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(54) Titre : ACIDE NUCLEIQUE ET FRAGMENTS D'ACIDE NUCLEIQUE CODANT DES POLYPEPTIDES AYANT UNE
ACTIVITE MYC DANS LES VEGETAUX
(54) Title: NUCLEIC ACID AND NUCLEIC ACID FRAGMENTS ENCODING POLYPEPTIDES HAVING MYC ACTIVITY IN
PLANTS

(57) **Abrégé/Abstract:**

The present invention relates to nucleic acids encoding flavonoid biosynthetic enzymes, flavonoid-regulating transcription factors and a flavonoid-specific membrane transporter in plants, and the use thereof for the modification of flavonoid biosynthesis in plants. The present invention also relates to constructs and vectors including such nucleic acids, and related polypeptides. More particularly, the protein involved in flavonoid biosynthesis is selected from the group consisting of: MADS box factor, WRKY box factor, MYC factor, TT1, HLH factor, MYB factor, FMT, UG3E, GST, OMT, RT, CYTb5, laccase, and ABC transporter proteins, and functionally active fragments and variants thereof.

ABSTRACT

The present invention relates to nucleic acids encoding flavonoid biosynthetic enzymes, flavonoid-regulating transcription factors and a
5 flavonoid-specific membrane transporter in plants, and the use thereof for the modification of flavonoid biosynthesis in plants. The present invention also relates to constructs and vectors including such nucleic acids, and related polypeptides. More particularly, the protein involved in flavonoid biosynthesis is selected from the group consisting of: MADS box factor, WRKY box factor,
10 MYC factor, TT1, HLH factor, MYB factor, FMT, UG3E, GST, OMT, RT, CYTb5, laccase, and ABC transporter proteins, and functionally active fragments and variants thereof.

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Nucleic Acid and Nucleic Acid Fragments Encoding Polypeptides having MYC Activity in Plants

The present invention relates to nucleic acid fragments encoding amino acid sequences for flavonoid biosynthetic enzymes in plants, and the use thereof for the modification of flavonoid biosynthesis in plants.

Flavonoids constitute a relatively diverse family of aromatic molecules that are derived from phenylalanine and malonyl-coenzyme A (CoA, via the fatty acid pathway). These compounds include six major subgroups that are found in most higher plants: the chalcones, flavones, flavonols, flavandiols, anthocyanins and condensed tannins (or proanthocyanidins). A seventh group, the aurones, is widespread, but not ubiquitous.

Some plant species also synthesize specialised forms of flavonoids, such as the isoflavonoids that are found in legumes and a small number of non-legume plants. Similarly, sorghum, maize and gloxinia are among the few species known to synthesize 3-deoxyanthocyanins (or phlobaphenes in the polymerised form). The stilbenes, which are closely related to flavonoids, are synthesised by another group of unrelated species that includes grape, peanut and pine.

Besides providing pigmentation to flowers, fruits, seeds, and leaves, flavonoids also have key roles in signalling between plants and microbes, in male fertility of some plant species, in defense as antimicrobial agents and feeding deterrents, and in UV protection.

Flavonoids also have significant activities when ingested by animals, and there is great interest in their potential health benefits, particularly for compounds such as isoflavonoids, which have been linked to anticancer benefits, and stilbenes that are believed to contribute to reduced heart disease.

The major branch pathways of flavonoid biosynthesis start with general phenylpropanoid metabolism and lead to the nine major subgroups: the colorless chalcones, aurones, isoflavonoids, flavones, flavonols, flavandiols, anthocyanins, condensed tannins, and phlobaphene pigments. The enzyme phenylalanine ammonia-

lyase (PAL) of the general phenylpropanoid pathway will lead to the production of cinnamic acid. Cinnamate-4-hydroxylase (C4H) will produce p-coumaric acid which will be converted through the action of 4-coumaroyl:CoA-ligase (4CL) to the production of 4-coumaroyl-CoA and malonyl-CoA. Chalcone synthase (CHS) uses malonyl CoA and 4-coumaroyl CoA as substrates. Chalcone reductase (CHR) balances the production of 5-hydroxy- or 5-deoxyflavonoids. The next enzyme, chalcone isomerase (CHI) catalyses ring closure to form a flavanone, but the reaction can also occur spontaneously. Further enzymes in the pathway are: flavanone 3-hydroxylase (F3H), dihydroflavonol 4-reductase (DFR), flavonoid 3'-hydroxylase (F3'H) and flavonoid 3', 5' hydroxylase (F3'5'H). A specific cytochrome b5 may act as an electron donor for F3'5'H enzymes.

In the branch of the phenylpropanoid pathway that is specific to condensed tannin and anthocyanin production, leucoanthocyanidins can be reduced to catechins by leucoanthocyanidin reductase (LAR) or to anthocyanidins by leucoanthocyanidin dioxygenase (LDOX). Anthocyanidins can be converted to anthocyanins by the addition of sugar groups, or to epicatechins by anthocyanidin reductase (ANR), encoded by the *BANYULS* gene. Catechins and epicatechins are the subunits of condensed tannins, which in *Arabidopsis* are thought to be transported into the vacuole by a multidrug secondary transporter-like protein, TRANSPARENT TESTA 12 (TT12), and polymerised by the activity of a laccase.

Enzymes in the flavonoid pathway have been found to be controlled by a range of transcription factors in *Arabidopsis*, maize and petunia. In *Arabidopsis*, condensed tannin biosynthesis requires the function of TRANSPARENT TESTA 2 (TT2), a R2R3 MYB family factor, TRANSPARENT TESTA 8 (TT8), a MYC/helix-loop-helix (bHLH) family factor and TRANSPARENT TESTA GLABRA 1 (TTG1), a WD40 family factor. These three proteins are thought to form a transcription complex that coordinately activates multiple flavonoid pathway enzymes in order to promote condensed tannin production in *Arabidopsis* seeds. Other myc and myb family transcription factors regulate distinct parts of the flavonoid pathway in maize, petunia and other plant species. Other transcription factors, including TRANSPARENT TESTA GLABRA 2 (TTG2) a WRKY box family member, TRANSPARENT TESTA 16 (TT16) a MADS box family member and TRANSPARENT TESTA 1 (TT1), a WIP family zinc finger factor,

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control the differentiation of condensed tannin-producing cells in the *Arabidopsis* seed coat. It is interesting that TTG2 also controls the development of trichomes in *Arabidopsis* and that glandular trichomes are the only sites of condensed tannin or monomer accumulation in vegetative organs of white clover.

A number of enzymes are involved in anthocyanin biosynthesis in plants. Anthocyanin biosynthesis begins in the cytoplasm with glycosylation and methylation of anthocyanidin molecules by flavonoid glycosyltransferases, rhamnosyltransferases and methyltransferases altering the hydrophilicity of their backbone as well as their stability and chemical properties. Addition of functional groups to flavonoids can also influence their intracellular transport and bioactivity. Expression of genes encoding glucosyltransferases has been shown to be critical for anthocyanin biosynthesis in some pigmented berries and in flower petals of some plants. Other sugar metabolism genes, including UDP glucose 4-epimerases, may be involved in the catabolism of complex carbohydrates to provide the sugar moieties used by glucosyltransferases and rhamnosyltransferases. Although anthocyanin biosynthesis occurs in the cytoplasm, anthocyanins accumulate in the vacuole of pigmented plant cells and there is evidence that specific glutathione-S-transferases and ATP-binding cassette (ABC) transporters of the multi-drug resistance-associated protein (MRP) family are involved in this subcellular transport.

While nucleic acid sequences encoding flavonoid methyltransferase (FMT), UDP glucose-3-epimerase (UG3E), glutathione-S-transferase (GST), O-methyltransferase (OMT), rhamnosyltransferase (RT), cytochrome b5 (CYTb5) and laccase-like enzymes, MADS box, WRKY, MYC, TT1, HLH and MYB transcription factors and ABC transporters, and like polypeptides, have been isolated for certain species of plants, there remains a need for materials useful in modifying flavonoid biosynthesis and metabolism; in modifying protein binding, metal chelation, anti-oxidation, and UV-light absorption; in modifying plant pigment production; in modifying plant defense to biotic stresses such as viruses, microorganisms, insects, fungal pathogens; in modifying forage quality, for example by disrupting protein foam and conferring protection from rumen pasture bloat, particularly in forage legumes, including alfalfa, medics and clovers, and for methods for their use.

It is an object of the present invention to overcome, or at least alleviate, one or more of the difficulties or deficiencies associated with the prior art.

In one aspect, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a polypeptide selected from the group consisting of flavonoid biosynthetic enzymes FMT, UG3E, GST, OMT, RT, CYTb5 and laccase, flavonoid biosynthesis-regulating transcription factors MADS box, WRKY, MYC, TT1, HLH and MYB, and an ABC transporter, from a clover (*Trifolium*) or medic (*Medicago*) species, complements thereof, sequences antisense thereto, and functionally active fragments and variants thereof.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of proteins which are related to FMTs, UG3Es, GSTs, OMTs, RTs, CYTb5s and laccase enzymes, MADS box, WRKY, MYC, TT1, HLH and MYB transcription factors and ABC transporters, or functionally active fragments or variants thereof. Such proteins are referred to herein as FMT-like, UG3E-like, GST-like, OMT-like, RT-like, CYTb5-like and laccase-like, MADS box-like, WRKY-like, MYC-like, TT1-like, HLH-like and MYB-like and ABC transporter-like, respectively.

By a -like polypeptide is meant that either one of both of the following criteria apply: (i) the gene which encodes the -like polypeptide is expressed in a similar manner to the polypeptide, and (ii) the -like polypeptide has similar functional activity to the polypeptide. In a preferred embodiment, the -like polypeptide has at least approximately 70%, preferably at least approximately 80%, more preferably at least approximately 90% identity to the polypeptide.

Also provided are substantially purified or isolated nucleic acids or nucleic acid fragments complementary or antisense to nucleic acid fragments encoding -like polypeptides.

More particularly, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a polypeptide selected from the group

consisting of flavonoid biosynthesis-regulating transcription factors MADS box, MADS box-like, WRKY, WRKY-like, MYC, MYC-like, TT1, TT1-like, HLH, HLH-like, MYB, and MYB -like; flavonoid biosynthetic enzymes FMT, FMT-like UG3E, UG3E-like, GST, GST-like, OMT, OMT-like, RT, RT-like, CYTb5, CYTb5-like, laccase and laccase-like; and flavonoid-related ABC transporter and ABC transporter-like protein; from a clover (*Trifolium*) or medic (*Medicago*) species; or a functionally active fragment or variant thereof.

The individual or simultaneous enhancement or otherwise manipulation of FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC-type transporter or like gene activities in plants may enhance, reduce or otherwise alter flavonoid biosynthesis or metabolism; may enhance, reduce or otherwise alter the plant capacity for protein binding, metal chelation, anti-oxidation, and UV-light absorption; may enhance, reduce or otherwise alter plant pigment production.

The individual or simultaneous enhancement or otherwise manipulation of FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC-type transporter or like gene activities in plants has significant consequences for a range of applications in, for example, plant production and plant protection. For example, it has applications in increasing plant tolerance and plant defense to biotic stresses such as viruses, microorganisms, insects and fungal pathogens; in improving plant forage quality, for example by disrupting protein foam and in conferring protection from rumen pasture bloat; in reducing digestion rates in the rumen and reducing parasitic load; in the production of plant compounds leading to health benefits, such as isoflavonoids, which have been linked to anticancer benefits, and stilbenes that are believed to contribute to reduced heart disease.

Methods for the manipulation of FMT, UG3E, GST, OMT, RT, CYTb5 and laccase, MADS box, WRKY, MYC, TT1, HLH and MYB and ABC-type transporter or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and medics (*Medicago* species) may facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to biotic stresses such as viruses, microorganisms, insects and fungal pathogens;

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altered pigmentation in flowers; forage legumes with enhanced herbage quality and bloat-safety; crops with enhanced isoflavonoid content leading to health benefits.

The use of transcription factors to modify multiple product-specific enzymes in the flavonoid pathway may be a useful alternative strategy to cloning genes encoding many enzymes and modifying their expression in transgenic plants.

While Applicant does not wish to be restricted by theory, the down-regulation of gene(s) encoding proteins involved in the addition of functional groups to anthocyanins and their transport to the vacuole may block the anthocyanin-specific branch of the flavonoid pathway in plants by a negative feedback mechanism. This may upregulate the condensed tannin pathway, which significantly overlaps with anthocyanin biosynthesis until the biosynthesis of leucoanthocyanidins. A metabolic engineering approach that combines the down-regulation of anthocyanin-related genes with over-expression of key genes involved in condensed tannin biosynthesis, such as BAN and LAR and optionally genes involved in the general flavonoid pathway may activate the condensed tannin pathway in anthocyanin-producing cells in the foliage of pasture legumes, conferring bloat-safety.

The clover (*Trifolium*) or medic (*Medicago*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Preferably, the species is white clover (*T. repens*) or alfalfa (*Medicago sativa*). White clover (*Trifolium repens* L.) and alfalfa (*Medicago sativa*) are key pasture legumes, in temperate climates throughout the world.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

Nucleic acids according to the invention may be full-length genes or part thereof, and are also referred to as "nucleic acid fragments" and "nucleotide sequences" in this

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specification. For convenience, the expression "nucleic acid or nucleic acid fragment" is used to cover all of these.

By 'substantially purified' is meant that the nucleic acid is free of the genes, which, in the naturally-occurring genome of the organism from which the nucleic acid of the invention is derived, flank the nucleic acid. The term therefore includes, for example, a nucleic acid which is incorporated into a vector; into an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote; or which exists as a separate molecule (eg. a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a nucleic acid which is part of a hybrid gene encoding additional polypeptide sequence. Preferably, the substantially purified nucleic acid is 90%, more preferably 95%, even more preferably 98% pure.

The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid present in a living plant is not isolated, but the same nucleic acid separated from some or all of the coexisting materials in the natural system, is isolated. Such nucleic acids could be part of a vector and/or such nucleic acids could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment.

Such nucleic acids or nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a polypeptide selected from the group consisting of FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC-type transporter proteins, or complementary or antisense to a sequence encoding said polypeptide, and including a nucleotide sequence selected from the group consisting of (a) the sequences shown in Figures 1, 3, 4, 6, 7, 9, 10, 12, 13, 15, 17, 20, 23, 25, 26, 28, 30, 32, 35, 37, 38, 40, 41, 43 45 and 48 hereto; (b) the complements of the sequences recited in (a); (c) the sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

By "functionally active" in relation to nucleic acids it is meant that the fragment or variant (such as an analogue, derivative or mutant) encodes a polypeptide which is capable of modifying flavonoid biosynthesis; in a plant. Such variants include naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the relevant part of the nucleotide sequence upon which the fragment or variant is based, more preferably at least approximately 90% identity, even more preferably at least approximately 95% identity, most preferably at least approximately 98% identity. Such functionally active variants and fragments include, for example, those having conservative nucleic acid changes. By 'conservative nucleic acid changes' is meant nucleic acid substitutions that result in conservation of the same amino acid in the encoded protein, due to the degeneracy of the genetic code. Such functionally active variants and fragments also include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. By 'conservative amino acid substitutions' is meant the substitution of an amino acid by another one of the same class, the classes being as follows:

Nonpolar: Ala, Val, Leu, Ile, Pro, Met Phe, Trp

Uncharged polar: Gly, Ser, Thr, Cys, Tyr, Asn, Gln

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Acidic: Asp, Glu

Basic: Lys, Arg, His

Other conservative amino acid substitutions may also be made as follows:

Aromatic: Phe, Tyr, His

Proton Donor: Asn, Gln, Lys, Arg, His, Trp

Proton Acceptor: Glu, Asp, Thr, Ser, Tyr, Asn, Gln

Preferably the fragment has a size of at least 30 nucleotides, more preferably at least 45 nucleotides, more preferably at least 60 nucleotides, more preferably at least 100 nucleotides, even more preferably at least 150 nucleotides.

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding an FMT or FMT-like protein, or complementary or antisense to a sequence encoding an FMT or FMT-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequences shown in Figures 1 and 3 hereto (Sequence ID Nos: 1 and 3-10); (b) the complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a UG3E or UG3E-like protein, or complementary or antisense to a sequence encoding a UG3E or UG3E-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequences shown in Figure 4 and 6 hereto (Sequence ID Nos: 11, 13 and 14); (b) the complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a GST or GST-like protein, or

complementary or antisense to a sequence encoding a GST or GST-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequences shown in Figures 7 and 9 hereto (Sequence ID Nos: 15, 17 and 18); (b) the complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding an OMT or OMT-like protein, or complementary or antisense to a sequence encoding an OMT or OMT-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequences shown in Figures 10 and 12 hereto (Sequence ID Nos: 19 and 21-29); (b) the complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding an RT or RT-like protein, or complementary or antisense to a sequence encoding a RT or RT-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequence shown in Figure 13 hereto (Sequence ID No: 30); (b) the complement of the sequence recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CYTb5 or CYTb5-like protein, or complementary or antisense to a sequence encoding a CYTb5 or CYTb5-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequence shown in Figure 15 hereto (Sequence ID No: 32); (b) the complement of the sequence recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a laccase or laccase-like protein, or complementary or antisense to a sequence encoding a laccase or laccase-like protein, and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 17 and 20 hereto (Sequence ID Nos: 34 and 36, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a MADS box or MADS box-like protein, or complementary or antisense to a sequence encoding a MADS box or MADS box-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequences shown in Figures 23 and 25 hereto (Sequence ID Nos: 38 and 40-43); (b) the complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a WRKY or WRKY-like protein, or complementary or antisense to a sequence encoding a WRKY or WRKY-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequence shown in Figure 26 hereto (Sequence ID No: 44); (b) the complement of the sequence recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a MYC or MYC-like protein, or complementary or antisense to a sequence encoding a MYC or MYC-like protein, and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 28, 30 and 32 hereto (Sequence ID Nos: 46, 48, 49 and 50); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences

recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a TT1 or TT1-like protein, or complementary or antisense to a sequence encoding a TT1 or TT1-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequences shown in Figures 35 and 37 hereto (Sequence ID Nos: 52, 54 and 55); (b) the complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding an HLH or HLH-like protein, or complementary or antisense to a sequence encoding an HLH or HLH-like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequences shown in Figures 38 and 40 hereto (Sequence ID Nos: 5, 56, 58 and 59); (b) the complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding a MYB or MYB-like protein, or complementary or antisense to a sequence encoding a MYB or MYB-like protein, and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 41, 43 and 45 hereto (Sequence ID Nos: 60, 62, 63 and 64); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment encoding an ABC transporter or ABC transporter-like protein, or complementary or antisense to a sequence encoding a ABC

transporter or ABC transporter -like protein, and including a nucleotide sequence selected from the group consisting of (a) the sequence shown in Figure 48 hereto (Sequence ID No: 66); (b) the complement of the sequence recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a particularly preferred embodiment, the present invention provides a substantially purified or isolated nucleic acid or nucleic acid fragment comprising a nucleotide sequence selected from the group consisting of the sequences shown in Figures 1, 3 4, 6 7, 9 10, 12, 13, 15, 17, 20, 23, 25, 26, 28, 30, 32, 35, 37, 38, 39, 41, 43, 45 and 48 hereto; and the sequences complementary and antisense thereto.

Nucleic acids or nucleic acid fragments encoding at least a portion of FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC-type transporter orthologs have been isolated and identified. The nucleic acids or nucleic acid fragments of the present invention may be used to isolate cDNAs and genes encoding homologous proteins from the same or other plant species. Isolation of homologous genes using sequence-dependent protocols, such as methods of nucleic acid hybridisation, and methods of DNA and RNA amplification as exemplified by various uses of nucleic acid amplification technologies (e.g. polymerase chain reaction, ligase chain reaction), is well known in the art.

For example, genes encoding other FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC-type transporter proteins, either as cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to

amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol (Frohman *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:8998, the entire disclosure of which is incorporated herein by reference) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated (Ohara *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:5673; Loh *et al.* (1989) *Science* 243:217, the entire disclosures of which are incorporated herein by reference). Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a second aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*) or medic (*Medicago*), species, selected from the group consisting of FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC transporter and like proteins; and functionally active fragments and variants thereof.

The clover (*Trifolium*) or medic (*Medicago*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Preferably, the species is white clover (*T. repens*) or alfalfa (*M. sativa*).

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In a preferred embodiment, the present invention provides a substantially purified or isolated polypeptide selected from the group consisting of FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC transporter polypeptides, said polypeptide including an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 11, 14, 16, 18, 21, 24, 27, 29, 33, 36, 39, 42, 46 and 49 hereto, and functionally active fragments and variants thereof.

By "functionally active" in relation to polypeptides it is meant that the fragment or variant has one or more of the biological properties of the polypeptide upon which the fragment or variant is based. Additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the relevant part of the amino acid sequence upon which the fragment or variant is based, more preferably at least approximately 90% identity, even more preferably at least approximately 95% identity, most preferably at least approximately 98% identity. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. By 'conservative amino acid substitutions' is meant the substitution of an amino acid by another one of the same class, the classes being as follows:

Nonpolar: Ala, Val, Leu, Ile, Pro, Met Phe, Trp

Uncharged polar: Gly, Ser, Thr, Cys, Tyr, Asn, Gln

Acidic: Asp, Glu

Basic: Lys, Arg, His

Other conservative amino acid substitutions may also be made as follows:

Aromatic: Phe, Tyr, His

Proton Donor: Asn, Gln, Lys, Arg, His, Trp

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Proton Acceptor: Glu, Asp, Thr, Ser, Tyr, Asn, Gln

Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, more preferably at least 20 amino acids, more preferably at least 50 amino acids.

In a preferred embodiment, the present invention provides a substantially purified or isolated FMT or FMT-like polypeptide including an amino acid sequence shown in Figure 2 hereto (Sequence ID No: 2); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated UG3E or UG3E -like polypeptide including an amino acid sequence shown in Figure 5 hereto (Sequence ID No: 12); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated GST or GST -like polypeptide including an amino acid sequence shown in Figure 8 hereto (Sequence ID No: 16); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated OMT or OMT-like polypeptide including an amino acid sequence shown in Figure 11 hereto (Sequence ID No: 20); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated RT or RT-like polypeptide including an amino acid sequence shown in Figure 14 hereto (Sequence ID No: 31); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated CYTb5 or CYTb5-like polypeptide including an amino acid sequence shown in Figure 16 hereto (Sequence ID No: 33); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated laccase or laccase-like polypeptide including an amino acid sequence selected from the group consisting of sequences shown in Figures 18 and 21 hereto (Sequence ID Nos: 35 and 37, respectively); and functionally active fragments and variants thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated MADS box or MADS box-like polypeptide including an amino acid sequence shown in Figure 24 hereto (Sequence ID No: 39); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated WRKY or WRKY-like polypeptide including an amino acid sequence shown in Figure 27 hereto (Sequence ID No: 45); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated MYC or MYC-like polypeptide including an amino acid sequence selected from the group consisting of sequences shown in Figures 29 and 33 hereto (Sequence ID Nos: 47 and 51, respectively); and functionally active fragments and variants thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated TT1 or TT1-like polypeptide including an amino acid sequence shown in Figure 36 hereto (Sequence ID No: 53); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated HLH or HLH-like polypeptide including an amino acid sequence shown in Figure 39 hereto (Sequence ID No: 57); or a functionally active fragment or variant thereof.

In a preferred embodiment, the present invention provides a substantially purified or isolated MYB or MYB-like polypeptide including an amino acid sequence selected from the group consisting of sequences shown in Figures 42 and 46 hereto (Sequence ID Nos: 61 and 65, respectively); and functionally active fragments and variants thereof.

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In a preferred embodiment, the present invention provides a substantially purified or isolated ABC transporter or ABC transporter-like polypeptide including an amino acid sequence shown in Figure 49 hereto (Sequence ID No: 67); or a functionally active fragment or variant thereof.

In a particularly preferred embodiment, the present invention provides a substantially purified or isolated polypeptide comprising an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 11, 14, 16, 18, 21, 24, 27, 29, 33, 36, 39, 42, 46 and 49 hereto.

In a further embodiment of this aspect of the invention, there is provided a polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing polypeptides are known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention said method including sequencing nucleic acid fragments from a nucleic acid library.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragment may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

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In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa and medics. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to biotic stresses such as viruses, microorganisms, insects, fungal pathogens; in relation to forage quality; in relation to bloat safety; in relation to condensed tannin content; in relation to plant pigmentation. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa and medics.

In a still further aspect of the present invention there is provided a construct including a nucleic acid or nucleic acid fragment according to the present invention.

The term "construct" as used herein refers to an artificially assembled or isolated nucleic acid molecule which includes the gene of interest. In general a construct may include the gene or genes of interest, a marker gene which in some cases can also be the gene of interest and appropriate regulatory sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes vectors but should not be seen as being limited thereto.

In a still further aspect of the present invention there is provided a vector including a nucleic acid or nucleic acid fragment according to the present invention.

The term "vector" as used herein encompasses both cloning and expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

In a preferred embodiment of this aspect of the invention, the vector may include a regulatory element such as a promoter, a nucleic acid or nucleic acid fragment according to the present invention and a terminator; said regulatory element, nucleic acid or nucleic acid fragment and terminator being operatively linked.

By "operatively linked" is meant that said regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of

the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter.

A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (*nos*) and the octopine synthase (*ocs*) genes.

The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (*ori*), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene], and reporter genes (such as beta-glucuronidase (GUS) gene (*gusA*)). The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

The vectors of the present invention may be incorporated into a variety of plants, including dicotyledons (such as arabidopsis, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea), monocotyledons (such as grasses from the genera *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley) and gymnosperms. In a preferred embodiment, the vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

Techniques for incorporating the vectors of the present invention into plant cells (for example by transduction, transfection or transformation) are well known to those skilled in the art. Such techniques include *Agrobacterium* mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, a vector or construct, nucleic acid or nucleic acid fragment of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable species, including dicotyledons, monocotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a dicotyledon, preferably

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forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*).

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell or plant of the present invention and preferably including e.g. transformed with, a vector or construct, nucleic acid or nucleic acid fragment of the present invention.

In a further aspect of the present invention there is provided a method of modifying flavonoid biosynthesis or metabolism; of modifying protein binding, metal chelation, anti-oxidation or UV-light absorption; of modifying plant pigment production; of modifying plant defense to biotic stresses such as viruses, microorganisms, insects, fungal pathogens; or of modifying forage quality by disrupting protein foam and conferring protection from rumen pasture bloat; said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or vector according to the present invention.

By "an effective amount" it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

Using the methods and materials of the present invention, flavonoid biosynthesis or metabolism, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, microorganisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety; isoflavonoid content leading to health benefits, may be increased, decreased or otherwise altered, in a transformed plant relative to an untransformed control plant, for

example by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention, preferably to overexpress the polypeptide or in sense suppression. They may be decreased or otherwise altered, for example by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

One or more nucleic acids of the present invention may be used in the methods, constructs and vectors of the present invention, optionally in combination with one or more nucleic acids described in Applicant's earlier patent applications AU 2002333038, PCT/AU2006/001020 and PCT/AU2006/001590.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus nucleotide sequence of *TrFMTa* (SEQ ID No: 1)

Figure 2 shows the deduced amino acid sequence of *TrFMTa* (SEQ ID No: 2).

Figure 3 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrFMTa* (SEQ ID Nos: 3-10).

Figure 4 shows the consensus nucleotide sequence of *TrUG3Ea* (SEQ ID No: 11).

Figure 5 shows the deduced amino acid sequence of *TrUG3Ea* (SEQ ID No: 12).

Figure 6 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrUG3Ea* (SEQ ID Nos: 13 and 14).

Figure 7 shows the consensus nucleotide sequence of *TrGSTa* (SEQ ID No: 15).

Figure 8 shows the deduced amino acid sequence of TrGSTa (SEQ ID No: 16).

Figure 9 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrGSTa* (SEQ ID Nos: 17 and 18).

Figure 10 shows the consensus nucleotide sequence of *TrOMTa* (SEQ ID No: 19).

Figure 11 shows the deduced amino acid sequence of TrOMTa (SEQ ID No: 20).

Figure 12 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrOMTa* (SEQ ID Nos: 21-29).

Figure 13 shows the nucleotide sequence of *TrRTa* (SEQ ID No: 30).

Figure 14 shows the deduced amino acid sequence of TrRTa (SEQ ID No: 31).

Figure 15 shows the nucleotide sequence of *TrCYTb5a* (SEQ ID No: 32).

Figure 16 shows the deduced amino acid sequence of TrCyTb5a (SEQ ID No: 33).

Figure 17 shows the nucleotide sequence of *TrLACa* (SEQ ID No: 34).

Figure 18 shows the deduced amino acid sequence of TrLACa (SEQ ID No: 35).

Figure 19 shows a plasmid map of the cDNA encoding *TrLACa*.

Figure 20 shows the full nucleotide sequence of the white clover *TrLACa* cDNA (SEQ ID No: 36).

Figure 21 shows the deduced amino acid sequence of the *TrLACa* cDNA (SEQ ID No: 37).

Figure 22 shows plasmid maps of the cDNA encoding *TrLACa* in the sense and antisense orientations in the pPZP221 binary transformation vector

Figure 23 shows the consensus nucleotide sequence of *TrMADSa* (SEQ ID No: 38).

Figure 24 shows the deduced amino acid sequence of *TrMADSa* (SEQ ID No: 39).

Figure 25 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrMADSa* (SEQ ID Nos: 40-43).

Figure 26 shows the nucleotide sequence of *TrWRKYa* (SEQ ID No: 44).

Figure 27 shows the deduced amino acid sequence of *TrWRKYa* (SEQ ID No: 45).

Figure 28 shows the consensus nucleotide sequence of *TrMYCa* (SEQ ID No: 46).

Figure 29 shows the deduced amino acid sequence of *TrMYCa* (SEQ ID No: 47).

Figure 30 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrMYCa* (SEQ ID Nos: 48-49).

Figure 31 shows a plasmid map of the cDNA encoding *TrMYCa*

Figure 32 shows the full nucleotide sequence of the *TrMYCa* cDNA (SEQ ID No: 50).

Figure 33 shows the deduced amino acid sequence of the *TrMYCa* cDNA (SEQ ID No: 51).

Figure 34 shows plasmid maps of the cDNA encoding *TrMYCa* in the sense and antisense orientations in the pPZP221 binary transformation vector

Figure 35 shows the consensus nucleotide sequence of *TrTT1a* (SEQ ID No: 52).

Figure 36 shows the deduced amino acid sequence of *TrTT1a* (SEQ ID No: 53).

Figure 37 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrTT1a* (SEQ ID Nos: 54-55).

Figure 38 shows the consensus nucleotide sequence of *TrHLHa* (SEQ ID No: 56).

Figure 39 shows the deduced amino acid sequence of *TrHLHa* (SEQ ID No: 57).

Figure 40 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrHLHa* (SEQ ID Nos: 58 and 59).

Figure 41 shows the consensus nucleotide sequence of *TrMYBa* (SEQ ID No: 60).

Figure 42 shows the deduced amino acid sequence of *TrMYBa* (SEQ ID No: 61).

Figure 43 shows the nucleotide sequences of nucleic acid fragments contributing to the consensus sequence of *TrMYBa* (SEQ ID Nos: 62-63).

Figure 44 shows a plasmid map of the cDNA encoding *TrMYBa*.

Figure 45 shows the full nucleotide sequence of the *TrMYBa* cDNA (SEQ ID No: 64).

Figure 46 shows the deduced amino acid sequence of the *TrMYBa* cDNA (SEQ ID No: 65).

Figure 47 shows plasmid maps of the cDNA encoding *TrMYBa* in the sense and antisense orientations in the pPZP221 binary transformation vector

Figure 48 shows the nucleotide sequence of *TrABCa* (SEQ ID No: 66).

Figure 49 shows the deduced amino acid sequence of *TrABCa* (SEQ ID No: 67).

Figure 50 shows a plasmid map of the pDONR221 GATEWAY entry vector (Invitrogen, Carlsbad, USA).

Figure 51 shows the steps of selection during *Agrobacterium*-mediated white clover transformation

Figure 52 shows 4-dimethylaminocinnemaldehyde (DMACA) staining patterns in *Trifolium repens* (cv 'Mink') leaf and immature inflorescence tissue and in *Lotus corniculatus* (cv 'Draco') leaf tissue

Figure 53 shows the results of microarray (lines) and real-time RT-PCR (bars) analyses of *TrMYB24a* expression in upper and lower halves of white clover (cv Mink) inflorescences at three stages of development (upper panel). Real-time RT-PCR analysis was also used to test *TrMYB24a* expression in sepals (dark bars) or remaining floral organs (florets without sepals; light bars) from florets at 4 stages of development (lower panel). More particularly, the graphs show expression of *TrMYB24a* normalised against expression of the elongation factor 1 alpha (EF-1 α) control gene. Complementary DNA from white clover (cv Mink) upper, lower and whole buds was tested by real-time RT-PCR using SYBR Green chemistry, primer sets designed using cDNA clones of flavonoid-related genes (Table 4). Microarray analysis was performed using custom-made 12K Combimatrix slides containing oligonucleotide probes based on white clover cDNA sequences. All experiments were performed in triplicate.

Figure 54 shows an alignment of the conserved R2 and R3 MYB domains of *TrMYB24a* and corresponding regions of R2R3 MYB proteins from the plant species *Petunia hybrida*, *Antirrhinum majus*, *Arabidopsis thaliana*, *Vitis vinifera*, *Zea mays*, *Oryza sativa*, *Lycopersicon esculentum* and *Picea mariana*.

Figure 55 shows a phylogenetic tree based on parsimony, comparing the amino acid sequences of *TrMYB24a* and R2R3 MYB proteins from the plant species *Malus domestica*, *Arabidopsis thaliana*, *Gossypium hirsutum*, *Zea mays*, *Petunia hybrida*, *Vitis vinifera*, *Antirrhinum majus*, *Oryza sativa*, *Lycopersicon esculentum* and *Antirrhinum majus*.

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Example 1

Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC transporter and like proteins from white clover (*Trifolium repens*)

cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) were prepared. The characteristics of the white clover libraries are described below (Table 1).

TABLE 1

cDNA libraries from white clover (*Trifolium repens*)

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 & 28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated plants
04wc	Cut leaf and stem collected after 0, 1, 4, 6 & 14 h after cutting
05wc	Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at –80°C, imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials
15wc	Senescing stolon
16wc	Senescing leaf

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into *Escherichia coli* Epicurian coli XL10-Gold ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser.

Example 2

DNA sequence analyses

cDNA clones encoding FMT, UG3E, GST, OMT, RT, CYTb5, MADS, WRKY, MYC, TT1, HLH, MYB, ABC and -like proteins were identified by conducting a BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) search. The DNA sequence was translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the Uniprot protein sequence database using the BLASTx algorithm (v 2.0.1) (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.

Example 3

Identification and full-length sequencing of cDNAs encoding white clover FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC transporter and like proteins

To fully characterise for the purposes of the generation of probes for hybridisation experiments and the generation of transformation vectors, a set of cDNAs encoding white clover FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC transporter and like proteins are identified and fully sequenced by the following method.

Full-length or partial cDNAs were identified from our EST sequence database using relevant published sequences (NCBI databank) as queries for BLAST searches. Full-length cDNAs were identified by alignment of the query and hit sequences using Sequencher (Gene Codes Corp., Ann Arbor, MI 48108, USA). The original cDNA in the pGEM-T easy vector is then used to transform chemically competent DH5 alpha cells (Invitrogen, Carlsbad, USA). At least two colonies per transformation are picked for initial sequencing with M13F and M13R primers. The resulting sequences are aligned with the original EST sequence using Sequencher to confirm identity and one of the two

clones is picked for full-length sequencing, usually the one with the best initial sequencing result.

Sequencing is completed by primer walking, i.e. oligonucleotide primers are designed to the initial sequence and used for further sequencing from the 5' end. In most instances, an extended poly-A tail necessitates the sequencing of the cDNA to be completed from the 5' end.

Contigs are then assembled in Sequencher. The contigs include at least the 5' end of the original EST sequence and extend to at least the poly-A tail at the 3' end of the cDNA.

Plasmid maps and the full cDNA sequences of white clover laccase, MYCa and MYB24a were obtained by this method (Figures 19, 20, 31, 44, 45 and Table 2).

Plasmid maps and full or partial cDNA sequences of white clover FMT, UG3E, GST, OMT, RT, CYTb5, MADS box, WRKY, TT1, HLH and ABC transporter and like genes in the pGEM-T Easy vector are obtained by this method.

TABLE 2

Primers used for sequencing of full-length cDNAs

gene name	clone ID	sequencing primer	primer sequence (5'>3')	SEQ ID No:
TrLACa	14wc1IsC08	14wc1IsC08.f1	CAGCATACATAACCCAATG	90
TrLACa	14wc1IsC08	14wc1IsC08.f2	GAATGGTGGAAATCAGATAC	91
TrMYCa	05wc1KsD09	05wc1KsD09.f1	ACGACTATTCCGGCTCTT	92
TrMYCa	05wc1KsD09	05wc1KsD09.f2	CTGAACAAGAACACCGTAGA	93
TrMYCa	05wc1KsD09	05wc1KsD09.f3a	GCAATTAGGTAGTAATTCTACT	94
TrMYCa	05wc1KsD09	05wc1KsD09.f3b	CTACTGTAATTACTCATCAAG	95

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TrMYCa	05wc1KsD09	05wc1KsD09.f4	GCTCCTAGTGTTGTTTCATG	96
TrMYCa	05wc1KsD09	05wc1KsD09.f5	CTCCGAATTCGAGAGGAAG	97
TrMYCa	05wc1KsD09	05wc1KsD09.f6	ATCATACTACTGAGCTG	98
TrMYCa	05wc1KsD09	05wc1KsD09.r1	GCTTGAAGACGTTGTTGG	99
TrMYB24a	07wc3SsF02	07wc3SsF02.r1	CAGGTAGTTTTGATGCTATG	100

Example 4

Development of binary transformation vectors containing chimeric genes with cDNA sequences from white clover FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC transporter and like proteins

To alter the expression of the proteins involved in flavonoid biosynthesis or metabolism, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, through antisense and/or sense suppression technology and for over-expression of these key proteins in transgenic plants, a set of sense and antisense binary transformation vectors is produced by the following method.

cDNA fragments are generated by high fidelity PCR using the original pGEM-T Easy plasmid cDNA as a template. The primers used contain attB1 and attB2 GATEWAY® recombination sites for directional cloning into the target vector. After PCR amplification and purification of the products, the cDNA fragments are cloned into the recombination site of the pDONR221TM vector (Figure 50) using BP GATEWAY® technology (Invitrogen, Carlsbad, USA). The pPZP221 binary vector (Hajdukiewicz et al., 1994, The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. *Plant Mol. Biol.* **25**:989-994.) was modified to contain the 35S2 cassette from pKYLX71:35S2 as follows. pKYLX71:35S2 was cut with ClaI. The 5' overhang was filled in using Klenow and the blunt end was A-tailed with Taq polymerase. After cutting

with EcoRI, the 2kb fragment with an EcoRI-compatible and a 3'-A tail was gel-purified. pPZP221 was cut with HindIII and the resulting 5' overhang filled in and T-tailed with Taq polymerase. The remainder of the original pPZP221 multi-cloning site was removed by digestion with EcoRI, and the expression cassette cloned into the EcoRI site and the 3' T overhang restoring the HindIII site. This binary vector contains between the left and right border the plant selectable marker gene *aaaC1* under the control of the 35S promoter and 35S terminator and the pKYLX71:35S2-derived expression cassette with a CaMV 35S promoter with a duplicated enhancer region and an *rbcS* terminator. This vector was GATEWAY®-enabled by digesting it with XbaI and blunt-ended using Klenow DNA polymerase, allowing the RfA recombination cassette to be cloned in the sense or antisense orientation between the enhanced 35S promoter and the *rbcS* terminator.

The orientation of the constructs (sense or antisense) is checked by restriction enzyme digestion and sequencing. Transformation vectors containing chimeric genes using full-length open reading frame cDNAs in sense and antisense orientations under the control of the CaMV 35S2 promoter are generated (Figures 22, 34 and 47).

TABLE 3

List of primers used to PCR-amplify the open reading frames of flavonoid-related genes from white clover and expression cassettes used in binary transformation vectors

gene name	clone ID	primer	primer sequence (5'→3')	SEQ ID No:
<i>TrLACa</i>	14wclIsC08	<i>TrLACa.attB1.f</i>	GGGGACAAGTTTGTACAAAAAAGCA GGCTTCATGGCCACGGCGCAATTTC G	101
<i>TrLACa</i>	14wclIsC08	<i>TrLACa.attB2.r</i>	GGGGACCACTTTGTACAAGAAAGCT GGGTCTCAACACTTAGGAAGGTCAC TTGG	102

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TrMYCa	05wc1KsD09	TrMYCa.attB1.f	GGGGACAAGTTTGTACAAAAAAGCA GGCTTCATGAATCTTTGGAGCGACG AGAACTC	103
TrMYCa	05wc1KsD09	TrMYCa.attB2.r	GGGGACCACTTTGTACAAGAAAGCT GGGTCTTATTGAACATCCCCAACTT TAGAGGAC	104
TrMYB24a	07wc3SsF02	TrMYB24a.attB1.f	GGGGACAAGTTTGTACAAAAAAGCA GGCTTCATGGGAAGAGCTCCTTGTT GTGAC	105
TrMYB24a	07wc3SsF02	TrMYB24a.attB2.r	GGGGACCACTTTGTACAAGAAAGCT GGGTCTCAATTTGTCTTAATGTCAG CATAAC	106

Example 5

Production and analysis of transgenic white clover plants carrying chimeric white clover FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC transporter and like genes involved in flavonoid biosynthesis

Transgenic white clover plants carrying white clover genes involved in flavonoid biosynthesis or metabolism, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, are produced by the following method.

pPZP221-based transformation vectors with cDNAs comprising the full open reading frame sequences in sense and antisense orientations under the control of the CaMV 35S promoter with duplicated enhancer region (35S2) are generated as detailed in Example 4.

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Agrobacterium-mediated gene transfer experiments are performed using these transformation vectors.

Preparation of white clover cotyledonary explants

White clover (cv 'Mink') seeds are rinsed for 5 minutes in running tap water and incubated twice, for 5 minutes in 70% v/v ethanol in a 120 ml tissue culture container with gentle shaking. The same container is used to incubate the seeds for 2 minutes in 1% sodium hypochlorite (1:3 ratio of Domestos™ bleach in water) with gentle shaking. The seeds are then rinsed six times in sterile water in a laminar flow hood and incubated for 18 hours at 4°C in the dark. Cotyledonary explants are extracted using 10 ml syringes attached to 21 G needles (Terumo, Japan) under a dissecting microscope in a laminar flow hood. Both layers of the seed coat are peeled away, the end of the hypocotyl is cut off and the cotyledons with approximately 4 mm of hypocotyl are separated and transferred to a 90 x 90 x 20 mm petri dish containing MGL medium.

Preparation of Agrobacterium

Agrobacterium tumefaciens strain AGL-1 containing each PZP221-derived binary expression vector is streaked on LB medium containing 50 µg/ml rifampicin and 100 µg/ml spectinomycin and grown at 27 °C for 48 hours. A single colony is used to inoculate 5 ml of LB medium containing 50 µg/ml rifampicin and 100 µg/ml spectinomycin and grown over night at 27 °C and 250 rpm on an orbital shaker. The overnight culture is used as an inoculum for 40 ml of YEP medium containing 100 µg/ml spectinomycin and 40 mg/l acetosyringone. Incubation is over night at 27 °C and 250 rpm on an orbital shaker in a 250 ml Erlenmeyer flask.

The overnight cultures are centrifuged for 15 min at 5500 xg and the supernatant discarded. The cells are resuspended in MGL media with 40 mg/l acetosyringone to a volume corresponding to an OD₆₀₀ reading of 0.4. The cells are then incubated at 27 °C and 250 rpm until the OD₆₀₀ reading reaches 0.8.

Cocultivation and selection of white clover transformants

The MGL medium is removed from the petri dish containing white clover cotyledonary explants and replaced with the prepared *Agrobacterium* suspension using a sterile serological pipette. The petri dish is sealed with laboratory film, covered with aluminium foil and incubated with gentle shaking for 45 min. The dish is opened in the laminar flow hood and the *Agrobacterium* suspension removed with a pipette. The explants are then transferred to plates containing RM73 media with 40 mg/l acetosyringone (Table 1) and incubated for 3 days in a plant tissue culture room at 22°C with a 16 hour photoperiod. After this, the explants are transferred, with the hypocotyl end in the media, to plates containing RM73 media with 75 mg/l gentamicin and 250 mg/l cefotaxime. The explants are transferred to fresh plates every two weeks for 6-8 weeks. Shoots are then transferred to 120 ml tissue culture vessels containing RIM media (Table 2) with 75 mg/l gentamicin and 250 mg/l cefotaxime. When roots develop, the plantlets are transferred to pots of soil and after 2 weeks of recovery in a misting bench, are grown under standard glasshouse conditions.

Preparation of genomic DNA

1-2 leaflets of white clover plants recovered from the transformation process are harvested and freeze-dried. The tissue is homogenised on a Retsch MM300 mixer mill, then centrifuged for 10 min at 1700xg to collect cell debris. Genomic DNA is isolated from the supernatant using Wizard Magnetic 96 DNA Plant System kits (Promega) on a Biomek FX (Beckman Coulter). 5 µl of the sample (50 µl) is then analysed on an agarose gel to check the yield and the quality of the genomic DNA.

Analysis of DNA from putative transgenic lines using real-time PCR

Genomic DNA is analysed for the presence of the transgene by real-time PCR using SYBR Green chemistry. PCR primer pairs were designed to detect the *aacC1* gentamycin resistance gene in the transferred T-DNA region using MacVector (Accelrys). The sequences of these primers are as follows:

pPZPaacC1-1f 5'-TCAAGTATGGGCATCATTCGCAC-3' (SEQ ID No: 107)

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pPZPaacC1-1.r 5'-TGCTCAAACCGGGCAGAACG-3' (SEQ ID No: 108)

2.5 µl of each genomic DNA sample is run in a 25 µl PCR reaction including SYBR Green on an ABI (Applied Biosystems) together with samples containing DNA isolated from wild type white clover plants (cv 'Mink', negative control), samples containing buffer instead of DNA (buffer control) and samples containing the plasmid used for transformation (positive plasmid control).

TABLE 4

Composition of RM73 tissue culture media, pH 5.75

Component	[Stock]	For 1 litre
MS Macronutrients	10 x	100 mL
MS Micronutrients	100 x	10 mL
MS Vitamins	100 x	10 mL
TDZ	100 mM	50 µL
NAA	1 mM	0.5 mL
Sucrose (BDH Chemicals)	-	30 g
Agar	-	8 g

TABLE 5

Composition of root-inducing tissue culture media (RIM73), pH 5.75

Component	[Stock]	For 1 litre
MS macronutrients	10 x	100 mL
MS micronutrients	100 x	10 mL
MS vitamins	100 x	10 mL
Indole-3-butyric acid	1 mM	1.2 mL
Sucrose (BDH Chemicals)	-	15 g
Agar (Becton-Dickinson)	-	8 g

Example 6

Analysis of condensed tannins and their monomers in the leaves of transgenic white clover plants carrying chimeric white clover FMT, UG3E, GST, OMT, RT, CYTb5, laccase, MADS box, WRKY, MYC, TT1, HLH, MYB and ABC transporter and like genes involved in flavonoid biosynthesis

Accumulation of condensed tannins and their monomers is analysed qualitatively in leaves of transgenic and wild type (cv 'Mink') white clover plants using 4-dimethylaminocinnemaldehyde (DMACA) staining according to the following method.

Two mature leaflets from each plant are decolourised in absolute ethanol in 6-well tissue culture plates for 3 hours with gentle shaking. The ethanol is removed and replaced with a 0.01% w/v solution of DMACA (Fluka), freshly made up in absolute ethanol with 2.4% v/v concentrated hydrochloric acid. After 1 hour of incubation with gentle shaking, the leaflets are rinsed with distilled water and mounted in 50% glycerol for analysis with a dissecting microscope (Figure 52). Wild type white clover plants show blue staining in epidermal cells in the floral organs and in trichomes. *Lotus corniculatus* (cv 'Draco'), a forage legume with a 'bloat-safe' level of condensed tannins in the leaves, shows blue staining of approximately 50% of mesophyll cells in leaves. Achieving a level of condensed tannins in white clover leaves that is comparable to the level seen in leaves of *L. corniculatus* by metabolic engineering would be agronomically valuable.

DMACA staining can detect economically significant levels of condensed tannins and their monomers in the leaves of established bloat-safe forage legumes. However, the condensation of catechin monomers to form condensed tannins and their transport from the cytoplasm to the vacuole is poorly understood. Hence, modifying the regulation of known enzymes and transcription factors in the flavonoid pathway may up-regulate catechin levels but not increase condensed tannin levels, and therefore, bloat-safety. The PVPP-butanol-HCl assay detects only condensed tannins, relying on the ability of condensed tannins, but not their monomers to bind to PVPP. The detailed method is as follows.

Clover leaf and inflorescence (positive control) tissue is snap-frozen and ground to a fine powder in a mortar and pestle under liquid nitrogen. After grinding, 0.75 g of the powder from each sample is transferred to a 14 ml screw-cap centrifuge tube (Falcon), vortex-mixed with 1.5 ml of extraction buffer containing 80% v/v methanol in distilled water with 5.3 mM sodium bisulfite. Samples are mixed for 5 hours on a mixing wheel before centrifugation at 3000 xg for 10 minutes. A 1 ml aliquot of each supernatant is transferred to a 1.5 ml microcentrifuge tube and reduced to 0.25 ml in a vacuum centrifuge. Equal volumes of the sample are added to each of two 1.5 ml microcentrifuge tubes containing 25 mg of polyvinyl polypyrrolidone (PVPP). Each mixture is vortex-mixed intermittently for 15 min and centrifuged for 1 min at maximum speed in a microcentrifuge. After removal of the supernatant, the pellet is washed four times with 1 ml of methanol, with a 1 min centrifugation step at maximum speed in a microcentrifuge between each wash. A freshly-made 70:30 (v/v) solution of butanol and concentrated hydrochloric acid is added to each pellet and one tube of the mixture is incubated for 1 hour at 70°C, whereas the other tube is incubated at ambient temperature. The difference in the absorbance (530 nm) between the two tubes from each plant sample is proportional to the level of condensed tannins in the sample. This assay can be quantitated with a condensed tannin of known concentration.

Example 7

Analysis of the temporal and spatial pattern of flavonoid-related gene expression.

Biochemical, molecular and microscopic analyses suggest that at least two proanthocyanidin (PA) and two anthocyanin (ANT) pathways are active in developing white clover florets. A PA pathway which is developmentally regulated in epidermal cells of IW with accumulation of flavan-3-ol monomers peaking at the stage 3 and sharply down-regulated at the later stages; another PA pathway is active in the trichomes located in sepals at all six developmental stages; an ANT pathway which is developmentally and light-regulated in epidermal cells of IW at the stages 4-6 and ANT pathway that is active at all stages in a small group of cells in sepals (Figure 53).

We monitored the expression pattern of 12,000 *T. repens* genes at six stages of inflorescence development using custom-made CombiMatrix oligonucleotide arrays in order to identify flavonoid genes differentially expressed in developing white clover florets. Each gene was represented by a sequence-specific, 30-40 base pair oligonucleotide. This approach aimed to determine which flavonoid-related genes and isoforms are most likely to be involved in condensed tannin production, or in the production of other flavonoids, and could therefore be targeted for overexpression or downregulation in the metabolic engineering of bloat-safe white clover. The expression of the *TrMYB24a* gene peaked at stage 3 (50% open inflorescence, upper half) and then declined (Figure 53).

Real-time RT-PCR is a recently developed technique that allows more quantitative analyses of gene expression than Northern or conventional RT-PCR experiments. Essentially, real-time RT-PCR with SYBR Green chemistry and gene-specific primers involves the automatic measurement of the level of a fluorescent PCR product generated from a cDNA species over each cycle. The abundance of each template is proportional to the amplification rate. Therefore, a threshold corresponding to the start of the exponential phase of PCR allows the relative abundance of target genes to be standardised against a uniformly expressed 'housekeeping' gene in each tissue and compared to a negative control without a template. Real-time RT-PCR with SYBR Green chemistry has been used successfully by others in the field to quantify the expression of four flavonoid-related genes in *Lotus corniculatus* plants exposed to different light regimes (Paolocci et al., 2005, Light and an exogenous transcription factor qualitatively and quantitatively affect the biosynthetic pathway of condensed tannins in *Lotus corniculatus* leaves. J. Exp. Bot. **56**: 1093-1103).

A Real-Time RT-PCR strategy involving with SYBR Green chemistry and absolute quantification was used to validate the microarray results. Real-time RT-PCR was also used to test whether expression of the *TrMYB24a* gene is restricted to the inner whorls (IW) of white clover florets at inflorescence stages 3, 4, 5 and 6, correlating with PA production.

The full-length cDNA sequences encoding *TrMYB24a* and *TrEF1 α* were used as input data for the Primer Express (Applied Biosystems, Foster City, USA) primer design program, using the default settings, no 3' GC clamp and a predicted amplicon size of 50-150 base pairs. Primers close to the 3' ends of the input sequences are preferred, due to the likelihood of a large number of cDNA molecules derived from clover samples being incomplete at the 5' end.

The specificity of the primer sets was tested using 1 ul of plasmid DNA (0.01 ng/ul) from the original cDNA cloned into pGEM-T Easy or autoclaved, purified water, 12.5 ul 2x SYBR Green Master Mix (Applied Biosystems), 0.5 ul each of the forward and reverse primers (10 uM) and 10.5 ul of autoclaved, purified water (Sartorius AG, Goettingen, Germany). Real-time PCR was performed in 96-well optical PCR plates (Applied Biosystems) using the Stratagene MX3000P cycler and the following cycling parameters: 95°C for 10 min, 40 cycles of 95°C for 30 sec and 60°C for 1 min, followed by 55°C for 1 min and 95°C for 1 min. Primer sets generally amplified a satisfactory level of products from the corresponding cDNA templates with a cycle threshold cut-off of 24 cycles. The primer sets were generally isoform-specific.

Total RNA was extracted from white clover tissues using a CTAB-based method (Chang, S., Puryear, J. and Cairney, J. (1993). A simple and efficient method for isolating RNA from pine trees. *Plant Mol Biol Rep* 11:113-116) and contaminating genomic DNA was digested on the column using the optional on-column DNase digestion method from the RNeasy kit (QIAGEN GmbH, Hilden, Germany) according to the manufacturers' instructions. Complementary DNA (cDNA) is synthesised from 0.5 ug of total RNA using the Quantitect Reverse Transcriptase Kit (QIAGEN GmbH). Real-time RT-PCR reactions are set up and run as described earlier using 1 ul of cDNA, plasmid control DNA or autoclaved, purified water as the template.

Real-time RT-PCR results supported the expression profile of *TrMYB24a* seen in the microarray experiment. *TrMYB24a* was also found to be expressed at a significantly higher level in inner whorls than in sepals (Figure 53).

TABLE 6

List of primers designed for Real-time RT-PCR analysis of condensed tannin-rich organs of white clover, based on the cDNA sequences of white clover genes

Gene name	Clone ID	primer 1 (forward)	primer 2 (reverse)
<i>TrEF-1α</i>	14wc2PsG04	TCGAGAAGGAAGCTGCTGAAA (SEQ ID No. 109)	CCCAGGCATACTTGAATGACCT (SEQ ID No. 110)
<i>TrMYB24a</i>	07wc3SsF02	TGAATCTTTGGAACCACTAATGGA (SEQ ID No. 111)	AAGCAACAACCTTGAAGCAAATCA (SEQ ID No. 112)

Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

CLAIMS:

1. A substantially purified or isolated nucleic acid or nucleic acid fragment encoding a MYC protein, or complementary or antisense to a sequence encoding a MYC protein, said nucleic acid or nucleic acid fragment comprising a nucleotide sequence selected from the group consisting of

- (a) Sequence ID Nos: 46, 48, 49 and 50;
- (b) full-length complements of the sequences recited in (a);
- (c) sequences antisense to the sequences recited in (a) and (b) having a size of at least 60 nucleotides and having antisense activity;
- (d) functionally active fragments of the sequences recited in (a), having a size of at least 60 nucleotides; and encoding a polypeptide with MYC activity; and
- (e) functionally active variants of the sequences recited in (a) and (d), wherein said functionally active variants have at least 95% identity to the sequence recited in (a) or (d); and encode a polypeptide with MYC activity.

2. The nucleic acid or nucleic acid fragment according to claim 1, wherein said functionally active fragments have a size of at least 100 nucleotides and said functionally active variants have at least 95% identity to the sequence recited in (a) or (d).

3. The nucleic acid or nucleic acid fragment according to claim 1, wherein said functionally active fragments have a size of at least 150 nucleotides and said functionally active variants have at least 98% identity to the sequence recited in (a) or (d).

4. The nucleic acid or nucleic acid fragment according to claim 1, wherein said nucleic acid or nucleic acid fragment comprises a nucleotide sequence selected from the group consisting of sequences shown in Sequence ID Nos: 46, 48, 49 and 50.

5. The nucleic acid or nucleic acid fragment according to any one of claims 1 to 4, wherein said nucleic acid is from a *Trifolium* or *Medicago* species.

6. The nucleic acid or nucleic acid fragment according to claim 5, wherein said nucleic acid is from a *Trifolium* species.

7. The nucleic acid or nucleic acid fragment according to claim 6, wherein said *Trifolium* species is *Trifolium repens*.

8. A polypeptide encoded by the nucleic acid or nucleic acid fragment according to any one of claims 1 to 7.

9. A construct comprising the nucleic acid or nucleic acid fragment according to any one of claims 1 to 7.

10. A vector comprising the nucleic acid or nucleic acid fragment according to claims 1 to 7.

11. The vector according to claim 10, further comprising a promoter and a terminator, said promoter, said nucleic acid or nucleic acid fragment and said terminator being operatively linked.

12. A plant cell comprising the construct according to claim 9 or the vector according to claim 10 or 11.

13. A substantially purified or isolated MYC polypeptide, said polypeptide comprising an amino acid sequence selected from the group consisting of

(a) Sequence ID Nos: 47 and 51;

(b) functionally active fragments of the sequences recited in (a) having a size of at least 50 amino acids; and having MYC activity; and

(c) functionally active variants of the sequences recited in (a) and (b), said functionally active variants having at least 95% identity to the sequence recited in (a) or (b) and having MYC activity.

14. The polypeptide according to claim 13, wherein said functionally active variants have at least 98% identity to the sequences recited in (a) and (b).

15. The polypeptide according to claim 13, wherein said polypeptide comprises an amino acid sequence selected from

(a) Sequence ID Nos: 47 and 51; and

(b) functionally active fragments of the sequences recited in (a) having a size of at least 50 amino acids; and having MYC activity.

16. The polypeptide according to claim 13, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of Sequence ID Nos: 47 and 51.

17. The polypeptide according to any one of claims 13 to 16, wherein said polypeptide is from a *Trifolium* or *Medicago* species.

18. The polypeptide according to claim 17, wherein said polypeptide is from a *Trifolium* species.

19. The polypeptide according to claim 18, wherein said *Trifolium* species is *Trifolium repens*.

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FIGURE 1

	*	20	*	40	*	60	
TrFMTa :	ATCTCTCAACAGTTCCTTAACCCCATTTTCATATCATTTCTTAAGTAACAGATCTCATCTT						: 60
	*	80	*	100	*	120	
TrFMTa :	TCGATCCATCATCTAAATTTTCTTCCTTTCTTAATTTGCTTAATATTATTTTACGATCC						: 120
	*	140	*	160	*	180	
TrFMTa :	AAGGTTCTAGATGGCAAACCAAGTGCTGCTGATAATAGGACTAGAAGTTCTGTGCAGAT						: 180
	*	200	*	220	*	240	
TrFMTa :	CTTTATAGTAGTTGGTTTGTGCTGTTTCTTCTATATATTGGGAGCGTGGCAAAGAAGTGG						: 240
	*	260	*	280	*	300	
TrFMTa :	ATTTGGAAAAGGAGATAGCATAGCATTAGAGATTACCAAGAATAATGCTGAATGTGATGT						: 300
	*	320	*	340	*	360	
TrFMTa :	AGTTCCAAATTTAAGTTTTGATTCACACCATGCTGGAGAAGTTAGTCAAATCGATGAATC						: 360
	*	380	*	400	*	420	
TrFMTa :	TGATTCAAAGGCTAAGGTGTTTAAACCGTGTGATGCTCGTTATACGGATTACACTCCGTG						: 420
	*	440	*	460	*	480	
TrFMTa :	TCAAGATCAACGTCGTGCTATGACATTTCTAGAGAAAACATGAACTATAGAGAGAGACA						: 480
	*	500	*	520	*	540	
TrFMTa :	TTGCCCTCCAGAGGAAGAGAAGTTACACTGTATGATCCCTGCACCAAAGGTTATGTAAC						: 540
	*	560	*	580	*	600	
TrFMTa :	ACCTTTTCCATGGCCTAAGAGTAGGGATTATGTTCTTATGCTAATGCACCCTACAAGAG						: 600
	*	620	*	640	*	660	
TrFMTa :	TCTCACAGTTGAGAAGGCCATTGAGAATTGGATCCAATATGAGGGAAATGTGTTAAGATT						: 660
	*	680	*	700	*	720	
TrFMTa :	CCCTGGTGGTGGAACCTCAATTTCTCAAGGTGCTGATAAATATATTGATCAACTTGCATC						: 720
	*	740	*	760	*	780	
TrFMTa :	TGTGGTTCCTATAGATGATGGGACGGTTAGGACGGCGCTTGACACCGGTTGTGGGGTTGC						: 780

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TrFMTa : AAGTTGGGGTGCATATCTCTGGAGCAGAAATGTTGTTGCCATGTCGTTTGCACCAAGGGA : 840

TrFMTa : CTCTCATGAAGCACAAGTGCAATTTGCTCTTGAAAGGGGTGTACCTGCTGTTATTGGTGT : 900

TrFMTa : TCTTGGAACAATAAAGTTGCCATATCCATCTAGAGCCTTCGACATGGCTCATTTGCTCTCG : 960

TrFMTa : CTGTTTGATTCCGTGGGGAGCAAATGCTGGAATATATATGATGGAAGTTGATAGAGTTCT : 1020

TrFMTa : AAGGCCTGGTGGTTATTGGGTGCTTCTGGTCCTCCAATCAATTGGAAGGTCAACTACAA : 1080

TrFMTa : ACCATGGCAAAGACCAAAGGAGGAACTCGAGGAAGAACAAGAAATATTGAAGAGGTTGC : 1140

TrFMTa : TAAGAACTTTCCTGGGAGAAGAAGTCTGAGAAGGCTGAAATTGCCATTTGGCAAAAGAC : 1200

TrFMTa : TACCGACTCTGAATCTTGTCGTAGCAGACAAGATGACTCCAGTGTAGAATTTTGTGAAGC : 1260

TrFMTa : ATCAGATCCTGATGATGTCTGGTATAAGAAAATGGAGGCCTGTGTTACTCCAACACCTAA : 1320

TrFMTa : AGTTTTGGGTGGTGATCTTAAACCATTTCCAAACAGGCTATATGCGATCCCTCCTAGAGT : 1380

TrFMTa : TTCTAGTGGTTCTATTCTCTGGAGTTTCTTCTGAGACATACCAGAATGATAACAAAGAGTG : 1440

TrFMTa : GAAAAAGCATGTCAGTGCTTACAAGAAAATTAATTCACCTCTTGGATTCCGGTAGATATCG : 1500

TrFMTa : CAACATTATGGATATGAATGCTGGTTTGGGTAGTTTCGCTGCAGCTATTCATTCGTCGAA : 1560

TrFMTa : ATCATGGGTCATGAATGTTGTGCCAACTATAGCTGAGAAAAGTACTCTCGGTGCGATATA : 1620

TrFMTa : TGAGCGAGGACTGATTGGCATCTATCATGATTGGTGTGAAGCCTTTTCCACATATCCAAG : 1680

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TrFMTa : AACATACGATCTCATTTCATGCTAATGGCCTCTTTAGTCTGTACAAGGATAAATGCAATAC : 1740

TrFMTa : AGAAGACATTCTTCTCGAAATGGACCGGATTTTGCACAGGAGGTGCTGTCATAATCCG : 1800

TrFMTa : CGACGAAGTCGATGTATTAATTCAGGTAAAGAAATTAATCGGAGGAATGAGATGGAATAT : 1860

TrFMTa : GAAATTAGTTGATCATGAAGATGGTCCTCTTGTTTCCTGAGAAAGTACTAATTGCTGTCAA : 1920

TrFMTa : ACAGTATTGGGTTACTGATGGAAATTCACATCAACACAATAATCACTGAAAAACAAGTT : 1980

TrFMTa : GAATTTACATCCCTACCCTTATCTATATACAACAATAGTCAAAGAGTTCATATGGTTTTG : 2040

TrFMTa : TGTCATCATCACAATA : 2057

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FIGURE 2

* 20 * 40 * 60
 TrFMTa : MAKPSAADNRTRSSVQIFIVVGLCCFFYILGAWQRSFGKGDSTALEITKNNAECDVVPN : 60

* 80 * 100 * 120
 TrFMTa : LSFDSHHAGEVSQIDESDSKAKVFKPCDARYTDYTPCQDQRRAMTFPRENMNYRERHCPP : 120

* 140 * 160 * 180
 TrFMTa : EEEKLHCMIPAPKGYVTFPPWPKSRDYVPYANAPYKSLTVEKAIQNWIQYEGNVLRFPGG : 180

* 200 * 220 * 240
 TrFMTa : GTQFPQGADKYIDQLASVVPIDDGTVRTALDTGCGVASWGAYLWSRNVVAMSFAPRDSHE : 240

* 260 * 280 * 300
 TrFMTa : AQVQFALERGVPVAVIGVLGTIKLPYPSRAFDMAHCSRCLIPWGANAGIYMMEVDRVLRPG : 300

* 320 * 340 * 360
 TrFMTa : GYWVLSGPPINWKVNYKPWQRPKEELEEEQRNIEEVAKKLSWEKKSEKAEIAIWQKTDS : 360

* 380 * 400 * 420
 TrFMTa : ESCRSRQDDSSVEFCEASDPDDVWYKKMEACVTPTPKVLGGDLKPFNRLYAIPPRVSSG : 420

* 440 * 460 * 480
 TrFMTa : SIPGVSSSETYQNDNKEWKKHVSAYKKINSLDSEGRYRNIMDMNAGLGSFAAAIHSSKSWV : 480

* 500 * 520 * 540
 TrFMTa : MNVVPTIAEKSTLGAIYERGLIGIYHDWCEAFSTYPRTYDLIHANGLFSLYKDKCNTEDI : 540

* 560 * 580 * 600
 TrFMTa : LLEMDRILRPEGAVIIRDEVVLIQVKKLIGGMRWNMKLVHDHEDGPLVPEKVLIQVAVKQYW : 600

*
 TrFMTa : VTDGNSTSTQ : 610

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FIGURE 3

		*	20	*	40	*	60	
TrFMTa1 :	ATCTCTCAACAGTTCCTTAACCCCATTTTCATATCATTCTTAAGTAACAGATCTCATCTT	:	60					
TrFMTa2 :	-----	:	-					
TrFMTa3 :	-----	:	-					
TrFMTa4 :	-----	:	-					
TrFMTa5 :	-----	:	-					
TrFMTa6 :	-----	:	-					
TrFMTa7 :	-----	:	-					
TrFMTa8 :	-----	:	-					
	ATCTCTCAACAGTTCCTTAACCCCATTTTCATATCATTCTTAAGTAACAGATCTCATCTT							
		*	80	*	100	*	120	
TrFMTa1 :	TCGATCCATCATCTAAATTTTCTTCCTTTCTTAATTGCTTAATATTATTTTACGATCC	:	120					
TrFMTa2 :	-----	:	-					
TrFMTa3 :	-----	:	-					
TrFMTa4 :	-----	:	-					
TrFMTa5 :	-----	:	-					
TrFMTa6 :	-----	:	-					
TrFMTa7 :	-----	:	-					
TrFMTa8 :	-----	:	-					
	TCGATCCATCATCTAAATTTTCTTCCTTTCTTAATTGCTTAATATTATTTTACGATCC							
		*	140	*	160	*	180	
TrFMTa1 :	AAGGTTCTAGATGGCAAACCAAGTGCTGCTGATAATAGGACTAGAAGTTCTGTGCAGAT	:	180					
TrFMTa2 :	-----	:	-					
TrFMTa3 :	-----	:	-					
TrFMTa4 :	-----	:	-					
TrFMTa5 :	-----	:	-					
TrFMTa6 :	-----	:	-					
TrFMTa7 :	-----	:	-					
TrFMTa8 :	-----	:	-					
	AAGGTTCTAGATGGCAAACCAAGTGCTGCTGATAATAGGACTAGAAGTTCTGTGCAGAT							
		*	200	*	220	*	240	
TrFMTa1 :	CTTTATAGTAGTTGGTTTGTGCTGTTTCTTCTATATATTGGGAGCGTGGCAAAGAAGTGG	:	240					
TrFMTa2 :	-----	:	-					
TrFMTa3 :	-----	:	-					
TrFMTa4 :	-----	:	-					
TrFMTa5 :	-----	:	-					
TrFMTa6 :	-----	:	-					
TrFMTa7 :	-----	:	-					
TrFMTa8 :	-----	:	-					
	CTTTATAGTAGTTGGTTTGTGCTGTTTCTTCTATATATTGGGAGCGTGGCAAAGAAGTGG							
		*	260	*	280	*	300	
TrFMTa1 :	ATTTGGAAAAGGAGATAGCATAGCATTAGAGATTACCAAGAATAATGCTGAATGTGATGT	:	300					
TrFMTa2 :	-----	:	-					
TrFMTa3 :	-----	:	-					
TrFMTa4 :	-----	:	-					
TrFMTa5 :	-----	:	-					
TrFMTa6 :	-----	:	-					
TrFMTa7 :	-----	:	-					
TrFMTa8 :	-----	:	-					
	ATTTGGAAAAGGAGATAGCATAGCATTAGAGATTACCAAGAATAATGCTGAATGTGATGT							

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      *           320           *           340           *           360
TrFMTa1 : AGTTCCAAATTTAAGTTTTGATTCACACCATGCTGGAGAAGTTAGTCAAATCGATGAATC : 360
TrFMTa2 : -----
TrFMTa3 : -----
TrFMTa4 : -----
TrFMTa5 : -----
TrFMTa6 : -----
TrFMTa7 : -----
TrFMTa8 : -----
      AGTTCCAAATTTAAGTTTTGATTCACACCATGCTGGAGAAGTTAGTCAAATCGATGAATC

      *           380           *           400           *           420
TrFMTa1 : TGATTCAAAGGCTAAGGTGTTTAAACCGGTGATGCTCGTTATACGATTACACTCCGTG : 420
TrFMTa2 : -----AGGCTAAGGTGTTTAAACCGGTGATGCTCGTTATACGGATTACACTCCGTG : 52
TrFMTa3 : -----GTGTTTAAACCGGTGATGCTCGTTATACGGATTACACTCCGTG : 44
TrFMTa4 : -----
TrFMTa5 : -----
TrFMTa6 : -----
TrFMTa7 : -----
TrFMTa8 : -----
      TGATTCAAAGGCTAAGGTGTTTAAACCGGTGATGCTCGTTATACGGATTACACTCCGTG

      *           440           *           460           *           480
TrFMTa1 : TCAAGATCAACGTCGTGCTATGACCTTCCGAGAGAAAACATGAACTATAGAGAGAGACA : 480
TrFMTa2 : TCAAGATCAACGTCGTGCTATGACATTTCCCTAGAGAAAACATGAACTATAGAGAGAGACA : 112
TrFMTa3 : TCAAGATCAACGTCGTGCTATGACATTTCCCTAGAGAAAACATGAACTATAGAGAGAGACA : 104
TrFMTa4 : -----
TrFMTa5 : -----
TrFMTa6 : -----
TrFMTa7 : -----
TrFMTa8 : -----
      TCAAGATCAACGTCGTGCTATGACATTTCCCTAGAGAAAACATGAACTATAGAGAGAGACA

      *           500           *           520           *           540
TrFMTa1 : TTGCCCTCCAGAGGAAGAGAAGTTACACTGTATGATCCCTGCACCAAAGGTTATGTAAC : 540
TrFMTa2 : TTGCCCTCCAGAGGAAGAGAAGTTACACTGTATGATCCCTGCACCAAAGGTTATGTAAC : 172
TrFMTa3 : TTGCCCTCCAGAGGAAGAGAAGTTACACTGTATGATCCCTGCACCAAAGGTTATGTAAC : 164
TrFMTa4 : -----
TrFMTa5 : -----
TrFMTa6 : -----
TrFMTa7 : -----
TrFMTa8 : -----
      TTGCCCTCCAGAGGAAGAGAAGTTACACTGTATGATCCCTGCACCAAAGGTTATGTAAC

      *           560           *           580           *           600
TrFMTa1 : ACCTTTTCCATGGCCTAAGAGTAGGGAT----- : 568
TrFMTa2 : ACCTTTTCCATGGCCTAAGAGTAGGGATTATGTTTCCTTATGCTAATGCACCCTACAAGAG : 232
TrFMTa3 : ACCTTTTCCATGGCCTAAGAGTAGGGATTATGTTTCCTTATGCTAATGCACCCTACAAGAG : 224
TrFMTa4 : -----
TrFMTa5 : -----
TrFMTa6 : -----
TrFMTa7 : -----
TrFMTa8 : -----
      ACCTTTTCCATGGCCTAAGAGTAGGGATTATGTTTCCTTATGCTAATGCACCCTACAAGAG
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      *           620           *           640           *           660
TrFMTa1 : ----- : -
TrFMTa2 : TCTCACAGTTGAGAAGGCCATTTCAGAATTGGATCCAATATGAGGGAAATGTGTTAAGATT : 292
TrFMTa3 : TCTCACAGTTGAGAAGGCCATTTCAGAATTGGATCCAATATGAGGGAAATGTGTTAAGATT : 284
TrFMTa4 : ----- : -
TrFMTa5 : ----- : -
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          TCTCACAGTTGAGAAGGCCATTTCAGAATTGGATCCAATATGAGGGAAATGTGTTAAGATT

      *           680           *           700           *           720
TrFMTa1 : ----- : -
TrFMTa2 : CCCTGGTGGTGGAAGTCAATTTCTCAAGGTGCTGATAAATATATTGATCAACTTGCATC : 352
TrFMTa3 : CCCTGGTGGTGGAAGTCAATTTCTCAAGGTGCTGATAAATATATTGATCAACTTGCATC : 344
TrFMTa4 : ----- : -
TrFMTa5 : ----- : -
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          CCCTGGTGGTGGAAGTCAATTTCTCAAGGTGCTGATAAATATATTGATCAACTTGCATC

      *           740           *           760           *           780
TrFMTa1 : ----- : -
TrFMTa2 : TGTGGTTCCTATAGATGATGGGACGGTTAGGACGGCGCTTGACACCGGTTGTGGGGTTGC : 412
TrFMTa3 : TGTGGTTCCTATAGATGATGGGACGGTTAGGACGGCGCTTGACACCGGTTGTGGGGTTGC : 390
TrFMTa4 : ----- : -
TrFMTa5 : ----- : -
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          TGTGGTTCCTATAGATGATGGGACGGTTAGGACGGCGCTTGACACCGGTTGTGGGGTTGC

      *           800           *           820           *           840
TrFMTa1 : ----- : -
TrFMTa2 : AAGTTGGGGTGCATATCTCTGGAGCAGAAATGTTGTTGCCATGTCGTTTGCACCAAGGGA : 472
TrFMTa3 : ----- : -
TrFMTa4 : ----- : -
TrFMTa5 : ----- : -
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          AAGTTGGGGTGCATATCTCTGGAGCAGAAATGTTGTTGCCATGTCGTTTGCACCAAGGGA

      *           860           *           880           *           900
TrFMTa1 : ----- : -
TrFMTa2 : CTCTCATGAAGCACAAGTGAATTTGCTCTTGAAAGGGGTGTACCTGCTGTTATTGGTGT : 532
TrFMTa3 : ----- : -
TrFMTa4 : -----GTGCAATTTGCTCTTGAA- GGGGTGTACCTGCTGTTATTGGTGT : 43
TrFMTa5 : ----- : -
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          CTCTCATGAAGCACAAGTGAATTTGCTCTTGAAAGGGGTGTACCTGCTGTTATTGGTGT

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      *      920      *      940      *      960
TrFMTa1 : ----- : -
TrFMTa2 : TCTTGGAACAATAAAGTTGCCATATCCATCTAGAGCCTTCGACATGG----- : 579
TrFMTa3 : ----- : -
TrFMTa4 : TCTTGGAACAATAAAGTTGCCATATCCATCTAGAGCCTTCGACATGGCTCATTGCTCTCG : 103
TrFMTa5 : ----- : -
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          TCTTGGAACAATAAAGTTGCCATATCCATCTAGAGCCTTCGACATGGCTCATTGCTCTCG

      *      980      *      1000      *      1020
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : CTGTTTGATTCCCGTGGGGAGCAAATGCTGGAATATATATGATGGAAGTTGATAGAGTTCT : 163
TrFMTa5 : ----- : -
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          CTGTTTGATTCCCGTGGGGAGCAAATGCTGGAATATATATGATGGAAGTTGATAGAGTTCT

      *      1040      *      1060      *      1080
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : AAGGCCTGGTGGTTATTGGGTGCTTTCTGGTCCTCCAATCAATTGGAAGGTCAACTACAA : 223
TrFMTa5 : ----- : -
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          AAGGCCTGGTGGTTATTGGGTGCTTTCTGGTCCTCCAATCAATTGGAAGGTCAACTACAA

      *      1100      *      1120      *      1140
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : ACCATGGCAAAGACCAAAGGAGGAACTCGAGGAAGAACAAAGAAATATTGAAGAGGTTGC : 283
TrFMTa5 : -----TTGAAGAGGTTGC : 13
TrFMTa6 : ----- : -
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          ACCATGGCAAAGACCAAAGGAGGAACTCGAGGAAGAACAAAGAAATATTGAAGAGGTTGC

      *      1160      *      1180      *      1200
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : TAAGAACTTTCTGGGAGAAGAAGTCTGAGAAGGCTGAAATTGCCATTTGGCAAAGAC : 343
TrFMTa5 : TAAGAACTTTCTGGGAGAAGAAGTCTGAGAAGGCTGAAATTGCCATTTGGCAAAGAC : 73
TrFMTa6 : ---GAAACTTTCTGGGAGAAGAAGTCTGAGAAGGCTGAAATTGCCATTTGGCAAAGAC : 57
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          TAAGAACTTTCTGGGAGAAGAAGTCTGAGAAGGCTGAAATTGCCATTTGGCAAAGAC
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      *      1220      *      1240      *      1260
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : TACGACTCTGAATCTTGTCTAGCAGACAAGATGACTCCAGTGTAGAATTTTGTGAAGC : 403
TrFMTa5 : TACCGACTCTGAATCTTGTCTAGCAGACAAGATGACTCCAGTGTAGAATTTTGTGAAGC : 133
TrFMTa6 : TACCGACTCTGAATCTTGTCTAGCAGACAAGATGACTCCAGTGTAGAATTTTGTGAAGC : 117
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          TACCGACTCTGAATCTTGTCTAGCAGACAAGATGACTCCAGTGTAGAATTTTGTGAAGC

      *      1280      *      1300      *      1320
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : ATCAGATCCTGATGAGGCTCTGGTATAAGAAAATGGAGGCCCTGTGTTACTCCAACACCTAA : 463
TrFMTa5 : ATCAGATCCTGATGATGTCTGGTATAAGAAAATGGAGGCCCTGTGTTACTCCAACACCTAA : 193
TrFMTa6 : ATCAGATCCTGATGATGTCTGGTATAAGAAAATGGAGGCCCTGTGTTACTCCAACACCTAA : 177
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          ATCAGATCCTGATGATGTCTGGTATAAGAAAATGGAGGCCCTGTGTTACTCCAACACCTAA

      *      1340      *      1360      *      1380
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : AGTTTTGGGTGGTGATCTTAAACCATTTCCAAACAGGCTATATGCGATCCCTCCTAGAGT : 523
TrFMTa5 : AGTTTTGGGTGGTGATCTTAAACCATTTCCAAACAGGCTATATGCGATCCCTCCTAGAGT : 253
TrFMTa6 : AGTTTTGGGTGGTGATCTTAAACCATTTCCAAACAGGCTATATGCGATCCCTCCTAGAGT : 237
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          AGTTTTGGGTGGTGATCTTAAACCATTTCCAAACAGGCTATATGCGATCCCTCCTAGAGT

      *      1400      *      1420      *      1440
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : TTCTAGTGGTTCTATTCCCTGGAGTTTCTTCTGAGACATAACCAGAATGA----- : 571
TrFMTa5 : TTCTAGTGGTTCTATTCCCTGGAGTTTCTTCTGAGACATAACCAGAATGATAACAAAGAGTG : 313
TrFMTa6 : TTCTAGTGGTTCTATTCCCTGGAGTTTCTTCTGAGACATAACCAGAATGATAACAAAGAGTG : 297
TrFMTa7 : ----- : -
TrFMTa8 : ----- : -
          TTCTAGTGGTTCTATTCCCTGGAGTTTCTTCTGAGACATAACCAGAATGATAACAAAGAGTG

      *      1460      *      1480      *      1500
TrFMTa1 : ----- : -
TrFMTa2 : ----- : -
TrFMTa3 : ----- : -
TrFMTa4 : ----- : -
TrFMTa5 : GAAAAAGCATGTCAGTGCTTACAAGAAAATTAATTCACCTCTTGGATTCCGGTAGATATCG : 373
TrFMTa6 : GAAAAAGCATGTCAGTGCTTACAAGAAAATTAATTCACCTCTTGGATTCCGGTAGATATCG : 357
TrFMTa7 : ----- : 9
TrFMTa8 : ----- : 5
          GAAAAAGCATGTCAGTGCTTACAAGAAAATTAATTCACCTCTTGGATTCCGGTAGATATCG

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	*	1520	*	1540	*	1560	
TrFMTa1 :	-----		-----		-----		-
TrFMTa2 :	-----		-----		-----		-
TrFMTa3 :	-----		-----		-----		-
TrFMTa4 :	-----		-----		-----		-
TrFMTa5 :	CAACATTATGGATATGAATGCTGGTTTGGGTAGTTTCGCTGCAGCTATTCATTCGTCGAA						: 433
TrFMTa6 :	CAACATTATGGATATGAATGCTGGTTTGGGTAGTTTCGCTGCAGCTATTCATTCGTCGAA						: 417
TrFMTa7 :	CAACATTATGGATATGAATGCTGGTTTGGGTAGTTTCGCTGCAGCTATTCATTCGTCGAA						: 69
TrFMTa8 :	CAACATTATGGATATGAATGCTGGTTTGGGTAGTTTCGCTGCAGCTATTCATTCGTCGAA						: 65
	CAACATTATGGATATGAATGCTGGTTTGGGTAGTTTCGCTGCAGCTATTCATTCGTCGAA						
	*	1580	*	1600	*	1620	
TrFMTa1 :	-----		-----		-----		-
TrFMTa2 :	-----		-----		-----		-
TrFMTa3 :	-----		-----		-----		-
TrFMTa4 :	-----		-----		-----		-
TrFMTa5 :	ATCATGGGTCATGAATGTTGTGCCAACTATAGCTGAGAAAAGTACTCTCGGTGCGATATA						: 493
TrFMTa6 :	ATCATGGGTCATGAATGTTGTGCCAACTATAGCTGAGAAAAGTACTCTCGGTGCGATATA						: 477
TrFMTa7 :	ATCATGGGTCATGAATGTTGTGCCAACTATAGCTGAGAAAAGTACTCTCGGTGCGATATA						: 128
TrFMTa8 :	ATCATGGGTCATGAATGTTGTGCCAACTATAGCTGAGAAAAGTACTCTCGGTGCGATATA						: 125
	ATCATGGGTCATGAATGTTGTGCCAACTATAGCTGAGAAAAGTACTCTCGGTGCGATATA						
	*	1640	*	1660	*	1680	
TrFMTa1 :	-----		-----		-----		-
TrFMTa2 :	-----		-----		-----		-
TrFMTa3 :	-----		-----		-----		-
TrFMTa4 :	-----		-----		-----		-
TrFMTa5 :	TGAGCGAGGACTGATTGGCATCTATCATGATTGGTGTGAAGCCTTTCCACATATCCAAG						: 553
TrFMTa6 :	TGAGCGAGGACTGATTGGCATCTATCATGATTGGTGTGAAGCCTTTCCACATATCCAAG						: 537
TrFMTa7 :	TGAGCGAGGACTGATTGGCATCTATCATGATTGGTGTGAAGCCTTTCCACATATCCAAG						: 188
TrFMTa8 :	TGAGCGAGGACTGATTGGCATCTATCATGATTGGTGTGAAGCCTTTCCACATATCCAAG						: 185
	TGAGCGAGGACTGATTGGCATCTATCATGATTGGTGTGAAGCCTTTCCACATATCCAAG						
	*	1700	*	1720	*	1740	
TrFMTa1 :	-----		-----		-----		-
TrFMTa2 :	-----		-----		-----		-
TrFMTa3 :	-----		-----		-----		-
TrFMTa4 :	-----		-----		-----		-
TrFMTa5 :	AACATACGATCTCATTCATGCTAATGGCCTCTTTAGTCTGTACAAG						: 599
TrFMTa6 :	AACATACGATCTCATTCATGCTAATGGCCTCTTTAGTCTGTACAAGGATAAATG						: 591
TrFMTa7 :	AACATACGATCTCATTCATGCTAATGGCCTCTTTAGTCTGTACAAGGATAAATGCAATAC						: 248
TrFMTa8 :	AACATACGATCTCATTCATGCTAATGGCCTCTTTAGTCTGTACAAGGATAAATGCAATAC						: 245
	AACATACGATCTCATTCATGCTAATGGCCTCTTTAGTCTGTACAAGGATAAATGCAATAC						
	*	1760	*	1780	*	1800	
TrFMTa1 :	-----		-----		-----		-
TrFMTa2 :	-----		-----		-----		-
TrFMTa3 :	-----		-----		-----		-
TrFMTa4 :	-----		-----		-----		-
TrFMTa5 :	-----		-----		-----		-
TrFMTa6 :	-----		-----		-----		-
TrFMTa7 :	AGAAGACATTCTTCTCGAAATGGACCGGATTTTGCGACCAGAAGGTGCTGTCATAATCCG						: 308
TrFMTa8 :	AGAAGACATTCTTCTCGAAATGGACCGGATTTTGCGACCAGAAGGTGCTGTCATAATCCG						: 305
	AGAAGACATTCTTCTCGAAATGGACCGGATTTTGCGACCAGAAGGTGCTGTCATAATCCG						

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	*	1820	*	1840	*	1860	
TrFMTa1	:	-----		-----		-----	-
TrFMTa2	:	-----		-----		-----	-
TrFMTa3	:	-----		-----		-----	-
TrFMTa4	:	-----		-----		-----	-
TrFMTa5	:	-----		-----		-----	-
TrFMTa6	:	-----		-----		-----	-
TrFMTa7	:	CGACGAAGTCGATGTATTAATTCAGGTAAAGAAATTAATCGGAGGAATGAGATGGAATAT					: 368
TrFMTa8	:	CGACGAAGTCGATGTATTAATTCAGGTAAAGAAATTAATCGGAGGAATGAGATGGAATAT					: 365
		CGACGAAGTCGATGTATTAATTCAGGTAAAGAAATTAATCGGAGGAATGAGATGGAATAT					

	*	1880	*	1900	*	1920	
TrFMTa1	:	-----		-----		-----	-
TrFMTa2	:	-----		-----		-----	-
TrFMTa3	:	-----		-----		-----	-
TrFMTa4	:	-----		-----		-----	-
TrFMTa5	:	-----		-----		-----	-
TrFMTa6	:	-----		-----		-----	-
TrFMTa7	:	GAAATTAGTTGATCATGAAGATGGTCCTCTTGTTCCCTGAGAAAGTACTAATTGCTGTCAA					: 428
TrFMTa8	:	GAAATTAGTTGATCATGAAGATGGTCCTCTTGTTCCCTGAGAAAGTACTAATTGCTGTCAA					: 425
		GAAATTAGTTGATCATGAAGATGGTCCTCTTGTTCCCTGAGAAAGTACTAATTGCTGTCAA					

	*	1940	*	1960	*	1980	
TrFMTa1	:	-----		-----		-----	-
TrFMTa2	:	-----		-----		-----	-
TrFMTa3	:	-----		-----		-----	-
TrFMTa4	:	-----		-----		-----	-
TrFMTa5	:	-----		-----		-----	-
TrFMTa6	:	-----		-----		-----	-
TrFMTa7	:	ACAGTATTGGGTTACTGATGGAAATTCCACATCAACACAATAATCACTGAAAAACAAGTT					: 488
TrFMTa8	:	ACAGTATTGGGTTACTGATGGAAATTCCACATCAACACAATAATCACTGAAAAACAAGTT					: 485
		ACAGTATTGGGTTACTGATGGAAATTCCACATCAACACAATAATCACTGAAAAACAAGTT					

	*	2000	*	2020	*	2040	
TrFMTa1	:	-----		-----		-----	-
TrFMTa2	:	-----		-----		-----	-
TrFMTa3	:	-----		-----		-----	-
TrFMTa4	:	-----		-----		-----	-
TrFMTa5	:	-----		-----		-----	-
TrFMTa6	:	-----		-----		-----	-
TrFMTa7	:	GAATTTACATCCCTACCCTTATCTATATACAACAATAGTCAAAGAGTTCATATGGTTTTG					: 548
TrFMTa8	:	GAATTTACATCCCTACCCTTATCTATATACAACAATAGTCAAAGAGTTCATATGGT-----					: 541
		GAATTTACATCCCTACCCTTATCTATATACAACAATAGTCAAAGAGTTCATATGGTTTTG					

	*		
TrFMTa1	:	-----	-
TrFMTa2	:	-----	-
TrFMTa3	:	-----	-
TrFMTa4	:	-----	-
TrFMTa5	:	-----	-
TrFMTa6	:	-----	-
TrFMTa7	:	TGTCATCATCACAATA	: 565
TrFMTa8	:	-----	-
		TGTCATCATCACAATA	

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FIGURE 4

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      *      20      *      40      *      60
TrUG3Ea : CATCATCTGCAACTGTTTATGGCACACCTGAAAAGATACCTTGTGAGGAGGATTTC AATT : 60

      *      80      *      100     *      120
TrUG3Ea : TATAAGCCATGAATCCATATGGACGGACCAAGCTTTTCCTCGAAGAAATCGCACGAGATA : 120

      *      140     *      160     *      180
TrUG3Ea : TTCAGAAAGCTGAGCCAGAATGGAGGATCATTTTACTGAGATACTTCAATCCAGTTGGGG : 180

      *      200     *      220     *      240
TrUG3Ea : CCCATGAAAGCGGTAGACTCGGTGAAGATCCCAAGGGCATCCCAAATAATCTCATGCCTT : 240

      *      260     *      280     *      300
TrUG3Ea : ATATACAGCGTGTAGCTGTTGAAAGATTACCCGAGCTCAATGTATATGGTCATGATTATC : 300

      *      320     *      340     *      360
TrUG3Ea : CTACGAGGGATGGTTCTGCGATTTCGGGACTATATCCATGTGATGGACTTAGCAGATGGTC : 360

      *      380     *      400     *      420
TrUG3Ea : ACATTGCTGCATTGAGAAAGCTTTTCACAACAGAAAACATAGGTTGTGCTGCTTACAACT : 420

      *      440     *      460     *      480
TrUG3Ea : TGGGAACTGGTCGTGGTACATCTGTACTTGAAATGGTTGATGCATTTGAGAAAGCTTCTG : 480

      *      500     *      520     *      540
TrUG3Ea : GCAAGAAAATTCCAGTGAAATTGTGTCCACGAAGGGCGGGAGATGCTACGGAGGTTTATG : 540

      *      560     *
TrUG3Ea : CATCTACAGAGAGAGCTGAGAAAGAACTTGG : 571

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FIGURE 5

 * 20 * 40 * 60
TrUG3Ea : MNPYGRTKLFLEEIARDIQKAEPEWRIILLRYFNPVGAHESGRLGEDPKGIPNNLMPYIQ : 60

 * 80 * 100 * 120
TrUG3Ea : RVAVERLPVLNVYGHDPTRDGSAIRDYIHVMDLADGHIAALRKLEFTTENIGCAAYNLGT : 120

 * 140 * 160
TrUG3Ea : GRGTSVLEMVDAFEKASGKKIPVKLCPRRAGDATEVYASTERAEKEL : 167

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FIGURE 6

	* 20 * 40 * 60	
TrUG3Ea1 :	CATCATCTGCAACTGTTTATGGCACACCTGAAAAGATACCTTGTGAGGAGGATTTCAATT	: 60
TrUG3Ea2 :	--TCATCTGCAACTGTTTATGGCACACCTGAAAAGATACCTTGTGAGGAGGATTTCAATT	: 58
	CATCATCTGCAACTGTTTATGGCACACCTGAAAAGATACCTTGTGAGGAGGATTTCAATT	
	* 80 * 100 * 120	
TrUG3Ea1 :	TATAAGCCATGAATCCATATGGACGGACCAAGCTTTTCCTCGAAGAAATCGCACGAGATA	: 120
TrUG3Ea2 :	TATAAGCCATGAATCCATATGGACGGACCAAGCTTTTCCTCGAAGAAATCGCACGAGATA	: 118
	TATAAGCCATGAATCCATATGGACGGACCAAGCTTTTCCTCGAAGAAATCGCACGAGATA	
	* 140 * 160 * 180	
TrUG3Ea1 :	TTCAGAAAGCTGAGCCAGAATGGAGGATCATTTTACTGAGATACTTCAATCCAGTTGGGG	: 180
TrUG3Ea2 :	TTCAGAAAGCTGAGCCAGAATGGAGGATCATTTTACTGAGATACTTCAATCCAGTTGGGG	: 178
	TTCAGAAAGCTGAGCCAGAATGGAGGATCATTTTACTGAGATACTTCAATCCAGTTGGGG	
	* 200 * 220 * 240	
TrUG3Ea1 :	CCCATGAAAGCGGTAGACTCGGTGAAGATCCCAAGGGCATCCCAAATAATCTCATGCCTT	: 240
TrUG3Ea2 :	CCCATGAAAGCGGTAGACTCGGTGAAGATCCCAAGGGCATCCCAAATAATCTCATGCCTT	: 238
	CCCATGAAAGCGGTAGACTCGGTGAAGATCCCAAGGGCATCCCAAATAATCTCATGCCTT	
	* 260 * 280 * 300	
TrUG3Ea1 :	ATATACAGCGTGTAGCTGTTGAAAGATTACCCGAGCTCAATGTATATGGTCATGATTATC	: 300
TrUG3Ea2 :	ATATACAGCGTGTAGCTGTTGAAAGATTACCCGAGCTCAATGTATATGGTCATGATTATC	: 298
	ATATACAGCGTGTAGCTGTTGAAAGATTACCCGAGCTCAATGTATATGGTCATGATTATC	
	* 320 * 340 * 360	
TrUG3Ea1 :	CTACGAGGGATGGTTCTGCGATTCTGGGACTATATCCATGTGATGGACTTAGCAGATGGTC	: 360
TrUG3Ea2 :	CTACGAGGGATGGTTCTGCGATTCTGGGACTATATCCATGTGATGGACTTAGCAGATGGTC	: 358
	CTACGAGGGATGGTTCTGCGATTCTGGGACTATATCCATGTGATGGACTTAGCAGATGGTC	
	* 380 * 400 * 420	
TrUG3Ea1 :	ACATTGCTGCATTGAGAAAGCTTTTCACAACAGAAAACATAGGTTGTGCTGCTTACAAC	: 420
TrUG3Ea2 :	ACATTGCTGCATTGAGAAAGCTTTTCACAACAGAAAACATAGGTTGTGCTGCTTACAAC	: 418
	ACATTGCTGCATTGAGAAAGCTTTTCACAACAGAAAACATAGGTTGTGCTGCTTACAAC	
	* 440 * 460 * 480	
TrUG3Ea1 :	TGGGAACTGGTCGTGGTACATCTGTACTTGAAATGGTTGATGCATTTGAGAAAGCTTCTG	: 480
TrUG3Ea2 :	TGGGAACTGGTCGTGGTACATCTGTACTTGAAATGGTTGATGCATTTGAGAAAGCTTCTG	: 478
	TGGGAACTGGTCGTGGTACATCTGTACTTGAAATGGTTGATGCATTTGAGAAAGCTTCTG	
	* 500 * 520 * 540	
TrUG3Ea1 :	GCAAGAAAATTCCAGTGAAATTGTGTCCACGAAGGGCGGGAGATGCTACGGAGGTTTATG	: 540
TrUG3Ea2 :	GCAAGAAAATTCCAGTGAAATTGTGTCCACGAAGGGCGGGAGATGCTACGGAGGTTTATG	: 538
	GCAAGAAAATTCCAGTGAAATTGTGTCCACGAAGGGCGGGAGATGCTACGGAGGTTTATG	
	* 560 *	
TrUG3Ea1 :	CATCTACAGAGAGAGCTGAGAAAGAACTTGG	: 571
TrUG3Ea2 :	CATCT-----	: 543
	CATCTACAGAGAGAGCTGAGAAAGAACTTGG	

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FIGURE 7

TrGSTa : GAGTAATTCAACTTTCGATAATATATATATATATATCCTCCTTCTCTCTTGTGAAACATAT : 60

TrGSTa : ATTTCCCTTTTTTTTTTTTTCTTTTCAAAGAAACCATGGTAGTGAAGGTGTATGGTCCTCA : 120

TrGSTa : CTGTGCCTCAACCAAAGAGTGTGGTTTGTCTTGTGAGAAGGAAATAGAATTTGAGGT : 180

TrGSTa : TGTCCCTATTAATTTCTTAGAAGGAGAACAGAAGAATCCTGAGTACCTCAAATTACAGCC : 240

TrGSTa : TTTTGGAACCTCTTCCTGTGATTCAAGATGGAGACTATAACCCTTTATGAATCTCGTGCAAT : 300

TrGSTa : AATAAGATACTATGCTGAAAAATATAGATCTCAAGGGGTGAATTACTTGGAAGACAAT : 360

TrGSTa : AGAAGAAAAAGGTCTAGTGGAACAATGGTTAGAAGTTGAAGCACAAAACCTTTAACCCATC : 420

TrGSTa : AGCATACAACCTGGCCCTTCATATATTATTTCCCTTCACTACTAGCTGACAACACTCCAAA : 480

TrGSTa : TCCTAAGGTAATTGAAGAGAGTGAACCAAACTTGTGAAGGTTTTGAACATTTATGAAGA : 540

TrGSTa : GAGGCTATCAAAGAGCAAGTATTTGGCTGGTGATTT : 576

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FIGURE 8

TrGSTa : MVVKVYGPHCASTKRVLVCLVEKEIEFEVVPINFLEGEQKNPEYCLKLQPFGTLPVIQDGD : 60

TrGSTa : YTLYESRAIIRYYAEKYRSQGVELLGKTIEEKGLVEQWLEVEAQNFNPSAYNLALHILFP : 120

TrGSTa : SLLADNTPNPKVIEESEPKLVKVLNIYEERLSKSKYLAGD : 160

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FIGURE 10

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      *      20      *      40      *      60
TrOMTa : CACCTTGAGAATTATTGCGATCAAGATTGCAATGAAAATTTGGATAAGGCCATCCCTCC : 60

      *      80      *      100     *      120
TrOMTa : CTCCCCTCCTCTCTATATAAGTAGTTGGTTGGTTAGTGTCAATATAAGAAGAAAAACACA : 120

      *      140     *      160     *      180
TrOMTa : AACCAAACCATATATATAGTATCAATATCAATTAAGCTAGCTATTTCCAAATCAACATGG : 180

      *      200     *      220     *      240
TrOMTa : CTCCTTCAACAACTGAATCCAATAAACAACAAATCCCCAACGGAAAAGACAATCATCTAA : 240

      *      260     *      280     *      300
TrOMTa : AACCACAACAACAAGAAGAAGATGATGATGCCCTCGAATTTGCCACACAAATAACAGGTT : 300

      *      320     *      340     *      360
TrOMTa : CCATTGTTGTTCCATTGGCTTTGAGGTCAGCCATTGATCTTGGCATCTTTGACATCCTAG : 360

      *      380     *      400     *      420
TrOMTa : CCAAAGCTGGCGAAGGTGCAGAACTCTCTGCACAAGACATTGCTGTTAAGATTGGAACCA : 420

      *      440     *      460     *      480
TrOMTa : ACAACCCGGAAGCACCAACAATGTTGAATCGTCTTCTTAGGTTGTTGGCCAGTCACTCTA : 480

      *      500     *      520     *      540
TrOMTa : TTCTAAACTCCTCTGTTTCCTCAACAACATGATGATCAACAAATATTCTACAGCCTCTCCA : 540

      *      560     *      580     *      600
TrOMTa : ATCGCTCCAAATATTTTGTACCCGATGCTGACGGCATCTCGTTGGGACCCACCTTGGCAT : 600

      *      620     *      640     *      660
TrOMTa : TACTTCTCGACAATGTCTTCTACCAAAGCTGGTCGGAGCTGAAAGGAGCGATAGTGGAAG : 660

      *      680     *      700     *      720
TrOMTa : GAGGAATACCGTTCAATAGAGTATATGGAATGCATGCCTTTGAGTACCCACGTGTGGATC : 720

      *      740     *      760     *      780
TrOMTa : CAAGGTTCAATGATGTTTTCAACAAAGCTATGCTTAGTTCAACCACTATTAATATGAAGA : 780

      *      800     *      820     *      840
TrOMTa : GAATTCTTGAATTTTATCAAGGTTTTGAGCATGTCACTAAGTTGGTTGACGTTGGTGGTG : 840

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TrOMTa : GTCTTGGACATAACCTCAAATTGATCACAGCCAAATATTCCCATATTCATGGAATTAATT : 900

TrOMTa : TTGACTTGCCTCATGTGCTACAAAATGCTCCTAACTACCCAGGTGTTGAACACGTGGGAG : 960

TrOMTa : GAGATATGTTTGAGAGCGTTCCTACAGGGGATGCCATTTTATGAAGTGGATACTTCATG : 1020

TrOMTa : ATTGGAGTGATGAACACTGCTTGAAGCTGTTGAAAAATTGTTACAAAGCTATTCCTGAGA : 1080

TrOMTa : ATGGAAAGGTTATTGTTGTGGACACAATCCTTCCCACCACGCCCCGAGACAACAGGGAGCG : 1140

TrOMTa : CAAAGTTTGGTTTCTCGTCTGATCTTTTAATGATGACTCAAAATCCAGGAGGAAAAGAGA : 1200

TrOMTa : GAACTGAGCAGGAATTCATAAAATTGGCAAAGGATCTGGATTTCAGTGGCATCAAACCTA : 1260

TrOMTa : TATGTTGTGTCTGGACTATGGGTTAT : 1288

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FIGURE 11

TrOMTa : MAPSTTESNKQQIPNGKDNHLKPQQQEEDDDALEFATQITGSIVVPLALRSAIDLGI FDI : 60

TrOMTa : LAKAGEGAELSAQDI AVKIGTNNPEAPTMLNRLRL LASHSILNSSVPQQHDDQQIFYSL : 120

TrOMTa : SNRSKYFVTDADGISLGPTLALLLDNVFYQSWSELKGAIVEGGIPFN RVYGMHAFEYPRV : 180

TrOMTa : DPRFNDVFNKAMLSSTTINMKRILEFYQGFEHVTKLVDVGGGLGHN LKLITAKYSHIHGI : 240

TrOMTa : NFDLPHVLQNAPNYPGVEHVGGDMFESVPTGDAIFMKWILHDWSDEHCLKLLKN CYKAIP : 300

TrOMTa : ENGKVIVVDTILPTTPETTGS AKFGFSSDLLMMTQNP GGKERTEQEFIKLAKGSGFSGIK : 360

TrOMTa : PICCVSGLWV : 370

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FIGURE 12

		*	20	*	40	*	60	
TrOMTa1	:	CACCTTGAGAATTATTGCGATCAAGATTGCAATGAAAATTTTGGATAAGGCCATCCCTCC						: 60
TrOMTa2	:	-----CTCTCCCTCC						: 10
TrOMTa3	:	-----						: -
TrOMTa4	:	-----						: -
TrOMTa5	:	-----						: -
TrOMTa6	:	-----						: -
TrOMTa7	:	-----						: -
TrOMTa8	:	-----						: -
TrOMTa9	:	-----						: -
		CACCTTGAGAATTATTGCGATCAAGATTGCAATGAAAATTTTGGATAAGGCCATCCCTCC						
		*	80	*	100	*	120	
TrOMTa1	:	CTCCCCCTCCTCTCTATATAAGTAGTTGGTTGGTTAGTGTCAATATAAGAAGAAAAACACA						: 120
TrOMTa2	:	CTCCCCCTCCTCTCTATATAAGTAGTTGGTTGGTTAGTGTCAATATAAGAAGAAAAACACA						: 70
TrOMTa3	:	-----A						: 1
TrOMTa4	:	-----						: -
TrOMTa5	:	-----						: -
TrOMTa6	:	-----						: -
TrOMTa7	:	-----						: -
TrOMTa8	:	-----						: -
TrOMTa9	:	-----						: -
		CTCCCCCTCCTCTCTATATAAGTAGTTGGTTGGTTAGTGTCAATATAAGAAGAAAAACACA						
		*	140	*	160	*	180	
TrOMTa1	:	AACCAAACCATATATATAGTATCAATATCAATTAAGCTAGCTATTTCCAAATCAACATGG						: 180
TrOMTa2	:	AACCAAACCATATATATAGTATCAATATCAATTAAGCTAGCTATTTCCAAATCAACATGG						: 130
TrOMTa3	:	AACCAAACCATATATATAGTATCAATATCAATTAAGCTAGCTATTTCCAAATCAACATGG						: 61
TrOMTa4	:	-----AACCATATATATAGTATCAATATCAATTAAGCTAGCTATTTCCAAATCAACATGG						: 55
TrOMTa5	:	-----TTAAGCTAGCTATTTCCAAA-GAACATGG						: 28
TrOMTa6	:	-----CATGG						: 5
TrOMTa7	:	-----						: -
TrOMTa8	:	-----						: -
TrOMTa9	:	-----						: -
		AACCAAACCATATATATAGTATCAATATCAATTAAGCTAGCTATTTCCAAATCAACATGG						
		*	200	*	220	*	240	
TrOMTa1	:	CTCCTTCAACAACCTGAATCCAATAAACAACAAATCCCCAACGGAAAAGACAATCATCTAA						: 240
TrOMTa2	:	CTCCTTCAACAACCTGAATCCAATAAACAACAAATCCCCAACGGAAAAGACAATCATCTAA						: 190
TrOMTa3	:	CTCCTTCAACAACCTGCTGCTGCTGAATAAACAACAAATCCCCAACGGAAAAGACAATCATCTAA						: 121
TrOMTa4	:	CTCCTTCAACAACCTGAATCCAATAAACAACAAATCCCCAACGGAAAAGACAATCATCTAA						: 115
TrOMTa5	:	CTCCTTCAACAACCTGAATCC-ATAAACAACAAATCCCCAACGGAAAAGACAATCATCTAA						: 87
TrOMTa6	:	CTCCTT-AACAACCTGAATCCAATAAACAACAAATCCCCAACGGAAAAGACA-TCATCTAA						: 63
TrOMTa7	:	-----						: -
TrOMTa8	:	-----						: -
TrOMTa9	:	-----						: -
		CTCCTTCAACAACCTGAATCCAATAAACAACAAATCCCCAACGGAAAAGACAATCATCTAA						

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      *           260           *           280           *           300
TrOMTa1 : AACCACAACAACAAGAAGAAGATGATGATGCCCTCGAATTTGCCACACAAATAACAGGTT : 300
TrOMTa2 : AACCACAACAACAAGAAGAAGATGATGATGCCCTCGAATTTGCCACACAAATAACAGGTT : 250
TrOMTa3 : AACCACAACAACAAGAAGAAGATGATGATGCCCTCGAATTTGCCACACAAATAACAGGTT : 181
TrOMTa4 : AACCACAACAACAAGAAGAAGATGATGATGCCCTCGAATTTGCCACACAAATAACAGGTT : 175
TrOMTa5 : AACCACAACAACAAGAAGAAGATGATGATGCCCTCGAATTTGCCACACAAATAACAGGTT : 147
TrOMTa6 : AACCACAACAACAAGAAGAAGATGATGATGCCCTCGAATTTGCCACACAAATAACAGGTT : 123
TrOMTa7 : ----- : -
TrOMTa8 : ----- : -
TrOMTa9 : ----- : -
      AACCACAACAACAAGAAGAAGATGATGATGCCCTCGAATTTGCCACACAAATAACAGGTT

      *           320           *           340           *           360
TrOMTa1 : CCATTGTTGTTCCATTGGCTTTGAGGTCAGCCATTGATCTTGGCATCTTTGACATCCTAG : 360
TrOMTa2 : CCATTGTTGTTCCATTGGCTTTGAGGTCAGCCATTGATCTTGGCATCTTTGACATCCTAG : 310
TrOMTa3 : CCATTGTTGTTCCATTGGCTTTGAGGTCAGCCATTGATCTTGGCATCTTTGACATCCTAG : 241
TrOMTa4 : CCATTGTTGTTCCATTGGCTTTGAGGTCAGCCATTGATCTTGGCATCTTTGACATCCTAG : 235
TrOMTa5 : CCATTGTTGTTCCATTGGCTTTGAGGTCAGCCATTGATCTTGGCATCTTTGACATCCTAG : 207
TrOMTa6 : CCATTGTTGTTCCATTGGCTTTGAGGTCAGCCATTGATCTTGGCATCTTTGACATCCTAG : 183
TrOMTa7 : ----- : -
TrOMTa8 : ----- : -
TrOMTa9 : ----- : -
      CCATTGTTGTTCCATTGGCTTTGAGGTCAGCCATTGATCTTGGCATCTTTGACATCCTAG

      *           380           *           400           *           420
TrOMTa1 : CCAAAGCTGGCGAAGGTGCAGAACTCTCTGCACAAGACATTGCTGTTAAGATTGGAACCA : 420
TrOMTa2 : CCAAAGCTGGCGAAGGTGCAGAACTCTCTGCACAAGACATTGCTGTTAAGATTGGAACCA : 370
TrOMTa3 : CCAAAGCTGGCGAAGGTGCAGAACTCTCTGCACAAGACATTGCTGTTAAGATTGGAACCA : 301
TrOMTa4 : CCAAAGCTGGCGAAGGTGCAGAACTCTCTGCACAAGACATTGCTGTTAAGATTGGAACCA : 295
TrOMTa5 : CCAAAGCTGGCGAAGGTGCAGAACTCTCTGCACAAGACATTGCTGTTAAGATTGGAACCA : 267
TrOMTa6 : CCAAAGCTGGCGAAGGTGCAGAACTCTCTGCACAAGACATTGCTGTTAAGATTGGAACCA : 243
TrOMTa7 : ----- : -
TrOMTa8 : ----- : -
TrOMTa9 : ----- : -
      CCAAAGCTGGCGAAGGTGCAGAACTCTCTGCACAAGACATTGCTGTTAAGATTGGAACCA

      *           440           *           460           *           480
TrOMTa1 : ACAACCCGGAAGCACCAACAATGTTGAATCGTCTTCTTAGGTTGTTGGCCAGTCACTCTA : 480
TrOMTa2 : ACAACCCGGAAGCACCAACAATGTTGAATCGTCTTCTTAGGTTGTTGGCCAGTCACTCTA : 430
TrOMTa3 : ACAACCCGGAAGCACCAACAATGTTGAATCGTCTTCTTAGGTTGTTGGCCAGTCACTCTA : 361
TrOMTa4 : ACAACCCGGAAGCACCAACAATGTTGAATCGTCTTCTTAGGTTGTTGGCCAGTCACTCTA : 355
TrOMTa5 : ACAACCCGGAAGCACCAACAATGTTGAATCGTCTTCTTAGGTTGTTGGCCAGTCACTCTA : 327
TrOMTa6 : ACAACCCGGAAGCACCAACAATGTTGAATCGTCTTCTTAGGTTGTTGGCCAGTCACTCTA : 303
TrOMTa7 : ----- : -
TrOMTa8 : ----- : -
TrOMTa9 : ----- : -
      ACAACCCGGAAGCACCAACAATGTTGAATCGTCTTCTTAGGTTGTTGGCCAGTCACTCTA

      *           500           *           520           *           540
TrOMTa1 : TTCTAAACTCCTCTGTTTCCTCAACAACATGATGATCAACAAATATTCTACAGCCTCTCCA : 540
TrOMTa2 : TTCTAAACTCCTCTGTTTCCTCAACAACATGATGATCAACAAATATTCTACAGCCTCTCCA : 490
TrOMTa3 : TTCTAAACTCCTCTGTTTCCTCAACAACATGATGATCAACAAATATTCTACAGCCTCTCCA : 421
TrOMTa4 : TTCTAAACTCCTCTGTTTCCTCAACAACATGATGATCAACAAATATTCTACAGCCTCTCCA : 415
TrOMTa5 : TTCTAAACTCCTCTGTTTCCTCAACAACATGATGATCAACAAATATTCTACAGCCTCTCCA : 387
TrOMTa6 : TTCTAAACTCCTCTGTTTCCTCAACAACATGATGATCAACAAATATTCTACAGCCTCTCCA : 363
TrOMTa7 : ----- : -
TrOMTa8 : ----- : -
TrOMTa9 : ----- : -
      TTCTAAACTCCTCTGTTTCCTCAACAACATGATGATCAACAAATATTCTACAGCCTCTCCA

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      *           560           *           580           *           600
TrOMTa1 : ATCGCTCCAAATATTTTGTACCGATGCTGACGGCATCTCGTT----- : 583
TrOMTa2 : ATCGCTCCAAATATTTTGTACCGATGCTGACGGCATCTCGTTGGGACCCACCTT----- : 545
TrOMTa3 : ATCGCTCCAAATATTTTGTACCGATGCTGACGGCATCTCGTTGGGACCCACCTTGGCAT : 481
TrOMTa4 : ATCGCTCCAAATATTTTGTACCGATGCTGACGGCATCTCGTTGGGACCCACCTTGGCAT : 475
TrOMTa5 : ATCGCTCCAAATATTTTGTACCGATGCTGACGGCATCTCGTTGGGACCCACCTTGGCAT : 447
TrOMTa6 : ATCGCTCCAAATATTTTGTACCGATGCTGACGGCATCTCGTTGGGACCCACCTTGGCAT : 423
TrOMTa7 : ATCGCTCCAAATATTTTGTACCGATGCTGACGGCATCTCGTTGGGACCCACCTTGGCAT : 66
TrOMTa8 : ----- : -
TrOMTa9 : ----- : -
      ATCGCTCCAAATATTTTGTACCGATGCTGACGGCATCTCGTTGGGACCCACCTTGGCAT

      *           620           *           640           *           660
TrOMTa1 : ----- : -
TrOMTa2 : ----- : -
TrOMTa3 : TACTTCTCGACAATGTCTTCTACCAAAGCTGGTCCGAGCTGAAAGGAGCGATAGTGGAAG : 541
TrOMTa4 : TACTTCTCGACAATGTCTTCTACCAAAGCTGGTCCGAGCTGAAAGGAGCGATAGTGGAAG : 535
TrOMTa5 : TACTTCTCGACAATGTCTTCTACCAAAGCTGGTCCGAGCTGAAAGGAGCGATAGTGGAAG : 507
TrOMTa6 : TACTTCTCGACAATGTCTTCTACCAAAGCTGGTCCGAGCTGAAAGGAGCGATAGTGGAAG : 483
TrOMTa7 : TACTTCTCGACAATGTCTTCTACCAAAGCTGGTCCGAGCTGAAAGGAGCGATAGTGGAAG : 126
TrOMTa8 : -----AGTGGAAG : 8
TrOMTa9 : ----- : -
      TACTTCTCGACAATGTCTTCTACCAAAGCTGGTCCGAGCTGAAAGGAGCGATAGTGGAAG

      *           680           *           700           *           720
TrOMTa1 : ----- : -
TrOMTa2 : ----- : -
TrOMTa3 : GAGGAATACCGTTCAATAGAGTATATGGAATGCATGCCCTTTGAGTACCCACGTGTGGATC : 601
TrOMTa4 : GAGGAATACCGTTCAATAGAGTATATGGAATGCATGCCCTTTGAGTACCCACGTGTGGATC : 595
TrOMTa5 : GAGGAATACCGTT----- : 519
TrOMTa6 : GAGGAATACCGTTCAATAGAGTATATGGAATGCATGCCCTTTGAGTACCCACGTGTGGATC : 524
TrOMTa7 : GAGGAATACCGTTCAATAGAGTATATGGAATGCATGCCCTTTGAGTACCCACGTGTGGATC : 186
TrOMTa8 : GAGGAATACCGTTCAATAGAGTATATGGAATGCATGCCCTTTGAGTACCCACGTGTGGATC : 68
TrOMTa9 : -----GGAATGCATGCCCTTTGAGTACCCACGTGTGGATC : 33
      GAGGAATACCGTTCAATAGAGTATATGGAATGCATGCCCTTTGAGTACCCACGTGTGGATC

      *           740           *           760           *           780
TrOMTa1 : ----- : -
TrOMTa2 : ----- : -
TrOMTa3 : CAAGGTTCAATGATGTTTTCAACAAAGCTATGCTTAGTTCAACCACTATTAATATGAAGA : 661
TrOMTa4 : CAAGGTTCAATGATGTTT----- : 613
TrOMTa5 : ----- : -
TrOMTa6 : ----- : 188
TrOMTa7 : CA----- : 128
TrOMTa8 : CAAGGTTCAATGATGTTTTCAACAAAGCTATGCTTAGTTCAACCACTATTAATATGAAGA : 91
TrOMTa9 : CA-GGTTCAATGATGTTTTCAACAAAGCTATGCTTAGTTCAACCACTATTAATATGAAGA
      CAAGGTTCAATGATGTTTTCAACAAAGCTATGCTTAGTTCAACCACTATTAATATGAAGA

      *           800           *           820           *           840
TrOMTa1 : ----- : -
TrOMTa2 : ----- : 699
TrOMTa3 : GAATTCTTGAATTTTATCAAGGTTT-GAGCATGTCACTA----- : -
TrOMTa4 : ----- : -
TrOMTa5 : ----- : -
TrOMTa6 : ----- : -
TrOMTa7 : ----- : 188
TrOMTa8 : GAATTCTTGAATTTTATCAAGGTTTTGAGCATGTCACTAAGTTGGTTGACGTTGGTGGTG : 150
TrOMTa9 : GAATTCTTGAATTTTATCAAGGTTTTGAGCATGTCACTAAGTTGGTTGACGTTGGTGGTG
      GAATTCTTGAATTTTATCAAGGTTTTGAGCATGTCACTAAGTTGGTTGACGTTGGTGGTG

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	*	860	*	880	*	900	
TrOMTa1	:	-----		-----		-----	:
TrOMTa2	:	-----		-----		-----	:
TrOMTa3	:	-----		-----		-----	:
TrOMTa4	:	-----		-----		-----	:
TrOMTa5	:	-----		-----		-----	:
TrOMTa6	:	-----		-----		-----	:
TrOMTa7	:	-----		-----		-----	:
TrOMTa8	:	GTCTTGGACATAACCTCAAATTGATCACAGCCAAATATTCCATATTTCATGGAATTAATT					:
TrOMTa9	:	GTCTTGGACATAACCTCAAATTGATCACAGCCAAATATTCCCATATTTCATGGAATTAATT					:
		GTCTTGGACATAACCTCAAATTGATCACAGCCAAATATTCCCATATTTCATGGAATTAATT					
		*	920	*	940	*	960
TrOMTa1	:	-----		-----		-----	:
TrOMTa2	:	-----		-----		-----	:
TrOMTa3	:	-----		-----		-----	:
TrOMTa4	:	-----		-----		-----	:
TrOMTa5	:	-----		-----		-----	:
TrOMTa6	:	-----		-----		-----	:
TrOMTa7	:	-----		-----		-----	:
TrOMTa8	:	TTGACTTGCCTCATGTGCTACAAAATGCTCCTAACTACCCAGGTGTTGAACACGTGGGAG					:
TrOMTa9	:	TTGACTTGCCTCATGTGCTACAAAATGCTCCTAACTACCCAGGTGTTGAACACGTGGGAG					:
		TTGACTTGCCTCATGTGCTACAAAATGCTCCTAACTACCCAGGTGTTGAACACGTGGGAG					
		*	980	*	1000	*	1020
TrOMTa1	:	-----		-----		-----	:
TrOMTa2	:	-----		-----		-----	:
TrOMTa3	:	-----		-----		-----	:
TrOMTa4	:	-----		-----		-----	:
TrOMTa5	:	-----		-----		-----	:
TrOMTa6	:	-----		-----		-----	:
TrOMTa7	:	-----		-----		-----	:
TrOMTa8	:	GAGATATGTTTGAGAGCGTTCCTACAGGGGATGCCATTTTATGAAGTGGATACTTCATG					:
TrOMTa9	:	GAGATATGTTTGAGAGCGTTCCTACAGGGGATGCCATTTTATGAAGTGGATACTTCATG					:
		GAGATATGTTTGAGAGCGTTCCTACAGGGGATGCCATTTTATGAAGTGGATACTTCATG					
		*	1040	*	1060	*	1080
TrOMTa1	:	-----		-----		-----	:
TrOMTa2	:	-----		-----		-----	:
TrOMTa3	:	-----		-----		-----	:
TrOMTa4	:	-----		-----		-----	:
TrOMTa5	:	-----		-----		-----	:
TrOMTa6	:	-----		-----		-----	:
TrOMTa7	:	-----		-----		-----	:
TrOMTa8	:	ATTGGAGTGATGAACACTGCTTGAAGCTGTTGAAAAATTGTTACAAAGCTATTCCTGAGA					:
TrOMTa9	:	ATTGGAGTGATGAACACTGCTTGAAGCTGTTGAAAAATTGTTACAAAGCTATTCCTGAGA					:
		ATTGGAGTGATGAACACTGCTTGAAGCTGTTGAAAAATTGTTACAAAGCTATTCCTGAGA					
		*	1100	*	1120	*	1140
TrOMTa1	:	-----		-----		-----	:
TrOMTa2	:	-----		-----		-----	:
TrOMTa3	:	-----		-----		-----	:
TrOMTa4	:	-----		-----		-----	:
TrOMTa5	:	-----		-----		-----	:
TrOMTa6	:	-----		-----		-----	:
TrOMTa7	:	-----		-----		-----	:
TrOMTa8	:	ATGGAAAGGTTATTGTTGTGGACACAATCCTTCCCACCAATGCCCGAGACAACAGGGAGCG					:
TrOMTa9	:	ATGGAAAGGTTATTGTTGTGGACACAATCCTTCCCACCAATGCCCGAGACAACAGGGAGCG					:
		ATGGAAAGGTTATTGTTGTGGACACAATCCTTCCCACCAATGCCCGAGACAACAGGGAGCG					

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      *      1160      *      1180      *      1200
TrOMTa1 : ----- : -
TrOMTa2 : ----- : -
TrOMTa3 : ----- : -
TrOMTa4 : ----- : -
TrOMTa5 : ----- : -
TrOMTa6 : ----- : -
TrOMTa7 : ----- : -
TrOMTa8 : CAAAGTTTGGTTTCTCGTCTGATCTTTTAATGATGACTCAAAATCCAGGAGGAAAAGAGA : 548
TrOMTa9 : CAAAGTTTGGTTTCTCGTCTGATCTTTTAATGATGACTCAAAATCCAGGAGGAAAAGAGA : 510
          CAAAGTTTGGTTTCTCGTCTGATCTTTTAATGATGACTCAAAATCCAGGAGGAAAAGAGA

      *      1220      *      1240      *      1260
TrOMTa1 : ----- : -
TrOMTa2 : ----- : -
TrOMTa3 : ----- : -
TrOMTa4 : ----- : -
TrOMTa5 : ----- : -
TrOMTa6 : ----- : -
TrOMTa7 : ----- : -
TrOMTa8 : GAACTGAGCAGGAATTCATAAAATTGGCAAAAGGATCTGC----- : 588
TrOMTa9 : GAACTGAGCAGGAATTCATAAAATTGGCAAAAGGATCTGGATTTCAGTGGCATCAAACCTA : 570
          GAACTGAGCAGGAATTCATAAAATTGGCAAAAGGATCTGGATTTCAGTGGCATCAAACCTA

      *      1280
TrOMTa1 : ----- : -
TrOMTa2 : ----- : -
TrOMTa3 : ----- : -
TrOMTa4 : ----- : -
TrOMTa5 : ----- : -
TrOMTa6 : ----- : -
TrOMTa7 : ----- : -
TrOMTa8 : ----- : -
TrOMTa9 : TATGTTGTGTGTCTGGACTATGGGTTAT : 598
          TATGTTGTGTGTCTGGACTATGGGTTAT
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FIGURE 13

TrRTa : TTGTGGATAAAAGAGTGGTTGGACAAGCAACCACGTAGCACGGTATTATATGTGGCTTTT : 60

TrRTa : GGTAGTGAAGCAAAACCAAGTCAAGAAGAAGTCACTAAGATAGCTTTTGGGTTGGAGGAA : 120

TrRTa : TCAAAGATTCCGTTCTTTTGGGTCCTTAGGGTTCAGCGTGGACCAACTGACAATGTGGTG : 180

TrRTa : TTGCAGCTGCCAGAAGGGTTTGAGGAGCGAAACAAGGGCGCGGAGTGGTATGCACTGAT : 240

TrRTa : TGGGCTCCGCAAGTGAAAATAATGGGTCACGTGGCAGTTGGTGGGTTCTTGACTCATGCT : 300

TrRTa : GGTTGGACATCAGTTGTGGAGGCTGTTCAAAATGAAAAGCCACTTGTGCTACTAACATTT : 360

TrRTa : CTTGCAGATCAAGGAATAAATGCGAGGGTGTGGAGGAAAAGAAGATGGGTTACTCAGTG : 420

TrRTa : CCTAGGGATGAACGAGATGGGTCATTACAAAGTGAAGTGGCTGCTTCGATTAGACTA : 480

TrRTa : GTTATGCTTGAAGAAGAGGGAAGAATCTACAAGGAAAAGATTAAAGAGATGAAGGACTTG : 540

TrRTa : TTCG : 544

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FIGURE 14

TrRTa : LWIKEWLDKQPRSTVLYVAFGSEAKPSQEEVTKIAFGLEESKIPFFWVLRVQRGPTDNVV : 60

TrRTa : LQLPEGFEERNKGRGVVCTDWAPQVKIMGHVAVGGFLTHAGWTSVVEAVQNEKPLVLLTF : 120

TrRTa : LADQGINARVLEEKKMGYSVPRDERDGSFTSDSVAASIRLVMLEEEGRIYKEKIKEMKDL : 180

TrRTa : F : 181

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FIGURE 15

TrCYTb5a : TAATAACATTATTATTATTGCTCCTCTAAAGCTCAAACCTCATTTACAACCATGGCAAAT : 60

TrCYTb5a : CAAAAGGTTTTCACCCTCTCACAAATCTCCCAACACAAGTCCAACAAAACTGTTGGCTT : 120

TrCYTb5a : GTAATCAACGACAGAGTGTTGAACGTGACAAAGTTTTTGGAGGAACATCCAGGAGGAGAA : 180

TrCYTb5a : GAGGTAATTCTAGAGGTTGCAGGGAAAGATGCCACAAAGGAGTTTGATGATATTGGACAT : 240

TrCYTb5a : AGTAAAGCAGCTCAAAATTTAGTCCTCAAATATCAAGTTGGTGTACTTGAAGGTGCCAAG : 300

TrCYTb5a : GTTGAAAAGATTGATAATATGGATTTTGTGAGGACAAGGAGTCCAAGAGCAAAGAAATG : 360

TrCYTb5a : AGTGCTTTTGTGTGTCAAAGAGGATACTAGTTCCAAAACCTGCAACATTTTGTAGAGTTGTTT : 420

TrCYTb5a : GTGCCATTTCTTTTGTCTTTATCTATTTTGGTTACAGTGTCATCACCAGAGCAGACACT : 480

TrCYTb5a : GTTGGTTACTAAATCATGGGGGATGTCTAGACCTTGGTCTGTG : 523

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FIGURE 16

TrCYTb5a : HYYYCSSKAQTSFTTMANQKVFTLSQISQHKSNKNCWLVINDRVNLNVTKFLEEHPGGEEV : 60

TrCYTb5a : ILEVAGKDATKEFDDIGHSKAAQNLVLKYQVGVLGAKVEKIDNMDFVEDKESKSKEMSA : 120

TrCYTb5a : FVVKEDTSSKTATFLELFVFPFLFAFIYFGYSVITRADTVGY : 161

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FIGURE 17

TrLACa : CATAGAAGAAGCTCTATAGCAACATTTCTTTGTTGAGTAGAGGTATATAACTCAAAAG : 58

TrLACa : GGTTGCTATGGCCACGGCGCAATTTCTGAATTATACTATTGTTGGTAGCATGTTTGCTT : 116

TrLACa : CCATTTTCTGTTGATGCTACGGTTCGACACTACAAGTTCAATGTTGTGTTGAAAAATG : 174

TrLACa : CCACAAGATTGTGTTCAACCAACCAATTGTAACCATAAATGGAAAATCCCCAGGTCC : 232

TrLACa : CACCATCTATGCTAGAGAAGATGACAATGTTCTAATTAAGGTTGTCAACCATGTCAAA : 290

TrLACa : TACAATGTTAGCATACTGGCATGGTGTCAAACAACTAAGAACGGGTTGGGCCGACG : 348

TrLACa : GGCCAGCATAACCAATGTCCAATTCAACCGGGTCAGGCCTATGTTTACAACTT : 406

TrLACa : CACTCTTACAGGCCAGAGAGGCACACTTTGGTGGCATGCTCATATTCTTTGGCTTAGA : 464

TrLACa : GCCACTGTCCATGGTGCCTTGGTCATTTTACCAAAGCTTGGAGTTCCTTACCCTTTTC : 522

TrLACa : CCAAACCTCATATGGAACAAGTTATTGTATTAGGT : 557

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FIGURE 18

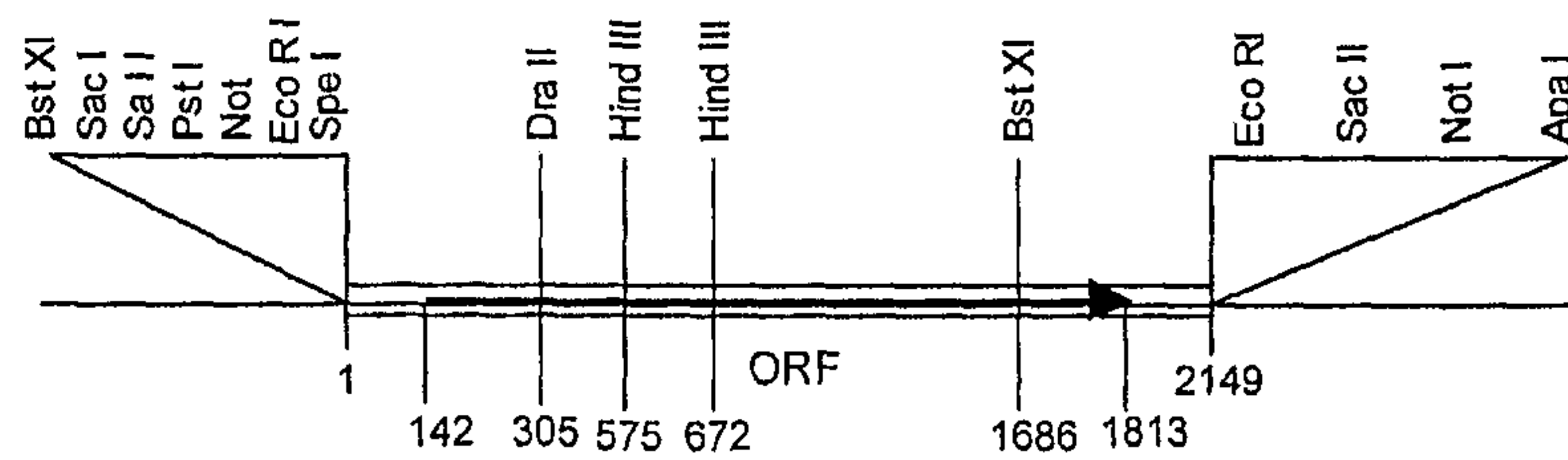
TrLACa : MATAQFRIILLLVACLLPFSVDATVRHYKFENVVLKNATRLCSTKPIVTINGKSPGPTIYA : 60

TrLACa : REDDNVLIKVVNVHVKYNVSIHWHGVKQLRTGWADGPAYITQCPIQPGQAYVYNFTLTGQR : 120

TrLACa : GTLWWHAHILWLRATVHGALVILPKLGVPYPFPKPHMEQVIVLG : 164

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FIGURE 19

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FIGURE 20

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      *      20      *      40      *
TrLACa : TAAGCAGTGGTAACAACGCAGAGTACGCGGGGATTGCATTGCATTTTCAAGAGAGTGA : 58

      60      *      80      *      100      *
TrLACa : TCACTAGCCAGCATAGAGAAGCTCTATAGCAACATTTCTTTGTTGAGTAGAGGTATA : 116

      120      *      140      *      160      *
TrLACa : TAACTCAAAAGGGTTGCTATGGCCACGGCGCAATTTCTGAATTATACTATTGTTGGTAG : 174

      180      *      200      *      220      *
TrLACa : CATGTTTGCTTCCATTTTCTGTTGATGCTACGGTTCGACACTACAAGTTCAATGTTGT : 232

      240      *      260      *      280      *
TrLACa : GTTGAAAAATGCCACAAGATTGTGTTCAACCAAACCAATTGTAACCATAAATGGAAAA : 290

      300      *      320      *      340
TrLACa : TCCCCAGGTCCCACCATCTATGCTAGAGAAGATGACAATGTTCTAATTAAGGTTGTCA : 348

      *      360      *      380      *      400
TrLACa : ACCATGTCAAATACAATGTTAGCATACACTGGCATGGTGTCAAACAATAAGAACGGG : 406

      *      420      *      440      *      460
TrLACa : TTGGGCCGACGGGCCAGCATACATAACCCAATGTCCAATTCAACCGGGTCAGGCCTAT : 464

      *      480      *      500      *      520
TrLACa : GTTTACAACCTTCACTCTTACAGGCCAGAGAGGCACACTTTGGTGGCATGCTCATATTC : 522

      *      540      *      560      *      580
TrLACa : TTTGGCTTAGAGCCACTGTCCATGGTGCCTTGGTCATTTTACCAAAGCTTGGAGTTCC : 580

      *      600      *      620      *
TrLACa : TTACCCTTTTCCCAAACCTCATATGGAACAAGTTATTGTATTAGGTGAATGGTGGAAA : 638

      640      *      660      *      680      *
TrLACa : TCAGATACCGAGGCTATAATAAATGAAGCTTTAAATCTGGATTAGCTCCAAATATTT : 696

      700      *      720      *      740      *
TrLACa : CTGATGCTCACACAATCAATGGTCTTCCAGGGTCTGGCCAAGGTTGTGCTTCACAAGA : 754

      760      *      780      *      800      *
TrLACa : TGGATTCTCATTGGAAGTTCAACAAAAAACCCTACTTACTAAGAATCATCAATGCT : 812

      820      *      840      *      860      *
TrLACa : GCACTCAATGAAGAACTCTTTTTCAAAATTGCAAACCATCAATTAAGTGTGTTGAAG : 870

      880      *      900      *      920
TrLACa : TTGATGCAACTTATGTAAAACCATTCAAACTGACACAATTGTTATAGCACCTGGCCA : 928

      *      940      *      960      *      980
TrLACa : AACCACAAACGTGCTTTTAGAAACCAACAAGCACTAGGAACTACTTAATTGCAGCT : 986

      *      1000      *      1020      *      1040
TrLACa : TCTCCTTTCATGGATGCACCAATTGTTGTTGACAACAAACTGCCATTGCCACATTAC : 1044

      *      1060      *      1080      *      1100
TrLACa : ACTATTCAAACACACTTGGTTCACAGTCACTTCCTTAACCTTCTTTACCTCCAAAAA : 1102

      *      1120      *      1140      *      1160

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TrLACa : TGCTACTCCAATTGCTAATACTTTCACAGATTCTCTTAGAGGCTTAACTCGAAAAA : 1160

TrLACa : TATCCGGCTAATGTTCCCTTTAAAGATTGATAATAAATTATTATTCACTGTTTCTCTTG : 1218

TrLACa : GTATTAATCCTTGTCTACATGTGTCAATAATAGTCGCGTCGTAGCTGATTTCAACAA : 1276

TrLACa : TGTTACATTCGTGATGCCGAAAACCGCGCTTATTCAAGCACATTTTTTTAAGATTAAA : 1334

TrLACa : GGAGTTTTTAGTGATGATTTTCCTGGAAATCCTCCTGTGGTGTATAATTTTACTGGGA : 1392

TrLACa : CACAGTTGACAAATTTTGGGACTACTAAAGGGACAAGGCTTTATAGACTTGCTTATAA : 1450

TrLACa : TTCTACTGTTGAATTGGTTTTGCAAGATACTGGAATGATAACACCTGAGAATCATCCT : 1508

TrLACa : ATTCATCTTCATGGATTCAATTTCTTTGTAGTTGGTAGTGGTAAAGGGAACCTTGATT : 1566

TrLACa : CTAAAAAGATGCAAAAAAGTTTAATCTTGTTGATCCTGTTGAGAGGAATACTGTTGG : 1624

TrLACa : TGTTCCGGCCGGAGGTTGGACTGCTATCAGATTCAGGGCTGATAATCCAGGGGTGTGG : 1682

TrLACa : TTTATGCATTGTCATTTGGAGATTCATAACAATGGGGACTAAAGATGGCTTTTGTTG : 1740

TrLACa : TGGACAATGGTAAAGGCCCAAATGAATCTCTATTACCACCTCCAAGTGACCTTCCTAA : 1798

TrLACa : GTGTTGAGGAAAGTACCAATTAACATTCAATGTTATTTGAAGAGAACAACATATTTTA : 1856

TrLACa : ATGGAAGGATTAAACAAGGCAAATGACAAGATTTTCTTGGAATATGGAAAGAATAAGA : 1914

TrLACa : TGTCCAATTTTCTTATAAAAAAAAATGTCCAATTGACATTTATTGGTATATTTTAAT : 1972

TrLACa : TCCTTTTAGTTGTATTATTTTCATTGTTTGTACCCATCTTCTTCTTCTTGAAAGATA : 2030

TrLACa : TTTTAGGGTTAATCAAAATTTTAAGAATTTTAAAGAAATCTTTTCTTTTGTTGCC : 2085

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FIGURE 21

* 20 * 40 * 60
 TrLACa : MATAQFRIILLLVACLLPFSVDATVRHYKFNVVLKNATRLCSTKPIVTINGKSPGPTIYA : 60

* 80 * 100 * 120
 TrLACa : REDDNVLIKVVNVHVKNVSIHWHGVKQLRTGWADGPAYITQCPIQPGQAYVYNFTLTGQR : 120

* 140 * 160 * 180
 TrLACa : GTLWWHAHILWLRATVHGALVILPKLGVPYPFPKPHMEQVIVLGEWWKSDTEAINEALK : 180

* 200 * 220 * 240
 TrLACa : SGLAPNISDAHTINGLPGSGQGCASQDGFSLLEVQQKKTYLLRIINAALNEELFFKIANHQ : 240

* 260 * 280 * 300
 TrLACa : LTVVEVDATYVVKPKTDTIVIAPGQTTNVLLLETKQALGNLYLIAASPFMDAPIVVDNKTAI : 300

* 320 * 340 * 360
 TrLACa : ATLHYSNTLGSTVTSLSLPPKNATPIANTFTDSLRLGNSKKYPANVPLKIDNKLLFTVS : 360

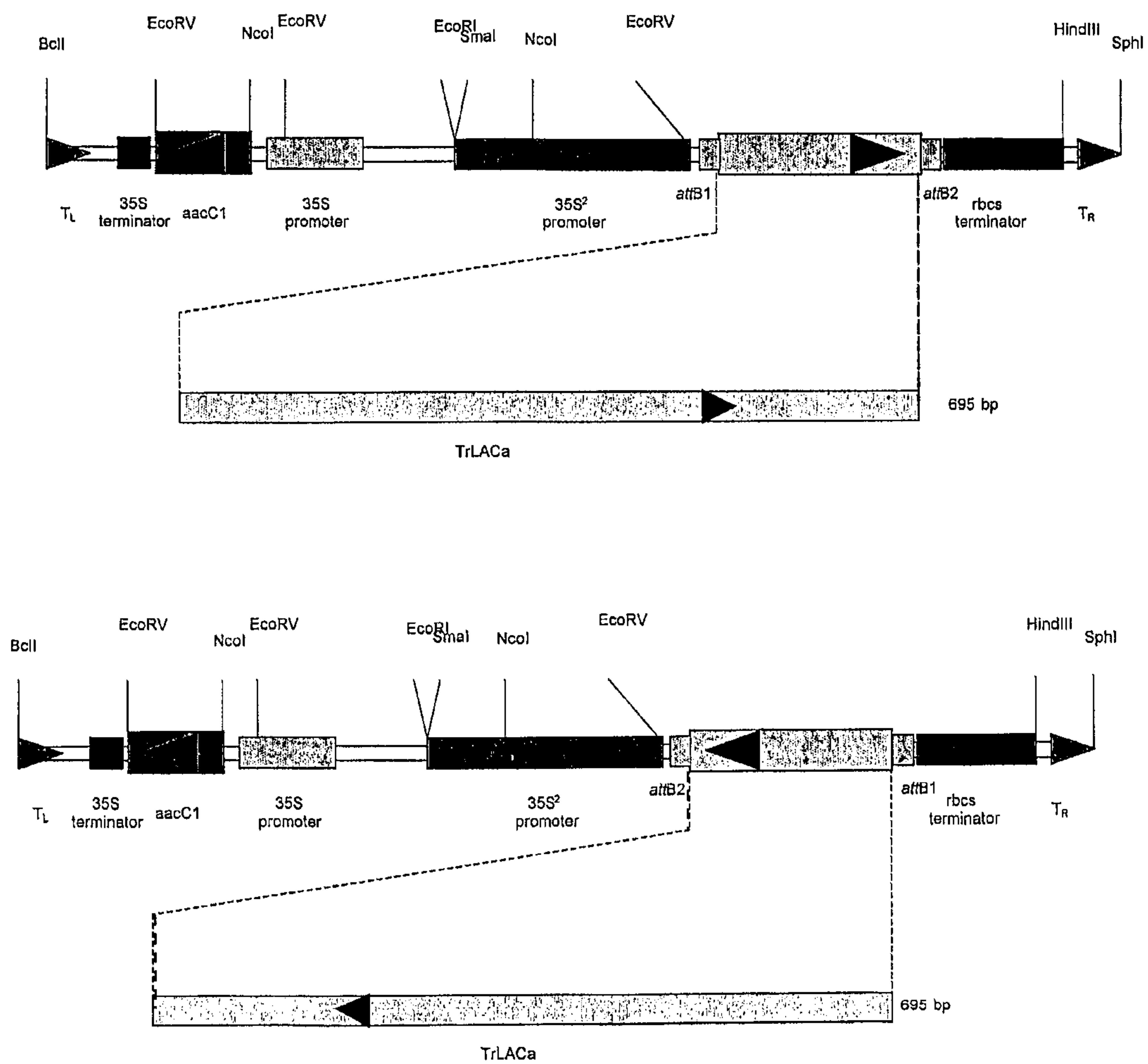
* 380 * 400 * 420
 TrLACa : LGINPCPTCVNNSRVVADFNNVTFVMPKTALIQAHFFKIKGVFSDDFPGNPPVVYNFTGT : 420

* 440 * 460 * 480
 TrLACa : QLTNFGTTKGTRLYRLAYNSTVELVLQDTGMITPENHPHILHGFNFFVVGSGKGNFDSKK : 480

* 500 * 520 * 540
 TrLACa : DAKKFNLVDPVERNTVGVPAGGWTAIRFRADNPGVWFMHCHLEIHTTWGLKMAFVVDNGK : 540

*
 TrLACa : GPNESLLPPPSDLPKC : 556

FIGURE 22



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FIGURE 23

TrMADSa : AGAGAAATGGGAAGAGGAAGAGTTGAATTGAAGAGAATTGAGAACAAAATCAACAGACAA : 60

TrMADSa : GTTACCTTTGCAAAACGAAGAAATGGTCTTTTGAAGAAAGCTTATGAACTTTCTGTTCTT : 120

TrMADSa : TGTGATGCTGAGGTTGCTCTCATCGTCTTCTCCAATAGAGGAAAACCTCTATGAGTTTTC : 180

TrMADSa : AGCACTTCTAGCATGCTCAAACTCTTGAGAGGTATCAGAAATGCAACTATGGAGCACCT : 240

TrMADSa : GAAGCTAATGTGACATCAAAGGAAGCTTTGGTATTGGAATTAAGCAGTCAACAAGAATAC : 300

TrMADSa : TTGAAGCTTAAGGCACGTTATGAATCTCTTCAACGCTCGCAAAGGAATCTTATGGGAGAA : 360

TrMADSa : GATCTTGGCCCTCTAAGTAGCAAAGATCTTGAACCACTTGAAAGGCAGCTAGATTCGTCC : 420

TrMADSa : TTGAAGCAAATCAGATCCACAAGGACCCAATTCATGCTGGATCAGCTTGGTGATCTTCAA : 480

TrMADSa : CGTAAGGAACACTTGCTATGTGAAGCAAACAGAGCTCTCAGACAAAGGATGGAAGGGTAT : 540

TrMADSa : CAAATAAATTCTCTCCAACCTGAATCTGAGTGCTGAAGATATGGGATATGGTCGTCATCAT : 600

TrMADSa : CCAGTTCACACCCAGGGTGATGAACTATTTCAACCAATTGAGTGCGAACCAACCTTACAA : 660

TrMADSa : ATTGGATATCAAGCTGATCCAGGATCAGTGGTGACAGCAGGCCCAAGCATGAATAATTTC : 720

TrMADSa : ATGGGTGGATGGTTACCATGATGATGTTAAAGTTATATATTGAGAACGAGTGTGAAGCAT : 780

TrMADSa : GCATAAAGATCAAATGAAAATTTGTAATACTAGCATGTTATATAATGGACTACACTAAAC : 840

TrMADSa : TATGTATTAGTGTCTACTTACTATGTAGGCAAATAATATAGTAA : 885

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FIGURE 24

TrMADSa : MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIVFSNRGKLYEFCST : 60

TrMADSa : SSMLKTLERYQKCNYGAPEANVTSKEALVLELSSQQEYLKLKARYESLQRSQRNLMGEDL : 120

TrMADSa : GPLSSKDLEPLERQLDSSLKQIRSTRTQFMLDQLGDLQRKEHLLCEANRALRQRMGYQI : 180

TrMADSa : NSLQLNLSAEDMGYGRHHPVHTQGDELFQPIECEPTLQIGYQADPGSVVTAGPSMNNFMG : 240

TrMADSa : GWLP : 244

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FIGURE 25

	*	20	*	40	*	60	
TrMADSa1 :	AGAGAAATGGGAAGAGGAAGAGTTGAATTGAAGAGAATTGAGAACAAAATCAACAGACAA						: 60
TrMADSa2 :	AGAGAAATGGGAAGAGGAAGAGTTGAATTGAAGAGAATTGAGAACAAAATCAACAGACAA						: 60
TrMADSa3 :	-----						: -
TrMADSa4 :	-----						: -
	AGAGAAATGGGAAGAGGAAGAGTTGAATTGAAGAGAATTGAGAACAAAATCAACAGACAA						
	*	80	*	100	*	120	
TrMADSa1 :	GTTACCTTTGCAAAACGAAGAAATGGTCTTTTGAAGAAAGCTTATGAACTTTCTGTTCTT						: 120
TrMADSa2 :	GTTACCTTTGCAAAACGAAGAAATGGTCTTTTGAAGAAAGCTTATGAACTTTCTGTTCTT						: 120
TrMADSa3 :	-----						: -
TrMADSa4 :	-----						: -
	GTTACCTTTGCAAAACGAAGAAATGGTCTTTTGAAGAAAGCTTATGAACTTTCTGTTCTT						
	*	140	*	160	*	180	
TrMADSa1 :	TGTGATGCTGAGGTTGCTCTCATCGTCTTCTCCAATAGAGGAAAACCTATGAGTTTTC						: 180
TrMADSa2 :	TGTGATGCTGAGGTTGCTCTCATCGTCTTCTCCAATAGAGGAAAACCTATGAGTTTTC						: 180
TrMADSa3 :	-----						: -
TrMADSa4 :	-----						: -
	TGTGATGCTGAGGTTGCTCTCATCGTCTTCTCCAATAGAGGAAAACCTATGAGTTTTC						
	*	200	*	220	*	240	
TrMADSa1 :	AGCACTTCTAGCATGCTCAAAACTCTTGAGAGGTATCAGAAATGCAACTATGGAGCACCT						: 240
TrMADSa2 :	AGCACTTCTAGCATGCTCAAAACTCTTGAGAGGTATCAGAAATGCAACTATGGAGCACCT						: 240
TrMADSa3 :	-----						: -
TrMADSa4 :	-----						: -
	AGCACTTCTAGCATGCTCAAAACTCTTGAGAGGTATCAGAAATGCAACTATGGAGCACCT						
	*	260	*	280	*	300	
TrMADSa1 :	GAAGCTAATGTGACATCAAAGGAAGCTTTGGTATTGGAATTAAGCAGTCAACAAGAATAC						: 300
TrMADSa2 :	GAAGCTAATGTGACATCAAAGGAAGCTTTGGTATTGGAATTAAGCAGTCAACAAGAATAC						: 300
TrMADSa3 :	-----GAATAC						: 6
TrMADSa4 :	-----						: -
	GAAGCTAATGTGACATCAAAGGAAGCTTTGGTATTGGAATTAAGCAGTCAACAAGAATAC						
	*	320	*	340	*	360	
TrMADSa1 :	TTGAAGCTTAAGGCACGTTATGAATCTCTTCAACGCTCGCAAAGGAATCTTATGGGAGAA						: 360
TrMADSa2 :	TTGAAGCTTAAGGCACGTTATGAATCTCTTCAACGCTCGCAAAGGAATCTTATGGGAGAA						: 360
TrMADSa3 :	TTGAAGCTTAAGGCACGTTATGAATCTCTTCAACGCTCGCAAAGGAATCTTATGGGAGAA						: 66
TrMADSa4 :	-----GTTATGAATCTCTTCAACGCTCGCAAAGGAATCTTATGGGAGAA						: 44
	TTGAAGCTTAAGGCACGTTATGAATCTCTTCAACGCTCGCAAAGGAATCTTATGGGAGAA						
	*	380	*	400	*	420	
TrMADSa1 :	GATCTTGGCCCTCTAAGTAGCAAAGATCTTGAACCACTTGAAAGGCAGCTAGATTCGTCC						: 420
TrMADSa2 :	GATCTTGGCCCTCTAAGTAGCAAAGATCTTGAACCACTTGAAAGGCAGCTAGATTCGTCC						: 420
TrMADSa3 :	GATCTTGGCCCTCTAAGTAGCAAAGATCTTGAACCACTTGAAAGGCAGCTAGATTCGTCC						: 126
TrMADSa4 :	GATCTTGGCCCTCTAAGTAGCAAAGATCTTGAACCACTTGAAAGGCAGCTAGATTCGTCC						: 104
	GATCTTGGCCCTCTAAGTAGCAAAGATCTTGAACCACTTGAAAGGCAGCTAGATTCGTCC						
	*	440	*	460	*	480	
TrMADSa1 :	TTGAAGCAAATCAGATCCACAAGGACCCAATTCATGCTGGATCAGCTTGGTGATCTTCAA						: 480
TrMADSa2 :	TTGAAGCAAATCAGATCCACAAGGACCCAATTCATGCTGGATCAGCTTGGTGATCTTCAA						: 480
TrMADSa3 :	TTGAAGCAAATCAGATCCACAAGGACCCAATTCATGCTGGATCAGCTTGGTGATCTTCAA						: 186
TrMADSa4 :	TTGAAGCAAATCAGATCCACAAGGACCCAATTCATGCTGGATCAGCTTGGTGATCTTCAA						: 164
	TTGAAGCAAATCAGATCCACAAGGACCCAATTCATGCTGGATCAGCTTGGTGATCTTCAA						

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      *      500      *      520      *      540
TrMADSa1 : CGTAAGGAACACTTGCTATGTGAAGCAAACAGAGCTCTCAGACAAAGGATGGAAGGGTAT : 540
TrMADSa2 : CGTAAGGAACACTTGCTATGTGAAGCAAACAGAGCTCTCAGACAAAGGATGGAAGGGTAT : 540
TrMADSa3 : CGTAAGGAACACTTGCTATGTGAAGCAAACAGAGCTCTCAGACAAAGGATGGAAGGGTAT : 246
TrMADSa4 : CGTAAGGAACACTTGCTATGTGAAGCAAACAGAGCTCTCAGACAAAGGATGGAAGGGTAT : 224
          CGTAAGGAACACTTGCTATGTGAAGCAAACAGAGCTCTCAGACAAAGGATGGAAGGGTAT

      *      560      *      580      *      600
TrMADSa1 : CAAATAAATTCTCTCCAACCTGAATCTGAGTGCTGAA----- : 576
TrMADSa2 : CAAATAAATTCTCTCCAACCTGAATCTGAGTGCTGAAGATATGG----- : 583
TrMADSa3 : CAAATAAATTCTCTCCAACCTGAATCTGAGTGCTGAAGATATGGGATATGGTCGTCATCAT : 306
TrMADSa4 : CAAATAAATTCTCTCCAACCTGAATCTGAGTGCTGAAGATATGGGATATGGTCGTCATCAT : 284
          CAAATAAATTCTCTCCAACCTGAATCTGAGTGCTGAAGATATGGGATATGGTCGTCATCAT

      *      620      *      640      *      660
TrMADSa1 : ----- : -
TrMADSa2 : ----- : -
TrMADSa3 : CCAGTTCACACCCAGGGTGATGAACTATTTCAACCAATTGAGTGCGAACC'AACCTTACAA : 366
TrMADSa4 : CCAGTTCACACCCAGGGTGATGAACTATTTCAACCAATTGAGTGCGAACC'AACCTTACAA : 344
          CCAGTTCACACCCAGGGTGATGAACTATTTCAACCAATTGAGTGCGAACC'AACCTTACAA

      *      680      *      700      *      720
TrMADSa1 : ----- : -
TrMADSa2 : ----- : -
TrMADSa3 : ATTGGATATCAAGCTGATCCAGGATCAGTGGTGACAGCAGGCCCAAGCATGAATAATTTTC : 426
TrMADSa4 : ATTGGATATCAAGCTGATCCAGGATCAGTGGTGACAGCAGGCCCAAGCATGAATAATTTTC : 404
          ATTGGATATCAAGCTGATCCAGGATCAGTGGTGACAGCAGGCCCAAGCATGAATAATTTTC

      *      740      *      760      *      780
TrMADSa1 : ----- : -
TrMADSa2 : ----- : -
TrMADSa3 : ATGGGTGGATGGTTACCATGATGATGTTAAAGTTATATATTGAGAACGAGTGTGAAGCAT : 486
TrMADSa4 : ATGGGTGGATGGTTACCATGATGATGTTAAAGTTATATATTGAGAACGAGTGTGAAGCAT : 464
          ATGGGTGGATGGTTACCATGATGATGTTAAAGTTATATATTGAGAACGAGTGTGAAGCAT

      *      800      *      820      *      840
TrMADSa1 : ----- : -
TrMADSa2 : ----- : -
TrMADSa3 : GCATAAAGATCAAATGAAAATTTGTAATACTAGCATGTTATATAATGGACTACACTAAAC : 546
TrMADSa4 : GCATAAAGATCAAATGAAAATTTGTAATACTAGCATGTTATATAATGGACTACACTAAAC : 524
          GCATAAAGATCAAATGAAAATTTGTAATACTAGCATGTTATATAATGGACTACACTAAAC

      *      860      *      880
TrMADSa1 : ----- : -
TrMADSa2 : ----- : -
TrMADSa3 : TATGTATTAGTGTCTACTTACTATG----- : 571
TrMADSa4 : TATGTATTAGTGTCTACTTACTATGTAGGCAAAATAATATAGTAA : 569
          TATGTATTAGTGTCTACTTACTATGTAGGCAAAATAATATAGTAA
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FIGURE 26

TrWRKYa : * 20 * 40 * 60
ATCTTCAAAAGATGCTTCTCATATTGATGTTAAACCCGGTAATGCCTCTAATATTCATGT : 60

TrWRKYa : * 80 * 100 * 120
TAAAAGGCAGAGTTATTTCTAAAACTATAAGGAAGGATACATCAAAGCAGAAAGGTAG : 120

TrWRKYa : * 140 * 160 * 180
CAAAGAAATCATGAAGCACAAATATGTATTTCAAACAAGGAGTCAGATCGATATACTAGA : 180

TrWRKYa : * 200 * 220 * 240
CGATGGGTTCCGATGGAGAAAGTACGGGGAAAAGTTGGTGAAAAACAACAAATATCCTAG : 240

TrWRKYa : * 260 * 280 * 300
AAGTTATTACAAATGCACTTATCCAGGCTGCAATGCAAAGAAACAATCCAAAGGAATTC : 300

TrWRKYa : * 320 * 340 * 360
CAACAGGATCATATTGTATAAACAACTTACGAGGGAATGCATATTCACCCTGTCCAGAA : 360

TrWRKYa : CTCAACTG : 368

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FIGURE 27

TrWRKYa : SSKDASHIDVKPGNASNIHVKKAEFLKTIRKDTSKQKGSKEIMKHKYVFQTRSQIDILD : 60

TrWRKYa : DGFRWRKYGEKLVKNNKYPRSYKCTYPGCNAKKQIQRNSKQDHIV : 106

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FIGURE 28

TrMYCa : CCTCTCTCTCTCTCTCTCCCCACTCCATTATCACCACCACACGGTCTCTTCTTCCTAAC : 60

TrMYCa : TTTCTCTTCTTCTCTTTCTTTCCCTAATTTACCTCCAAAATTAACCAAAAATAATAAT : 120

TrMYCa : AAAAATTCCATTTTCATGAATCTTTGGAGCGACGAGAACTCATCAGTGATGGAGGCTTTTA : 180

TrMYCa : TGACCTCATCCGATTTATCAACCTTATGGCCATCACAACCACAGCCGCCGTCGTCACAAC : 240

TrMYCa : CACCACAAACCACCACCGGATTCAACCAAGACACACTCCAACAACGTCTTCAAGCTTTAA : 300

TrMYCa : TCGAAGGCGCTTCCGAAATCTGGACTTACGCTATCTTCTGGCAACCTTCTTACGACTATT : 360

TrMYCa : CCGGCTCTTCTCTTCTCGGTTGGGGTGACGGTTATTACAAAGGCGAAGAAGACAAATCAA : 420

TrMYCa : AATCAAAATCCAAAGCTACTTCACCAGCTGAACAAGAACACCGTAGAAAAGTTCTCCGAG : 480

TrMYCa : AACTTAATTCTTTAATCTCCGGTAATCCAGCACCGGAAGAATCTTCCGTCGATGAAGAAG : 540

TrMYCa : TTACAGATACGGAATGGTTTTTTTTTAGTTTCTATGACTCAATCTTTTGTTAACGGAAGT : 600

TrMYCa : GGACTTCCTGGACAAGCTTATTTTAATTCAAC : 632

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FIGURE 29

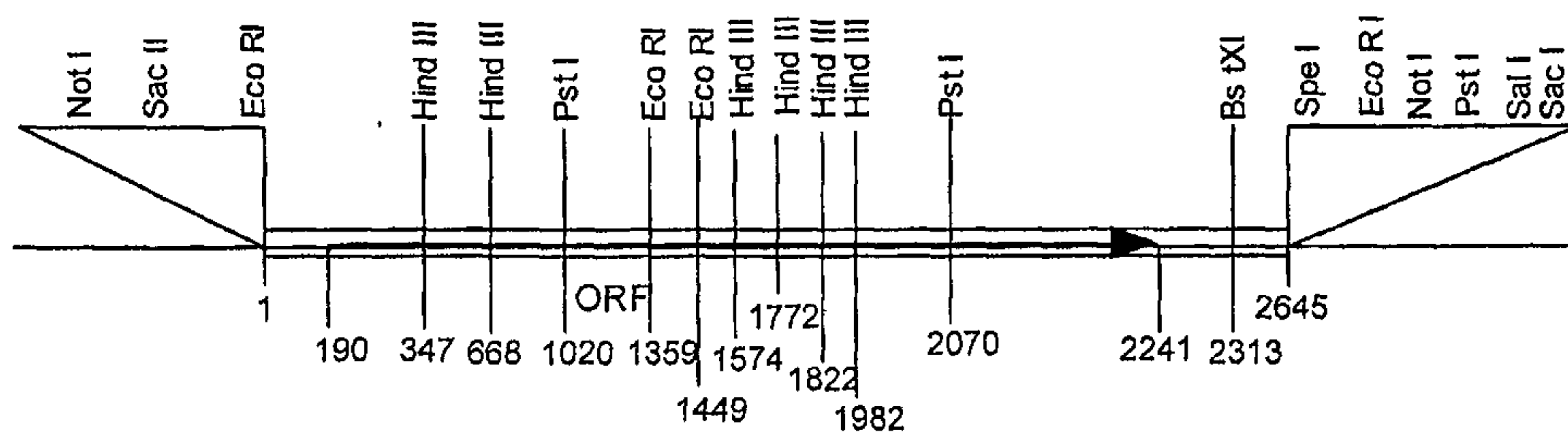
TrMYCa : MNLWSDENSSVMEAFMTSSDLSTLWPSQPQPPSSQPPQTTTGFNQDTLQQRLQALIEGAS : 60

TrMYCa : EIWTYAIFWQPSYDYSGSSLLGWGDGYKGEEDKSKSKSKATSPAQQEHRKVLRELNSL : 120

TrMYCa : ISGNPAPEESSVDEEVTDTWFFFSFYDSIFC : 152

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FIGURE 31

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FIGURE 32

TrMYCa : TAAGCAGTGGTAACAACGCAGAGTACGCGGGGATTCGTCTCTTTCTTCCTCTCTCTCTCT : 60

TrMYCa : CTCTCCCCCAATCCATTATCACCACCACACGGTCTCTTCTTCCTAACTTTCTCTTCTTCT : 120

TrMYCa : CTTTCTTTTCCCTAATTTACCTCCAAAATTAACCAAAAATAAATAATAAAAATTCCATTT : 180

TrMYCa : CATGAATCTTTGGAGCGACGAGAAGTCATCAGTGATGGAGGCTTTTATGACCTCTTCCGA : 240

TrMYCa : TTTATCAACCTTATGGCCATCACAACCACAGCCGCCGTCGTCACAACCACCACAAACCAC : 300

TrMYCa : CACCGGATTCAACCAAGACACACTCCAACAACGTCTTCAAGCTTTAATCGAAGGCGCTTC : 360

TrMYCa : CGAAATCTGGACTTACGCTATCTTCTGGCAACCTTCTTACGACTATTCCGGCTCTTCTCT : 420

TrMYCa : TCTCGGTTGGGGTGACGGTTATTACAAAGGCGAAGAAGACAAATCGAAATCAAATCCAA : 480

TrMYCa : AGCTACTTCACCAGCTGAACAAGAACACCGTAGAAAAGTTCTCCGAGAACTTAATTCTTT : 540

TrMYCa : AATCTCCGGTAATCCGGCACCGGAAGAATCTTCCGTCGATGAAGAAGTTACAGATACGGA : 600

TrMYCa : ATGGTTTTTTTTAGTTTCTATGACTCAATCTTTTGTTAACGGAAGTGGACTTCCTGGACA : 660

TrMYCa : AGCTTATTTTAATTCAACTCCGGTGTGGTTAGTCGGAGGTGAGAATCTCGCCCTCTCGGT : 720

TrMYCa : TTGCGAGAGGGCGAGACAAGGTCATGAACATGGTTTACAGACGCTGACGTGTATACCGTC : 780

TrMYCa : GGCGAACGGTGTTTTAGAGCTTGGATCTACTGAATTGATTTATCAGAATAACGATCTGAT : 840

TrMYCa : GAATAAAGTTAAGATGTTGTTTAATTTTAATAATAATTCTGATTTTGGATCTTCTTGGCA : 900

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TrMYCa : * 920 * 940 * 960
ATTAGGTAGTAATTCTACTGTAATTACTCATCAAGGTGAAAATGATCTTTCTTCAATTTG : 960

TrMYCa : * 980 * 1000 * 1020
GCTTAATGATCCTGAAACTAGAGATTCTGTTGATAATAATTCTCTTGCTGCAGCAACAAC : 1020

TrMYCa : * 1040 * 1060 * 1080
AACAACAACGACAACAAACACTTCAATTTCAATTCCAAGTCATCATCAGCAACAGCAACA : 1080

TrMYCa : * 1100 * 1120 * 1140
GCACCAGAACAATAGTAATAATCAGAGTTTGAGTGTGACGAAAACGATTCAATTTGAAAC : 1140

TrMYCa : * 1160 * 1180 * 1200
GCGTGGTTCAAGTACTTTAACAGAAGCTCCTAGTGTGTTTCATGTTTCAAGTAAGCAAAA : 1200

TrMYCa : * 1220 * 1240 * 1260
TCAACAAGGATTGTTTTCTAAAGAAATGAATCTTTTGGAGTACGGTGGGGGTAATAGTCA : 1260

TrMYCa : * 1280 * 1300 * 1320
GCAGCGTTCGTTGAAGCCGGAATCTGGTGAGATTTTGAGT'TTTGGTGGTGAGAGTAAAAA : 1320

TrMYCa : * 1340 * 1360 * 1380
GAGTTCTTATGTTGCTAATAATGGAAATTCGAATTCGAATTTTTTCTCTGGTCAATCACA : 1380

TrMYCa : * 1400 * 1420 * 1440
GTTAGTTTCAGTTGCTGAGGAGAATGGGAATGGAAATGGAAATGGGAAGAGGAGGTCTCC : 1440

TrMYCa : * 1460 * 1480 * 1500
GAATTCGAGAGGAAGCAATAATGATGATGGAATGCTATCTTTTACTTCTGGTGTAATTGT : 1500

TrMYCa : * 1520 * 1540 * 1560
TCCACCGGTGAATTTGAAATTCTCTGGTGGTACTGGTGGTGGTGATTCCGACCATTTCGGA : 1560

TrMYCa : * 1580 * 1600 * 1620
TCTTGAAGCTTCGGTGCTGAAGGAAGTGGATAGTAGTCGTGTGGTGGAGCCGGAGAAGAA : 1620

TrMYCa : * 1640 * 1660 * 1680
GCCGAGGAAGAGAGGGAGGAAACCGGCGAATGGAAGAGAGGAACCGTTGAATCATGTTGA : 1680

TrMYCa : * 1700 * 1720 * 1740
AGCCGAGAGACAACGAAGAGAGAAGCTGAATCAGAGATTCTATGCTCTTCGTGCAGTTGT : 1740

TrMYCa : * 1760 * 1780 * 1800
TCCTAATGTTTCAAAGATGGATAAAGCTTCACTTTTGGGTGATGCTATATCATACATTAC : 1800

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* 1820 * 1840 * 1860
 TrMYCa : TGAGCTGAAAACAAAGCTTGTGAAAAGTGAATCCGATAAAGATGAATTAGAAAAACAAC : 1860

* 1880 * 1900 * 1920
 TrMYCa : TGATGCAGTGAAGAATGAGCTTCAGAAAGTCAATGAAAAGTTCGTCTCATCCACCGCCTCA : 1920

* 1940 * 1960 * 1980
 TrMYCa : ACCTCAACAACACTACAACAACAACAAGTACCCGATAAACCTCTTCCAATCAAGCTTT : 1980

* 2000 * 2020 * 2040
 TrMYCa : AATCGATTTAGATATTGATGTGAAGATTATAGGTTGGGATGCAATGATAAGGGTCCAATG : 2040

* 2060 * 2080 * 2100
 TrMYCa : CAGTAAGAAAAACCACCCTGCAGCGAAGTTGATGGCGGCGTTGATGGAGCTTGACCTAGA : 2100

* 2120 * 2140 * 2160
 TrMYCa : AGTGCACCACGCAAGTGTTTCCGTGGTGAATGATTTGATGATACAACAAGCAACCGTGAA : 2160

* 2180 * 2200 * 2220
 TrMYCa : GATGGGGGGTCGTTTTTACACCCAGGAGCAGCTTCGGGCAGCATTGTCCTCTAAAGTTGG : 2220

* 2240 * 2260 * 2280
 TrMYCa : GGATGTTCAATAAAGTCTGTAAATTGCTGCAATGTGAAATTAATTGGGAATGTTATGTAT : 2280

* 2300 * 2320 * 2340
 TrMYCa : GTAAATTTCTCATTCCTCCATAATTTTGGGGCTCTGGGATATTTTACTGATTCCCGGTAA : 2340

* 2360 * 2380 * 2400
 TrMYCa : CTATGTAAACTAGAAGTGTCTTTGTTTTTGGTAGCTTAGTATGAATTTTGAGGTAATTTT : 2400

* 2420 * 2440 * 2460
 TrMYCa : ATTTGGGAATTTGTATGGAGATGAAGTACTAGAACTAGAGGTAGCGTCGATGAAGTAAGT : 2460

* 2480 * 2500 * 2520
 TrMYCa : AAAAATAAGTGTAATTTCTCCGCAATGCGTGCCCGTGTGTGTATATAGATGTTGTTGTA : 2520

* 2540 * 2560 *
 TrMYCa : TAATTCTCATAAATGGGTAAACATGGTGAAAATTCTGAATATTATTATTCTCAGCTTACC : 2579

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FIGURE 33

* 20 * 40 * 60
 TrMYCa : MNLWSDENSSVMEAFMTSSDLSTLWPSQPQPPSSQPPQTTTGFNQDTLQORLQALIEGAS : 60

* 80 * 100 * 120
 TrMYCa : EIWTYAIWFQPSYDYSGSSLLGWGDGYKGEEDKSKSKSKATSPAEQEHRRKVLRELNSL : 120

* 140 * 160 * 180
 TrMYCa : ISGNPAPEESSVDEEVTDTTEWFFLVSMQTQSFVNGSGLPGQAYFNSTPVWLVGGENLALSV : 180

* 200 * 220 * 240
 TrMYCa : CERARQGHEHGLQTLTCIPSANGVLELGSTELIYQNNDLMNKVKMLFNFNNNSDFGSSWQ : 240

* 260 * 280 * 300
 TrMYCa : LGSNSTVITHQGENDLSSIWLNDPETRDSVDNNSLAAATTTTTTTNTSISIPSHHQQQQQ : 300

* 320 * 340 * 360
 TrMYCa : HQNNSNNQSLSVTKTIQFETRGSSTLTEAPSVVHVSSKQNZQGLFSKEMNLLEYGGGNSQ : 360

* 380 * 400 * 420
 TrMYCa : QRSLKPESGEILSFGGESKKSSYVANNGNSNSNFFSGQSQLVSVAEENGNGNGKRRSP : 420

* 440 * 460 * 480
 TrMYCa : NSRGSNNDDGMLSFTSGVIVPPVNLKFSGGTGGGSDHSDLEASVVKEVDSSRVVEPEKK : 480

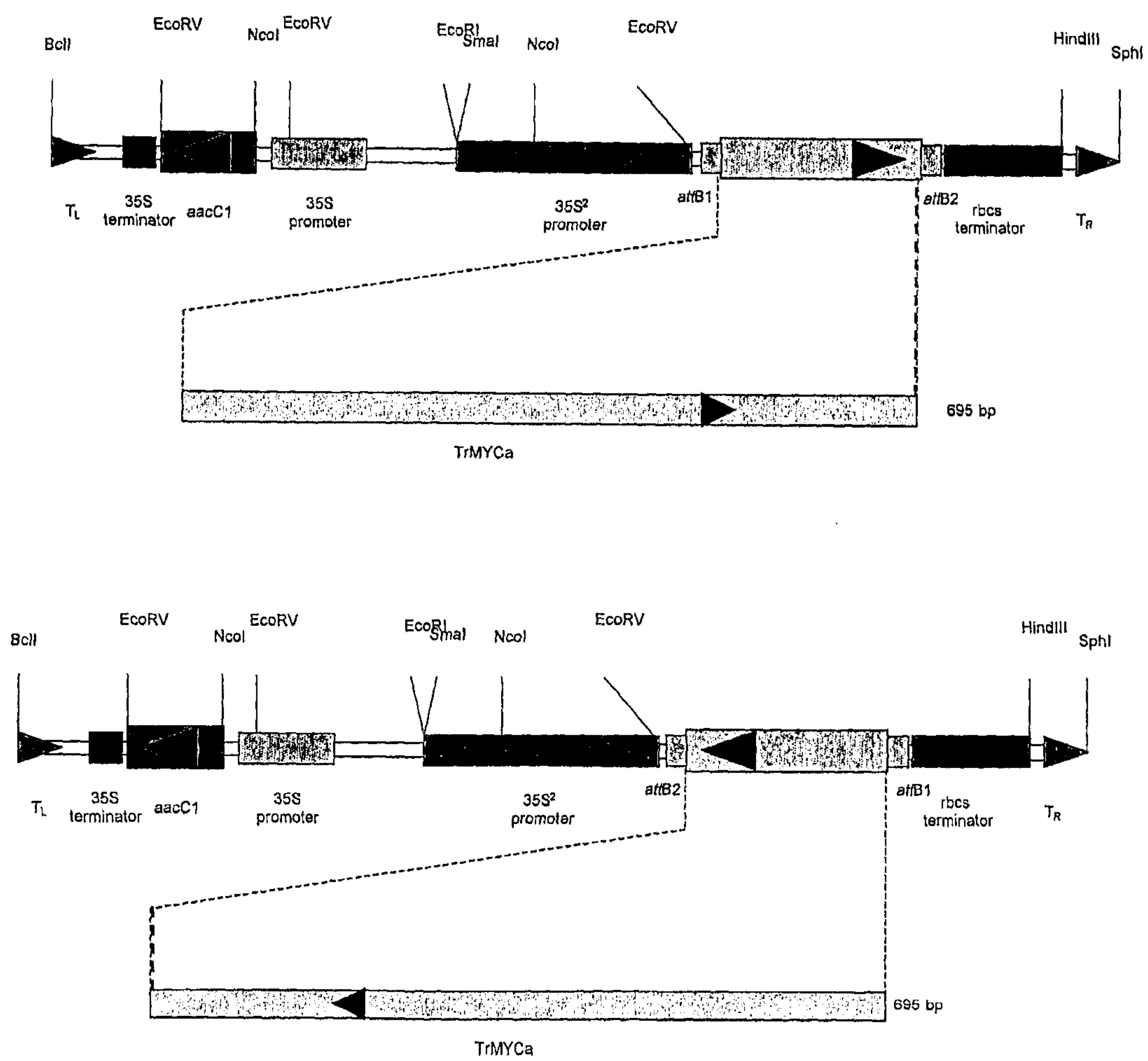
* 500 * 520 * 540
 TrMYCa : PRKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVPNVSKMDKASLLGDAISYIT : 540

* 560 * 580 * 600
 TrMYCa : ELKTKLVKTESDKDELEKQLDAVKNELQKVNENSSHPPPQPPQLQQQQQVPDPKSSNQAL : 600

* 620 * 640 * 660
 TrMYCa : IDLDIDVKIIGWDAMIRVQCSKKNHPAAKLMAALMELDLEVHHASVSVVNDLMIQQATVK : 660

* 680
 TrMYCa : MGGRFYTQEQLRAALSSKVGDVQ : 683

FIGURE 34



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FIGURE 35

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      *      20      *      40      *      60
TrTT1a : ATAAACCCTTTCTAGGGAGAGACTAATTGAATATATTGCACAAATCTAGGGACTCTATCT : 60

      *      80      *      100     *      120
TrTT1a : CACTCTAAACTAAGATGGGGGGGAGAGATAAGTGCAATGTAAAAGACAAGAATTTATAT : 120

      *      140     *      160     *      180
TrTT1a : CTTCAAACCCCAACTTTTCATTGAATGGCTCAAACCTTCTTCATCACTTTTCATCTTCTCCT : 180

      *      200     *      220     *      240
TrTT1a : TCATCATCTTTAACTCATCAACAAGAAATATCTCAAGAACTTTTCAGTTTTTACCCATC : 240

      *      260     *      280     *      300
TrTT1a : TATAGTGGAATTAAGTCCTTTGAGGAAAACCATGGGATGCAAAAGGAAGATTTAGAAGTA : 300

      *      320     *      340     *      360
TrTT1a : AAAGAAGAGAAAGTGGA AAAAGTAACTGTGGCTTTGCACATTGGATTGCCTAACATAGGA : 360

      *      380     *      400     *      420
TrTT1a : GGAGGTGAATCTTATGATCATGAAGAGAAGAATAAGGTTTTTGATGAGAACAATAAAGTT : 420

      *      440     *      460     *      480
TrTT1a : AATGAAAAAGAATTAAAGAAAAACTTGCATGGTTTTTGTTTTAAAGGAAGAAAGAAGGTTT : 480

      *      500     *      520     *      540
TrTT1a : TGGATACCAACTCCTGCTCAGATCCTTGTTGGACCTATGCAATTTGCTTGCTCCATATGC : 540

      *      560     *      580     *      600
TrTT1a : AACAAAGACTTTCAATAGATACAACAATATGCAGATGCATATGTGGGGACATGGATCAGAA : 600

TrTT1a : T : 601

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FIGURE 36

TrTT1a : M G G R D K C N V K D K N L Y L Q T P T F I E W L K P S S S L S S S P S S S L T H Q Q E I S Q E T F Q F L P I Y S G I K : 60

TrTT1a : S F E E N H G M Q K E D L E V K E E K V E K V T V A L H I G L P N I G G G E S Y D H E E K N K V F D E N N K V N E K E L : 120

TrTT1a : K K N L H G F C F K E E R R F W I P T P A Q I L V G P M Q F A C S I C N K T F N R Y N N M Q M H M W G H G S E : 175

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FIGURE 37

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      *      20      *      40      *      60
TrTT1a1 : ATAAACCCCTTCTAGGGAGAGACTAATTGAATATATTGCACAAATCTAGGGACTCTATCT : 60
TrTT1a2 : -TAAACCCCTTCTAGGGAGAGACTAATTGAATATATTGCACAAATCTAGGGACTCTATCT : 59
      ATAAACCCCTTCTAGGGAGAGACTAATTGAATATATTGCACAAATCTAGGGACTCTATCT

      *      80      *      100     *      120
TrTT1a1 : CACTCTAAAACTAAGATGGGTTTGAGAGATAAGTGCAATGTAAAAGACAAGAATTTATAT : 120
TrTT1a2 : CACTCTAAAACTAAGATGGGGGGGAGAGATAAGTGCAATGTAAAAGACAAGAATTTATAT : 119
      CACTCTAAAACTAAGATGGGGGGGAGAGATAAGTGCAATGTAAAAGACAAGAATTTATAT

      *      140     *      160     *      180
TrTT1a1 : CTTCAAACCCCAACTTTTCATTGAATGGCTCAAACCTTCTTCATCACTTTCATCTTCTCCT : 180
TrTT1a2 : CTTCAAACCCCAACTTTTCATTGAATGGCTCAAACCTTCTTCATCACTTTCATCTTCTCCT : 179
      CTTCAAACCCCAACTTTTCATTGAATGGCTCAAACCTTCTTCATCACTTTCATCTTCTCCT

      *      200     *      220     *      240
TrTT1a1 : TCATCATCTTTAACTCATCAACAAGAAATATCTCAAGAACTTTTCAGTTTTTACCCATC : 240
TrTT1a2 : TCATCATCTTTAACTCATCAACAAGAAATATCTCAAGAACTTTTCAGTTTTTACCCATC : 239
      TCATCATCTTTAACTCATCAACAAGAAATATCTCAAGAACTTTTCAGTTTTTACCCATC

      *      260     *      280     *      300
TrTT1a1 : TATAGTGGAATTAAGTCCTTTGAGGAAAACCATGGGATGCAAAAGGAAGATTTAGAAGTA : 300
TrTT1a2 : TATAGTGGAATTAAGTCCTTTGAGGAAAACCATGGGATGCAAAAGGAAGATTTAGAAGTA : 299
      TATAGTGGAATTAAGTCCTTTGAGGAAAACCATGGGATGCAAAAGGAAGATTTAGAAGTA

      *      320     *      340     *      360
TrTT1a1 : AAAGAAGAGAAAGTGGA AAAAGTA ACTGTGGCTTTGCACATTGGATTGCCTAACATAGGA : 360
TrTT1a2 : AAAGAAGAGAAAGTGGA AAAAGTA ACTGTGGCTTTGCACATTGGATTGCCTAACATAGGA : 359
      AAAGAAGAGAAAGTGGA AAAAGTA ACTGTGGCTTTGCACATTGGATTGCCTAACATAGGA

      *      380     *      400     *      420
TrTT1a1 : GGAGGTGAATCTTATGATCATGAAGAGAAGAATAAGGTTTTTGATGAGAACAATAAAGTT : 420
TrTT1a2 : GGAGGTGAATCTTATGATCATGAAGAGAAGAATAAGGTTTTTGATGAGAACAATAAAGTT : 419
      GGAGGTGAATCTTATGATCATGAAGAGAAGAATAAGGTTTTTGATGAGAACAATAAAGTT

      *      440     *      460     *      480
TrTT1a1 : AATGAAAAAGAATTAAAGAAAAACTTGCATGGTTTTTGTGTTTAAGGAAGAAAGAAGGTTT : 480
TrTT1a2 : AATGAAAAAGAATTAAAGAAAAACTTGCATGGTTTTTGTGTTTAAGGAAGAAAGAAGGTTT : 479
      AATGAAAAAGAATTAAAGAAAAACTTGCATGGTTTTTGTGTTTAAGGAAGAAAGAAGGTTT

      *      500     *      520     *      540
TrTT1a1 : TGGATACCAACTCCTGCTCAGATCCTTGTTGGACCTATGCAATTTGCTTGCTCCATATGC : 540
TrTT1a2 : TGGATACCAACTCCTGCTCAGATCCTTGTTGGACCTATGCAATTTGCTTGCTCCATATGC : 539
      TGGATACCAACTCCTGCTCAGATCCTTGTTGGACCTATGCAATTTGCTTGCTCCATATGC

      *      560     *      580     *      600
TrTT1a1 : AACAAAGACTTTCAATAGATACAACAATATGCAGATGCATATGTGGGGACATGGATCAGAA : 600
TrTT1a2 : AACAAAGACTTTCAATAGATACAACAATATGCAGATGCATATGTGGGGACATG----- : 591
      AACAAAGACTTTCAATAGATACAACAATATGCAGATGCATATGTGGGGACATGGATCAGAA

TrTT1a1 : T : 601
TrTT1a2 : - :
      T

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FIGURE 38

TrHLHa : TACACACACAACAAACAATATGGACATGGATTCAACAGGTGGTTCTTCTTGGTGGCTCTA : 60

TrHLHa : TGATTATGGCTATGATATTTCTGTTCTGACCTGATTTCATGCCTTCTGATCATCACTC : 120

TrHLHa : TCCTGCTTCTGTTTTACCTGGAATATGCCTCAGACTCATATCATCAAGCCTCCTTCCTC : 180

TrHLHa : CAATATCAGCTTGGAATGGAATACTCACTGGACTCAACTGTACTGGAAAGTGGTCCTTC : 240

TrHLHa : ATCAAAGCGCTTGGAATGGAATACTCACTGGATTCAACTGTACTGGAAAATGGCCCTTC : 300

TrHLHa : AAAGCGGTTAAAGACAGAATCATGTGCATCTGGCTCCAAGGCATGTCGCGAGAAACAGCG : 360

TrHLHa : CAGGGATAAACTGAATGACAAGTTTATGGAATTGAGTTCTGTCTTAGAGCCTGATACT : 420

TrHLHa : GCCCAAACAGACAAAGTTACCTTATTAAATGACGCGGTTTCGTGTGGTTACACAATTAAG : 480

TrHLHa : AAATGAAGCAGAAAGGCTGAAGGAAAGGAATGACGAATTGCGCGAAAAAGTTAAAGAACT : 540

TrHLHa : TAAGACTGAGAAAAATGAGCTTCGCGATGAGAAAAATAAGCTGAAGTTAGACAAAGAAAA : 600

TrHLHa : GTTGGACAGCAAGTGAAATTAACAAGTGACAGTCCAGCATCCTCTCGAATGCCATGGC : 660

TrHLHa : GGCTAAAGGACAATCTGCTGCTAACCACAAGCTGATGCCTTTCATTGGTTATCCTGGAAT : 720

TrHLHa : TTCGGTGTGGCAGTTTATGTCACCTGCTACAGTTGATACATCACAGGA : 768

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FIGURE 39

TrHLHa : THTTNNMDMDSTGGSSCWLYDYGDISVPAPDFMPSDHHSPASVFTWNMPQTHIIKPPSS : 60

TrHLHa : NISLEMEYSLDSTVLESGPSSKRLEMEYSLDSTVLENGPSKRLKTESCASGSKACREKQR : 120

TrHLHa : RDKLNDKFMELSSVLEPDTLPKTDKVTLLNDAVRVVTQLRNEAERLKERNDELREKVKE : 180

TrHLHa : KTEKNELRDEKNKLIKLDKEKLEQQVKLTSVQSSILSNAMAAKGQSAANHKLMPFIGYPGI : 240

TrHLHa : SVWQFMSPATVDTSQ : 255

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FIGURE 40

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      *           20           *           40           *           60
TrHLHa1 : TACACACACAACAAACAATATGGACATGGATTCAACGGTGGTTCTTCTTGTGGCTCTA : 60
TrHLHa2 : -----ACACAACAACAAACAATATGGACATGGATTCCACAGGTGGTTCTTCTTGTGGCTCTA : 55
          TACACACACAACAAACAATATGGACATGGATTCAACAGGTGGTTCTTCTTGTGGCTCTA

      *           80           *           100          *           120
TrHLHa1 : TGATTATGGCTATGATATTTCTGTTTCCTGCACCTGATTTTCATGCCTTCTG---ATCACTC : 117
TrHLHa2 : TGATTATGGCTATGATATTTCTGTTTCCTGCACCTGATTTTCATGCTTCTGATCATCACTC : 115
          TGATTATGGCTATGATATTTCTGTTTCCTGCACCTGATTTTCATGCCTTCTGATCATCACTC

      *           140          *           160          *           180
TrHLHa1 : TCCTGCTTCTGTTTTTCACCTGGAATATGCCTCAGACTCATATCATCAAGCCTCCTTCCTC : 177
TrHLHa2 : TCCTGCTTCTGTTTTTCACCTGGAATATGCCTCAGACTCATATCATCAAGCCTCCTTCCTC : 175
          TCCTGCTTCTGTTTTTCACCTGGAATATGCCTCAGACTCATATCATCAAGCCTCCTTCCTC

      *           200          *           220          *           240
TrHLHa1 : CAATATCAGCTTGGAAATGGAATACTCACTGGACTCAACTGTACTGGAAAGTGGTCCTTC : 237
TrHLHa2 : CAATATCAGCTTGGAAATGGAATACTCACTGGACTCAACTGTACTGGAAAGTGGTCCTTC : 235
          CAATATCAGCTTGGAAATGGAATACTCACTGGACTCAACTGTACTGGAAAGTGGTCCTTC

      *           260          *           280          *           300
TrHLHa1 : ATCAAAGCGCTTGGAAATGGAATACTCACTGGATTCAACTGTACTGGAAATGGCCCTTC : 297
TrHLHa2 : A---AAGCGCTTGGAAATGGAATACTCACTGGATTCAACTGTACTGGAAATGGCCCTTC : 292
          ATCAAAGCGCTTGGAAATGGAATACTCACTGGATTCAACTGTACTGGAAATGGCCCTTC

      *           320          *           340          *           360
TrHLHa1 : AAAGCGGTTAAAGACAGAATCATGTGCATCTGGCTCCAAGGCATGTCGCGAGAAATGGCG : 357
TrHLHa2 : AAAGCGGTTAAAGACAGAATCATGTGCATCTGGCTCCAAGGCATGTCGCGAGAAACAGCG : 352
          AAAGCGGTTAAAGACAGAATCATGTGCATCTGGCTCCAAGGCATGTCGCGAGAAACAGCG

      *           380          *           400          *           420
TrHLHa1 : CAGGGATAAACTGAATGACAAGTTTATGGAATTGAGTTCTGTCTTAGAGCCTGATACACT : 417
TrHLHa2 : CAGGGATAAACTGAATGACAAGTTTATGGAATTGAGTTCTGTCTTAGAGCCTGATACACT : 412
          CAGGGATAAACTGAATGACAAGTTTATGGAATTGAGTTCTGTCTTAGAGCCTGATACACT

      *           440          *           460          *           480
TrHLHa1 : GCCCAAACAGACAAAGTTACCTTATTAAATGACGCGGTTTCGTGTGGTTACCAATTAAG : 477
TrHLHa2 : GCCCAAACAGACAAAGTTACCTTATTAAATGACGCGGTTTCGTGTGGTTACACAATTAAG : 472
          GCCCAAACAGACAAAGTTACCTTATTAAATGACGCGGTTTCGTGTGGTTACACAATTAAG

      *           500          *           520          *           540
TrHLHa1 : AAATGAAGCAGAAAGGCTGAAGGAAAGGAATGACGAATTGCGCGAAAAAGTTAAAGAACT : 537
TrHLHa2 : AAATGAAGCAGAAAGGCTGAAGGAAAGGAATGACGAATTGCGCGAAAAAGTTAAGAACT : 532
          AAATGAAGCAGAAAGGCTGAAGGAAAGGAATGACGAATTGCGCGAAAAAGTTAAAGAACT

      *           560          *           580          *           600
TrHLHa1 : TAAGCTGAGAAATGAGCTTCGCGATGAGAAAAATAAGCTGAAGTTAGACAAAGAAAA : 597
TrHLHa2 : TAAGCTGAGAAAAATGAGCTTCGCGATGAGAAAAATAAGCTGAAGTTAGACAAAGAAAA : 592
          TAAGCTGAGAAAAATGAGCTTCGCGATGAGAAAAATAAGCTGAAGTTAGACAAAGAAAA

      *           620          *           640          *           660
TrHLHa1 : GTTGAACAGCAAGTGAAATTAACAAGTGTACAGTCCAGCTCCTCTCGGATGCCATGGC : 657
TrHLHa2 : GTTGAACAGCAAGTGAAATTAACAAGTGTACAGTCCAGCATCCTCTCGAATGCCATGGC : 652
          GTTGAACAGCAAGTGAAATTAACAAGTGTACAGTCCAGCATCCTCTCGAATGCCATGGC

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                                *      680      *      700      *      720
TrHLHa1 : G----- : 658
TrHLHa2 : GGCTAAAGGACAATCTGCTGCTAACCACAAGCTGATGCCTTTCATTGGTTATCCTGGAAT : 712
          GGCTAAAGGACAATCTGCTGCTAACCACAAGCTGATGCCTTTCATTGGTTATCCTGGAAT

                                *      740      *      760
TrHLHa1 : ----- : -
TrHLHa2 : TTCGGTGTGGCAGTTTATGTACCTGCTACAGTTGATACATCACAGGA : 760
          TTCGGTGTGGCAGTTTATGTACCTGCTACAGTTGATACATCACAGGA
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FIGURE 41

TrMYB24a : TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGCTATGGGAAGCAGCTCCTTGTTGTGACAAAGAC : 60

TrMYB24a : AAAGTTAAGAGAGGACCATGGTCTCCTGATGAAGATGCAAACTCAAGAATTATTTAGCA : 120

TrMYB24a : ATTCATGGCACTGTTGGAAATTGGATTGCATTGCCTAAAAAGCTGGCCTTAAGCGGTGT : 180

TrMYB24a : GGAAAGAGTTGTCGTCTAAGGTGGCTGAATTATCTTAGGCCTGACATCAAACATGGAAGC : 240

TrMYB24a : TTTACTGAGGAAGAAGATACCATCATTTGTACCCTCTATGCTCAAATGGGTAGCAGATGG : 300

TrMYB24a : TCTGCCATAGCATCAAACTACCTGGGAGAACAGACAATGATGTAAAAAACTATTGGAAC : 360

TrMYB24a : ACAAACTGAAGAAGAAATTATGGCAGGAAAAGTTGGCCTCAAATCATTGACTGAAAAT : 420

TrMYB24a : GACAATACTGTCCCTTCAACCCCATCAGTGACTCAAATTGCAACATTATGTTAGACAAT : 480

TrMYB24a : AATTTTGATGCTAGTTATGGATTCAAGAATAATGAAAAAACATTGGTTTTGATCAAATT : 540

TrMYB24a : CATGATGTTGGTGTCTCAGAAATTGGTGCAAGTAACAACAATATTGATATTAAT : 594

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FIGURE 42

TrMYB24a : ERERERERLWEAAPCCDKDKVKRGPWSPDEDAKLKNYLAIHGTVGWNWIALPKKAGLKRCG : 60

TrMYB24a : KSCRLRWLNLYLRPDIKHGSFTEEDTIICTLYAQMGSRWSAIASKLPGRDNDVKNYWNT : 120

TrMYB24a : KLKKKIMAGKVGLKSLTENDNTVPSTPSVTQNCNIMLDNNFDASYGFKNNEKNIGFDQIH : 180

TrMYB24a : DVGVSSEIGASNNNIDIN : 197

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FIGURE 43

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      *      20      *      40      *      60
TrMYB24a1 : TGAGAGAGAGAGAGAGAGAGAGAGAGAGGCTATGGGAAG-AGCTCCTTGTGTGACAAAGACA :
60
TrMYB24a2 : -----GAGAGAGAGAGAGGCTATGGGAAGCAGCTCCTTGTGTGACAAAGACA :
48
      TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGCTATGGGAAGCAGCTCCTTGTGTGACAAAGACA

      *      80      *      100      *      120
TrMYB24a1 : AAGTTAAGAGAGGACCATGGTCTCCTGATGAAGATGCAAACTCAAGAATTATTTAGCAAT :
121
TrMYB24a2 : AAGTTAAGAGAGGACCATGGTCTCCTGATGAAGATGCAAACTCAAGAATTATTTAGCAAT :
109
      AAGTTAAGAGAGGACCATGGTCTCCTGATGAAGATGCAAACTCAAGAATTATTTAGCAAT

      *      140      *      160      *      180
TrMYB24a1 : TCATGGCACTGTTGGAAATTGGATTGCATTGCCTAAAAAAGCTGGCCTTAAGCGGTGTGGA :
182
TrMYB24a2 : TCATGGCACTGTTGGAAATTGGATTGCATTGCCTAAAAAAGCTGGCCTTAAGCGGTGTGGA :
170
      TCATGGCACTGTTGGAAATTGGATTGCATTGCCTAAAAAAGCTGGCCTTAAGCGGTGTGGA

      *      200      *      220      *      240
TrMYB24a1 : AAGAGTTGTCGTCTAAGGTGGCTGAATTATCTTAGGCCTGACATCAAACATGGAAGCTTTA :
243
TrMYB24a2 : AAGAGTTGTCGTCTAAGGTGGCTGAATTATCTTAGGCCTGACATCAAACATGGAAGCTTTA :
231
      AAGAGTTGTCGTCTAAGGTGGCTGAATTATCTTAGGCCTGACATCAAACATGGAAGCTTTA

      *      260      *      280      *      300
TrMYB24a1 : CTGAGGAAGAAGATACCATCATTTGTACCCTCTATGCTCAAATGGGTAGCAGATGGTCTGC :
304
TrMYB24a2 : CTGAGGAAGAAGATACCATCATTTGTACCCTCTATGCTCAAATGGGTAGCAGATGGTCTGC :
292
      CTGAGGAAGAAGATACCATCATTTGTACCCTCTATGCTCAAATGGGTAGCAGATGGTCTGC

      *      320      *      340      *      360
TrMYB24a1 : CATAGCATCAAACTACCTGGGAGAACAGACAATGATGTAAAAAACTATTGGAACACAAAA :
365
TrMYB24a2 : CATAGCATCAAACTACCTGGGAGAACAGACAATGATGTAAAAAACTATTGGAACACAAAA :
353
      CATAGCATCAAACTACCTGGGAGAACAGACAATGATGTAAAAAACTATTGGAACACAAAA

      *      380      *      400      *      420
TrMYB24a1 : CTGAAGAAGAAAATTATGGCAGGAAAAGTTGGCCTCAAATCATTGACTGAAAATGACAATA :
426
TrMYB24a2 : CTGAAGAAGAAAATTATGGCAGGAAAAGTTGGCCTCAAATCATTGACTGAAAATGACAATA :
414
      CTGAAGAAGAAAATTATGGCAGGAAAAGTTGGCCTCAAATCATTGACTGAAAATGACAATA

      *      440      *      460      *      480
TrMYB24a1 : CTGTCCCTTCAACCCCATCAGTGACTCAAATTGCAACATTATGTTAGACAATAATTTTGA :
487
TrMYB24a2 : CTGTCCCTTCAACCCCATCAGTGACTCAAATTGCAACATTATGTTAGACAATAATTTTGA :
475
      CTGTCCCTTCAACCCCATCAGTGACTCAAATTGCAACATTATGTTAGACAATAATTTTGA

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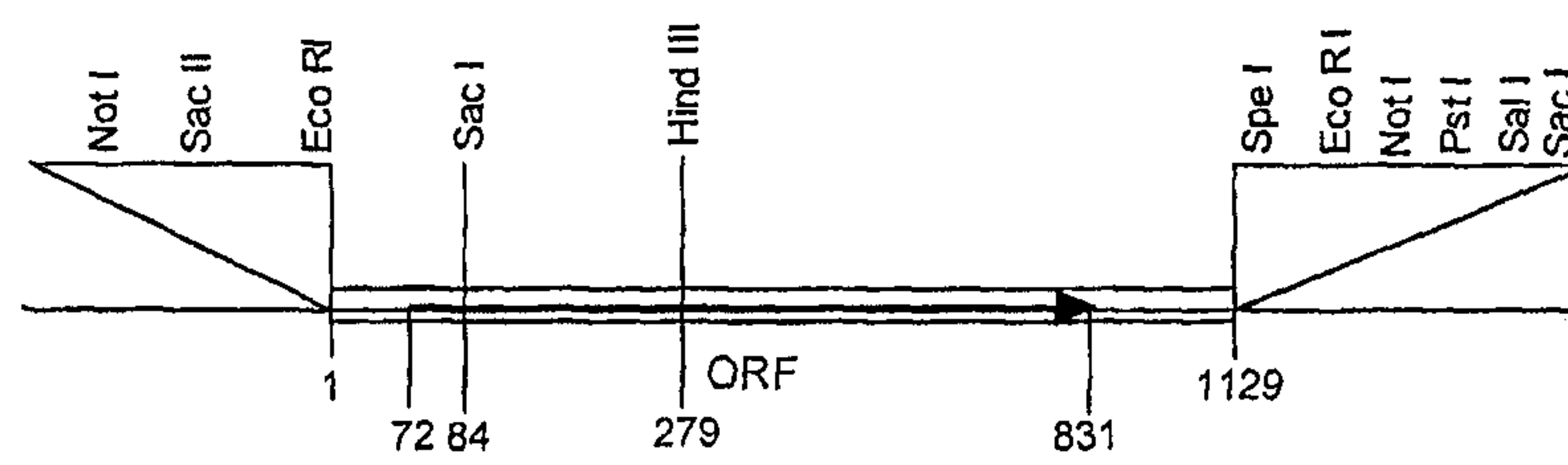
      *      500      *      520      *      540
TrMYB24a1 : TGCTAGTTATGGATTCAAGAATAATGAAAAAACATTGGTTTTGATCAAATTCATGATGTT :
548
TrMYB24a2 : TGCTAGTTATGGATTCAAGAATAATGAAAAAACATTGGTTTTGATCAAATTCATGATGTT :
536
      TGCTAGTTATGGATTCAAGAATAATGAAAAAACATTGGTTTTGATCAAATTCATGATGTT

      *      560      *      580      *
TrMYB24a1 : GGTGTCTCAGAAATTGGTGC----- : 568
TrMYB24a2 : GGTGTCTCAGAAATTGGTGCAAGTAACAACAATATTGATATTAAT : 581
      GGTGTCTCAGAAATTGGTGCAAGTAACAACAATATTGATATTAAT
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FIGURE 44



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FIGURE 45

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      *      20      *      40      *      60
TrMYB24a : TAAGCAGTGGTAACAACGCAGAGTACGCGGGGGAGTGAGAGAGAGAGAGAGAGAGAGA : 60

      *      80      *      100     *      120
TrMYB24a : GGCTATGGGAAGAGCTCCTTGTGTGACAAAGACAAAGTTAAGAGAGGACCATGGTCTCC :120

      *      140     *      160     *      180
TrMYB24a : TGATGAAGATGCAAACTCAAGAATTATTTAGCAATTCATGGCACTGTTGGAAATTGGAT :180

      *      200     *      220     *      240
TrMYB24a : TGCATTGCCTAAAAAGCTGGCCTTAAGCGGTGTGGAAAGAGTTGTCGTCTAAGGTGGCT :240

      *      260     *      280     *      300
TrMYB24a : GAATTATCTTAGGCCTGACATCAAACATGGAAGCTTTACTGAGGAAGAAGATACCATCAT :300

      *      320     *      340     *      360
TrMYB24a : TTGTACCCTCTATGCTCAAATGGGTAGCAGATGGTCTGCCATAGCATCAAACTACCTGG :360

      *      380     *      400     *      420
TrMYB24a : GAGAACAGACAATGATGTAAAAAACTATTGGAACACAAAAGTGAAGAAGAAAATTATGGC :420

      *      440     *      460     *      480
TrMYB24a : AGGAAAAGTTGGCCTCAAATCATTGACTGAAAATGACAATACTGTCCCTTCAACCCCATC :480

      *      500     *      520     *      540
TrMYB24a : AGTGACTCAAAATTGCAACATTATGTTAGACAATAATTTTGATGCTAGTTATGGATTCAA :540

      *      560     *      580     *      600
TrMYB24a : GAATAATGAAAAAACATTGGTTTTGATCAAATTCATGATGTTGGTGTCTCAGAAATTGG :600

      *      620     *      640     *      660
TrMYB24a : TGCAAGTAACAACAATATTGATATTAATCCTATGGTGTCAATATCTCAAGACAATTCAAG :660

      *      680     *      700     *      720
TrMYB24a : CATTGGAGTGAACAACAATTGTGTATCACTTCAAGATCAAGCTGGTGATGAATCTTTGGA :720

      *      740     *      760     *      780
TrMYB24a : ACCACTAATGGATTTTGGCTTTGGAGTTGGTAGTGATTTTGCTTCAAGTTGTTGCTTTCC :780

      *      800     *      820     *      840
TrMYB24a : TGAGTGGGTTGATTTTAGTTATGCTGACATTAAGACAAATTGACTGGTTCAAAATCTTGC :840

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TrMYB24a : * 860 * 880 * 900
ATTGTCTAGTTCTAGTAATTAAATATGGGATTAATTAATTATGTAATAGCAAAATTACAT :900

TrMYB24a : * 920 * 940 * 960
TACATAGGTGAAATATTTTTAGTTTTGCTAAGTATTAAATTTAATTTTTCTTCCAACAAT :960

TrMYB24a : * 980 * 1000 * 1020
AAATTGGTCTGAGTGATAAACATTTTAAGTCCCTTAAGCAGTTAGTCGGGGATTGCAAGT :1020

TrMYB24a : * 1040
TCTTCAACAAAATTTATTCATCATT : 1045

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FIGURE 46

TrMYB24a : MGRAPCCDKDKVKRGFWSPDEDAKLKNYLAIHGTVGWNWIALPKKAGLKRCGKSCRLRWLN : 60

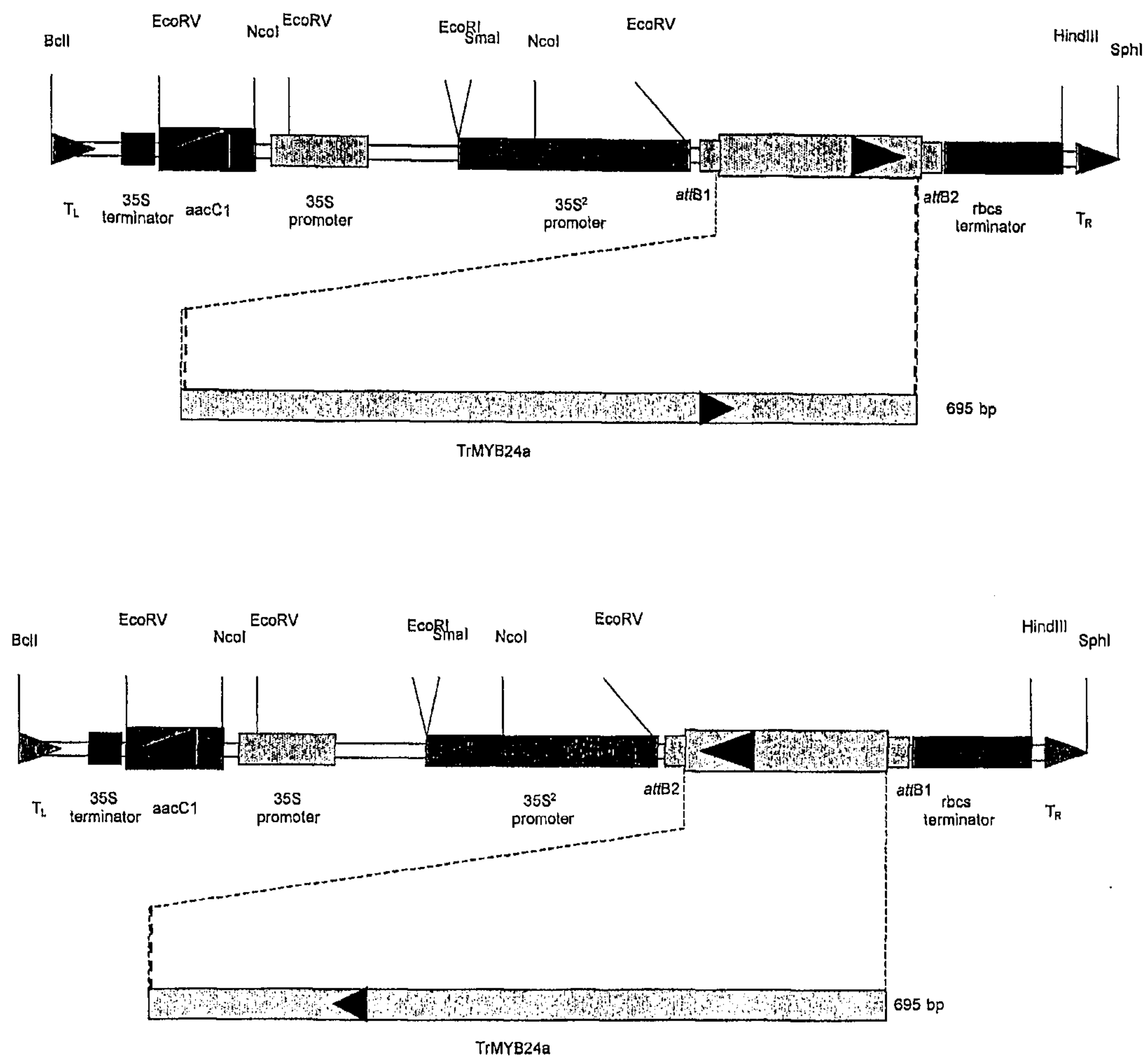
TrMYB24a : YLRPDIKHGSFTEEDTIICTLYAQMGSRWSAIAASKLPGRTDNDVKNYWNTKLKKKIMAG : 120

TrMYB24a : KVGLKSLTENDNTVPSTPSVTQNCNIMLDNNFDASYGFKNNEKNIGFDQIHDVGVSEIGA : 180

TrMYB24a : SNNNIDINPMVSIQDNSSIGVNNNCVSLQDQAGDESLEPLMDFGFGVGSDFASSCCFPE : 240

TrMYB24a : WVDFSYADIKTN : 252

FIGURE 47



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FIGURE 48

TrABCa : AGCTGCATGGAAAATTGCCGATAAGTCTCCTCCTCAGAATTGGCCGAGTCATGGCACTAT : 60

TrABCa : AGAGTTAAATAATTTACAGGTTAGGTACAGGCCAAACACTCCTCTAGTTCTTAAGGGAAT : 120

TrABCa : CTCTCTAACCATTGAAGGTGGAGAAAAAGTTGGTGTCTGGTTCGTACAGGAAGTGGAAA : 180

TrABCa : ATCAACACTTATTCAAGTGTTATTTAGATTAATTGAGCCTTCAGCTGGTAAAATTATTAT : 240

TrABCa : TGATGGTATCAATATTTCCAATATTGGCCTTCATGATTTAAGGTCACGTTTTTGGGAATTAT : 300

TrABCa : ACCACAAGAGCCTGTCTCTTTCAAGGAACAGTAAGAACCAATATTGACCCTCTTGGAGT : 360

TrABCa : ATATTCAGAAGAAGAAATTTGGAAGAGTCTCGAGCGCTGCCAATTGAAAGAAGTGGTGGC : 420

TrABCa : TGCAAAGCCTGAGAACTCGAGGCTTCAGTGGTTGATGGTGGAGACAATTGGAGTGTGGG : 480

TrABCa : ACAAAGACAGCTTCTATGCTTAGGAAGGATCATGCTAAAACGAAGCCAAATACTATTTCAT : 540

TrABCa : GGACGAAGCAACAGCATCTGTCTGATTACAAACTGATGCTGTAATACAA : 589

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FIGURE 49

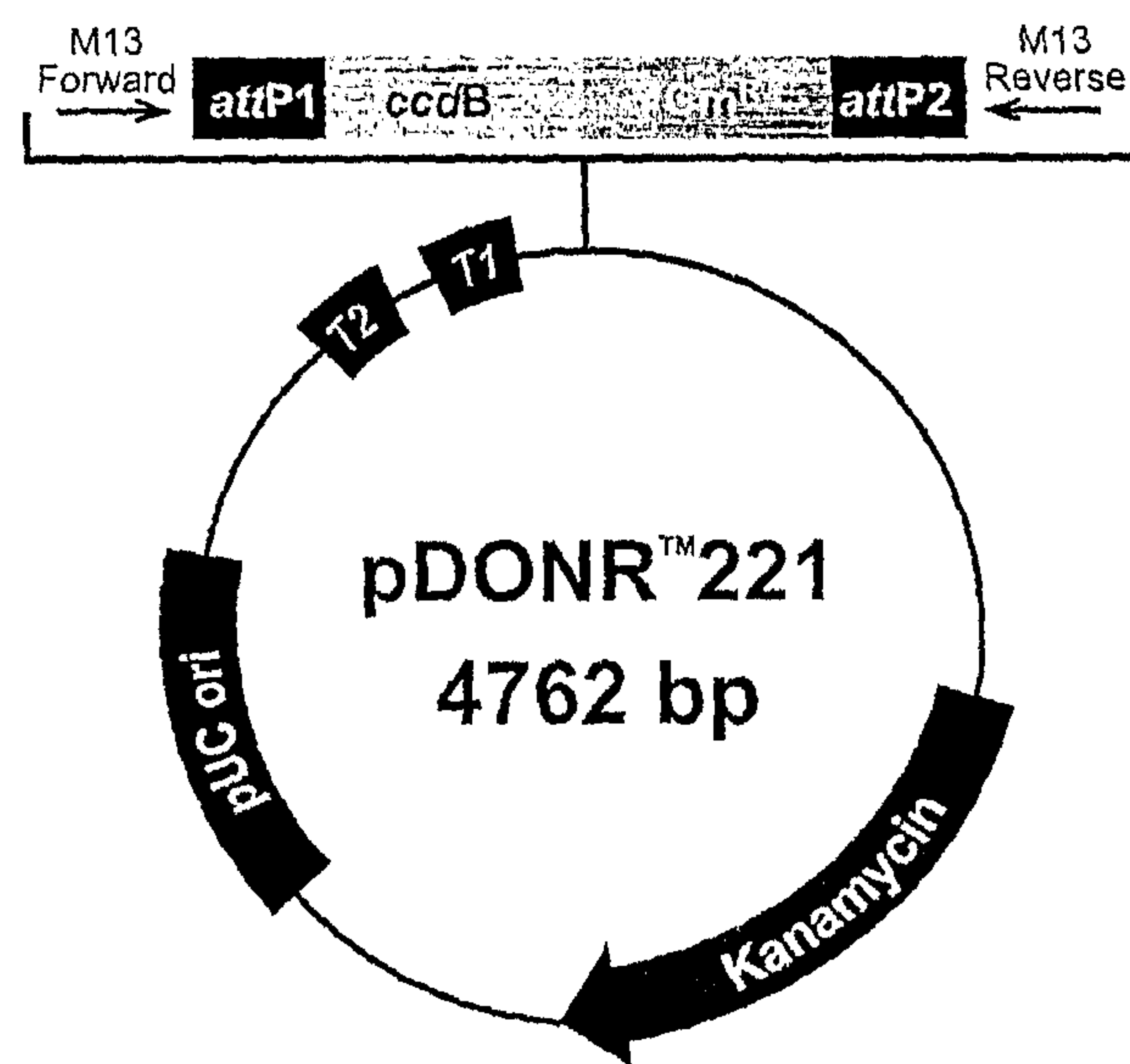
TrABCa : AAWKIADKSPQNWPSHG^{*}20^{*}40^{*}60TIELNNLQVRYRPNTPLVLKGISLTIEGGEKVG^{*}VVGRTGSGK : 60

TrABCa : STLIQVLFR^{*}80^{*}100^{*}120LIEPSAGKIIIDGINISNIGLHDLRSRFGIIPQE^{*}PVLFQGTVRTNIDPLGV : 120

TrABCa : YSEEEIWKSLERCQLKEV^{*}140^{*}160^{*}180VAAKPEKLEASVVDGGDNWSVGQRQLLCLGRIMLKRSQILFM : 180

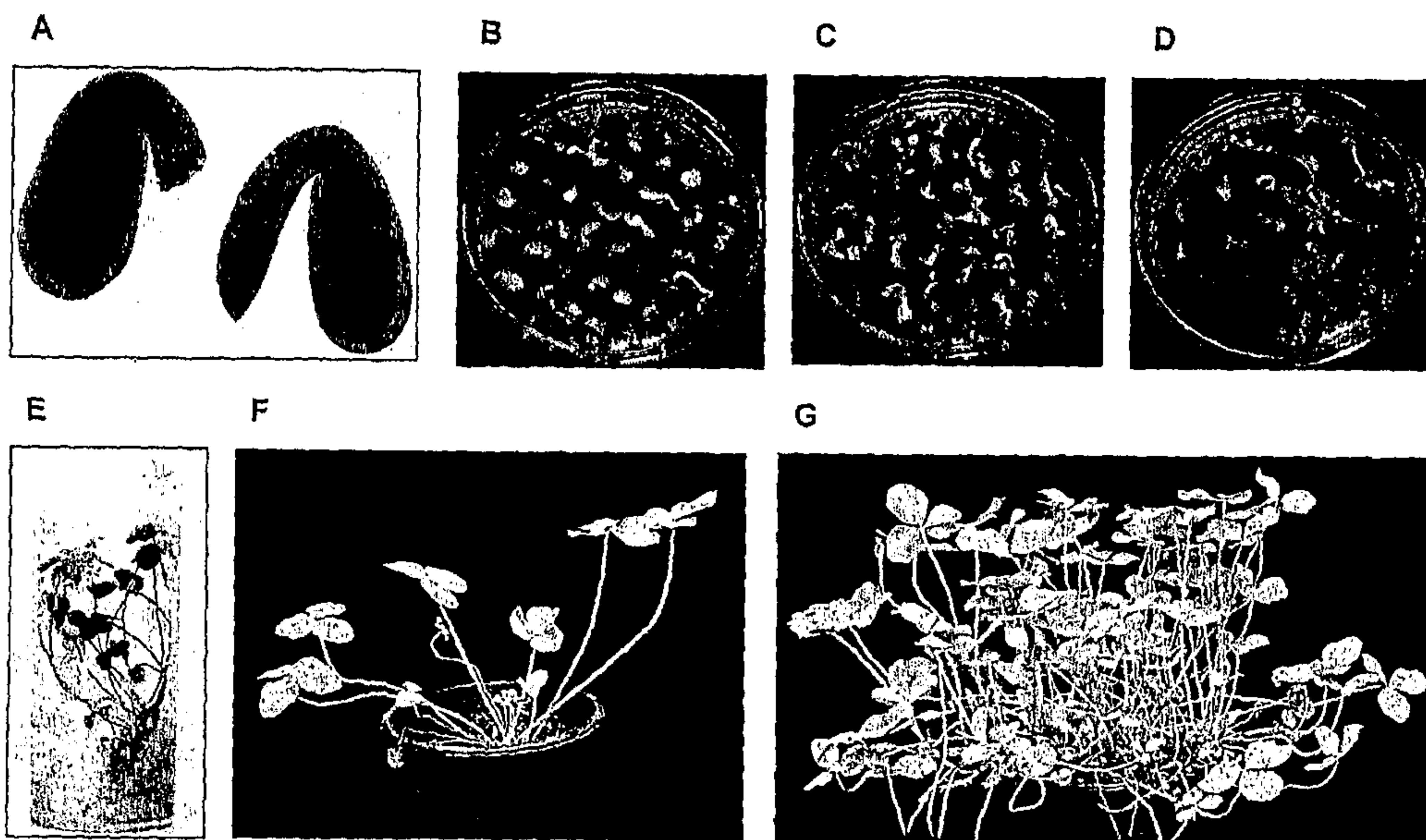
TrABCa : DEATASVDSQTDAVIQ^{*} : 196

FIGURE 50



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Figure 51

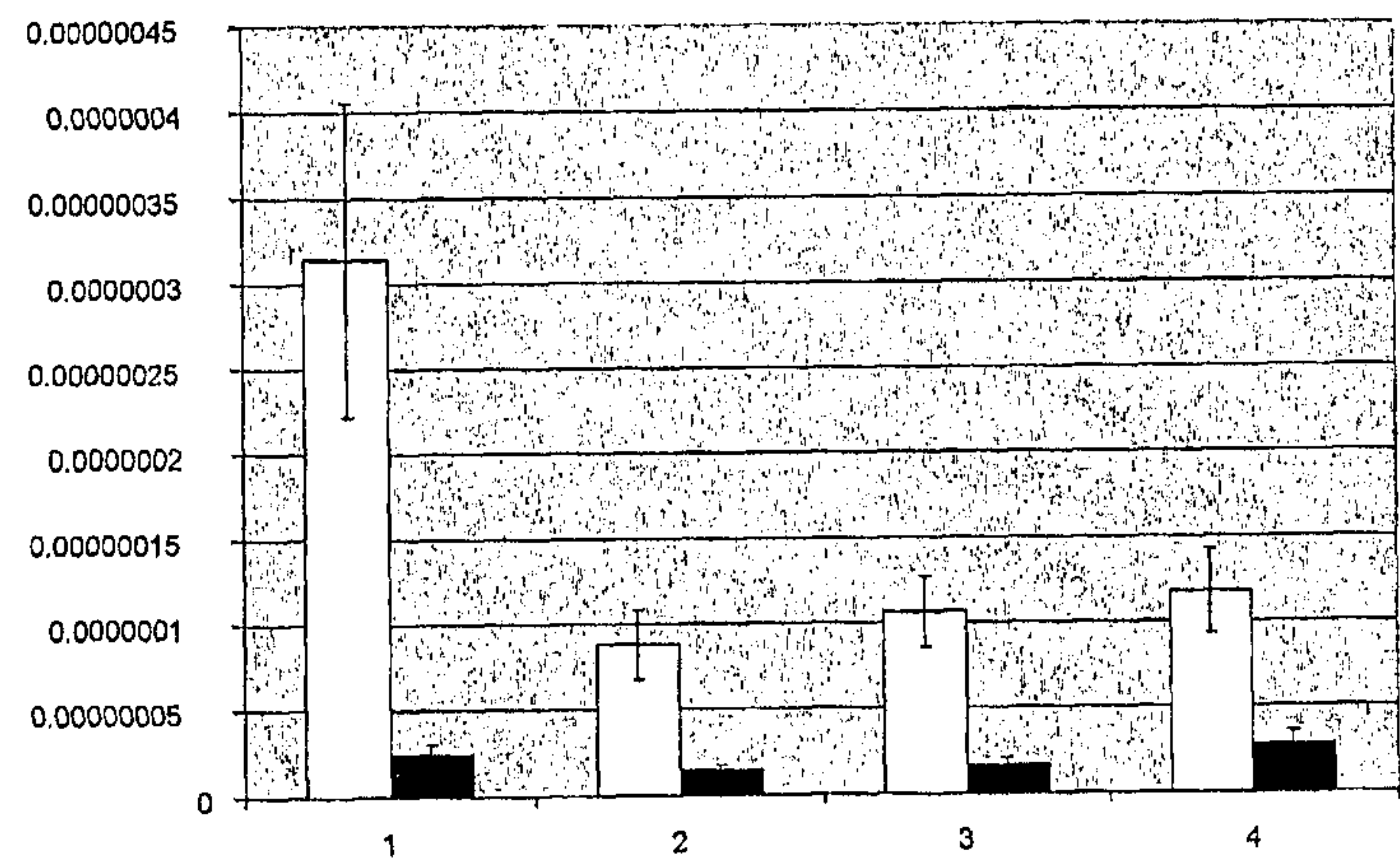
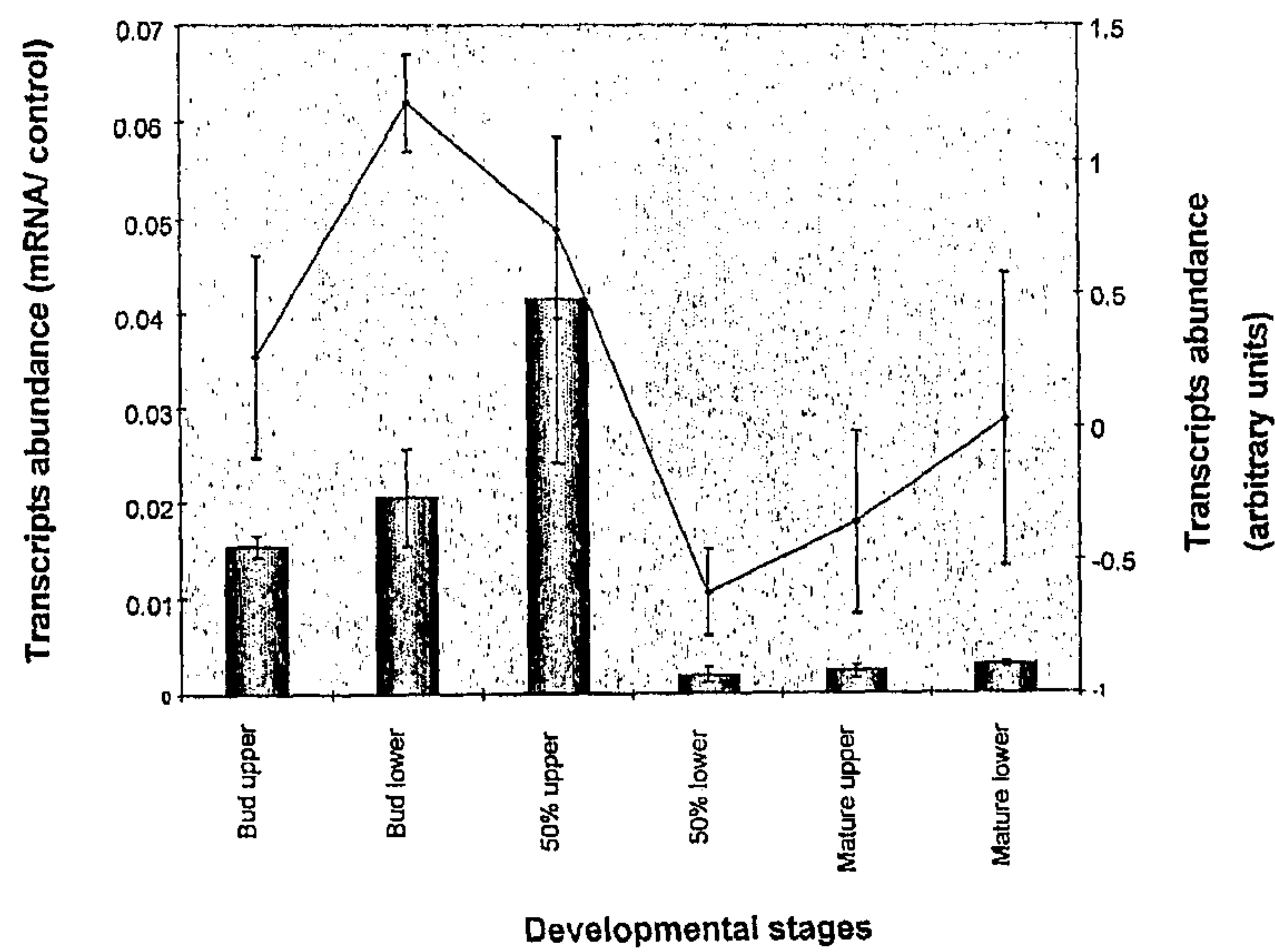
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Figure 52



Figure 53



Developmental stages



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FIGURE 54

TrMYB24a : VKRGPWSPDEDAKLKNYLAIHGTVGNWIALPKKAGLKRCGKSCRLRWLNLYL: 62
 PhMYB1_Z13 : LKKGPTWPEEDOKLLAYIEEHG-EGSWRALPAKAGLORCGKSCRLRWLNLYL: 61
 AmMIXTA_CA : VKKGPWTYDEDOKLLAYIEEHG-EGSWRSLPKKAGLORCGKSCRLRWLNLYL: 61
 AtGL1_P279 : VKKGLWTVEEDNILMDYVKNHG-TGQWNRIVRKGLKRCGKSCRLRWLNLYL: 63
 AtWER_CAC0 : VKKGLWTVEEDKILMDYVKAHG-KGHWNRIAKKGLKRCGKSCRLRWLNLYL: 65
 AtTT2_Q9FJ : LNRGAWTDHEDKILRDYITTHG-EGKWSTLPNQAAGLKRCGKSCRLRWLNLYL: 63
 VvMYBPA1_A : LHRGSWTAREDELLTKYIQAHG-EGHWRSLPKKAGLORCGKSCRLRWLNLYL: 61
 AtMYB111_A : LKRGRTWAEDEEILTKYIQAHG-EGSWRSLPKKAGLORCGKSCRLRWLNLYL: 61
 ZmP_P27898 : LKRGRTWAEEDQLLANYIAAHG-EGSWRSLPKKAGLORCGKSCRLRWLNLYL: 61
 ZmC1_AAA33 : VKRGAWTSKEDDALAAYVKAHG-EGKWREVPQKAGLORCGKSCRLRWLNLYL: 61
 VvMYB5A_AA : LKRGPTWPEEDELANYVKEG-EGRWRTLPKRAGLORCGKSCRLRWLNLYL: 69
 VvMYB5B_Q5 : LKRGPTWPEEDEVLANVYKKEG-EGRWRTLPKRAGLORCGKSCRLRWLNLYL: 74
 PH4_AAY513 : LKRGPTWPEEDELNTYINKEG-EGRWRTLPKRAGLORCGKSCRLRWLNLYL: 72
 AtMYB5_U26 : MKRGPWTVEEDEILVSFKKEG-EGRWRTLPKRAGLORCGKSCRLRWLNLYL: 72
 OsMYB4_D88 : LKRGPTWPEEDEVLAFFVAREG-CDRWRTLPKRAGLORCGKSCRLRWLNLYL: 69
 VvMYBA1_BA : VRKGAWTQEEDEVLLRKGIKMYG-EGKWHTVPKRAGLORCGKSCRLRWLNLYL: 55
 VvMYBA2_BA : VRKGAWTQEEDEVLLRKGIKMYG-EGKWHTVPKRAGLORCGKSCRLRWLNLYL: 55
 PhAN2_AAF6 : VRKGAWTQEEDEVLLRKGIKMYG-EGKWHTVPKRAGLORCGKSCRLRWLNLYL: 60
 LeANT1_AAQ : VRKGAWTQEEDEVLLRKGIKMYG-EGKWHTVPKRAGLORCGKSCRLRWLNLYL: 60
 AtPAP1_AAG : LKRGAWTQEEDEVLLRKGIKMYG-EGKWHTVPKRAGLORCGKSCRLRWLNLYL: 57
 AtPAP2_AAG : LKRGAWTQEEDEVLLRKGIKMYG-EGKWHTVPKRAGLORCGKSCRLRWLNLYL: 57
 PmMBF1_AAA : LKRGAWTQEEDEVLLRKGIKMYG-EGKWHTVPKRAGLORCGKSCRLRWLNLYL: 61
 644GP53P2E126L615624HG3EG4WR36P44AG64RCGKSCR6RW6NLYL

TrMYB24a : RPDIKRGSTTEDEDTIITLVAOMGSRWSAIASKLPGRTDNIVKNYWNTKLSKK: 116
 PhMYB1_Z13 : RPDIKRGSTTEDEDTIITLVAOMGSRWSAIASKLPGRTDNIVKNYWNTKLSKK: 115
 AmMIXTA_CA : RPDIKRGSTTEDEDTIITLVAOMGSRWSAIASKLPGRTDNIVKNYWNTKLSKK: 115
 AtGL1_P279 : SPNVKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 117
 AtWER_CAC0 : SPNVKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 119
 AtTT2_Q9FJ : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 117
 VvMYBPA1_A : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 115
 AtMYB111_A : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 115
 ZmP_P27898 : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 115
 ZmC1_AAA33 : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 115
 VvMYB5A_AA : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 123
 VvMYB5B_Q5 : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 128
 PH4_AAY513 : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 126
 AtMYB5_U26 : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 126
 OsMYB4_D88 : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 123
 VvMYBA1_BA : KPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 109
 VvMYBA2_BA : KPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 109
 PhAN2_AAF6 : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 114
 LeANT1_AAQ : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 114
 AtPAP1_AAG : KPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 111
 AtPAP2_AAG : KPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 111
 PmMBF1_AAA : RPDIKRGNTTEDEDTIIRLHKLGNRWSLIAGRLPGRTDNIVKNYWNTKLSKK: 115
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