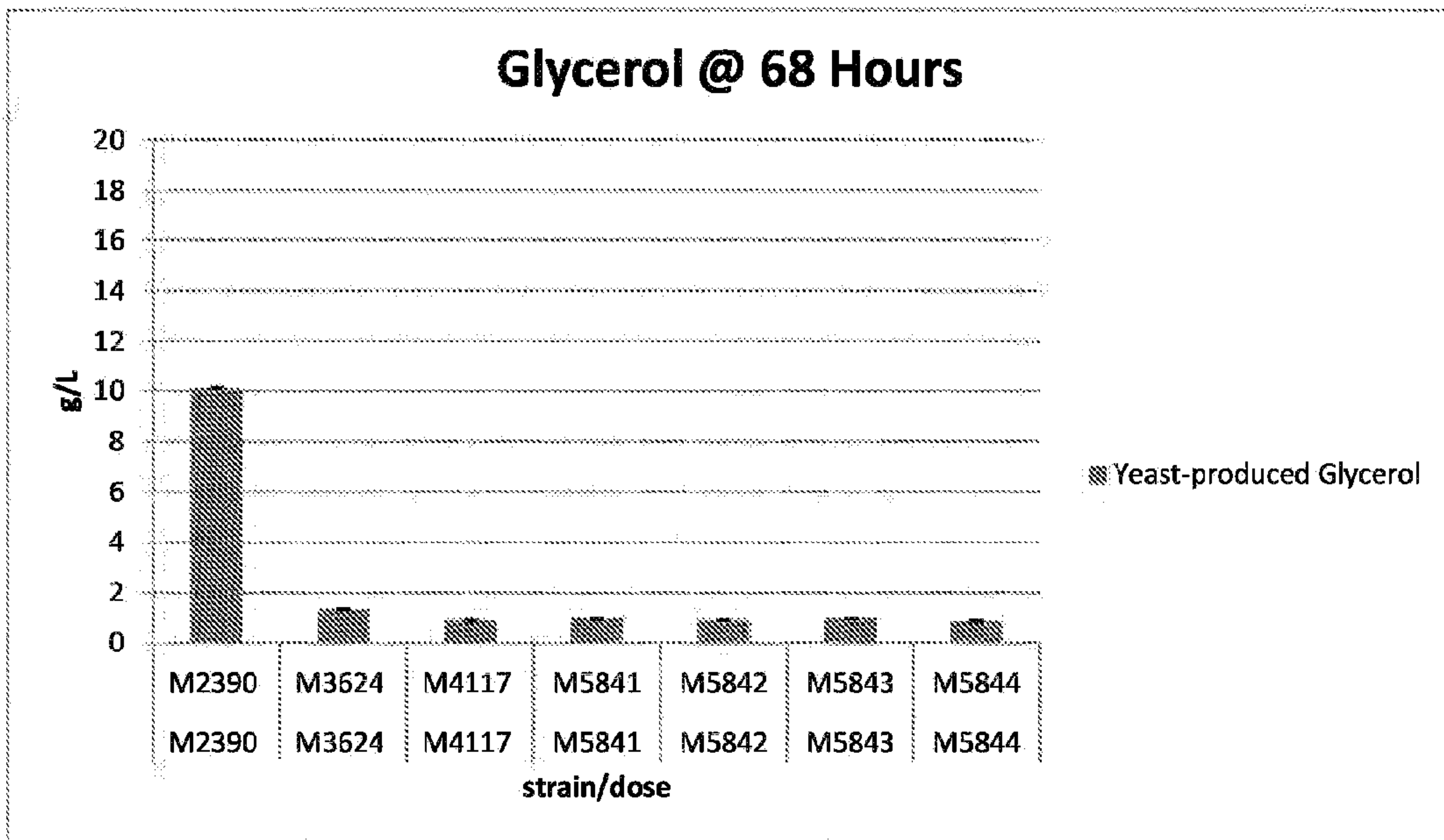


FIGURE 74