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POSTDOCTORAL STUDIES

Karol Geraldina Rivera

AUTEUR DE LA THÈSE / AUTHOR OF THESIS

M.Sc. (Biology)

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TITRE DE LA THÈSE / TITLE OF THESIS

K. Seifert

DIRECTEUR (DIRECTRICE) DE LA THÈSE / THESIS SUPERVISOR

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M. Smith

Gary W. Slater

Le Doyen de la Faculté des études supérieures et postdoctorales / Dean of the Faculty of Graduate and Postdoctoral Studies

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Karol Geraldina Rivera

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List of Abbreviations and Acronyms

BenA – β -tubulin

BI – bayesian inference

BIONJ – neighbour joining algorithm that takes into account biological data

BLAST – basic local alignment tool

blastx - search protein database using a translated nucleotide query

bp – base pairs

CaM – calmodulin

CI – consistency index

CoxI – *cytochrome c oxidase subunit 1*

CREA – creatine ammonia agar

CYA – Czapek's yeast agar

CZ – Czapek's agar

DNA – deoxyribonucleic acid

E-value – expected value

GTR+G – General time reversible substitution nucleotide model with gamma distribution

GTR+G+I – general time reversible substitution nucleotide model with gamma distribution and proportion of invariable sites.

HI – homoplasy index

ITS – the internal transcribed spacer region of the nuclear ribosomal repeat

L – tree length

MAFFT* – multiple alignment program for amino acid or nucleic acid sequences; online program

MEA – malt extract agar

MEGA* – Molecular Evolutionary Gene Analyses; software

ML – maximum likelihood

MP – maximum parsimony

NJ – neighbour-joining

nt - nucleotide

OA – oatmeal agar

PAUP* - Phylogenetic Analyses Using Parsimony* and other methods; software

PCR – polymerase chain reaction

p-distance – proportion of nucleotide site distance

p-value – partition analyses value

RC – retention consistency index

RI – retention index

SYM+I – symmetrical substitution model with proportional invariable sites and a gamma distribution

tblastx - search translated nucleotide database using a translated nucleotide query

TBR – tree bisection and reconnection algorithm

TEF1- α – *translation elongation factor 1- α*

YES – yeast extract sugar agar

Abstract

Cytochrome c oxidase subunit 1 (*Cox1*) is the barcode for many animal groups, protists, and macroalgae. Previously in fungi, the efficiency of *Cox1* as a genetic marker was only analysed in *Penicillium* subgenus *Penicillium* and *Leohumicola* spp. In this thesis, two species isolated from the intestinal tracts of caterpillars from Costa Rica, and two potential species complexes, *P. sclerotiorum* and *P. oxalicum* belonging to *Penicillium* subgenus *Aspergilloides* and *Furcatum*, were studied using the Genealogical Concordance Concept (GCC) recognition criterion and barcoding methods. Analyses with β -tubulin (*BenA*), the nuclear internal transcriber spacer (ITS) region, *Cox1*, translation elongation factor 1- α (*TEF1- α*), and calmodulin (CaM) revealed that the *Penicillium* species isolated from Costa Rica are undescribed, and that *P. sclerotiorum* is a complex of seven phylogenetic species (including the Costa Rican species) that fit the prevailing morphological concept of *P. sclerotiorum*. The phylogenetic species were compared and newly discovered diagnostic morphological characters were used to create a taxonomic key to the species of the complex. The new species are formally described as *P. guanacastense*, *P. mallochii*, *P. krugii*, *P. cainii*, *P. jacksonii* and *P. ciebiessum*. Analyses of multiple strains of *P. oxalicum* revealed that it is a single phylogenetic species, despite having a world wide distribution, an unusually high degree of morphological variation, and a diversity of ecological roles.

Cox1 proved to be a good barcode for identifying the selected *Penicillium* groups, and provided a species level resolution of 83.3%. ITS provided the same resolving ability. *BenA* (91.7%), *TEF1- α* (100%) and CaM (100%) provided a higher species level

resolution than *Cox1*, but *BenA*, *TEF1- α* , and CaM were difficult to amplify or sequence for some *Penicillium* groups. A secondary barcode marker is suggested in addition to *Cox1* for *Penicillium*.

Résumé

Le cytochrome oxydase c sous-unité 1 (*Cox1*) est le code-barre d'ADN le plus utilisé pour de nombreux groupes d'animaux, de protistes et des macroalgues. Chez les champignons, l'efficacité du marqueur *Cox1* n'a été avant tout investiguée que sur les espèces de *Penicillium* sous-genre *Penicillium* et de *Leohumicola*. Dans cette thèse, deux espèces isolées du tractus intestinal de chenilles provenant du Costa Rica, ainsi que deux complexes d'espèces potentiels, *P. sclerotiorum* et *P. oxalicum* appartenant au genre *Penicillium* sous-genre *Aspergilloides* et *Furcatum*, ont été étudiées en utilisant le critère de reconnaissance du Concept de Concordance Généalogique (CCG) et les méthodes de code-barres. Analyses avec la β -tubuline (*BenA*), entretoise transcrite interne (ITS) region, *Cox1*, facteur d'élongation de traduction 1- α (*TEF1- α*), et calmoduline (CaM) ont révélé que les espèces de *Penicillium* provenant du Costa Rica n'ont pas encore été décrites, et que *P. sclerotiorum* constitue un complexe de sept espèces phylogénétiques (comprenant les espèces du Costa Rica) qui correspond au concept morphologique prévalant de *P. sclerotiorum*. Les espèces phylogénétiques ont été comparées et des caractéristiques morphologiques utilisées pour le diagnostique et récemment découvertes ont été utilisés afin d'élaborer une clé de classification des espèces de ce complexe. Les nouvelles espèces sont formellement décrites comme *P. guanacastense*, *P. mallochii*, *P. krugii*, *P. cainii*, *P. jacksonii* et *P. ciebiessum*. L'analyse de plusieurs souches de *P. oxalicum* a révélé qu'il s'agit d'une seule espèce phylogénétique, en dépit de sa large distribution à travers le monde, de son degré élevé inhabituel de variation morphologique et de la diversité de ses rôles écologiques.

Cox1 s'est avéré être un bon code-barre pour l'identification des groupes de *Penicillium* sélectionnés et a fourni une résolution au niveau de l'espèces de 83.3%. Une résolution analogue a été obtenue avec ITS. *BenA* (91.7%), *TEF1- α* (100%) et CaM (100%) ont affiché une résolution plus élevée que *Cox1*. Cependant, l'amplification et le séquençage de *BenA*, *TEF1- α* et CaM ont été difficiles pour certains groupes de *Penicillium*. Un second marqueur de code-barre a été suggéré en plus de *Cox1* pour le *Penicillium*.

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Chapter 1: General Introduction

1.1 Fungi

Fungi are a major clade in the Tree of Life (Maddison *et al.* 2006). Their circumscription includes eukaryotic, heterotrophic, absorptive organisms that develop diffuse, branched, tubular bodies and reproduce by means of spores (Kendrick 2000). At one point, fungi and fungi-like organisms were thought to belong to the kingdom *Plantae*. The lack of photosynthesis, nutrition mode, and microscopic features placed fungi in a separate kingdom (Whittaker 1969). Molecular phylogenetic analyses revealed that fungi are more closely related to animals than plants (Wainright *et al.* 1993; Baldauf and Palmer 1993; Berbee and Taylor 1993; Lang *et al.* 2002; Lutzoni *et al.* 2004; James *et al.* 2006).

Taxonomy is divided into eight main ranks: domain, kingdom, phylum (animals) or divisions (plants and fungi), class, order, family, genus, and species. The major divisions in fungi are: the *Ascomycota*, which produce meiospores in sac like structures called asci (singular: ascus); the *Basidiomycota*, which produce meiospores externally by the formation of specialized club-shaped cells called basidia (singular: basidium); the *Zygomycota*, where the name is derived from the fusion of compatible gametangia to form a zygosporangium (plural: zygosporangia), which develops a thick wall for protection against unfavourable conditions; the *Glomeromycota*, asexual fungi that are characterized by the formation of arbuscular mycorrhizas; and the *Chytridiomycota*, the most primitive group of fungi, which are characterized by the presence of flagella in meiospores and mitospores. Phylogenetic analyses of DNA sequences excluded several

lineages that were considered fungi, such as the *Myxomycota*, which belong to the kingdom *Protista*, and the *Oomycota* which belong to the kingdom *Straminipila*. Phylogenetic analyses with DNA sequences have included *Microsporidia*, which was originally thought to be a protist, but is now believed to have diverged from the *Zygomycota* (Keeling *et al.* 2000; Keeling 2003; Keeling and Fast 2005)

Hawksworth (1993, 2001) estimated that there are 1.5 M species of fungi worldwide. The estimate was based on a 1:6 ratio of plants to fungi in the British Isles and an estimate of 250,000 plants worldwide. The described species represents 7% (100,000) of the estimated number of species (Crous *et al.* 2006). The undescribed species are believed to be in poorly explored habitats and niches that include plant and animal hosts, soil, wood, and rainforest litter (Hyde 2001). Some of the undescribed species may be morphologically cryptic, hiding in known morphologically defined species.

1.2 Anamorphic Fungi

Fungi can reproduce through asexual and sexual means via spores, which are produced on specialized structure or in fruiting bodies (Figure 1.1). Asexual reproduction is achieved by the production of vegetative spores (mitospores or conidia) or through mycelial fragmentation. In the case of anamorphic (mitosporic) fungi, asexual reproduction is the only known means of propagation (Figure 1.1). Sexual reproduction has not been observed in these fungi. Sexual reproduction through meiosis is achieved by cell fusion of vegetative hyphae of compatible individuals. Fungi that sexually reproduce with other compatible individuals (heterothallic) or themselves (homothallic)

and are referred to as teleomorphic (meiosporic) fungi. The whole fungus (holomorph) includes asexual and sexual states if present (Figure 1.1B).

The absence of a meiosporic state for mitotic fungi poses a problem in fungal nomenclature and taxonomy. Fungal names and classification are based on the morphology of the fruiting structures produced during sexual reproduction. Article 59 in Chapter VI of the International Code of Botanical Nomenclature, which governs the naming of fungi, allows for taxon names to be given to anamorphic fungi (Sigler and Hawksworth 1987). For example, *Aspergillus niger* Tiegh. has no known sexual cycle, thus the name *Aspergillus niger* is considered a valid taxon name. Its close relative, *Emericella nidulans* (Eidam) Vuill., which has a sexual state, also has an *Aspergillus* asexual state. Hence both names, *E. nidulans* and *A. nidulans*, are valid, but when referring to the holomorph, the teleomorph taxon name in *Emericella* Berk., is used. Hence, the fungus is referred to as *E. nidulans*.

1.3 The Genus *Penicillium*

Penicillium is classified as an anamorphic genus in the division *Ascomycota* (order *Eurotiales*, class *Eurotiomycetes*, family *Trichocomaceae*). The genus name is derived from the Latin word *penicillus*, which means little brush. Link (1809) described the genus and three species, *P. glaucum*, *P. candidum* and *P. expansum*, which produced brush like conidiophore (asexual fruiting structure) in his “Observationes in Ordines plantarum naturales”. *Penicillium expansum*, the common apple rot fungus, was selected to represent the type of the genus (Thom 1910; Raper and Thom 1949; Pitt 1979; Samson and Pitt 1985).

The International Code of Botanical Nomenclature does not accept names published before 1 January 1821, and the genus name '*Penicillium* Link' cannot stand alone. The name *Penicillium* was used by Gray and Fries after 1 January 1821, who attributed the name to Link. Starting in 1980, the code gave special status to some of Fries' work, which included *Penicillium*. Thus the correct name for the genus is "*Penicillium* Link:Fries".

Penicillium colonies on media plates are fast growing, achieving typically 20–40 mm in colony diam., after incubating for 7 d at 25°C in the dark. *Penicillium* colonies are in shades of green, and consist of a dense felt of conidiophores. Colony texture can be velvety, when conidiophores arise from the substrate; lanose, when conidiophores arise from aerial hyphae in the colony; funiculose, when conidiophores arise from prostrate, bundled hyphae; or synnematos, with conidiophores that arise from bundled hyphae. Conidiophores are hyaline, smooth to rough-walled, and have four branching patterns (Figure 1.2). To determine the branching pattern, the number of branch points starting from the tip of the phialide along the main axis of the conidiophores, are counted (Figure 1.3). The simplest type of conidiophore, monoverticillate, has one whorl of phialides (Figure 1.2). Phialides are conidiogenous cells that may be flask-shaped or lanceolate, with a neck that can be short or long. Conidia are one-celled and hyaline, and arise in long, dry chains from phialides. The more complex conidiophore branching patterns are biverticillate (one-staged), terverticillate (two-staged) and quaverticillate (three-staged) (Figure 1.2). In these conidiophore types, the cell connecting the stipe to the phialide is referred to as the metulae (Figure 1.2). The metulae are absent in monoverticillate conidiophores.

Penicillium belongs to an anamorphic group of fungi called Hyphomycetes, which are sometimes referred to as moulds. Hyphomycete identification is primarily based on microscopic morphology: conidial morphology, especially septation, shape, size, colour and cell wall texture, conidial arrangement as they are borne from conidiogenous cells (phialides), and the presence of sporodochia or synnemata, which are asexual fruiting structures. Several hyphomycetes resemble *Penicillium*. (1) *Geosmithia* Pitt, which differs from *Penicillium* by the formation of conidia borne as cylinders from rough-walled phialides that lack collula (necks) in the phialides (Pitt, 1979b). (2) *Merimbla* Pitt and Hocking, which differs from *Penicillium* by the absence of shades of green in the colonies (Pitt and Hocking 1979). (3) *Thysanophora* Kendrick, which is found on the needles of conifers and produces stout, dark brown conidiophores (Kendrick 1961). (4) *Paecilomyces* Bainer, which differs from *Penicillium* by having phialides with long necks. (5) *Trichoderma* Persoon, which differs from *Penicillium* in that conidia are borne in slimy heads. (6) *Aspergillus*, which differs from *Penicillium*, because its conidiophores have an apical swelling.

Penicillin, which is produced by *P. chrysogenum* Thom, was first discovered by Alexander Fleming in 1929 and found to inhibit the growth of gram negative bacteria (Fleming 1929). Little attention was paid to penicillin until Howard Florey in the late 1930's realized its potential as an antibiotic. Florey, along with Ernst Chain, purified and concentrated the compound. Penicillin saved the lives of many soldiers during World War II who were dying from infected wounds, earning Fleming, Florey and Chain the Nobel Prize in Medicine in 1949 (Lax 2005).

The need for large scale production of penicillin for the war effort led Florey and his colleague Norman Heatley to the USDA Northern Regional Research Laboratory (NRRL) in Peoria, Illinois to seek the help of microbiologist Kenneth Raper. Raper and his associates initiated a broad program of research for *Penicillium* to (1) develop a more productive culture medium, (2) to find moulds capable of producing increased yields of penicillin, and (3) to develop methods for the production of penicillin submerged culture. This led to the publication of the monograph *The Manual of the Penicillia* by Raper and Thom (1949). This monograph followed the conceptual framework of *The Penicillia* by Thom (1930), but included species that were described since 1930.

Thom (1930) and Raper and Thom (1949) divided the genus *Penicillium* into four groups: the Monoverticillata, which consisted of monoverticillate conidiophores; the Asymmetrica, which consisted of irregular, one-sided or asymmetrical conidiophores with one or more branch points; the Biverticillata-Symmetrica, which consisted of symmetrically biverticillate conidiophores; and the Polyverticillata, which consisted of symmetrical conidiophores with many branching points. Ramirez's (1982) monograph, *The Manual and Atlas to the Penicillia*, closely followed Thom (1930) and Raper and Thom (1949), adding new species that were described since Raper and Thom (1949).

Thom (1930), Raper and Thom (1949), and Ramirez (1982) did not use the taxonomic rank of subgenus to divide *Penicillium*, which was used in earlier work by Dierckx (1901) and Biourge (1923). Pitt (1979a) used the taxonomic rankings of subgenera, section and series, and broadened species concepts. *Penicillium* was divided into four subgenera based on conidiophore morphology and branching pattern, subgenus *Aspergilloides* Dierckx, subgenus *Biverticillium* Dierckx, subg. *Furcatum* Pitt and

subgenus *Penicillium*. Monoverticillate conidiophores are characteristics of *Penicillium* species belonging to subgenus *Aspergilloides*. Some monoverticillate conidiophores are vesiculate conidiophores, which have a small swollen head at the apex of the stipe, where the phialides arise. Biverticillate conidiophores are characteristic of subgenera *Biverticillium* and *Furcatum*. The two groups can be differentiated by colony diameter on 25% glycerol agar (G25N; Pitt 1979a) medium, phialide shape, the number of metulae per stipe, and phialide to metula length (Pitt 2000). Subgenus *Biverticillium* and *Furcatum* section *Furcatum* Pitt are characterized by 'regular' and 'well-defined' conidiophores, with a whorl of metulae. Furthermore, conidiophores tend to be more symmetrical and phialides acerose in subgenus *Biverticillium* than *Furcatum*. Subgenus *Furcatum* section *Diviricatum* Pitt also has biverticillate conidiophores, but, they are irregular and ill-defined (Figure 1.4). *Penicillium* subgenus *Penicillium* is characterized by terverticillate and quaterverticillate conidiophores that are asymmetrical, with flask-shaped phialides.

Penicillium is associated with two meiosporic genera, *Eupenicillium* Ludwig and *Talaromyces* Benjamin (Figure 1.5). *Eupenicillium* species are characterized by the production of cleistothecial ascocarps, which are sclerotium-like (Figure 1.5). The ascocarp initials consist of modified cells in the crotch of a tree-like network of hyphae. The ascocarp matures from the center outwards. The asci are borne singly in the centre of the ascocarp on short branches of the ascogenous hyphae. Occasionally asci appear end to end, but this is an exception (Dodge 1933). The genus is further characterized by producing ascospores with or without a well-defined furrow (Figure 1.5).

Talaromyces species are characterized by the production of cleistothecial ascocarps, which are formed by interlacing hyphae that can be closely knit or loose, but not fused. The ascocarp expands by intercalary growth of the hyphae that form the wall, and is of indeterminate growth. In addition, there are multiple points within the ascocarp at which the ascogenous hyphae and asci are initiated. The genus is further characterized by the end to end arrangements of the asci to form chains, and spiny ascospores.

In addition to being morphologically different, *Eupenicillium* and *Talaromyces* species have different cell wall composition and structure (Table 1.1; Gomez-Miranda *et al.* 1988; Leal *et al.* 1991; Leal *et al.* 1997) and produce of different ubiquinones (Table 1.1; Kirashi *et al.* 1991).

1.4 Notes on *Penicillium* Biology

1.4.1 Commercial Uses

Soil fungi, such as *Penicillium*, are particularly promising in pharmaceutical potential because their biocenotic competitiveness is often based on the production of antibiotics and other inhibitory substances. Penicillin is not the only antibiotic discovered from a *Penicillium* species. Griseofulvin, an antifungal drug (Hiddlest 1970) and a potential chemotherapeutic agent (Panda *et al.* 2005; Singh *et al.* 2008), was discovered in *P. griseofulvum* Dierckx. Six additional tumor cell inhibiting compounds have been discovered from *P. pinophilum* Thom (3-O-methylfunicone; De Stefano *et al.* 1999), *P. sizovae* Baghd (oxaxine derivative; Ciavatta *et al.* 2006), *P. canescens* Sopp (Sch 642305 and cuvulic acid; Nicoletti *et al.* 2008) and *P. glabrum* (Wehmer) Westling (asterric acid and sulochrin; Nicoletti *et al.* 2008).

Penicillium species have also shown other commercial value. Some are used for the fermentation of foods, such as the production of Camembert, Roquefort, and Gorgonzola cheeses by *P. camemberti* Sopp and *P. roquefortii* Thom (Babel 1957). Other species are valued for the uptake of heavy metals (*P. ochrochloron* Biourge and *P. arenicola* Chalab), their ability to inoculate soil as biofertilizers (*P. bilaiae* Chalab and *P. oxalicum* Currie & Thom), transformation of organic compounds (*P. sclerotiorum*), and the production of organic compounds (*P. simplicissimum* (Oudem.) Thom) and enzymes (*P. janthinellum* Biourge and *P. griseoroseum* Dierckx) (Pitt 1979a).

1.4.2 Habitats and Substrates

Penicillium species cause food spoilage, particularly species belonging to *Penicillium* subgenus *Penicillium* (Samson *et al.* 2004). Species belonging to this subgenus can be found in cereals, seeds, wheat, flour, rice, barley and maize (Pitt 1979a). Consuming foods contaminated with *Penicillium* might be hazardous because some species produce mycotoxins. The ability of these *Penicillium* species to grow on seeds depends on their ability to grow in low humidity and to colonize rapidly by aerial dispersion while the seeds are sufficiently moist (Pitt 1979a).

Penicillium species also affect the bulbs and fruits of plants, like *P. expansum* (*Malus pumila* and *Pyrus communis*; apples and pears; Pitt 1979a), *P. digitatum* (Pers.) Sacc. (*Citrus sinensis* and *C. aurantium*; oranges; Pitt 1979a), *P. hirsutum* Dierckx (bulbous iris; Pitt 1979a) and *P. allii* Vincent & Pitt (*Allium sativum*; garlic; Valdez *et al.* 2006). They are also plant pathogens, such as *P. oxalicum*, which causes cucumber stem rot (van Stekelenburg 1998; Jarvis *et al.* 1990; O'Neill *et al.* 1991; Jarvis and Ferguson 1992; Menzies *et al.* 1995) and blue ear rot of corn (Caldwell *et al.* 1981). *Penicillium*

species are also animal pathogens. *Penicillium marneffe* Segretain, which causes death in the Vietnamese bamboo rats (Pitt 1979a), and is a pathogen of immune suppressed patients. Also *P. corylophilum* Dierckx, *P. fellutanum* Biourge, *P. implicatum* Biourge, *P. janthinellum*, *P. viridicatum* Westling and *P. waksmanii* Zalessky may be potential pathogens of mosquitos (*Aedes aegypti*, *Aedes fluviatilis*, *Anopheles aquasalis* and *Culex quinquefasciatus*) (da Costa *et al.* 1999).

As it is for many fungi, soil is the primary habitat for *Penicillium* species. Some species like *P. lividum* Westling and *P. montanense* Chr. & Backus have been isolated only from woodland soil, while species like *P. janthanellum* have rarely been isolated from substances other than soil (Pitt 1979a). The process governing these dependencies is unknown (Pitt 1979a). Species belonging to *Talaromyces* and *Eupenicillium* are primarily isolated from soil. This is most likely due to the hydrophilic nature of the ascospores, making dispersal through soil and water preferable to air (Pitt 1979a). On the other hand, *Penicillium* conidial size is smaller in comparison to ascospores, making air dispersal effective (Pitt 1979a).

Penicillium species are also isolated from the air and dust of indoor environments, which includes homes, public buildings, and other human environments. Exposures to *Penicillium* and other moulds are a major health concern. Most of these biocontaminants are transported from outdoor sources, and can grow and amplify indoors. Building material or accumulated soil provides nutrients for growth. *Penicillium* growth can still occur indoors even if air relative humidity is low as long as there is sufficient moisture available on a given surface (Pasanen *et al.* 1991). *Penicillium* species also grow on

ceiling tiles as long as the relative humidity of 85% and the moisture content is greater than 2.2% (Chang *et al.* 1995).

1.5 Molecular Advances in *Penicillium* Taxonomy

For 200 years fungal taxonomists have relied on morphological analyses to identify species. Advances in molecular biology in the 1980s led to the production of gene sequences for identification and the construction of phylogenies for species delimitation. Gene sequences are of great value for *Penicillium* identification because there are 1,088 described species (www.indexfungorum.com); however, there are only 223 accepted species (Pitt and Samson 2000). The molecular identification of fungi began when White *et al.* (1990) designed PCR primers that work for most groups of fungi for the ribosomal genes: the large subunit (LSU or 28S); the small subunit (SSU or 18S); and the internal transcribed spacer (ITS) region, which comprises two variable spacers ITS1 and ITS2 which bracket the conserved 5.8S region. The SSU and LSU regions are highly conserved, and are used for higher taxonomic resolution. The variability of the ITS1 and ITS2 spacers, have made the ITS region the default marker of choice for species level taxonomic studies in fungi (Hibbett 1992), with the exception of yeasts, where the LSU is the standard for identification (Linton *et al.* 2006).

Since White *et al.* (1990), many other genes have been sequenced. The international, multi-laboratory consortium, Assembling the Fungal Tree of Life (AFToL; Blackwell *et al.* 2006), sequenced the translation elongation factor 1- α (*TEF1- α*), calmodulin (CaM), β -tubulin (*BenA*), ribosomal polymerase B1 and B2 (*RPB1*, *RPB2*), the small mitochondrial ribosomal operon (mtSSU), and the ATP synthase 6 (ATP6) to develop a phylogeny for the fungi. More than 1000 fungal species were sampled,

representing all five fungal divisions (Lutzoni *et al.* 2004). AFToL sequenced ITS to provide a reference framework for an identification database. All AFToL results were published in the December 2007 issue of *Mycologia*. Several AFToL2 projects have started that focus on fungal classes that require denser sampling and the sequencing of additional genes to answer questions of basal fungal phylogeny.

1.5.1 *Penicillium* Phylogenies

Phylogenetic analyses with the nuclear ribosomal genes revealed that *Eupenicillium* and *Talaromyces* are phylogenetically distinct (Berbee *et al.* 1995). Phylogenetic analyses with the mtSSU and ITS regions revealed that *Talaromyces* and *Penicillium* subgenus *Biverticillium* species form one monophyletic group (LoBuglio *et al.* 1993). *Eupenicillium* species and *Penicillium* species from subgenera *Penicillium*, *Furcatum* and *Aspergilloides* form another group (LoBuglio *et al.* 1993, 1994; LoBuglio and Taylor 1993). Analyses with the nuclear ITS and 28S regions revealed that subgenus *Penicillium* forms one monophyletic group, while subgenera *Aspergilloides* and *Furcatum* are paraphyletic (Peterson 2000). The monophyly of subgenus *Penicillium* is also supported by the ITS region (Seifert and Levesque 2004), the *BenA* gene (Samson *et al.* 2004) and CaM (Wang and Zhuang 2007). Thus the morphological groupings of subgenera *Penicillium* and *Biverticillium* are well supported by DNA sequence phylogenetic analyses, but are not supported for subgenera *Aspergilloides* and *Furcatum*.

Peterson (2000) constructed a phylogeny of selected *Penicillium* ex-type strains, which excluded *Talaromyces* and *Penicillium* subgenus *Biverticillium* species based on ITS and 28S sequence data using maximum parsimony. The study concluded that there are six clades of ‘*Eupenicillium* species’, each with strong bootstrap support ($\geq 80\%$).

Wang and Zhuang (2007) constructed a phylogeny using CaM of all *Penicillium* groups, including *Talaromyces* and *Biverticillium*, but did not include ex-type strains. Tree topologies using maximum parsimony and neighbour joining methods were similar, and revealed the same six clades described by Peterson (2000). Wang and Zhuang (2007) observed two clades of *Talaromyces* species.

1.5.2 DNA Barcoding

The concept of DNA barcoding as a tool for species identification and scientific research has been successfully applied to animals (Hebert *et al.* 2004; Ward *et al.* 2005; Hajibabaei *et al.* 2004; Barrett and Hebert 2004; Smith *et al.* 2008; Huange *et al.* 2007), oomycetes (Martin and Tooley 2003), and algae (Saunders 2008) (Table 2). The mitochondrial gene, cytochrome c oxidase subunit 1 (*Cox1*), provided distinct sequences for many studied taxa (Table 1.2).

The *Cox1* gene in animals is approximately 1,400–1,500 bp, but a region near the 5' end of the gene is sufficient for species resolution (Hebert *et al.* 2003). The region was chosen because of lack of introns, limited exposure to recombinations, and haploid mode of inheritance (Saccone *et al.* 1999; Hebert *et al.* 2003). *Cox1* is an ideal barcode because there are many copies of the mitochondrial genome in a cell, and it is one of the two protein coding genes found in all eukaryotes, the other being cytochrome *b*. *Cox1* is the larger of the two, and has the slowest rate of change in amino acid sequences (Lynch and Jarrell 1993), making the gene conserved but variable enough to provide species level resolution.

The Consortium for the Barcode of Life (CBOL) is an international initiative of natural history museums, herbaria, government agencies and research organizations.

CBOL promotes the development of DNA barcoding by helping to launch barcode projects in a wide variety of taxonomic groups. A DNA barcode can be defined as a short gene sequence (500–600 bp or less) from a standardized region from the genome for species identification. CBOL recognizes that *Cox1* might not work well for all taxonomic groups. This is true for land plants, where families differ by only a few base pairs (Cowen *et al.* 2006). Megakaryocyte-associated tyrosine kinase (*matK*) has been proposed as a potential barcode for plants (Newmasters *et al.* 2008), followed by secondary genes specific to taxonomic groups. Thus CBOL has set specific standards for genes to be considered as barcodes. The gene must have low variation within a species, with a considerable amount of interspecific variation to allow for species discrimination. The gene must also be short enough to mitigate amplification and sequencing problems. Furthermore, for a sequence to be considered a barcode by the Barcode of Life Database (BOLD; www.barcodeoflife.org), the specimen sample should include an authoritative identification, a voucher specimen (e.g. photograph, museum specimen, DNA), and collection information. A colourful representation of DNA barcodes based on four colours representing the four different base pairs can be obtained from the online program FINGERPRINT (Lou and Golding 2007) hosted by McMaster University, funded by the Barcode of Life Systems Database (BOLD) .

The ‘All Fungi Barcode of Life Planning Workshop’ held at the Smithsonian’s Conservation and Research Centre at Front Royal, Virginia, USA in 2007, endorsed ITS as the fungal barcode. ITS primers work well for most fungal groups, making the region easy to sequence and amplify, making it an ideal barcode. Also there are a large number

of reference sequences in GenBank. The use of ITS as the fungal barcode has yet to be proposed to CBOL, however, BOLD is accepting ITS sequences in their database.

The only fungal studies to date to investigate potential of *Cox1* as a fungal marker were Seifert *et al.* (2007) for *Penicillium* subgenus *Penicillium* and Nguyen and Seifert (2008) for *Leohumicola*. *BenA*, *Cox1*, and ITS were tested and provided 80%, 66%, and 25% species specific barcodes for subgenus *Penicillium*, and resolved all *Leohumicola* spp. *Cox1* has been rejected as a barcode for fungi due to the presence of mobile introns in the barcoding region in *Cox1* (Hamari *et al.* 2002) and the presence of multiple copies in some fungal groups (Gilmore *et al.* 2009). Introns were observed in only 1% of the *Penicillium* species tested by Seifert *et al.* (2007) and in three out of the 53 *Leohumicola* strains examined by Nguyen and Seifert (2008). *Cox1* was found to be an adequate fungal marker for these groups.

1.6 What is a ‘fungal species’?

Once all described *Penicillium* species have been barcoded, the identification and recognition of undescribed species will be simple, but what is a species? A species can be defined as the most basic taxonomic rank in biological classification. At least twenty-two species concepts were developed to aid in the recognition of species. The most widely used species concepts in fungi, which are discussed in this thesis, are the Biological Species Concept (BSC), Morphological Species Concept (MSC), Phylogenetic Species Concept (PSC) and the Genealogical Concordance Concept (GCC). Mayden (1997) divided species concepts into theoretical and operational concepts. Theoretical concepts represent events such as evolution and natural selection that are not easily seen in the laboratory or in nature (Mayden 1997). Operational concepts are those

representing data and observations, such as round versus square, which can be used to delimit species (Mayden 1997). The BSC, MSC, PSC and GCC are operational concepts that use ‘recognition’ criteria such as mating, morphological characters and gene trees that can be used to delimit species (Taylor *et al.* 2000).

1.6.1 Biological Species Concept

According to the BSC, a species is a group of interbreeding natural populations that is reproductively isolated from other such groups (Mayr and Ashlock 1991); speciation results from reproductive isolation (Mayr 1963). The BSC is applied when there is mating between individuals, and then mating individuals are assigned to species (Taylor *et al.* 2000). The BSC is not applicable to anamorphic and homothallic fungi like *Penicillium*. Another drawback of the BSC is that genetically isolated groups in nature that retain the ancestral trait of interbreeding are considered a single species (Taylor *et al.* 2000). Matings in the laboratory do not necessarily reflect natural matings because of physical, behavioural, or geographical constraints. Natural matings may also not be observed in the laboratory because environmental cues may be missing. Natural matings may also be difficult to detect because the fruiting bodies are microscopic and may be rare. Thus negative matings may not provide a conclusive answer on conspecificity.

1.6.2 Morphological Species Concept

The MSC has been the dominant concept in taxonomy for 200 years. Species are defined on the basis of their morphological distinctiveness (Mayr 1997), and are referred to as morphological species. The majority of the described fungal species have been distinguished based on morphological characters (Hawksworth *et al.* 1996), or other phenotypic characters such as growth in different temperatures (Pitt 1973; Pitt 1979a) and

the production of secondary metabolites (Frisvad and Filtenborg 1989; Frisvad *et al.* 1990; Frisvad *et al.* 2008). A problem with the MSC involves sibling or cryptic species, which are difficult to distinguish using morphological analyses.

Thom (1930) introduced the standardization of media for the description and identification of *Penicillium* species using Czapek's Agar (CZ) and Malt Yeast Extract Agar (MEA) for colony and microscopic morphological analyses. Pitt (1973) introduced the growth media Czapek's Yeast Extract Agar (CYA), a modification of Thom's (1930) original CZ and 25% glycerol agar (G25N) for colony analyses. Pitt (1979a) also grew *Penicillium* isolates on CYA and G25N at different temperatures (5°C, 15°C, 25°C, and 37°C) for 7 d in the dark for identification. Additional media have been introduced for *Penicillium* diagnosis, such as Yeast Extract Sucrose (YES) medium (Filtenborg *et al.* 1990) and Creatine Ammonia (CREA) medium (Frisvad 1993). *Penicillium* strains are grown in the dark for 7 days at 25°C on MEA and CYA for microscopic and colony morphology for species descriptions. Additional media are used to differentiate among morphologically similar species.

Secondary metabolite profiling has also been used in the description and classification of some *Penicillium* species. This is performed by growing isolates on CYA or YES for extraction for High Performance Liquid Chromatography (HPLC) and Thin Layer Chromatography (TLC). Secondary metabolite profiles have been used to characterize, classify and identify many members of *Penicillium* subgenus *Penicillium* (Clemmensen *et al.* 2007; Dorge *et al.* 2000; Filtenborg and Frisvad 1990; Frisvad *et al.* 2008; Larsen and Frisvad 1995; Smedsgaard *et al.* 2004, Stolk *et al.* 1990), *Talaromyces* species and *Penicillium* subgenus *Furcatum* (Frisvad *et al.* 1990).

1.6.3 The Phylogenetic Species Concepts

Cracraft (1983) defined the PSC as “a diagnosable cluster of individuals within which there is a parental pattern of ancestry and descent”. The application of this definition includes the need for a synapomorphy, which is a shared derived character present among all members of a group but not present in others (Rosen 1978). This concept can be applied to anamorphs and teleomorphs. Morphological characters can be coded numerically and can be used for phylogenetic analyses, however, difficulties may arise when coding for qualitative characters, eg. conidia globose or subglobose. Sequence data have also been used in phylogenetic analyses for tree construction to delimit species. A few examples in fungi are the *P. aurantiogriseum* Dierckx complex, where *BenA* was used to delimit species (Seifert and Louis-Seize 2000); and *P. roqueforti* and *P. carneum* (Frisvad) Frisvad, where ITS provided sufficient variation to resolve the limit of the species (Boysen *et al.* 1996).

The problem with the PSC is that the limit of a species is subjective (Figure 1.6). For example if a gene is polymorphic, and has alleles A and B, individuals with the allele A are considered one species while individuals with allele B are considered another (Figure 1.6). Without any additional information, such as the ability to interbreed which many fungi cannot be tested for, one would not know if the gene was polymorphic within a species, or fixed for alternate alleles in two species (Taylor *et al.* 2000).

1.6.4 The Genealogical Concordance Concept

Mayden (1997) introduced the idea of multiple gene genealogies to remove the subjectivity in determining species from the PSC. Mayden (1997) called this modification of the PSC the GCC. A requirement of the GCC recognition criteria is that

gene recombination does not occur within the gene (Taylor *et al.* 2000). Tree topology is the same where the different gene trees are concordant. This is due to fixation of formerly polymorphic loci following genetic isolation; the concordant branches represent species (Taylor *et al.* 2000). Recombination among individuals within a species is represented by conflict among the gene tree branches (Figure 1.7). The transition from concordant to incongruent branches determines species boundaries (Figure 1.7; Taylor *et al.* 2000).

The transition from concordance to conflict cannot occur in a truly clonal species. As much as one-fifth of fungi are anamorphic and are thought to be clonal (Taylor *et al.* 2000). Examinations of several anamorphic fungi have found that they are recombining in nature in addition to reproducing clonally (Anderson and Kohn, 1998; Taylor *et al.* 1999a, b, 2000). Even a low level of recombination can lead to conflict among gene genealogies (Taylor *et al.* 2000)

The GCC is widely used in fungi, and has been applied to anamorphs and teleomorphs (Taylor *et al.* 2000). Studies with the teleomorphic fungus *Gibberella fujikuroi* (Sawada) Wollenw (anamorph: *Fusarium*) complex suggests that species recognized by the BSC are also recognized by the GCC (O' Donnell *et al.* 1999). In *Penicillium*, gene genealogies have been used to delimitate new species, such as *P. pimentouense* Peterson (Peterson *et al.* 1999), *P. brocae* Peterson, Pérez, Vega and Infante (Peterson *et al.* 2002), *P. coffeae* Peterson, Vega, Posada and Nagai (Peterson *et al.* 2005), *P. astrolabium* Serra and Peterson and *P. neocrassum* Serra and Peterson (Serra and Peterson 2007). The most commonly used genetic markers are CaM, *BenA*, *TEF-1 α* and ITS.

1.7 Research Objectives and Hypothesis

Thesis Objective

The aim of this thesis was to assess the effectiveness of *Cox1* as a species marker or DNA barcode in comparison to four nuclear genes (ITS, *BenA*, *TEF1- α* and CaM) known to provide species level resolution in *Penicillium* species belonging to subgenera *Aspergilloides* and *Furcatum*. Species boundaries and phylogenetic relationships among species were determined using morphological characters and the Genealogical Concordance Concept (GCC) recognition criterion.

Thesis Hypothesis

1) *Cox1* is an effective species marker for the selected *Penicillium* groups and can be used to identify species recognized by the GCC recognition criteria.

This hypothesis is based on the previous study by Seifert *et al.* (2007), where it was determined that *Cox1* is an effective marker in *Penicillium* subgenus *Penicillium*. Although the selected *Penicillium* groups are relatively distant to subgenus *Penicillium*, similar results are expected.

Chapter 2: *Penicillium mallochii* and *P. guanacastense*, two new species isolated from Costa Rican caterpillars.

Chapter Objective

The objective of this study was to determine if *Penicillium* isolates collected from the intestinal tract of caterpillars from the Área de Conservación Guanacaste, Costa Rica are two undescribed species as determined by preliminary analyses with *BenA*. Twenty-five isolates of *P. mallochii* were isolated from *Rothschildia lebeau* and *Citheronia lobesis*; and two strains of *P. guanacastense* were collected from two unidentified

caterpillars belonging to the family *Noctuidae*. Species were resolved using the GCC recognition criteria using maximum-parsimony (MP), maximum-likelihood (ML), and Bayesian inference (BI) gene trees, and morphological characters. Species descriptions are provided.

Chapter 3: A Taxonomic and Phylogenetic Revision of the *Penicillium sclerotiorum*

Chapter Objective

Genetic variation was observed in *BenA*, ITS, *Cox1*, *TEF1- α* and CaM in 39 strains identified as *P. sclerotiorum*. The GCC recognition criterion was used to resolve species boundaries using MP, ML, and BI gene trees for six phylogenetic species. Morphological characters were also used to resolve species boundaries. Morphological descriptions and a taxonomic key to the group are provided. Phylogenetic relationships were inferred from combined gene trees using MP ML and BI analyses.

Chapter 4: Multiple gene genealogies reveal *Penicillium oxalicum* is a single phylogenetic species.

Chapter Objective

The objective in this chapter was to determine the number of phylogenetic species conforming to the morphological species concept of *P. oxalicum*. Preliminary analyses of the *BenA* gene indicated the presence of three species. As well, *P. oxalicum* causes cucumber stem rot and blue ear of corn. Some strains have been identified as potential biocontrol agents against tomato root rot caused by *Fusarium oxysporum* and *Verticillium* species (Pascual *et al.* 1997), and strawberry mildew (De Cal *et al.* 2003). The wide variety of biological roles played by this species, may suggest the presence of cryptic

species as indicated by *BenA*. Species were resolved using the GCC recognition criteria using MP, ML, and BI gene trees.

Table 1.1: Ubiquinone and cell wall composition in *Eupenicillium* and *Talaromyces*.

Character	<i>Eupenicillium</i>	<i>Talaromyces</i>	References
<u>Ubiquinone</u>	Q-9, Q-10	Q-9, Q-10(H2), Q10(H4)	Kirashi <i>et al.</i> 1991
<u>Cell Wall</u>			
Glucose (%)	78	48–64	Gomez-Miranda <i>et al.</i> 1988
Galactose (%)	13 –15	25–39	Gomez-Miranda <i>et al.</i> 1988
<u>Cell Wall Fraction S</u>			
% fraction S amount of cell wall dry weight	13–18	4–12	Gomez-Miranda <i>et al.</i> 1988
Galactose (%)	13–15	25–26	Gomez-Miranda <i>et al.</i> 1988
Glucose (%)	25–27	64–67	Gomez-Miranda <i>et al.</i> 1988
α -glucan absorption	850 cm ⁻¹	820 cm ⁻¹	Gomez-Miranda <i>et al.</i> 1988
Aditols obtained by complete Smith degradation of polysaccharides	glucose	glycerol erithrodol theritol arabinitol mannose galactose glucose	Gomez-Miranda <i>et al.</i> 1998

Table 1. 2: Percentage of species specific *Cox1* sequences in 11 eukaryotic taxa.

Taxa	Number of Species Tested	Percentage of Species Specific Sequences	References
North American Birds	521	100	Hebert <i>et al.</i> 2004
Korean Birds	92	100	Yoo <i>et al.</i> 2006
Australian Marine Fish	207	100	Ward <i>et al.</i> 2005
Spiders	203	100	Barrett and Hebert 2004
Moths and Butterflies	521	97.6	Hajibabaei <i>et al.</i> 2004
Amphibians	7	94	Smith <i>et al.</i> 2008
Earth worms	36	100	Huang <i>et al.</i> 2007
Crustaceans	150	95	Costa <i>et al.</i> 2007
Red Macroalgae	26	100	Saunders <i>et al.</i> 2007
Ciliates	51	96	Chantangsi <i>et al.</i> 2007
<i>Phytophthora</i>	13	100	Martin <i>et al.</i> 2003

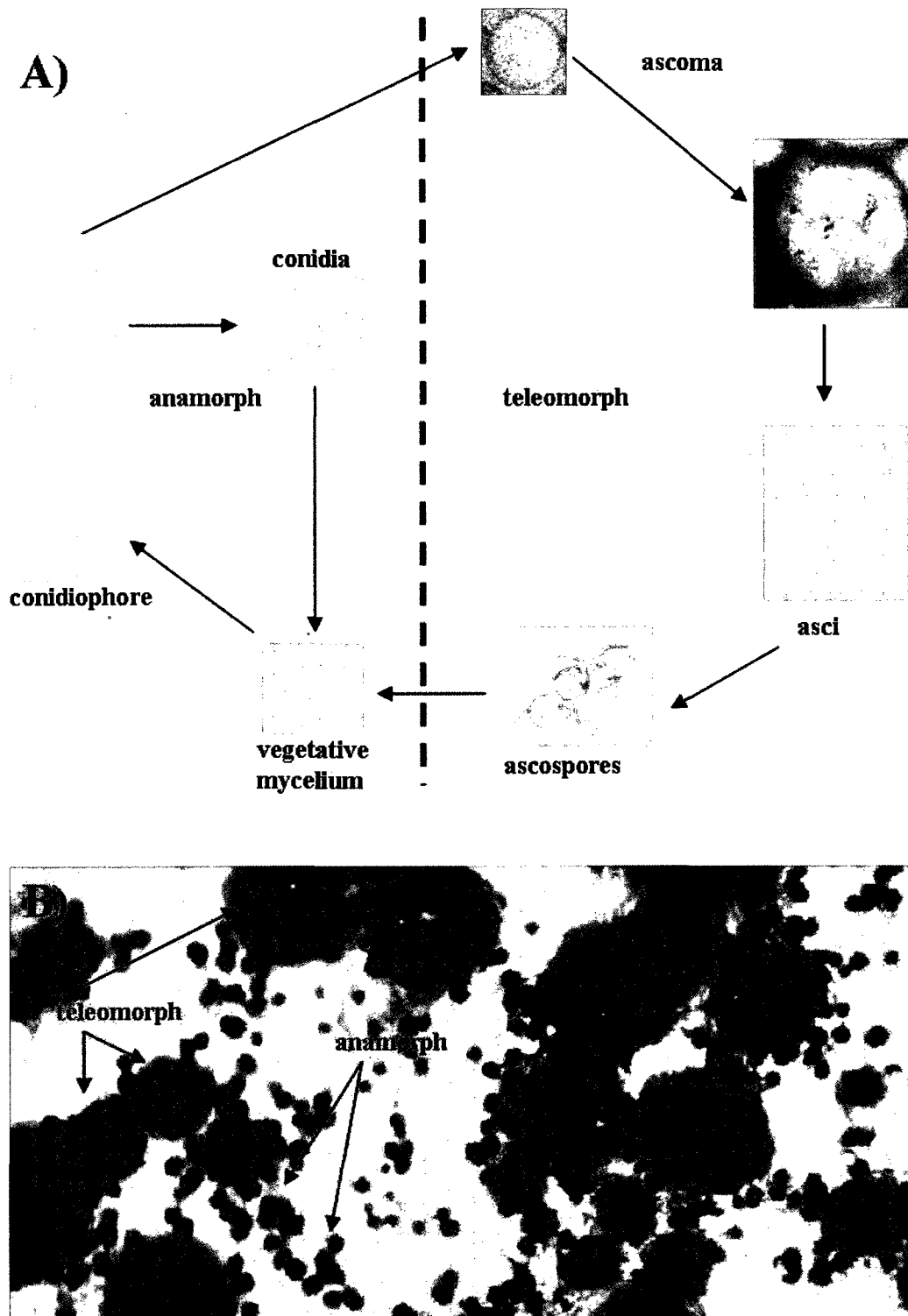


Figure 1.1: A–B) The life cycle of a typical anamorphic fungus, demonstrating the anamorph and teleomorph relations.

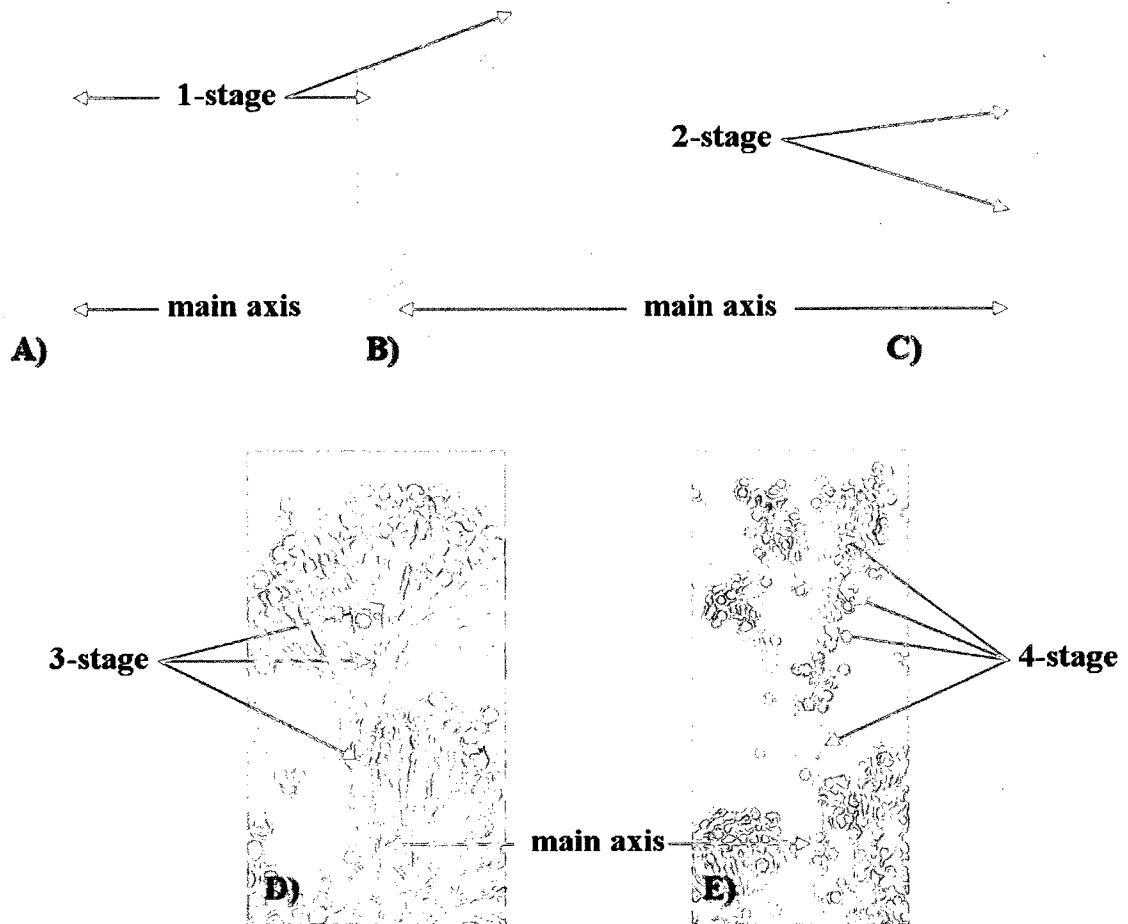


Figure 1.2: Conidiophore types in *Penicillium*. A–B) Monoverticillate (simple), C) biverticillate (one-stage), D) terverticillate (two-stage), and E) quaterverticillate (three-stage).

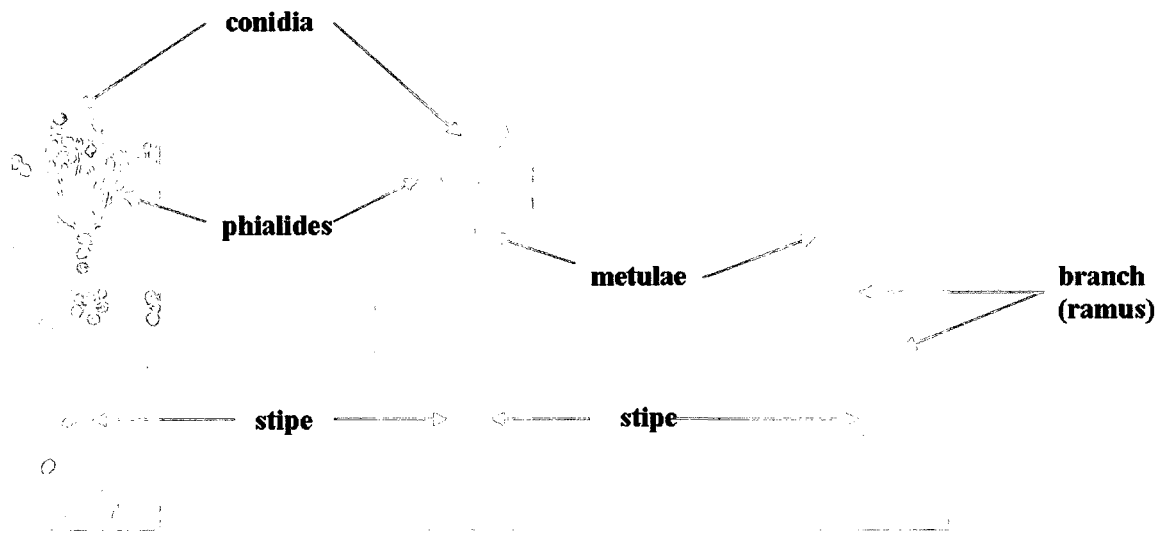


Figure 1.3: Microscopic structures of *Penicillium* conidiophores.



Figure 1.4: Typical conidiophore of subgenus *Furcatum* section *Divaricatum*.

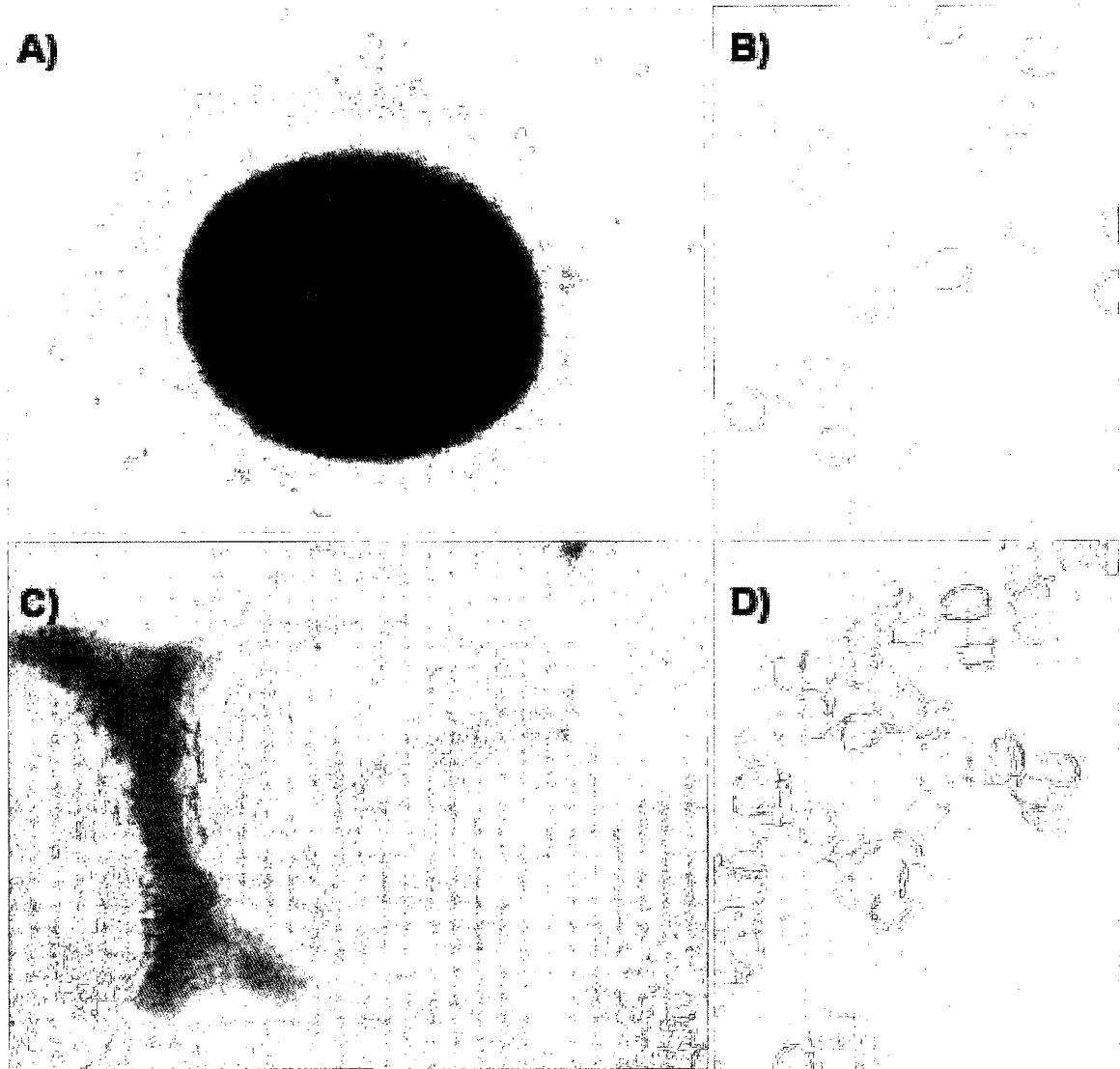


Figure 1.5: *Penicillium* teleomorphs. *Talaromyces*. (A) Ascocarp and (B) ascospores. *Eupenicillium*. (C) Ascocarps and (D) ascospores.

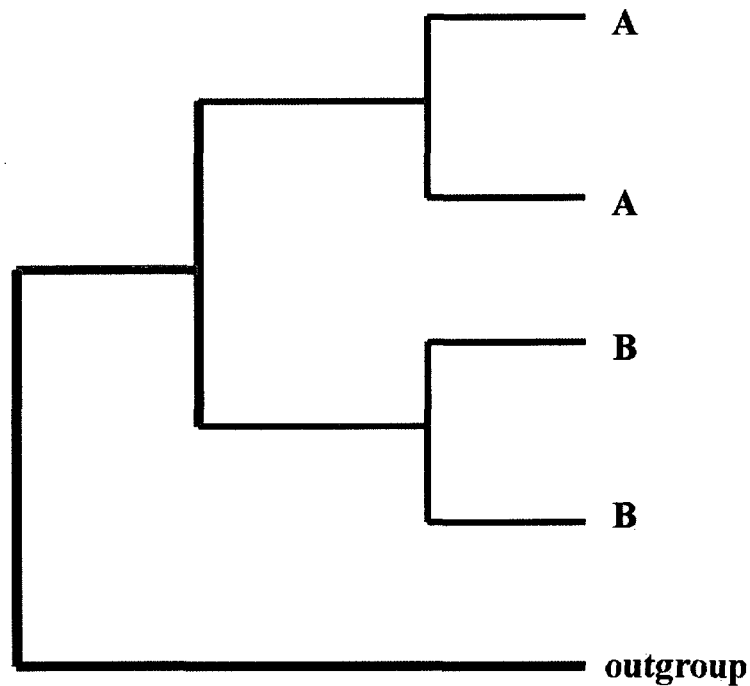


Figure 1.6: Uncertainty in species limits using a single gene genealogy. Phylogenetic analysis of a single gene can be used to group individuals into monophyletic groups, which may represent species. The limit of the species is uncertain in this figure. If the limit is at the red line, it implies that alleles A and B represent intraspecific variation. If the species limit is at the blue line, it suggests that alleles A and B are fixed in two genetically isolated populations.

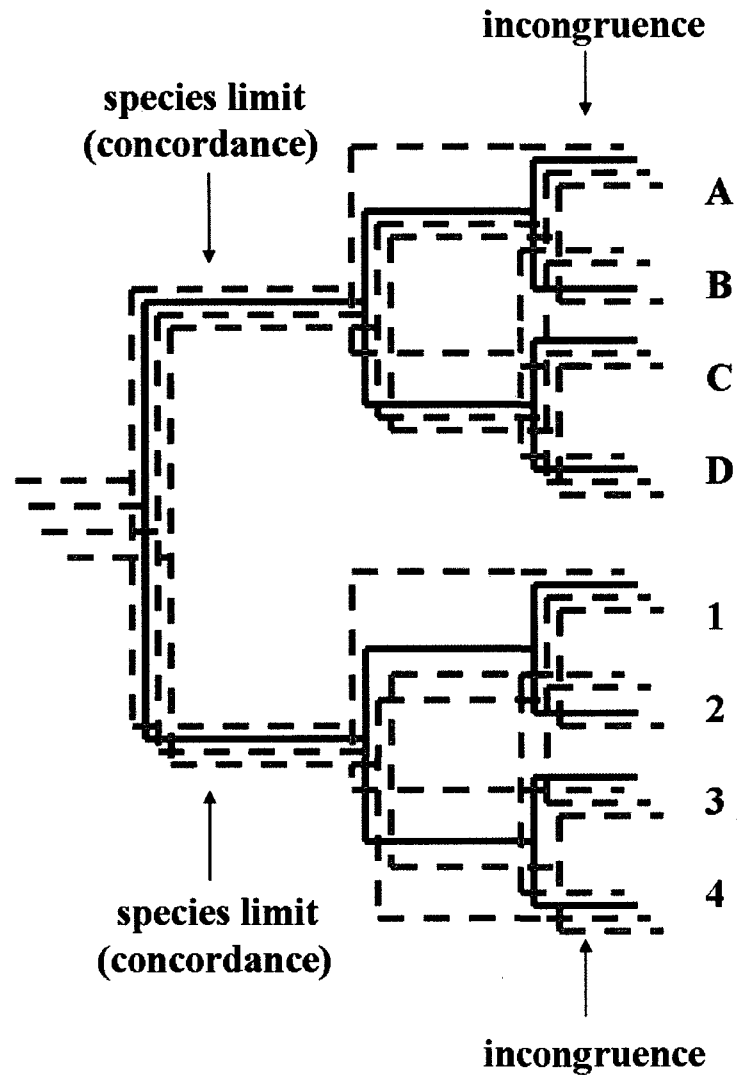


Figure 1.7: Four gene genealogies demonstrating concordance and incongruity in branches used to delimit species. Each line colour represents a different gene genealogy. The letters represent one species, while the numbers represent a different species.

Chapter 2: *Penicillium mallochii* and *P. guanacastense*, two new species isolated from Costa Rican caterpillars

Karol G. Rivera, Joel Díaz, Felipe Díaz-Chaverria, Maria Garcia, Mirjam Urb, R. Gregg Thorn, and Keith A. Seifert

2.1 Abstract

Twenty-five strains of *Penicillium mallochii* and two strains of *P. guanacastense* were isolated from the intestinal tracts of leaf-eating caterpillars from the Área de Conservación Guanacaste, Costa Rica. *Penicillium mallochii* was isolated from *Rothschildia lebeau* and *Cithorenia lobesis*, two large caterpillars belonging to the *Saturnidae* family. *Penicillium guanacastense* was isolated from two unidentified caterpillars belonging to the *Noontidae* family. Phylogenetic analyses of β -tubulin (*BenA*), the nuclear ribosomal internal transcribed (ITS) spacer, cytochrome c oxidase subunit 1 (*Cox1*), translation elongation factor 1- α (*TEF1- α*) and calmodulin (CaM) using the Genealogical Concordance Concept (GCC) recognition criterion revealed that the two species are distinct, and are closely related to *P. sclerotiorum*, which they resemble morphologically, differing in vesicle width. *Cox1* resolved the two species, but did not provide the strong statistical support as did *BenA*, *TEF1- α* and CaM, but had a higher statistical support than ITS. Morphological analyses placed the two species in *Penicillium* subgenus *Aspergilloides* series *Glabra*.

2.2 Introduction

In 2005, *Penicillium* strains isolated from the intestinal tracts of caterpillars from the Área de Conservación Guanacaste, Costa Rica, were received at the Eastern Cereal

and Oilseed Research Centre (ECORC) in Ottawa from Dr. R. Gregg Thorn from the University of Western Ontario. The fungi were compared with previously described species using cultural characters, microscopy and DNA sequence data from β -tubulin (*BenA*), cytochrome c oxidase subunit 1 (*Cox1*), translation elongation factor 1- α (*TEF1- α*), calmodulin (CaM), and the nuclear internal transcribed spacer (ITS) region. In this chapter, the isolates are described as two new species belonging to *Penicillium* subgenus *Aspergilloides*, *P. mallochii* and *P. guanacastense*.

2.3 Materials and Methods

Rothschildia lebeau, *Cithorenia lobesis* and unidentified caterpillars feeding on *Spondias mombis* and *Cochlospermum vitifolium* were collected by Joel Díaz, Felipe Díaz-Chaverria, and Maria Garcia from the Área de Conservación Guanacaste, Costa Rica. Caterpillars were surface sterilized with ddH₂O and ethanol to minimize contamination. The intestinal tracts of the caterpillars were then removed and dissected into three parts; the foregut, midgut and hindgut. Faeces were collected for fungal isolation from caterpillars kept in sterile Petri dishes before dissection. Gut contents and faeces were dispersed in sterile distilled water and serially diluted in sterile distilled water prior to plating onto rose bengal agar. Fungal colonies were plated onto Malt Extract Agar (MEA; Pitt 1979a; refer to Appendix 1 for medium recipe) until a pure culture was obtained. Cultures were brought to Canada by Dr. Thorn, where Mirjam Urb with the aid of Dr. Seifert from Agriculture and Agri-Food Canada, Ottawa identified the strains as undescribed *Penicillium* species using morphological analyses and preliminary *BenA* phylogenetic data.

Penicillium mallochii was isolated twenty-five times from the intestinal tract and frass from two caterpillar species, *Rothschildia lebeau* or *Cithorenia lobesis* (Table 2.1). *Penicillium guanacastense* was isolated two times from unidentified caterpillars belonging to the family *Noontidae* (Table 2.1). Cultures were preserved in 4°C and -80°C in water and 10% glycerol. Both strains of *P. guanacastense* and 12 strains of *P. mallochii* were submitted to the Canadian Collection of Fungal Cultures (CCFC or DAOM) for preservation (Table 2.1). Cultures not deposited in the CCFC are currently being held in the personal research collection of Keith A. Seifert (KAS).

2.3.1 Morphological Analyses

Isolates were grown in the dark at 25°C for 7 d on malt extract (MEA) and Czapek's agar (CYA; Pitt 1979a; refer to Appendix 1 for medium recipe). All strains were 3-point inoculated twice on all media. Colony descriptions and measurements were made for all colonies. Colony diameters were measured, and colony colours determined using Korrnerup and Wanscher (1978) colour references. Colony photographs were taken with a Nikon Coolpix E 5000 camera under incandescent lighting conditions using a copy stand.

Microscopic examinations were performed using an Olympus BX 50 light microscope on colonies grown on MEA mounted in 85% lactic acid. Microscopic photographs and character measurements were taken with an Evolution MP Media Cybernetics Camera with the aid of the camera digital analyzing software Image-Pro Plus v. 6 (Media Cybernetics, MD, U.S.A.). Using Image-Pro Plus, 10 manual measurements were made for phialides, stipe, metulae and vesicle, and 25 automated measurements for conidia. Length to width conidia ratios were plotted using Excel from the Microsoft

2003 Home Edition for *P. mallochii*, *P. guanacastense*, and *P. sclerotiorum*. Twenty-five spore measurements were used for each strain.

2.3.2 DNA Isolation, PCR Amplification and Sequencing

DNA was extracted from strains grown on MEA and CYA using the UltraCleanTM Microbial DNA Isolation Kit (MO BIO Laboratories, Inc., Montreal, CA) following the manufacturer's protocol. *BenA* was amplified with primers Bt2a and Bt2b (Glass & Donaldson 1995), ITS with primers ITS1 and ITS4 (White *et al.* 1990), *CoxI* with primers PF and AR (Seifert *et al.* 2007), *TEF1-α* with primers EF1c and EF6 (Peterson *et al.* 2004), and CaM was amplified with primers CMD5 and CMD6 (Hong *et al.* 2006).

PCR reactions were performed in 10 µl reaction mixtures containing 1 µl genomic DNA, 1X PCR Buffer, 0.1 mM of dNTPs, 0.08 µM of each primer, and 0.5X Taq polymerase. Amplifications were performed in a TGradient (Biometra, Montreal, Canada) or a Genius (Techne, Duxford, Cambridge) thermocycler. The temperature cycling parameters for ITS, *CoxI*, *BenA* were 95°C for 1 min for denaturation followed by primer annealing at 56°C for 45 s and primer extension at 72°C for 1:30 min for a total of 35 cycles, plus a final 10 min elongation step at 72°C. The temperature cycling parameters for *TEF-1α* and CaM were 94°C for 1 min for denaturation, 62°C for 30 s for annealing, 72°C for 1:30 min for primer extension for 42 cycles, plus a final elongation step 72°C for 10 min. PCR products were visually examined by gel electrophoresis in a 1% agarose gel containing ethidium bromide (0.05 µg/mL).

Two strains of *P. herquei*, CBS 336.48 and CBS 110644, produced two bands (approximately 360 bp and 470 bp in length) for *BenA*. The PCR products with multiple

bands were cloned using Promega's pGEM®-T Vector Kit and JM109 High Efficiency Competent Cells (Madison, WI, U.S.A) following the manufacturer's protocol. Fifteen transformed colonies were selected for PCR and sequencing.

Sequencing reactions were performed directly from PCR products in both directions with the forward and reverse primers. The sequencing reaction total volume of 10 µl contained 1 µl of amplicon, 0.5 µl of ready-made BigDye terminator mix v. 7 (Applied Biosystems, Foster City, CA, USA), 0.161 µM of primer, and 0.125X BigDye buffer v. 7 (Applied Biosystems, Foster City, CA, USA). Reactions were performed in a TGradient (Biometra, Montreal, QC, Canada) or in a Genius (Techne, Duxford, Cambridge) thermocycler, programmed for 95°C for 1 min for denaturation, followed by primer annealing at 56°C for 30 s and primer extension at 72°C for 1 min for a total of 30 cycles, plus a final 10 min elongation step at 72°C. Sequence reaction mixtures were then sent to the ECORC Mycology Sequencing Facility (Ottawa, ON, Canada) for analyses. Sequence reaction mixtures were precipitated using ethanol/EDTA/sodium acetate precipitation. Samples were analyzed on an ABI 30XL Genetic Analyzer (Applied Biosystems, Foster City, California, USA).

Penicillium mallochii and *P. guanacastense* ITS and *BenA* sequences were compared with sequences in GenBank using the Basic Local Assignment Systems Tool (BLAST). Both *P. mallochii* and *P. guanacastense* sequences had 99% sequence similarity to *P. sclerotiorum* and an E-value of zero. *Penicillium sclerotiorum* is part of Group 3 of the six *Penicillium* groups described by Peterson (2000). Five strains per species for Group 3 (*P. sclerotiorum* van Beyma, *Eupenicillium hirayamae* Udagawa, *P. bilaiae* Chaleb., *P. adametzii* Zalesky, and *P. herquei* Bainier & Sartory), were obtained

from the Centraalbureau voor Schimmelcultures (CBS) in Utrecht, Netherlands, and the Agriculture Research Service Culture Collection (NRRL) in Peoria, IL, USA as freeze-dried cultures (Table 2.1). Freeze-dried cultures were resuspended on ddH₂O for two hours and then plated on MEA for revival.

2.3.3 Phylogenetic Analyses

Consensus sequences were assembled using the DNA sequence assembly software Sequencher v. 4.8 (Genes Codes Corporation, MI, U.S.A.). Alignments were constructed using the online version of MAFFT v. 6 (<http://align.bmr.kyushu-u.ac.jp/mafft/software/>), and manual adjustments were made to optimize homology in BioEdit 7.0.9 (Hall, 1999). Alignments were subjected to maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI) analyses.

MP analyses were performed using heuristic searches in PAUP v. 4 (Swofford 2002) with the tree bisection-reconnection (TBR) branch swapping algorithm. Uninformative characters were removed for all analyses, gaps were treated as missing data, and maxtrees were set to 5000. Consensus trees were calculated, and the robustness of the gene trees was tested using a full heuristic search, saving 10 trees per replicate (1000 replicates were performed). Bootstrap values are represented in per cent.

ML analyses were performed using the computer program Phylogenies for Maximum Likelihood (PhyML) v. 2.4.4 (Guidon and Gascuel 2003). Tree searches for each alignment were run under the nucleotide substitution model obtained from ModelTest 3.7, using the Akaike Information Criteria (AIC) (Posada and Crandall 1998), and starting from a tree obtained for branch swapping using the modified neighbor joining algorithm BIONJ (Gascuel 1997) as implemented by PhyML. Gaps are treated

as missing data by the programs. The robustness for each tree was tested by performing 1000 bootstrap replicates. Bootstrap values are represented as frequencies. BI analyses for each alignment were performed using MrBayes v. 3.1.2 (Huelsenbeck and Ronquist 2001), under the same model conditions as those selected for ML. All Bayesian analyses were performed using random starting trees, and were run for four chains with one million generations for all genes (burnin chains = 250). Gaps were treated as missing data

2.4 Results

DNA sequences were obtained for all genes and strains, except for CaM sequences for *P. adametzii* strains, because amplification was not observed after PCR. PCR reactions for *P. adametzii* were performed with denaturation temperatures as low as 40°C for 1 min with primers CF4 and CF5 (Peterson *et al.* 2004), CF4 and CMD6, and CMD5 and CF5, however, amplification was not observed (see Appendix 2 for primer sequences). Not all strains of *E. hirayamae* (CBS 478.66, CBS 247.67 and CBS 277.70) and *P. herquei* (CBS 167019) were used in the construction of the sequence alignments. Sequence analyses revealed that these strain were misidentified or contaminated. Two strains of *P. herquei*, CBS 336.48 and CBS 110644, revealed multiple bands in gel electrophoresis in amplicons of the *BenA* gene. Two copies of the *BenA* gene were obtained; similar nucleotide sequences to the *P. herquei* ex-type strain were selected for the construction of sequence alignments.

The length of the alignments for *BenA*, ITS, *Cox1*, *TEF1- α* , and CaM in bp were 565, 574, 604, 1009, and 620 respectively. The sequence lengths of *P. mallochii* for *BenA*, ITS, *Cox1*, *TEF1- α* , and CaM in bp were 565, 566, 604, 989, and 610 respectively.

The nucleotide sequence lengths of *P. guanacastense* for *BenA*, ITS, *Cox1*, *TEF1- α* , and CaM in bp were 477, 545, 576, 725, and 522 respectively.

For *BenA*, the MP and BI trees yielded strong statistical support for *P. mallochii* and *P. guanacastense* with 100% bootstrap support (Figure 2.1) and posterior probabilities of 1.00 (Figure 2.3). The ML also provided strong bootstrap support, 0.998 and 1.00, for *P. mallochii* and *P. guanacastense* (Figure 2.2). *BenA* trees revealed two groups of *P. mallochii* strains that are not present in the other gene trees. In the MP tree, the groups had 86% and 70% bootstrap support (Figure 2.1); in the ML tree the groups had 0.866 and 0.814 bootstrap support (Figure 2.2); and in the BI trees, the groups had posterior probabilities of 0.74 and 0.66 (Figure 2.3).

The ITS trees did not provide resolution for *P. mallochii* strains (Figure 2.4–2.6). For *P. guanacastense*, the ITS trees provided strong statistical support. The MP tree provided 100% bootstrap support (Figure 2.4), the ML tree provided 1.00 bootstrap support (Figure 2.5), and the BI tree provided a posterior probability of 1.00 (Figure 2.6).

For *Cox1*, the MP and ML tree yielded strong bootstrap support for *P. mallochii* and *P. guanacastense* (MP–85% and 100%; ML–0.986 and 0.996) (Figure 2.7–2.8). The posterior probability was strong for *P. guanacastense*, 1.00, and low for *P. mallochii*, 0.53 (Figure 2.9).

The *TEF1- α* MP and ML revealed strong bootstrap values for *P. mallochii* and *P. guanacastense* (MP–91% and 100%; ML–0.975 and 1.00) (Figure 2.10–2.11). The posterior probability in the BI tree were strong for *P. mallochii* and *P. guanacastense*, 0.87 and 1.00 (Figure 2.12). The CaM MP, ML and BI trees also had strong statistical support (100%, 1.00, and 1.00) for both species (Figure 2.–2.15).

Combined gene data analyses results are presented in Chapter 3 of this thesis because the two species form part of the *P. sclerotiorum* complex. The placement of *P. mallochii* and *P. guanacastense* in Peterson's *Penicillium* Group 3 and the *P. sclerotiorum* complex phylogeny are also discussed. The morphological species description for *P. mallochii* and *P. guanacastense* are included in the Taxonomy section of this chapter. Strain KAS 2597 was not included in the morphological species description for *P. mallochii* because it was sterile and precluded morphological examination.

To differentiate between conidial size in *P. mallochii* and *P. guanacastense*, and its closest relative *P. sclerotiorum*, the average length to width ratio for conidia for each strain was plotted (Figure 2.16). The conidia measurements for *P. mallochii* and *P. guanacastense* overlapped with one another, except for five strains of *P. mallochii*. The length and width for these five strains is greater than the rest of the *P. mallochii* strains, and all *P. guanacastense* and *P. sclerotiorum* strains. The two *P. guanacastense* strains did not overlap with strains from other species; however, this is probably due to a limited sample size. More strains are needed to determine if conidial size is a useful character to distinguish between the three species.

2.5 Taxonomy

***Penicillium mallochii* Rivera, Urb & Seifert, prov. sp. nov.¹** Figures 2.17– 2.21

Colonies on CYA after 7 days at 25°C: typically 29–39 mm in diam.; dense and velutinous, sometimes with aerial mycelium in the centre; moderately sulcate with 4–7 sulcations, often with 2–5 wrinkles in the centre; approximately 1 mm deep; conidia

¹ The name does not constitute a valid publication of the new species name according to the regulations of the International Code of Botanical Nomenclature, which requires that new species be published in the formal scientific literature, accompanied by a Latin diagnosis.

turquoise grey to greenish grey (24–25D2–3), concentric rings of different shades of these colours present; clear yellow exudate droplets produced in moderate amounts by some strains, absent in others; vivid orange clear soluble pigment present in some strains, absent in others; 2–3 mm of white mycelia at the margin, margin entire; reverse deep yellow (4A8), reddish orange (4A6–7) or golden yellow to orange (5–6A–B6–8) in the centre, light to pastel yellow (3–4A4–5) at the margins.

Colonies on MEA after 7 days at 25°C: 24–35 mm in diam., less commonly 19–26 mm in diam.; planar, velutinous, no aerial mycelia; conidia grayish green to dull green (25–30B–E3–7), no exudates or soluble pigments present; reverse grayish green (30C5), grayish yellow (1–2B–C3–8), yellow (2–3A6–7), deep yellow (4A8) and orange (6A–B6–8), near the margins paler shades of these colours; margin entire.

Individual monoverticillate conidiophores on MEA borne from agar surface, smooth to finely roughened, septate stipes 53–380 μm long, 2–4 μm wide; most strains unbranched; in branched strains, 10% of the conidiophores are branched, branches 14–44 $\times$ 1.5–2 μm ; vesiculate, 4–6 μm in diam ($\bar{x}$ for different strains = $4.5\text{--}6.0 \pm 0.71 \mu\text{m}$, $n = 25$). Conidiogenous cells phialidic, in whorls of 12–22, ampulliform with a collula, 7–10 (–16) $\times$ 2–3 (–4) μm . Conidia globose to subglobose, finely roughened, 2.5–3.5 $\times$ 2–2.5 μm ; range of $\bar{x}$ for different strains = $2.6\text{--}3.4 \pm 0.01 \times 2.3\text{--}2.4 \pm 0.01$, $n = 25$; L/W mean ratio 1.15:1.

Cultures examined: DAOM 239917 (ex-type), DAOM 239918, DAOM 239919, DAOM 239920, DAOM 239921, DAOM 239922, DAOM 229924, DAOM 229926, DAOM 229925, DAOM 229926, DAOM 229927, DAOM 229928, DAOM 229929, KAS 2601, KAS 2606, KAS 2612, KAS 2615, KAS 2630, KAS 3183, KAS 3186, KAS

3187, DAOM 239925, KAS 3190, KAS 3191, KAS 3193. Refer to Table 2.1 for more details.

Etymology: The species was named after David Malloch, who was a faculty member of the University of Toronto and is currently at the Natural History Museum in Newfoundland. He is a great teacher of mycology, and has immensely influenced the field. I consider myself fortunate to have been in his undergraduate classes while at the University of Toronto.

Substrate: *Rothschildia lebeau* and *Cithorenia lobesis* intestinal tracts and feces.

Geographical distribution: Área de Conservación Guanacaste, Santa Rosa, Costa Rica.

***Penicillium guanacastense* Rivera, Urb & Seifert prov. sp. nov.**¹ Figures 2.22–2.24

Colonies on CYA after 7 days at 25°C: 25–33 in diam., dense and velutinous, with 5–8 sulcations, sectors with poor sporulation, moderately sulcate especially at the margins, 2–3 radial wrinkles present in one strain; conidia greenish grey (25–30B–E2), yellow concentric ring near the margins, followed by a bluish grey concentric ring towards the centre, clear exudate droplets produced in moderate amounts and soluble pigments by one strain, absent in the other; 2–3 mm of white mycelium at the margin, margin entire; reverse orange yellow to orange (4–6B7–8).

Colonies on MEA after 7 days at 25°C: 29–33 mm in diam., planar and velutinous, no aerial mycelia observed; conidia greenish grey (25–30B–E2), with no exudates or soluble pigments present; reverse yellowish white (2–4B2), orange (6B7–8) and light brown (6–7D4–8), near the margin lighter shades of these colours.

Individual monoverticillate conidiophores on MEA borne directly from agar surface; finely roughed, septate stipes, 86–97 μm long, 2.5–3 μm wide; strains branched or unbranched, 90% of conidiophores unbranched; vesiculate, 4–5.5 μm (x for different strains = $4.5\text{--}4.65 \pm 0.5 \mu\text{m}$). Conidiogenous cells phialidic, in whorls of 14–18, ampulliform with distinguishable collula, $8.5\text{--}12 \times 2\text{--}3.5 \mu\text{m}$. Conidia globose, finely roughened, 2.5–3 μm in diam (x for different strains $2.7\text{--}2.8 \pm 0.01 \times 2.5\text{--}2.6 \pm 0.01 \mu\text{m}$, $n = 25$), L/W mean ratio 1.1:1.

Cultures Examined: DAOM 239912, DAOM 2399. Refer to Table 2.1 for more details.

Etymology: The species was named after the Área de Conservación Guanacaste, a World Heritage Site in the northwestern part of Costa Rica, where the species was isolated.

Substrate: intestinal tracts of wild caterpillars belonging to the family *Noontidae*.

Geographical distribution: Área de Conservación Guanacaste, Santa Rosa, Costa Rica.

2.6 Discussion

Penicillium mallochii and *P. guanacastense* are phylogenetically related and morphologically resemble *P. sclerotiorum*. All three species have vesiculate monoverticillate conidiophores and vivid orange to red colony colours. Morphological analyses placed the two species in *Penicillium* subgenus *Aspergilloides* Dierckx series *Glabra* Pitt. All species in this series produce long, vesiculate stipes bearing monoverticillate conidiophores. On closer inspection, *P. sclerotiorum* is vesiculate while *P. mallochii* and *P. guanacastense* are moderately vesiculate, with *P. mallochii* being

more conspicuously vesiculate than *P. guanacastense*. Furthermore, *P. sclerotiorum* has ellipsoidal conidia, while *P. mallochii* and *P. guanacastense* have subglobose conidia. Also some strains of *P. sclerotiorum* produce sclerotia, which were not observed in any *P. mallochii* and *P. guanacastense* strains. However, sclerotia production is not a good distinguishing characteristic.

To differentiate further amongst the species, the average conidia length to width measurements were plotted (Figure 2.16). The conidial measurements for the species overlapped, and did not help to differentiate the species. There are, however, ecological differences. *Penicillium mallochii* strains were isolated from caterpillars belonging to the family *Saturniidae*, while *P. guanacastense* strains were isolated from caterpillars belonging to the family *Noontidae*. On the other hand, *P. sclerotiorum* strains were isolated from the soil and the air.

Overall the gene trees suggested that *P. mallochii* and *P. guanacastense* are distinct species that formed coherent monophyletic groups. The ITS MP and BI trees did not resolve *P. mallochii* from the branch that grouped *P. guanacastense* and *P. sclerotiorum*. The ML tree resolved the three species, but with low bootstrap support. *BenA*, *TEF1- α* , and *CaM* resolved the species using all three phylogenetic methods, with strong statistical support. *Cox1* resolved all the species with strong statistical support, with the exception of the BI tree, where *P. mallochii* had a posterior probability of 0.53.

Penicillium mallochii and *P. guanacastense* conformed to the Genealogical Concordance Concept recognition criterion. As mentioned previously, *Cox1* resolved *P. mallochii* and *P. guanacastense*, as well as the rest of the *Penicillium* species belonging

to Peterson's (2000) *Penicillium* Group 3. Thus *Cox1* is an effective DNA marker for this group.

Table 2.1: Fungal strains examined in Chapter 2 for morphological and molecular analyses.

Species	Culture	Country	Province/State	Region	Substrate
<i>Penicillium mallochii</i>	DAOM 239917*	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Spondias mombis</i>
	DAOM 239918	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM, MG, HG
	DAOM 239919	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Cithorenia lobesis</i> /MG
	DAOM 239920	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM
	DAOM 239921	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM, MG
	DAOM 239922	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /frass
	DAOM 239924	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Cithorenia lobesis</i> /FM, MG, HG
	DAOM 239925	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM, MG, HG
	DAOM 239926	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /frass
	DAOM 239927	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM, MG, HG
	DAOM 239928	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Cithorenia lobesis</i> /FM, MG, HG
	DAOM 239929	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM
	KAS 2597	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM, MG, HG
	KAS 2601	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Cithorenia lobesis</i> /MG
	KAS 2606	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Cithorenia lobesis</i> /FM, MG, HG
	KAS 2612	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Cithorenia lobesis</i> /FM, MG, HG
	KAS 2615	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /frass
	KAS 2630	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /frass
	KAS 3183	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FG
	KAS 3186	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Cithorenia lobesis</i> /FG, MG, HG
	KAS 3187	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FG
	DAOM 239925	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FG, MG, HG
	KAS 3190	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FG, MG, HG

Species	Culture	Country	Province/State	Region	Substrate
	KAS 3193	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rolhschildia lebeau</i> /FG, MG, HG
	KAS 3191	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rolhschildia lebeau</i> /FG, MG, HG
<i>Penicillium guanacastense</i>	DAOM 239912*	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	wild caterpillar belonging to the <i>Noonitidae</i> /FG, MG, HG
	DAOM 2399	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	wild caterpillar belonging to the <i>Noonitidae</i> /FG, MG, HG
<i>Penicillium sclerotiorum</i>	NRRL 2087*	Indonesia	Java	Buitenzorg	air
	NRRL 32583	USA	Hawaii	Kuauai	coffee seeding crown
	DAOM 239930				pineapple soil
	DAOM 239931	Australia	Queensland	Barron Falls	forest soil
	DAOM 239932	Australia	Queensland	Barron Falls	forest soil
<i>Eupenicillium hirayamae</i>	CBS 229.60*	Thailand			milled rice
	CBS 238.68	South Africa		corn meal	
<i>Penicillium adametzii</i>	CBS 209.28*	Poland	Poznan		soil under conifers
	KAS 3463	Malaysia	Kedah		forest soil
	KAS 3464	Malaysia	Kedah		forest soil
	KAS 3465	Malaysia	Kedah		forest soil
	KAS 3466	Malaysia	Kedah		forest soil
<i>Penicillium bilaiae</i>	NRRL 3391*	Russia	Kiev		soil
	LEQ 1642	Canada	Saskatchewan		Soil
	LEQ 1643	Canada	Saskatchewan		soil
	LEQ 1644	Canada	Saskatchewan		soil

Species	Culture	Country	Province/State	Region	Substrate
	LEQ 1848	Canada	Ontario	Ottawa	soil
<i>Penicillium herquei</i>	CBS 336.48	France			<i>Agauri prifolia</i>
	CBS 6.22				
	CBS 347. 51 *	Japan	Nehira	Osaka Univ. Fac. Techn.	wakamoto corn and rice cake
	CBS 110644	USA	Wisconsin		forest soil
<i>Eupenicillium levitum</i>	NRRL 705 *	USA	New York		modeling clay

FG – Foregut; MG – midgut; HG – hindgut.

* represents the ex-type strain.

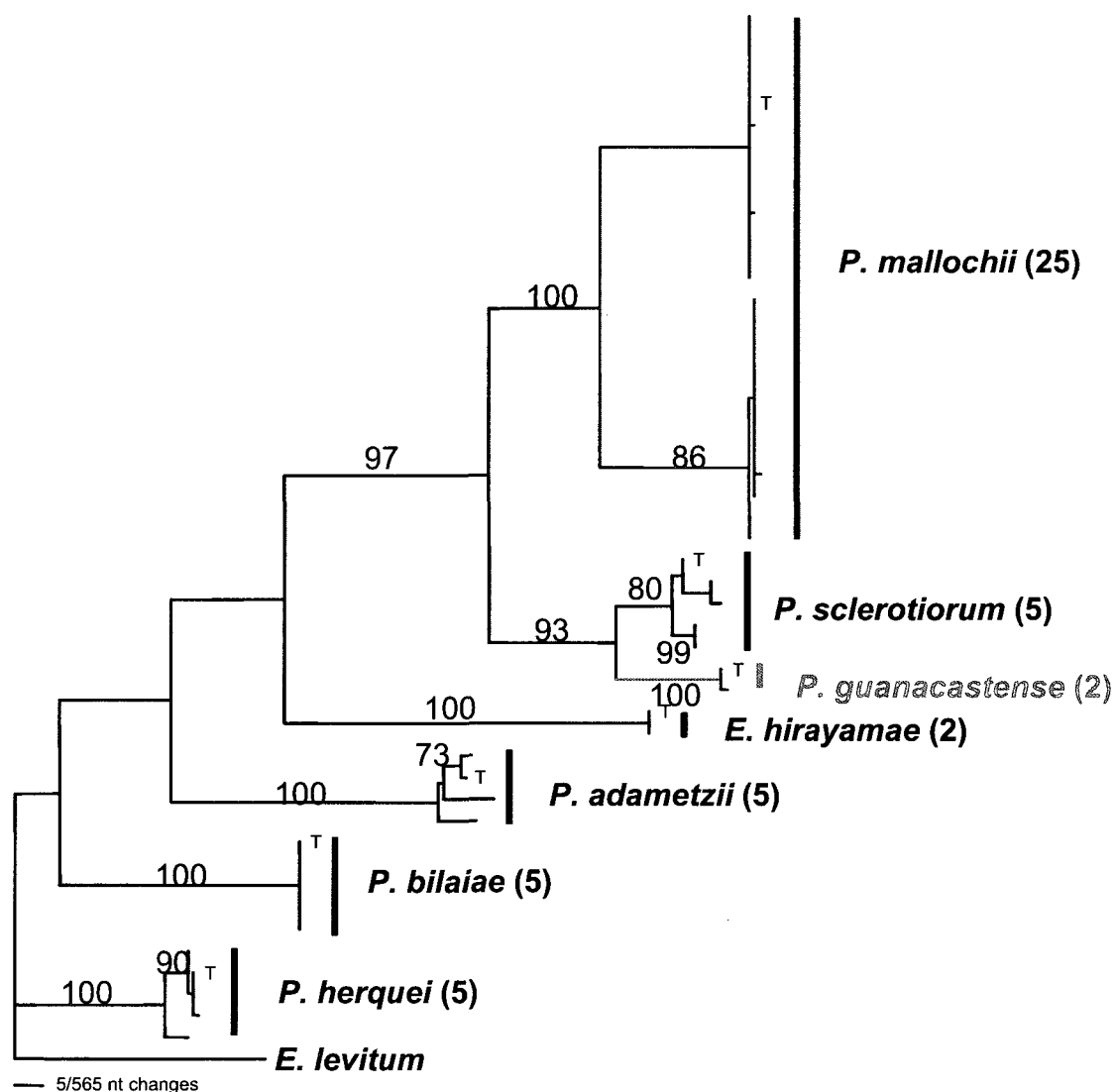


Figure 2.1: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *BenA* sequences. One out one most parsimonious trees (L=357, CI=0.723, RI=0.933, RC=0.674, and HI=0.277). A heuristic search and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. The number in parenthesis represents the number of strains; T represents the ex-type strain.

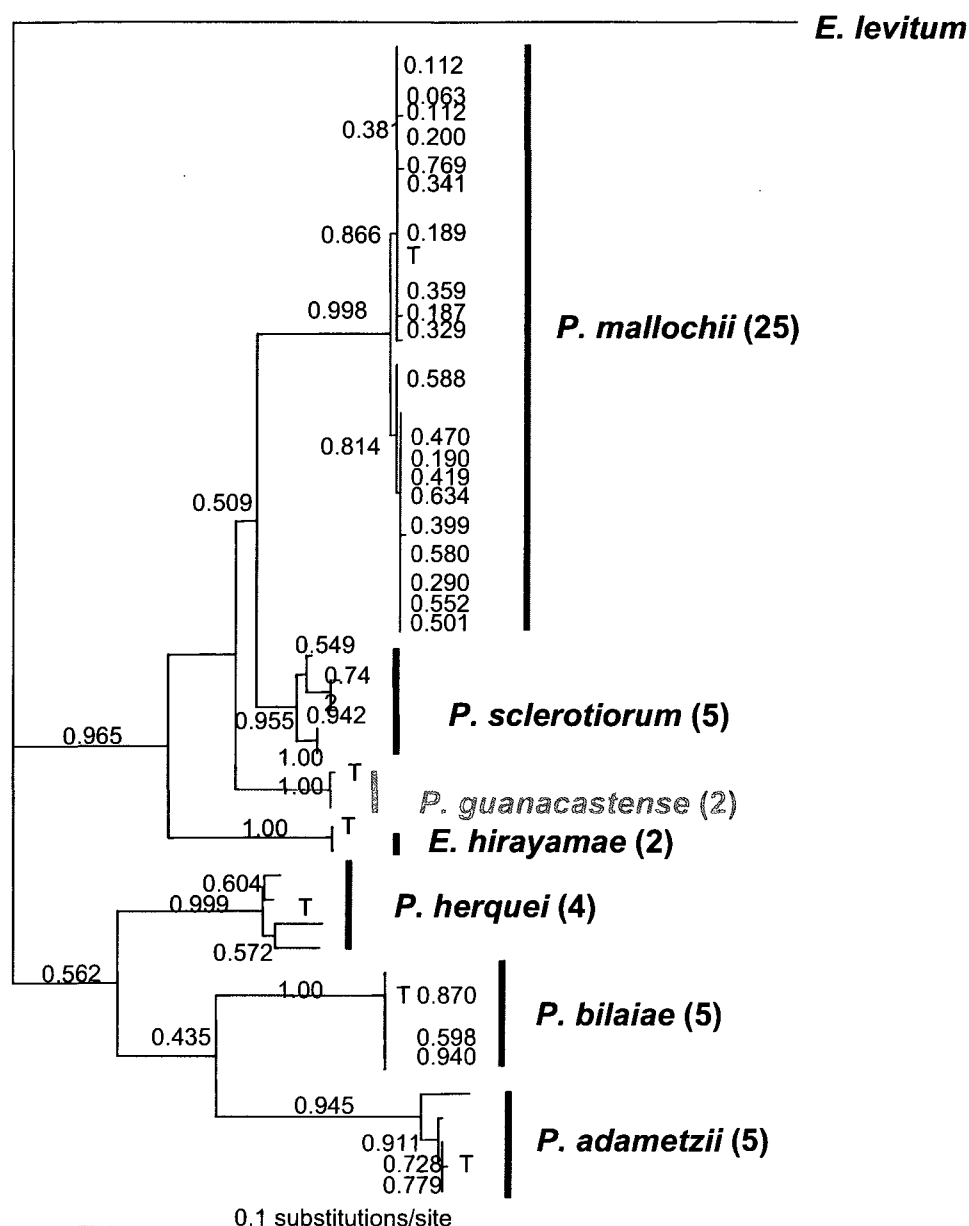


Figure 2.2: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *BenA* sequences. The tree was constructed using the HKY+I+G nucleotide substitution model, 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

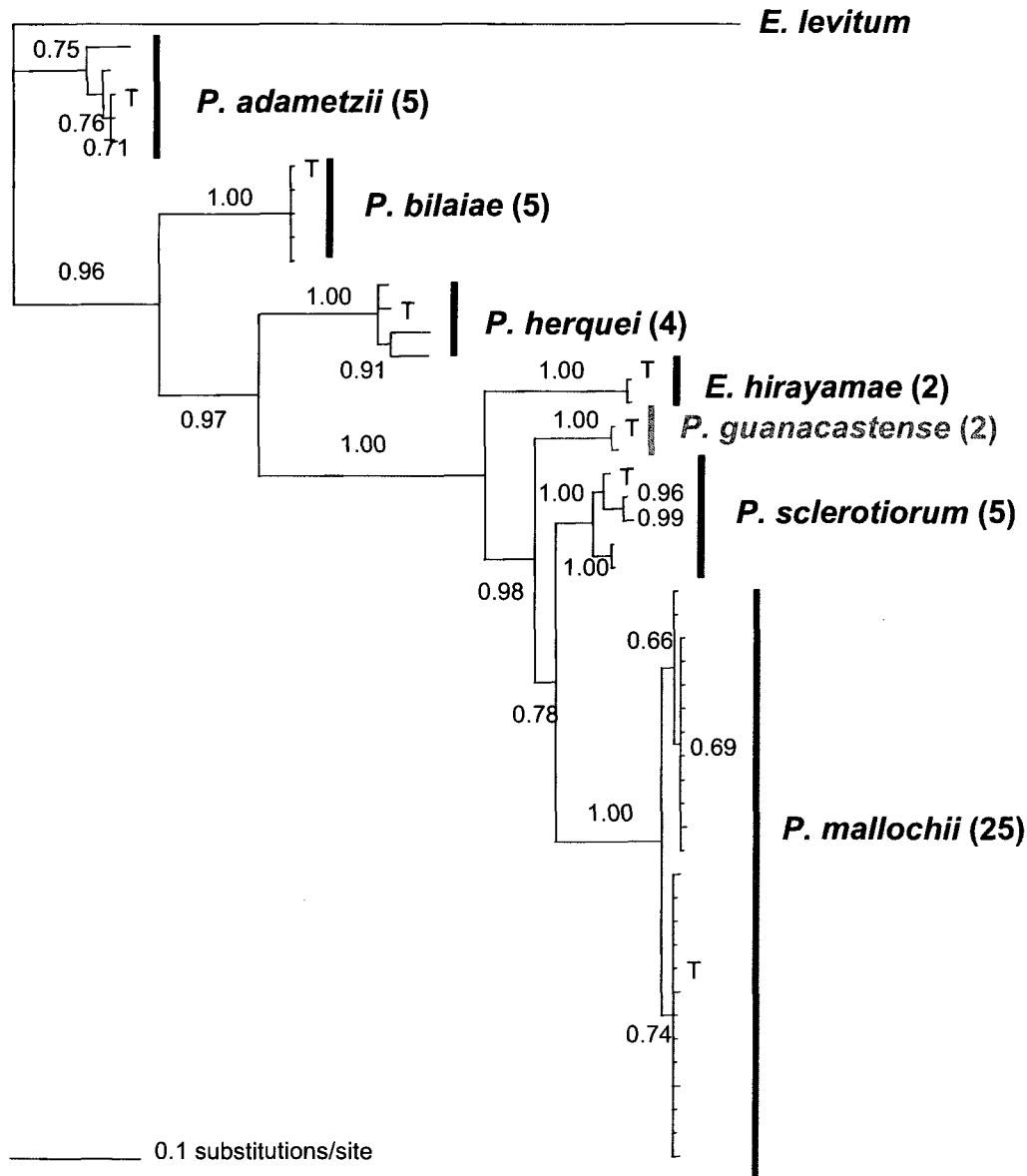


Figure 2.3: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *BenA* sequences. The tree was constructed using the HKY+I+G nucleotide substitution model. Posterior probabilities are shown, the number in parenthesis represents the number of strains; T represents the ex-type strain.

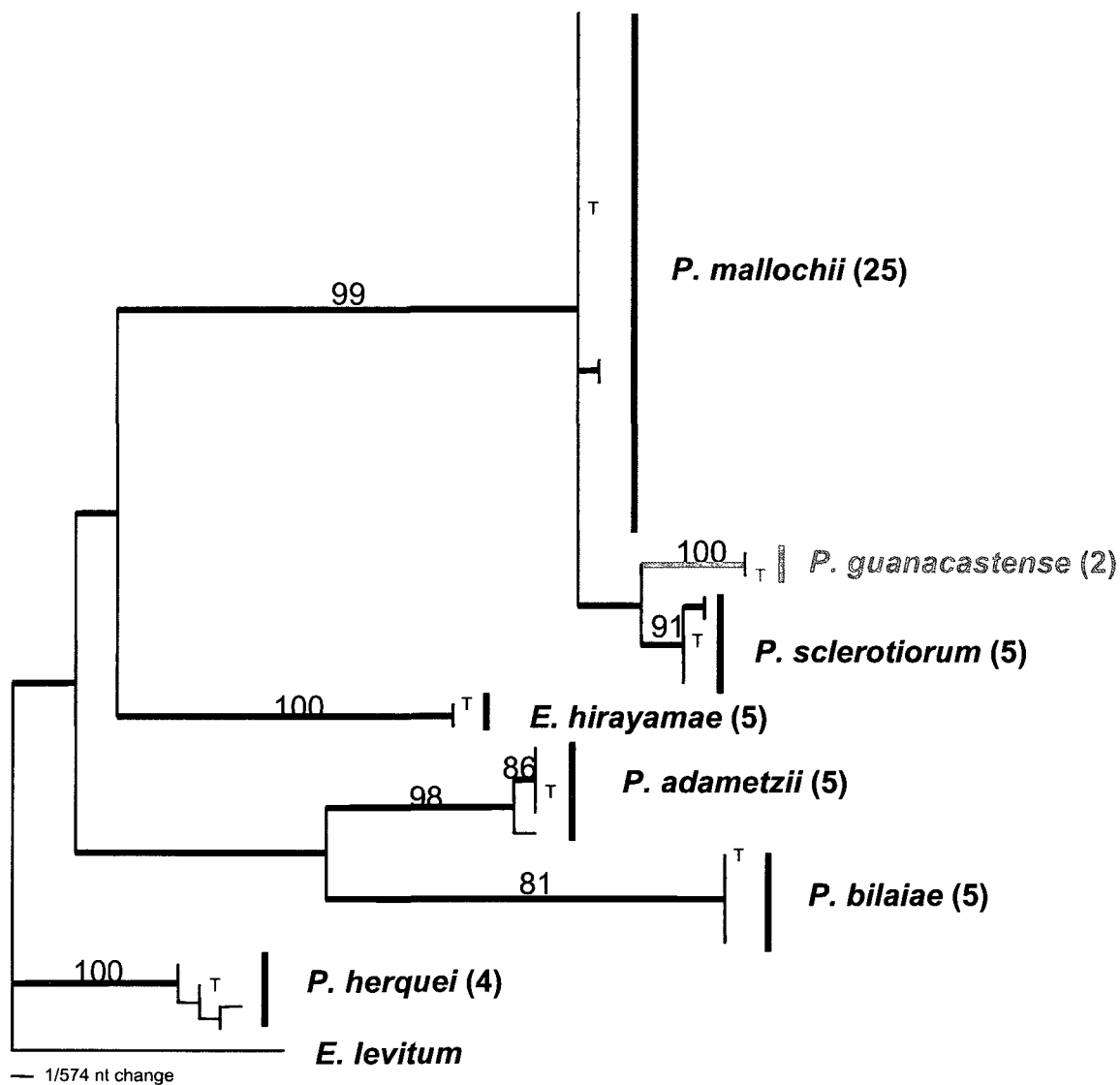


Figure 2.4: Maximum parsimony gene tree for species of Peterson's (2000) Group 3 of *Penicillium*, showing the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned ITS sequences. One out of 500 most parsimonious trees (L=105, CI=0.75, RI=0.93, RC=0.706, HI=0.248). A heuristic search and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

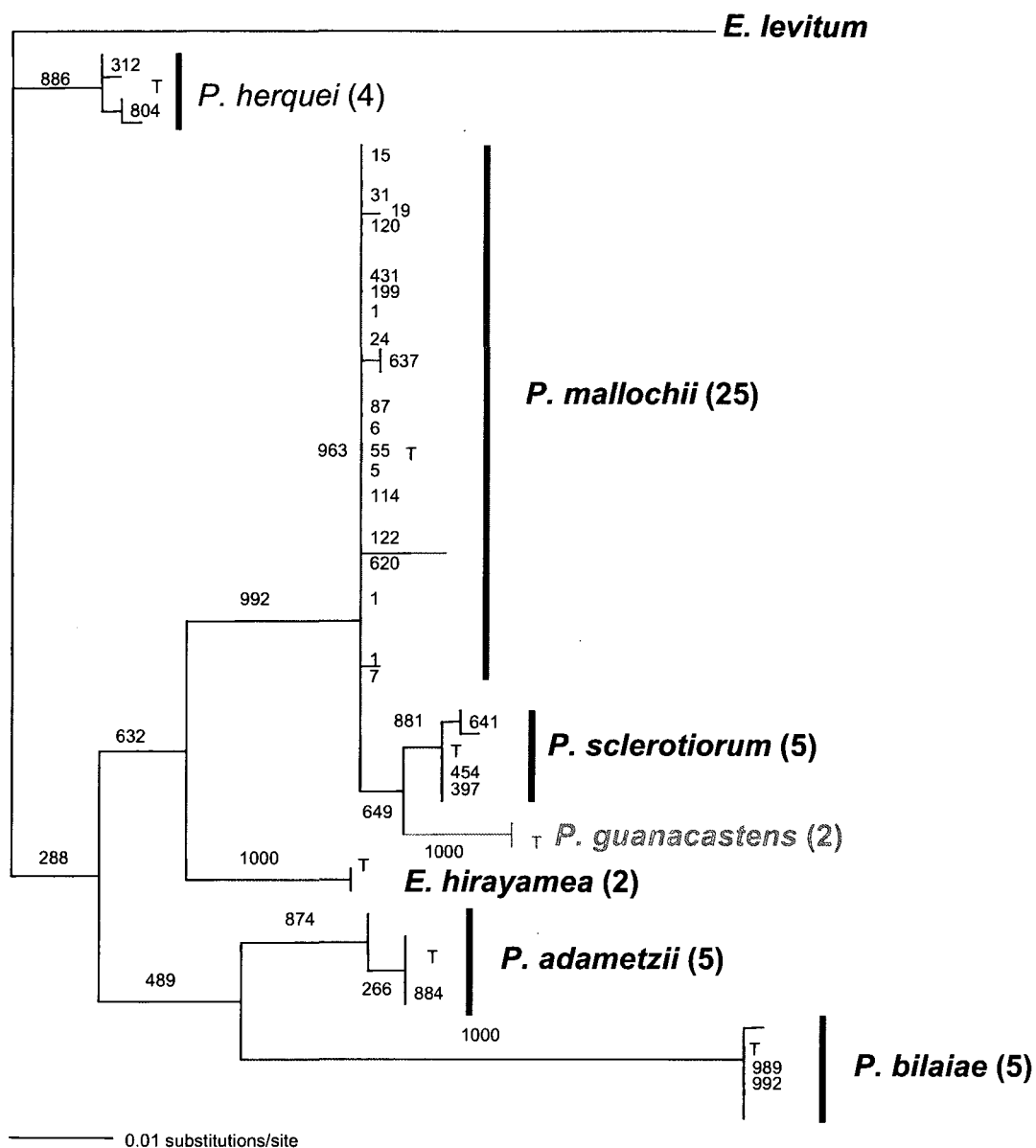


Figure 2.5: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned ITS sequences. The tree was constructed using the GTR+G nucleotide substitution model; 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

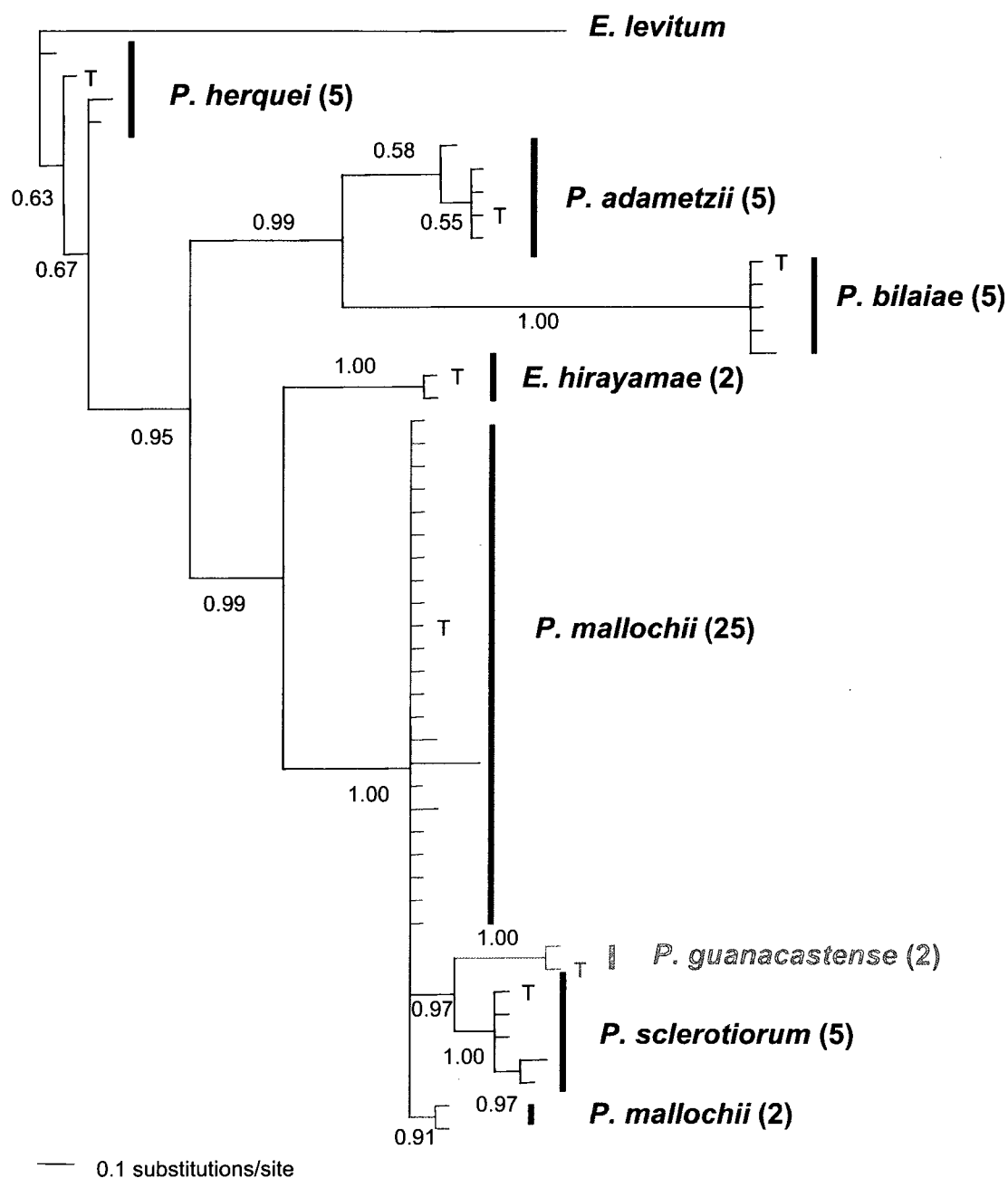


Figure 2.6: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned ITS sequences. Tree was constructed using the GTR+G nucleotide substitution model. Posterior probabilities are shown, the number in parenthesis besides the species name represents the number of strains; T represents the ex-type strain.

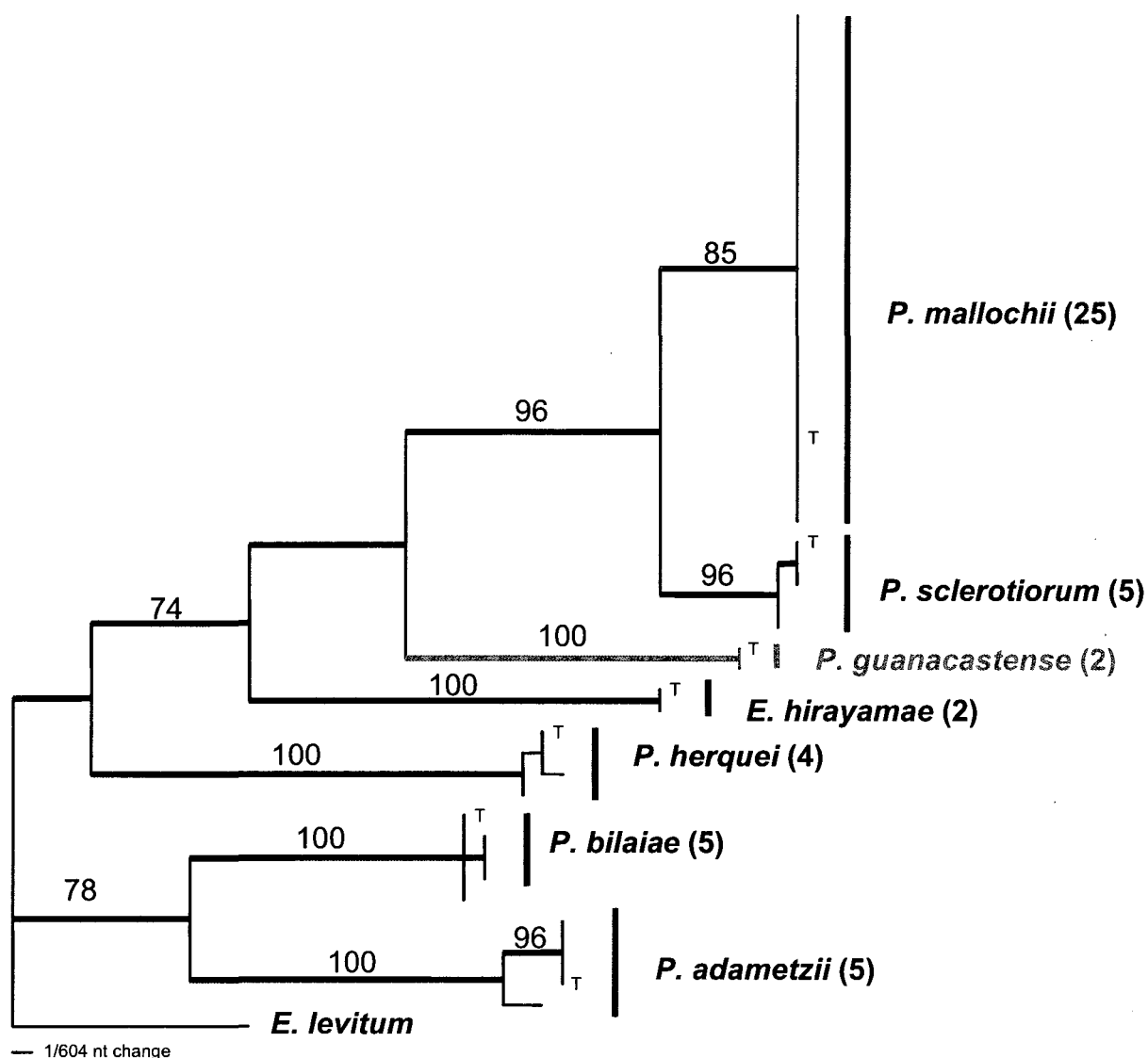


Figure 2.7: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *Cox1* sequences. One out of eight most parsimonious trees (L=0, CI=0.692, RI=0.932, RC=0.645, HI=0.308). A heuristic search and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

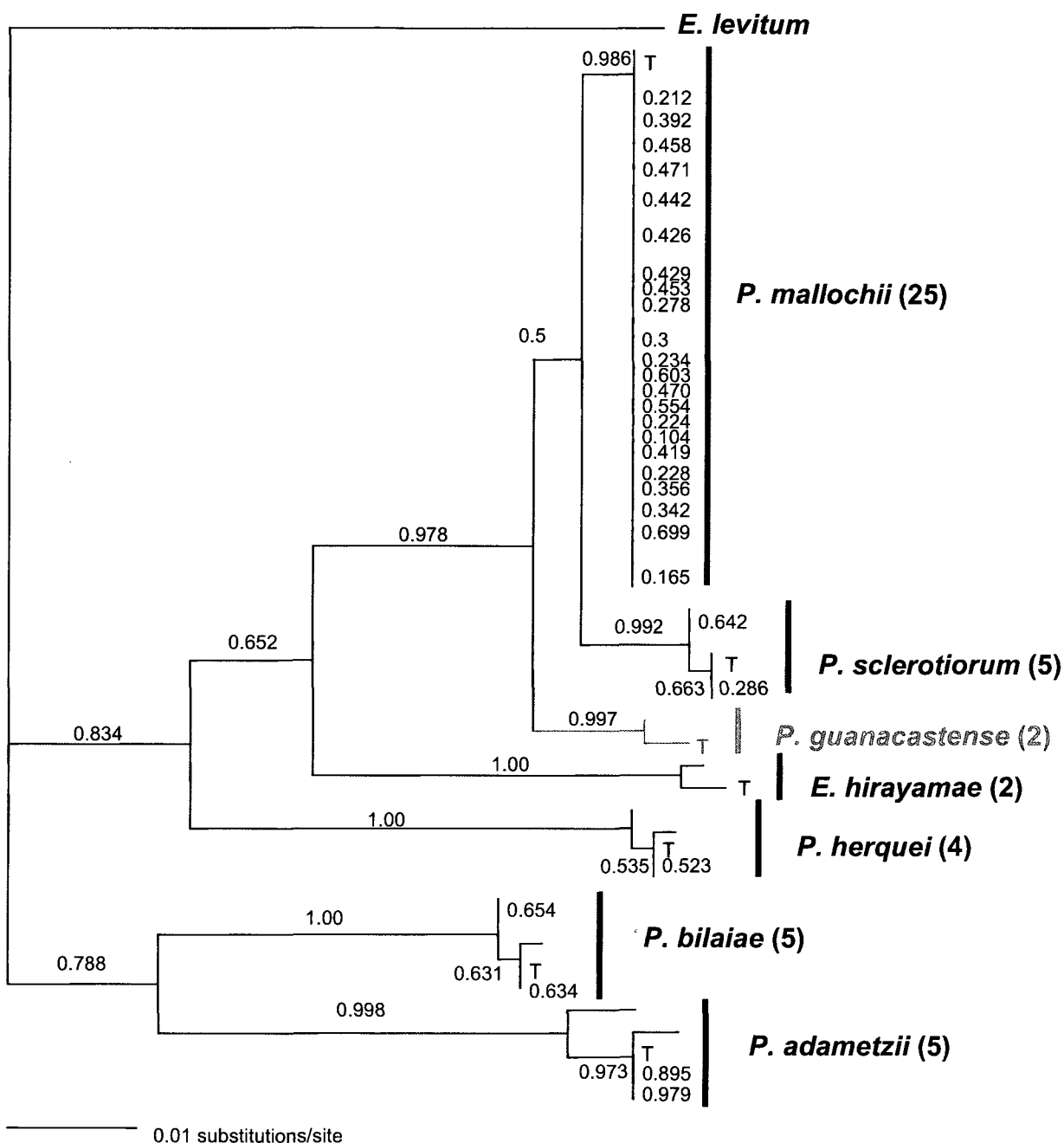


Figure 2.8: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *Cox1* sequences. The tree was constructed using the GTR+G nucleotide substitution model; 1000 bootstrap replicates were performed. The number besides the species name represents the number of strains; T represents the ex-type strain.

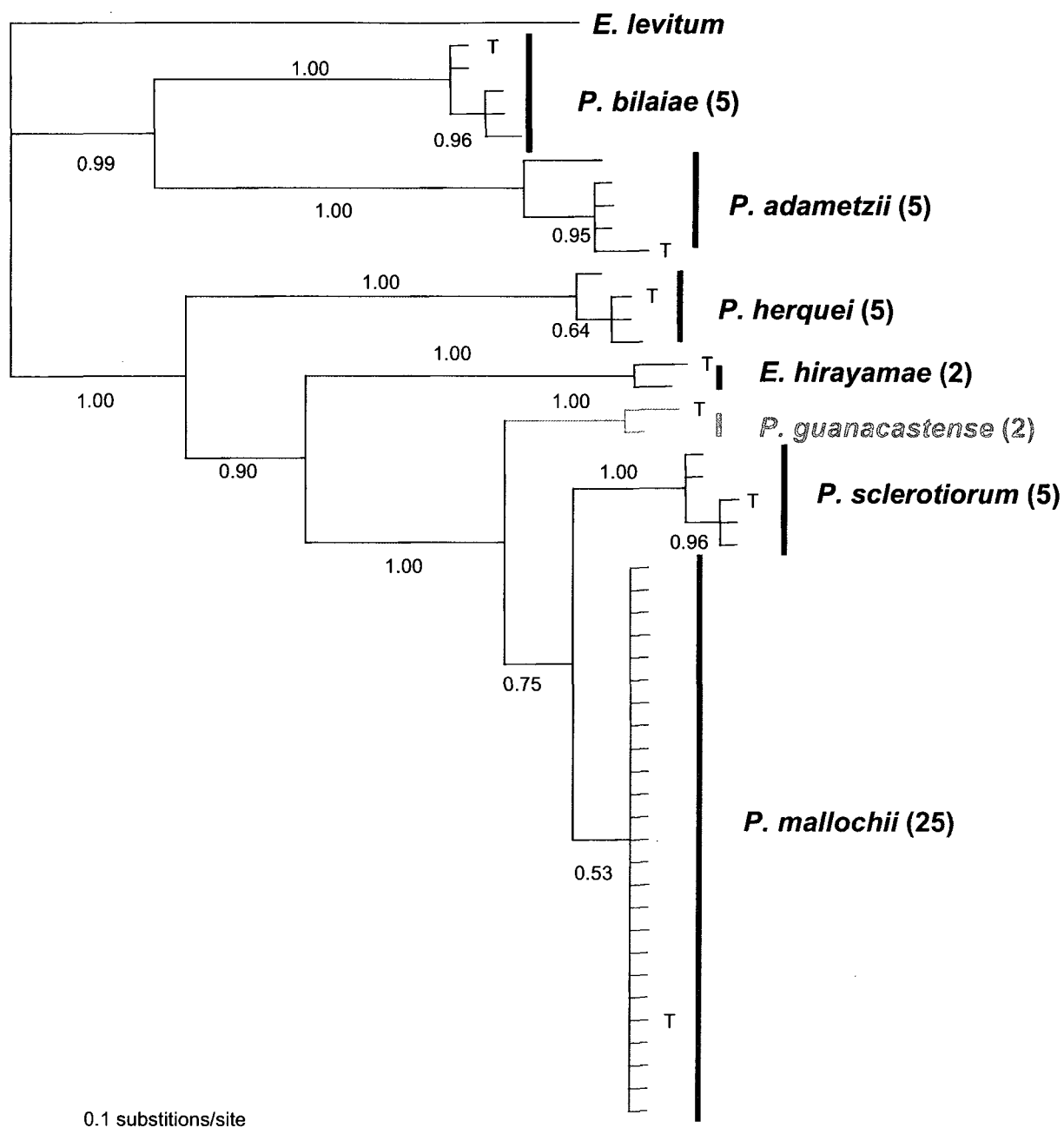


Figure 2.9: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *Cox1* sequences. Tree was constructed using the GTR+G nucleotide substitution model. Posterior probabilities are shown, the number in parenthesis represents the number of strains; T represents ex-type strain.

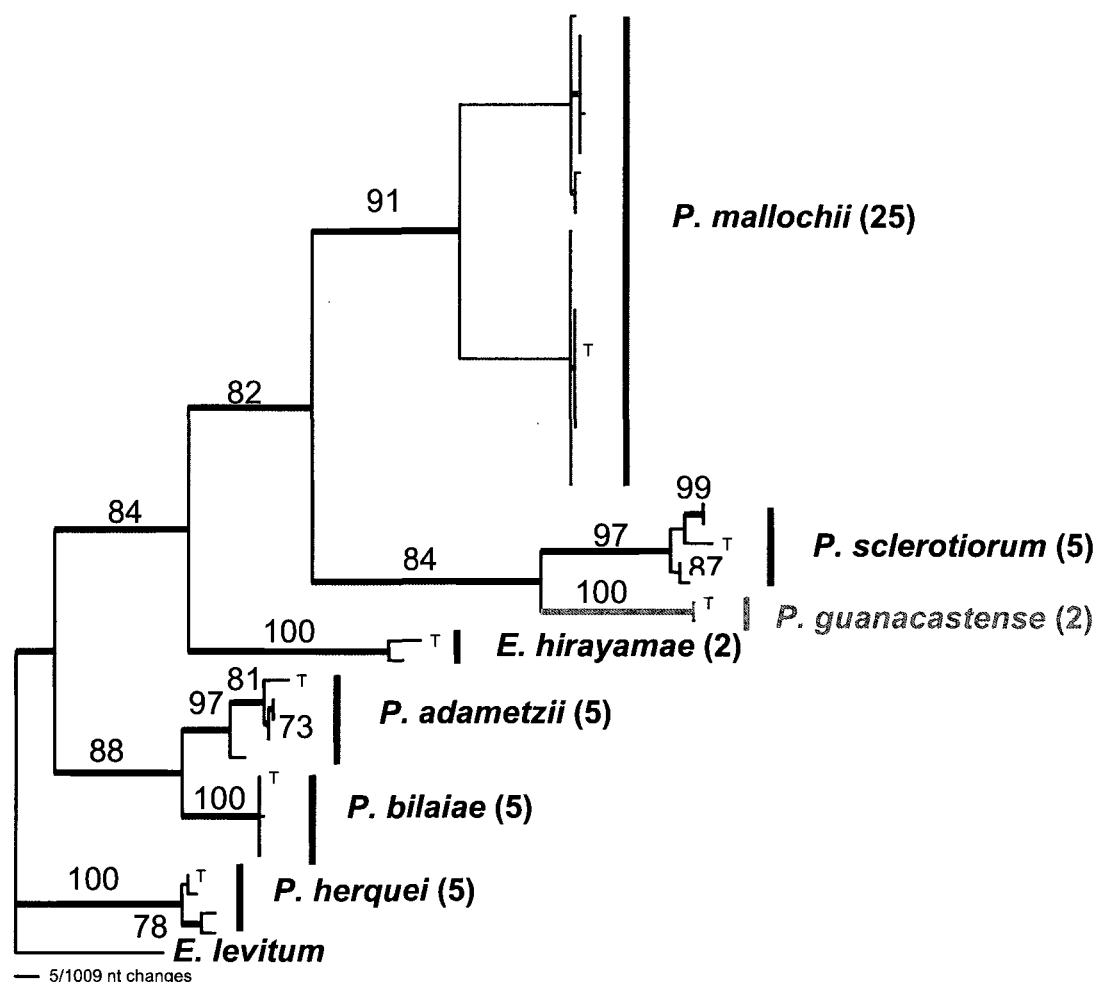


Figure 2.10: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *TEF1-α* sequences. One out of 5000 most parsimonious trees (L=352, CI=0.759, RI=0.915, RC=0.694, HI=0.241). A heuristic search and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

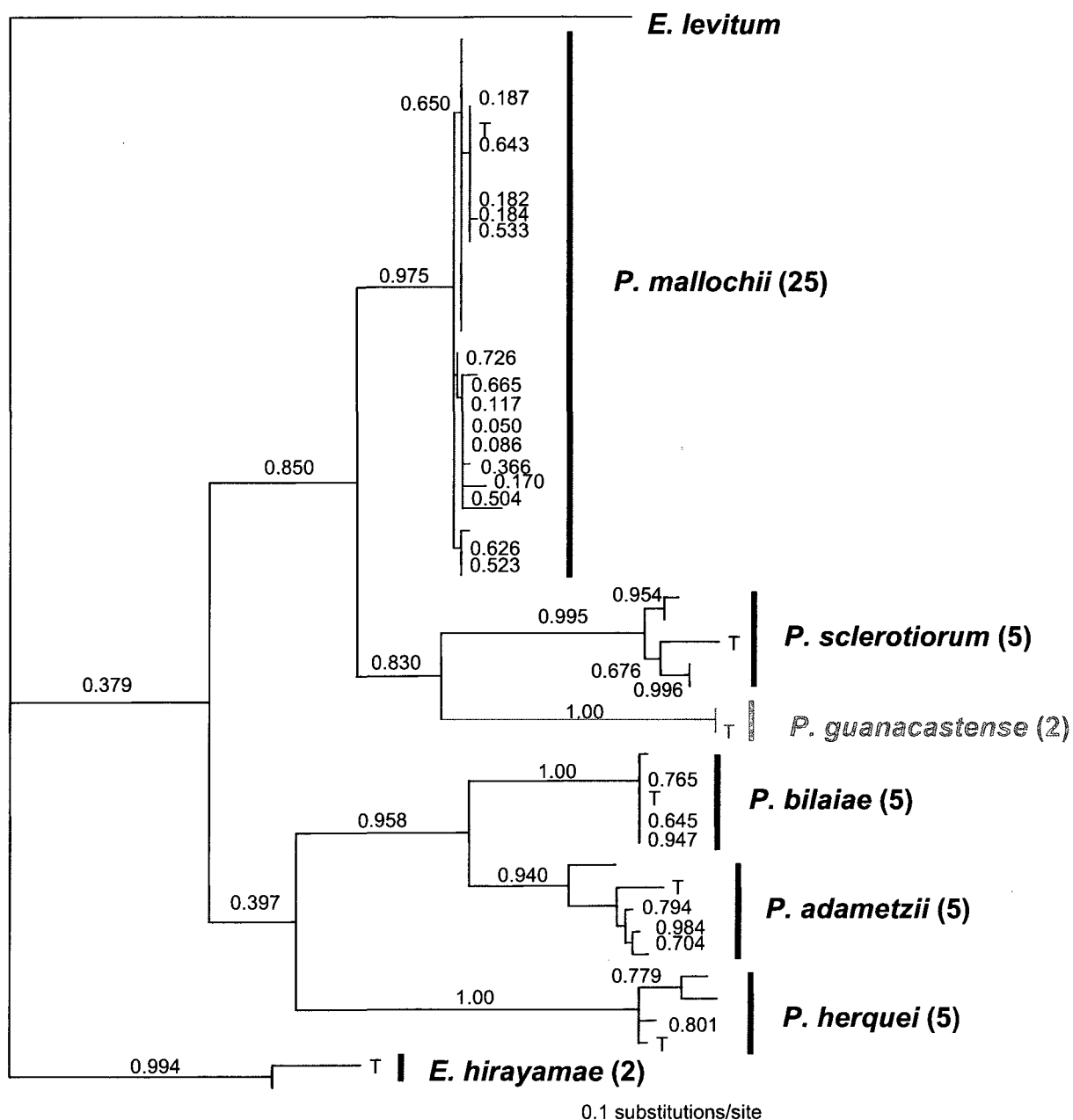


Figure 2.11: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *TEF1-α* sequences. The tree was constructed using the GTR+G nucleotide substitution model; 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

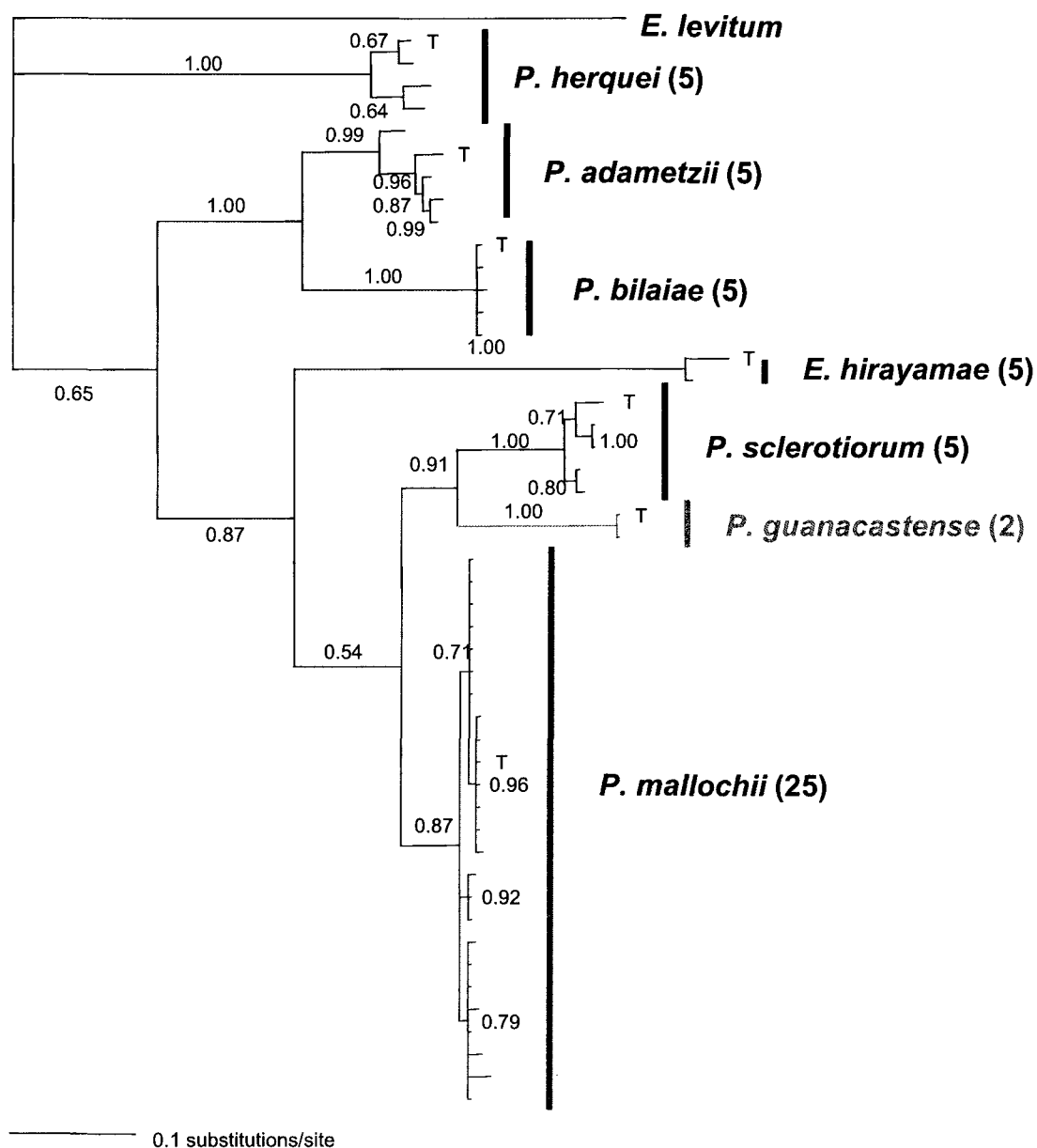


Figure 2.12: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned *TEFI-α* sequences. The tree was constructed using the GTR+G nucleotide substitution model. Posterior probabilities are shown, the number in parenthesis represents the number of strains; T represents the ex-type strain.

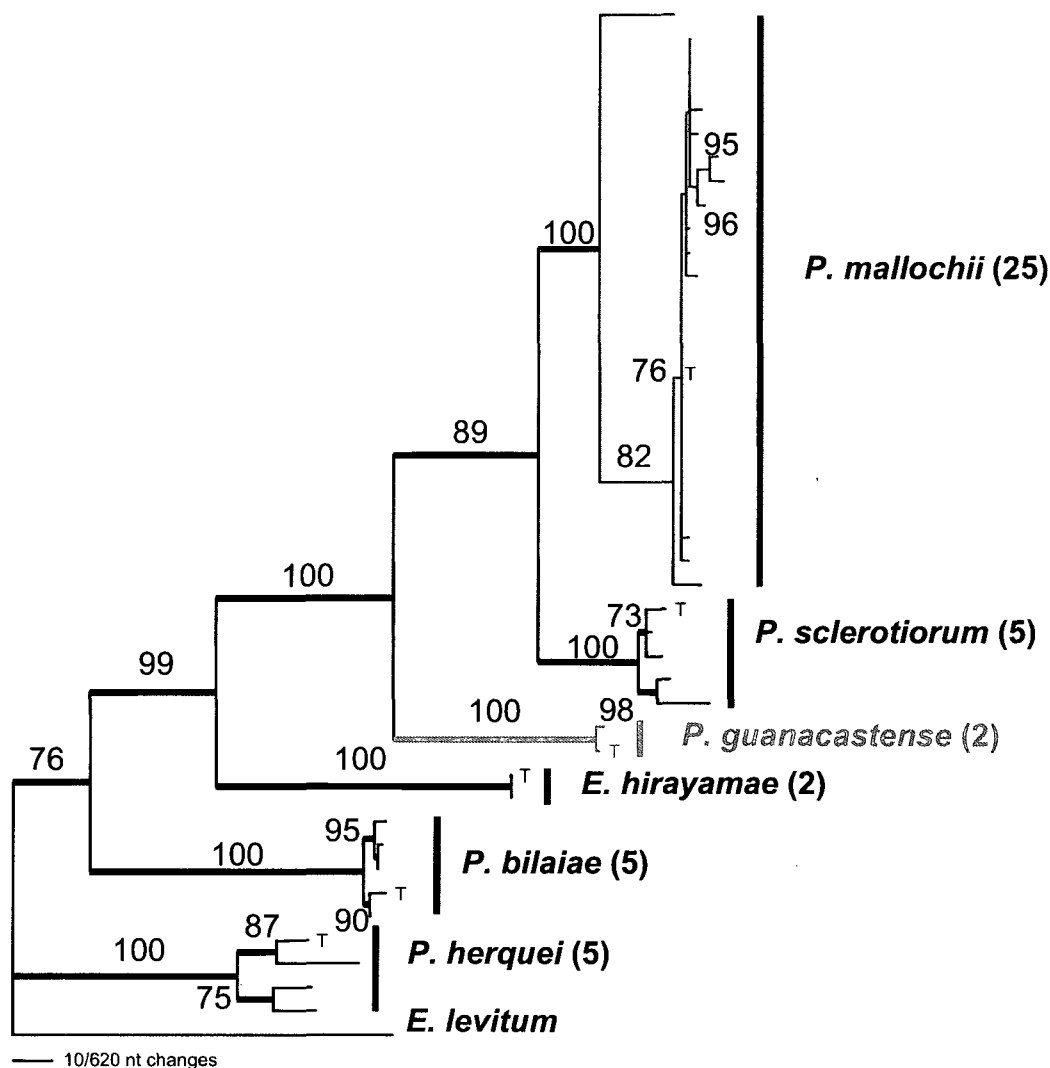


Figure 2: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned CaM sequences. One out of 5000 most parsimonious trees (L=105, CI=0.750, RI=0.930, RC=0.706, HI=0.248). A heuristic search and 1000 bootstrap replicates were performed, bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

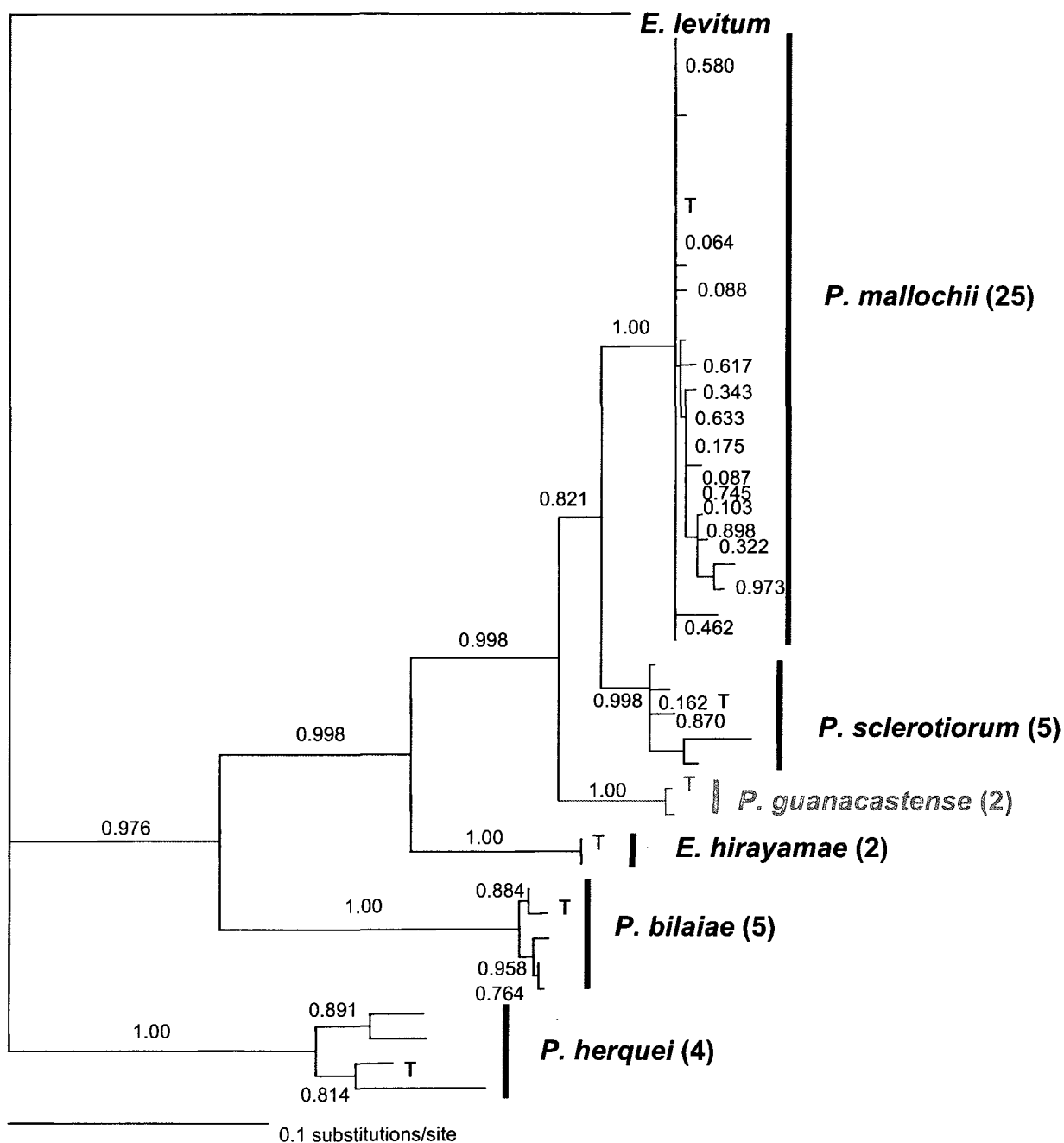


Figure 2.14: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned CaM sequences. The tree was constructed using the GTR+G nucleotide substitution model; 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

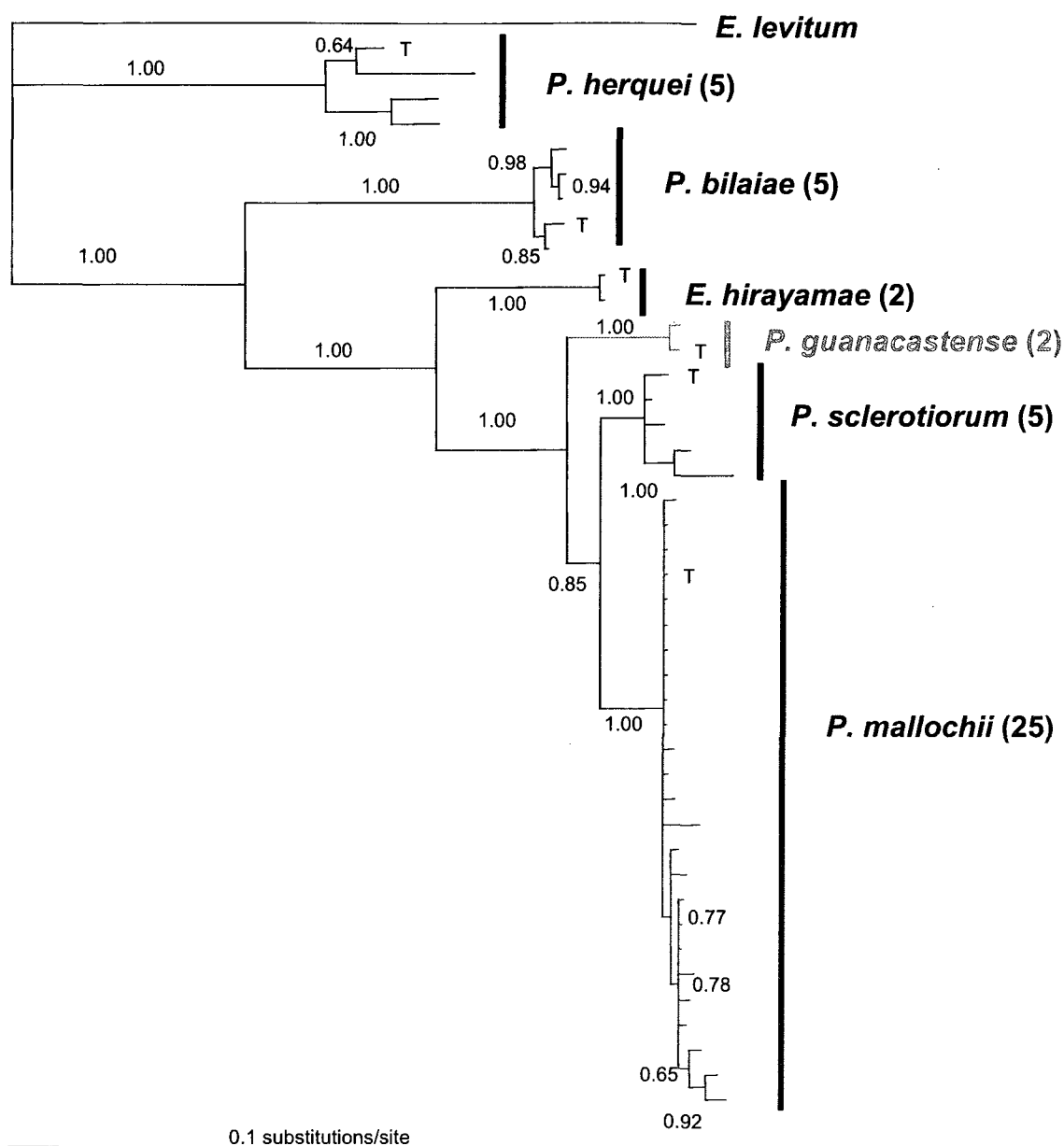


Figure 2.15: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of the new species *P. mallochii* and *P. guanacastense*, based on aligned CaM sequences. The tree was constructed using the GTR+G nucleotide substitution model. Posterior probabilities are shown, the number in parenthesis represents the number of strains; T represents the ex-type strain.

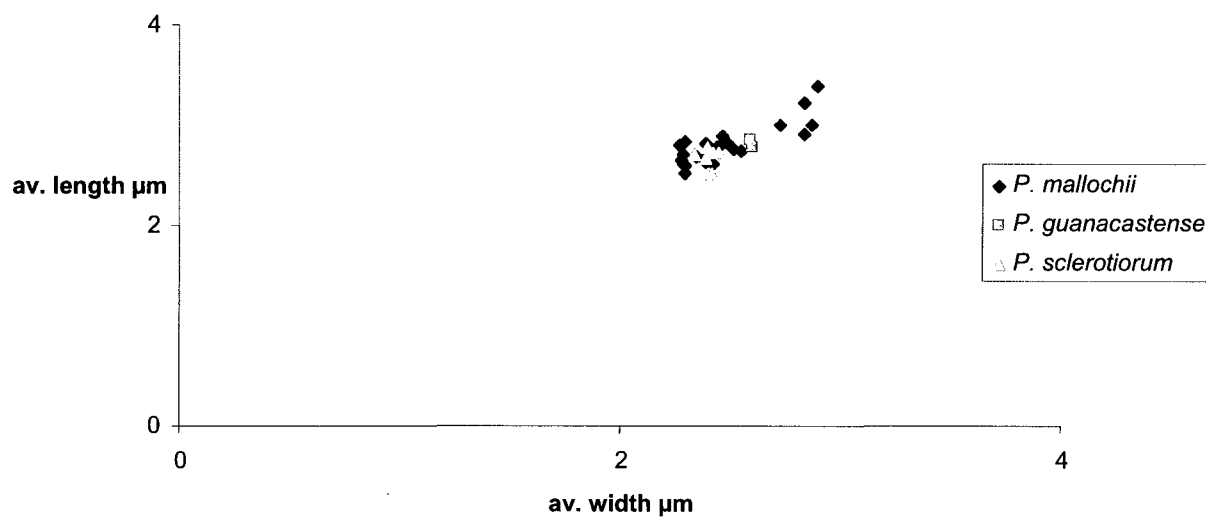


Figure 2.16: Scatter plot of average conidia length to width ratio for *P. sclerotiorum*, *P. mallochii* and *P. guanacastense*.

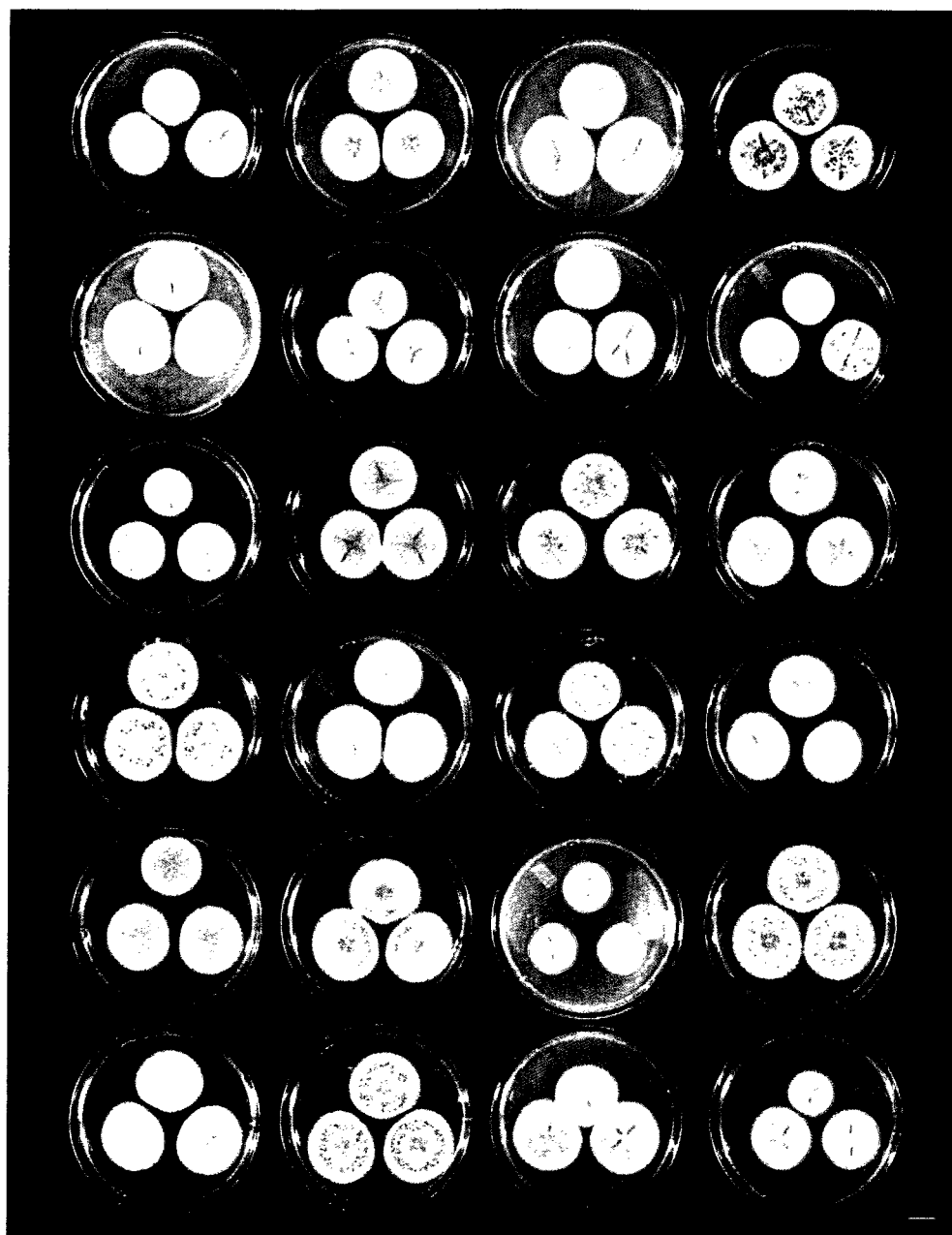


Figure 2.17: Colony obverse of *P. mallochii* strains grown on CYA in the dark at 25°C for 7 d. Rows left to right: DAOM 239918, DAOM 239919, KAS 2606, DAOM 239920, DAOM 239921, KAS 2612, KAS 2615, DAOM 239924, KAS 2630, KAS 3183, DAOM 239917 (ex-type), DAOM 239924, KAS 3186, KAS 3187, DAOM 239925, DAOM 239925, KAS 3190, KAS 3191, DAOM 239926, KAS 3193, DAOM 239927, DAOM 239928, DAOM 239929, KAS 2601. Scale bar = 10 mm.

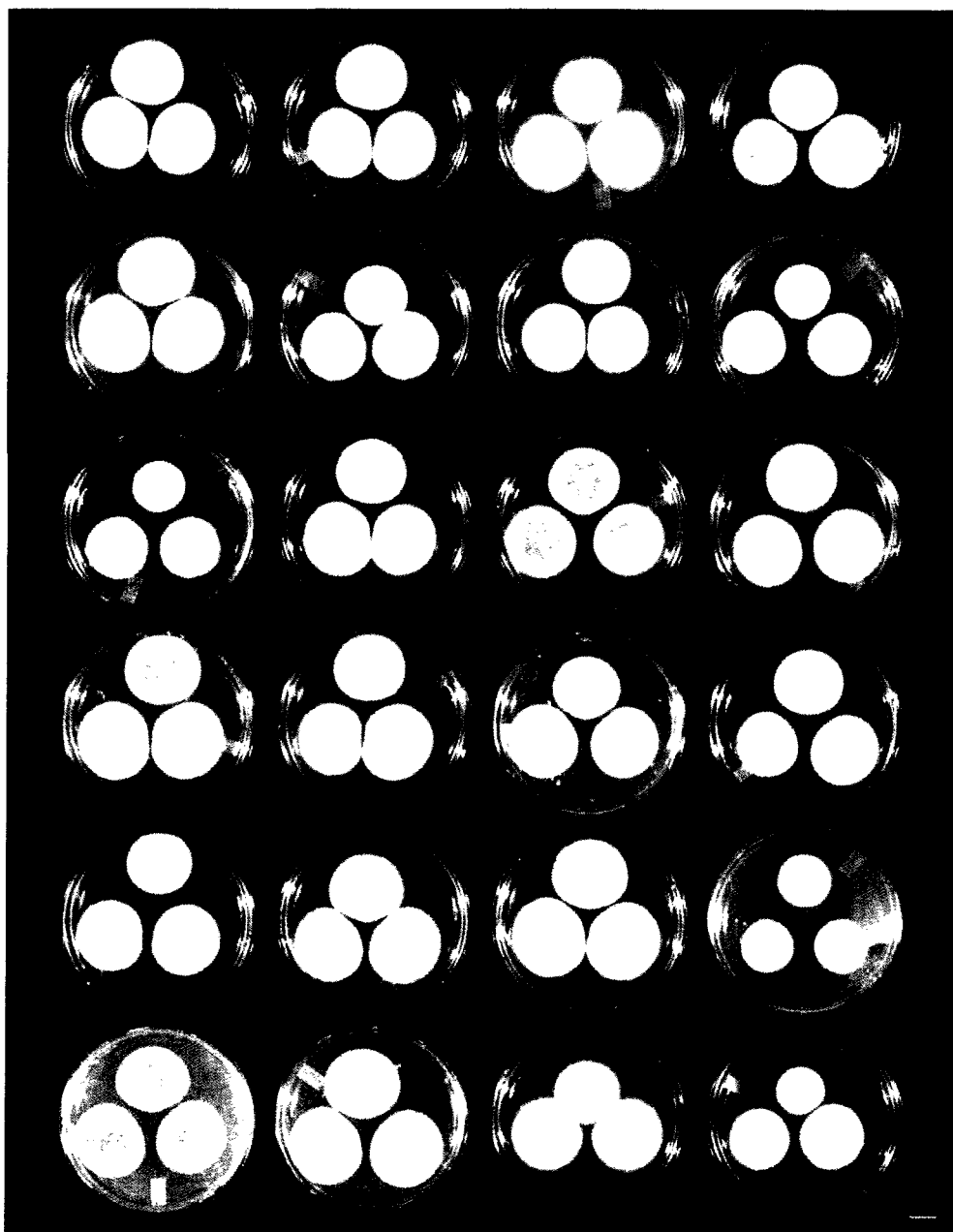


Figure 2.18: Colony reverse of *P. mallochii* strains grown on CYA in the dark at 25°C for 7 d. Rows left to right: DAOM 239918, DAOM 239919, KAS 2606, DAOM 239920, DAOM 239921, KAS 2612, KAS 2615, DAOM 239924, KAS 2630, KAS 3183, DAOM 239917 (ex-type), DAOM 239924, KAS 3186, KAS 3187, DAOM 239925, DAOM 239925, KAS 3190, KAS 3191, DAOM 239926, KAS 3193, DAOM 239927, DAOM 239928, DAOM 239929, KAS 2601. Scale bar = 10 mm.

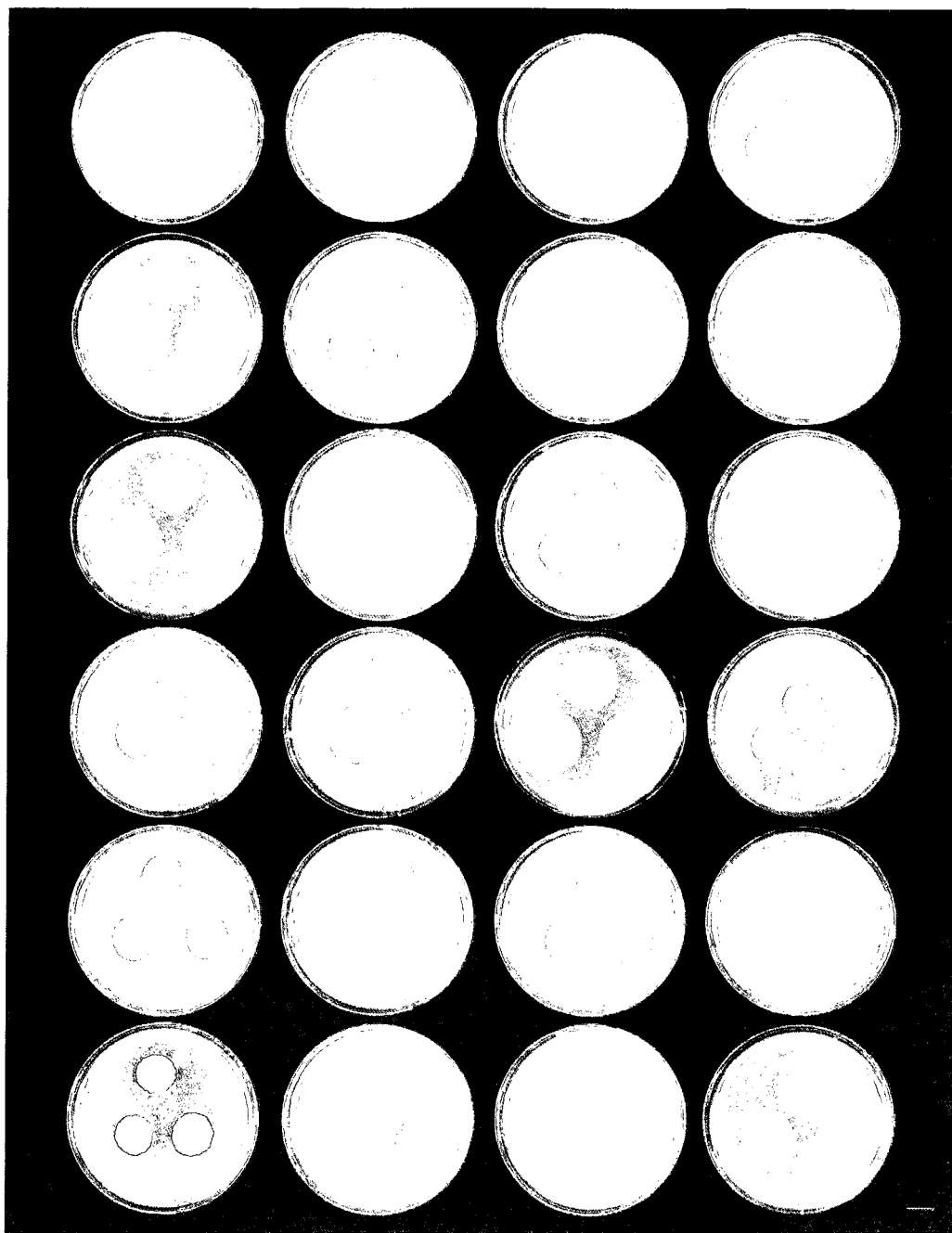


Figure 2.19: Colony obverse of *P. mallochii* strains grown on MEA in the dark at 25°C for 7 d. Rows left to right: DAOM 239918, DAOM 239919, KAS 2606, DAOM 239920, DAOM 239921, KAS 2612, KAS 2615, DAOM 239924, KAS 2630, KAS 3183, DAOM 239917 (ex-type), DAOM 239924, KAS 3186, KAS 3187, DAOM 239925, DAOM 239925, KAS 3190, KAS 3191, DAOM 239926, KAS 3193, DAOM 239927, DAOM 239928, DAOM 239929, KAS 2601. Scale bar = 10 mm.

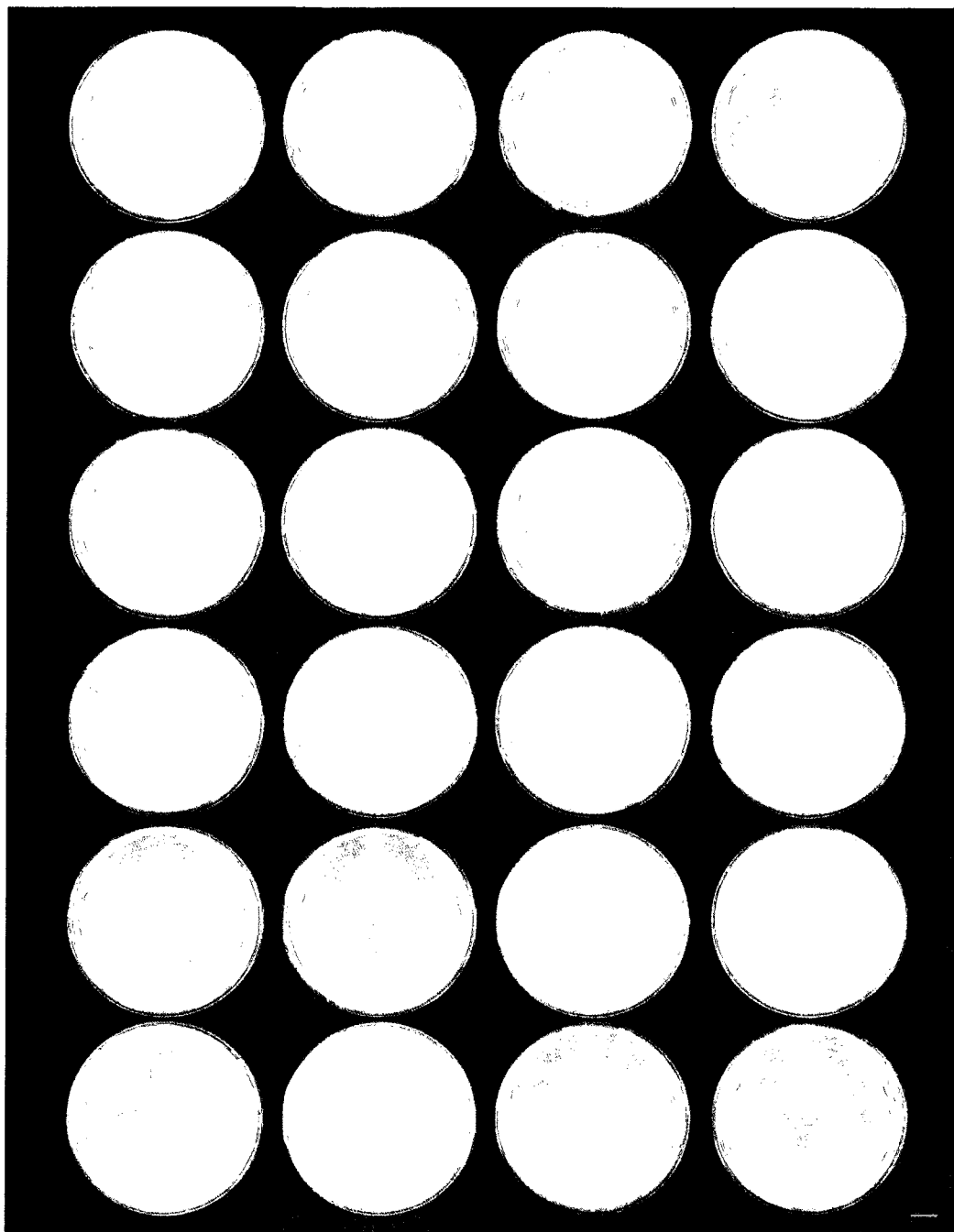


Figure 2.20: Colony reverse of the *P. mallochii* strains grown on MEA in the dark at 25°C for 7 d. Rows left to right: DAOM 239918, DAOM 239919, KAS 2606, DAOM 239920, DAOM 239921, KAS 2612, KAS 2615, DAOM 239924, KAS 2630, KAS 3183, DAOM 239917 (ex-type), DAOM 239924, KAS 3186, KAS 3187, DAOM 239925, DAOM 239925, KAS 3190, KAS 3191, DAOM 239926, KAS 3193, DAOM 239927, DAOM 239928, DAOM 239929, KAS 2601. Scale bar = 10 mm.

Figure 2.21: Differential interference contrast microscopic photographs of conidiophores (A–E) and conidia (F) of *P. mallochii* ex-type strain. Scale = 10 μm .

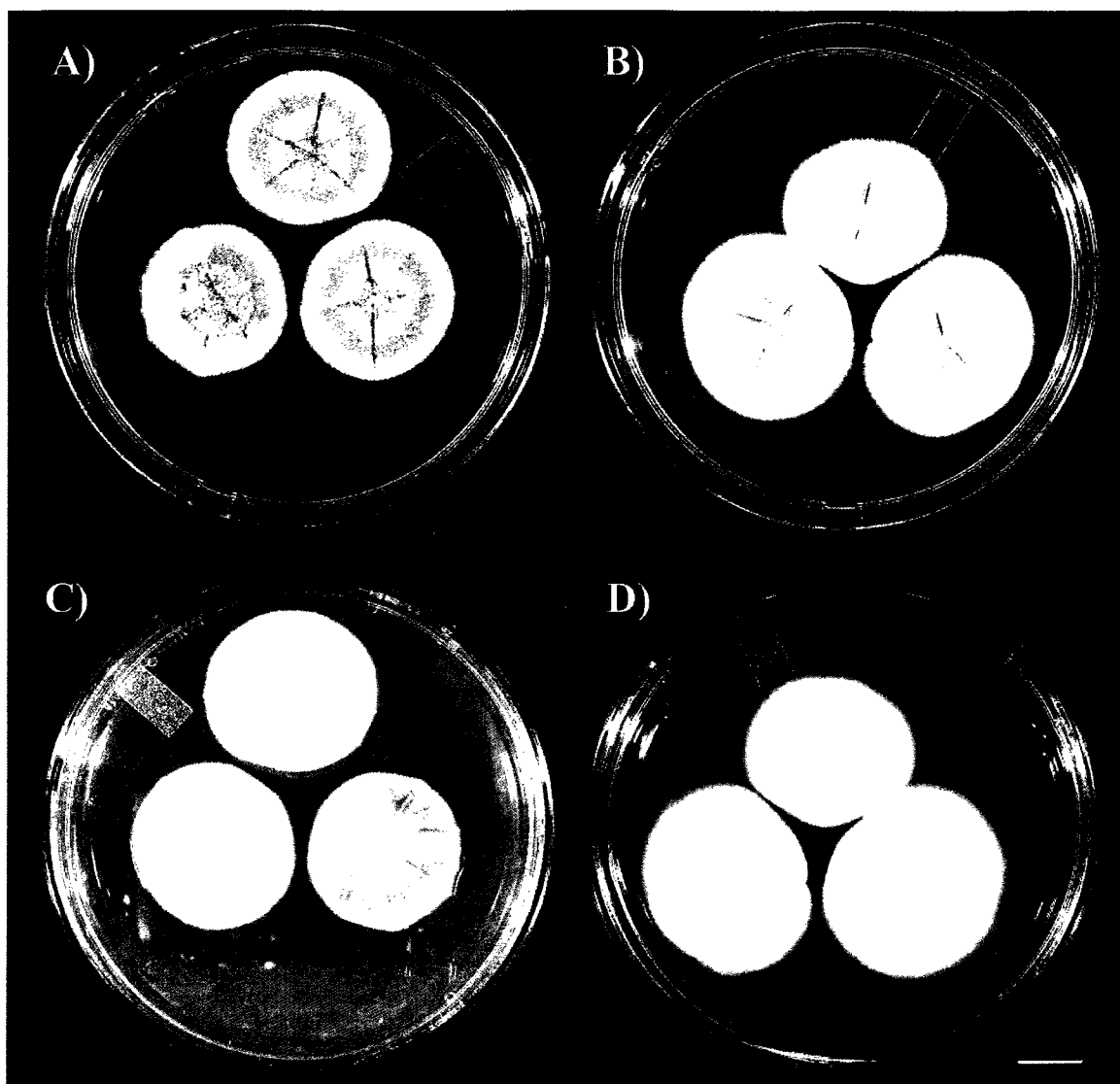


Figure 2.22: *Penicillium guanacastense* strains on CYA grown for 7 d at 25°C in the dark. A–B) Left to right: DAOM 239912 (ex-type) and DAOM 2399 obverse. C–D) Left to right: DAOM 239912 and DAOM 2399 reverse. Scale bar = 10 mm.

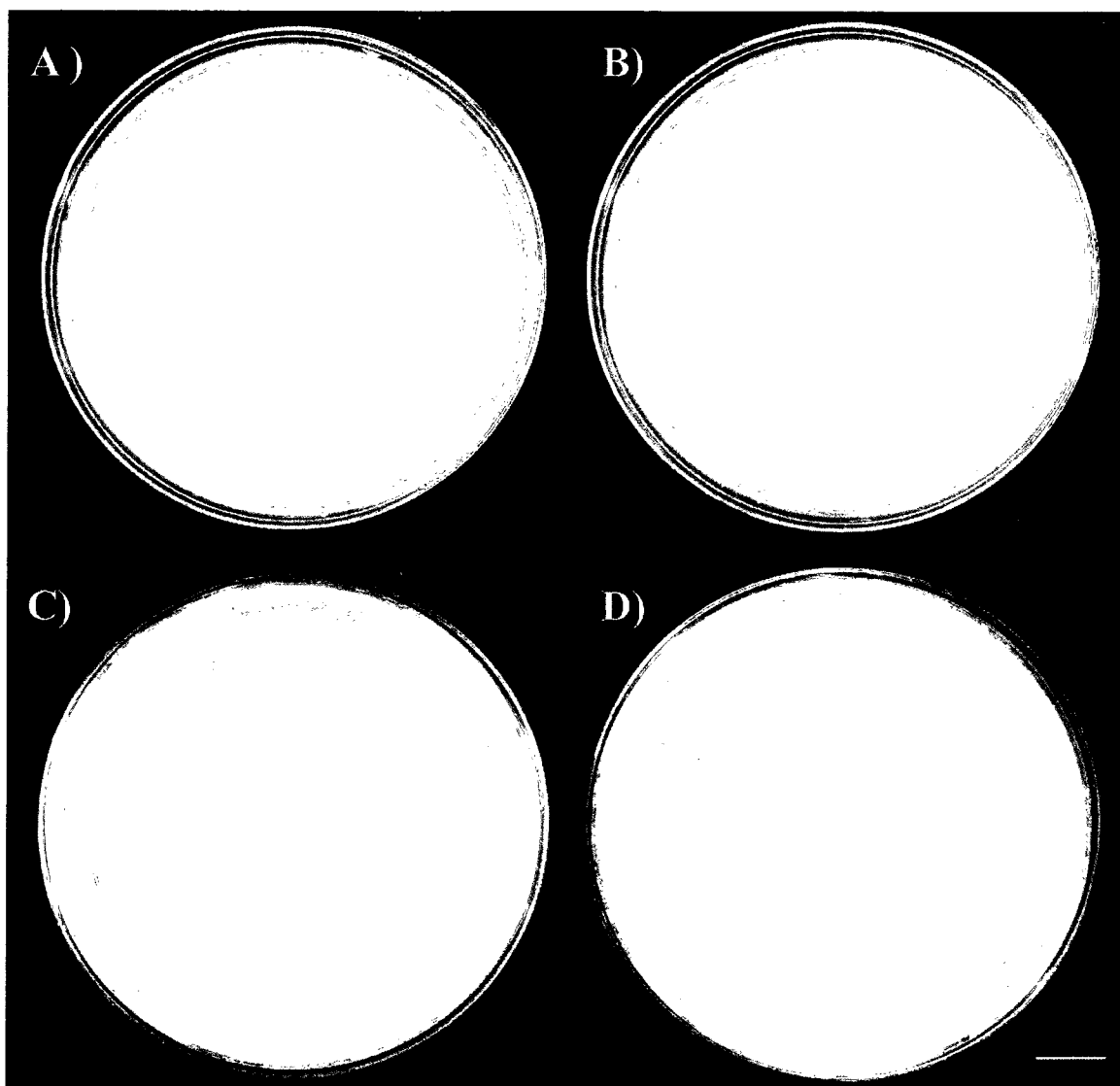


Figure 2.23: *Penicillium guanacastense* strains on MEA grown for 7 d at 25°C in the dark. A–B) Left to right: DAOM 239912 (ex-type) and DAOM 2399 obverse. C–D) Left to right: DAOM 239912 and DAOM 2399 reverse. Scale bar = 10 mm.

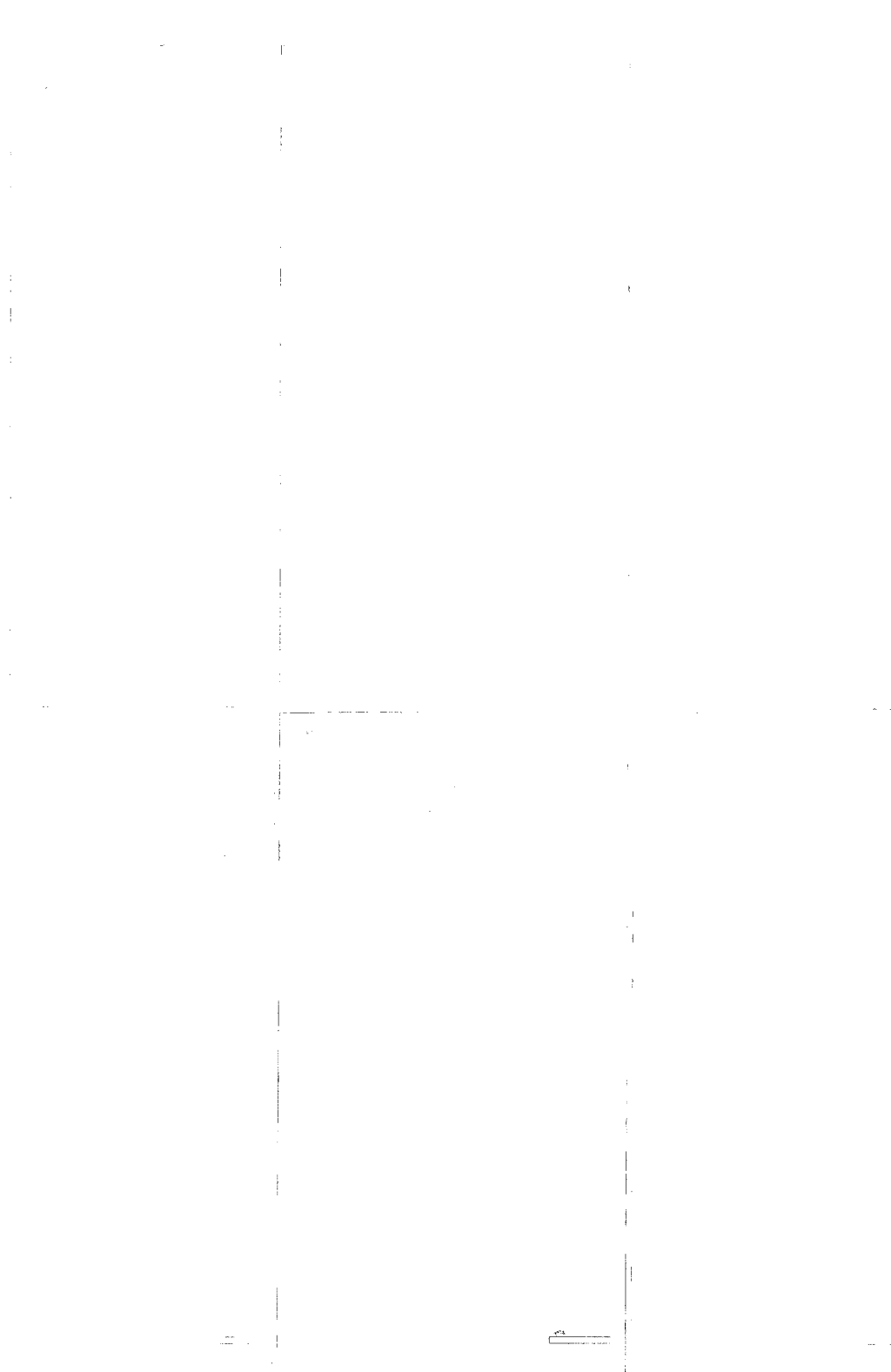


Figure 2.24: Differential interference contrast microscopic photographs of conidiophores (A–B) and conidia (D) of *P. guanacastense* ex-type strain. Scale = 10 μm .

Chapter 3: A Taxonomic and Phylogenetic Revision of the *Penicillium sclerotiorum* complex

Karol G. Rivera and Keith A. Seifert

3.1 Abstract

Penicillium sclerotiorum is a monoverticillate *Penicillium* with vivid orange to red colony colours and vesiculate conidiophores, which is characterized by the production of sclerotia by some strains. Strains are also known to produce antimicrobial compounds and endothelin antagonists. Multigene phylogenetic analyses with β -tubulin (*BenA*), the nuclear ribosomal internal transcribed spacer (ITS) region, cytochrome c oxidase subunit 1 (*Cox1*), translation elongation factor 1- α (*TEF1- α*) and calmodulin (CaM) of 29 strains revealed the presence of four previously unidentified phylogenetic species closely related to *P. sclerotiorum*. The new species are described and named *P. krugii*, *P. jacksonii*, *P. cainii*, and *P. ciebiessum*. *Penicillium mallochii* and *P. guanacastense*, described in Chapter 2, also form part of this group. All seven species are morphologically similar, but on closer examination, morphological differences are observed in conidial shape, vesicle size and colony colour on different media. The species resolving ability of *Cox1* was compared to the Genealogical Concordance Concept (GCC) recognition criterion. *TEF1- α* and CaM resolved all species in this group. *Cox1* did not resolve *P. mallochii*, *P. krugii* and *P. jacksonii*. According to Stolk and Samson (1983), *P. adametzioides* and *P. multicolor* are synonyms of *P. sclerotiorum*, but multigene phylogenetic analyses, along with morphological examinations, determined that they are distinct species outside of the *P. sclerotiorum* complex.

3.2 Introduction

Penicillium sclerotiorum van Beyma was first isolated from the air in Java, Indonesia, and described by J.F.H. Beyma in 1937. The species epithet reflects the production of sclerotia (singular *sclerotium*; Figure 3.1), which is originally derived from the Greek word *sklērotēs*, which means hardness. Sclerotia are round, compact masses of hardened cells that can remain dormant for long periods until conditions are favourable for survival. Sclerotia are considered immature or vestigial ascomata, and may not be produced in all strains of a species. The development of ascospores can be medium dependant; usually sclerotia producing strains are grown on Oatmeal Agar (OA), and ascoma development may take months. *Penicillium sclerotiorum* has monoverticillate conidiophores, placing it in *Penicillium* subgenus *Aspergilloides* (Pitt 1979a).

In subgenus *Aspergilloides*, *Penicillium sclerotiorum* was placed into section *Aspergilloides* Dierckx series *Glabra* Pitt by Pitt (1979a). Section *Aspergilloides* is characterized by the presence of vesiculate conidiophores. Series *Glabra* is characterized by colony diameters greater than 30 mm in CYA after 7 d at 25°C in the dark. *Penicillium sclerotiorum* is the only member in series *Glabra* that has vivid orange to red colony colours, and is one out of three species in this series to produce sclerotia. The other two species are *P. thomii* K.M. Maire and *P. macrosclerotiorum* L. Wang, X.M. Zhang, W.Y. Zhuang. Stolk and Samson (1983) placed *P. adametzioides* S. Abe ex G. Sm., *P. multicolor* Grigorievá-Manoilová and Poradielová, and *P. implicatum* var. *aureomarginatum* Thom as synonyms of *P. sclerotiorum*.

Secondary metabolites with antibacterial and antifungal activities were reported for some strains of *P. sclerotiorum*; sclerotin (MacCurtin and Reilly 1940),

isochromphilone VI (De Lucca *et al.* 2008), and pencolide (De Lucca *et al.* 2008). Pairet *et al.* (1995) reported that two azapholines produced by *P. sclerotiorum* are endothelin antagonists of endothelin-A and endothelin-B receptors. Endothelins are vasoconstriction peptides that have been implicated in hypertension, heart failure, renal failure, pulmonary hypertension, ischemia, and cerebral vasospasms.

Penicillium sclerotiorum strains have been isolated from many parts of the world, such as Indonesia, China, Florida, USA, India, Puerto Rico, South Africa, Mexico, Vietnam and Canada. Apparently it has a world wide distribution, but it has been reported infrequently (Pitt 1979a; Ramirez 1980). Isolates are commonly found in soil, and occasionally in fabrics (Pitt 1979a). Air sampling revealed higher concentrations of *P. sclerotiorum* in outdoors than indoor environments (Sawane and Saoji 2004). Furthermore, the species has been isolated from dust samples from homes (Vesper *et al.* 2005), diseased grape berries and stems (De Lucca *et al.* 2008), and is believed to be a coffee berry endophyte of *Coffea arabica* (Vega *et al.* 2006).

Penicillium sclerotiorum is part of Peterson's (2000) Group 3 of *Penicillium*, which include species from subgenus *Aspergilloides* and *Furcatum* Pitt: *P. herquei* Bainer and Sartory, *P. adametzii* Zalesky, *P. sclerotiorum*, *P. bilaiae* Chaleb., and *E. hirayamae* Udagawa. Group 3 species also includes the newly described species, *P. mallochii* Rivera, Urb and Seifert and *P. guanacastense* Rivera, Urb and Seifert, from Chapter 2. All species, except *P. herquei*, have monoverticillate conidiophores and are part of *Penicillium* subgenus *Aspergilloides*. *Penicillium herquei* has biverticillate conidiophores and is part of *Penicillium* subgenus *Furcatum* ser. *Furcatum* Pitt (Pitt 1979a).

Penicillium mallochii Rivera, Urb and Seifert and *P. guanacastense* Rivera, Urb and Seifert, two species isolated from caterpillars from Costa Rica, conformed to the morphological species concept of *P. sclerotiorum*. The two species are distinct according to the GCC recognition criterion as demonstrated by gene genealogies with β -tubulin (*BenA*), cytochrome c oxidase subunit 1 (*Cox1*), the internal transcriber spacer (ITS) region, translation elongation factor 1- α (*TEF1- α*), and calmodulin (CaM). In this study, 29 strains identified as *P. sclerotiorum* were obtained to determine the existence of more phylogenetic species. Four additional phylogenetic species conforming to the GCC recognition criterion were identified and are described as new species in this chapter; *P. krugii*, *P. jacksonii*, *P. cainii* and *P. ciebiessum*. In this thesis *P. krugii*, *P. jacksonii*, *P. cainii*, *P. ciebiessum*, *P. mallochii*, *P. guanacastense*, and *P. sclerotiorum* will be referred to as the *P. sclerotiorum* complex. The species resolving ability of *Cox1* was compared to the GCC recognition criterion, and a taxonomic and phylogenetic revision of the *P. sclerotiorum* complex is provided.

3.3 Materials and Methods

Strains identified as *P. sclerotiorum* were obtained from several sources including the Centraalbureau voor Schimmelcultures (CBS), the Northern Regional Research Laboratory (NRRL), and the personal research collections of Keith Seifert (Ottawa, ON, Canada), David Malloch (Toronto, ON, Canada), and Robert A. Samson (Utrecht, Netherlands). Some of the strains studied in this chapter were deposited in Canadian Collection of Fungal Cultures (CCFC). Strains not deposited in the CCFC were deposited in the personal research collection of Keith A. Seifert. Refer to Table 3.1 for a list of all strains used in this study.

Strains from CBS and NRRL were revived from freeze dried vials by resuspending in ddH₂O for two hours and then plating onto Malt Extract Agar (MEA; Pitt 1979a; refer to Appendix 1 for medium recipe). Strains from the David Malloch collection were revived from slants preserved in mineral oil by plating on MEA. Strains from the Robert A. Samson collection were obtained as living slants on MEA medium. All strains were stored at 4°C and –80°C for future use, except for the strains from the Keith A. Seifert Collection which were already stored in water and 10% glycerol at 4°C and –80°C.

Several attempts were made to isolate strains of the *P. sclerotiorum* complex by treating soil with ethanol and heat (65°C) to select for sclerotia producing fungi. Soils were also sprinkled and diluted with ddH₂O on MEA and Dichloran 18% Glycerol Agar (DG-18). DG-18 is a selective medium that slows the growth of fast growing fungi like *Rhizopus* species (Samson *et al.* 2004). Soil samples originated from the Agriculture and Agri-Food Canada Central Experimental Farm, Ottawa, Ontario, Canada. Some *P. sclerotiorum* strains (DAOM 239931 and DAOM 239932) and all *P. krugii* strains were isolated from ethanol treated soils from Australia (Houbraken, pers. comm.). I sampled 20 homes, in addition to the K.W. Neatby Building in Agriculture and Agri-Food Canada building, in Ottawa with a volumetric portable air sampler using MEA or DG-18 plates for *P. sclerotiorum* isolates. No strains of *P. sclerotiorum* were isolated.

3.3.1 Morphological Analyses

All strains were 3-point inoculated onto MEA, Czapek's Yeast Agar (CYA; Pitt, 1973), Czapek's Agar (CZ; Raper and Thom, 1949), Yeast Extract Sucrose Agar (YES; Filtenborg *et al.* 1990), Oatmeal Agar (OA) and Creatine Ammonia Agar (CREA;

Frisvad 1993) (refer to Appendix 1 for media recipes). Plates were then incubated in the dark at 25°C for 7 days. Strains were grown on MEA and CYA for colony species characterization, but only colonies grown on MEA were used for microscopic species characterization. CZ was used to determine sporulation and growth in the absence of ammonia. YES was used to stimulate colony pigmentation by enhancing secondary metabolite production. OA was used to stimulate the development of sclerotia and ascomata. CREA was used to determine organic acid production. Colony measurements and descriptions were taken in all media for *P. sclerotiorum*, *P. krugii*, *P. jacksoni*, *P. cainii*, and *P. ciebiessum*. Colony photographs were taken using a copy stand and a Nikon Coolpix P5000 camera under incandescence lighting conditions.

Microscopic examinations were performed on an Olympus BX 50 light microscope on colonies grown on MEA mounted in lactic acid. Microscopic photographs and character measurements (conidia, phialide, stipe, branch, vesicle, sclerotia, sclerotia cells) were taken with an Evolution MP Media Cybernetics Camera with the aid of the digital analyzing software Image-Pro Plus v6 (Media Cybernetics, MD, U.S.A.). Ten manual measurements for all characters were made, with the exception of conidia where 25 automated measurements were made for each strain.

2.3.2. Molecular and Phylogenetic Analyses

Genomic DNA was extracted for all 29 strains using the MoBio DNA Extraction kit (Montreal, Canada) following manufacturer's protocol from strains grown on MEA or CYA. *BenA* was amplified and sequenced with primers Bt2a and Bt2b (Glass and Donaldson 1995), ITS with primers ITS1 and ITS4 (White *et al.* 1990), *Cox1* with primers PF and AR (Seifert *et al.* 2007), *TEF1- α* with primers EF1c and EF6 (Peterson

et al. 2004), and CaM was amplified with primers CMD5 and CMD6 (Hong *et al.* 2006). Refer to Appendix 2 for primer sequences. PCR and sequencing reactions were performed in a Genius (Techne, Duxford, Cambridge), TGradient (MBI, Montreal Canada) or TGradient 3000 (MBI, Montreal, Canada) following the thermocycler parameters described in Chapter 2. Consensus sequences were assembled using the DNA sequence assembly software Sequencher v 4.8 (Genes Codes Corporation, MI, USA) and SeqMan in the LASERGENE package v. 8 (DNASTAR Inc., Madison, WI, USA).

As previously mentioned in Chapter 2, *P. sclerotiorum* is part of Group 3 of the six *Penicillium* groups described by Peterson (2000). Gene sequences obtained for Group 3 species, along with sequences obtained from six strains of *P. mallochii* and two strains of *P. guanacastense*, were included in the phylogenetic analyses. Alignments and maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI) analyses were performed following the procedures described in chapter two.

A partition homogeneity test (PHT) was performed in PAUP v. 4 (Swofford 2002) using all genes. Missing CaM sequences for *P. adamatzii* strains and missing *TEF1- α* sequences for strains DAOM 239916 and CBS 426.65 were replaced by N's. Parsimony parameters were set to TBR, 1000 replicates, 10 trees saved per replicate, and maxtrees were set to 5000.

3.4 Results

Multigene phylogenetic analyses with *BenA*, ITS, *Cox1*, *TEF1- α* and CaM revealed that strains previously identified as *P. sclerotiorum* by other researchers comprise a species complex. The results were used to determine the monophyly and the phylogenetic relationships of the species in the complex. The complex includes *P.*

sclerotiorum, the newly described species in this chapter, *P. krugii*, *P. jacksonii*, *P. cainii* and *P. ciebiessum*, and the newly described species from Chapter 2, *P. mallochii* and *P. guanacastense*. The morphological species descriptions for *P. krugii*, *P. jacksonii*, *P. cainii*, *P. ciebiessum* and the revised species description for *P. sclerotiorum* are provided in the Taxonomy section. Comparative colony and microscopic characters of all *P. sclerotiorum* complex species were provided (Table 3.2). Sclerotia and ascoma development were examined in MEA, CYA, CZ, YES, CREA and OA. The morphology of phylogenetically isolated strains that are part of the *P. sclerotiorum* complex, such as CBS 248.65, was also examined. As well, *P. sclerotiorum* strains previously named or identified as *P. adamatzioides* and *P. multicolor* were also examined.

The length of the *BenA* alignment was 565 bp. The nucleotide sequence lengths for the ex-type strains for *P. sclerotiorum*, *P. krugii*, *P. jacksonii*, *P. cainii* and *P. ciebiessum* were 489, 491, 565, 481, and 485 bp. Strong statistical support was observed for *P. jacksonii*, *P. cainii* and *P. ciebiessum* in the MP, ML and BI *BenA* gene trees (Figure 3.2–3.4) with 100% bootstrap support, 1.00 bootstrap support, and a posterior probability of 1.00 for all three species. *Penicillium krugii* strains did not form a coherent monophyletic group, with the exception of four strains, DAOM 239939, DAOM 239940, DAOM 239943, and DAOM 239946. Strong statistical support was observed in the ML and BI trees with 0.89 bootstrap support and a posterior probability of 1.00 for these strains; strong statistical support was not observed in the MP tree. *Penicillium sclerotiorum* strains formed a coherent monophyletic group without strong statistical support in any of the trees.

The length of the ITS alignment was 574 bp. The nucleotide sequence lengths for the ex-type strains of *P. sclerotiorum*, *P. krugii*, *P. jacksoni*, *P. cainii* and *P. ciebiessum* were 573, 531, 569, 577 and 564 bp. In the MP and ML ITS trees (Figure 3.5–3.7), *P. krugii*, *P. jacksonii* and *P. mallochii* strains formed coherent monophyletic groups without strong bootstrap support, but were not resolved in the BI tree (Figure 3.8). *Penicillium sclerotiorum*, *P. cainii* and *P. ciebiessum* strains form coherent monophyletic groups without strong bootstrap support in the MP tree, with statistical support greater than 0.8 in the ML and BI trees, with the exception of *P. cainii* in the BI tree, which had a posterior probability of 0.63.

The length of the *Cox1* alignment was 604 bp. The nucleotide sequence lengths for the ex-type strains of *P. sclerotiorum*, *P. krugii*, *P. jacksoni*, *P. cainii* and *P. ciebiessum* were 599, 573, 604, 582 and 597 bp. The MP, ML, and BI trees (Figure 3.8–3.10) did not resolve *P. krugii* and *P. mallochii* strains. Strong statistical support was observed for all trees in *P. sclerotiorum*, *P. jacksonii*, *P. cainii* and *P. ciebiessum*.

The length of the *TEF1- α* alignment was 1009 bp. The nucleotide sequence lengths for the ex-type strains of *P. sclerotiorum*, *P. krugii*, *P. jacksoni*, *P. cainii* and *P. ciebiessum* were 786, 573, 725, 800 and 806 bp. In the *TEF1- α* MP tree (Figure 3.11), *P. krugii* formed a cohesive monophyletic group with no strong bootstrap support. The ML (Figure 3.12) and BI (Figure 3.13) trees did not yield strong statistical support either, with 0.666 bootstrap support and a posterior probability of 0.55. Statistical support for the MP, ML and BI trees was observed for *P. sclerotiorum*, *P. jacksonii*, *P. cainii*, and *P. ciebiessum* (Figures 3.11–3.13) with bootstrap values greater than 80% for the MP tree

(Figure 3.11) and 0.8 for the ML tree (Figure 3.12), and posterior probabilities of 1.00 for the BI tree (Figure 3.13).

The length of the CaM alignment was 620 bp. The nucleotide sequence length in bp for the ex-type strains of for *P. sclerotiorum*, *P. krugii*, *P. jacksonii*, *P. cainii* and *P. ciebiessum* were 517, 521, 521, and 520. The CaM MP tree (Figure 3.14) shows that *P. krugii* forms a cohesive monophyletic group, with the exception of KAS 3479 and DAOM 239922, without strong bootstrap support. This was not observed in the ML (Figure 3.15) and BI (Figure 3.16) trees, where *P. krugii* strains formed cohesive monophyletic groupings, with a bootstrap support of 0.675 and a posterior probability 0.92. For *P. sclerotiorum*, a coherent monophyletic group is observed without strong bootstrap support. In the ML and BI trees, strong statistical support is observed for *P. sclerotiorum*, 0.933 and 0.92. Strong statistical support was observed for *P. jacksonii*, *P. cainii* and *P. ciebiessum* in the MP, ML and BI trees.

The PHT value for the combined data set was 0.0001, suggesting that the data sets are incongruent. PHT values for gene pairs are depicted in Table 3.3. Gene combinations that were congruent were *BenA* and *TEF1- α* , ITS and *TEF1- α* , and *Cox1* and ITS (Table 3.3). All CaM combinations with other genes were not congruent, except for ITS. CaM sequences were excluded from the construction of the phylogeny using MP, ML and BI analyses (Figure 3.17 –3.19). In all trees, *P. mallochii* and *P. krugii* were closely related. In the MP and BI trees, *P. sclerotiorum* and *P. guanacastense* were closely related, without strong statistical support (Figures 3.17 and 3.19). In the ML tree *P. sclerotiorum* grouped with *P. cainii*, *P. ciebiessum*, and *P. jacksonii*, but strong statistical support was not observed (Figure 3.18). In the MP and BI trees, *P. cainii* and

P. ciebiessum were grouped together, in turn grouping with *P. jacksonii*, all had strong statistical support (Figures 3.17 and 3.19).

In all trees, *P. sclerotiorum* strains formed two distinct monophyletic groups, A and B (Figure 3.2–3.16). Strong statistical support was observed in all genes trees, except for *Cox1* which only yielded a strong posterior probability (0.99) for group B in the BI gene tree. In the combined gene trees, strong statistical values were observed for both groups. Group B strains were not treated as a separate species in this chapter. Cultures were sterile and precluded examination of microscopic and colony characters. Morphological variation was observed in group A strains (Figure 3.21), which may correlate with geographic origin (Table 3.1).

All *P. krugii* strains produced sclerotia on all media. Only four *P. sclerotiorum* strains, NRRL 2074, DAOM 239930, DAOM 239931 and DAOM 239932 produced sclerotia on all media. *Penicillium cainii*, *P. ciebiessum*, *P. mallochii* and *P. guanacastense* strains did not produce sclerotia on any medium, including OA. All strains were left for eight months in the dark at 25°C in OA; ascomata were not produced.

Strain CBS 248.65 was also identified as *P. sclerotiorum*. The strain did not group with *P. sclerotiorum* ex-type group or any of the newly described species, but it is part of the *P. sclerotiorum* complex. The strain produced the typical vivid orange to red reverse colony colours described for *P. sclerotiorum* on MEA, CYA, CZ and YES (Figure 3.22). The strain conformed to the GCC recognition criterion and represents a phylogenetic species that is part of the *P. sclerotiorum* complex. The name *P. sclerotiorum* is not accepted for this strain, and the name *Penicillium* sp. was used in this thesis.

Strains CBS 313.59 and DAOM 239916 were initially identified as *P. sclerotiorum*, but individual gene trees (Figures 3.2–3.16) and combined gene trees (Figures 3.17–3.19) revealed that they represent a different species. CBS 313.59, which is sterile, is the ex-type strain of *P. adametzioides*, a synonym of *P. sclerotiorum* according to Stolk and Samson (1983). Combined LSU and ITS data placed the ex-type strain *P. adametzioides* in Peterson's (2000) *Penicillium* Group 3 (Peterson, 2000). *Penicillium adametzioides* strain DAOM 239916 produced an extensive amount of red soluble pigment, yellow aerial mycelium towards the colony centre in CYA and YES, and stipe lengths ranging from 60–90µm (Figure 3.20). Stipe length for the *Penicillium sclerotiorum* ex-type group ranged from 193–393 µm. *Penicillium adametzioides* as a synonym for *P. sclerotiorum* is not accepted in this thesis.

CBS 501.73 is the ex-type strain of *P. multicolor*, which is also a synonym of *P. sclerotiorum* according to Stolk and Samson (1983). Preliminary phylogenetic analyses with *BenA*, ITS, *Cox1*, *TEF1-α*, and CaM determined that the strain CBS 501.73 falls outside Peterson's (2000), with the outgroup. BLAST results from *BenA*, ITS, *TEF1-α* and CaM sequences had 100% sequence similarity to *P. fellutanum*. *Penicillium fellutanum* was not placed in any of Peterson's (2000) six *Penicillium* group, but is the sister taxon, along with *P. charlesii*, to Group 2 of *Penicillium*. The CBS strain did not produce the vivid red to orange colony colours or vesiculate conidiophores usually observed in *P. sclerotiorum* (Figure 3.21). Soluble pigments and exudates were not observed (Figure 3.21). The growth rate was 13–15 mm in CYA, MEA and CZ in comparison to 18–40 mm in *P. sclerotiorum* strains (Figure 3.22), except in YES. *Penicillium multicolor* is not accepted as a synonym for *P. sclerotiorum* in this thesis.

3.5 Taxonomy

Penicillium sclerotiorum van Beyma

Figures 3.23–3.27

Colonies on CYA after 7 days at 25°C: 18–40 mm diam., low and velutinous, sporulation when present dense, when sporulation absent sclerotia present, sclerotia orange, aerial mycelium absent, 8–11 sulcations and 2–3 wrinkles present in some strains, approximately 1 mm deep, conidia when present greenish grey (25–27E2), clear light yellow exudate droplets present in some strains in moderate amounts, soluble pigments present in some strains; reverse orange to reddish yellow (3A7– 4A6), brown (7E4–8) or pale, some strains with darker colours turning orange towards the centre; margin entire.

Colonies on MEA after 7 days at 25°C: 15–32 mm diam., planar, when sporulating strictly velutinous, aerial mycelium absent, conidia grey (25–28D–F1) or greyish green (25–28C2), exudates and soluble pigments not produced; sclerotia present in some strains, orange, in some strains yellow towards the centre; reverse orange (6B7–8), reddish orange (7A–B7–8), reddish yellow (4A6) or pale (1A2); margin entire.

Colonies on CZ after 7 days at 25°C: resembling CYA, but differing in 15–30 mm diam., sclerotia dark or reddish orange, sulcations when present 3–7, exudate droplets when present light yellow to red, reverse colour in some strains yellowish white (1– 4A2–3).

Colonies on YES after 7 days at 25°C: (20–) 33–38 (–44) mm diam., with a raised concentric ring of mycelium; conidia turquoise grey (24B–F2), grey (27B1), greenish grey (25–27C–D2); 16–20 sulcations and 6–8 wrinkles present in some strains; light orange and orange sclerotia present in some strains; exudates and soluble pigments not

produced; reverse reddish yellow (4A6–7), orange (7C8) turning pastel yellow (3A4) near the margins or pale yellow (4A3); margin entire.

Colonies on CREA after 7 days at 25°C: (13–) 20–28 mm diam., moderate growth, good yellow acid production, sporulation sparse, aerial mycelium present, sclerotia present in some strains; entire medium yellow after two and three week; no base production.

Individual conidiophores on MEA borne directly from agar surface, with smooth to finely roughened, septate stipes (88–) 193–393 μm long, 2–3 μm wide, branching not present, vesiculate (width: range 4–7 μm , x for different strains = $4.6\text{--}5.9 \pm 0.6$). Phialides in whorls of (10–) 16–29, ampulliform to cylindrical, 8–11 x 2.5–3 μm , short to long necks, periclinal thickenings not obvious. Conidia produced in columns, ellipsoidal, 2–3 μm diam (x for different strains = $2.5\text{--}3.0 \pm 0.1$ x $2\text{--}2.5 \pm 0.1$ μm , $n = 25$) L/W ratio 1.3:1, finely roughened. Sclerotia on MEA subglobose to ellipsoidal, 180–320 μm ; sclerotial cells 7–11 x 5–8 μm .

Specimens examined: NRRL 2087 (ex-type)*, NRRL 32583, DAOM 239930, DAOM 239931*, DAOM 239932*. Refer to Table 3.1.

* indicates sclerotia producing strains.

Substrate: air, forest soil, coffee berry (*Coffea arabica*).

Geographical distribution: Indonesia, Australia, Hawaii (USA).

Commentary: *Penicillium sclerotiorum* is morphologically similar to *P. thomii*, if colony pigmentation is disregarded, and is the only species within the *P. sclerotiorum* complex with ellipsoidal conidia. It can be further distinguished by the white and orange colonies on CZ, along with orange and greenish grey colonies on CYA. The species conformed to the GCC concept recognition criterion and is resolved by *Cox1*. Two

possible phylogenetic species are observed in all gene trees, one comprised of the ex-type group (A), and the other comprised of sterile strains (B; CBS 138.64, CBS 258.55, and CBS 118889) that are not included in the morphological description of *P. sclerotiorum* presented above. Strains identified in the production of azapholines (Pairet *et al.* 1995) and antimicrobial compounds (MacCurtin and Riley 1940; De Lucca *et al.* 2008) were not available for this study because they were not deposited in a culture collection. Thus it is unclear which of the phylogenetic species in this thesis actually produce these potentially useful compounds.

***Penicillium krugii* Rivera and Seifert, prov. sp. nov.¹** Figure 3.22, 3.28–3.30

Colonies on CYA after 7 days at 25°C: 30–38 mm diam., sporulation absent, 5–9 sulcations, with 2–3 radial wrinkles, one strain with 7–9 radial wrinkles, approximately 1 mm deep, mycelia white (1–3A1), sclerotia white, aerial mycelium not present, clear light yellow exudate droplets produced in low to moderate amounts, soluble pigments absent; reverse reddish yellow to orange (4–6AB7–8) and yellowish grey (3–4B2) towards the edges, stellate with radial wrinkles; margin entire.

Colonies on MEA after 7 days at 25°C: 26–36 mm diam., planar, low and velutinous, aerial mycelium not present; conidia greenish grey (24–27DE 3–5); sclerotia orange, yellow towards the centre, and white towards the edges; conidia and sclerotia sectoring in some strains; reverse orange (5–6B8), vivid yellow (3A8), yellowish grey (3–4B2) towards the centre; margin entire.

Colonies on CZ after 7 days at 25°C: 15–23 mm diam., occasionally 10–19 mm diam., velutinous and dense, sparse to negligible sporulation, conidia greenish grey (25–

¹ The name does not constitute a valid publication of the new species name according to the regulations of the International Code of Botanical Nomenclature, which requires that new species be published in the formal scientific literature, accompanied by a Latin diagnosis.

27D2), clear light yellow exudates droplets in low amounts produced, soluble pigments absent, 4–6 sulcations and 1–2 radial wrinkles present in some strains; sclerotia white; reverse yellow to deep yellow (3A6–8) and orange (5–6B8), some strains yellowish white (3A3–3) and pastel yellow (3A4) towards the centre; margin entire.

Colonies on YES after 7 days at 25°C: 28–38 mm diam., sporulation poor, velutinous, conidia greenish grey (25D2), 11–17 sulcations and 6–10 radial wrinkles, clear yellow exudates droplets produced in low amounts by some strains, soluble pigments not produced, sclerotia white; white mycelia at the margins 1 mm; reverse yellow and (3A3–4) and orange (5–6B8), some strains pastel yellow towards the edges (3A3–4), stellate with radial wrinkles or wrinkled; margin entire.

Colonies on CREA after 7 days at 25°C: 14–22 (–27) diam., sparse sporulation, weak growth and good yellow acid production, aerial mycelium present in some strains, sclerotia present; entire medium turned yellow after two weeks, no base production.

Individual monoverticillate conidiophores on MEA borne from agar surface; smooth to finely roughened, septate stipes, 88–229 μm long, 2–2.5 μm wide, branching not present, vesiculate (width: range 4–6 μm , x for different strains = $4.6\text{--}5.4 \pm 0.3 \mu\text{m}$). Phialides in whorls of 14–35, ampulliform to cylindrical, 7–11 $\times$ 2–3 (–5) μm , short to distinguishable necks, periclinal thickenings not obvious. Conidia borne in chains, globose to subglobose, 2–3 μm diam (x for different strains = $2.7\text{--}2.9 \pm 0.01 \times 2.3\text{--}2.5 \pm 0.01 \mu\text{m}$, $n = 25$), L/W ratio 1.1:1, finely roughened. Sclerotia examined on MEA, subglobose to ellipsoidal, 136–552 $\times$ 131–433 μm ; sclerotial cell length 3.5–8 $\times$ 3–6 μm . Sclerotia were produced on all media examined.

Specimens Examined: DAOM 239939, DAOM 239940, DAOM 239941, DAOM 239942, DAOM 239943 (ex-type), DAOM 239944, DAOM 239945, DAOM 239946, DAOM 239946, KAS 3479.

Etymology: The species was named after John Krug, who was a faculty member at the University of Toronto and a research associate at the Royal Ontario Museum (ROM). For three years I had the privilege of working for him at the Mycology Herbarium part-time during my undergraduate studies. He introduced me to the world of fungal taxonomy, and made me appreciate the diversity within the fungi. Like his PhD supervisor, R.F. Cain, he was a specialist on coprophilous fungi, but was an avid lichen collector. His lichen collection was deposited at the Mycology Herbarium at the ROM, which included specimens from all over the world.

Substrate: forest soil.

Geographical distribution: Kedah, Malaysia.

Commentary: *Penicillium krugii* differs from all species in the *P. sclerotiorum* complex in the production of white colonies and sclerotia in CYA and CZ. All strains produced organic acids in CREA, except for strain DAOM 239944. *Penicillium krugii* is morphologically similar to *P. sclerotiorum*; both have vivid yellow to orange reverse colony colours; *P. krugii* differs by its subglobose conidia and conspicuously vesiculate conidiophores. Multigene phylogenetic analyses revealed that *P. krugii* is closely phylogenetically related to *P. mallochii*. *Penicillium krugii* strains were not resolved by *BenA* or *Cox1*. *TEF1- α* provided species resolution in all phylogenetic analyses; ITS for MP and ML trees; and CaM for ML and BI trees.

***Penicillium jacksonii* Rivera and Seifert prov. sp. nov.¹**

Figures 3.22, 3.31–3.33

Colonies on CYA after 7 days at 25°C: 26–30 (–36) mm diam., dense and velutinous, white aerial mycelium in the centre (2–3 mm diam); 6–13 sulcations, 16–17 sulcations near the margin in some strains some strains, 2–3 radial wrinkles, approximately 1 mm deep; conidia greenish grey (25–27E2), with bluish grey (22D–F2) concentric rings; clear light yellow exudates droplets produced in low amounts in some strains; soluble pigments not produced, 2–3 mm of white mycelium at the margin; sclerotia not observed; reverse light yellow (5C8), yellowish grey (3–4B2), orange grey (6B7–8), some near the edges yellowish grey (3–4B2) and yellowish white (1A2–3), stellate with some radial wrinkles; margin entire.

Colonies on MEA after 7 days at 25°C: 23–35 (–40) mm diam., planar and moderately dense, velutinous, sclerotia not observed; conidia greenish grey (25–27E2); exudates and soluble pigments not produced; reverse orange yellow to orange (4–6B7–8), brownish orange (7C7–8), pastel yellow or reddish yellow (4A6–7) near the edges; margin entire.

Colonies on CZ after 7 days at 25°C: resembling CYA, 17–25 mm diam., some strains floccose at the centre, 5–6 sulcations and 2–3 wrinkles in some strains, mycelia 1–2 mm; reverse reddish yellow (4A7) and brownish yellow (5C8) in some strains.

Colonies on YES after 7 days at 25°C: 29–33 mm diam., less commonly 34–36 mm diam., dense and velutinous; densely sulcate, especially near the edges (15–21), 7–9 radial wrinkles; clear vivid yellow exudate droplets produced in low amounts in some strains; conidia greenish grey (25–26D–E2) and turquoise grey (24D2), concentric rings of different shades of turquoise grey present in some strains; mycelia 2–3 mm; sclerotia

not produced; reverse reddish yellow (7B8), orange (6B8), greyish yellow (2–4B3), some strains yellowish grey (2B–C3) or dull yellow (3B3–4) towards the edges, wrinkled towards the centre with visible sulcations and radial wrinkles towards the edges; margin entire.

Colonies on CREA after 7 days at 25°C: 23–29 mm diam., sporulation sparse, aerial mycelium not observed, moderate growth and good yellow acid production; entire medium yellow after two and three week; no base production.

Individual conidiophores on MEA borne from agar surface, rough septate stipes, 31–134 μm long, 2–3 μm wide, 90% unbranched, moderately vesiculate (width: range 4–6, $\bar{x}$ for different strains = $4.6\text{--}5.0 \pm 0.3$); metulae when present 22–55 μm long, 2–3 μm wide. Phialides in whorls of 15–23 (– 28), ampulliform, 7–10 x 2–3 μm , distinguishable collarette. Conidia borne in columns, globose, smooth, 2–3 μm diam ($\bar{x}$ for different strains $2.6\text{--}2.7 \times 2.3\text{--}2.6 \pm 0.01 \mu\text{m}$), L/W mean ratio 1.1:1.

Specimens Examined: DAOM 239933, DAOM 239934, DAOM 239935 (ex-type), DAOM 239936.

Etymology: The species was named after H.S. Jackson, a faculty member of the University of Toronto. H.S. Jackson worked mostly on rusts, but was an avid collector of fungi of all groups, especially of the Basidiomycota, that were deposited at the ROM. While working at the ROM I came across his drawings, fungal specimens and handwriting many times. He was R.F. Cain's PhD supervisor.

Substrate: rainforest soil.

Geographic distribution: Queensland, Australia.

Commentary: *Penicillium jacksonii* colony morphology resembles *P. mallochii*, *P. guanacastense*, *P. cainii*, and *P. sclerotiorum* in CYA and MEA. In CZ it resembles *P. mallochii* and *P. guanacastense*. Microscopically it does not have the conspicuous vesiculate stipes observed in *P. mallochii*, *P. guanacastense* and *P. cainii*. *Penicillium jacksonii* conformed to the GCC recognition criterion and is resolved by *Cox1*. Strong statistical support is observed for all gene trees, except ITS where strains form a coherent monophyletic group in all phylogenetic analyses.

***Penicillium cainii* Rivera and Seifert sp. nov.¹**

Figures 3.22, 3.36–3.37

Colonies on CYA after 7 days at 25°C: 23–29 mm diam., dense and velutinous, 14–18 sulcations, 1–2 radial wrinkles in some strains, approximately 1 mm deep; conidia deep blue to deep green (23–27E2); 1–2 mm of white mycelia at the margin; clear yellow exudates produced in moderate amounts in some strains, soluble pigments not produced; sclerotia absent; reverse golden yellow (5B7) and brownish yellow (5C8–9), yellowish white (2–3A2) towards the edges; margin entire.

Colonies on MEA after 7 days at 25°C: 28–35 mm diam., planar, dense and velutinous, aerial mycelium not present; conidia greenish grey (28E2) and dull green (27C–D2–4), exudate and soluble pigments not produced; sclerotia not produced; reverse orange to dark orange (5A–B8), yellowish white (2–3A2) towards the edges, margin entire.

Colonies on CZ after 7 days at 25°C: 18–21 mm diam., dense and velutinous; no visible sulcations and radial wrinkles; conidia turquoise grey (24B–F2), with a concentric ring of paler shades of this colour towards the centre, 2 mm of white mycelia at the margin; vivid clear yellow exudate droplets produced in moderate amounts in the centre

of the colony, soluble pigments not observed; sclerotia not produced; reverse brownish yellow (5–6C8), turning yellowish grey (3–4B2) towards the edges, margin entire.

Colonies on YES after 7 days at 25°C: 31–34 mm diam., dense and velutinous, 21–23 sulcations and 8–10 radial wrinkles; conidia greenish grey (27D–F2); clear dark orange exudates droplets produced in negligible amounts in some strains, soluble pigments not produced; 2 mm of white mycelia at the margin; reverse brownish orange to reddish orange (7BD8), greyish brown (2B3) towards the edges, wrinkled towards the centre; margin entire.

Colonies on CREA after 7 days at 25°C: 25–31 mm diam., sporulation sparse, aerial mycelium not observed, weak growth and good yellow acid production; entire medium yellow after two weeks, base production not observed.

Individual conidiophores on MEA borne from agar surface, rough septate stipes, vesiculate, 69–79 μm length, 2.5–3 μm wide, conidiophores branched and unbranched strains; in branched strains, 10% of conidiophores branched, metulae 31–34 μm in length. Phialides in whorls of (13–) 18–29, ampulliform, 7.5–10 $\times$ 2–3 μm , with a distinguishable neck and with inconspicuous periclinal thickening. Conidia globose, 2.0–2.5 μm diam (x for different strains = $2.3\text{--}2.4 \pm 2.1\text{--}2.2 \pm 0.035 \mu\text{m}$), L/W mean ratio 2.1:1, finely roughened.

Specimens Examined: DAOM 239914 (ex-type), DAOM 239915.

Etymology: This species was named after Roy F. Cain, a faculty member of the University of Toronto. He was a world authority on coprophilous Ascomycota, and was an avid collector of fungi of all groups. His collection was deposited at the Mycology Herbarium at the ROM. Cain was David Malloch's and John Krug's PhD supervisor.

Substrate: soil, forest rich in *Jungladaceae*.

Geographical distribution: Niagara Falls, ON., Canada.

Commentary: *Penicillium cainii* colony morphology resembles *P. sclerotiorum*, *P. mallochii*, *P. guanacastense*, and *P. jacksonii* on CYA, MEA, and YES. Colony morphology on CZ differs from the rest of the species in *P. sclerotiorum* complex by a concentric ring of a light shade of turquoise grey and clear yellow exudate droplets in the centre of the colony. Microscopic characters resemble *P. mallochii*, *P. guanacastense*, and *P. krugii*. Each species had a similar number of phialides and had vesiculate conidiophores. *Penicillium cainii* differs by having clavate vesicles and conspicuously roughened stipe. The species conformed to the GCC recognition criterion and is resolved by *Cox1*. All genes provided strong statistical support for all phylogenetic analyses.

***Penicillium ciebiessum* Rivera and Seifert prov. sp. nov.¹** Figures 3.22, 3.34–3.35

Colonies on CYA after 7 day at 25°C: 30–33 mm diam., dense and velutinous sporulation dense, aerial mycelium present towards the centre, 10–11 sulcations, radial wrinkles not visible, approximately 1 mm deep; conidia deep green (25–26E2), concentric rings of paler shades of these colours; clear yellow exudate droplets produced in low amounts in some strains, soluble pigments not produced; margin 1–3 mm of white mycelia; reverse yellow (3A6–7), vivid yellow (2–3A8), near the edges yellowish white (2A2); margin entire.

Colonies on MEA after 7 days at 25°C: 31–37 mm diam., planar and velutinous, moderately dense, sporulation good; conidia dull green (26–27E3), concentric ring near the edges of a paler shade of this colour; reverse pale, margin entire.

Colonies on CZ after 7 days at 25°C: 19–23 (–30) mm diam., dense and velutinous, sporulation good, aerial mycelium present throughout the colony, one strain floccose near the centre, sulcations and radial wrinkles not present; vivid clear yellow exudates droplets in low amounts produced in some strains; soluble pigments observed; margin 1–2 mm of white mycelia near the margin; conidia greenish grey (26–27E2); reverse brownish yellow (5C8–9), deep yellow (4A8), yellowish white towards the edges (1A2); margin entire.

Colonies on YES after 7 days at 25°C: 30–32 mm diam., dense, sporulation good, velutinous, aerial mycelia absent; 8–10 sulcations, 19–23 sulcations towards the edges, 6–9 radial wrinkles; conidia greenish grey (25E2), concentric rings of paler shades of this colour present in some strains, white patches present occasionally; exudate droplets and soluble pigments not produced; reverse yellowish white (3A2) or reddish yellow (4A6); margin entire.

Colonies on CREA after 7 days at 25°C: 26–33 mm diam., sporulation poor, aerial mycelium not produced, weak growth and good yellow acid production; entire medium yellow after two weeks, base production not observed.

Individual conidiophores on MEA borne from agar surface, smooth to rough, septate stipes, 83–134 μm in length, 2–3 μm wide, branched and unbranched strains, vesiculate (width: range 3–6 μm , $\bar{x}$ for different strains = $4.4\text{--}4.7 \pm 0.4 \mu\text{m}$); 65% of conidiophores branched, when branched metulae 28–48 μm in length. Conidiogenous cells phialidic in whorls of 11–19, ampulliform, 6–5 (–13) μm length, 2–3 μm wide, distinguishable collarette and inconspicuous periclinal thickening. Conidia globose, 2.5–

3 μm diam (x for different strains = $2.8 \times 2.5\text{--}2.6 \pm 0.035 \mu\text{m}$), L/W mean ratio 1.1:1, finely roughened.

Specimens examined: DAOM 239937 (ex-type), DAOM 239938.

Etymology: This species was named after the Centraalbureau voor Schimmelcultures (CBS). I am extremely grateful to everyone there for their help and support, and for sending me the strains. Without them this chapter of my thesis would not exist.

Substrate: forest soil.

Geographical distribution: Queensland, Australia.

Commentary: *Penicillium ciebiessum* colonies were morphologically similar to *P. mallochii*, *P. guanacastense*, *P. jacksonii* and *P. cainii* in CYA, MEA and YES. Colony morphology on CZ and microscopic characters on MEA were similar to *P. jacksonii*, differing in weak growth on CREA. The species conformed to the GCC recognition criterion and was resolved by *Cox1*. All genes provided strong statistical support for all phylogenetic analyses.

3.6 Discussion

In this chapter, four additional species conforming to Pitt's (1979a) morphological species concept of *P. sclerotiorum* were identified. Phylogenetic analyses of *BenA*, ITS, *Cox1*, *TEF1- α* and CaM determined that all species conformed to the GCC recognition criterion. *Cox1* provided species resolution for all species except for *P. krugii* and *P. mallochii*. ITS did not provide species level resolution for *P. mallochii* and *P. krugii*. Gene tree analyses also indicated the presence of two coherent monophyletic groups with strong statistical support for *BenA*, *TEF1- α* , and CaM within *P. sclerotiorum*.

One group consisted of strains NRRL 2074 (ex-type), NRRL 31583, DAOM 239930, DAOM 239931, and DAOM 239932. The other consisted of strains CBS 258.55, CBS 128.64, and CBS 11889. The latter group was not described as a distinct species in this thesis because the strains were sterile, preventing morphological descriptions.

The homogeneity partition test (HPT) indicated that CaM was not congruent with the other genes (Table 3.3). Thus CaM was not included in combined phylogenetic analyses by maximum parsimony, maximum likelihood, and Bayesian inference. Although the phylogeny differed among the genes, the species groupings remained constant. All species conformed to the GCC species recognition criterion.

Careful examination of colony and microscopic characters revealed subtle morphological differences among the species. The diagnostic characters were used to construct an identification key at the end of the chapter. *Penicillium sclerotiorum* was characterized by orange and white colony colours on CZ; *P. krugii* strains produced sclerotia on all examined media and white colonies on CYA and CZ; *P. jacksonii* produced a small vesicle on the conidiophore, roughened stipes, concentric rings and exudate droplets in the centre of the colony on CZ; *P. cainii* had a clavate vesicle and roughened stipes; and *P. ciebiessum* had moderately vesiculate stipes and roughened stipes. *Penicillium mallochii* and *P. guanacastense* are similar in colony and microscopic character morphology, but conidiophores of *P. mallochii* were more conspicuously vesiculate and *P. guanacastense* had a mycelial margin of approximately 3 mm on CZ.

Some species indicated potentially informative geographical distribution patterns. *Penicillium krugii* was collected from Kdah, Malaysia; *P. jacksonii* and *P. ciebiessum* were collected from Queensland, Australia; and *P. cainii* was collected from Niagara

Falls, Ontario. *Penicillium mallochii* and *P. guanacastense* were collected from the Área de Conservación Guanacaste, Costa Rica, but from hosts that belonged to different insect families. Our knowledge of these newly recognized species is preliminary, and their actual geographical distributions may or may not eventually overlap with the distribution of other species. *Penicillium sclerotiorum* strains had a broader geographical distribution (Table 3.1) and demonstrated greater morphological variation than the other species (Figure 3.25–3.26). Not all strains of *P. sclerotiorum* produced sclerotia, but all sclerotia producing strains produced sclerotia on all media (NRRL 2087, DAOM 239931 and DAOM 239932).

Sclerotia formation depends not only on the strain and the species as observed in *P. sclerotiorum* and *P. krugii*, but on medium and growth conditions. Experiments with other species, such as *Aspergillus caelatus*, have shown that a pH of 6–10 and temperatures of 28–30°C are optimal for sclerotia formation (McAlpin 2004). Carbon and nitrogen concentration may also be important because sclerotia production peaked at a C:N ratio of 8.6 (McAlpin 2004). Sucrose was found to suppress sclerotia formation by 12% (McAlpin 2004). Similar results were observed in other *Aspergillus* species (Rudolph 1962), *Sclerotinia rolfii* (Wheeler and Sharan 1965), and *Verticillium* species (Wyllie and de Vay 1970).

The use of secondary metabolite profiles to distinguish between *Penicillium* species is a common practice. It has proven useful in *Penicillium* subgenus *Penicillium*, where it distinguished the species comprising the *P. roquefortii* complex (*P. paneum*, *P. cameum*, and *P. roquefortii*), all having similar morphologies (Nielsen *et al.* 2006). Secondary metabolite profiling, which was not performed for this thesis, may or may not

further distinguish the species in the *P. sclerotiorum* complex. Furthermore, the pharmaceutical potential within the *P. sclerotiorum* complex should also be investigated.

The designation of *P. adametzioides* and *P. multicolor* as synonyms of *P. sclerotiorum* according to Stolk and Samson (1983) was not accepted in this thesis. *Penicillium adametzioides* is a distinct phylogenetic species, which was also noted by Peterson (2000) using ITS and LSU combined phylogenetic data. Morphologically, *P. adametzioides*, does not resemble *P. sclerotiorum* or any of the species studied in this chapter. Morphological analyses were not performed for the ex-type of *P. multicolor*, CBS 501.73, because it was sterile (no production of sexual or asexual structures). Pitt (1979a) did not address *P. multicolor* in his monograph because the original description of Grigorieva-Manoilova and Poradielova (1915) described it as producing colonies with a purple reverse, 3–5 phialides, and short nonvesiculate conidiophores. The isolates examined by Thom and Raper (1949) had long vesiculate conidiophores, up to 16 phialides, and yellow to orange-red colony reverse; resembling the morphological species concept of *P. sclerotiorum*. BLAST results of *BenA* and ITS sequences of the ex-type strain of *P. multicolor* suggested similarity to *P. fellutanum*. Thus, *P. adametzioides* and *P. multicolor* are not accepted as synonyms of *P. sclerotiorum* in this thesis.

The strain CBS 248.65 was identified as *P. sclerotiorum* but did not group with the *P. sclerotiorum* strains or any of the other species studied in this chapter. The gene trees indicated that the strain is another species within the *P. sclerotiorum* complex, but a second strain is needed to make a species description. The presence of a phylogenetically isolated strain may indicate the presence of more species fitting the morphological species concept of *P. sclerotiorum*.

3.7 Taxonomic Key

- 1a. Colonies on CYA white, with orange and grey sclerotia *P. krugii*
- 1b. Colonies on CYA in shades of green or orange red 2
- 2a. Colony reverse colours on CYA and MEA pale. *P. ciebiessum*
- 2b. Colony reverse colours yellow to red vivid colours 3
- 3a. Colonies on CYA sulcate, exudates present; on CZ exudate droplets concentrated in the centre of colony, a concentric ring turning darker shades towards the edges, stipes clearly roughened *P. cainii*
- 3b. Colonies on CYA sulcate, exudate droplets present or absent; on CZ exudate droplets dispersed throughout the colony; stipes smooth to finely roughened . . . 4
- 4a. Sporulation on CREA sparse *P. jacksonii*
- 4b. Sporulation moderate on CREA 5
- 5a. Colonies on CZ white or orange, sclerotia present or absent, conidia ellipsoidal *P. sclerotiorum*
- 5a. Colony on CZ green, sclerotia usually absent, conidia globose 6
- 6a. Conidiophores moderately vesiculate; colony on YES more wrinkled than sulcate *P. mallochii*
- 6b. Conidiophores moderately; vesiculate colony on YES sulcate *P. guanacastense*

Note: *P. mallochii* and *P. guanacastense* colony photographs of CYA, MEA, CZ, YES and CREA are depicted in Figure 3.11.

Table 3.1: Fungal strains examined in Chapter 3 for morphological and molecular analyses.

Species	Culture	Country	Province/State	Region	Substrate
<i>Penicillium canii</i>	DAOM 239914*	Canada	Ontario	Niagara, Niagara Falls, Fireman's Park	soil, forest rich in Jungladaceae
	DAOM 239915	Canada	Ontario	Niagara, Niagara Falls, Fireman's Park	soil, forest rich in Jungladaceae
<i>Penicillium ciebiessum</i>	DAOM 239937*	Australia	Queensland	Barrine Lake	forest soil
	DAOM 239938	Australia	Queensland	Barrine Lake	forest soil
<i>Penicillium guanacastense</i>	DAOM 239912*	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	wild caterpillar belonging to the <i>Noontidae</i> /FG, MG, HG
	DAOM 239913	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	wild caterpillar belonging to the <i>Noontidae</i> /FG, MG, HG
<i>Penicillium jacksonii</i>	DAOM 239933	Australia	Queensland	Barron Falls	forest soil
	DAOM 239934	Australia	Queensland	Atherton	forest soil
<i>Penicillium krugii</i>	DAOM 239935	Australia	Queensland	Atherton	rainforest soil
	DAOM 239936	Australia	Queensland	Atherton	rainforest soil
	DAOM 239939	Malaysia	Kedah	Langkawi	rainforest soil
	DAOM 239940	Malaysia	Kedah	Langkawi	forest soil
	DAOM 239941	Malaysia	Kedah	Langkawi	forest soil
	DAOM 239942	Malaysia	Kedah	Langkawi	forest soil
	DAOM 239943*	Malaysia	Kedah	Langkawi	forest soil
	DAOM 239944	Malaysia	Kedah	Langkawi	forest soil
	DAOM 239945	Malaysia	Kedah	Langkawi	forest soil
	DAOM 239946	Malaysia	Kedah	Langkawi	forest soil
<i>Penicillium mallochii</i>	KAS 3479	Malaysia	Kedah	Langkawi	forest soil
	DAOM 239917*	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Spondias mombis</i>
	DAOM 239919	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Cithorenia lobesis</i> /MG
	DAOM 239920	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM
	DAOM 239925	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FM, MG, HG
	DAOM 239926	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /frass
	DAOM 239927	Costa Rica	Santa Rosa	Área de Conservación Guanacaste	<i>Rothschildia lebeau</i> /FG, MG, HG
	NRRL 2087*	Indonesia	Java	Buitenzorg	air
	NRRL 32583	USA	Hawaii	Kuauai, Kuauai Coffee Co.	coffee seedling crown

Species	Culture	Country	Province/State	Region	Substrate
	DAOM 239930				pineapple soil
	DAOM 239931	Australia	Queensland	Barron Falls	forest soil
	DAOM 239932	Australia	Queensland	Barron Falls	forest soil
	CBS 128.65	Zaire	Leopoldville	Nsang-Ngidinga River	forest litter
	CBS 258.55	Turkey	Istanbul		culture contaminant
	CBS 118889	Korea			
<i>Eupenicillium hirayamae</i>	CBS 229.60*	Thailand			milled rice
	CBS 238.68	South Africa			corn meal
<i>Penicillium adametzii</i>	CBS 209.28*	Poland	Poznan		soil contaminant
	KAS 3463	Malaysia	Kedah		forest soil
	KAS 3464	Malaysia	Kedah		forest soil
	KAS 3465	Malaysia	Kedah		forest soil
	KAS 3466	Malaysia	Kedah		forest soil
<i>Penicillium bilaiae</i>	NRRL 3391*	Russia	Kiev		soil
	LEQ 1642	Canada	Saskatchewan	Saskatoon	soil
	LEQ 1643	Canada	Saskatchewan	Saskatoon	soil
	LEQ 1644	Canada	Saskatchewan	Saskatoon	soil
	LEQ 1848	Canada	Ontario	Ottawa	soil
<i>Penicillium herquei</i>	CBS 336.48	France			<i>Agauri prifolia</i>
	CBS 136.22				
	CBS 347. 51*	Japan	Nehira	Osaka Univ. Fac Techn.	wakamoto corn and rice cake
	CBS 110644	USA	Wisconsin		forest soil
<i>Penicillium adametziodies</i>	DAOM 239916	Canada	Ontario	Niagara, Vineland,	Riesling grapes
	CBS 313.59*	Japan			soil
<i>Penicillium multicolor</i>	CBS 501.73*				
<i>Penicillium</i> sp.	CBS 248.65	South Africa			corn meal
<i>Eupenicillium levitum</i>	NRRL 705*	USA	New York		modeling clay

FG – foregut; MG – midgut; HG – hindgut.

* represents the ex-type strain.

Table 3.2: Comparative summary of colony and microscopic characters of species in the *P. sclerotiorum* complex.

Species	Colony characters			Microscopic characters			
	CYA		diam (mm)	sclerotia	stipe	vesicles	roughening
	Colours						
<i>P. sclerotiorum</i>	greenish grey/orange		18–40	present	smooth to finely roughened	vesiculate	finely roughened
<i>P. krugii</i>	white		30–38	present	smooth to finely roughened	vesiculate	finely roughened
<i>P. jacksonii</i>	greenish grey		26–36	absent	roughened	moderately vesiculate	smooth
<i>P. cainii</i>	deep blue to deep green		23–29	absent	roughened	vesiculate	finely roughened
<i>P. ciebiessum</i>	deep green		30–33	absent	smooth to roughened	vesiculate	finely roughened
<i>P. mallochii</i>	turquoise grey/greenish grey		29–39	absent	smooth to finely roughened	vesiculate	finely roughened
<i>P. guanacastense</i>	greenish grey		25–33	absent	finely roughened	vesiculate	finely roughened
							shape
							subglobose to ellipsoidal
							globose to subglobose
							globose
							globose
							globose
							globose to subglobose
							globose

Table 3.3: Gene to gene partition homogeneity test (PHT) values using PAUP v. 4

	<i>BenA</i>	ITS	<i>CoxI</i>	<i>TEF1-α</i>	CaM
<i>BenA</i>		0.12	0.16	0.51	0.001
ITS			0.72	0.85	0.349
<i>CoxI</i>				0.225	0.031
<i>TEF1-α</i>					0.002
CaM					

Note: values greater than 0.05 indicate congruence.

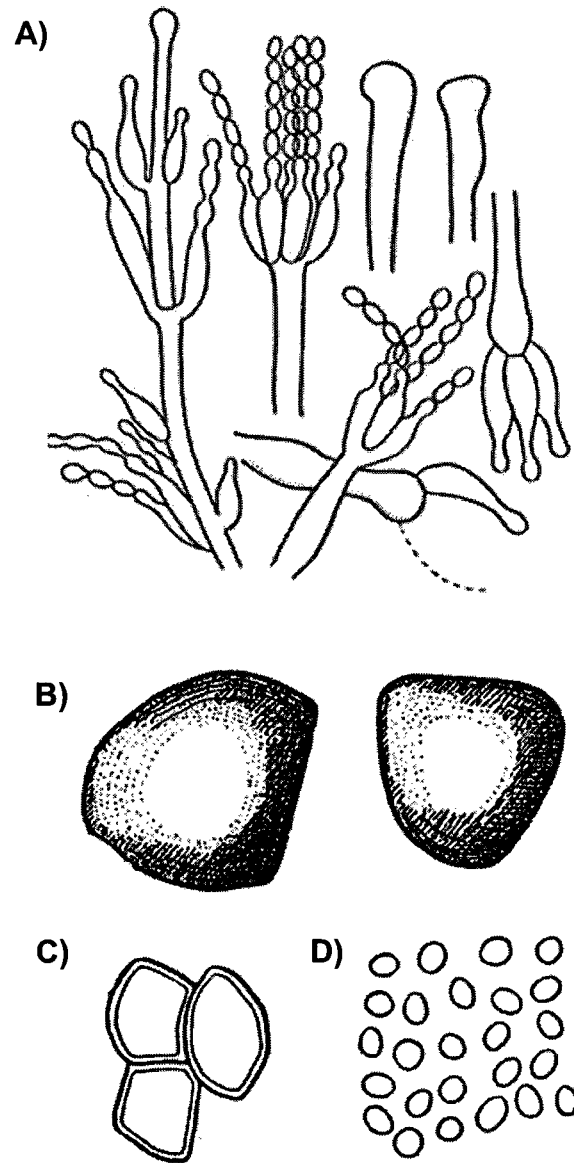


Figure 3.1: Original microscopic drawing of conidiophores (A), sclerotia (B), sclerotia cells (C), and conidia (D) of *P. sclerotiorum* by van Beyma (1937).

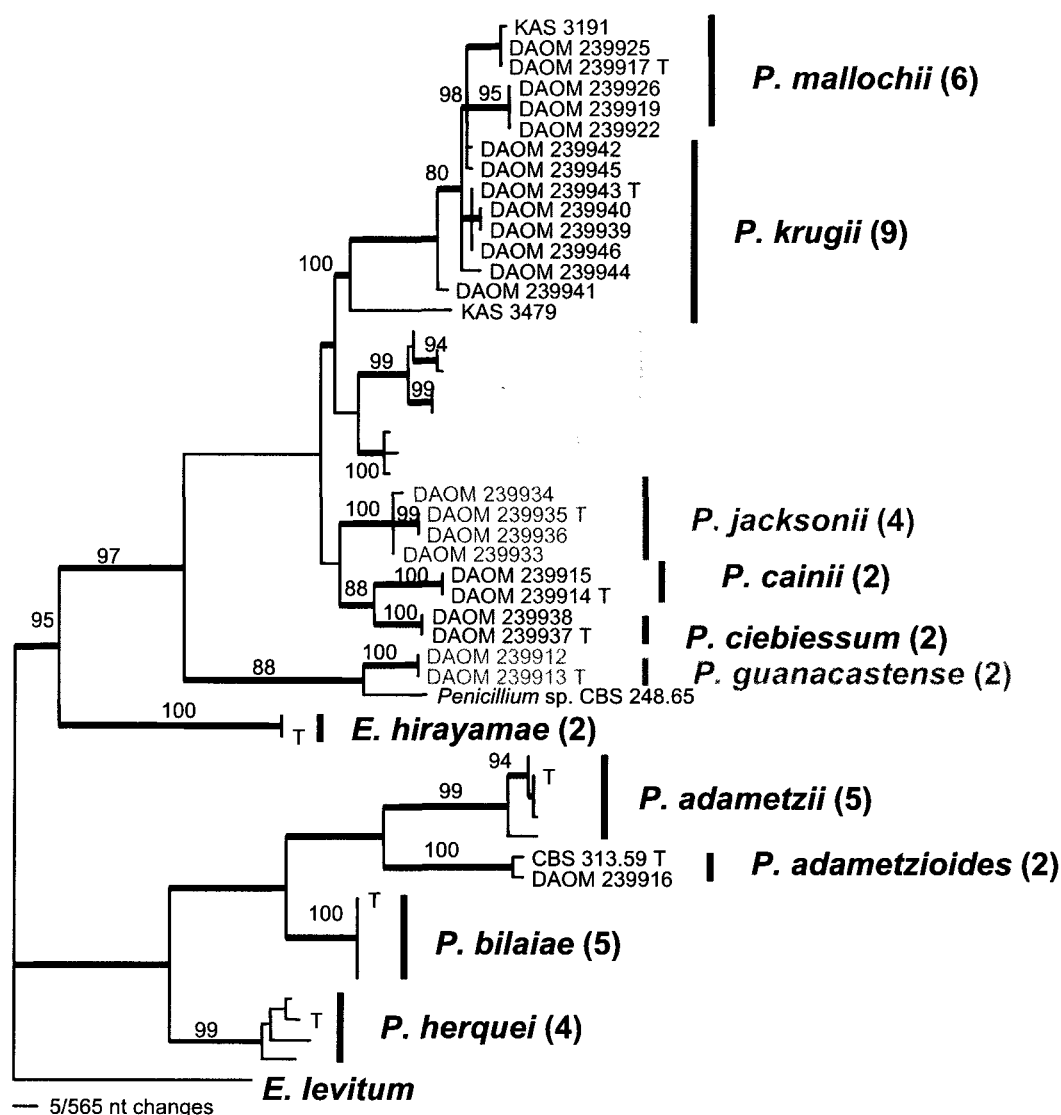


Figure 3.2: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *BenA* sequences. One out of 720 most parsimonious trees (L=537, CI=0.646, RI=0.895, RC=0.578, HI=0.354). A heuristic search with 185 informative characters and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

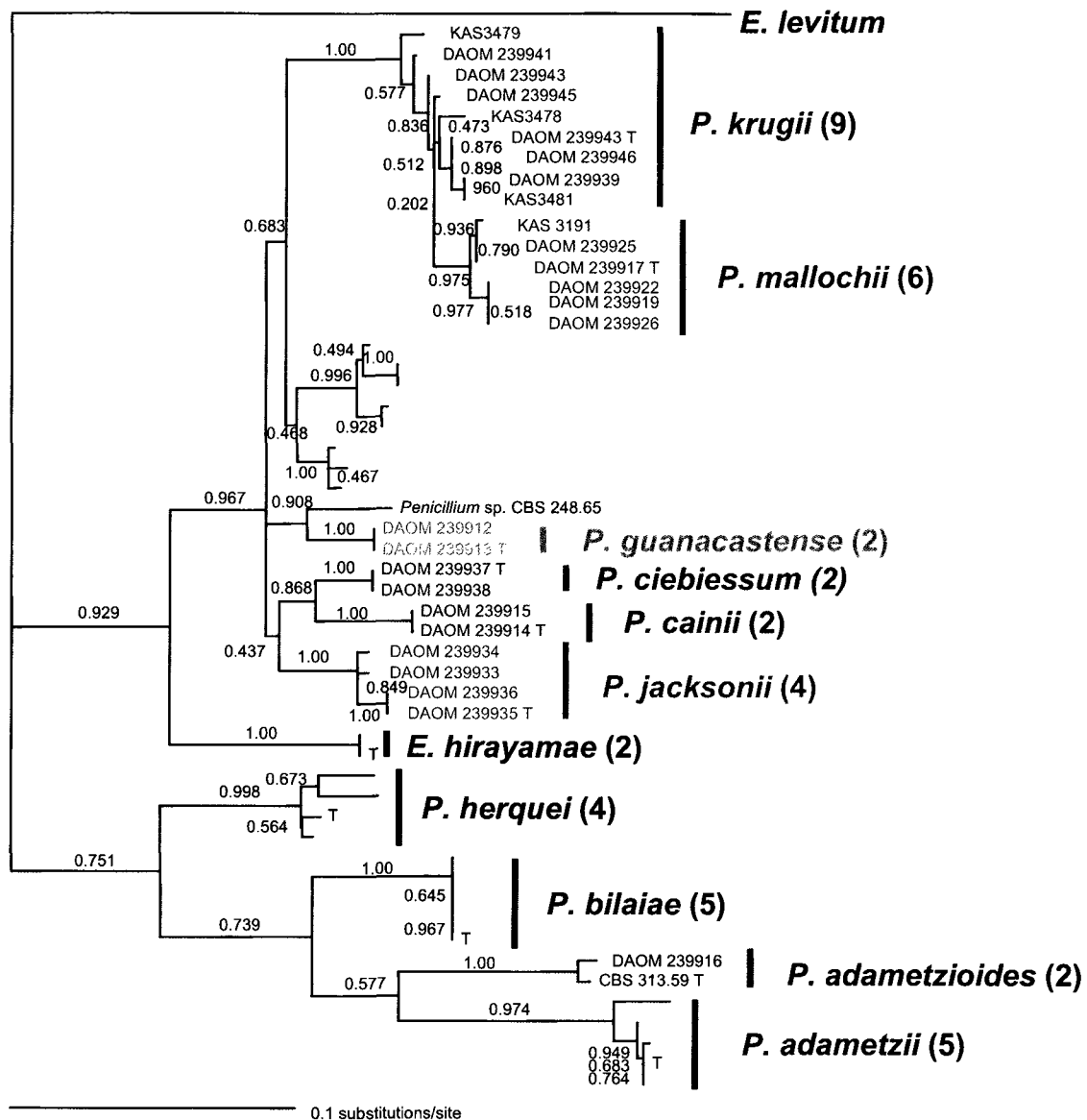


Figure 3.3: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *BenA* sequences. The tree was constructed using the GTR+G nucleotide substitution model; 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; the T represents the ex-type strain.

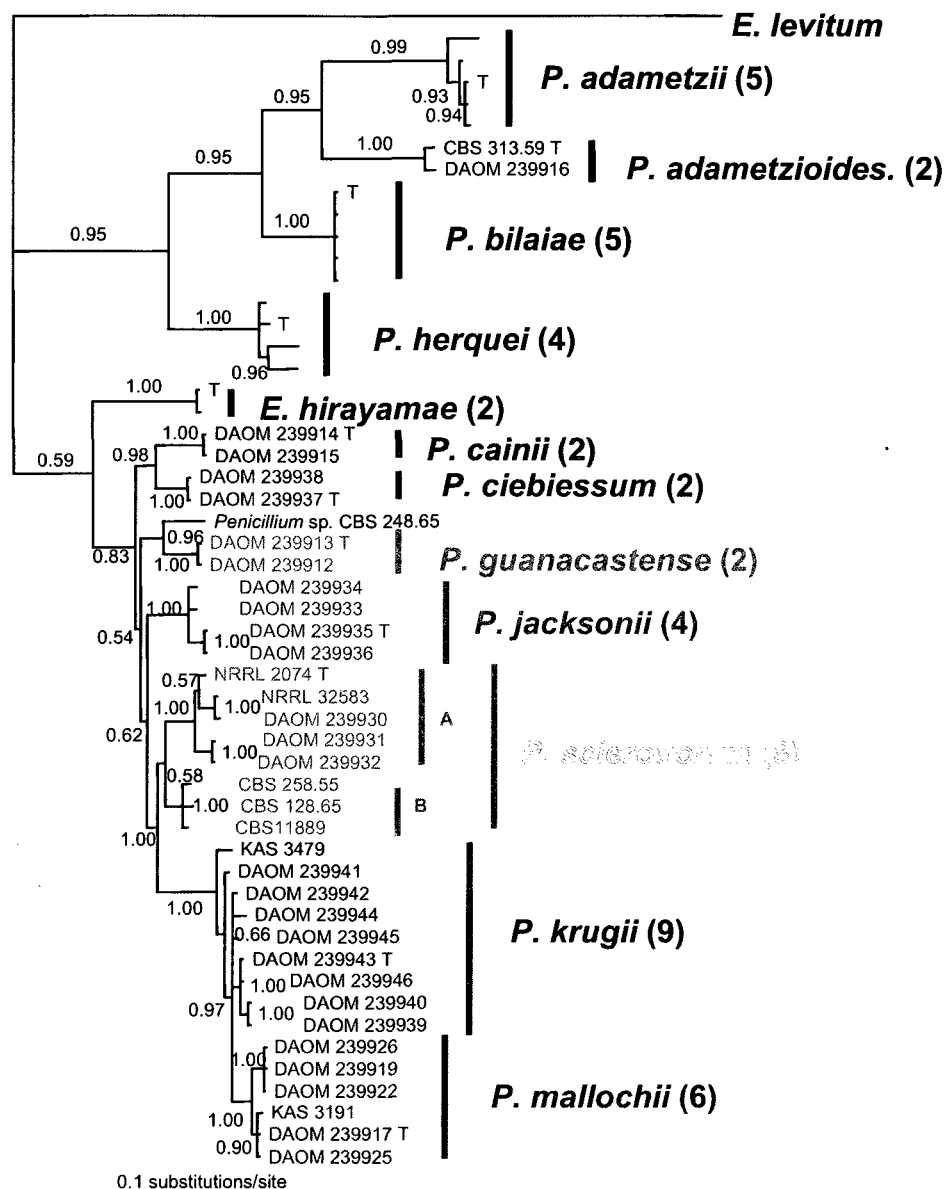


Figure 3.4: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium* Group 3, demonstrating the position of *P. sclerotiorum* complex species, based on *BenA* sequences. The tree was constructed using the GTR+G nucleotide substitution model. Posterior probabilities are presented. The number in parenthesis represents the number of strains; the T represents the ex-type strain.

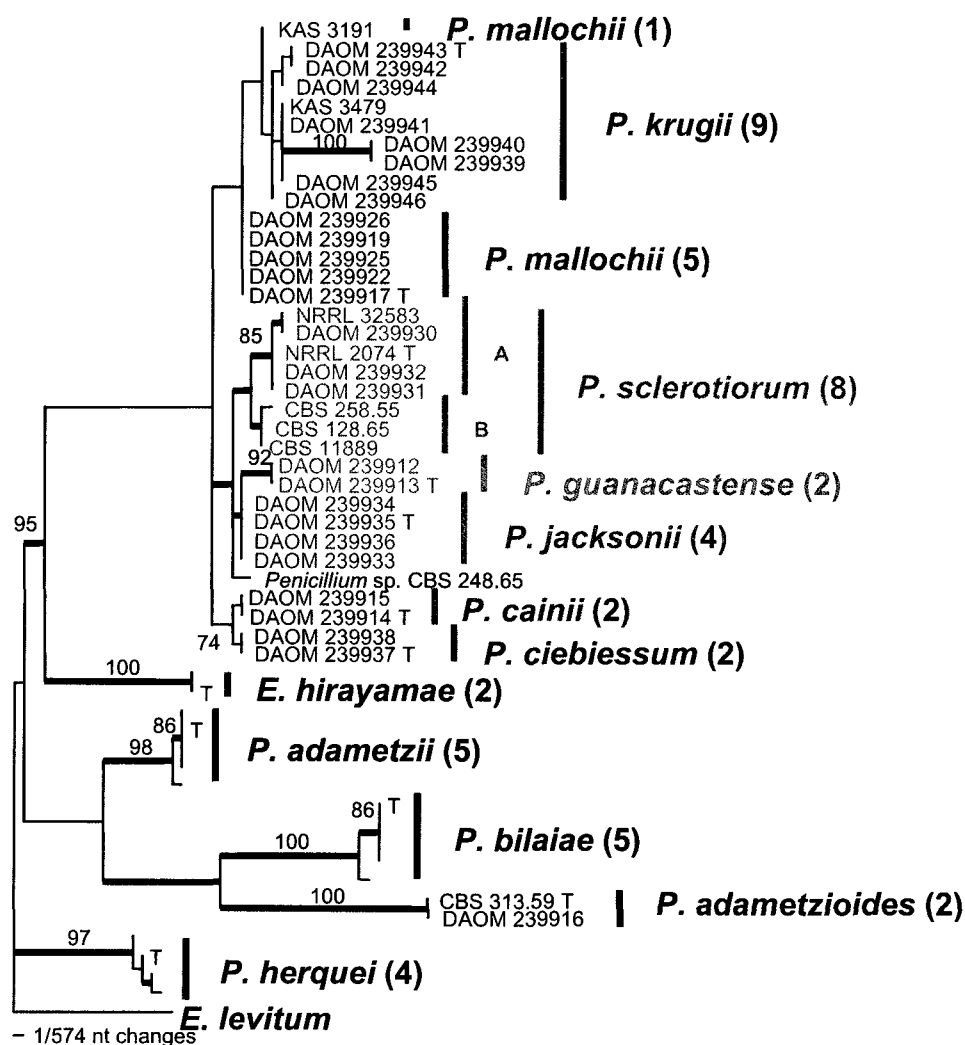


Figure 3.5: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on ITS sequences. One out of 5000 most parsimonious trees (L=156, CI=0.667, RI=0.909, RC=0.606, HI=0.333). A heuristic search with 85 parsimony informative characters and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; the T represents the ex-type strain.

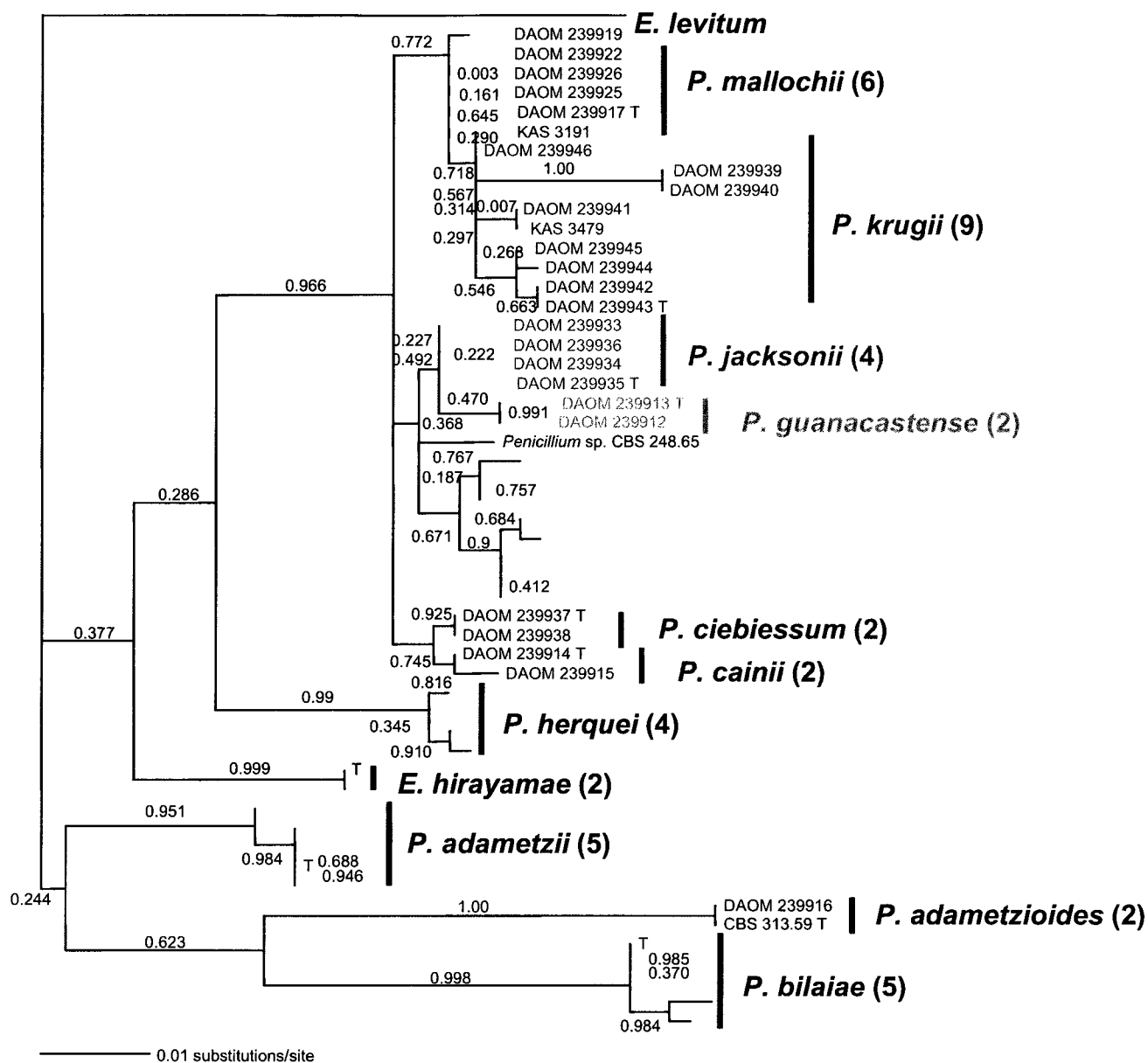


Figure 3.6: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on ITS sequences. The tree was constructed using the GTR+G nucleotide substitution model; 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

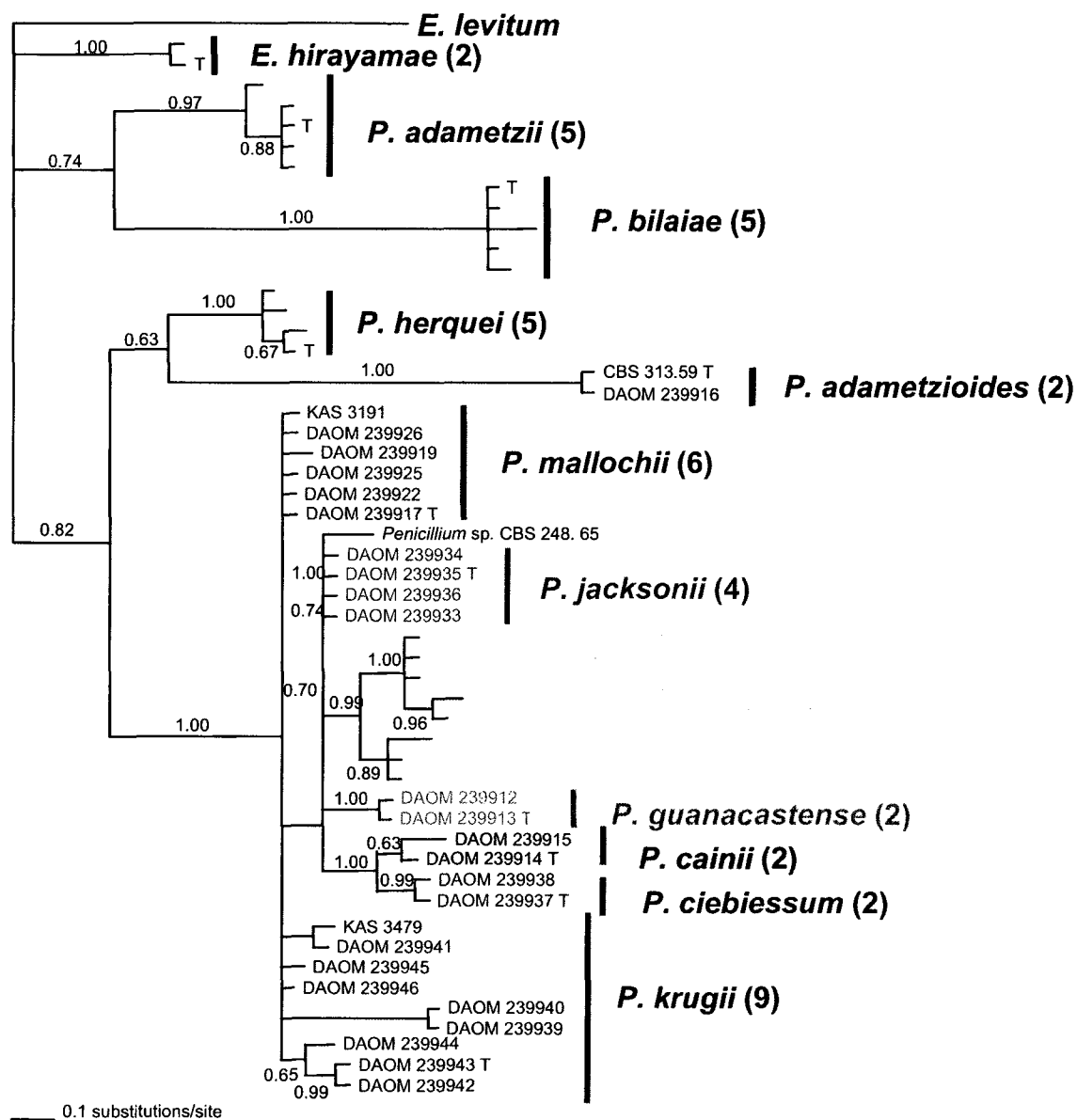


Figure 3.7: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex based on ITS sequences. The tree was constructed using the GTR+G nucleotide substitution model. Posterior probabilities are presented. The number in parenthesis represents the number of strains; T represents the ex-type strain.

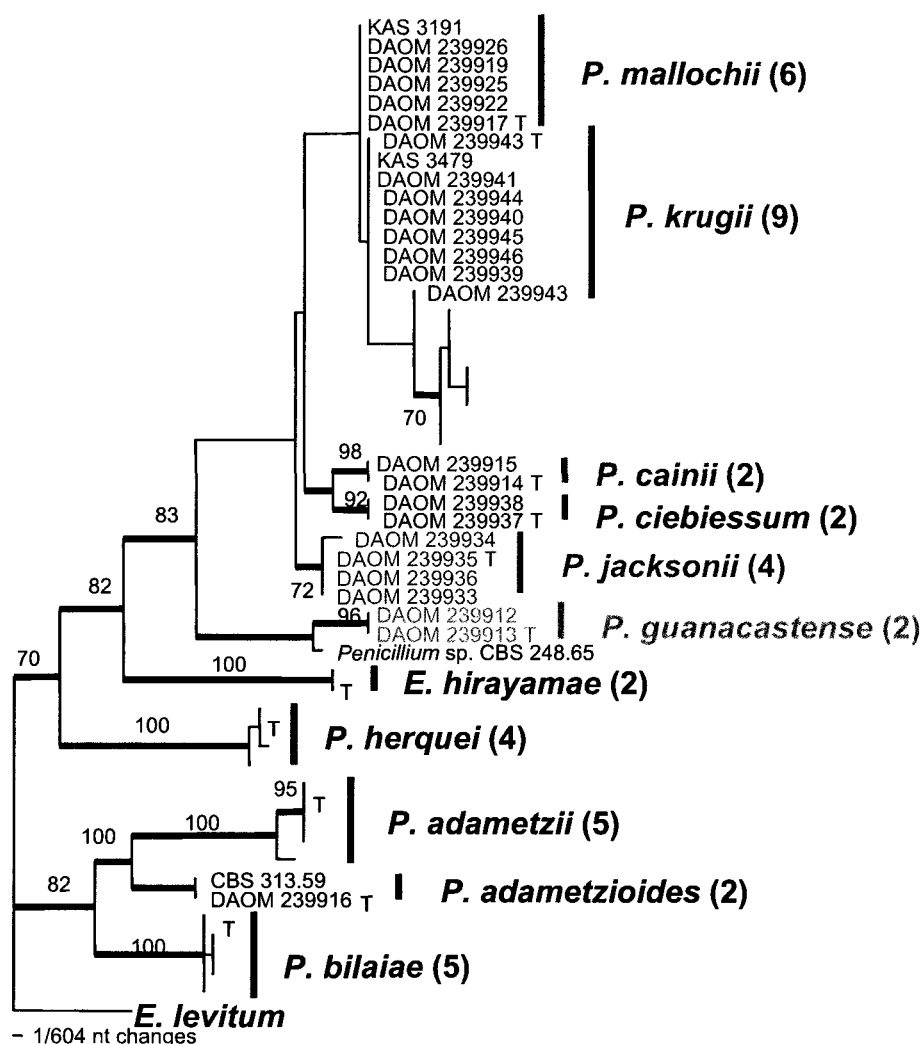


Figure 3.8: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *CoxI* sequences. One out of 244 most parsimonious trees (L=164, CI=0.579, RI=0.905, RC=0.524, HI=0.421). A heuristic search with 84 parsimony informative characters and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

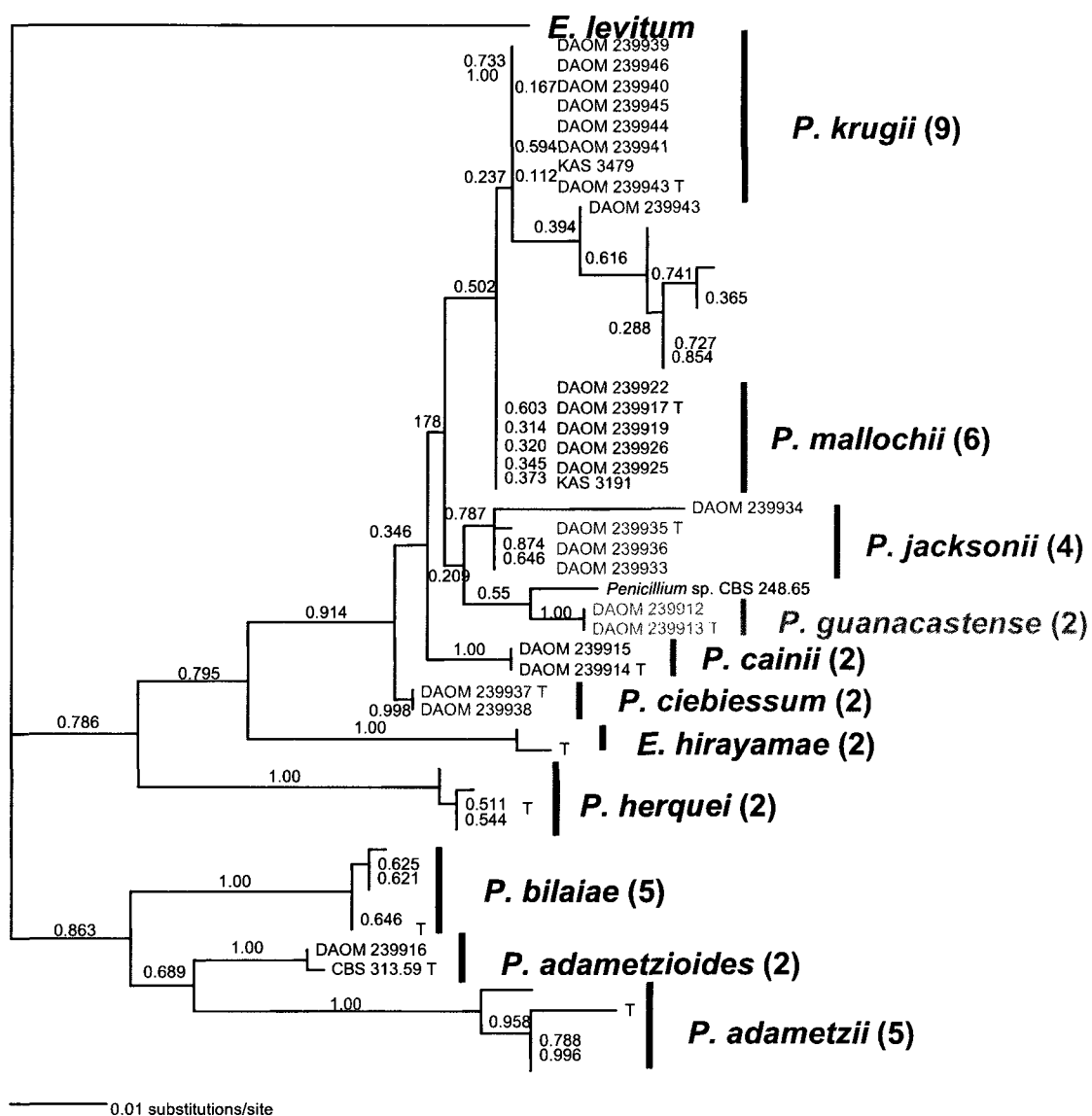


Figure 3.9: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *Cox1* sequences. The tree was constructed using the GTR+G nucleotide substitution model, 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

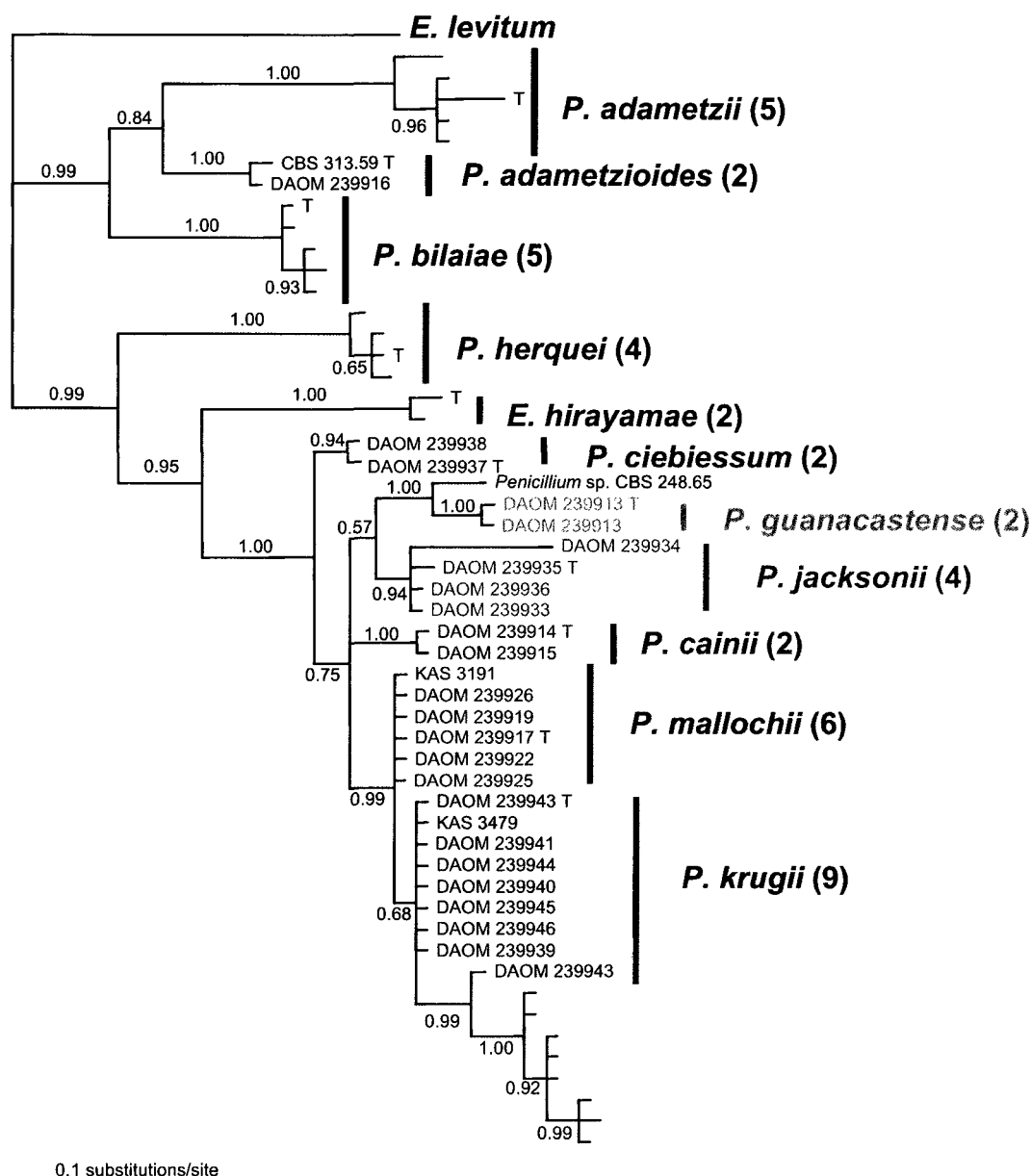


Figure 3.10: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *Cox1* sequences. The tree was constructed using the GTR+G nucleotide substitution model. Posterior probabilities are presented. The number in parenthesis represents the number of strains; T represents the ex-type strains.

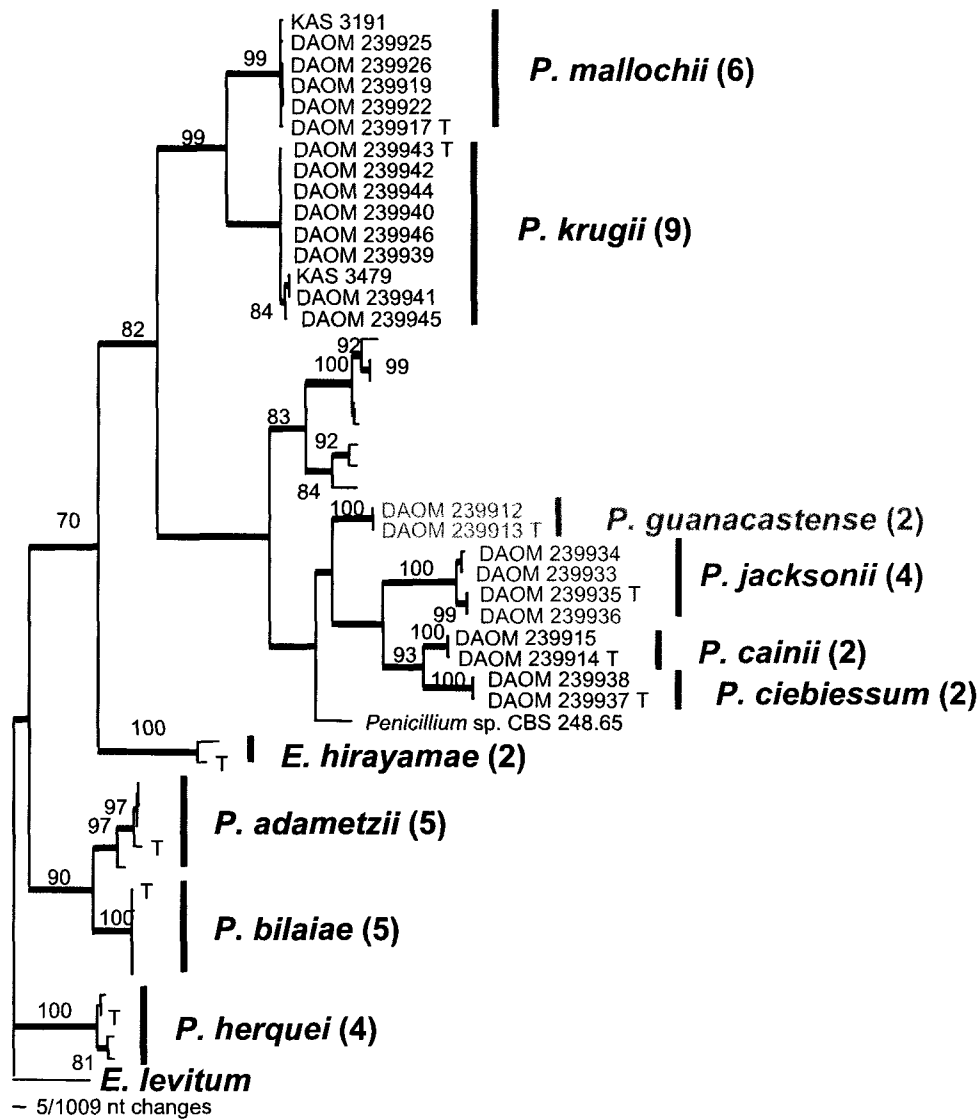


Figure 3.11: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *TEF1-α* sequences. One out of 6 most parsimonious trees (L=244, CI=0.689, RI=0.898, RC=0.619, HI=0.311). A heuristic search with 244 parsimony informative characters and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

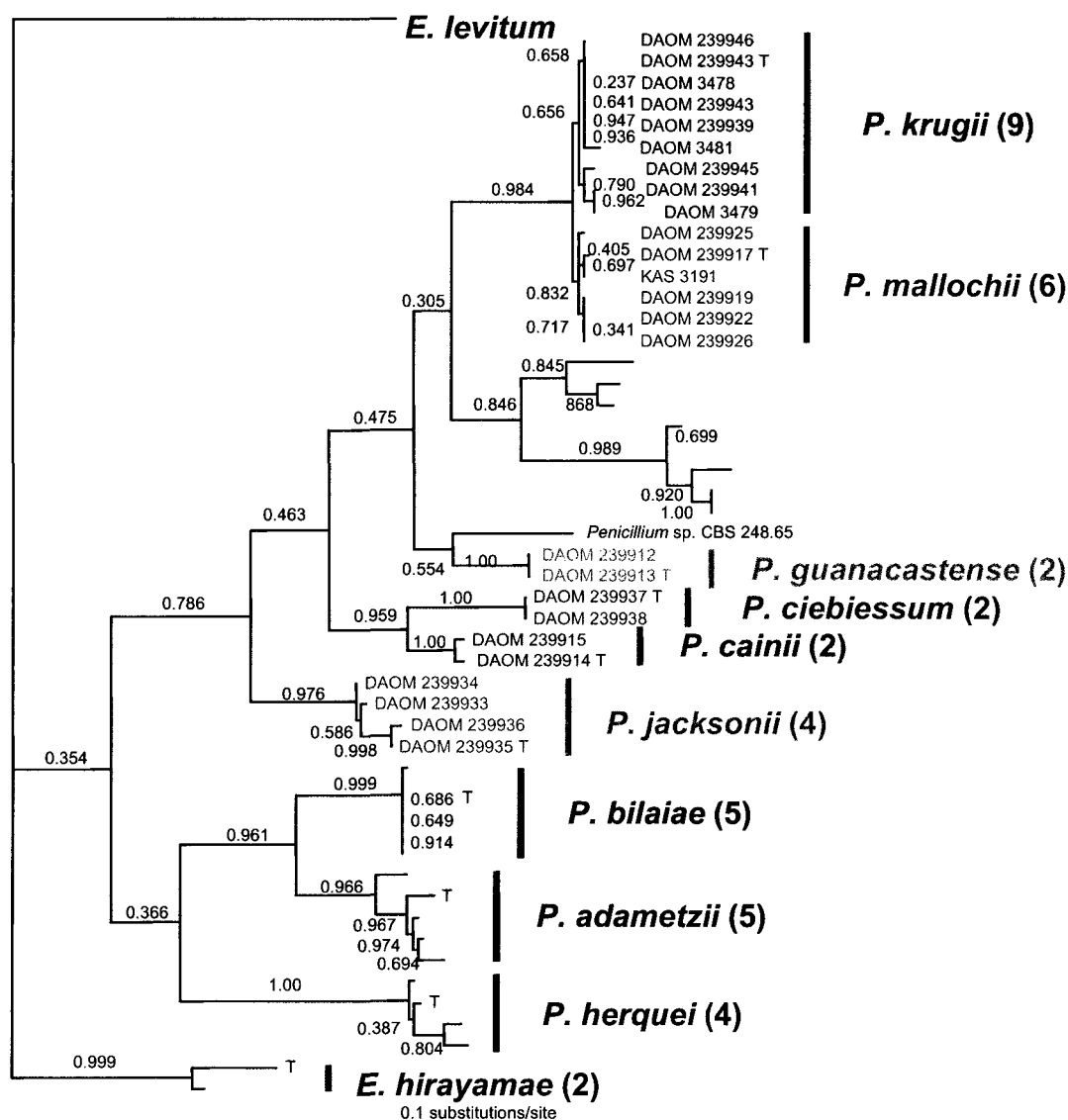


Figure 3.12: Maximum likelihood gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *TEF1-α* sequences. The tree was constructed using the GTR+G+I nucleotide substitution model, 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

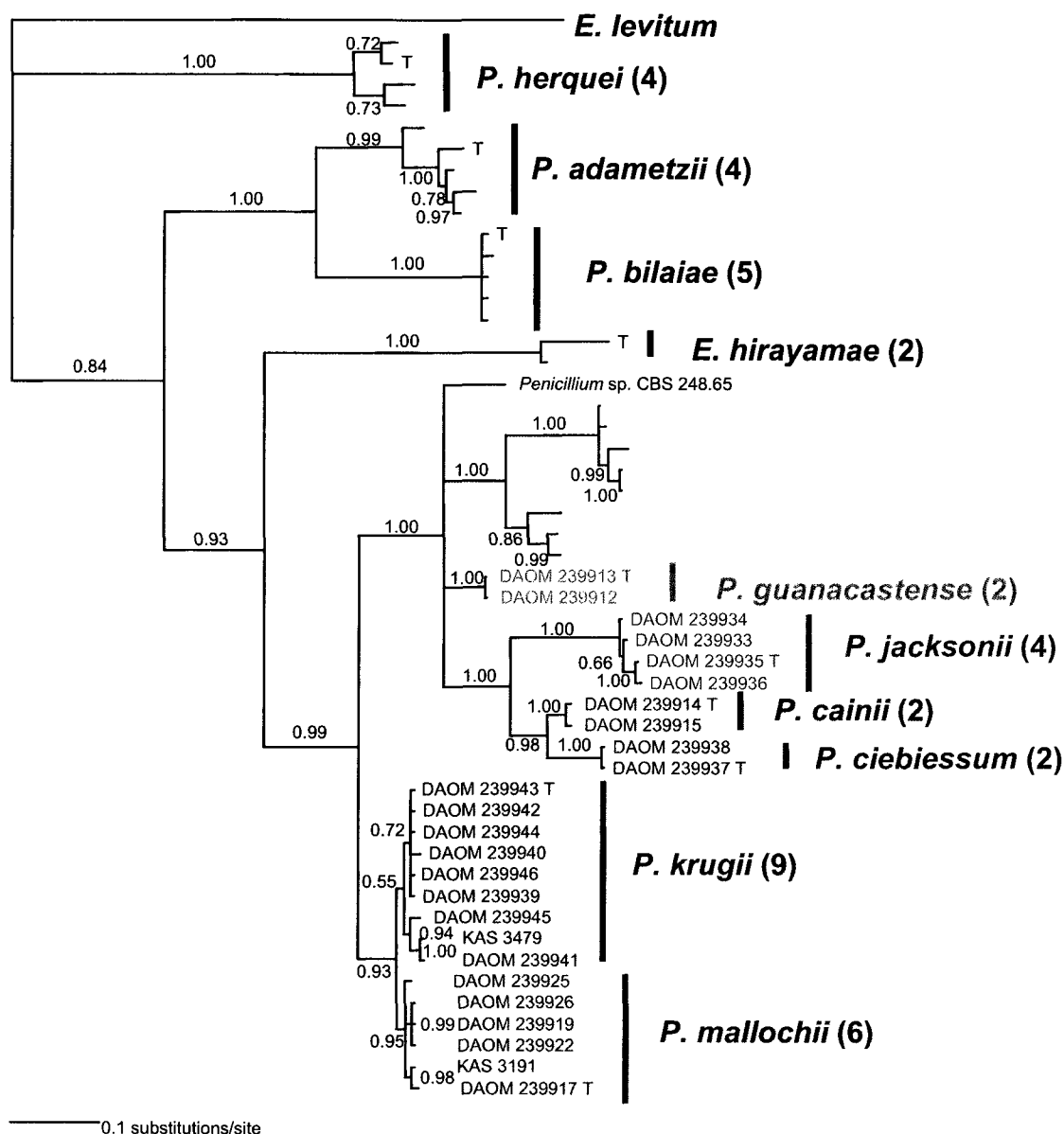


Figure 3.13: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *TEF1-α* sequences. The tree was constructed using the GTR+G+I nucleotide substitution model. Posterior probabilities are demonstrated, the number in parenthesis represents the number of strains; T represents the ex-type strain.

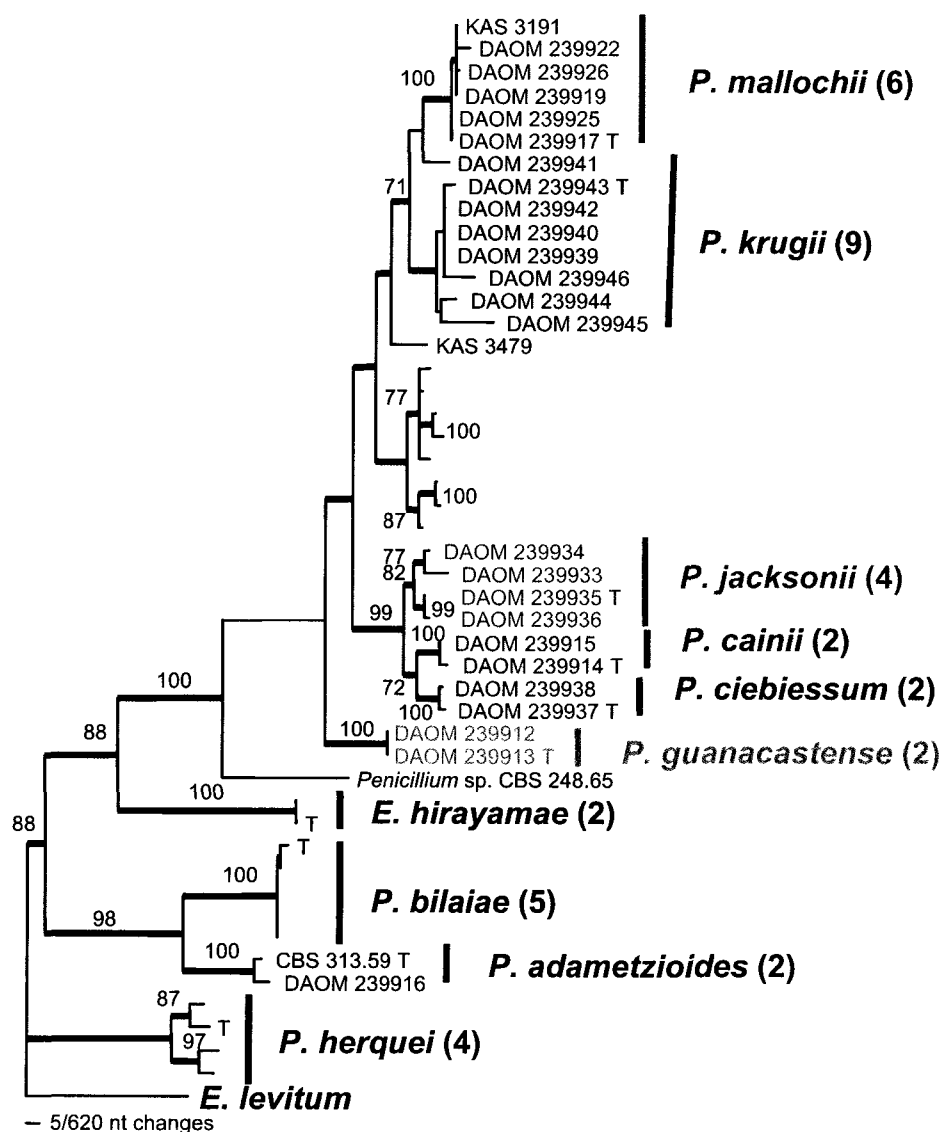


Figure 3.14: Maximum parsimony gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on CaM sequences. One out of 500 most parsimonious trees (L=639, CI=0.604, RI=0.855, RC=0.516, HI=0.396). A heuristic search with 244 parsimony informative characters and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

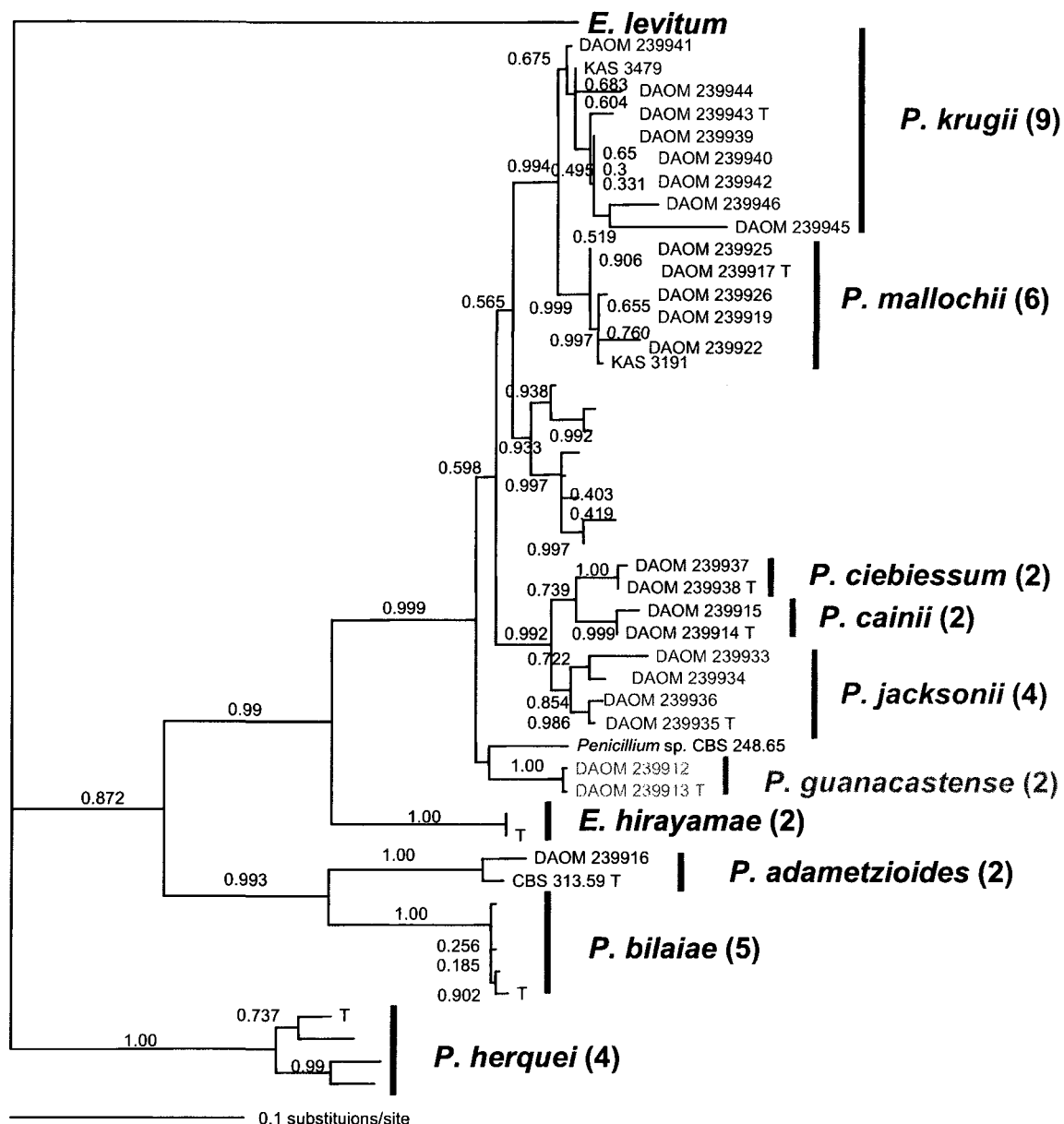


Figure 3.15: Maximum likelihood tree gene of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on CaM sequences. The tree was constructed using the GTR+G nucleotide substitution model, 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

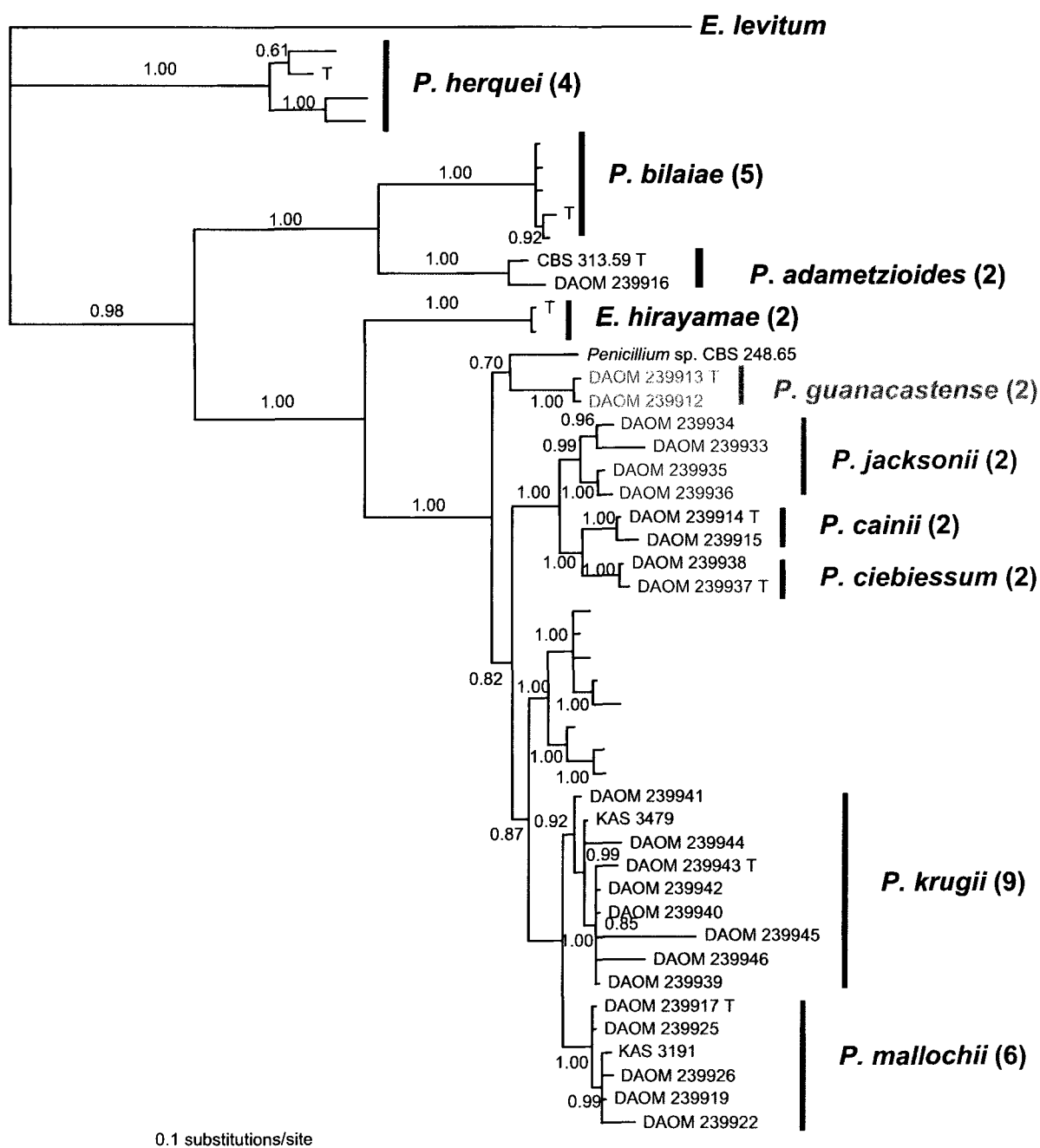


Figure 3.16: Bayesian inference gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on CaM sequences. The tree was constructed using the GTR+G nucleotide substitution model. Posterior probabilities are demonstrated, the number in parenthesis represents the number of strains; T represents the ex-type strains.

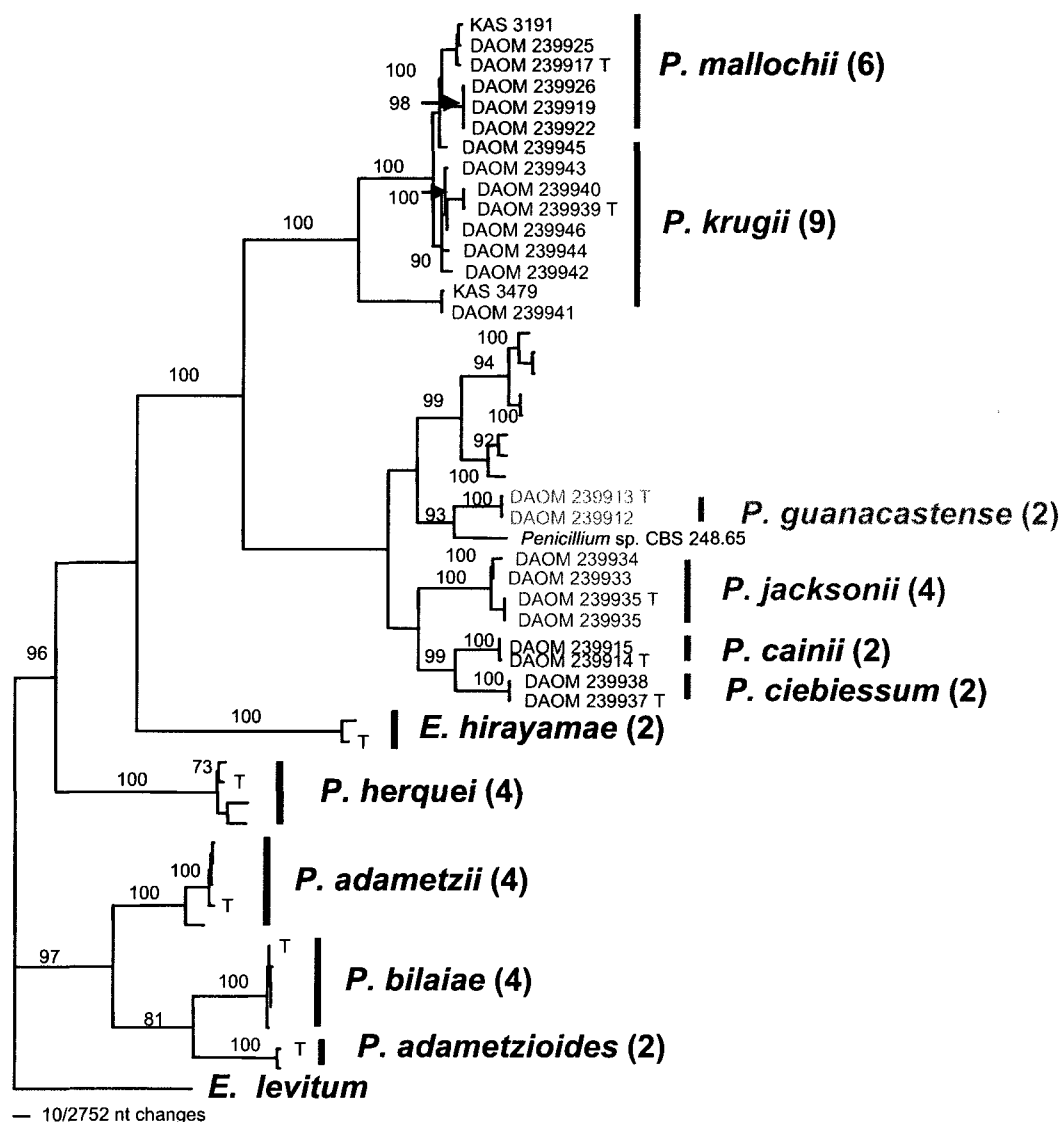


Figure 3.17: Maximum parsimony combined gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *BenA*, ITS, *Cox1*, and *TEF1-α* sequences. One out of one most parsimonious tree (L=2047, CI = 0.616, RI = 0.878, RC = 0.541, HI = 0.384). A heuristic search with 819 parsimony informative characters and 1000 bootstrap replicates were performed; bootstrap values above 70% are presented. Thickened lines represent strict consensus branches. The number in parenthesis represents the number of strains; T represents the ex-type strain.

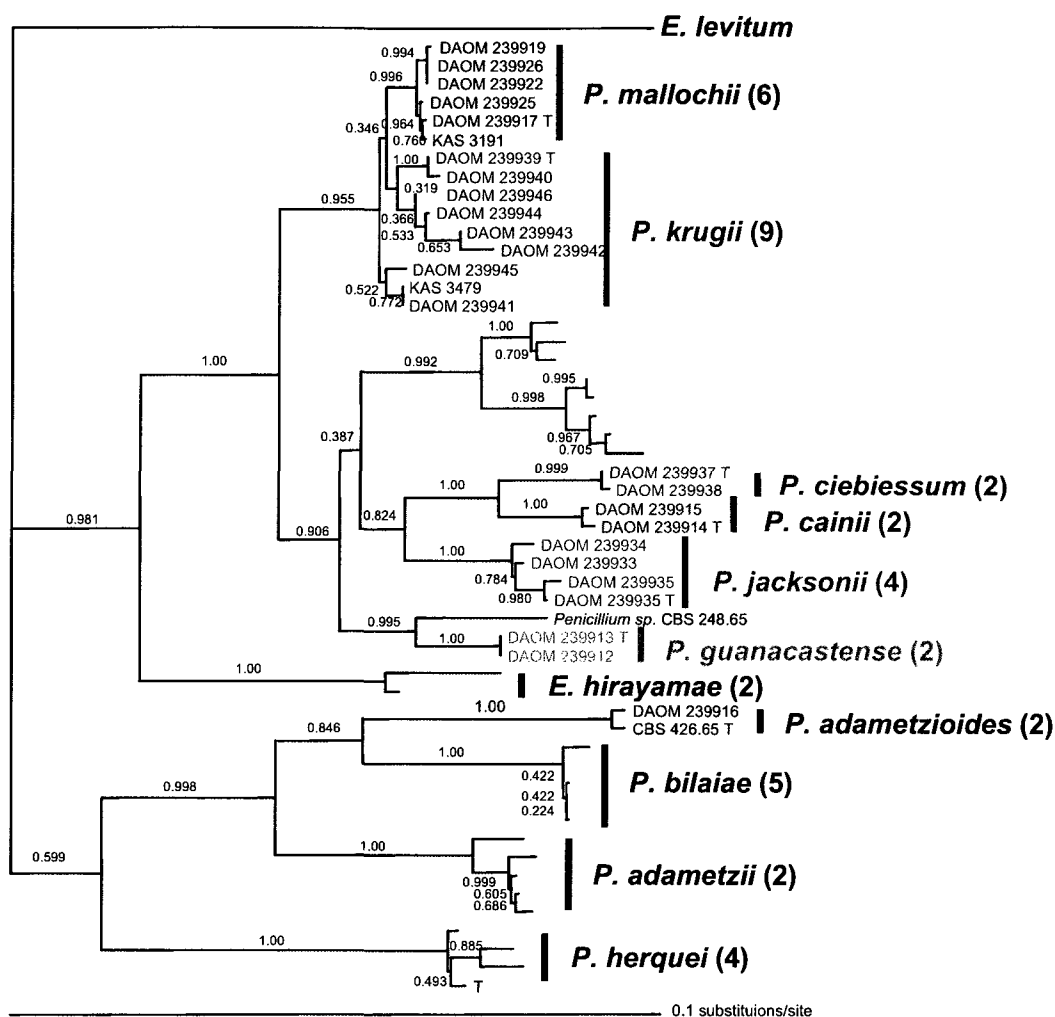


Figure 3.18: Maximum likelihood combined gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *BenA*, ITS, *Cox1*, and *TEF1-α* sequences. The tree was constructed using the GTR+G nucleotide substitution model, 1000 bootstrap replicates were performed. The number in parenthesis represents the number of strains; T represents the ex-type strain.

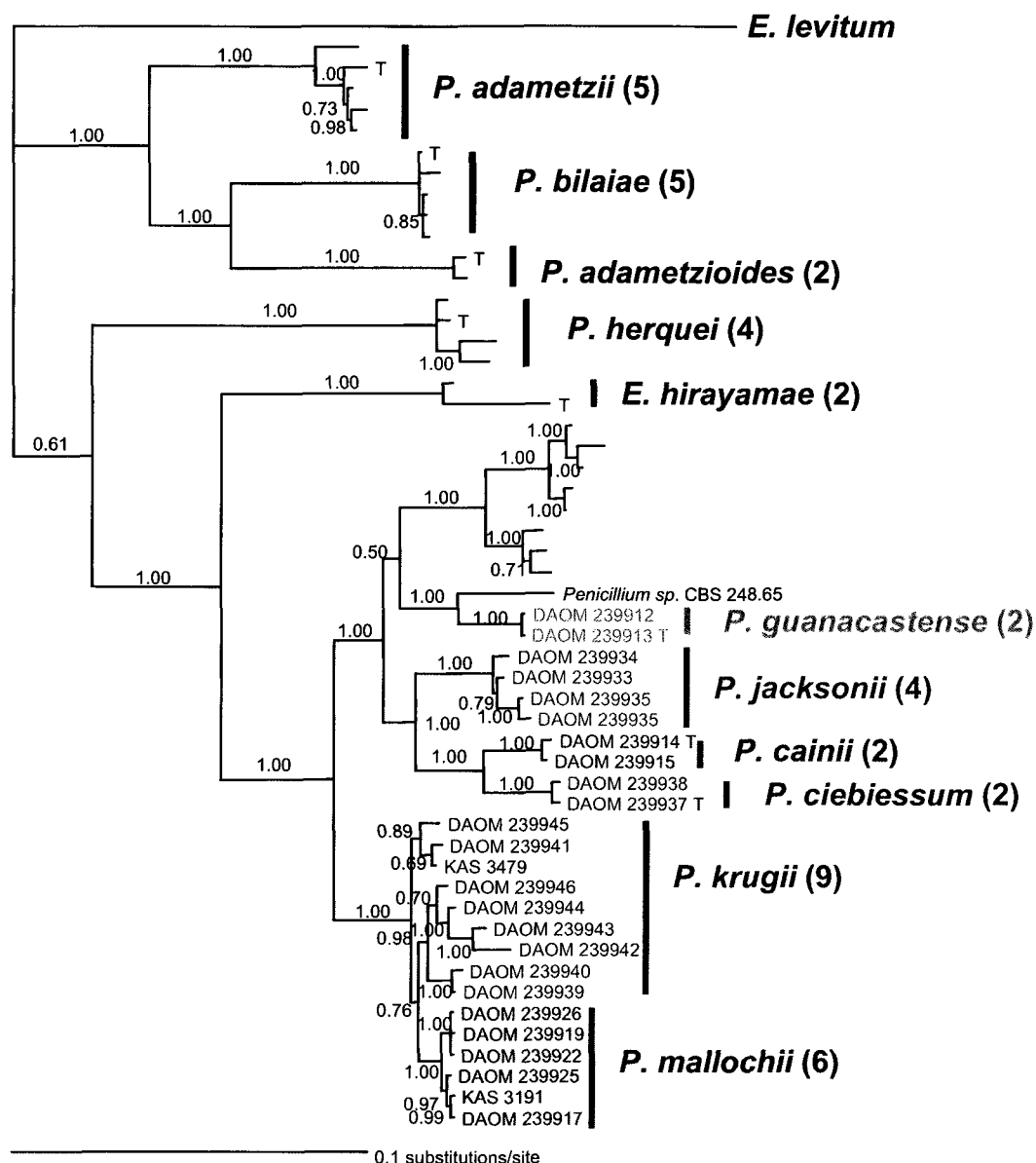


Figure 3.19: Bayesian inference combined gene tree of species in Peterson's (2000) Group 3 of *Penicillium*, demonstrating the position of *P. sclerotiorum* complex species based on *BenA*, ITS, *Cox1*, and *TEF1-α* sequences. The tree was constructed using the GTR+G nucleotide substitution model, except for *TEF1-α* where the GTR+G+I was implemented. Posterior probabilities are demonstrated, the number in parenthesis represents the number of strains; T represents the ex-type strain.

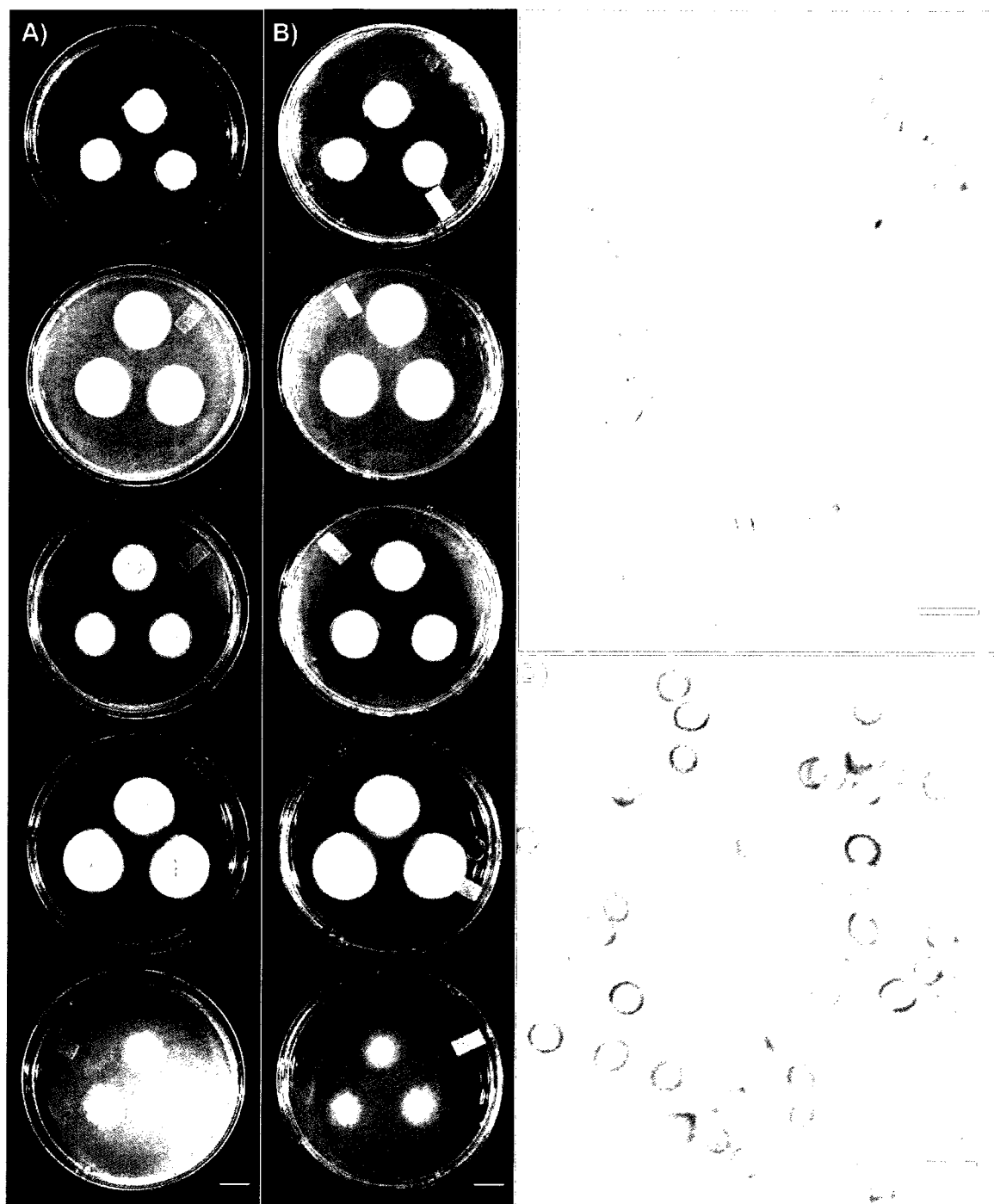


Figure 3.20: Colony (A–B) and microscopic (C–D) photographs of *P. adametzioides* strain DAOM 239916. Obverse (A) and (B) reverse colony photographs of CYA, MEA, CZ, YES and CREA, scale bar = 20 mm. Microscopic photographs of conidiophores (C) and conidia (D), scale bar = 10 μ m.

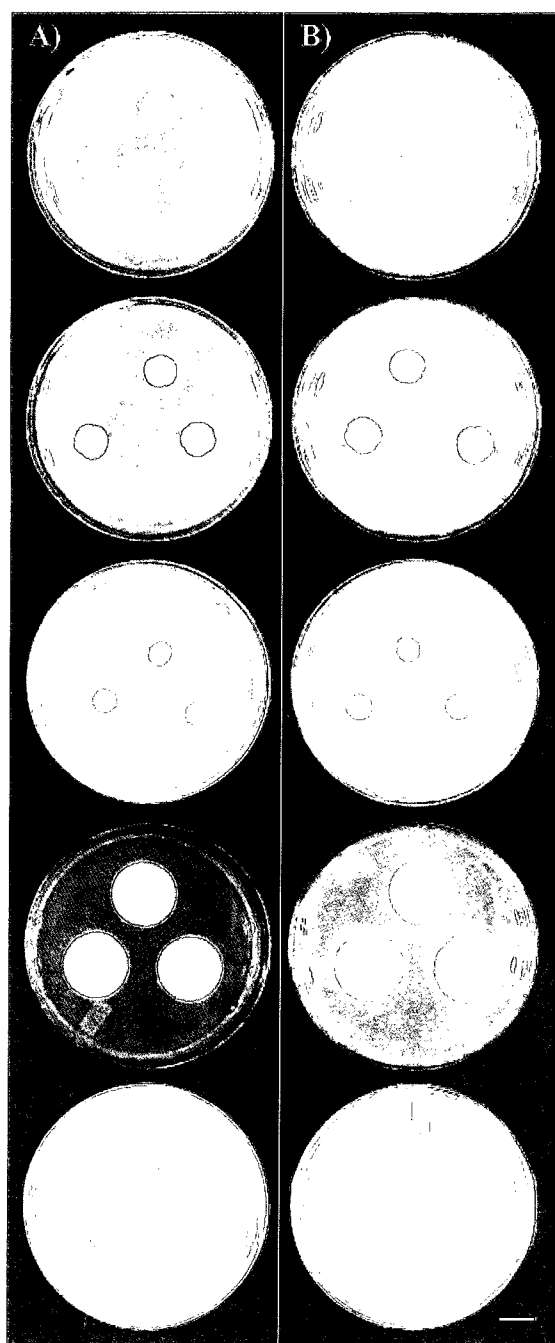


Figure 3.21: Colony (A–B) and microscopic (C–D) photographs of *P. multicolor* ex-type strain. Obverse (A) and (B) reverse colony photographs of CYA, MEA, CZ, YES and CREA, scale bar = 20 mm. Microscopic photographs of conidiophores (C) and conidia (D), scale bar = 10 μ m.

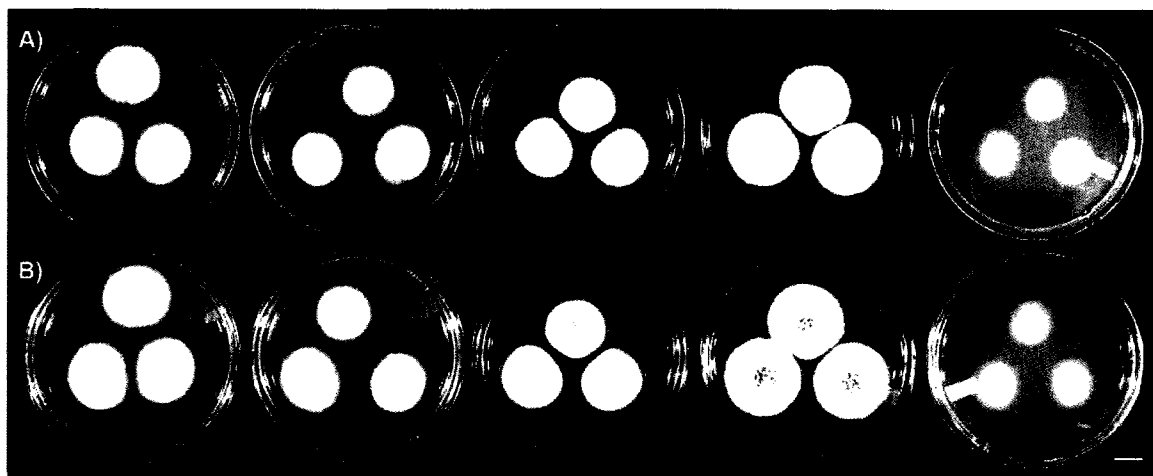


Figure 3.22: *Penicillium* sp. strain CBS 248.65 obverse (A) and reverse (B) colony photographs. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

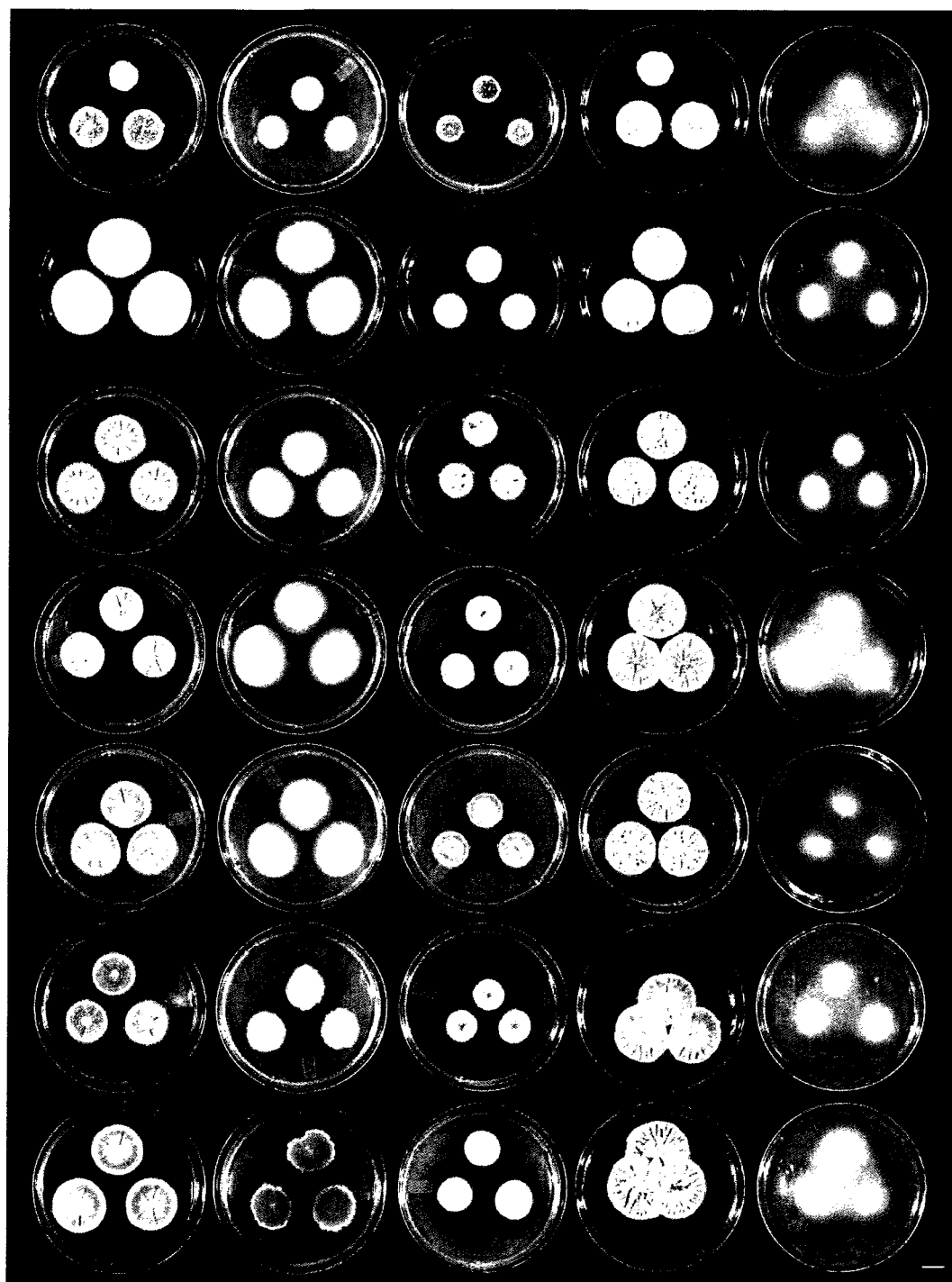


Figure 3.23: Colony obverse of the ex-type strains in the *P. sclerotiorum* complex grown at 25°C in the dark for 7 d. Columns top to bottom: *P. sclerotiorum*, *P. krugii*, *P. jacksonii*, *P. cainii*, *P. ciebiessum*, *P. mallochii* and *P. guanacastense*. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

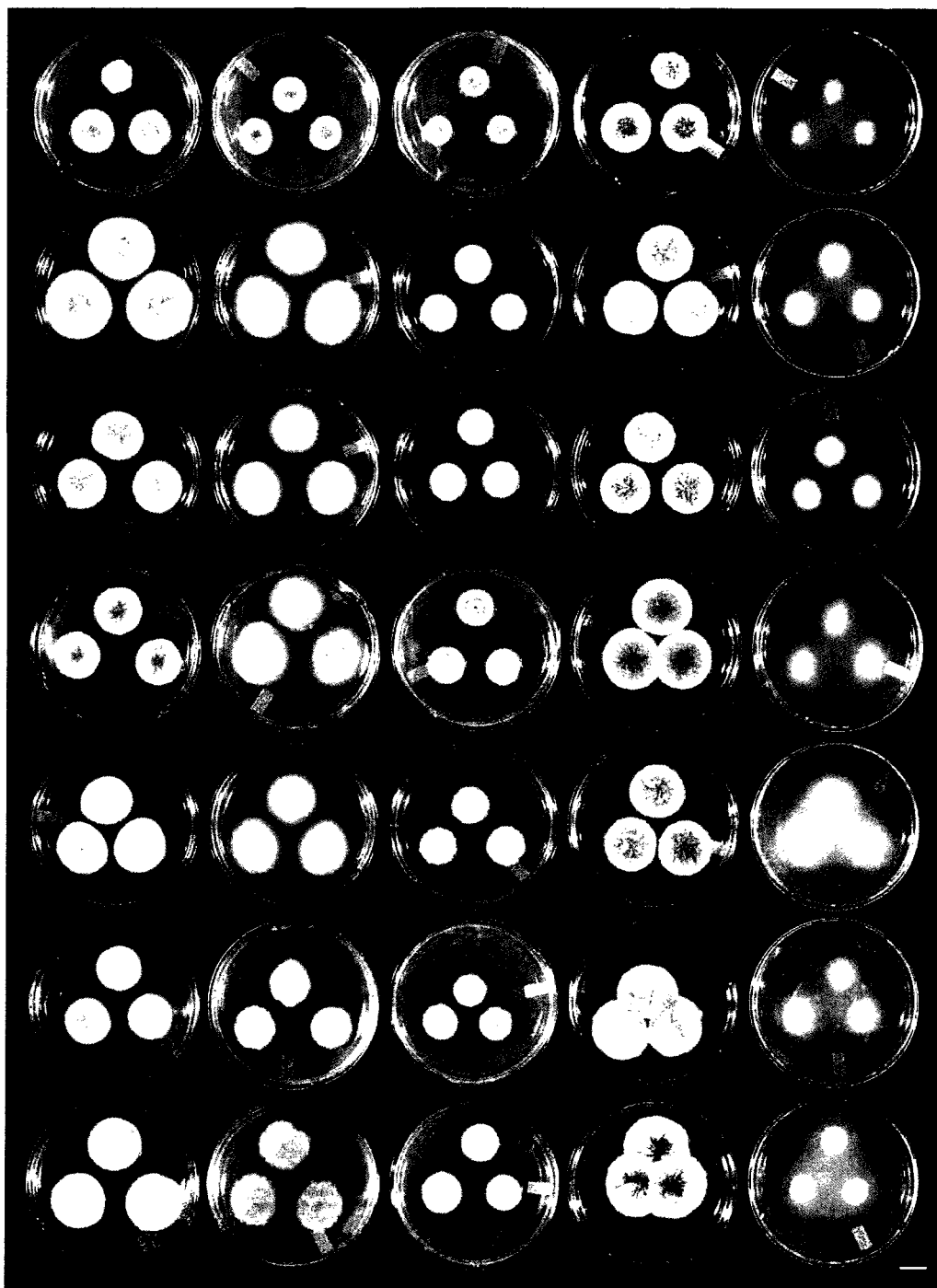


Figure 3.24: Colony reverse of the ex-type strains in the *P. sclerotiorum* complex grown at 25°C in the dark for 7 d. Columns top to bottom: *P. sclerotiorum*, *P. krugii*, *P. jacksonii*, *P. cainii*, *P. ciebiessum*, *P. mallochii* and *P. guanacastense*. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

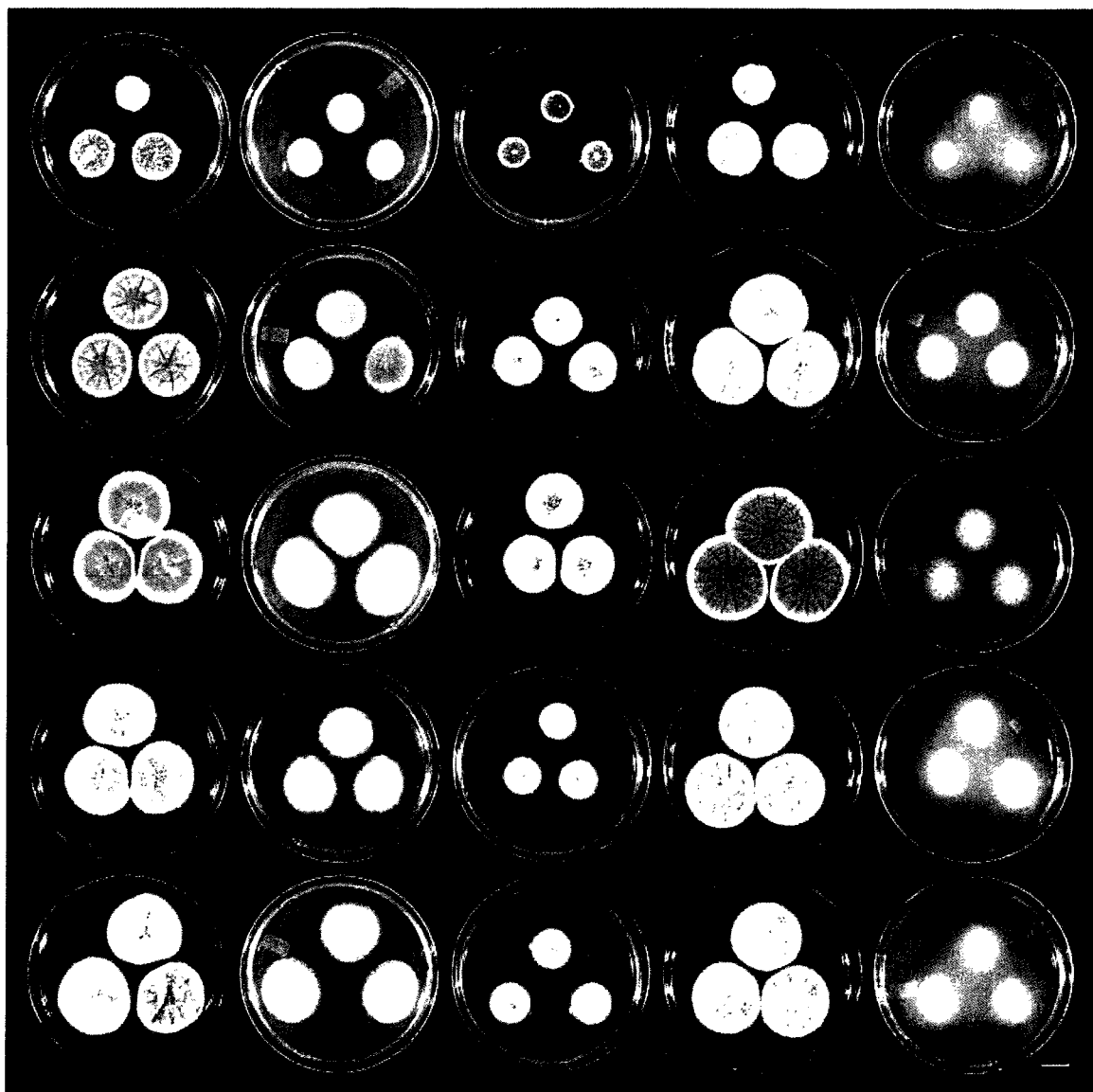


Figure 3.25: Colony obverse of *P. sclerotiorum* strains grown at 25°C in the dark for 7 d. Columns top to bottom: NRRL 2087 (ex-type), NRRL 32583, DAOM 239930, DAOM 239931 and DAOM 239932. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

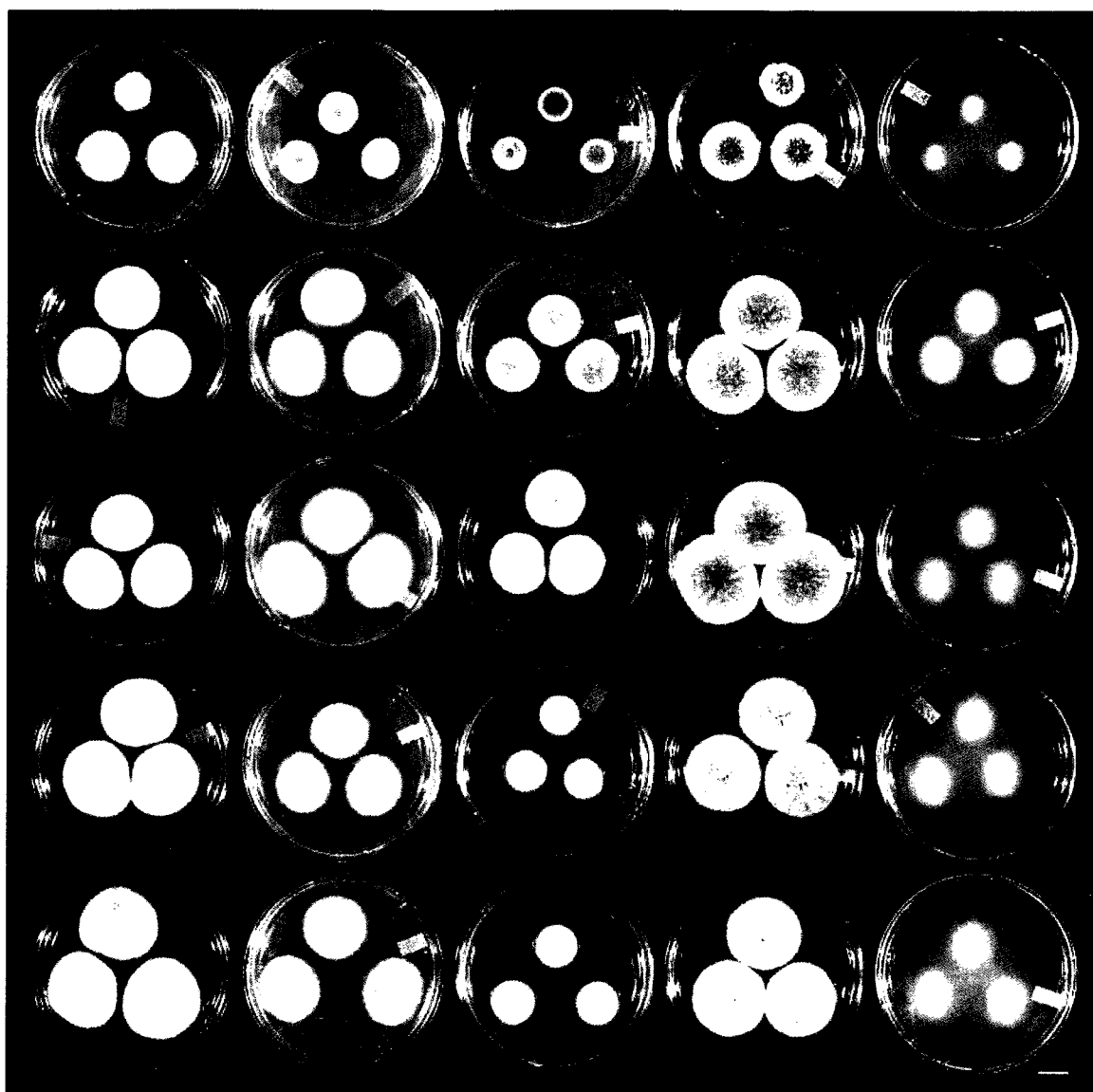


Figure 3.26: Colony reverse of *P. sclerotiorum* strains grown at 25°C in the dark for 7 d. Columns top to bottom: NRRL 2087 (ex-type), NRRL 32583, DAOM 239930, DAOM 239931 and DAOM 239932. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

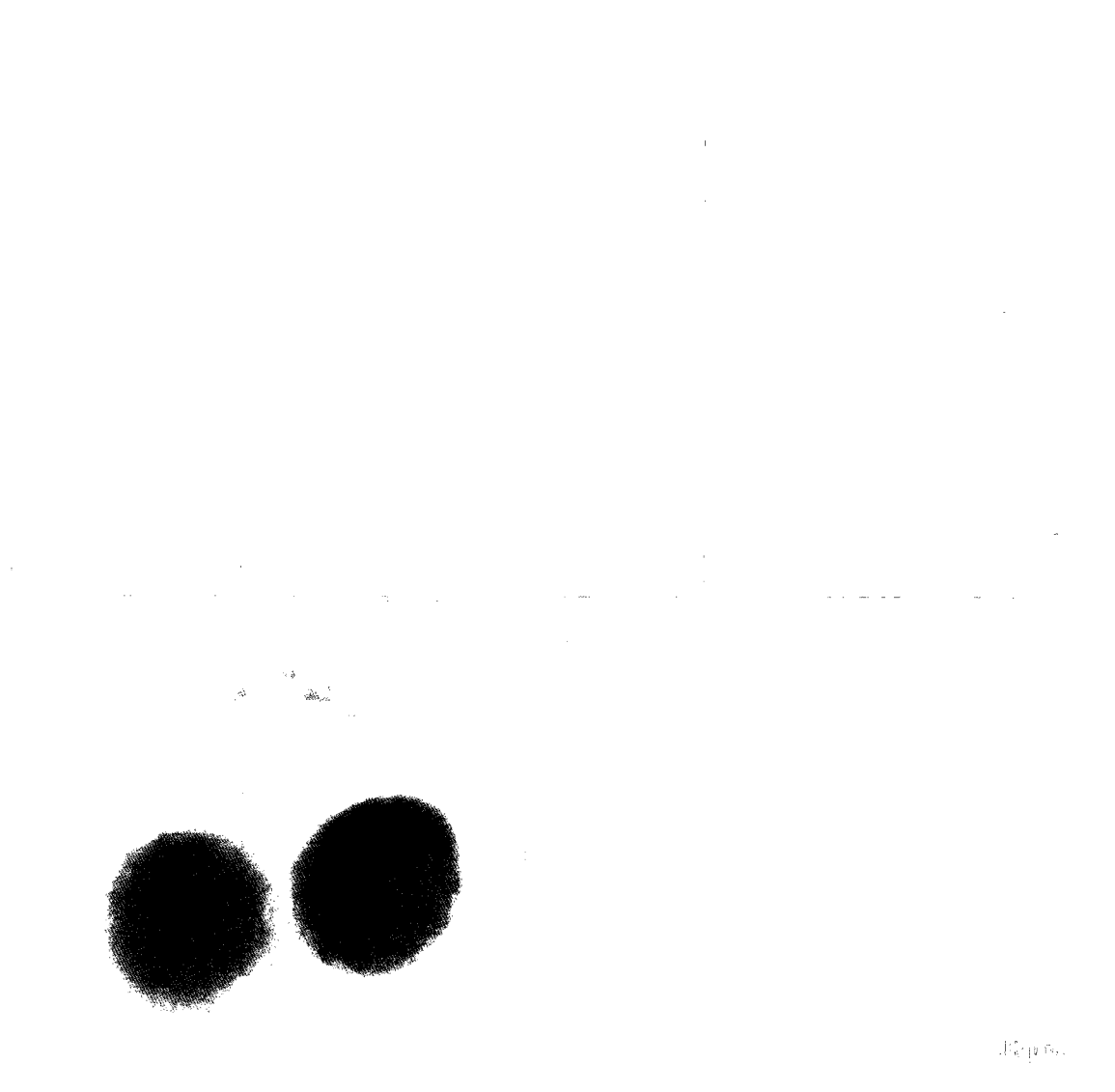


Figure 3.27: *Penicillium sclerotiorum*. Microscopic differential interference contrast photographs of the ex-type strain (NRRL 2087) of conidiophores (A–C), conidia (D), sclerotia (E) and sclerotial cells (F).

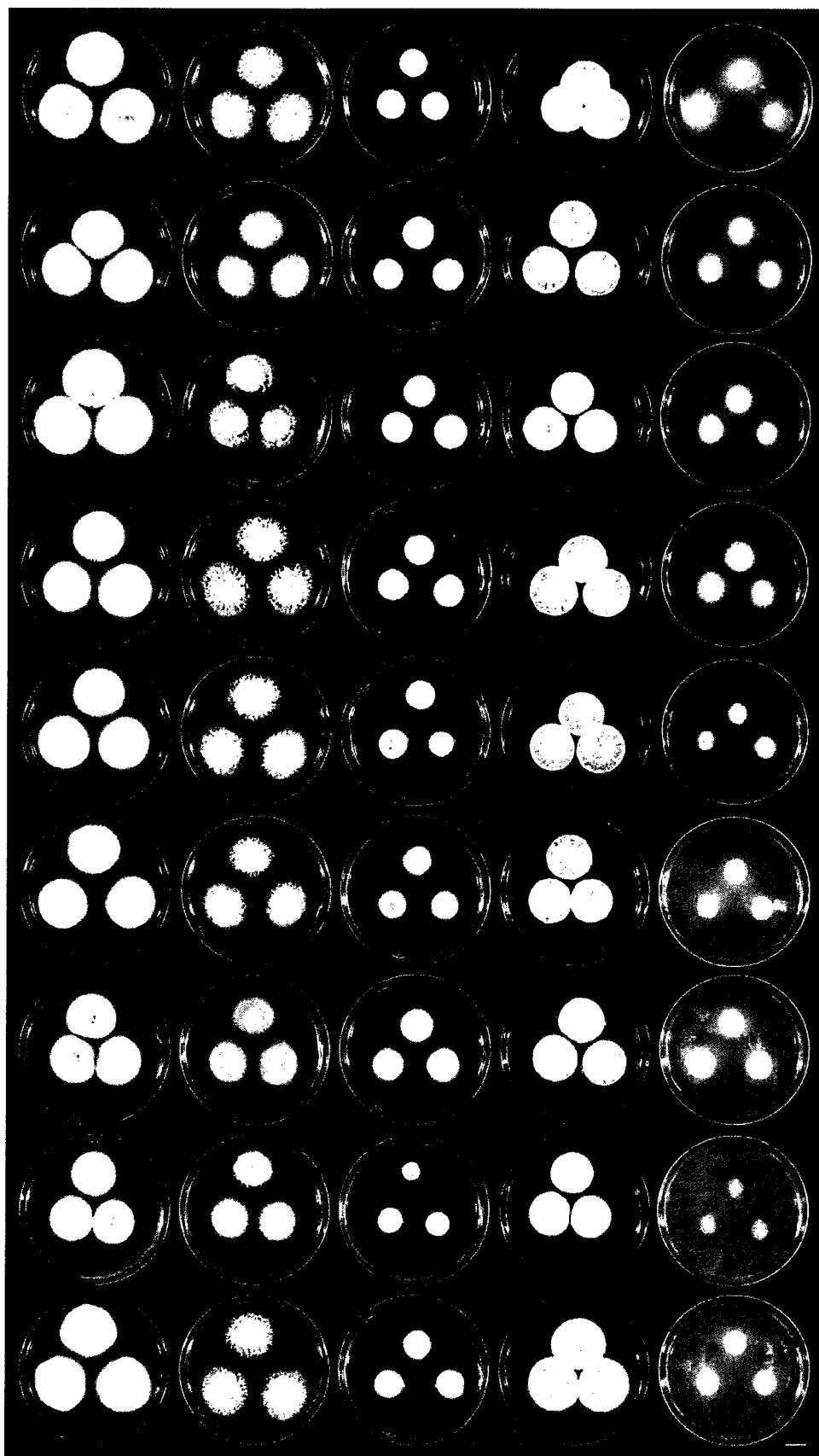


Figure 3.28: Colony obverse of *P. krugii* strains grown at 25°C in the dark for 7 d. Columns top to bottom: DAOM 239942, DAOM 239943, DAOM 239944, KAS 3479, DAOM 239939 (ex-type), DAOM 239940, DAOM 239941, DAOM 239945, DAOM 239946. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

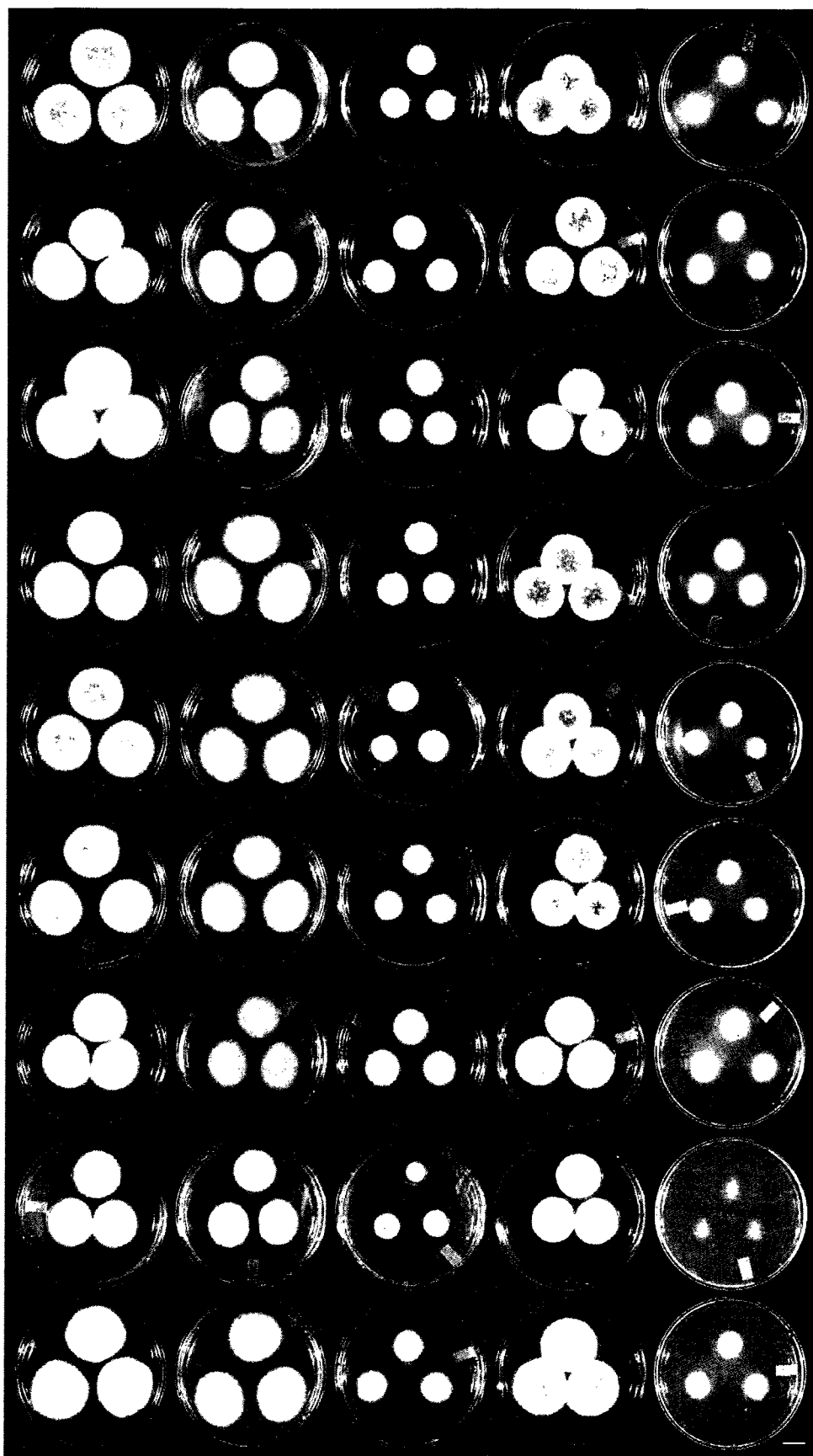


Figure 3.29: Colony reverse of *P. krugii* strains grown at 25°C in the dark for 7 d. Columns top to bottom: DAOM 239942, DAOM 239943, DAOM 239944, KAS 3479, DAOM 239939 (ex-type), DAOM 239940, DAOM 239941, DAOM 239945, DAOM 239946. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

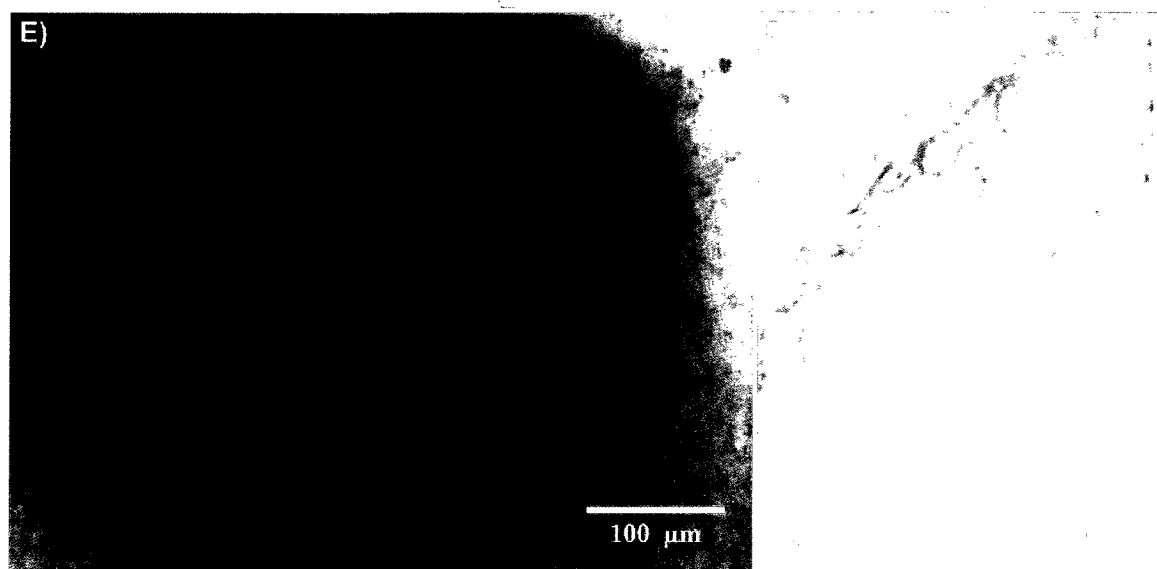


Figure 3.30: *Penicillium krugii*. Microscopic differential interference contrast photographs of the ex-type strain (DAOM 239943) of conidiophores (A–C), conidia (D), sclerotia (E) and sclerotial cells (F).

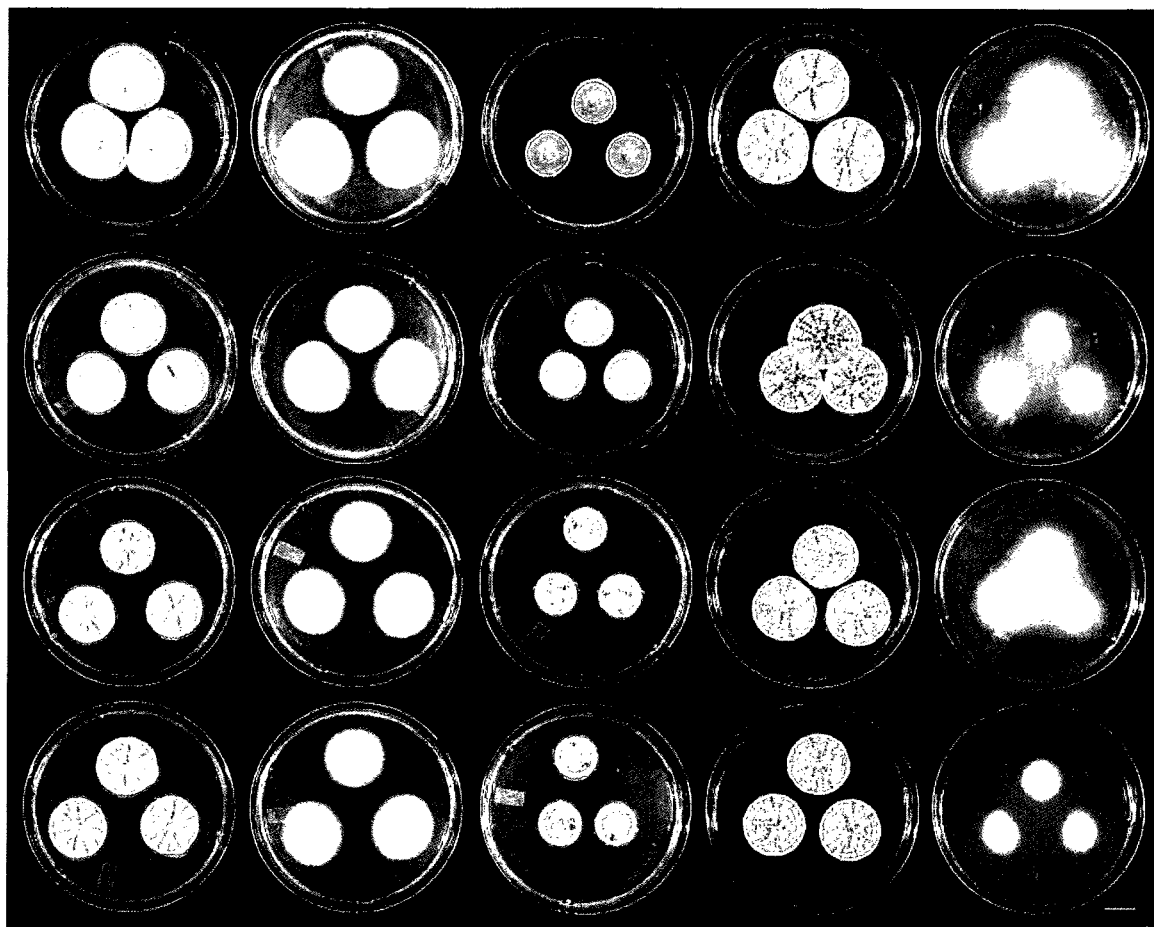


Figure 3.31: Colony obverse of *P. jacksonii* strains grown at 25°C in the dark for 7 d. Columns top to bottom: DAOM 239933, DAOM 239934, DAOM 239935 (ex-type) and DAOM 239936. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

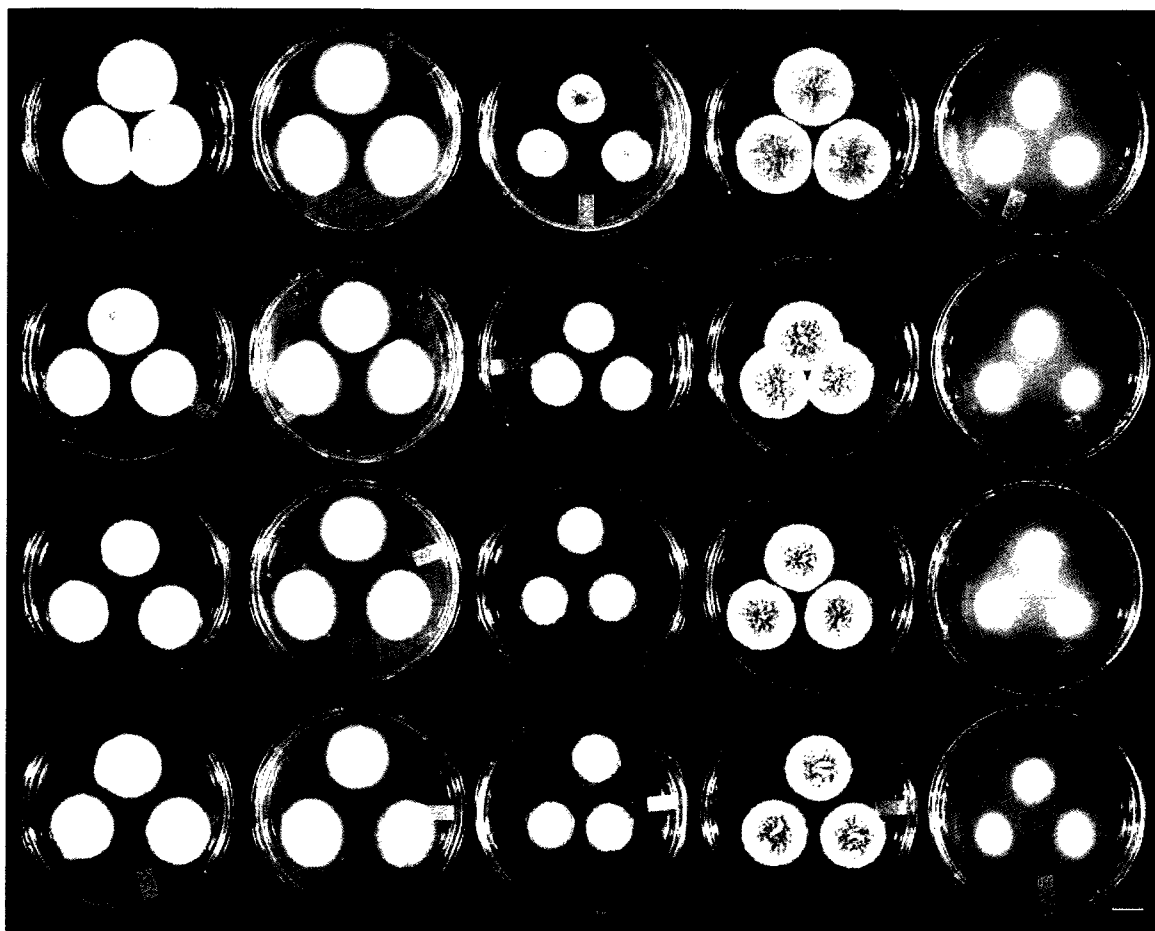


Figure 3.32: Colony reverse of *P. jacksonii* strains grown at 25°C in the dark for 7 d. Columns top to bottom: DAOM 239933, DAOM 239934, DAOM 239935 (ex-type) and DAOM 239936. Rows left to right: CYA, MEA, CZ, YES and CREA. Scale bar = 10 mm.

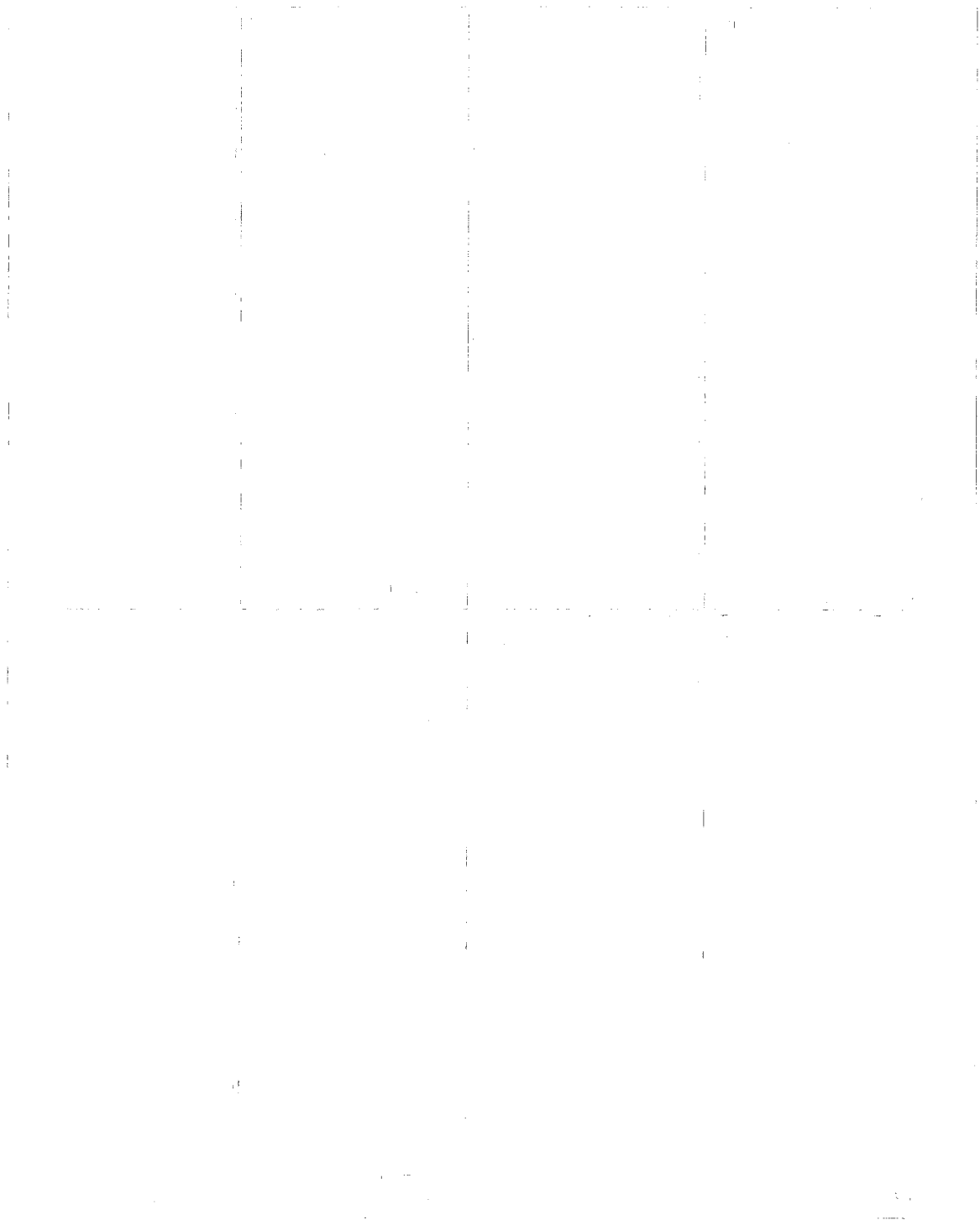


Figure 3.33: *Penicillium jacksonii*. Microscopic differential interference contrast photographs of ex-type strain (DAOM 239935) of conidiophores (A–G) and conidia (D).

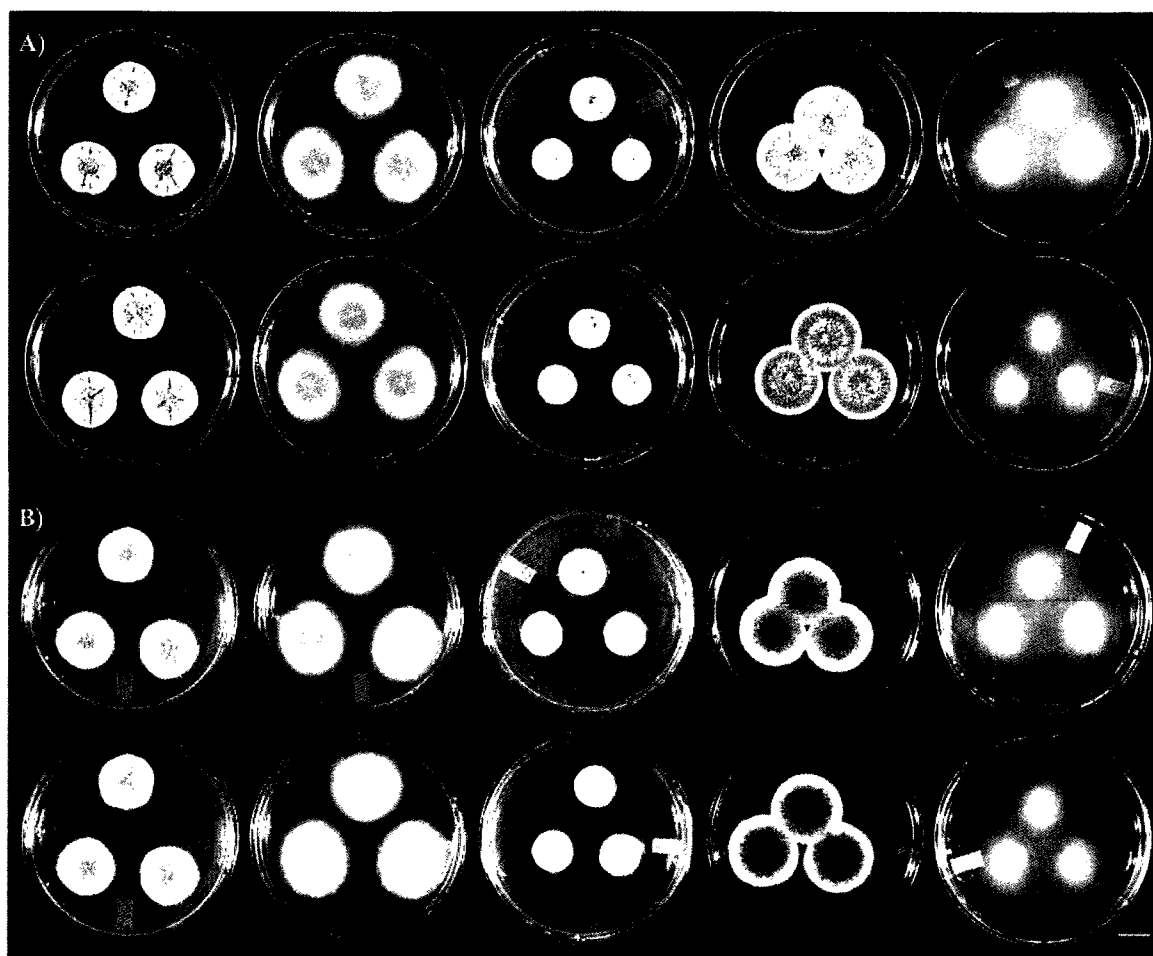


Figure 3.34: *Penicillium cainii* strains grown at 25°C in the dark for 7 d, obverse (A) and reverse (B) colony photographs. First and second rows: DAOM 239914 (ex-type) and DAOM 239915. Columns left to right: CYA, MEA, CZ, YES, and CREA. Scale = 10 mm.

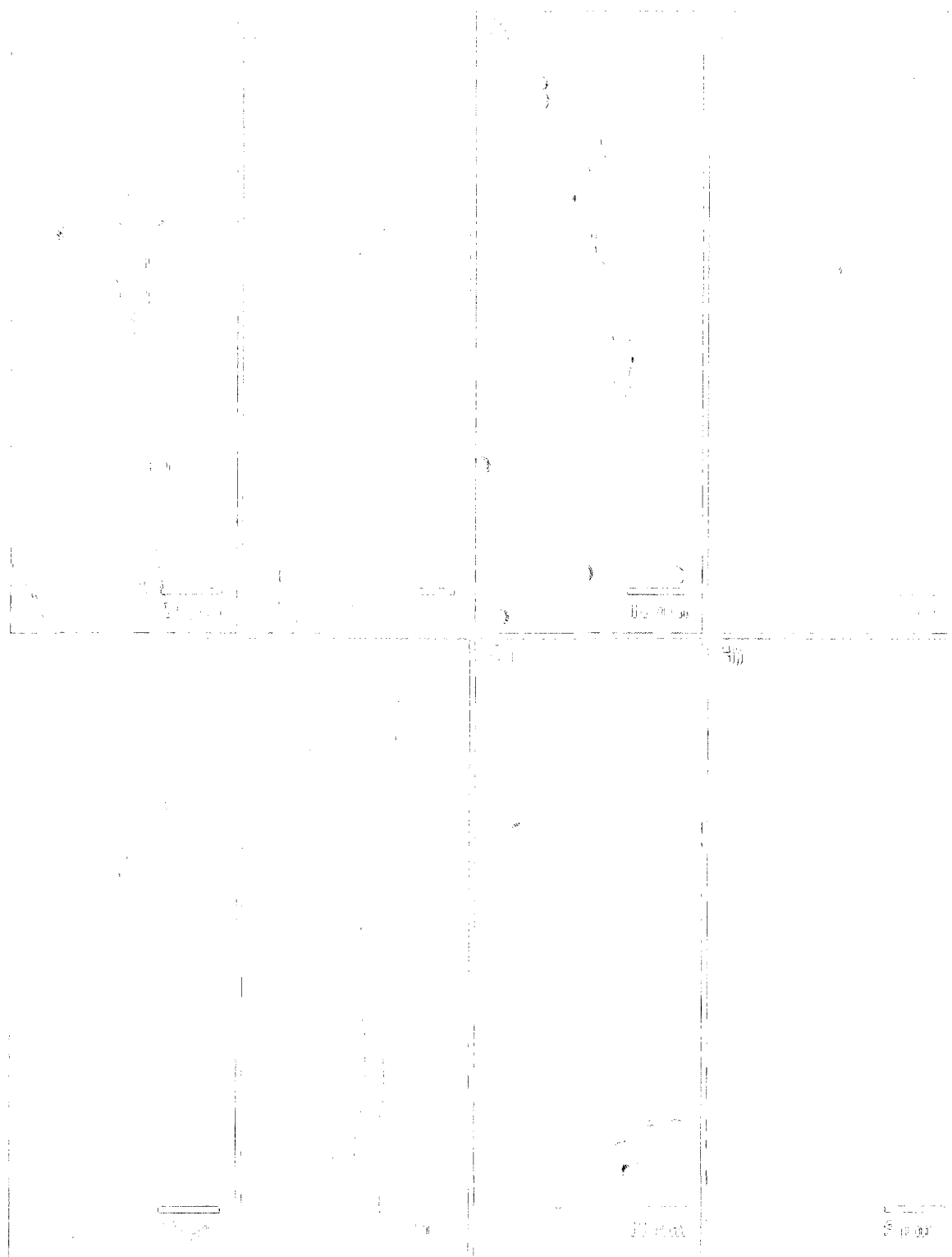


Figure 3.35: *Penicillium cainii*. Microscopic differential interference contrast photographs of the ex-type strain (DAOM 239914) of conidiophores (A–G) and conidia (H).

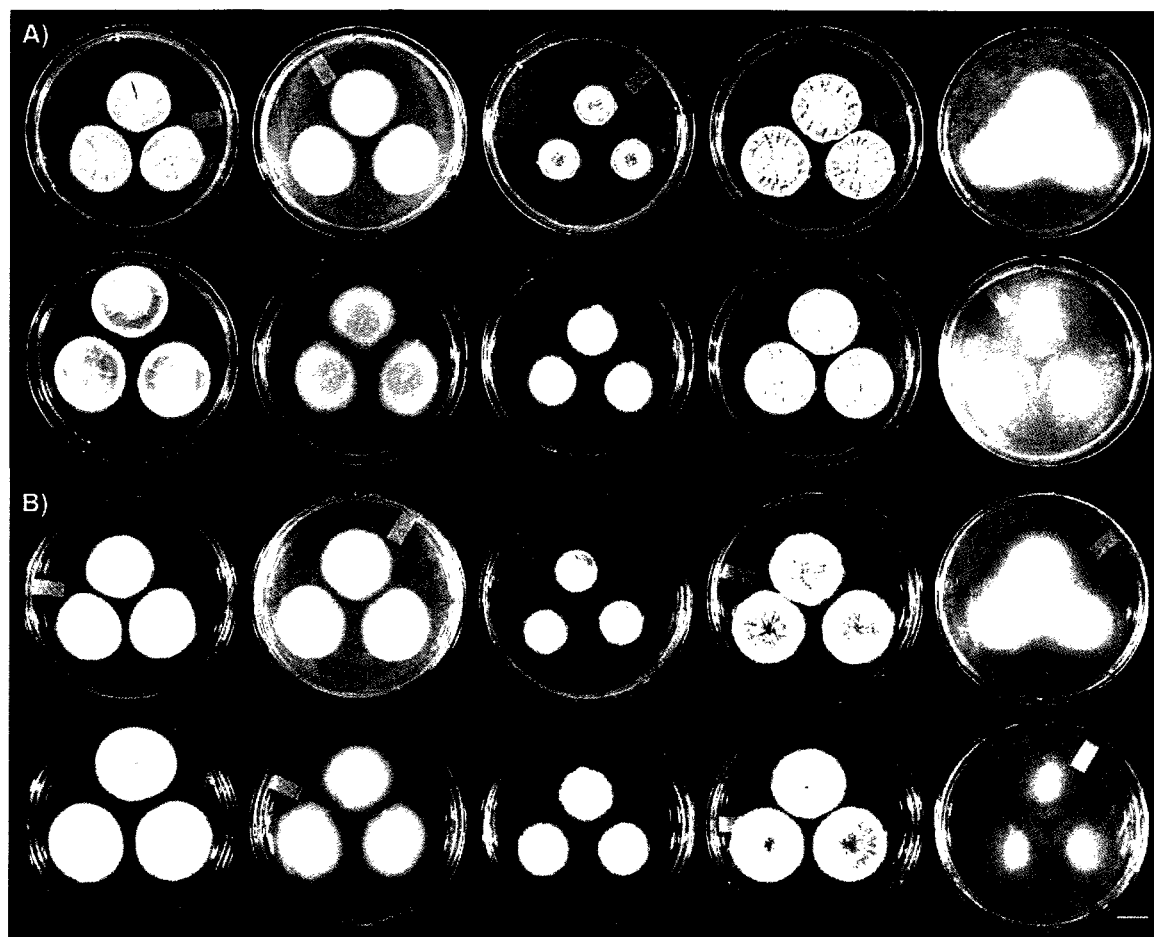


Figure 3.36: *Penicillium ciebiessum* strains grown at 25°C in the dark for 7 d, obverse (A) and reverse (B) photographs. First and second rows: DAOM 239937 (ex-type) and DAOM 239937. Columns left to right: CYA, MEA, CZ, YES, and CREA. Scale = 10 mm.

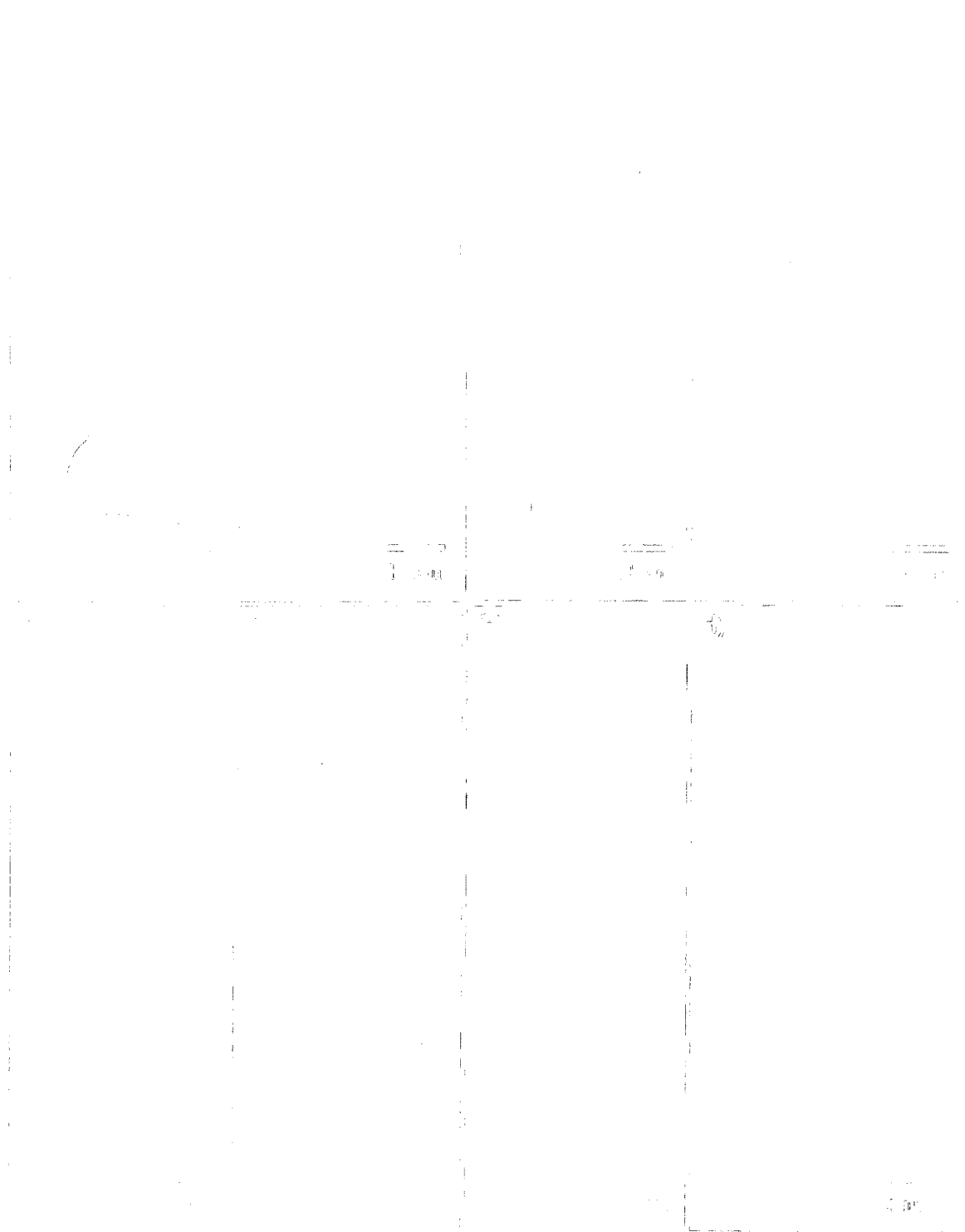


Figure 3.37: *Penicillium ciebiessum*. Microscopic differential interference contrast photographs of ex-type strain (DAOM 239939) of conidiophores (A–C) and conidia (D).

Chapter 4: Multiple gene genealogies reveal that *Penicillium oxalicum* is a single phylogenetic species

Karol G. Rivera and Keith A. Seifert

4.1 Abstract

Penicillium oxalicum is a cosmopolitan fungus that plays many ecological roles, ranging from a pathogen to a biocontrol agent. The species has been noted for morphological variation, especially in conidiophore morphology, where the presence of mono-, bi- and terverticillate conidiophores has been reported. Preliminary phylogenetic analyses with β -tubulin (*BenA*) revealed the presence of four possible phylogenetic species. The nuclear ribosomal internal transcribed spacer (ITS) region, cytochrome c oxidase subunit 1 (*Cox1*), translation elongation factor 1- α (*TEF1- α*) and calmodulin (CaM) gene genealogies were constructed using maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI) for 38 strains. The three groups observed in *BenA* were not present in the rest of the genes. Two groups were observed in the ITS, *TEF1- α* and CaM gene trees, but did not have strong statistical support in all analyses. Only one group was observed for *Cox1*. The lack of congruency in tree topologies across the gene genealogies suggested that *P. oxalicum* is a single phylogenetic species, with great morphological variability. Further investigation of *BenA* in four strains led to the detection of paralogs that were retrieved by cloning, which may represent functional genes or pseudogenes. The DNA sequence of the paralogs did not resemble any of the previous sequences identified as *P. oxalicum*. It is suggested that the groupings observed in the *BenA* may represent different allelic morphs or additional paralogs.

4.2 Introduction

Penicillium oxalicum was first described by James N. Currie and Charles Thom (1915). The species epithet reflects the production of oxalic acid. Thom (1930) and Raper and Thom (1949) placed the species in section *Asymmetrica* subsection *Velutina*. They described and keyed out *P. oxalicum* as a terverticillate species, but did not mention rami. Currie and Thom (1915) observed only biverticillate conidiophores (Figure 4.1). Careful examination of the species by Pitt (1979a) determined that it has biverticillate conidiophores and roughened, ellipsoidal conidia. Pitt (1979a) classified this species in subgenus *Furcatum* Pitt series *Furcatum* Pitt section *Oxalica* Pitt.

Penicillium oxalicum has been isolated from many parts of the world, such as Africa, Australia, Canada, China, Denmark, Egypt, India, Korea, Netherlands, Norway, Taiwan, Iran, Pakistan, Puerto Rico, Slovenia, South Africa, Sweden and USA. It is most commonly found in soil (Pitt 1979a), decaying vegetation (Pitt 1979a) and indoor air from homes (Vesper *et al.* 2005; Sawane and Saoji 2004). It has also been isolated from air in Indian grain shops (Sawane and Saoji 2005) and hospitals (Sing *et al.* 1994), sweet corn kernels (Baird *et al.* 1996), poultry feeds (Magnoli 1998), luncheon meat (Ismail and Zaky 1999), sausages (Iacumin *et al.* 2009) and stored yams (Ikotum 1984). *Penicillium oxalicum* has also been isolated from and is believed to be an endophyte of *Coffea arabica* leaves, where its role remains unknown (Vega *et al.* 2006); and from growth medium used for greenhouse cultivation of English cucumbers (*Cucumis sativus* L), where its presence is correlated with increase root growth (Menzies *et al.* 2005).

Penicillium oxalicum is a reported pathogen of the sugarcane aphid pest *Ceratovacuna lanigera* Zehntner (Fang and Tang 1986). It is also a plant pathogen. In

maize, it causes ear rot that can be seen as a blue-green powder that grows between the kernel and the cob surface. Infected kernels become bleached, streaked and have reduced germinability (Caldwell *et al.* 1981). It also causes cucumber stem rot, which was first reported in the Leamington area of southwestern Ontario, Canada in 1988 (Jarvis and Ferguson 1992). The disease has also been reported in British Columbia, Canada (Jarvis *et al.* 1990; Menzies *et al.* 1995), England (O'Neill *et al.* 1991), and Scandinavia (van Steekelenburg 1988). A lesions starts as a white powdery sporulation on stubs left after fruit picking, leaf trimming and side-shoot trimming, which then turn into a blue green powdery sporulation (O'Neill *et al.* 1991). Not all strains of *P. oxalicum* cause the disease (Menzies *et al.* 1995).

Although *P. oxalicum* is a plant pathogen, it has potential beneficial uses. The conidia of *Penicillium oxalicum* are an effective biocontrol against wilt of tomato caused by *Fusarium oxysporum* f. sp. *lycopersici* (Sacc.) Snyder & H.N. Hansen (De Cal *et al.* 1997, 2000) and *Verticillium dahliae* Kleb., (Larena *et al.* 2003; Sabuquillo *et al.* 2005). Greenhouse and field experiments revealed 22–64 % reduction in wilt of tomato in *P. oxalicum* treated plants (Sabuquillo *et al.* 2005). There was no significant difference between biological and pesticide chemical treatments (Sabuquillo *et al.* 2005). *Penicillium oxalicum* may also be an effective biocontrol treatment for strawberry powdery mildew (De Cal *et al.* 2008). Strawberry cultivars and lines treated with *P. oxalicum* conidia have shown a significant reduction in the amount of powdery mildew in growth chambers and open-field nurseries of strawberries (De Cal *et al.* 2008).

Penicillium oxalicum also produces antifungal substances that suppress the mycelial growth of plant pathogenic fungi such as *Sclerotinia sclerotiorum* (Lib.) de

Bary, *S. minor* Jagger, *S. nivalis* I. Saito, *Alternaria alternata* (Fr.) Keissl., *Gibberella zeae* (Schwein.) Petch, *Fusarium oxysporum* f.sp. *vasifectum* W.C. Snyder and H.N. Hansen, *Sclerotium rolfsii* Sacc., *Botrytis cinera* Pers., *Bipolaris maydis* (Y. Nisik. and C. Miyake) Shoemaker and *Monilinia laxa* (Aderh. and Ruhland) Honey (Yang *et al.* 2008). It also inhibits the growth of *Colletotrichum gloeosporioides* (Penz.) Penz., and Sacc., a pathogen of guava (*Psidium guajava* L.), where *P. oxalicum* is considered a phylloplane fungus (Pandey *et al.* 1993).

Ochrotoxin A (OTA) is a toxin produced by some *Aspergillus* and *Penicillium* species, including *P. oxalicum* (Iacumin *et al.* 2009; Vega *et al.* 2006). Human exposure to this toxin occurs mainly through consumption of cereals, grapes, coffee and cocoa (Amézqueta *et al.* 2009). Factors that affect fungal growth and OTA production are temperature, nutrient availability, moisture content and the amount of time the product remains under adverse conditions (Amézqueta *et al.* 2009). It is nephrotoxic, hepatotoxic, genotoxic, teratogenic and immunotoxic to animals (Mateo *et al.* 2007). Its carcinogenicity in rats and mice is well-established (Castegnaro *et al.* 1998; Pfohl-Leszkowicz *et al.* 1998).

Combined DNA sequence data analyses of the ITS and LSU regions by maximum parsimony (MP) revealed that *P. oxalicum* falls in Petersons' (2000) Group 5 of *Penicillium*, where it is a phylogenetically isolated species. Group 5 species are classified in *Penicillium* subgenera *Aspergilloides* Dierckx and *Furcatum*.

Preliminary analyses of the β -tubulin (*BenA*) gene suggested a moderate amount of genetic variation in *P. oxalicum*, indicating the existence of at least three phylogenetically distinct genotypes that may have different ecological or pathological

behaviours (Seifert, unpublished data). *BenA* has been used to analyze the phylogeny of *Penicillium* subgenus *Penicillium* (Samson *et al.* 2004) and has been useful in identifying species complexes in *P. roquefortii* Thom (Samson *et al.* 2004), and *P. aurantiogriseum* Dierckx groups (Seifert and Louis-Seize 2000), which correlated with groups identified using secondary metabolite profiles (Nielsen *et al.* 2007; Lund and Frisvad 1992). In this study, four additional genes were sequenced, cytochrome c oxidase subunit 1 (*Cox1*), the ribosomal internal transcribed spacer (ITS) region, translation elongation factor 1- α (*TEF1- α*), and calmodulin (CaM) to confirm the existence of three phylogenetic species using the Genealogical Concordance Concept (GCC) recognition criterion.

4.3 Materials and Methods

Thirty-eight strains identified as *P. oxalicum* were obtained from the Canadian Collection of Fungal Cultures (CCFC), the Centraalbureau voor Schimmelcultures (CBS), Northern Regional Research Laboratory (NRRL), Food Science Australia Culture Collection (FRR), and the personal research collections of David Malloch, Robert A. Samson and Jim Menzies. Strains from CBS and NRRL were received as freeze dried cultures and resuspended in ddH₂O for two hours, then plated onto Malt Yeast Extract Agar (MEA; Pitt 1979a). Strains from the David Malloch collection were revived from slants preserved in mineral oil by plating onto MEA. Strains from Australia, Robert A. Samson and Jim Menzies were obtained as living slants on MEA media. All strains were stored at 4°C and –80°C in ddH₂O and 10% glycerol for future use. Cultures from the David Malloch and Jim Menzies collections were deposited into the Canadian Collection of Fungal Cultures (CCFC).

4.3.1 Morphological Analyses

Three-point inoculations were made for all strains onto MEA and Czpeck's Yeast Agar (CYA; Pitt 1973) (refer to Appendix 1 for media recipe). Plates were then incubated in the dark at 25°C for 7 d. Gross morphological characterization for all strains was observed on MEA and CYA, while microscopic characterization was observed only on MEA. All morphological analyses and photographs were taken following the procedures described in Chapter 2.

4.3.2 Molecular and Phylogenetic Analyses

Genomic DNA extraction for target gene amplification, *BenA*, ITS, *Cox1*, *TEF1- α* and CaM for all strains was performed following the procedures described in Chapter 2. *BenA* was amplified with primers Bt2a and Bt2b; for strains that did not amplify, primers T10 and T222 were used (Glass and Donaldson 1995). The ITS region was amplified with ITS1 and ITS4 (White *et al.* 1990). *Cox1* was amplified with PF and AR (Seifert *et al.* 2007). *TEF1- α* was amplified with EF1c and EF6 (Peterson *et al.* 2004). CaM with CF1 and CF4 (Peterson *et al.* 2004). See Appendix 2 for primer sequences.

PCR mixture reactions and thermocycling parameters were performed following the procedures described in Chapter 2 with the exception of the thermocycling parameters for CaM. The PCR profile for CaM was modified to 95°C for 1 min for denaturation, 50°C for 1 min for primer annealing, 72°C for 1:30 min for primer extension for 40 cycles, and a final elongation step for 10 min at 72°C. Multiple amplification bands were observed during gel electrophoresis for *BenA* with Bt2a and Bt2b for strains CBS 347.68, CBS 460.67, FRR 1268 and FRR 1391. The PCR products were cloned following the procedures described in Chapter 2.

Successful PCR products were sequenced directly in both directions with the forward and reversed primers for *BenA*, *Cox1*, *TEF1- α* , and ITS. Primer CMD5 (Hong *et al.* 2006) and PoxalCMD2R (5'–GGG GAA ATR AAG CCG TTG TTA–3') were used as internal sequencing primers because multiple peaks were observed in sequence chromatograms. Primer PoxalCMD2R was designed using the sequences obtained from the forward primer CMD5, with the aid of the online primer designing tool in the Integrated Technologies DNA website (www.idtdna.com). Sequence reactions were analyzed and assembled as described in Chapter 2. Sequence alignments were constructed and subjected to maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI) analyses (see Chapter 2).

4.3.3 BLAST and Phylogenetic Analyses for *BenA* Clone Sequences

Basic local alignment system tools (BLAST) nucleotide searches were conducted using the nblast tool on sequences obtained from the cloning of *BenA* products that yielded multiple bands during gel electrophoresis. The DNA sequences were translated using the computer program BioEdit v. 7 (Hall 1999) to search the translated nucleotide sequence and protein databases from GenBank using the tblastx and blastx tools for top matches. Distinct nucleotide sequences obtained from cloning were used to construct an alignment for MP, ML and BI phylogenetic analyses as described in Chapter 2.

4.4 Results

4.4.1 Morphological Results

Branching patterns on strains grown on MEA were examined. Approximately 94%, 60%, and 8% of the strains examined in this study had bi-, mono- and terverticillate conidiophores (Table 4.2). Currie and Thom (1915), Pitt (1979a) and Ramirez (1980)

observed that the ex-type strain produced mono- and biverticillate conidiophores. Biverticillate conidiophores were predominant in all strains, approximately 20% and 80% of the conidiophores were mono- and biverticillate, with two exceptions, NRRL 787 (ex-type) and CBS 336.50. In the terverticillate strains, CBS 300.97, CBS 358.48 and CBS 114222, approximately 5% of the conidiophores were terverticillate. In this study the strain NRRL 787 (ex-type) produced monoverticillate conidiophores only (Figure 4.2C). This is probably a symptom of cultural degradation, which was evidenced by the sparse sporulation compared with other strains (Figure 4.5). The only other strain to produce monoverticillate conidiophores only was CBS 336.50.

In biverticillate conidiophores, metulae were in whorls of 2–6 ranging in 16–22 x 3–5 μm and phialides in whorls of 7–12 (–14) ranging from 8.5–12.5 x 2.5–3.5 μm . The observations did not differ greatly from Pitt's (1979a) species description, with metulae in whorls of 2–6 ranging in 15–25 (–30) x 3.5–4.5 μm and phialides in whorls of 10–15 (–20) x 3.0–3.5 μm . Conidia were ellipsoidal ($x = 3.5\text{--}6 \times 2.5\text{--}3.5 \mu\text{m}$), smooth to finely roughened; similar observations were made by Pitt (1979a). Stipes ranged from 200–400 x 2.5–3.5 μm , however, Pitt (1979a) observed stipes of 3.5–5 μm in width.

Colony morphology was also examined in strains grown on CYA and MEA in the dark at 25°C for 7 days. Colony diameter for strains grown on CYA ranged from 20–62 mm, compared with 35–60 mm (Pitt 1979a). The number of sulcations per colony ranged from 0–30 (Figure 4.2); sulcations have not been previously reported. Colony diameters on MEA ranged from 19–61 mm (Figure 4.3–4.6), compared with 20–50 mm (Pitt 1979a). Colony colours for obverse (greyish green, 25–26C3) and reverse (pale to

yellow, brown, orange or pinkish) views match those previously described (Figure 4.4, 4.6).

4.4.2 Multigene Phylogenetic Results

BenA sequences were obtained for all strains. The mean sequence length was 495 bp. There are at least three groupings observed in the MP, ML and BI trees (Figures 4.7–4.9). In the MP tree, groups 1 and 2 formed coherent monophyletic groups without strong bootstrap support, while group 3 had 100% bootstrap support. In the ML tree, strong bootstrap support is observed for groups 2 and 3, 0.813 and 1.00, while strains in group 1 did not form a monophyletic group (Figure 4.8). In the BI tree, group 2 and 3 formed monophyletic groups with posterior probabilities of 0.99 and 1.00. Group 1 was not resolved (Figure 4.9). In all *BenA* trees, the sequence for CBS 219.30 was genetically isolated from all other sequences.

The ITS mean sequence length was 561 bp. Two groups of strains, A and B, were observed in the MP, ML and BI trees (Figures 4.10–4.12) with weak statistical support. Group A strains formed a coherent monophyletic group in all trees; group B strains were not resolved.

The *CoxI* mean sequence length was 591 bp. The MP and ML trees formed a coherent monophyletic of all *P. oxalicum* strains, except for DAOM 239956 and DAOM 230057, without strong bootstrap support (Figures 4.13–4.14). In the BI tree, the strains did not form a monophyletic group (Figure 4.15).

TEF1-α sequences were obtained for 36 strains. The chromatogram quality was poor for FRR 1268, CBS 114222 and DAOM 178627, and thus they were not included in the sequence alignments. The *TEF1-α* mean sequence length was 651 bp. The MP and

ML trees yielded two groups of strains, as observed in the ITS trees, that formed two coherent monophyletic groups without strong bootstrap support (Figure 4.16–4.18). Only group A in the ML tree had strong bootstrap support with 0.996 (Figure 4.17). In the BI tree, only the strains in group A formed a coherent monophyletic group with a moderate posterior probability of 0.86 (Figure 4.18).

CaM sequences were obtained for 36 strains. Sequences were not obtained for CBS 118872 and DAOM 239955 strains because there was no PCR amplification. The CaM mean sequence length was 809 bp. In the CaM MP tree, the two groups observed in the ITS and *TEF1- α* gene trees, A and B, were also observed (Figure 4.19). Only group A had strong bootstrap support, 100%. In the ML and BI trees, only strains in group A formed a coherent monophyletic group with strong statistical support, 0.998 and 1.00 (Figure 4.20–4.21). Group B strains formed a coherent monophyletic group without strong bootstrap support, except for strains FRR 1058, CBS 218.30 and DAOM 239950 (Figure 4. 20–4.21).

4.4.3. BLAST and Phylogenetic Results for *BenA* Clone Sequences

The *BenA* amplification products for FRR 1268, FRR 1391, CBS 347.68 and CBS 460.67 yielded multiple bands during gel electrophoresis. The amplification products were cloned, and four different nucleotide sequence copies were recovered (Table 4.3). Only nucleotide sequence 1 was similar to previously obtained *P. oxalicum BenA* sequences, and was used for the construction of the alignment in section 4.4.3.

BLAST searches for sequences 2 (468 bp), 3 (372 bp) and 4 (440 bp) determined that they were fungal *BenA* (Table 4.4). The top five nucleotide, translated nucleotide and protein BLAST results for each sequence are given Table 4.4, Table 4.5 and Table

4.6. The sequences were also aligned with at least three representatives from the three *BenA* groupings observed in section 4.4.3 for MP, ML and BI analyses. The alignment was 491 bp in length. Sequences 2, 3 and 4 aligned at positions 90–140, 220–330, and 340–591. Sequences 4 and 2 were phylogenetically isolated, while sequence 3 grouped with strain CBS 219.30 (Figure 4.22).

4.5 Discussion

Penicillium oxalicum is a morphologically distinctive fungus that can be easily identified by roughened ellipsoidal conidia, the predominance of biverticillate conidiophores, and its pale to yellow, orange, or pinkish colony reverse colours on CYA. As mentioned previously, *P. oxalicum*, is cosmopolitan, and has been isolated from a variety of substrates. The variety of ecological roles, the morphological variation described in the literature, and the preliminary *BenA* study by Seifert (unpublished) using neighbour joining (NJ) analyses suggested the existence of more than one phylogenetic species fitting the morphospecies concept of *P. oxalicum*.

The increased number of strains sampled in this study confirmed the initial results that at least three distinct groups exist in the *BenA* gene tree. The groupings, however, were not observed in the other gene trees. The ITS, *TEF1- α* and CaM gene trees revealed two groups, A and B, that differed from those observed in *BenA*. Group A strains formed a coherent monophyletic groups in all trees, with strong statistical support in the *TEF1- α* BI and all CaM trees. Group B strains did not form coherent monophyletic groups in all trees, except for the *TEF1- α* MP and ML trees and the CaM MP tree. Geographical distributions and morphological characters do not correlate with any of the

groupings observed in *BenA* or in ITS, *TEF1- α* , and CaM. No clear groupings of strains were observed in the *CoxI* gene trees.

Comparison of phylogenetic tree topologies of multiple genes has been promoted as a method of fungal species recognition, termed the Genealogical Concordance Concept (GCC; Taylor *et al.* 2000). In the GCC, congruent tree topologies over multiple loci indicate reproductive isolation, which indicates phylogenetic species (Scott and Chakraborty 2006). The incongruence observed for the five genes analyzed here indicates a single phylogenetic species. The groupings observed in the ITS, *TEF1- α* and CaM trees were not present in the other genes trees, nor was strong statistical support observed in any of the phylogenetic analyses.

Although *P. oxalicum* is one phylogenetic species following the GCC recognition criterion, it demonstrated greater morphological variation than previously described. Colony sulcations on CYA and a wider range of colony diameters were observed. The presence of mono- and terverticillate conidiophores previously described in the literature was confirmed. *Penicillium oxalicum* strains can either produce mono- or biverticillate conidiophores only, mono- and biverticillate conidiophores, or all three conidiophore types. In *Penicillium* taxonomy, the most differentiated branching pattern determines the conidiophore type. Terverticillate conidiophores were only present in three out of 38 strains, and made up 8% of the conidiophores in those strains. Biverticillate conidiophores were prevalent in most strains and were found in greater abundance than monoverticillate conidiophores, making the placement of *P. oxalicum* in subgenus *Furcatum* by Pitt (1979a) rather than subgenera *Aspergilloides* and *Penicillium*, appropriate.

Currie and Thom (1915) reported monoverticillate and biverticillate conidiophores, with roughened, ellipsoidal conidia for the ex-type strain of *P. oxalicum*. Raper and Thom (1949) examined the ex-type strain, NRRL 787, along with NRRL 790, NRRL 1836 and NRRL 2139. Their studied demonstrated that *P. oxalicum* also has terverticillate conidiophores. Pitt (1979a) examined nine strains, including the ex-type strain, IMI 39750, IMI 93376, IMI 15255, FRR 669, FRR 670, FRR 1058, FRR 1195, and FRR 1218. Only strains FRR 1058, FRR 1195 and FRR 1218 were examined in this study. Monoverticillate and biverticillate conidiophores were seen by Pitt (1979a) and Ramirez (1980), but the latter author only examined the ex-type strain.

Penicillium oxalicum plays a variety of ecological roles, ranging from a pathogen to a biological control agent. The species has been isolated from all over the world from a wide variety of substrates and habitats (Table 4.1). Correlations between geographical localities, ecological roles and phylogenetic species are often observed in fungal species. For example, *Fusarium graminearum* Schwabe (teleomorph = *Gibberella zeae* Schwein), which causes wheat scab, was thought to be pandemic. *BenA*, *TEF1-α*, ammonia ligase, reductase, 3-O-acetyltransferase and phosphate permase gene genealogies recovered seven geographically structured lineages representing phylogenetically distinct species (O'Donnell *et al.* 2000). This was not the case for *P. oxalicum*. *Botrytis cinera* Persoon has also been isolated from many parts of the world and different substrates, and is a grey mold on over 200 hosts (Fournier *et al.* 2005). Gene genealogies of five nuclear genes, *BenA*, ITS, the *Bc-hch* locus (a homolog of the vegetative incompatibility locus of *Neurospora crassa* Shear and B.O. Dodge), CYP51 (C-14α demethylase, the target gene for DMIs fungicides), and the 63R locus (a noncoding region) determined that it is one

phylogenetic species conforming to the GCC recognition criterion (Fournier *et al.* 2005) like *P. oxalicum*.

BenA has proven to be a useful genetic marker in fungi. It has been used in the construction of multiple gene phylogenies of the family *Botryosphaeriaceae* (Taylor *et al.* 2009); the order the order *Orbiliiales* (Li *et al.* 2005); and the genera *Alternaria* Nees. (Peever *et al.* 2004), *Colletotrichum* Corda (Lubbe *et al.* 2004), *Hypoxylon* Bull., (Hsieh *et al.* 2005), *Trichoderma* Pers., (Kullnig-Gradnager *et al.* 2002), and *Penicillium* subgenus *Penicillium* Pitt (Samson *et al.* 2004). It has been used to delimit cryptic species in *Botryosphaeria dothidea* (Moug.) Ces and Not., (Slippers *et al.* 2004), *Chrysosporthe cubensis* (Bruner) Gryzenh. and Wingf., (Gryzenhout *et al.* 2006), *Paxillus involutus* (Batsch) Fr. (Hedh *et al.* 2008), *Tuber indicum* Cooke and Massee (Wang *et al.* 2006) and *Fusarium graminearum* (O'Donnell *et al.* 2000).

As mentioned previously, *BenA* has proven to be a useful marker in the study of *Penicillium*. Seifert *et al.* (2007) reported that *BenA* has a higher species resolving ability than ITS and *Cox1* in *Penicillium* subgenus *Penicillium*. In this chapter, it was demonstrated that the topology of the *BenA* trees was inconsistent with that suggested by other genes. It is possible that *BenA* is polymorphic in *P. oxalicum*, with each group in the gene trees representing a different allele. Different *BenA* alleles have been reported in other fungal groups, such as *Erysiphe necator* Schwein. (Amrani and Corio-Costet 2005) and *Septoria nodorum* (Berk.) Berk. (Colley *et al.* 1991).

Four different nucleotide sequences were obtained from the cloning of *BenA* PCR products for CBS 347.68, CBS 460.67, FRR 1268 and FRR 1511 strains. Sequence 1 was similar to previously obtained *BenA* sequences; sequence 2, 3, and 4 were not.

Sequences 2, 3, and 4 yielded different BLAST results for nucleotide sequence (Table 4.4), translated nucleotide sequence (Table 4.5) and protein (Table 4.6) searches, and are probably pseudogenes, i.e. non-functional copies. Sequences 2, 3, and 4 aligned at three different regions with the other *P. oxalicum* sequences. Phylogenetic analyses revealed that sequence 3 grouped with CBS 219.30 strain, but the sequences differ by four nucleotides, suggesting that a paralog sequence was recovered. This may suggest that the groups observed in the *BenA* gene trees may not be different alleles as previously suggested in this chapter, but different paralogs. Cloning of *BenA* PCR products for all *P. oxalicum* strains is needed to recover all the paralogs present, as well as increasing the number of colonies selected for cloning. Overall, the results suggested the presence of at least four *BenA* homologs in *P. oxalicum*.

Only a few homologs of *BenA* are known from fungi (Begerow *et al.* 2004). Paralogs have been reported from *Colletotrichum* spp., *Emericella nidulans* (Eidam) Vuil., *Galactomyces geotrichum* (E.E. Butler and L.J. Petersen) Redhead and Malloch, *Saccharomyces cerevisiae* Gasp, *Trichoderma viride* Pers., (Ayliffe *et al.* 2001). More than one transcribed copy of *BenA* has been reported in fungi, including *Schizophyllum commune* Fr. (Russo *et al.* 1992) and *Microsporidia* (Keeling 2003; Keeling and Fast 2005). In *S. commune*, the two *BenA* copies were transcribed, however, one copy was transcribed only during the active growth of young mycelia. To determine if sequences 2, 3 and 4 are pseudogenes as suggested in this chapter, gene expression analyses would have to be performed to determine functionality.

Table 4.1: *Penicillium oxalicum* strains examined and sequenced in Chapter 4 of this thesis.

Species	Collection No.	Country	State/Province	Locality	Substrate
<i>P. oxalicum</i>	NRRL 787*	USA	Connecticut		soil
	NRRL 35183	Colombia	Chinchina	Caldas	coffee leaves
	DAOM 178627	Canada	Quebec	Longeuil	menstrual sponge
	DAOM 213171	Canada			
	DAOM 213268	Canada	Manitoba	Westbourne	stored grain
	DAOM 214729	Canada	British Columbia	Agassiz	<i>Cucumis sativis</i> roots
	DAOM 226577	Canada			
	DAOM 226606	Canada			
	DAOM 239948	Canada	Ontario	Chatham-Kent, Wallaceburg	house dust
	DAOM 239949	Canada	Ontario	Chatham-Kent, Wallaceburg	house dust
	DAOM 239950	Canada	Ontario	Chatham-Kent, Wallaceburg	house dust
	DAOM 239951	Canada	Ontario	Chatham-Kent, Wallaceburg	house dust
	DAOM 239952	Canada	Ontario	Chatham-Kent, Wallaceburg	house dust
	DAOM 239953	Canada	Ontario	Chatham-Kent, Wallaceburg	house dust
	DAOM 239954	Canada	Ontario	Chatham-Kent, Wallaceburg	house dust
	DAOM 239955	Canada	British Columbia	Metropolitan Vancouver, Richmond	<i>Cucumis sativis</i> stem
	DAOM 239956	Canada	British Columbia	Metropolitan Vancouver, Richmond	<i>Cucumis sativis</i> stem
	DAOM 239957	Canada	British Columbia	Metropolitan Vancouver, Richmond	<i>Cucumis sativis</i> stem
	96111148	Canada			
	CBS 219.30	USA	Connecticut		soil
	CBS 300.97	Slovenia			soil
	CBS 301.97	Denmark			juice of elderberry
	CBS 336.50	France			<i>Hedera helix</i> litter
	CBS 347.68	Pakistan			
	CBS 358.48	USA	Wisconsin		Danish blue cheese
	CBS 460.67	South Africa			<i>Aloe</i>
	CBS 708.88	Norway			<i>Cucurbita</i>
	CBS 838.96	Netherlands			<i>Shiso purper</i>
	CBS 102405	Taiwan			

Species	Collection No.	Country	State/Province	Locality	Substrate
	CBS 114222	Iran	Saterloo		<i>Hordeum vulgare</i> leaf
	CBS 118872	Korea	Daejeon		soil of onion field
	FRR 1058	Australia	Queensland	Toowoomba	poultry feed
	FRR 1391	Australia			
	FRR 1511	Australia			
	FRR 2695	Australia			fish
	KAS 3458	Australia			soil
	KAS 3458	Australia			soil
	KAS 3460	Australia			soil
<i>E. reticulisporum</i>	NRRL 3447	Japan	Oshima Islands	Molomachi	soil

* indicate the ex-type strain.

Table 4.2: Conidiophore types present in examined strains of *P. oxalicum*.

Collection No.	Conidiophore Type		
	Monoverticillate	Biverticillate	Terverticillate
NRRL 787*	X		
NRRL 35183		X	
DAOM 178627		X	
DAOM 213171	X	X	
DAOM 213268	X	X	
DAOM 214729	X	X	
DAOM 226577		X	
DAOM 226606	X	X	
DAOM 239948	X	X	
DAOM 239949	X	X	
DAOM 239950		X	
DAOM 239951		X	
DAOM 239952	X	X	
DAOM 239953	X	X	
DAOM 239954		X	
DAOM 239955		X	
DAOM 239956	X	X	
DAOM 239957		X	
96111148	X	X	
CBS 219.30	X	X	
CBS 300.97	X	X	X
CBS 301.97	X	X	
CBS 336.50	X		
CBS 347.68		X	
CBS 358.48		X	X
CBS 460.67	X	X	
CBS 708.88	X	X	
CBS 838.96		X	
CBS 102405	X	X	
CBS 114222		X	X
CBS 118872	X	X	
FRR 1058		X	
FRR 1391		X	
FRR 1511		X	
FRR 2695	X	X	
KAS 3458	X	X	
KAS 3459	X	X	
KAS 3460	X	X	

* indicate the ex-type strain.

Table 4.3: *Penicillium oxalicum* sequences obtained with primers Bt2A and Bt2B after the cloning of PCR products from four strains with multiple bands.

Sequences	Length (bp)	Strains
1*	495	CBS 347.68, FRR 1391, CBS 460.67
2	468	CBS 347.68, FRR 1268
3	372	CBS 347.68, FRR 1391, CBS 460.67
4	440	FRR 1268

* indicates sequences similar to previously obtained *P. oxalicum* *BenA* sequences from other strains.

Table 4.4: Top five nucleotide BLAST results for *P. oxalicum* DNA sequences obtained from the cloning of *BenA* PCR products with multiple bands.

Sequences	BLAST results	GenBank No.	Similarity (%)	E -value
2	<i>Hypoxylon crocopeplum</i>	AY951710	92	5e-53
	<i>Pestalotiopsis lespedezae</i>	EF055243	92	6e-52
	<i>Claviceps</i> sp. CRN03	EU274647	90	1e-49
	<i>Claviceps</i> sp. CRN 502	EU274646	90	1e-49
	<i>Claviceps</i> sp. CRN501	EU274645	90	1e-49
3	<i>Fusarium phaseoli</i>	DQ092469	99	0
	<i>Cercospora piaropi</i>	AF146117	99	9e-179
	<i>Acremonium strictum</i>	AY435441	90	2e-121
	<i>Acremonium strictum</i>	AY435440	90	2e-121
	<i>Cylindrocarpon</i> sp.	FM865808	85	3e-99
4	<i>Talaromyces wortmannii</i>	AY533533	94	0
	<i>Talaromyces trachyspermus</i>	AY753371	87	2e-102
	<i>Talaromyces bacillisporus</i>	AY753367	82	3e-100
	<i>Talaromyces bacillisporus</i>	AY753368	81	5e-97
	<i>Talaromyces trachyspermus</i>	FJ515300	86	4e-78

Note: Sequence 1 was not included because its nucleotide sequence resembled that of previously obtained *P. oxalicum* strains.

Table 4.5: Top five translated BLAST results for *P. oxalicum* DNA sequences obtained from the cloning of *BenA* PCR products with multiple bands.

Sequences	BLAST results	GenBank No.	E -value
2	<i>Penicillium polonicum</i>	EU128556	1e-33
	<i>Spencermartinsia viticola</i>	EU673103	3e-33
	<i>Spencermartinsia</i> sp.	EU673143	4e-33
	<i>Spencermartinsia</i> sp.	EU673142	4e-33
	<i>Diplodia corticola</i>	EU673117	1e-32
3	<i>Fusarium phaseoli</i>	DQ092469	4e-74
	<i>Cercospora piaropi</i>	AF146117	3e-69
	<i>Metarhizium flavoviride</i>	EU248827	5e-58
	<i>Acremonium chrysogenum</i>	X72789	7e-58
	<i>Metarhizium anisopliae</i>	EU248837	2e-57
4	<i>Talaromyces wortmannii</i>	AY533533	1e-72
	<i>Talaromyces trachyspermus</i>	AY753371	3e-55
	<i>Talaromyces bacillisporus</i>	AY753367	4e-55
	<i>Talaromyces bacillisporus</i>	AY753368	5e-54
	<i>Talaromyces trachyspermus</i>	FJ515300	1e-53

Note: Sequence 1 was not included because its nucleotide sequence resembled that of previously obtained *P. oxalicum* strains.

Table 4.6: Top five protein BLAST results for *P. oxalicum* DNA sequences obtained from the cloning of *BenA* PCR products with multiple bands.

Sequences	BLAST results	GenBank No.	E -value
2	<i>Coniothyrium zuluense</i>	AAQ24279	1e-33
	<i>Cladosporium langeronii</i>	ABQ53021	3e-33
	<i>Coniothyrium zuluense</i>	AAQ24280	4e-33
	<i>Coniothyrium zuluense</i>	AAQ24270	4e-33
	<i>Taphrina virginica</i>	AAF98250	1e-32
3	<i>Acremonium chrysogenum</i>	P41741	2e-46
	<i>Metarhizium anisopliae</i>	Q52NY7	4e-46
	<i>Epichloe typhina</i>	P17938	4e-46
	<i>Neotyphodium coenophialum</i>	P33127	4e-46
	<i>Neotyphodium coenophialum</i>	ABO28929	4e-46
4	<i>Aspergillus flavus</i>	EED50040	5e-35
	<i>Aspergillus terreus</i>	XP001210373	7e-28
	<i>Cladosporium</i> sp. PZ-2007g	ABQ53020	1e-27
	<i>Cladosporium</i> sp. PZ-2007f	ABQ52990	1e-27
	<i>Phymatotrichopsis omnivora</i>	ABU88907	1e-27

Note: Sequence 1 was not included because its nucleotide sequence resembled that of previously obtained *P. oxalicum* strains.

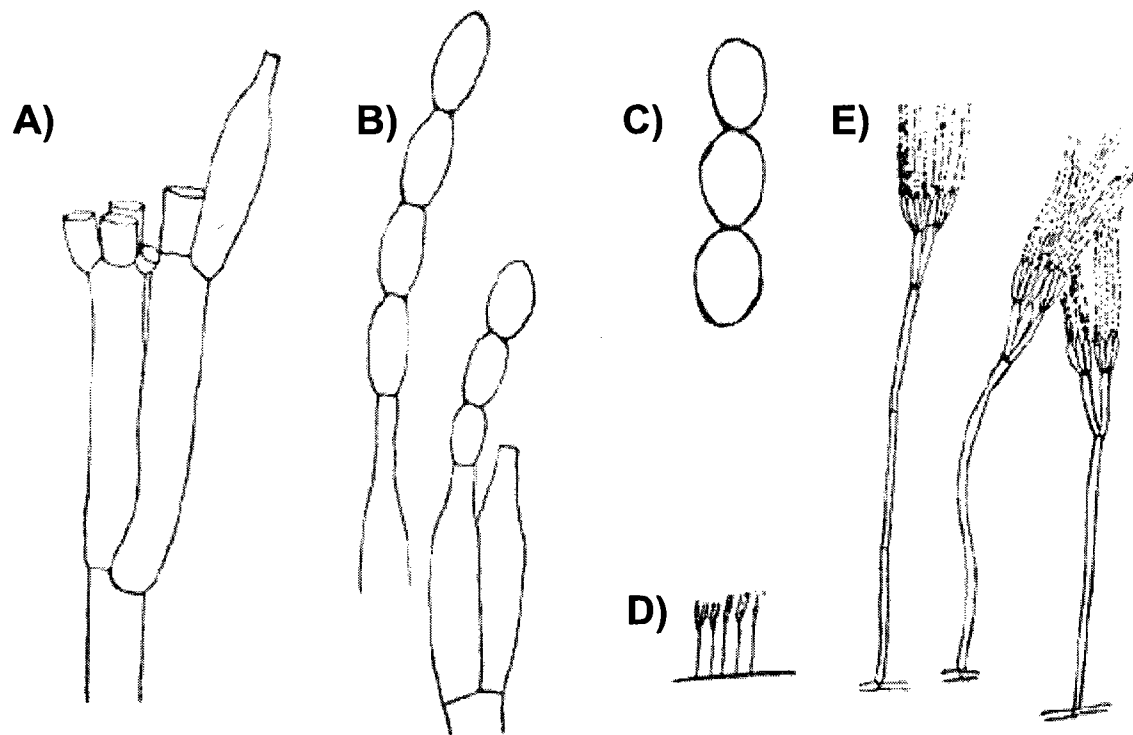


Figure 4.1: Original microscopic drawings of the *Penicillium oxalicum* ex-type strain by Currie and Thom (1915). A) Metulae; B) phialides and conidia; C) conidia; D–E) conidiophores.



Figure 4.2: Microscopic photographs of *P. oxalicum* using differential interference contrast. Typical biverticillate conidiophores (A) and conidia (B) observed in *P. oxalicum*, CBS 301.97. C) Monoverticillate conidiophore of the ex-type strain, NRRL 787. Conidiophore morphology observed in CBS 114222; monoverticillate (D), biverticillate (E–F), and terverticillate (D) conidiophores. Scale bar = 10 μ m.

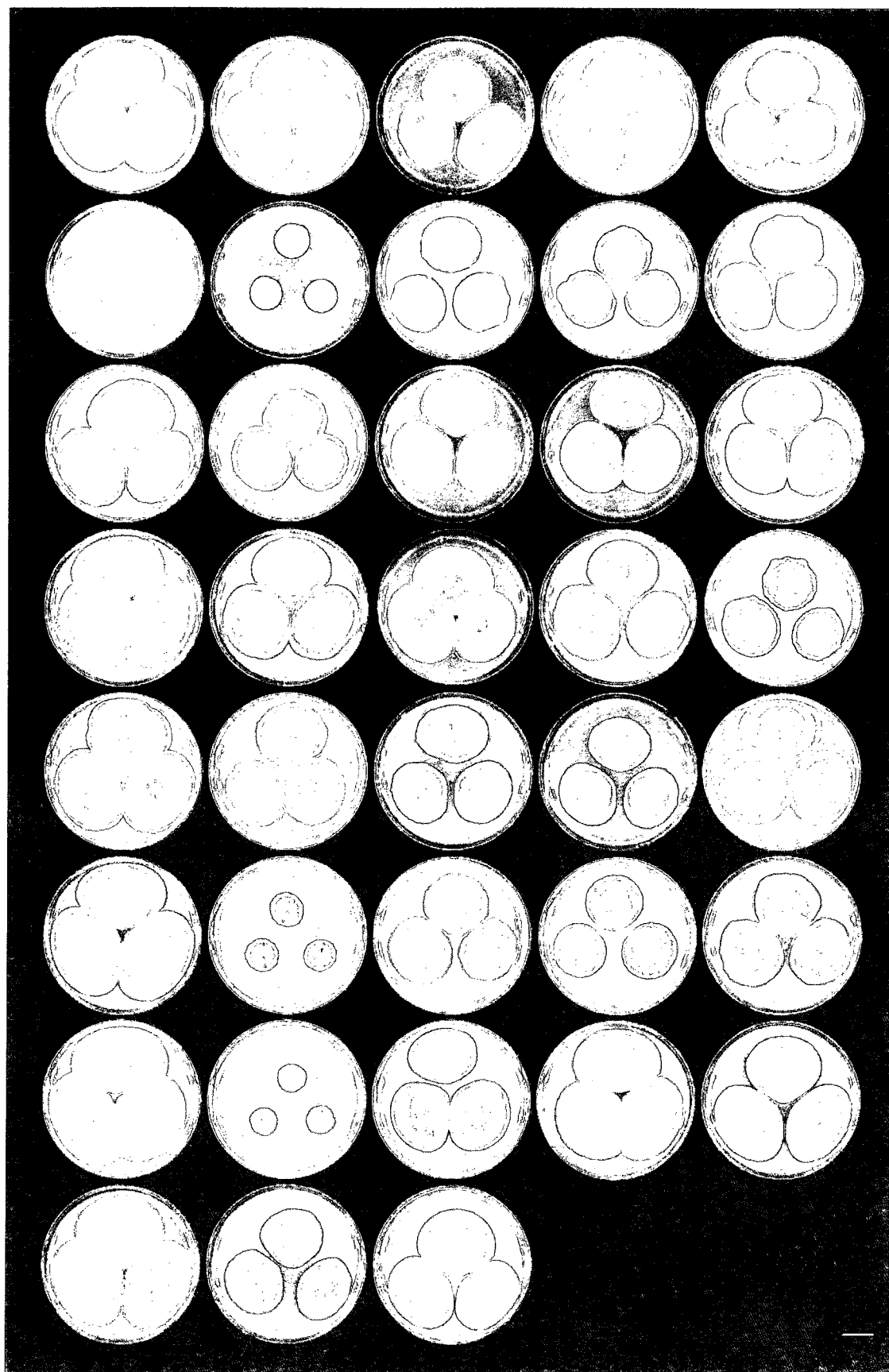


Figure 4.3: Colony obverse of *P. oxalicum* strains grown on CYA at 25°C in the dark for 7 d. Rows left to right: NRRL 787 (ex-type), DAOM 239952, DAOM 239948, DAOM 239953, DAOM 239953, DAOM 239949, DAOM 239950, DAOM 239951, 96111148, CBS 219.30, CBS 300.97, CBS 301.97, CBS 336.5, CBS 341.68, CBS 358.48, CBS 460.67, CBS 708.88, CBS 838.96, CBS 102405, CBS 114222, CBS 118832, DAOM 239955, DAOM 239956, DAOM 239957, DAOM 178627, DAOM 213171, DAOM 213265, DAOM 214729, DAOM 226577, DAOM 226606, FRR 1058, FRR 1391, FRR 1511, FRR 2695, KAS 3458, KAS 3459, KAS 3460, NRRL 32583. Scale bar = 10 mm.

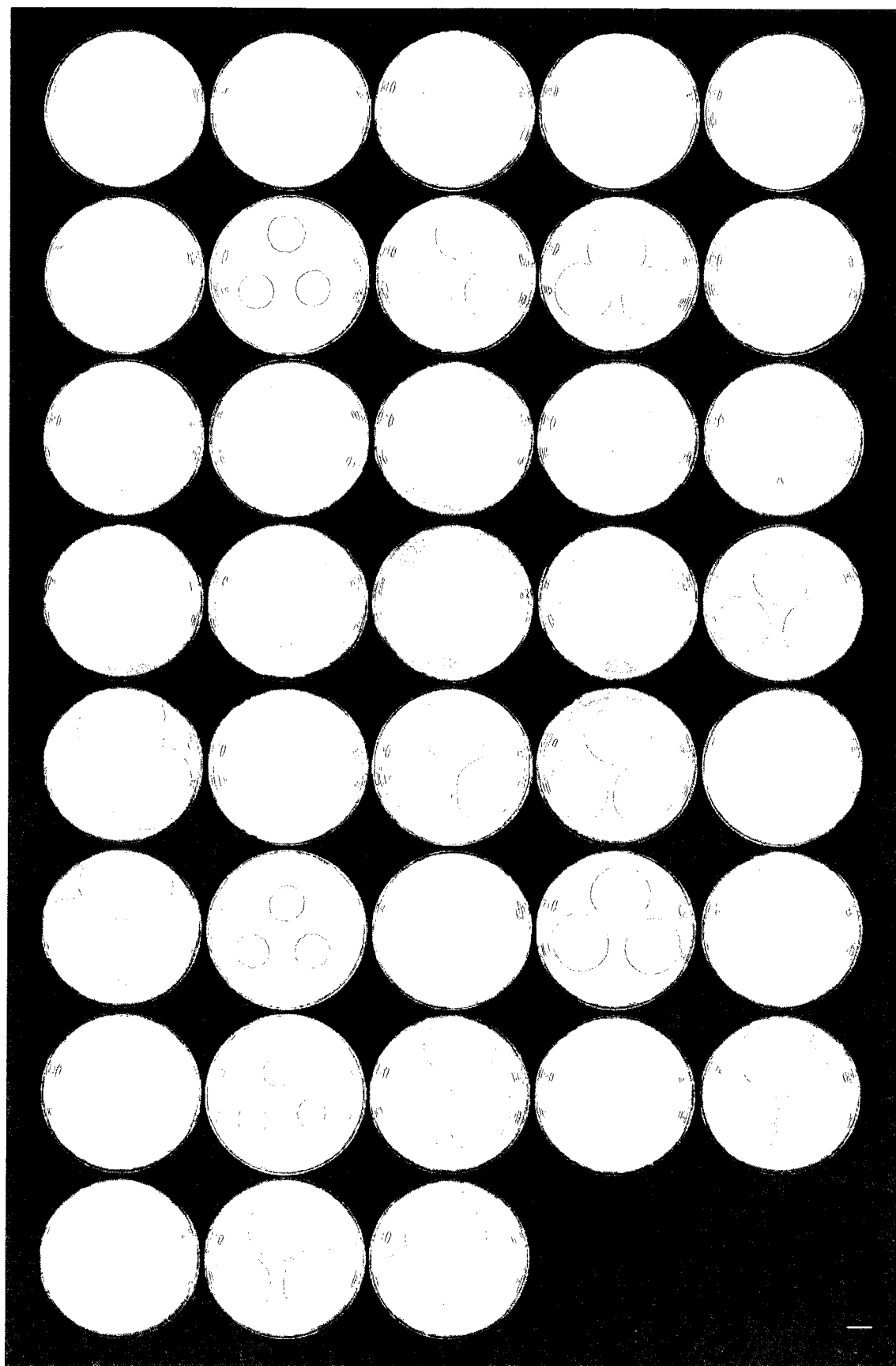


Figure 4.4: Colony reverse of *P. oxalicum* strains grown on CYA at 25°C in the dark for 7 d. Rows left to right: NRRL 787 (ex-type), DAOM 239952, DAOM 239948, DAOM 239953, DAOM 239953, DAOM 239949, DAOM 239950, DAOM 239951, 96111148, CBS 219.30, CBS 300.97, CBS 301.97, CBS 336.5, CBS 341.68, CBS 358.48, CBS 460.67, CBS 708.88, CBS 838.96, CBS 102405, CBS 114222, CBS 118832, DAOM 239955, DAOM 239956, DAOM 239957, DAOM 178627, DAOM 213171, DAOM 213265, DAOM214729, DAOM 226577, DAOM 226606, FRR 1058, FRR 1391, FRR 1511, FRR 2695, KAS 3458, KAS 3459, KAS 3460, NRRL 32583. Scale bar = 10 mm.

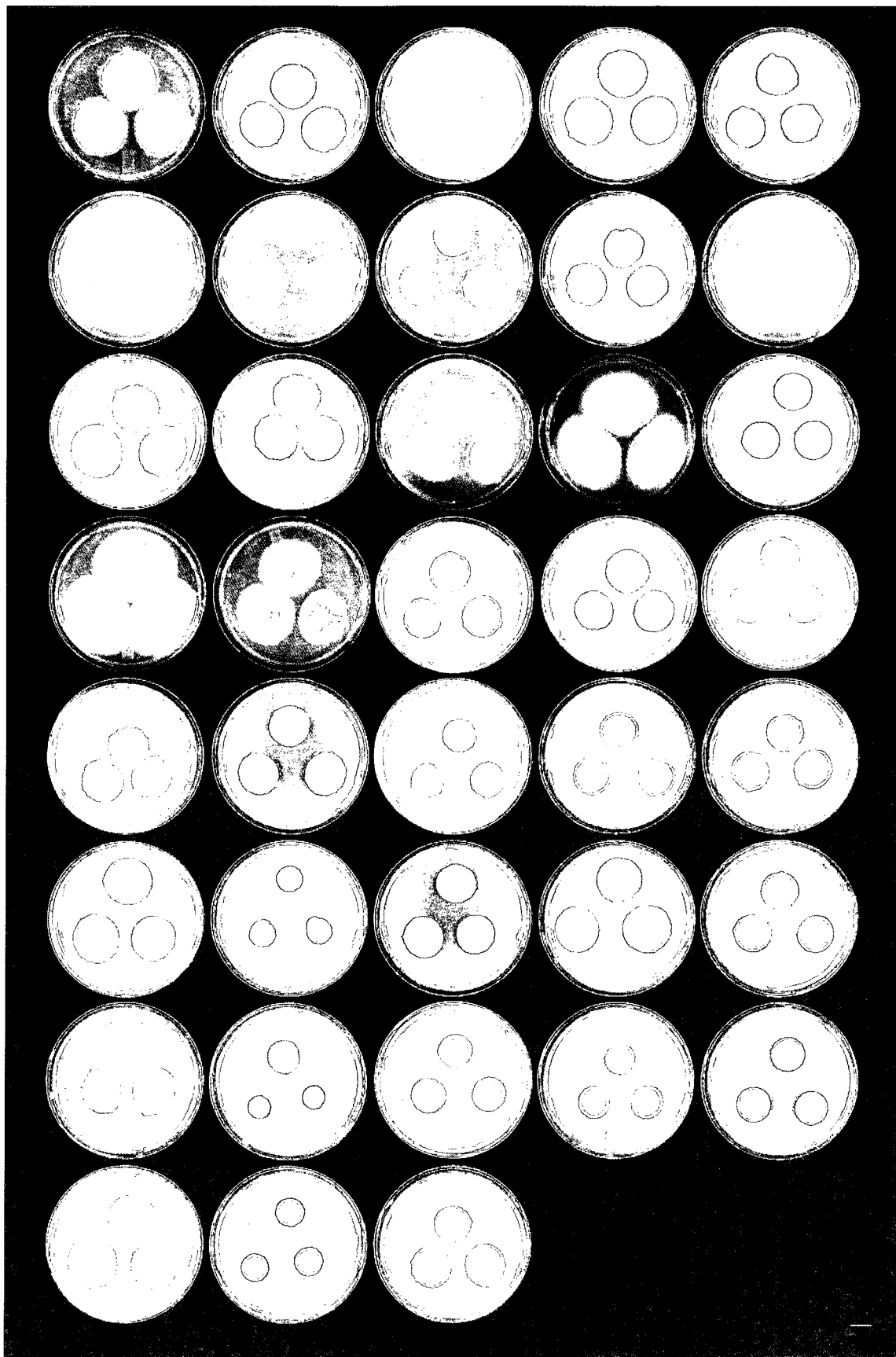


Figure 4.5: Colony obverse of *P. oxalicum* strains grown on MEA at 25°C in the dark for 7 d. Rows left to right: NRRL 787 (ex-type), DAOM 239952, DAOM 239948, DAOM 239953, DAOM 239953, DAOM 239949, DAOM 239950, DAOM 239951, 96111148, CBS 219.30, CBS 300.97, CBS 301.97, CBS 336.5, CBS 341.68, CBS 358.48, CBS 460.67, CBS 708.88, CBS 838.96, CBS 102405, CBS 114222, CBS 118832, DAOM 239955, DAOM 239956, DAOM 239957, DAOM 178627, DAOM 213171, DAOM 213265, DAOM 214729, DAOM 226577, DAOM 226606, FRR 1058, FRR 1391, FRR 1511, FRR 2695, KAS 3458, KAS 3459, KAS 3460, NRRL 32583.

Scale bar = 10 mm.

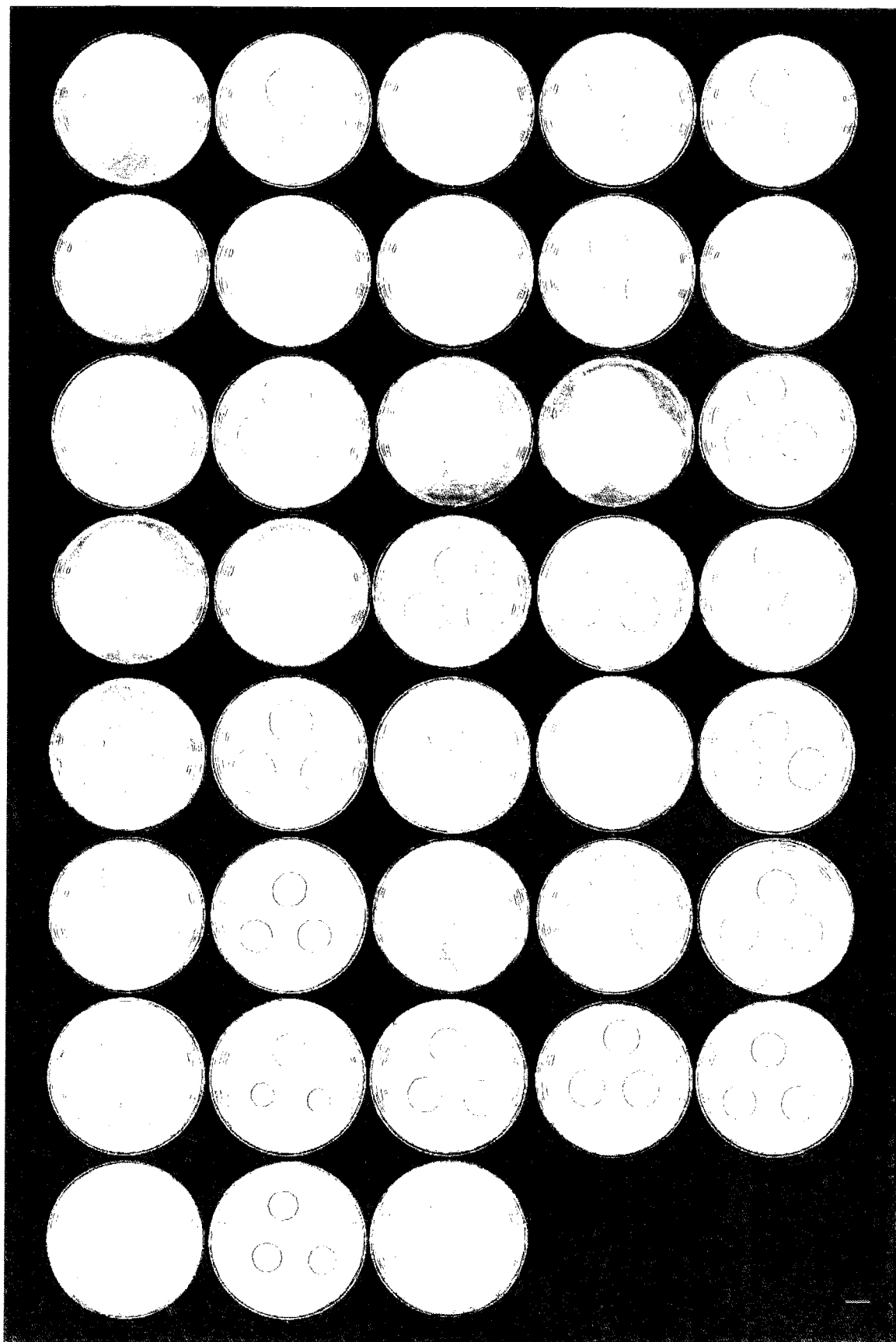


Figure 4.6: Colony reverse of *P. oxalicum* strains grown on MEA at 25°C in the dark for 7 d. Rows left to right: NRRL 787 (ex-type), DAOM 239952, DAOM 239948, DAOM 239953, DAOM 239953, DAOM 239949, DAOM 239950, DAOM 239951, 96111148, CBS 219.30, CBS 300.97, CBS 301.97, CBS 336.5, CBS 341.68, CBS 358.48, CBS 460.67, CBS 708.88, CBS 838.96, CBS 102405, CBS 114222, CBS 118832, DAOM 239955, DAOM 239956, DAOM 239957, DAOM 178627, DAOM 213171, DAOM 213265, DAOM 214729, DAOM 226577, DAOM 226606, FRR 1058, FRR 1391, FRR 1511, FRR 2695, KAS 3458, KAS 3459, KAS 3460, NRRL 32583. Scale bar = 10 mm.

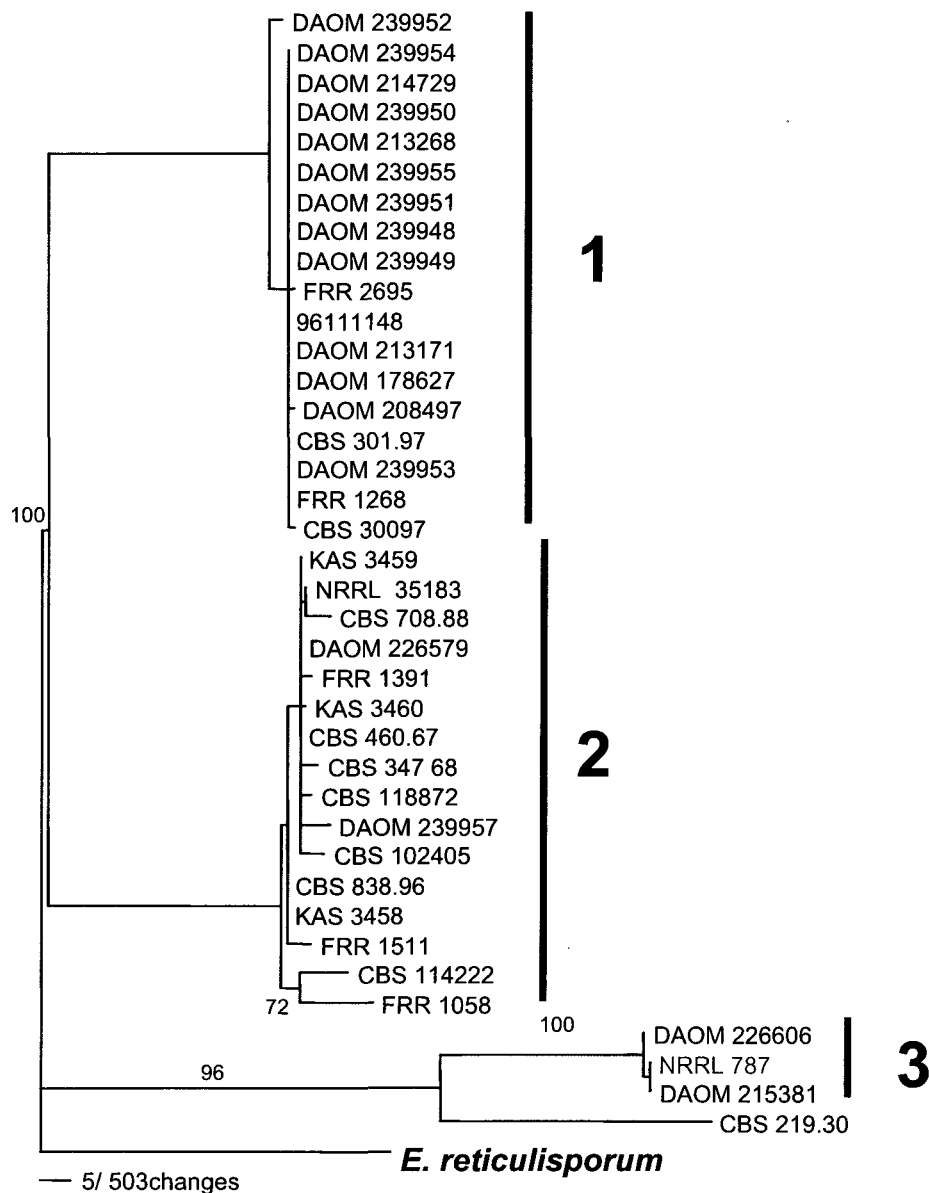


Figure 4.7: Maximum parsimony gene tree for *P. oxalicum* strains based on *BenA* sequences. One out 5000 most parsimonious rooted trees ($L=229$, $CI=0.856$, $RI=0.918$, $RC=0.785$, $HI=0.144$), all characters included. A heuristic search and 1000 bootstrap replicates were performed; bootstrap values of 70% above are presented. Thickened lines represent consensus branches. The strain in red is the ex-type.

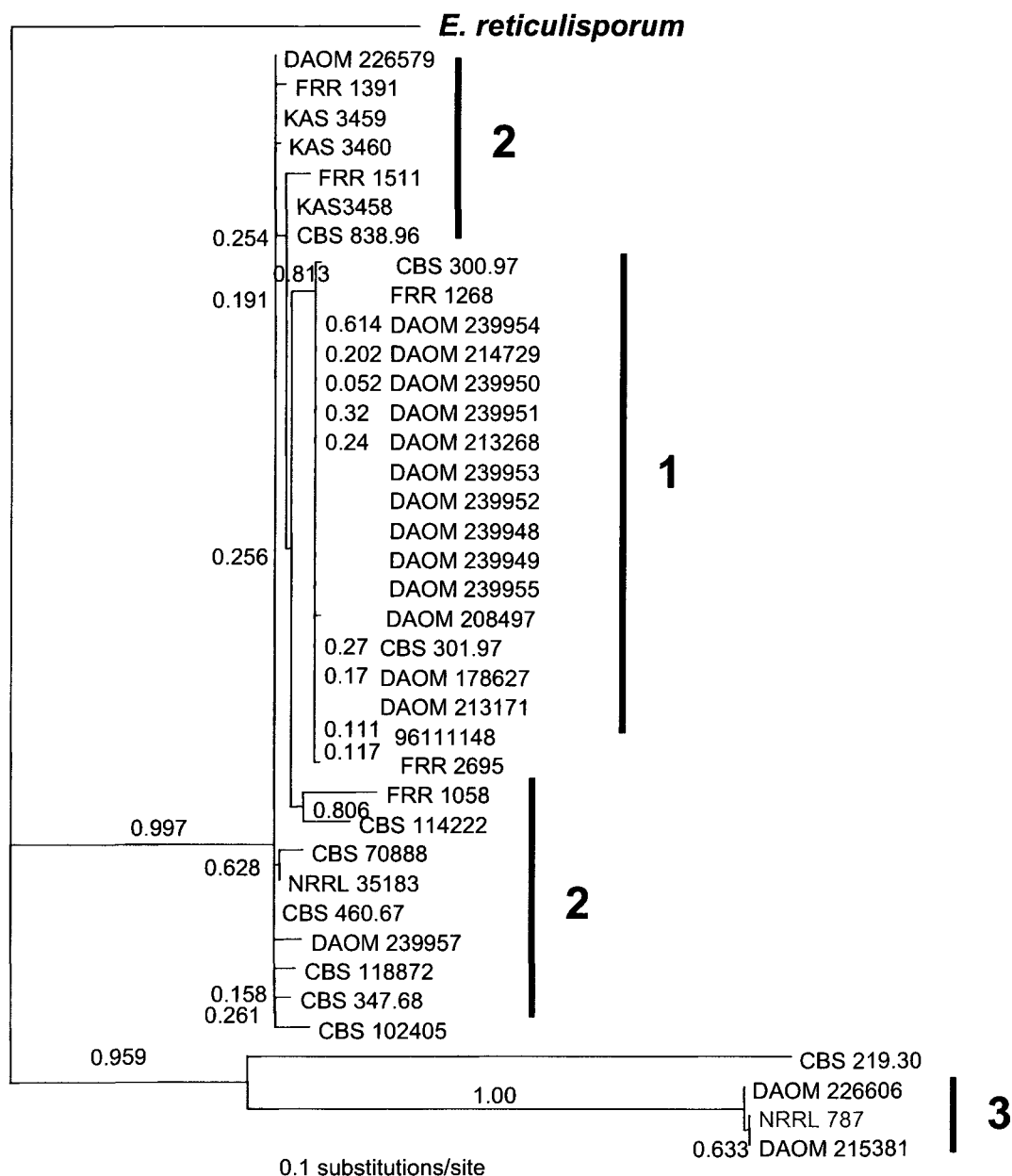


Figure 4.8: Maximum likelihood gene tree for *P. oxalicum* strains based on *BenA* sequences. The tree was constructed using the GTR+G nucleotide substitution model, with 1000 bootstrap replicates. The ex-type strain is depicted in red.

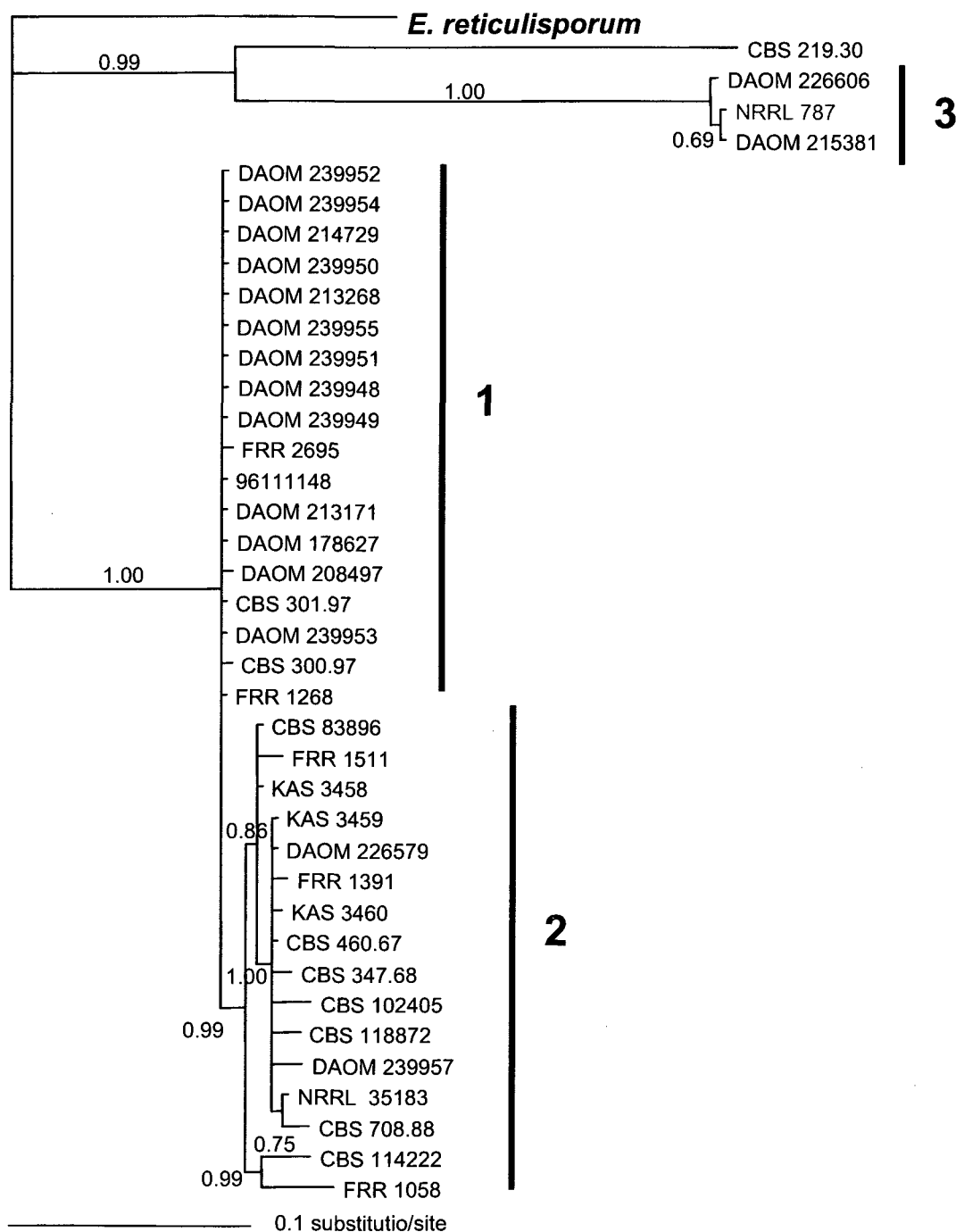


Figure 4.9: Bayesian inference gene tree for *P. oxalicum* strains based on *BenA* sequences. The tree was constructed using the GTR+G nucleotide substitution model. The ex-type strain is depicted in red.

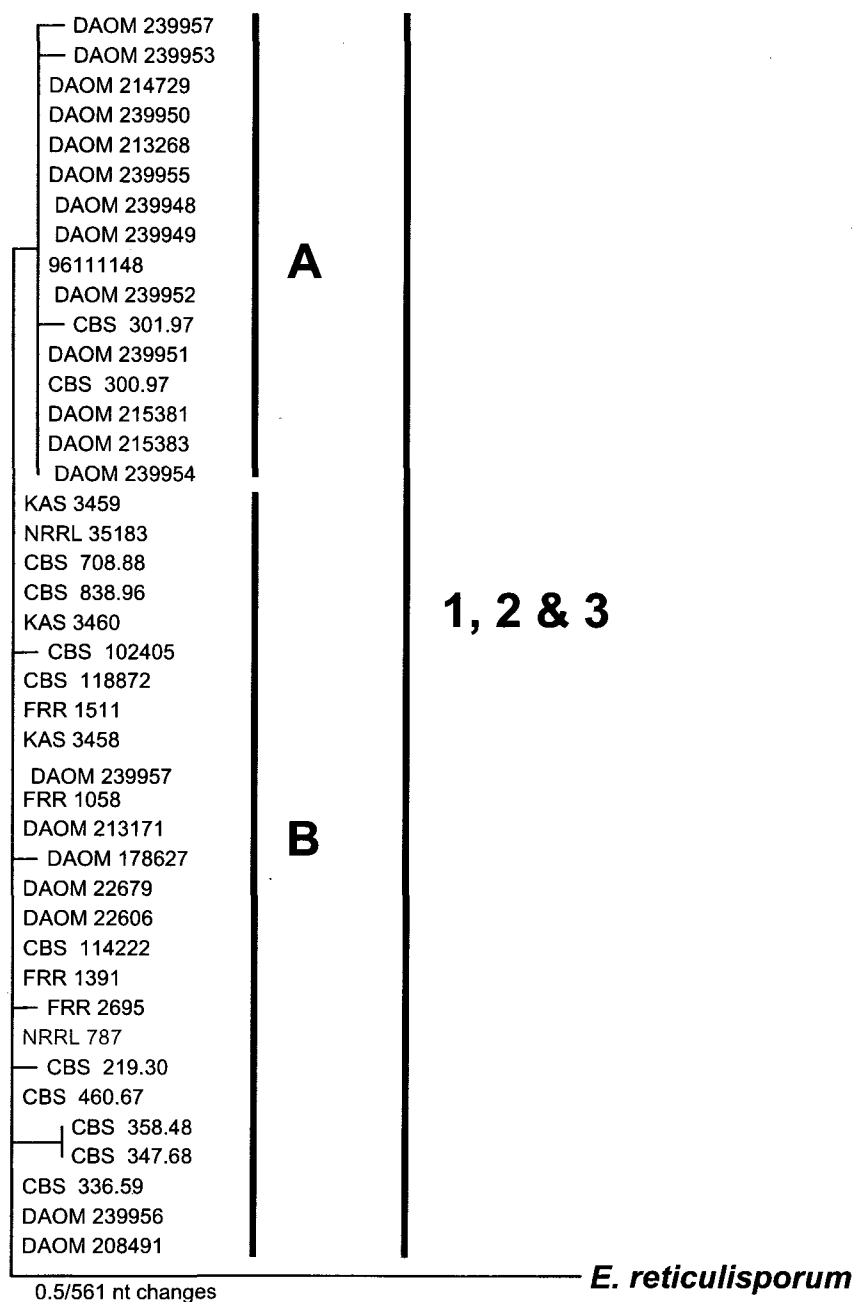


Figure 4.10: Maximum parsimony gene tree for *P. oxalicum* strains based on ITS sequences. One out 5000 most parsimonious trees ($L=2$, $CI=2$, $RI=1$, $RC=1$, $HI=0.$), all characters included. A heuristic search and 1000 bootstrap replicates were performed; bootstrap values above 70% were not present. Thickened lines represent consensus branches. The ex-type strain is depicted in red. A and B represent two groups of strains.

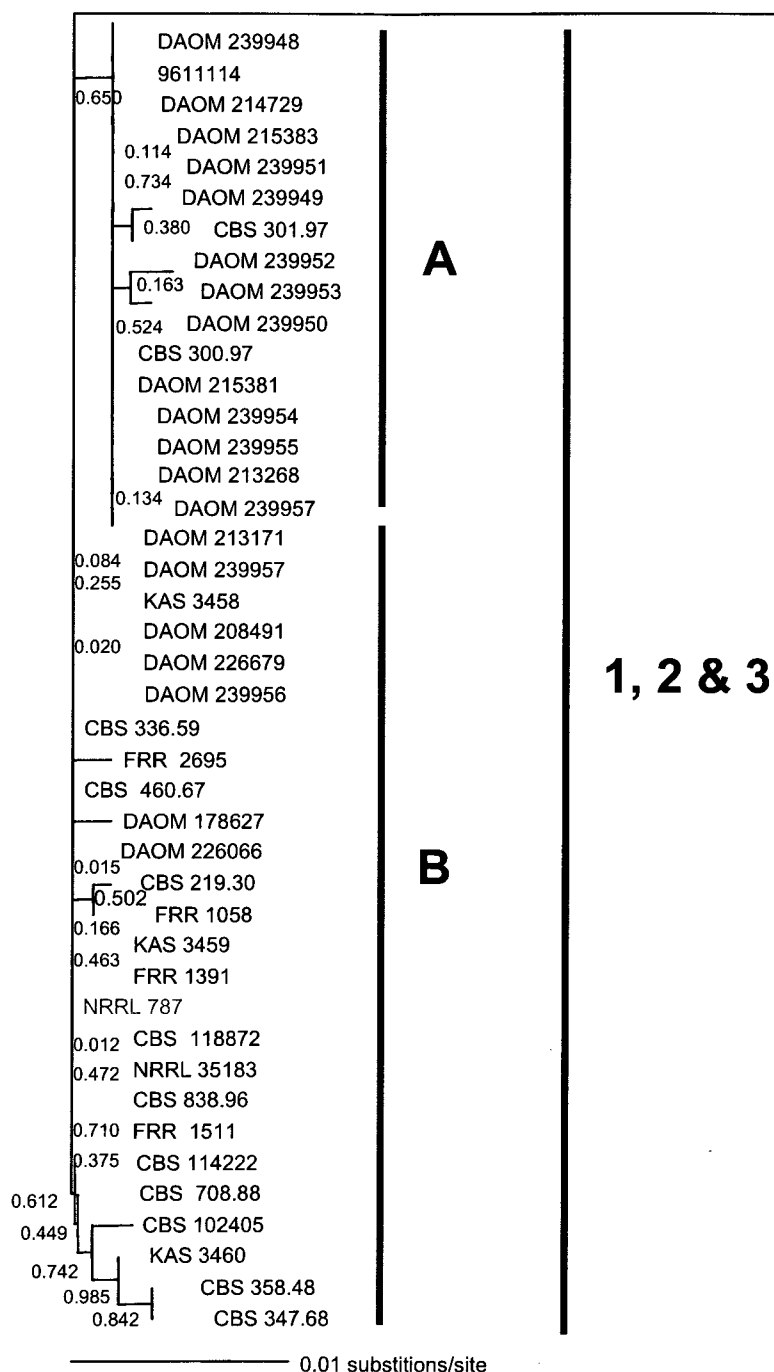


Figure 4.11: Maximum likelihood gene tree for *P. oxalicum* strains based on ITS sequences. The tree was constructed using the GTR+G nucleotide substitution model, with 1000 bootstrap replicates. The ex-type strain is depicted in red. A and B represent two groups of strains.

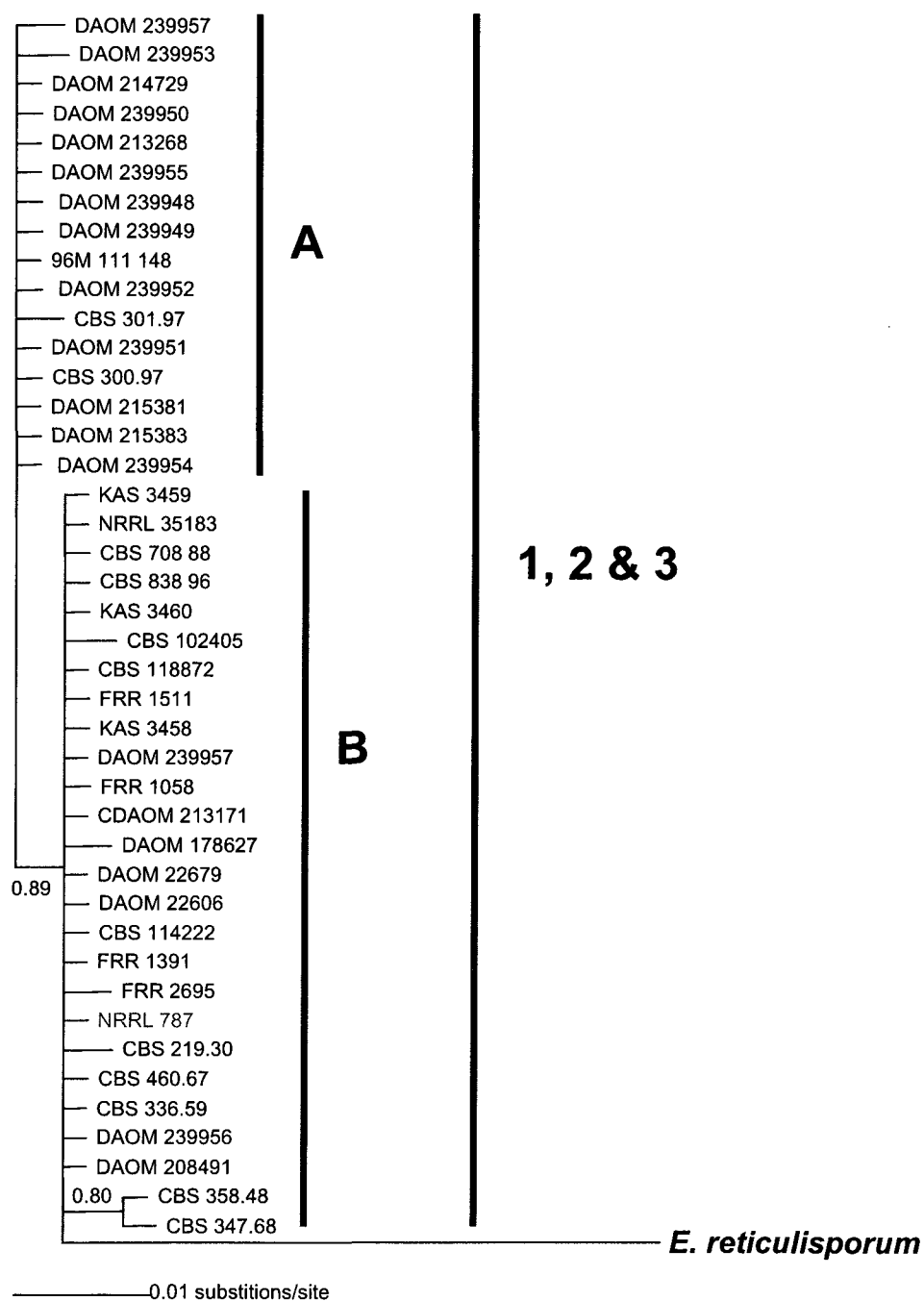


Figure 4.12: Bayesian inference gene tree for *P. oxalicum* strains based on ITS sequences. The tree was constructed using the GTR+G nucleotide substitution model. The ex-type strain is depicted in red. A and B represent two group of strains.

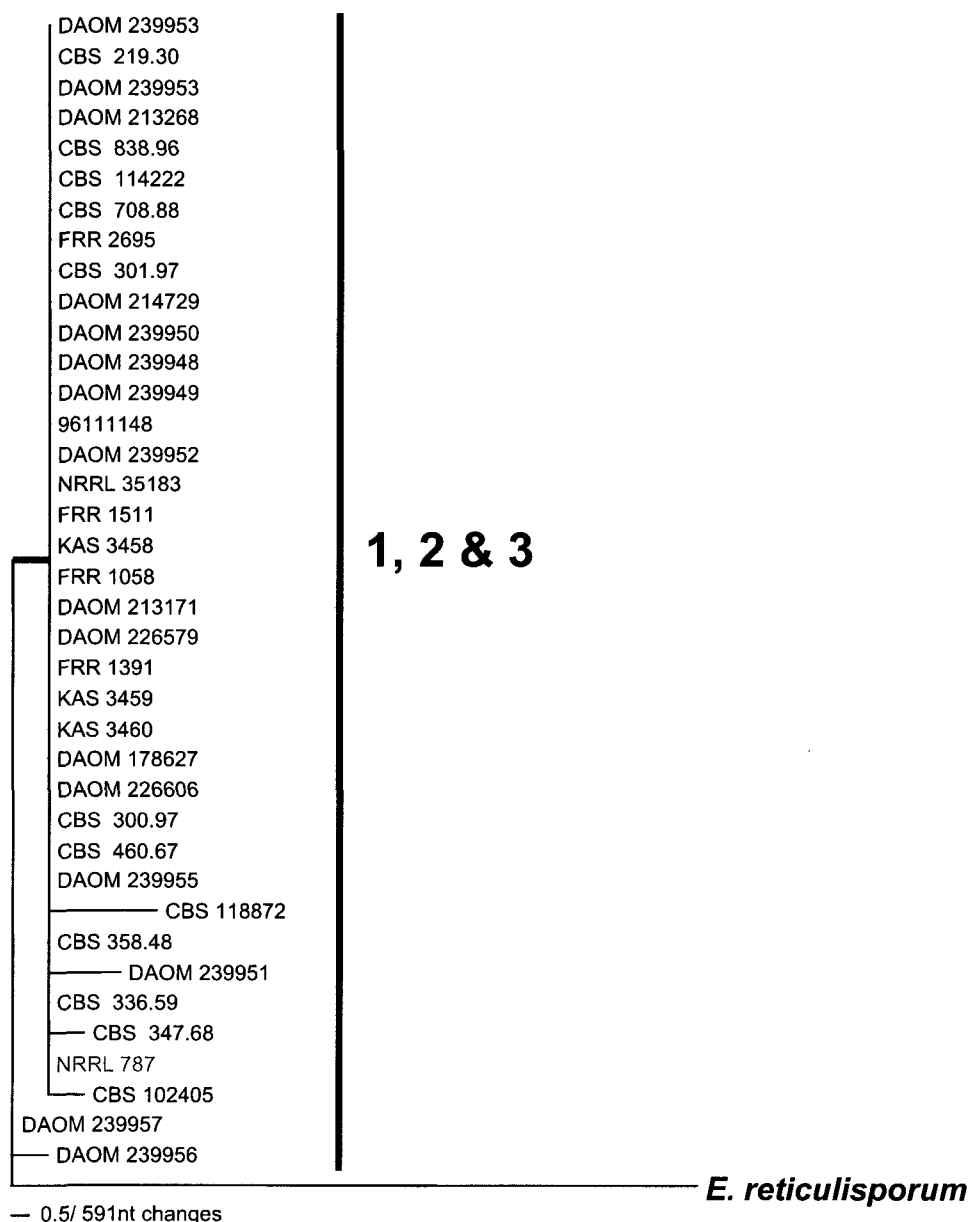


Figure 4.13: Maximum parsimony gene tree for *P. oxalicum* strains based on *Cox1* sequences. One out 5000 most parsimonious rooted trees (L=28, CI=1, RI=1, RC=1, HI=0.), all characters included, using a heuristic search. One thousand bootstrap replicates were performed, bootstrap values above 70% were not present. Thickened lines represent consensus branches. The ex-type strain is depicted in red. A and B represent two groups of strains.

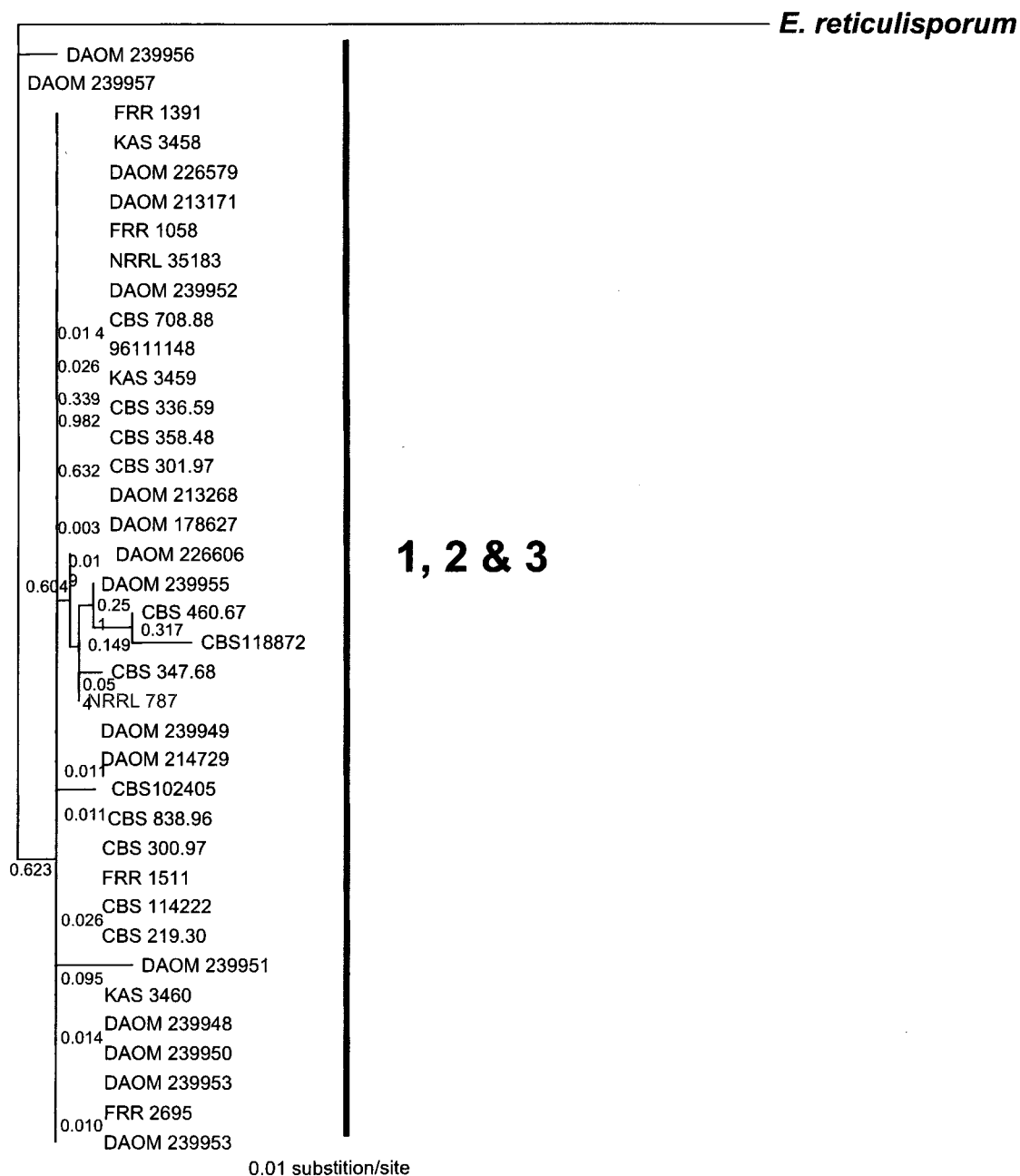


Figure 4.14: Maximum likelihood gene tree for *P. oxalicum* strains based on *Cox1* sequences. The tree was constructed using the GTR+G nucleotide substitution model, with 1000 bootstrap replicates. The ex-type strain is depicted in red.

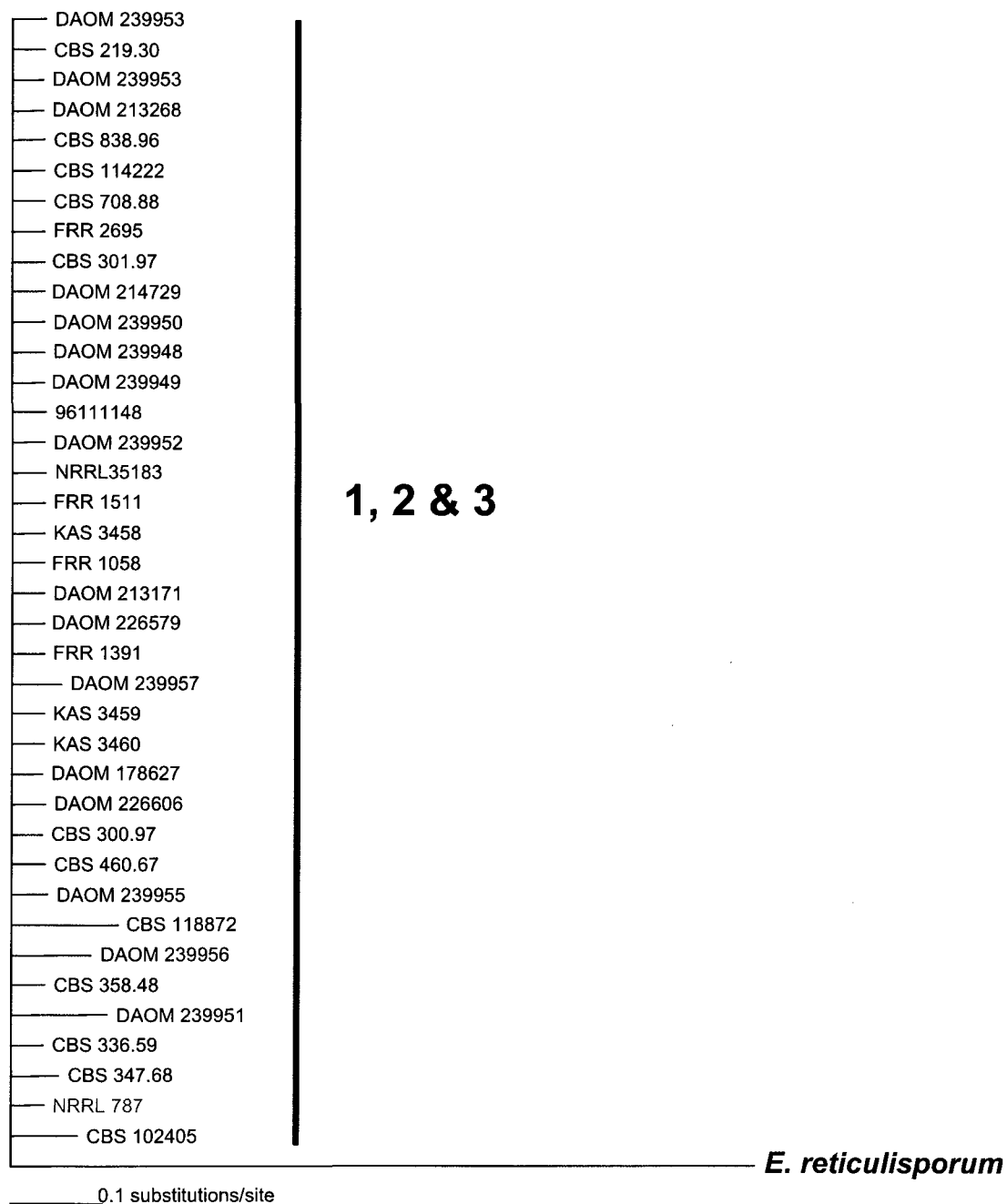


Figure 4.15: Bayesian inference gene tree for *P. oxalicum* strains based on *Cox1* sequences. The tree was constructed using the GTR+G nucleotide substitution model. The ex-type strain is depicted in red.

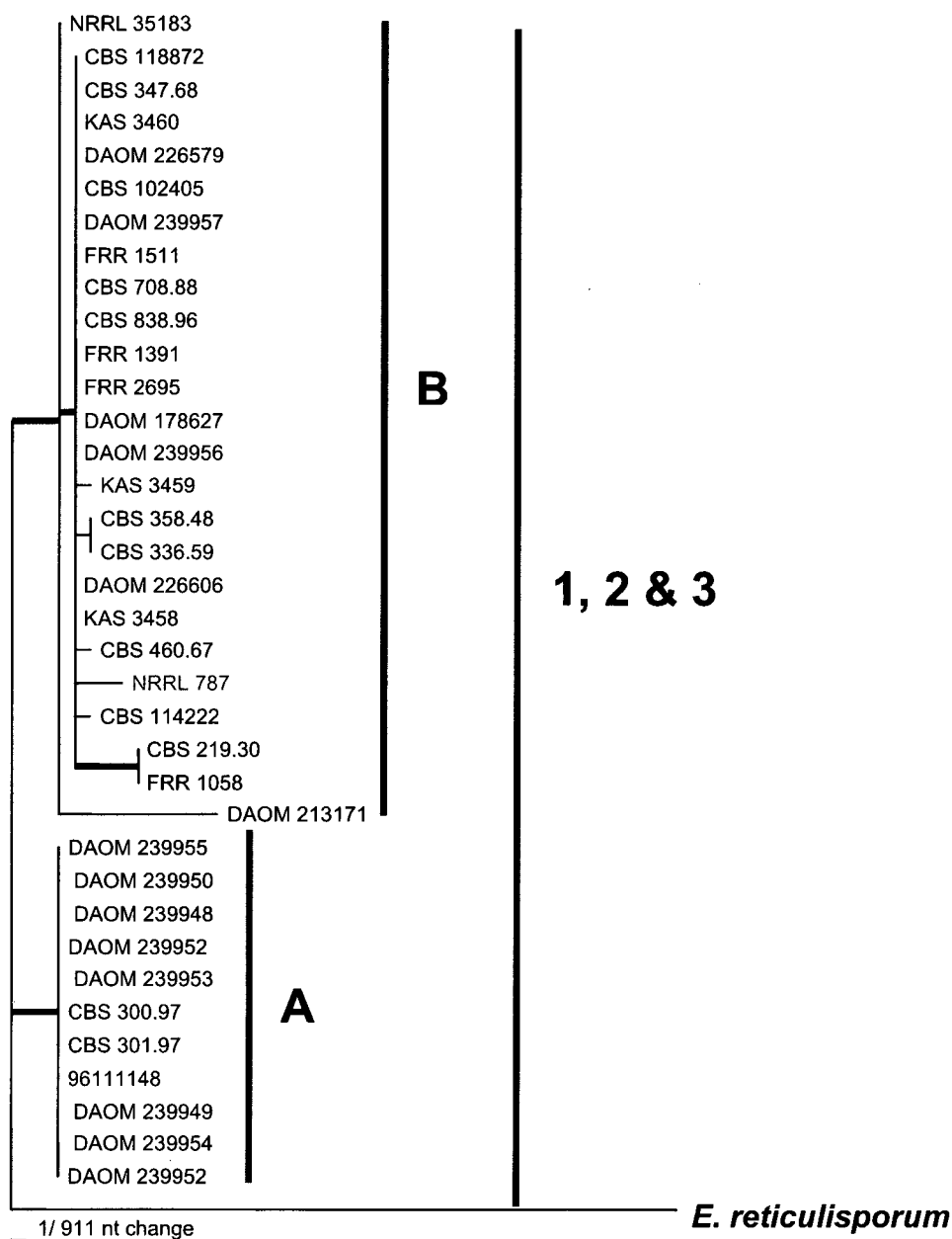


Figure 4.16: Maximum parsimony gene tree for *P. oxalicum* strains based on *TEF1-α* sequences. One out 5000 most parsimonious trees (L=334, CI=0.904, RI=0.920, RC=0.832, HI=0.096), all characters included, using a heuristic search. One thousand bootstrap replicates were performed, values above 70% were not present. Thickened lines represent consensus branches. The strain in red is the ex-type. A and B are two groups of strains.

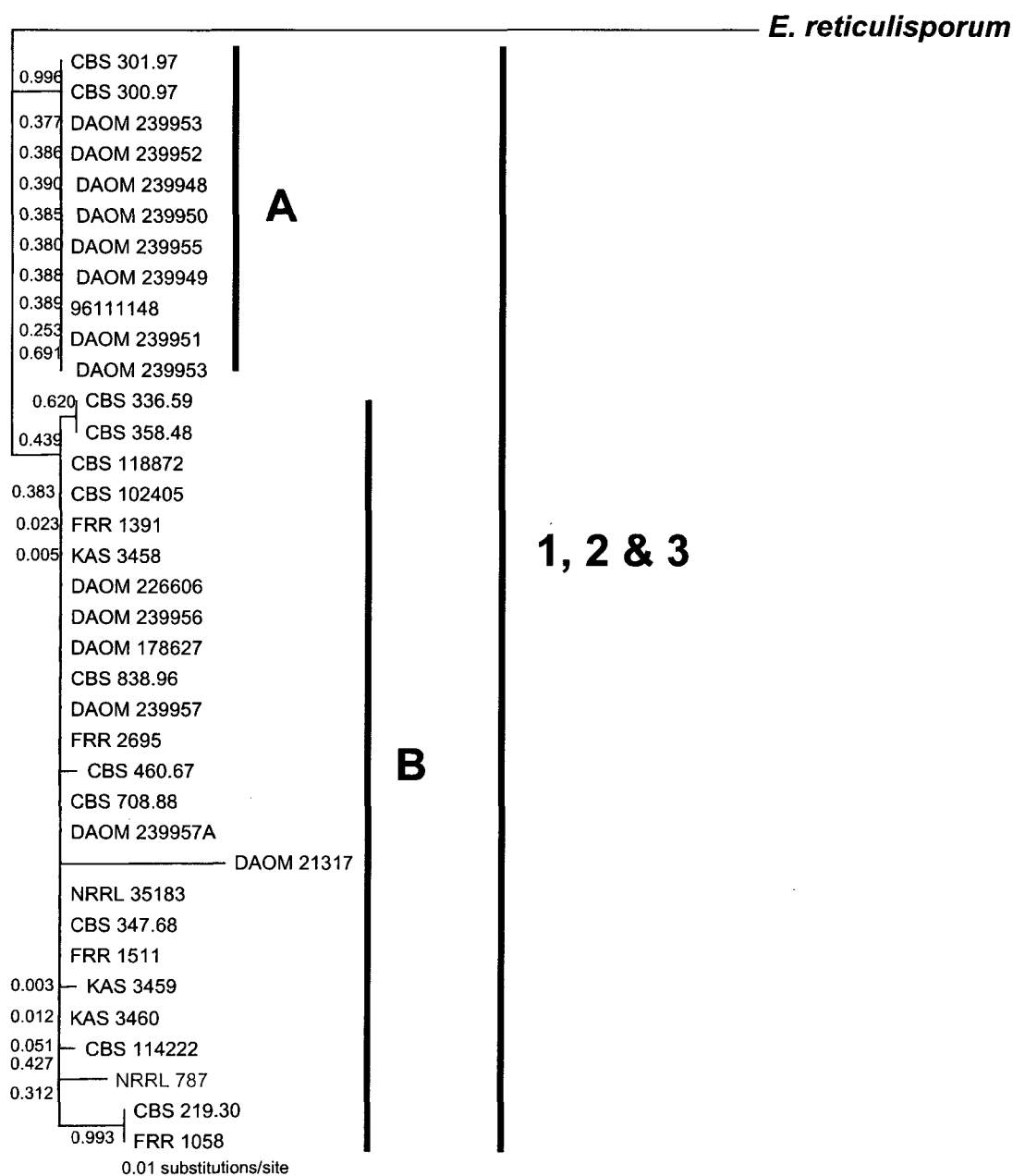


Figure 4.17: Maximum likelihood tree for *P. oxalicum* strains based on *TEF1-α* sequences. The tree was constructed using the GTR+G nucleotide substitution model, with 1000 bootstrap replicates. The ex-type strain is depicted in red. A and B are two groups of strains.

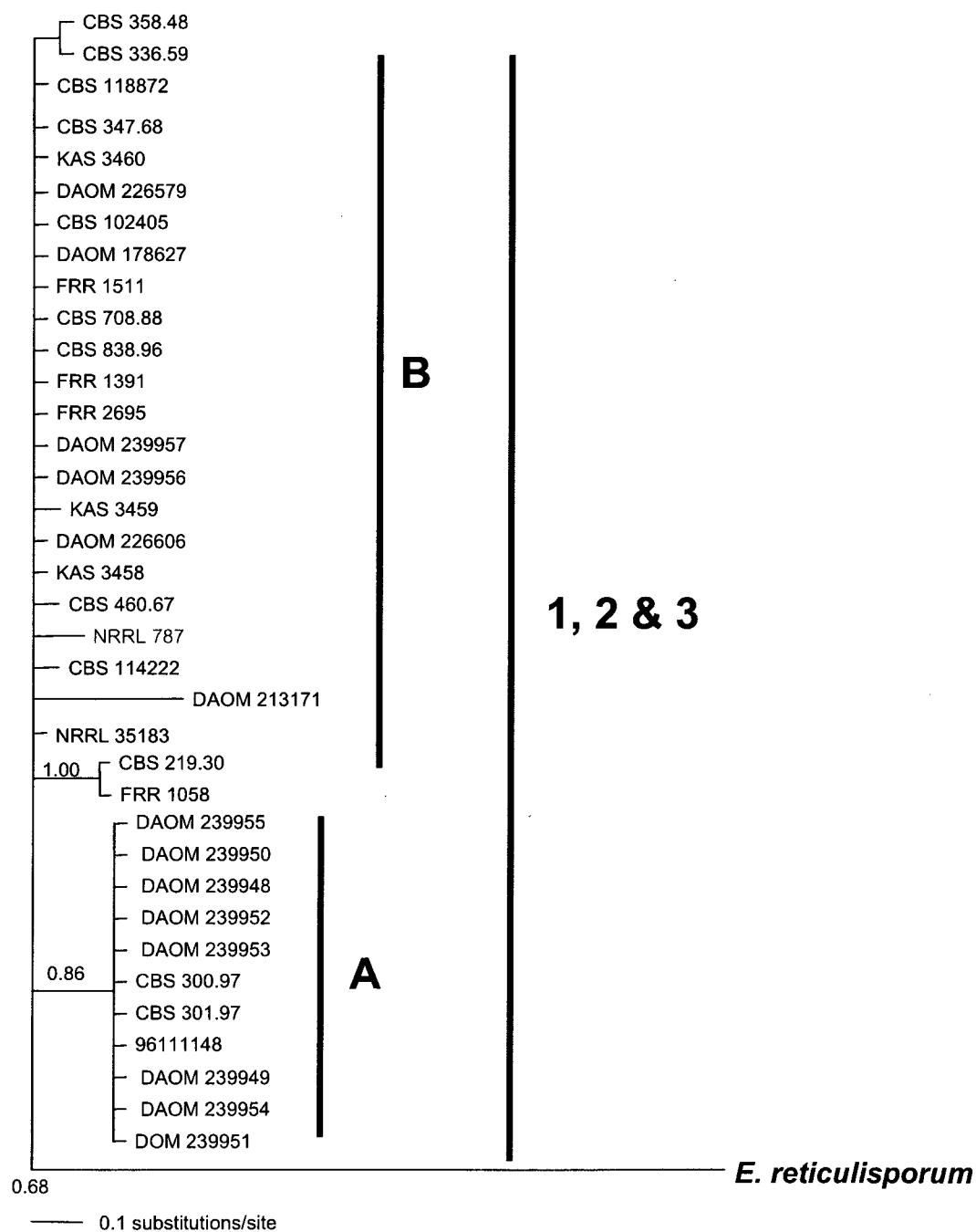


Figure 4.18: Bayesian inference tree for *P. oxalicum* strains based on *TEF1-α*. The tree was constructed using the GTR+G nucleotide substitution model. The ex-type strain is depicted in red.

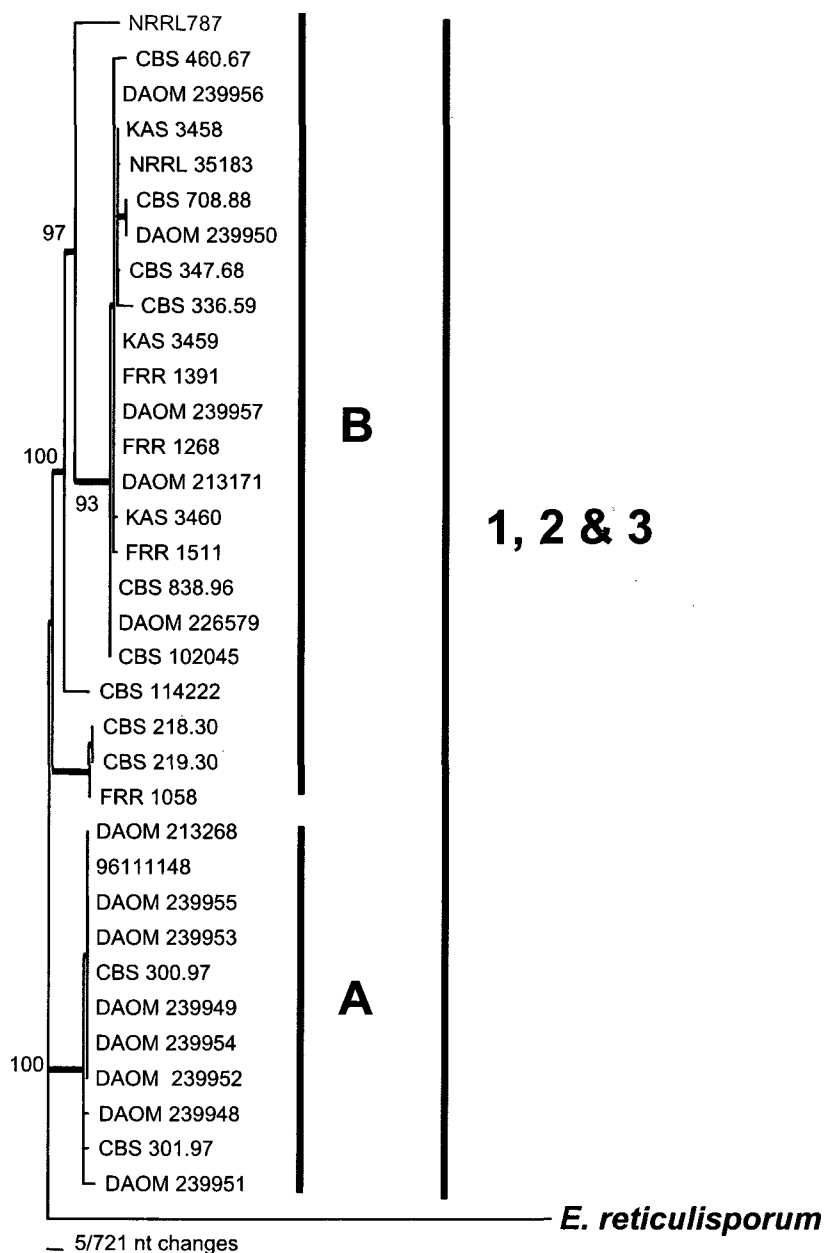


Figure 4.19: Maximum parsimony gene tree for *P. oxalicum* strains based on CaM sequences. One out 5000 most parsimonious trees ($L=23$, $CI=0.971$, $RI=0.967$, $RC=0.940$, $HI=0.029$), all characters included, using a heuristic search. One thousand bootstrap replicates were performed, bootstrap values above 70% were not present. Thickened lines represent consensus branches. The strain in red is the ex-type. A and B are two groups of strains.

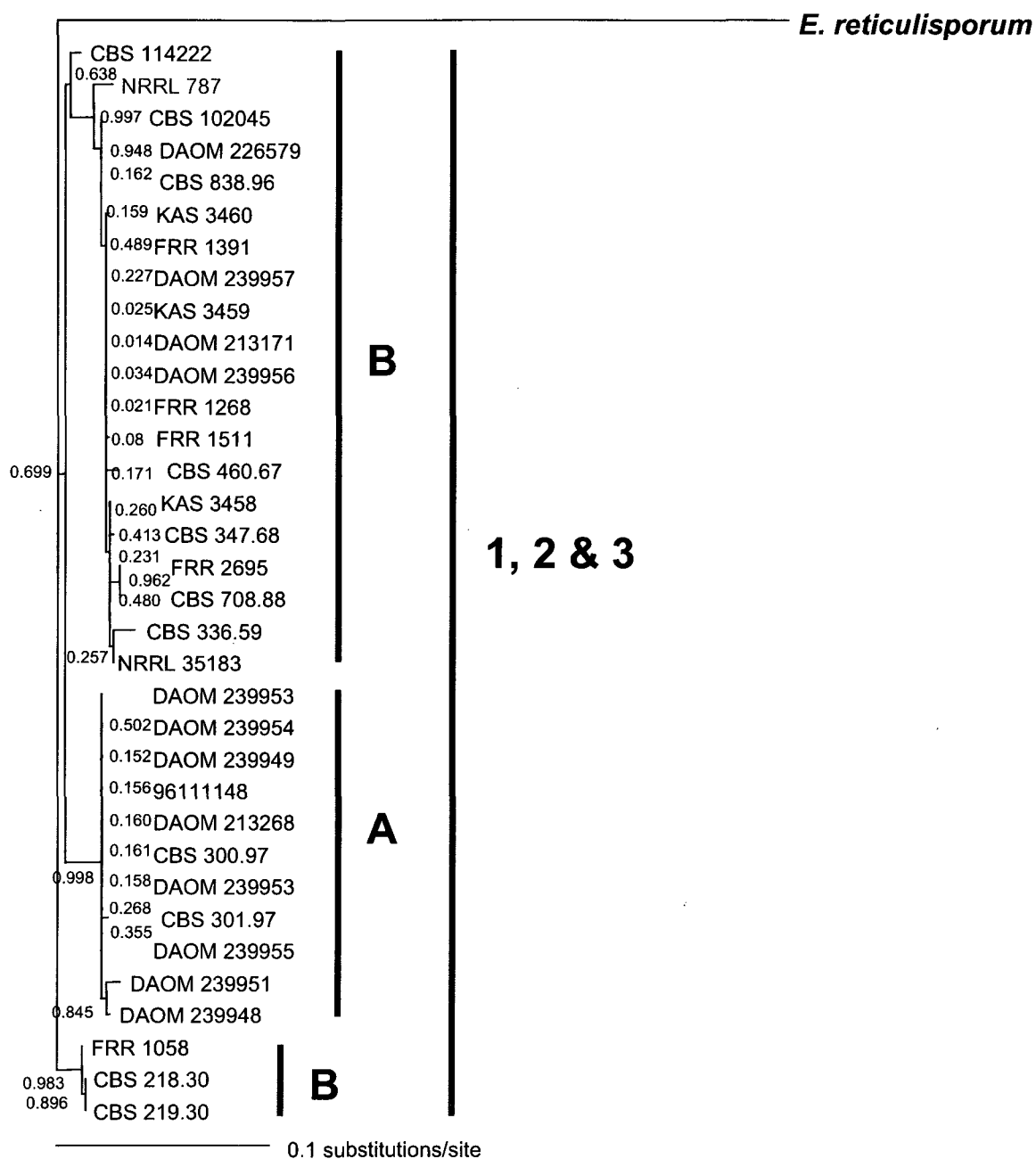


Figure 4.20: Maximum likelihood gene tree for *P. oxalicum* strains based on CaM sequences. The tree was constructed using the SYM+G nucleotide substitution model, with 1000 replicates. The ex-type strain is depicted in red. A and B are two groups of strains.

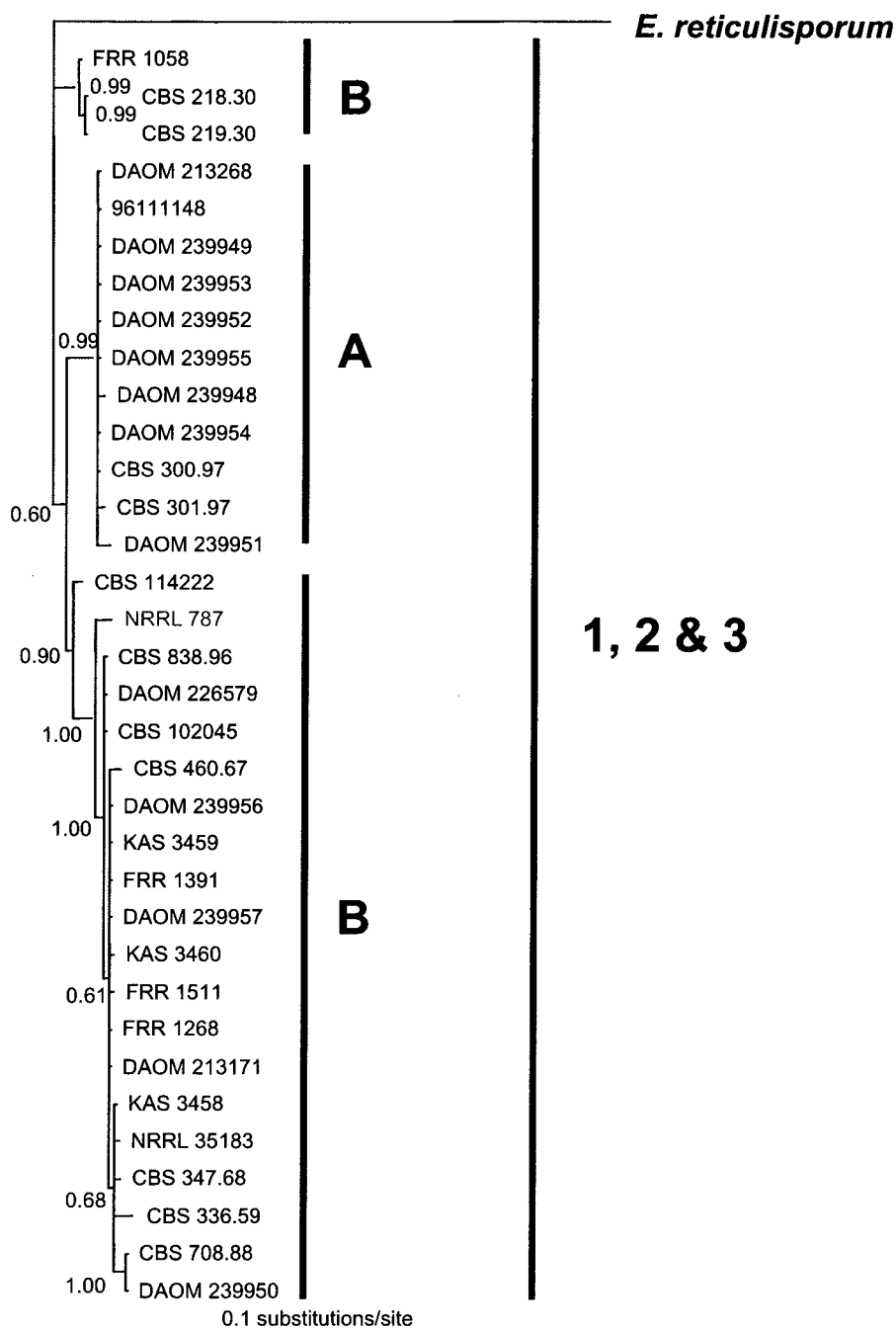


Figure 4.21: Bayesian inference gene tree for *P. oxalicum* strains based on CaM sequences. The tree was constructed using the SYM+G nucleotide substitution model. The ex-type strain is depicted in red. A and B represent two groups of strains.

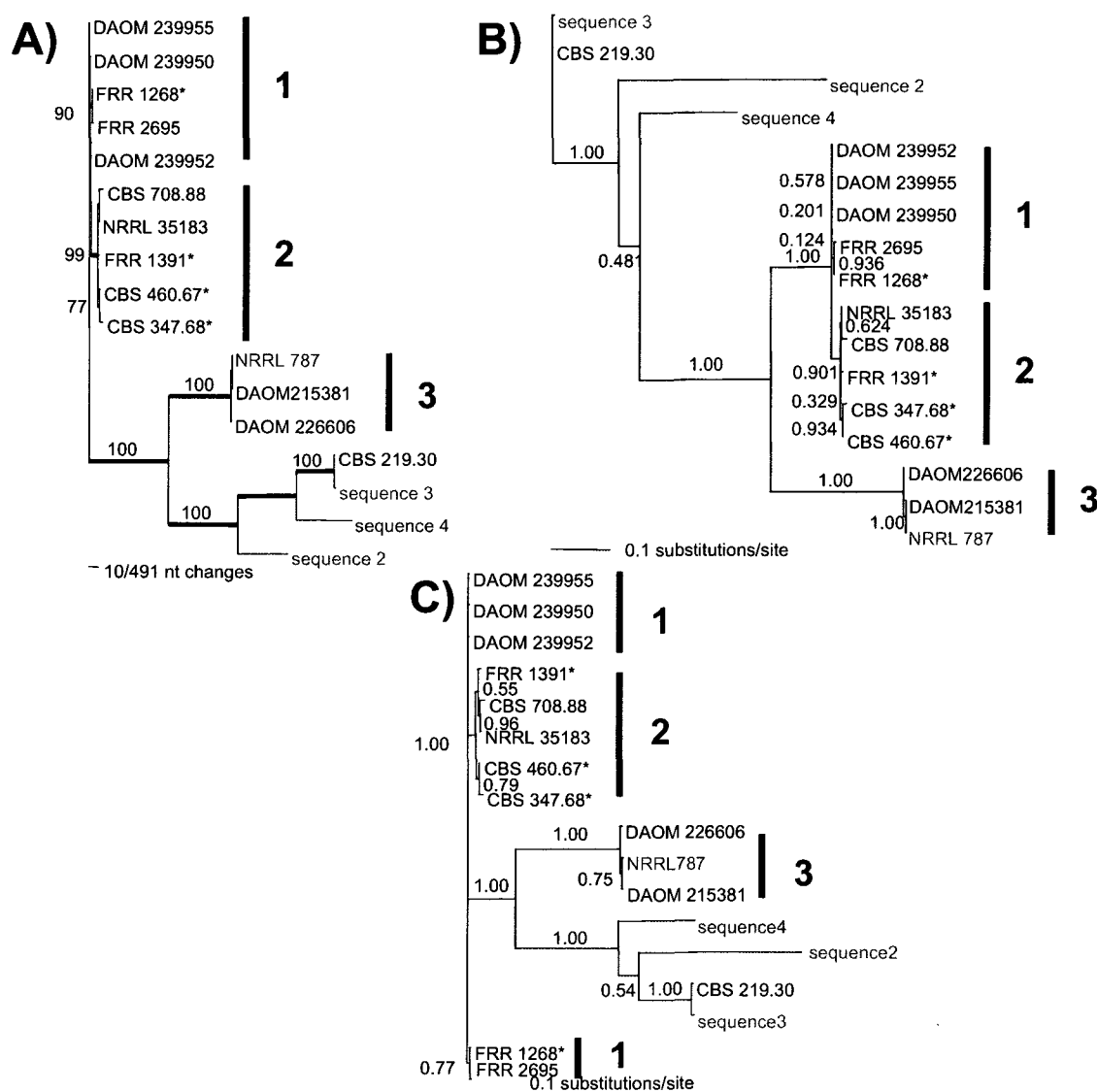


Figure 4.22: Maximum parsimony (A), maximum likelihood (B), and Bayesian inference (C) gene trees for *P. oxalium* based on *BenA* demonstrating the position of sequences 2, 3 and 4 within the three *BenA* groups. A) One out of 21 most parsimonious trees (L=186, CI=0.81, RI=0.89, CI=0.75, HI=0.25). One thousand bootstrap replicates were performed; bootstrap values above 70% are demonstrated. The ML (B) and BI (C) trees were constructed using the GTR+G nucleotide substitution model; one thousand and 1 M generations were performed. The ex-type strain sequence is depicted in red. The asteric (*) indicates sequences obtained from cloning.

Chapter 5: Discussion of DNA Barcodes for *Penicillium* species in subgenera *Aspergilloides* and *Furcatum*

The primary goal of this thesis was to discover undescribed, unknown and cryptic *Penicillium* species belonging to subgenera *Aspergilloides* and *Furcatum* using phylogenetic and barcoding methods. The β -tubulin (*BenA*), the nuclear ribosomal internal transcriber space (ITS) region, cytochrome c oxidase subunit 1 (*Cox1*), translation elongation factor 1- α (*TEF1- α*) and calmodulin (CaM) gene genealogies, along with morphological analyses, were used to determine species limits. The potential of the five genes as genetic barcode markers for Peterson's (2000) Group 3 of *Penicillium* was examined, with special attention to *Cox1* and ITS, using the Genealogical Concordance Concept (GCC) recognition criterion.

5.1 Barcoding *Penicillium*

DNA barcoding is a taxonomic method that uses a short region of DNA to identify organisms to the species level. A DNA barcode should be easily accessible (universally amplified/sequenced by standardized primers from a wide set of organisms), relatively short (~ 500–600 bp), simple to sequence, and easily alignable. The idea of a standardized molecular identification system emerged in the 1990s with the development of PCR-based approaches for species identification. The Barcode of Life project was the first attempt to create a universal system for a eukaryotic species inventory based on standardized molecular approaches, which then turned into the international initiative 'Consortium for the Barcode of Life' (CBOL). To achieve the CBOL objectives, species have to be taxonomically described and species limits resolved.

In fungi, the GCC determines species limits by comparing phylogenetic tree topologies of multiple genes (Figure 1.7). Under the GCC recognition criterion, congruent topologies across multiple gene genealogies indicate lineages that have developed under reproductive isolation, and are thus recognized as phylogenetic species (Scott and Chakraborty 2006). Incongruence indicates a genetically recombining, single phylogenetic species, with limited lineage development (Scott and Chakraborty 2006).

The GCC recognised *P. mallochii* and *P. guanacastense*, two species collected from the intestinal tract of caterpillars from Costa Rica, as undescribed, which were originally detected by preliminary *BenA* sequence data. All genes resolved the two species using maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI). The isolation of *P. mallochii* and *P. guanacastense* from different caterpillars may imply ecological preferences or roles. *Penicillium mallochii* was isolated from caterpillars belonging to the family Saturnidae, while *P. guanacastense* strains were isolated from caterpillars belonging to the family Noontidae. This may suggest substrate preference by the species, but more than two strains are needed for *P. guanacastense* to determine ecological relationships.

The GCC also recognized the species in the *P. sclerotiorum* complex, which also include *P. mallochii* and *P. guanacastense*: *P. krugii*, *P. jacksonii*, *P. cainii* and *P. ciebiessum*. All species within the complex are phylogenetically related and are morphologically similar in having yellow to orange vivid colony colours, and monoverticillate conidiophores. Closer inspection, however, revealed morphological differences that are useful in distinguishing the species (Table 3.2). Geographical

correlations for the groups exist, with the exception of *P. sclerotiorum*, which was isolated from all over the world (Table 3.1).

In *Penicillium*, *BenA* has been useful in identifying the *P. roquefortii* Thom (Samson *et al.* 2004), and *P. aurantiogriseum* Dierckx (Seifert and Louis-Seize 2000) complexes. It has been used in the construction many gene genealogies and phylogenies of many fungal groups (Serra and Peterson 2007; Peterson and Sigler *et al.* 2002, Wang *et al.* 2004). Preliminary DNA sequences analyses of *BenA* suggested the presence of three phylogenetic species for *P. oxalicum* Currie and Thom. In this thesis, analyses with multiple strains of *P. oxalicum* confirmed the preliminary results, but were not supported in ITS, *Cox1*, *TEF1- α* and CaM gene genealogies. The ITS, *TEF1- α* and CaM indicated two groups of strains, while *Cox1* yielded one group. Furthermore, geographical distribution and substrate isolation did not correlate with any of the groups observed in *BenA* or in the ITS, *TEF1- α* and CaM. The incongruence in gene tree topologies indicated that *P. oxalicum* is a single phylogenetic species that is cosmopolitan, plays many ecological roles and has great morphological variation.

In *Penicillium* subgenus *Penicillium*, *BenA* provided species level resolution for 80.1% of the species tested, while *Cox1* and ITS provided 67.1% and 24.5% (Seifert *et al.* 2007). Out of the three genes tested, *BenA* had the highest intraspecific and interspecific divergence, 0.83% and 14.4% (Seifert *et al.* 2007). *Cox1* had the lowest intraspecific and the second highest interspecific divergence, 0.06% and 5.6% (Seifert *et al.* 2007). ITS had an intraspecific and interspecific divergence of 0.51% and 24.5% (Seifert *et al.* 2007). *Cox1* provided good species level resolution, and the lack of introns

and gaps, make it a good barcode for *Penicillium* subgenus *Penicillium*. Seifert et al. (2007), however, suggested a second barcode gene is needed.

The potential of *BenA*, *Cox1*, ITS, *TEF1-α* and CaM as barcodes for Peterson's (2000) Group 3 of *Penicillium*, including the newly described species in this thesis, is analysed here. The species level resolution using MP, ML and BI were calculated using the gene trees from Chapter 3. The intraspecific and interspecific divergences, and the genetic distance (species level resolution) for all species were calculated using the alignments from Chapter 3 with MEGA (Molecular Evolutionary Genetic Analyses; Tamura *et al.* 2007) v. 8 using p-distances. The results are summarized in Table 5.1.

CaM and *TEF1-α* provide 100% species level resolution, while *BenA* provides 91.7% species level resolution. ITS and *Cox1* had a species level resolution of 83.3%. CaM had the highest intraspecific variation while *Cox1* had the lowest (Table 5.1). *Cox1* also had no gaps and no introns, while CaM had the highest number of gaps, interspecific divergence, and along with *TEF1-α*, the highest number of introns (Table 5.1). *Cox1* had the third highest interspecific variation, while ITS had the lowest.

From the five genes tested, *TEF1-α* and CaM had the highest species resolving ability. However, they had the greatest number of gaps and introns, making manual adjustments of sequences difficult. Thus they are not ideal barcodes, but are still good genetic markers nonetheless. *Cox1* and ITS had the lowest species resolving ability, but unlike ITS, *Cox1* had no gaps or introns. The results obtained by Seifert *et al.* (2007) suggested that *Cox1* had a better resolving ability than ITS, but this was not observed in this thesis. The species resolving ability of *Cox1* and ITS is approximately the same for Peterson's (2000) *Penicillium* Group 3, 83.3%; differing from the 67.1% and 24.5%

observed for *Cox1* and ITS for *Penicillium* subgenus *Penicillium* (Seifert *et al.* 2007). *BenA* resolved 91.7% of the species in *Penicillium* Group 3, and provided a species resolution of 80.1% for Seifert *et al.* (2007). The difference between results may be attributed to the different sampling sizes. The number of species used in this thesis was 11–12, while Seifert *et al.* (2007) used 49–70 species. Seifert *et al.* (2007) used five representatives for each species, whereas two to six representative strains were used in this thesis. Mobile introns, which are typically present in the fungal mitochondrial genome (Hamari *et al.* 2002) were not observed in the strains examined in this thesis and appeared in two strains examined by Seifert *et al.* (2007) identified as *P. arenicola* and *P. pinophilum*. The introns observed by Seifert *et al.* (2007) ranged from 1,100–1,200 bp. The introns in the two species were at the same sites, and aligned with one another.

Cox1 is also a good genetic barcode marker for *Leohumicola*, a slow growing, heat resistant genus (Hambleton *et al.* 2005; Nguyen and Seifert 2008). In *Leohumicola*, only three strains out of 53 examined by Nguyen and Seifert (2008) had mobile introns (~850 bp) in the barcoding region of *Cox1*. Overall, *Cox1* is a good barcode for *Penicillium* and *Leouimicola* spp. A second barcode marker, however, is needed to provide better species resolution for *Penicillium*. CaM and *TEF1-α* provided the highest species resolution, but had shortcomings. For CaM two different primers sets (CF4 and CF5; CMD5 and CMD6) were used to amplify and sequence *P. oxalicum* strains. *Penicillium adametzii* strains were not amplified using the primers for CaM. For *TEF1-α*, two strains of *P. oxalicum* had poor sequence signal and primers EF1c and EF6 did not amplify *P. adametzioides* during PCR. Furthermore, CaM and *TEF1-α* sequences had the highest

number of introns and gaps, making sequence alignment difficult. More gene regions need to be tested to find a second genetic barcode marker.

5.2 Future Research

DNA sequence data, along with morphological analyses and secondary metabolite profiling, are useful in *Penicillium* research. In *Penicillium* subgenus *Penicillium* species, species-specific secondary metabolite profiles were produced (Frisvad 1981; Frisvad & Fitenborg 1983, 1989; Lund & Frisvad *et al.* 1992; Smedsgaard *et al.* 2004). Secondary metabolite profiling may aid in delimiting the species in the *Penicillium sclerotiorum* complex, and may identify compounds unique to each species.

Penicillium sclerotiorum has been noted for the production of secondary metabolites with antibacterial and antifungal properties (MacCurtin and Reilly 1940; De Lucca *et al.* 2008); and for the production of a wide range of azapholine production, two of which are endothelin antagonists (Pairet *et al.* 1995). Species in the *P. sclerotiorum* complex maybe tested for novel anti-microbial substances or other molecular uses. A *Penicillium* species, *P. chrysogenum*, was the first organism known to produce an antimicrobial substance. This discovery was then later followed by the discovery of antifungal griseofulvum, which is produced by *P. griseofulvum*.

As discussed in Chapter 4, there have been many reports of *BenA* paralogs in fungi, some of which may be functional because they are transcribed. In this thesis, paralogs are reported in *Penicillium* for *P. oxalicum*, and were also observed in two strains of *P. herquei*, CBS 336.48 and CBS 110644, as noted in chapter two. One of the paralogs was approximately 470 bp long and was homologous to previously obtained *BenA* *P. herquei* sequences. The other paralog is approximately 360 bp long, the

nucleotide sequence was different from previously obtained *BenA P. herquei* sequences (Table 5.2) and resembled sequence 2 in chapter four, and is most likely a pseudogene as suggested in chapter four. The presence of the 360 bp paralog in two *Penicillium* species may suggest a duplication event in the ancestor of *Penicillium*, which was retained by these two species.

Table 5.1: Comparison of five potential markers for Peterson’s (2000) Group 3 of *Penicillium*.

Marker	No. of isolates	No. of species	Mean sequence length	Mean intraspecific divergence (%)	Range of means (%)	Mean interspecific divergence (%)	Range of means (%)	Species resolution (%) ^a	Mean no. of introns (approx)	Mean no. of gaps in alignment
<i>CoxI</i>	51	12	591	0.3	0 – 0.3	4.7	0.3 – 8.4	83.3	0	0
<i>BenA</i>	51	12	500	0.9	0 – 0.25	8.8	4.8 – 18.6	91.7	3	72
ITS	51	12	563	0.15	0 – 0.4	3.7	0.6 – 8.8	83.3	1	64
<i>TEF1-α</i>	49	11	738	0.5	0 – 1.1	4.4	0.3 – 8.4	100	4	91
CaM	47	11	520	1.7	0.1 – 2.2	14.3	3.9 – 26.5	100	4	285

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Appendix 1: Media Recipes. All media were autoclaved for at least 20 mins at 15 psi. The media was then poured onto 9 cm Petri plates under a laminar hood. Media was left at room temperature until it solidified. It was then stored at 4°C for future use.

Medium	Ingredients	½ L
CYA (Czapek Yeast Extract Agar; Pitt 1979)	K ₂ HPO ₄ Czapek concentrate ¹ Yeast Extract Sucrose Agar Trace elements ² dH ₂ O	0.5 g 5 mL 2.5 g 15 g 7.5 g 0.5 mL 0.5 L
MEA (Malt Extract Agar 2%; Pitt 1979a)	Malt Extract Agar Trace elements ² dH ₂ O	10 g 7.5 g 0.5 mL 0.5 L
CZ (Czapek Agar; Raper and Thom 1949)	K ₂ HPO ₄ Czapek concentrate ¹ Sucrose Agar Trace elements ² dH ₂ O	0.5 g 5 mL 15 g 7.5 g 0.5 mL 0.5 L
YES (Yeast Extract Sucrose Agar; Filtenborg <i>et al.</i> 1990) Note: Volume was brought up to 500 mL. The pH was adjusted to 6.4 – 6.6 before autoclaving by adding NaOH or HCl.	Sucrose Yeast extract MgSO ₄ ·7H ₂ O Trace elements Agar dH ₂ O	75 g 10 g 0.25 0.5 mL 10 g 425 mL
OA (Oatmeal Agar) Note: Oats were simmered for 1 h then poured using a cheese cloth.	Oats Agar dH ₂ O	15 g 7.5 g bring to 0.5 L

Medium	Ingredients	½ L
CREA (Creatine Sucrose Agar; Frisvad 1993) Note: The pH was adjusted to 8.0 using NaOH or HCl.	Creatine	1.5 g
	Sucrose	15 g
	KCl	0.25 g
	MgSO ₄ ·7H ₂ O	0.25 g
	FeSO ₄ ·7H ₂ O	0.005
	K ₂ HPO ₄	0.65 g
	Bromocresol purple	0.025 g
	Agar	7.5 g
	dH ₂ O	0.5 L
DG-18 (Dichloran 18% Glycerol Agar; Samson <i>et al.</i> 2004)	Peptone	2.5 g
	Glucose	5 g
	K ₂ HPO ₄	0.5 g
	MgSO ₄ ·7H ₂ O	0.25 g
	Dichloran (2% in ethanol)	0.5 mL
	Glycerol	110 g
	Chloramphenicol	0.05 g
	Agar	7.5 g
	dH ₂ O	0.5 L

¹ Czapek concentrate for 50 mL solution (Pitt 1979a): NaNO₃ – 15 g; KCL – 2.5 g; MgSO₄·7H₂O – 2.5 g; FeSO₄·7H₂O – 0.05 mg; and dH₂O – 50 mL. A magnetic stirrer was used to dissolve the ingredients. The solution was then stored at 4°C.

² Trace elements for 50 mL solution (Pitt 1979a): ZnSO₄ 7H₂O – 0.5 g; CuSO₄·5H₂O – 0.23; and dH₂O – 50 mL. A magnetic stirrer was used to dissolve the ingredients. The solution was then stored at 4°C.

Appendix 2: Primers Sequences

Gene	Forward Primer	Reverse Primers
<i>BenA</i>	Bt2A: 5'–ggtaaccaaatcggtgctgcttc–3' (Glass and Donaldson 1995)	Bt2B: 5'–aacctcagtgtagtgaccgttggc–3' (Glass and Donaldson 1995)
	T10: 5'–acgatagggtcacctccatgact–3' (O' Donnell and Cigelnik 1997)	T222: 5'–gaccggggaaacggagacagg–3' (O' Donnell and Cigelnik 1997)
ITS	ITS1: 5'–tccgtaggtgaacctgccg–3' (White <i>et al.</i> 1990)	ITS4: 5'–tcctccgctattgatatgc–3' (White <i>et al.</i> 1990)
<i>Cox1</i>	PF: 5'–gacaagaaaggtgattttatcttc–3' (Seifert <i>et al.</i> 2007)	AR: 5'–ggtaatgataataataataacagctg–3' (Seifert <i>et al.</i> 2007)
<i>TEF1-α</i>	EF1c: 5'–tcgtcggttatcgccacgctc–3' (Peterson <i>et al.</i> 2004)	EF6: 5'–cttstyccarcccttgcca–3' (Peterson <i>et al.</i> 2004)
CaM	CMD5: 5'–ccgagtacaaggargccttc–3' (Hong <i>et al.</i> 2006)	CMD6: 5'–ccgatrgaggtcatracgtgg–3' (Hong <i>et al.</i> 2006)
	CF1: 5'–gccgactctttgacygargar–3' (Peterson <i>et al.</i> 2004)	CF4: 5'ttytgcatcatragytggac–3' (Peterson <i>et al.</i> 2004)
		PoxalCMD2R: 5'–ggcggaaatraagccgttgta–3' (Rivera and Seifert 2009; sequence)

Appendix 3: Chapter 2 Multiple Sequence Alignments

Multiple *BenA* Sequence Alignment

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239918 GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS2615    GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239922 GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS2630    GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS2596    GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS3189    -----GGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239927 -----GGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239919 -----GGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS2606    GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239921 -----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS3190    -----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239917 -----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS3191    -----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS3183    -----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239928 GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS3193    -----GGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239926 -----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS3186    -----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239929 GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS3187    -----A-CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239925 -----A-CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS2601    -----GCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239924 -----GCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
KAS2612    GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
DAOM239920 -----GAGTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTC
NRRL2074   -----ATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
NRRL32583 GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
DAOM239930 -----ACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
DAOM239931 GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
DAOM239932 GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
DAOM239912 GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----TATC
DAOM239913 -----C-AAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----TATC
CBS229.60  GGTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----AGTC
CBS23865   -GTAA-CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----AGTC
KAS3463    GTAA--CCAAAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
CBS238.68  GTAA--CCAAAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
KAS3464    -----ATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
KAS3466    -----ATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
KAS3465    -----AATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
NRRL3391   GTAA--CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
AL1878     GTAA--CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
AL1644     GTAA--CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
AL1642     GTAA--CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
AL1643     GTAA--CCAAAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
CBS136.22  -TAA--CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
CBS347.51  -----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
CBS336.48  -TAA--CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
CBS110644  GTAA--CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC
NRRL705    GTAA--CC-AAATCGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATC

[      81      91      101      111      121      131      141      151      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239918 AATTG-GTGAACCTCAGGAACC----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCT-CGATGG
KAS2615    AATTG-GTGAACCTCAGGAACC----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCT-CGATGG
DAOM239922 AATTG-GTGAACCTCAGGAACC----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCT-CGATGG
KAS2630    AATTG-GTGAACCTCAGGAACC----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCT-CGATGG
KAS2596    AATTG-GTGAACCTCAGGAACC----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCT-CGATGG
KAS3189    AATTG-GTGAACCTCAGGAACC----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCT-CGATGG
DAOM239927 AATTG-GTGAACCTCAGGAACC----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCT-CGATGG

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NRRL32583 CGAGGGCCAGTAAGT-----ATCCATT-CAGTTGGAATTGAGTGATA---TGAGAAT-GG
 DAOM239930 CGAGGGCCAGTAAGT-----ATCCATT-CAGTTGGAATTGAGTGATA---TGAGAAT-GG
 DAOM239931 CGAGGGCCAGTAAGT-----ATCCATT-CGGTTGGAATTGAGTGATA---TGAGAAT-GG
 DAOM239932 CGAGGGCCAGTAAGT-----ATCCATT-CGGTTGGAATTGAGTGATA---TGAGAAT-GG
 DAOM239912 CGAGGGCCAGTAAGT-----ATCAATT-TGGTTGGAATTGGGTGATA---TGAGAAT-GG
 DAOM239913 CGAGGGCCAGTAAGT-----ATCAATT-TGGTTGGAATTGGGTGATA---TGAGAAT-GG
 CBS229.60 CGAGGGCCAGTAAGT-----ATCAATA-CGAGTGGGATTGGGTGATG---TGAGAAC-GG
 CBS23865 CGAGGGCCAGTAAGT-----ATCAATA-CGAGTGGGATTGGGTGATG---TGAGAAC-GG
 KAS3463 CGATGGCCAGTAAGT-----TTCTCGA-TTAAGTCGATTGGGTATGTGGTGGGAAT-GG
 CBS238.68 CGATGGCCAGTAAGT-----TTCTCGA-TTAAGTCGATTGGGTATGTGGTGGGAAT-GG
 KAS3464 CGATGGCCAGTAAGT-----TTCTCGA-TTAAGTCGATTGGGTATGTGGTGGGAAT-GG
 KAS3466 CGATGGCCAGTAAGT-----TTCTTGA-TTAAGTCGATTGGGTATGTGGTGGGAAT-GG
 KAS3465 CGATGGCCAGTAAGT-----TTCTCGA-TCAA-TCGATTGGGTATGTGGTGGGAAT-GG
 NRRL3391 CGATGGACAGTAAGT-----CTCGATCATCGACTCGATTGAATGAAGTGGTGGGAAT-GG
 AL1878 CGATGGACAGTAAGT-----CTCGATCATCGACTCGATTGAATGAAGTGGTGGGAAT-GG
 AL1644 CGATGGACAGTAAGT-----CTCGATCATCGACTCGATTGAATGAAGTGGTGGGAAT-GG
 AL1642 CGATGGACAGTAAGT-----CTCGATCATCGACTCGATTGAATGAAGTGGTGGGAAT-GG
 AL1643 CGATGGACAGTAAGT-----CTCGATCATCGACTCGATTGAATGAAGTGGTGGGAAT-GG
 CBS136.22 CGAAGGACAGTGAGT-----ATCAATA-TTAATGGAATTGAGTGACGAG-TAGGAAT-GG
 CBS347.51 CGAAGGACAGTGAGT-----ATCGATA-TTAATGGAATTGAGTGACGAG-TAGGAAT-GG
 CBS336.48 CGAAGGACAGTGAGT-----ATCGATA-TTAATGGAATTGAGTGACGAG-TAGGAAT-GG
 CBS110644 CGAAGGACAGTGAGT-----ATCAATA-TTAATGGAATTGAGTGACGAG-TAGGAAT-GG
 NRRL705 CGATGGCCAGTAAGTCTCTTCGATACCACTTGATACCTCT-----C-GACACGGAA-TGG

	241	251	261	271	281	291	301	311
DAOM239918	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS2615	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239922	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS2630	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS2596	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS3189	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239927	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239919	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS2606	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239921	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS3190	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239917	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS3191	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS3183	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239928	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS3193	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239926	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS3186	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239929	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS3187	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239925	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS2601	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239924	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
KAS2612	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
DAOM239920	CGGTCTGATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA					
NRRL2074	CGGTCTGACATTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
NRRL32583	CGGTCTGATA-TTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
DAOM239930	CGGTCTGATA-TTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
DAOM239931	CGGTCTGATA-TTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
DAOM239932	CGGTCTGATA-TTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
DAOM239912	CGGTCTGATA-----TTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
DAOM239913	CGGTCTGATA-----TTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
CBS229.60	CGGTCTGATA-----TTTTTC-TAGCTTTAC-	TGGCCAGTCTGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
CBS23865	CGGTCTGATA-----TTTTTC-TAGCTTTAC-	TGGCCAGTCTGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCA						
KAS3463	CGGTCTGATG-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
CBS238.68	CGGTCTGATG-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
KAS3464	CGGTCTGATG-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
KAS3466	CGGTCTGATG-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
KAS3465	CGGTCTGATG-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAATGTCTACTTCAACCA						
NRRL3391	CGGTCTGATA-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
AL1878	CGGTCTGATA-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
AL1644	CGGTCTGATA-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
AL1642	CGGTCTGATA-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
AL1643	CGGTCTGATA-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						
CBS136.22	CGGTCTGATA-----TTTTTC-TAGCTTCAC-	CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA						

CBS347.51 CGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA
 CBS336.48 CGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA
 CBS110644 CGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCTCCGACCTCCAGCTGGAGCGTATGAACGTCTACTTCAACCA
 NRRL705 CGGTCTGATA-----TTTTTGGTTAGCTACAA-TGGTACCTCCGACCTTCAGCTCGAGCGCCTGAACGTCTACTTCAACCA

	321	331	341	351	361	371	381	391	
[									]
[									]
DAOM239918	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
KAS2615	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
DAOM239922	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
KAS2630	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
KAS2596	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
KAS3189	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
DAOM239927	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
DAOM239919	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
KAS2606	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
DAOM239921	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
KAS3190	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
DAOM239917	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
KAS3191	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
KAS3183	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
DAOM239928	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
KAS3193	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
DAOM239926	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
KAS3186	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
DAOM239929	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
KAS3187	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
DAOM239925	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
KAS2601	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
DAOM239924	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
KAS2612	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGG-TTT		
DAOM239920	CGTAAG-----			TGTGG-AATCAACACTCCAA-ACTCGTCA----			ACCACATCTAATACAATGGT-TTT		
NRRL2074	CGTAAG-----			TGTGG-AATCGATACTCGAT-ACCTGCCA----			ACCCCGTCTAATATAATGGA-TTT		
NRRL32583	CGTAAG-----			TGTGG-AATCGATACTCCAT-ACCTGCCA----			ACCCCGTCTAATATAATGGA-TTT		
DAOM239930	CGTAAG-----			TGTGG-AATCGATACTCCAT-ACCTGCCA----			ACCCCGTCTAATATAATGGA-TTT		
DAOM239931	CGTAAG-----			TGTGG-AATCGATACTCGAT-ACCTGCCA----			ACCACGTCTAATATAATGGA-TTT		
DAOM239932	CGTAAG-----			TGTGG-AATCGATACTCGAT-ACCTGCCA----			ACCACGTCTAATATAATGGA-TTT		
DAOM239912	CGTAAG-----			TGTGGAAACCGACACTCGAT-ACCTTTCA----			AACACGTCTAATATGATGCA-TCCT		
DAOM239913	CGTAAG-----			TGTGGAAACCGACACTCGAT-ACCTTTCA----			AACACGTCTAATATGATGCA-TCCT		
CBS229.60	CGTAAG-----			TGTGG-AATCGATACCCGTA-ACGTTTAA----			ACCTCGTCTAATACAATTGA-TTT		
CBS23865	CGTAAG-----			TGTGG-AATCGATACCCGTA-ACGTTTAA----			ACCTCGTCTAATACAATTGA-TTT		
KAS3463	CGTAAG-----			TATGA-CATTGATATATTGA-ATAATTTCG----			ACCCTGTCTAATATTTTGGATT-T		
CBS238.68	CGTAAG-----			TATGA-CATTGATATATTGA-ATAATTTCG----			ACCCTGTCTAATATTTTGGATT-T		
KAS3464	CGTAAG-----			TATGA-CATTGATATATTGA-ATAATTTCG----			ACCCTGTCTAATATTTTGGATT-T		
KAS3466	CGTAAG-----			TATGA-CATTGATATATTGA-ATAATTTCG----			ACCCTGTCTAATATTTTGGATT-T		
KAS3465	CGTAAG-----			TATGA-CATTGATATATTGA-ATAATTTCG----			ACCCTGTCTAATATTTCTGGATT-C		
NRRL3391	CGTAAG-----			TGTGG-CATTGATATCCCGA-GTCACTCG----			AACACGGCTAATATGTCGGGTTTT		
AL1878	CGTAAG-----			TGTGG-CATTGATATCCCGA-GTCACTCG----			AACACGGCTAATATGTCGGGTTTT		
AL1644	CGTAAG-----			TGTGG-CATTGATATCCCGA-GTCACTCG----			AACACGGCTAATATGTCGGGTTTT		
AL1642	CGTAAG-----			TGTGG-CATTGATATCCCGA-GTCACTCG----			AACACGGCTAATATGTCGGGTTTT		
AL1643	CGTAAG-----			TGTGG-CATTGATATCCCGA-GTCACTCG----			AACACGGCTAATATGTCGGGTTTT		
CBS136.22	CGTAAG-----			TGTGG-AATCAATCTCACAATACATTTCG----			ACTCCGCCTAATATGATGGAAA--		
CBS347.51	CGTAAG-----			TGTGG-AATCAATCTCACAATACATTTCG----			ACTCCGCCTAATATGATGGAAA--		
CBS336.48	CGTAAG-----			TGTGG-AATCCATCTCACAATACATTTCG----			AATTCACCTAATAGGATTGAAA--		
CBS110644	CGTAAG-----			TGTGG-AATCATTACTCACAATACATTTCG----			ACTCCGCCTAATATGCTTGAAA-T		
NRRL705	CGTAAGTTGCGTGTCCATCCAACGAA-----			GAACACCCAGAATTA-----			AGCTAACCCATGGATGTTTTGTT		

	401	411	421	431	441	451	461	471	
[									]
[									]
DAOM239918	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
KAS2615	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
DAOM239922	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
KAS2630	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
KAS2596	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
KAS3189	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
DAOM239927	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
DAOM239919	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
KAS2606	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
DAOM239921	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
KAS3190	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							
DAOM239917	TCA-----	TAGGCCTCTGGTGACCGTTACGTTCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGT							

DAOM239913 CCGTGCT-GGTCCCTTCGGCAAGCTTTTCCGTCCCGAC-AACTTCGTCTTCGGTCAGTCTGG-TGCTGGTAACAACCTGGG
 CBS229.60 CCGTGCC-GGTCCCTTTGGAAAGCTTTTCCGTCCCGAC-AACTTTGTTTTTCGGTCAGTCCGG-TGCCGGTAACAACCTGGG
 CBS23865 CCGTGCC-GGTCCCTTTGGAAAGCTTTTCCGTCCCGAC-AACTTTGTTTTTCGGTCAGTCCGG-TGCCGGTAACAACCTGGG
 KAS3463 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTTGTTTTTCGGTCAGTCTGG-TGCTGGTAACAACCTGGG
 CBS238.68 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTTGTTTTTCGGTCAGTCTGG-TGCTGGTAACAACCTGGG
 KAS3464 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTTGTTTTTCGGTCAGTCTGG-TGCTGGTAACAACCTGGG
 KAS3466 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTTGTTTTTCGGTCAGTCTGG-TGCTGGTAACAACCTGGG
 KAS3465 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTTGTTTTTCGGTCAGTCTGG-TGCTGGTAACAACCTGGG
 NRRL3391 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 AL1878 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 AL1644 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 AL1642 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 AL1643 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 CBS136.22 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 CBS347.51 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 CBS336.48 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 CBS110644 CCGTGCC-GGTCCCTTCGGCAAGCTCTTCCGTCCCGAC-AACTTCGTTTTTCGGTCAGTCCGG-TGCTGGTAACAACCTGGG
 NRRL705 CCGTGCC-GGTCCCTTTGGCAAGCTCTTCCGTCCCGAC-AACTTCGTCTTCGGCCAGTCCGG-TGCCGGTAACAACCTGGG

[561 571]
 [| |]

DAOM239918 CCAAGGGTCACTACAC
 KAS2615 CCAAGGGTCACTACAC
 DAOM239922 CCAAGGGTCACTACAC
 KAS2630 CCAAGGGTCACTACAC
 KAS2596 CCAAGGGTCACTACAC
 KAS3189 CCAAGGGTCACTACAC
 DAOM239927 CCAAGGGTCACTACAC
 DAOM239919 CCAAGGGTCACTACAC
 KAS2606 CCAAGGGTCACTACAC
 DAOM239921 CCAAGGGTCACTACAC
 KAS3190 CCAAGGGTCACTACAC
 DAOM239917 CCAAGGGTCACTACAC
 KAS3191 CCAAGGGTCACTACAC
 KAS3183 CCAAGGGTCACTACAC
 DAOM239928 CCAAGGGTCACTACAC
 KAS3193 CCAAGGGTCACTACAC
 DAOM239926 CCAAGGGTCACTACAC
 KAS3186 CCAAGGGTCACTACAC
 DAOM239929 CCAAGGGTCACTACAC
 KAS3187 CCAAGGGTCACTACAC
 DAOM239925 CCAAGGGTCACTACAC
 KAS2601 CCAAGGGTCACTACAC
 DAOM239924 CCAAGGGTCACTACAC
 KAS2612 CCAAGGGTCACTACAC
 DAOM239920 CCAAGGGTCACTACAC
 NRRL2074 CCAAGGGTCACTACAC
 NRRL32583 CCAAGGGTCACTACAC
 DAOM239930 CCAAGGGTCACTACAC
 DAOM239931 CCAAGGGTCACTACAC
 DAOM239932 CCAAGGGTCACTACAC
 DAOM239912 CCAAGGGTCACTACAC
 DAOM239913 CCAAGGGTCACTACAC
 CBS229.60 CCAAGGGTCACTACAC
 CBS23865 CCAAGGGTCACTACAC
 KAS3463 CCAAGGGTCACTACAC
 CBS238.68 CCAAGGGTCACTACAC
 KAS3464 CCAAGGGTCACTACAC
 KAS3466 CCAAGGGTCACTACAC
 KAS3465 CCAAGGGTCACTACAC
 NRRL3391 CCAAGGGTCACTACAC
 AL1878 CCAAGGGTCACTACAC
 AL1644 CCAAGGGTCACTACAC
 AL1642 CCAAGGGTCACTACAC
 AL1643 CCAAGGGTCACTACAC
 CBS136.22 CCAAGGGTCACTACAC
 CBS347.51 CCAAGGGTCACTACAC
 CBS336.48 CCAAGGGTCACTACAC
 CBS110644 CCAAGGGTCACTACAC
 NRRL705 CCAAGGGTCACTACAC

Multiple ITS Sequence Alignment

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239918 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3190    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239928 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS2612    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS2596    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3187    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239925 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239920 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3191    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239917 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3183    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS2606    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3193    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239929 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3186    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239921 -----TCTGGGTCCACCTCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS2601    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239919 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS2615    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239927 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239922 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239924 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3189    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239926 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS2630    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239913 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239912 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
NRRL32583 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
NRRL2074  CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239930 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239931 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
DAOM239932 CATTACTG--AGTGAGGGCCCTCTGG-T-C--ACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
CBS23865  CATTACTG--AGTGAGGGCCCTCGGGTCCAACCTCCCACCCGTGTTTATTGCGTACCTTGGTTGCTTCGGCAGGCCCGCC-
CBS229.60 -----CTCCGG-T-C--ACCTCCCACCCGTGTTTATTGCGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3463   CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTATTGCGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS3466   CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTATTGCGTACCTTGGTTGCTTCGGCAGGCCCGCC-
CBS238.68 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTATTGCGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS34641  CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTATTGCGTACCTTGGTTGCTTCGGCAGGCCCGCC-
KAS34653  CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTATTGCGTACCTTGGTTGCTTCGGCAGGCCCGCC-
CBS136.22 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
CBS347.51 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
CBS110644 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
CBS336.48 CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGGCCCGCC-
NRRL3391  CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTC-TTGTACCATGTTGCTTCGGCAGGCCCGCC-
AL1878    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTC-TTGTACCATGTTGCTTCGGCAGGCCCGCC-
AL1642    CATTACTG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTC-TTGTACCATGTTGCTTCGGCAGGCCCGCC-
AL1644    CATTACTG--AGTGAGGGCC-TCTGG-T-CAACCTCCCACCCGTGTC-TTGTACCATGTTGCTTCGGCAGGCCCGCC-
AL1643    -----ACCTCCCACCCGTGTC-TTGTACCATGTTGCTTCGGCAGGCCCGCC-
NRRL705   CATTACCG--AGTGAGGGCCCTCTGGGTCCAACCTCCCACCCGTGTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCCG

[      81      91      101      111      121      131      141      151      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239918 TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
KAS3190    TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
DAOM239928 TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
KAS2612    TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
KAS2596    TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
KAS3187    TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
DAOM239925 TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
DAOM239920 TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
KAS3191    TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
DAOM239917 TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
KAS3183    TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
KAS2606    TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
KAS3193    TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT
DAOM239929 TCACGGCCGCC-GGGGGGCTTC-TGCCCCGGGGCCCGCGCTGCCGGAGACAATCTTGAACGCTGTCTGAAGAATGCAGT

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[illegible]


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KAS34653 C-GCCT--GCCGACCC-TCATCATCC--TTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTAAGCA
CBS136.22 C-GCCTTAGCCGACG---ACACAATCTTTTTTTTCAGGTTGACCTCGGATCAGGTAGG-----
CBS347.51 C-GCCTTAGCCGACG---ACACAATC-TTTTTTTTCAGGTTGACCTCGGATCAGGTAGG-----
CBS110644 C-GCCTTAGCCGACG---ACACAATC-TTTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTAAGCA
CBS336.48 C-GCCTTAGCCGACG---ACACAATC-TTTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTAAGCA
NRRL3391 C-GCTG--GCCGACCCCTCCAACCCCA---TTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTAAGCA
AL1878 C-GCTG--GCCGACCCCTCCAACCCCA---TTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTAAGCA
AL1642 C-GCTG--GCCGACCCCTCCAACCCCA---TTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTAAGCA
AL1644 C-GCTG--GCCGACCCCTCCAACCCCA---TTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTA---
AL1643 C-GCTG--GCCGACCCCTCCAACCCCA---TTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTAAGCA
NRRL705 C-GCCC--GCCGGCG---ACCCCATCAATCTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTAAGCA

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[ 561 ]
[ | ]

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DAOM239918 TATCAA
KAS3190 TATCAA
DAOM239928 TATCAA
KAS2612 TATCAA
KAS2596 TATCAA
KAS3187 TATCAA
DAOM239925 TATCAA
DAOM239920 TATCAA
KAS3191 TATCAA
DAOM239917 TATCAA
KAS3183 TATCAA
KAS2606 TATCAA
KAS3193 TATCAA
DAOM239929 TATCAA
KAS3186 TATCAA
DAOM239921 -----
KAS2601 TATCAA
DAOM239919 TATCAA
KAS2615 TATCAA
DAOM239927 -----
DAOM239922 TATCAA
DAOM239924 TATCAA
KAS3189 TATCAA
DAOM239926 TATCAA
KAS2630 TATCAA
DAOM239913 TATCAA
DAOM239912 TATCAA
NRRL32583 TATCAA
NRRL2074 TATCAA
DAOM239930 TATCAA
DAOM239931 TATCAA
DAOM239932 TATCAA
CBS23865 TATCAA
CBS229.60 TATCAA
KAS3463 TATCAA
KAS3466 TATCAA
CBS238.68 TATCAA
KAS34641 TATCAA
KAS34653 TATCAA
CBS136.22 -----
CBS347.51 -----
CBS110644 TATCAA
CBS336.48 TATCAA
NRRL3391 TATCAA
AL1878 TATCAA
AL1642 TATCAA
AL1644 -----
AL1643 TATCAA
NRRL705 TATCAA

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Multiple *CoxI* Sequence Alignment

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239918 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3190      GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239919 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239928 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239926 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS2630      GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239924 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239925 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS2606      GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS2601      --GATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3183      GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3193      GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239920 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS2596      GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTACACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3189      --GATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239927 --GATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS2612      -TGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3191      --GATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239922 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS2615      GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239917 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3186      GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3187      -TGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239921 -TGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239929 -TGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
NRRL2074     GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
NRRL32583    GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239931 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239930 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239932 GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239912 --GATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239913 --GATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS229.60     GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS238.68     GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS347.51     GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-CTTTTATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS136.22     GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-CTTTTATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS336.48     GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-CTTTTATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS110644     GTGATTTTATC-TTCAATGCT-AAAGATA-TAGGTAC-CTTTTATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
NRRL3391     GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGAAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
AL1643        GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGAAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
AL1644        GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGAAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
AL1878        GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGAAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
AL1642        GTGATTTTATC-TTCTAATGCAAAAGATATTGGAAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3463       GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3466       GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3464       GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3465       GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS238.68     ----TTTT-T--TT-TTATGCA-AAAGAAA-TTGGTAC-ATTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGA
NRRL705       GTGATTTTATC-TTCTAATGCT-AAAGATA-TTGGTAC-CTTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGA

[      81      91      101      111      121      131      141      151      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239918 ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
KAS3190      ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
DAOM239919 ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
DAOM239928 ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
DAOM239926 ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
KAS2630      ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
DAOM239924 ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
DAOM239925 ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
KAS2606      ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
KAS2601      ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
KAS3183      ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
KAS3193      ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT
DAOM239920 ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCCAGGAGTACAATATATATCAGATAATCAATTATATAAT

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CBS229.60 AGTATAATTACAGCC--CACGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATAGGAGGTTTTGGTAATTT
CBS238.68 AGTATAATTACAGCC--CACGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATAGGAGGTTTTGGTAATTT
CBS347.51 AGTATAATAACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAATTGGAGGTTTTGGTAATTT
CBS136.22 AGTATAATAACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAATTGGAGGTTTTGGTAATTT
CBS336.48 AGTATAATAACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAATTGGAGGTTTTGGTAATTT
CBS110644 AGTATAATAACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAATTGGAGGTTTTGGTAATTT
NRRL3391 AGTATAATTACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATGGTGGTTTTGGTAATTT
AL1643 AGTATAATTACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATGGTGGTTTTGGTAATTT
AL1644 AGTATAATTACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATGGTGGTTTTGGTAATTT
AL1878 AGTATAATTACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATGGTGGTTTTGGTAATTT
AL1642 AGTATAATTACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATGCCAGCATTAATGGTGGTTTTGGTAATTT
KAS3463 AGTATAGTAACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATAGGAGGTTTTGGTAATTT
KAS3466 AGTATAGTAACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATAGGAGGTTTTGGTAATTT
KAS3464 AGTATAGTAACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATAGGAGGTTTTGGTAATTT
KAS3465 AGTATAGTAACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATAGGAGGTTTTGGTAATTT
CBS238.68 AGTATAGTAACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAATAGGAGGTTTTGGTAATTT
NRRL705 AGTATAATAACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAATAGGTGGTTTTGGTAATTT

[illegible]

CBS110644 TA-GGTGCTATTAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGAATACGTTTACATAAAATTAGCGTTAT
 NRRL3391 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 AL1643 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 AL1644 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 AL1878 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 AL1642 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 KAS3463 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 KAS3466 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 KAS3464 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 KAS3465 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 CBS238.68 TA-GGAGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT
 NRRL705 TA-GGTGCTATGAATTTT-ATAACAACATATTTTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAAATTAGCGTTAT

	561	571	581	591	601
[					
[					
DAOM239918	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATT-----				
KAS3190	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATT-----				
DAOM239919	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239928	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239926	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS2630	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239924	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATT---				
DAOM239925	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATT---				
KAS2606	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTAT----				
KAS2601	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS3183	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS3193	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239920	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS2596	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT-				
KAS3189	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATT-----				
DAOM239927	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTAT----				
KAS2612	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS3191	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239922	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS2615	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239917	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS3186	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS3187	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239921	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATT---				
DAOM239929	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTAT-				
NRRL2074	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
NRRL32583	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239931	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239930	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239932	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
DAOM239912	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATATT-				
DAOM239913	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
CBS229.60	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
CBS238.68	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTA--TATTATTATT				
CBS347.51	TTG-G-ATGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT				
CBS136.22	TTG-G-ATGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT				
CBS336.48	TTG-G-ATGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT				
CBS110644	TTG-G-ATGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT				
NRRL3391	TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT				
AL1643	TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT				
AL1644	TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT				
AL1878	TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT				
AL1642	TTG-T-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT				
KAS3463	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTAT-				
KAS3466	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS3464	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
KAS3465	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
CBS238.68	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT				
NRRL705	TTG-G-ATGA-GCTGT-AGTTA-TTACAGCTG--TATTATTATT				

Multiple *TEF1-α* Sequence Alignment

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239924 TCG--CACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC
DAOM239918 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS2596   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS2606   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS3193   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
DAOM239920 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS3183   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
DAOM239917 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
DAOM239928 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
DAOM239921 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTA-----ACTCCATCGCTCC
DAOM239925 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS3190   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
DAOM239919 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC
DAOM239926 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC
KAS2612   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC
DAOM239922 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC
DAOM239927 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
DAOM239929 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS3191   TCGG--CACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS3186   T--GCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS2630   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC
KAS3189   TC--GCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACT--CAACGCTCC
KAS2601   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS3187   T--GGCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
KAS2615   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCA--CGCTCC
NRRL32583 TCG--CCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAATCCCCTCGCTCC
DAOM239930 TCGG--CACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAATCCCCTCGCTCC
NRRL2074   TCG--CCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAATCCCCTCGCTCC
DAOM239931 TCGG--CACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATCCCCTCGCTCC
DAOM239932 -----CGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATCCCCTCGCTCC
DAOM239912 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACCCAATTCCATCGATCC
DAOM239913 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACCAATCCATCGATCC
CBS229.60 TAGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCCCGC-----CAATCCCCTCGATCC
CBS238.68 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC
CBS238.68 TCGGCCACGTCGATTCCCGGCAAGTCCACCACCACCTGGT-----ACATCCCTCT
KAS3463   ACGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTTCAACCTCCTCCC-----CCCCCCA---CCTTTC
KAS3464   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTTCAACCTCCTCCC-----CCCCCCA---CCTTTC
KAS3466   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTTCAACCTCCTCCC-----CCCCCCA---CCTTTC
KAS3465   TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTTCAATCCCCCAA-----CCTTTC
---CCACGTCGATT-CCGGCAAGTCCACCACCACCTGGTAAAGTTTCAACC--TTAACACCTTCCCGATTAGGTAGCCAT
CBS136.22 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCTGGT-AAGTTTCAACC--TTCACACCTTCTCGATTAGGTAGCCAT
CBS336.48 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCTGGT-AAGTTATTCAATCTTCACACCTTCCCGATTAGGTAGCCAT
CBS110644 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCTGGT-AAGTTATTAAATCTTCACACCTTCCCGTTAGGTAGTCAT
NRRL3391  TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCT
AL1642    TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCT
AL1878    TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCT
AL1644    -C--GCCACGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCT
AL1643    -----CAGTCGATT-CCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCT
NRRL705   TCGGCCCTCGTCGATT-CCGGCAAGTCCACCACCACCTGGT-AAGCACCCCTCCTCCATCCGTCCTCGCCTCGCCCATCG
[      81     91     101     111     121     131     141     151     ]
[      |      |      |      |      |      |      |      |      ]
DAOM239924 -TTCCTCACTTCCATCGAACAACAT-----GACAGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
DAOM239918 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
KAS2596   -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
KAS2606   -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
KAS3193   -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
DAOM239920 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
KAS3183   -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
DAOM239917 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
DAOM239928 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
DAOM239921 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
DAOM239925 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
KAS3190   -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA
DAOM239919 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGA

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DAOM239926 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS2612 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 DAOM239922 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 DAOM239927 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 DAOM239929 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS3191 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS3186 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS2630 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS3189 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS2601 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS3187 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS2615 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 NRRL32583 -TGCCTCACATCCATCGAACAACAT-----GACTGATTTCATCATAATAGGACACTTGATCTACAAGTGCGGTGGTATCGA
 DAOM239930 -TGCCTCACATCCATCGAACAACAT-----GACTGATTTCATCATAATAGGACACTTGATCTACAAGTGCGGTGGTATCGA
 NRRL2074 -TGCCTCACATCCATCGAACAACAT-----GACTGATTTCATCATAATAGGACACTTGATCTACAAGTGCGGTGGTATCGA
 DAOM239931 -TGCCTCACATCCATCGAACAACAT-----GACTGATTTCATCATAATAGGACACTTGATCTACAAGTGCGGTGGTATCGA
 DAOM239932 -TGCCTCACATCCATCGAACAACAT-----GACTGATTTCATCATAATAGGACACTTGATCTACAAGTGCGGTGGTATCGA
 DAOM239912 -TTCCT-ATTTCCATCGAACAACAT-----GACTGATTTCATCAACACAGGACACTTGATCTACAAGTGCGGTGGTATCGA
 DAOM239913 -TTCCT-ATTTCCATCGAACAACAT-----GACTGATTTCATCAACACAGGACACTTGATCTACAAGTGCGGTGGTATCGA
 CBS229.60 ---TCTCTCTCATACCGAACAACAT-----AACTGATTTCATGAATATAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 CBS238.68 -TTCCTCACTTCCATCGAACAACAT-----GACTGATTTCATCAATGCAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 CBS238.68 -----CACATGATCTACAAGTGCGGTGGTATCGA
 KAS3463 CATT-----CCATCGAACAACAG-----AACTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS3464 CATT-----CCATCGAACAACAG-----AACTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS3466 CATT-----CCATCGAACAACAG-----AACTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 KAS3465 CATC-----CCATCGAACAAC-----AACTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 CBS347.51 GGT-----AACTAACAAAGCATAACAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 CBS136.22 GGT-----AACTAAC-AAGCATAACAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 CBS336.48 GGT-----AACTAAC-CAGCATAACAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 CBS110644 GGT-----AACTAAC-AAGCATAATAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 NRRL3391 ACCTTCCCATTTCCATCGAATAATAT-----AGCTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 AL1642 ACCTTCCCATTTCCATCGAATAATAT-----AGCTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 AL1878 ACCTTCCCATTTCCATCGAATAATAT-----AGCTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 AL1644 ACCTTCCCATTTCCATCGAATAATAT-----AGCTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 AL1643 ACCTTCCCATTTCCATCGAATAATAT-----AGCTGATTTCATCAATTTAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA
 NRRL705 AGGTTTCATCCTTCATCCGCAATGACAAAATACTGATTCTCCCGA-CAGGTCACCTTGATCTACAAGTGCGGTGGTATCGA

	161	171	181	191	201	211	221	231	
[									]
[									]
DAOM239924	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239918	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS2596	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS2606	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS3193	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239920	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS3183	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239917	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239928	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239921	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239925	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS3190	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239919	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239926	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS2612	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239922	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239927	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239929	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS3191	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS3186	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS2630	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS3189	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS2601	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS3187	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
KAS2615	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
NRRL32583	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239930	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
NRRL2074	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239931	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239932	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239912	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							
DAOM239913	CTCTCGTACCATCGAGAAGTTTCGAGA	-----							

CBS229.60 CTCTCGTACCATCGAGAAGTTCGAGA-----
 CBS238.68 CTCTCGTACCATCGAGAAGTTCGAGA-----
 CBS238.68 CCAGCGTACCATCGAGAAGTTCGAGA-----
 KAS3463 CTCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3464 CTCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3466 CTCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3465 CTCTCGTACCATCGAGAAGTTCGAGA-----
 CBS347.51 CTCTCGTACCATCGAGAAGTTCGAGA-----
 CBS136.22 CTCTCGTACCATCGAGAAGTTCGAGA-----
 CBS336.48 CTCTCGTACCATCGAGAAGTTCGAGA-----
 CBS110644 CTCTCGTACCATCGAGAAGTTCGAGA-----
 NRRL3391 CTCTCGTACCATCGAGAAGTTCGAGA-----
 AL1642 CTCTCGTACCATCGAGAAGTTCGAGA-----
 AL1878 CTCTCGTACCATCGAGAAGTTCGAGA-----
 AL1644 CTCTCGTACCATCGAGAAGTTCGAGA-----
 AL1643 CTCTCGTACCATCGAGAAGTTCGAGA-----
 NRRL705 CTCTCGTACCATCGAGAAGTTCGAGAAGGTACGGAATCACAATTTTCACTGCCCCCTCCTTGAGTGGGGTGGGGTCGTT

	241	251	261	271	281	291	301	311	
[									]
[									]
DAOM239924	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239918	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS2596	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS2606	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS3193	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239920	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS3183	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239917	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239928	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239921	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCG-C				
DAOM239925	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCG-C				
KAS3190	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCG-C				
DAOM239919	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239926	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS2612	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239922	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239927	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
DAOM239929	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS3191	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS3186	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS2630	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS3189	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS2601	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS3187	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
KAS2615	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
NRRL32583	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGAAAGGGTTCCTTCAAGGTACGGTCGCA--				
DAOM239930	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGAAAGGGTTCCTTCAAGGTACGGTCGCA--				
NRRL2074	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGAAAGGGTTCCTTCAAGGTACGGTCGCA--				
DAOM239931	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGAAAGGGTTCCTTCAAGGTACGGTCGCA--				
DAOM239932	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGAAAGGGTTCCTTCAAGGTACGGTCGCA--				
DAOM239912	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCACC				
DAOM239913	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCACC				
CBS229.60	-----	-----	-----	-----	AGGAGGCCGCTGAGCTCGGTAAGGGTTCCTTCAAGGTATGAGCCCA-T				
CBS238.68	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-C				
CBS238.68	-----	-----	-----	-----	AGGAGGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----				
KAS3463	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
KAS3464	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
KAS3466	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
KAS3465	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
CBS347.51	-----	-----	-----	-----	AGGAGGCCGCCGAGCTCGGTAAGGGTTCCTTCA-----				
CBS136.22	-----	-----	-----	-----	AGGAGGCCGCCGAGCTCGGTAAGGGTTCCTTCA-----				
CBS336.48	-----	-----	-----	-----	AGGAGGCCGCCGAGCTCGGTAAGGGTTCCTTCA-----				
CBS110644	-----	-----	-----	-----	AGGAGGCCGCCGAGCTCGGTAAGGGTTCCTTCA-----				
NRRL3391	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
AL1642	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
AL1878	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
AL1644	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
AL1643	-----	-----	-----	-----	AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----				
NRRL705	-----	-----	-----	-----	TCTCGCCTTGGAACATTGTGCTAACCCCTCACAGGAAGCCGCTGAGCTCGGCAAGGGTTCCTTCA-----				

[321 331 341 351 361 371 381 391]

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[ | | | | | | | ]
DAOM239924 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
DAOM239918 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
KAS2596 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
KAS2606 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
KAS3193 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
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KAS3183 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
DAOM239917 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
DAOM239928 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
DAOM239921 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
DAOM239925 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
KAS3190 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
DAOM239919 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
DAOM239926 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
KAS2612 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
DAOM239922 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
DAOM239927 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
DAOM239929 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
KAS3191 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
KAS3186 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
KAS2630 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
KAS3189 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
KAS2601 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
KAS3187 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTG
KAS2615 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTG
NRRL32583 CCACAACACTCCAAGTG--AAAAAATTTTCAAAGTGGATCAGCGAACTAACATCC--ACAATAGTACGCTTGGGTTCTTG
DAOM239930 CCACAACACTCCAAGTG--AAAAAATTTTCAAAGTGGATCAGCGAACTAACATCC--ACAATAGTACGCTTGGGTTCTTG
NRRL2074 CCACAACACTCCAAGTG--AAAAAATTTTCAAAGTGGATCAGCGAACTAACATCC--ACAATAGTACGCTTGGGTTCTTG
DAOM239931 CCACAACACCCCAAGTGAAAAAATTTTCAAAGTGGATCAGTCAACTAACATCT--ACAATAGTACGCTTGGGTTCTTG
DAOM239932 CCACAACACCCCAAGTGAAAAAATTTTCAAAGTGGATCAGTCAACTAACATCT--ACAATAGTACGCTTGGGTTCTTG
DAOM239912 ATTACAAATTTTCAC-----AAGTCTCTTAAAGTGGATC----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTG
DAOM239913 ATTACAAATTTTCAC-----AAGTCTCTTAAAGTGGATC----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTG
CBS229.60 GAACTATATCCTACACTCAATATGAAGCAACTAACATT-----CGCATTAGTACGCTTGGGTTCTTG
CBS238.68 CCCACAACCCATGTG-----AAAATTCTGAAGTGGGTC----AACTAACATCTGTCTGTATAGTACGCTTGGGTTCTTG
CBS238.68 -----AGTACGCTTGGGTTCTTG
KAS3463 -----AGTACGCTTGGGTTCTTG
KAS3464 -----AGTACGCTTGGGTTCTTG
KAS3466 -----AGTACGCTTGGGTTCTTG
KAS3465 -----AGTACGCTTGGGTTCTTG
CBS347.51 -----AGTACGCTTGGGTTCTTG
CBS136.22 -----AGTACGCTTGGGTTCTTG
CBS336.48 -----AGTACGCTTGGGTTCTTG
CBS110644 -----AGTACGCTTGGGTTCTTG
NRRL3391 -----AGTACGCTTGGGTTCTTG
AL1642 -----AGTACGCTTGGGTTCTTG
AL1878 -----AGTACGCTTGGGTTCTTG
AL1644 -----AGTACGCTTGGGTTCTTG
AL1643 -----AGTACGCTTGGGTTCTTG
NRRL705 -----AGTACGCTTGGGTTCTTG

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[ 401 411 421 431 441 451 461 471 ]
[ | | | | | | | ]
DAOM239924 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239918 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
KAS2596 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
KAS2606 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
KAS3193 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239920 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
KAS3183 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239917 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239928 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239921 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239925 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
KAS3190 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239919 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239926 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
KAS2612 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239922 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239927 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC
DAOM239929 ACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTC

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	481	491	501	511	521	531	541	551
DAOM239924	ACCGTCATT							
DAOM239918	ACCGTCATT							
KAS2596	ACCGTCATT							
KAS2606	ACCGTCATT							
KAS3193	ACCGTCATT							
DAOM239920	ACCGTCATT							
KAS3183	ACCGTCATT							
DAOM239917	ACCGTCATT							
DAOM239928	ACCGTCATT							
DAOM239921	ACCGTCATT							
DAOM239925	ACCGTCATT							
KAS3190	ACCGTCATT							
DAOM239919	ACCGTCATT							
DAOM239926	ACCGTCATT							
KAS2612	ACCGTCATT							
DAOM239922	ACCGTCATT							
DAOM239927	ACCGTCATT							
DAOM239929	ACCGTCATT							
KAS3191	ACCGTCATT							
KAS3186	ACCGTCATT							
KAS2630	ACCGTCATT							
KAS3189	ACCGTCATT							
KAS2601	ACCGTCATT							
KAS3187	ACCGTCATT							
KAS2615	ACCGTCATT							
NRRL32583	ACCGTCATT							
DAOM239930	ACCGTCATT							
NRRL2074	ACCGTCATT							
DAOM239931	ACCGTCATT							
DAOM239932	ACCGTCATT							
DAOM239912	ACCGTCATT							
DAOM239913	ACCGTCATT							
CBS229.60	ACCGTCATT							
CBS238.68	ACCGTCATT							
CBS238.68	ACCGTCATCGGTAAGAGAC-TTTC	CCGTTCAACATATCGGTCATAC-					ACACGCTAATATCTTCCATT	
KAS3463	ACCGTCATTGGTAAGCTTTATCCCTGAGCCCTCTTTATTCTCTTTTCAGCC						ATTAASCCCTTTTATC	
KAS3464	ACCGTCATTGGTAAGCTTTATCCCTGAGCCCTCTTTATTCTCTTTTCAGCC						ATTAACCCCTTTTATC	

KAS3466 ACCGTCATTGGTAAGCTTTATCCCTGAGCCCTCTTTATTCTCTTTCAGCC-----ATTAACCCCTTTTATC
 KAS3465 ACCGTCATTGGTAAGCTTTATCCCTGAGCCCTCTTTATTCTCTTTCAGCC-----ATTAACCCCTTTTATT
 CBS347.51 ACCGTCATC-----
 CBS136.22 ACCGTCATC-----
 CBS336.48 ACCGTCATC-----
 CBS110644 ACCGTCATC-----
 NRRL3391 ACCGTCATC-----
 AL1642 ACCGTCATC-----
 AL1878 ACCGTCATC-----
 AL1644 ACCGTCATC-----
 AL1643 ACCGTCATC-----
 NRRL705 ACCGTCATTGGTAAGAATTATCCC-ACCCACCATCTTCTCCATCCATCATGGACTCTCTGACTGACTCTTC---CTCCT

[	561	571	581	591	601	611	621	631	]
[									]

DAOM239924 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239918 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS2596 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS2606 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3193 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239920 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3183 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239917 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239928 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239921 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239925 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3190 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239919 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239926 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS2612 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239922 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239927 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239929 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3191 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3186 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS2630 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3189 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
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 KAS3187 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS2615 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 NRRL32583 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239930 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 NRRL2074 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239931 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239932 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239912 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 DAOM239913 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 CBS229.60 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 CBS238.68 ---GATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 CBS238.68 ACAGATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3463 TCAGACGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3464 TCAGACGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3466 TCAGACGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 KAS3465 TCAGATGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 CBS347.51 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 CBS136.22 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 CBS336.48 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 CBS110644 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 NRRL3391 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 AL1642 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 AL1878 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 AL1644 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 AL1643 ---GATGCCCCCGGTACCGTGATTTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT
 NRRL705 CTAGACGCCCCCGGTACCGTGACTTCATCAAGAACATGATCACTGGTACCTCCCAGGCCGATTGCGCTATTCTCATCAT

[	641	651	661	671	681	691	701	711	]
[									]

DAOM239924 CGCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCCCTTCTGGCTTTACCC
 DAOM239918 CGCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCCCTTCTGGCTTTACCC
 KAS2596 CGCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCCCTTCTGGCTTTACCC
 KAS2606 CGCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCCCTTCTGGCTTTACCC

	721	731	741	751	761	771	781	791
DAOM239924	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239918	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS2596	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS2606	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS3193	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239920	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS3183	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239917	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239928	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239921	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239925	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS3190	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239919	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239926	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS2612	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239922	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239927	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
DAOM239929	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS3191	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS3186	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS2630	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS3189	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						
KAS2601	TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----						

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KAS3187 TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT-----
KAS2615 TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT-----
NRRL32583 TCGGTGTCCGTGAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTATAACCTGCCTGACTACATGA
DAOM239930 TCGGTGTCCGTGAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTATAACCTGCCTGACTACATGA
NRRL2074 TCGGTGTCCGTGAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTCGTAACCTGTCTGACTACATGA
DAOM239931 TCGGTGTCCGTGAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTGTAACCTGCCTGACTACATGA
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DAOM239912 TCGGTGTCCGTGAGCTGATCGTTGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTTCTAATCCATGGCTACTTGAC
DAOM239913 TCGGTGTCCGTGAGCTGATCGTTGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTTCTAATCCATGGCTACTTGAC
CBS229.60 TTGGTGTCCGCCAGCTGATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
CBS238.68 TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT-----
CBS238.68 TCGGTGTAAAGCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT-----
KAS3463 TTGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGCAAGT-----
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CBS336.48 TCGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT-----
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[      801      811      821      831      841      851      861      871      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239924 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239918 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS2596 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS2606 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3193 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239920 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3183 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239917 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239928 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239921 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239925 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3190 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239919 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239926 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS2612 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239922 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239927 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239929 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3191 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3186 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS2630 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3189 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS2601 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3187 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS2615 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
NRRL32583 CATCCCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239930 CATCCCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
NRRL2074 CATCCCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239931 CATCCCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239932 CATCCCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239912 C---TCAACCAACAAATACTAATTACCTAAACAGGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
DAOM239913 C---TCAACCAACAAATACTAATTACCTAAACAGGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
CBS229.60 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
CBS238.68 -----GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
CBS238.68 -----GGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3463 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3464 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3466 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
KAS3465 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
CBS347.51 -----GGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
CBS136.22 -----GGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC
CBS336.48 -----GGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAACCTTC

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CBS110644 -----GGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAAC TTC
NRRL3391 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAAC TTC
AL1642 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAAC TTC
AL1878 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAAC TTC
AL1644 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAAC TTC
AL1643 -----GGGCTGAGGAGCGTTACAACGAGATTGTCAAGGAGACCTCCAAC TTC
NRRL705 -----GGTCTGAGGACCGTTACAACGAGATCGTCAAGGAGACCTCCAAC TTC

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[      881      891      901      911      921      931      941      951      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239924 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAACGGGTGACAACATGCTTGAGG
DAOM239918 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS2596 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS2606 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS3193 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239920 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS3183 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239917 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239928 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239921 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239925 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS3190 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239919 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239926 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS2612 ATCAAGAAGGTCGGCTACTACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239922 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239927 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239929 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS3191 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS3186 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS2630 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGG-TTCAAC-GGTGACAACATGCTTGAGG
KAS3189 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGG-TTCAAC-GGTGACTTGTAGCTTGAGG
KAS2601 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
KAS3187 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTGTCAAC-GGTGACAACATGCTTGAGG
KAS2615 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
NRRL32583 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239930 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGG-TTCAAC-GGTGACAACATGCTTGAGG
NRRL2074 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239931 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGG-TTCAAC-GGTGACAACATGCTTGAGG
DAOM239932 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGG-TTCAAC-GGTGACAACATGC-TGAGT
DAOM239912 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
DAOM239913 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGG
CBS229.60 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGC
CBS238.68 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCTCCCATCTCCGG-TTCAAC-GGTGACAACATGCTTGAGG
CBS238.68 ATCAAGAAGGTCGGCTACAACCCCAAGTCCGTTCCCTTCGTCCTCCCATCTCCGGATTCAAC-GGCGACAACATGCTCGAGG
KAS3463 ATCAAGAAGGTCGGCTACAACCCCAAGGGGTGTCCTTCGTTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTTGAGC
KAS3464 ATCAAGAAGGTCGGCTACAACCCCAAGGGGTGTCCTTCGTTCCCATCTCCGG-TTCAAC-GGTGACAACATGCTTGAGC
KAS3466 ATCAAGAAGGTCGGCTACAACCCCAAGGGGT-TCCCTTCGTTCCCATCTCCGG-TTCAAC-GGTGACAACATGCTTGAGC
KAS3465 ATCAAGAAGGTCGGCTACAACCCCAAGGGGTGTCCTTCGTTCCCATCTCCGG-TTCAAC-GGTGACAACATGCTTGAGC
CBS347.51 ATCAAGAAGGTCGGCTACAACCCCAAGAACGTTCCCTTCGTTCCATCTCCGGTTTCAAC-GGTGACAACATGCTCGAGC
CBS136.22 ATCAAGAAGGTCGGCTACAACCCCAAGAACGTTCCCTTCGTTCCATCTCCGGTTTCAAC-GGTGACAACATGCTCGAGC
CBS336.48 ATCAAGAAGGTCGGCTACAACCCCAAGAACGTTCCCTTCGTTCCATCTCCGGTTTCAAC-GGTGACAACATGCTCGAGC
CBS110644 ATCAAGAAGGTCGGCTACAACCCCAAGAACGTTCCCTTCGTTCCATCTCCGGTTTCAAC-GGTGACAACATGCTCGAGC
NRRL3391 ATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTGGAGC
AL1642 ATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTGGAGC
AL1878 ATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTGGAGC
AL1644 ATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTGGAGC
AL1643 ATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTCCTCCCATCTCCGGTTTCAAC-GGTGACAACATGCTGGAGC
NRRL705 ATCAAGAAGGTTGGCTACAACCCCAAGACCGTCCCTTCGTCCTCCCATCTCCGGCTTCAAC-GGTGACAACATGCTCGAGC

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[      961      971      981      ]
[      |      |      |      ]
DAOM239924 CCTCCCC-AACTGCCCTGGTACAAGG
DAOM239918 CCTCCCC-AACTGCCCTGGTACAAGG
KAS2596 CCTCCCC-AACTGCCCTGGTACAAGG
KAS2606 CCTCCCC-AACTGCCCTGGTACAAGG
KAS3193 CCTCCCC-AACTGCCCTGGTACAAGG
DAOM239920 CCTCCCC-AACTGCCCTGGTACAAGG
KAS3183 CCTCCCC-AACTGCCCTGGTACAAGG
DAOM239917 CCTCCCC-AACTGCCCTGGTACAAGG
DAOM239928 CCTCCCC-AACTGCCCTGGTACAAGG

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DAOM239921 CCTCCCCC-AACTGCCCTGGTACAAGG
DAOM239925 CCTCCCCC-AACTGCCCTGGTACAAGG
KAS3190 CCTCCCCC-AACTGCCCTGGTACAAGG
DAOM239919 CCTCCCCC-AACTGCCCTGGTACAAGG
DAOM239926 CCTCCCCC-AACTGCCCTGGTACAAGG
KAS2612 CCTCCCCC-AACTGCCCTGGTACAAGG
DAOM239922 CCTCCCCC-AACTGCCCTGGTACAAGG
DAOM239927 CCTCCCCC-AACTGCCCTGGTACA-GG
DAOM239929 CCTCCCCC-AACTGCCCTGGTACAAGG
KAS3191 CCTCCCCC-AACTGCCCTGGTACAAGG
KAS3186 CCTCCCCC-AACTGCCCTGGTACAAGG
KAS2630 CAACCCC--AACTG-CCCTGGTACAAGG
KAS3189 CCTCCCCC-AACTGCCCTGGTACA-GG
KAS2601 CCTCCCCC-AACTGCCCTGGTACAAGG
KAS3187 CCTCCCCC-AACTGCCCTGGTACA-GG
KAS2615 CCTCCCCC-AACTGCCCTGGTACAAGG
NRRL32583 CCTCCCCC-AACTGCCCTGGTACA-G
DAOM239930 CCTCCCCC-AACTGCCCTGGTACA-GG
NRRL2074 CCCCCCCC-AACTGCCCC-----
DAOM239931 CCTCCCCC-AACTG-CCCTGGTACA-GG
DAOM239932 CCCCCC-----
DAOM239932 CCTCCCCC-AACTGCCCTGGTACAAGG
DAOM239913 CCTCCCCC-AACTGCCCTGGTACAAGG
CBS229.60 CCTCCACC-AACTGCCCTGGTACAAGG
CBS238.68 CCTCCCCCAACTGCCCTGGTACAAGG
CBS238.68 TTTCACC-AACTGCCCTGGTACAAGG
KAS3463 CCTCCCCC-AACTGCCCTGGTACAAG-
KAS3464 CCTCCCCC-AACTGCCCTGGTACA-GG
KAS3466 CCTCCCCC-AACTGCCCTGG-ACAAG-
KAS3465 CCTCCCCC-AACTGCCCTGGTACAAGG
CBS347.51 CCTCCCTT-AACTGCCCTGGTACAAGG
CBS136.22 CCTCCCTT-AACTGCCCTGGTACAAGG
CBS336.48 CCTCCCTT-AACTGCCCTGGTACAAGG
CBS110644 CCTCCCTT-AACTGCCCTGGTACAAGG
NRRL3391 CCTCTTCC-AACTGCCCTGGTACAAG-
AL1642 CCTCTTCC-AACTGCCCTGGTACAAG-
AL1878 CCTCTTCC-AACTGCCCTGGTACAAG-
AL1644 CCTCTTCC-AACTGCCCTGGTACAAGG
AL1643 CCTCTTCC-AACTGCCCTGGTACAAGG
NRRL705 CCTCCCCC-AACTGCCCTGGTACA--

Multiple CaM Sequence Alignment

	1	11	21	31	41	51	61	71	
[									]
DAOM239918	A-GGAGGCCCTTGTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACTGGGATTT-		
DAOM239919	-----						AGATCTGTA-ACT-GGATTT-		
KAS2601	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAS3183	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239917	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239927	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CAGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239920	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239928	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239925	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAS3186	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CAGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAS3193	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAS2630	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239924	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239929	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CAGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAS3189	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCTA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAs3187	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAS3190	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CAC-TCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239926	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAS2606	-----								
DAOM239921	-----CCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
DAOM239922	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-GCT-GGATTTT		
KAS2612	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACCTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		
KAS2615	A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG----						AAGATCTGTA-ACT-GGATTT-		

KAS3191 A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCAA--CACGTCGATTGG-----AAGACTCTGTA-ACT-GGATTT-
 KAS2596 A-GGAGGCATTCTCCCTCTTT--GTAAAGT--ACTCCAA--CACGTCGATTGG-----AAGTACTGTA-ACT-GGATTTA
 NRRL2074 -----C--GT-AAGT--ACTTCCA--CGCGTCGATTGA-----AACCCCTCGTG-ACT-GGATTT-
 NRRL32583 A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCCA--CGCGTCGATTGA-----AACCCCTCGTG-ACT-GGATTT-
 DAOM239930 A-GGAGGCCCTTCTCCCTCTTT--GT-AAGT--ACTCCCA--CGCGTCGATTGA-----AACCCCTCGTG-ACT-GGATTT-
 DAOM239931 A-GGAGGCCCTTCTCCCTCTTTGTA-AAGT--ACTCTCA--CGCGTCGATTGA-----AACCCCTCGTG-ACT-GGATTT-
 DAOM239932 -----TCCCTCTTTT--GT-AAGTAAATTCTCA--CGCGTCGATTGA-----AACCCCTCGTG-TCT-GGATTT-
 DAOM239913 ---AGAGCCTTCTCCCTCTTT--GT-AAGT--GCCCCCA--CGCATCGATTGG-----AAGACTCGTG-ACT-GGATTT-
 DAOM239912 -----CTTCTCCCTCTTT--GT-AAGT--GCCCCCA--CGCATCGATTGA-----AAGACTCGTG-ACT-GGATTT-
 CBS229.60 A-GGAGGCCCTTCTCCCTTTT--GT-AAGT--GTCCCGA--CCTGTCGATTG-----AAGACCCATG-ACT-GGATTT-
 CBS238.68 -----CTTCTCCCTTTT--GT-AAGT--GTCCCGA--CCTGTCGATTG-----AAGACCCATG-ACT-GGATTT-
 AL1642 A-GGAGGCATTCTCCCTTTGT-----GGT--GCCCGAT--TTCGTTGATTGG-AAAAAAGCGTCG-CCT-GGAATC-
 AL1644 A-GGAGGCATTCTCCCTGTTT--GT-GAGT--GCCCGAT--TTCGTTGATTGG-AAAAAAGCGTCG-CCT-GGAATC-
 AL1878 A-GGAGGCATTCTCCCTGTTT--GT-GAGT--GCCCGAT--TTCGTTGATTGG-AAAAAAGCGTCG-CCT-GGAATC-
 NRRL3447 AGGAAGGCATTCTCCCTGTTTTGT-GAGT--GCCCGA--TTCGTTGATTGGAAAAAAGCGTCG-CCT-GGAATC-
 AL1643 A-GGAGGCATTCTCCCTGTTTTGT-GAGT--GCCCGATTTCGTTGATTGGAAAAAAGCGTCGCCCT-GGAATC-
 CBS347.51 --AGGAGCCTTCTCCTGTTT--GT-AAGT--TCTTCGA--TCCTTCCATTGA-----ATGCCGTGGTTT--AAATTC-
 CBS336.48 A-AGAGCCTTCTCCTGTTT--GT-AAGT--TTATAGA--TCCTTCCATTGC-----ATACTGTGTTTTT-AAATTC-
 CBS110644 A-GGAGGCATTCTCCTGTTT--GT-AAGT--TCATAGA--TCCTTCCATTGG-----ATACTGTGTTTT--AAATTC-
 CBS136.22 A-G-----TCTTCGA--TCTTTC--ATTA-----ATGCCGTGGTTC-A-AAATTC-
 NRRL705 --AGGAGCCTTCTCCTGTTGT-----GAGT--GCCTCAG--ACGCGTCGATTGAC---AATCTCCGATCGGG-AAAACAG

DAOM239918 AATGCTGAT---GGATATGTTCTCC--GGAAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239919 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS2601 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS3183 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239917 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239927 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239920 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239928 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239925 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS3186 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS3193 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS2630 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239924 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239929 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS3189 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS3187 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS3190 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239926 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS2606 -----TCC--GGCAA-TAG-GA--CAAGGGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239921 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 DAOM239922 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS2612 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS2615 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS3191 GATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 KAS2596 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGCGATGGTTAGTGCACCGTC-GGCGATTT
 NRRL2074 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGTGTGTTAGTGCACCGTC-GGCGATTT
 NRRL32583 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGTGTGTTAGTGCACCGTC-GGCGATTT
 DAOM239930 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGTGTGTTAGTGCACCGTC-GGCGATTT
 DAOM239931 AATGCTGAT---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGTGTGTTAGTGCACCGTC-GGCGATTT
 DAOM239932 AATGCTGAA---GGATATGTTCTCC--GGCAA-TAG-GA--CAA-GGATGGTGTGTTAGTGCACCGTC-GGCGATTT
 DAOM239913 AATGCTGAT---GGATATGTTCTCC--GGCGA-TAG-GA--CAA-GGATGGTGTGTTAGTGCACCGTC-GGCGATTT
 DAOM239912 AATGCTGAT---GGATATGTTCTCC--GGCGA-TAG-GA--CAA-GGATGGTGTGTTAGTGCACCGTC-GGCGATTT
 CBS229.60 --ATACTGAT---AAATACGTTCTGC--TTCAA-TAG-GA--CAA-GGACGGCGATGGTGAGTGCGACCGTC-TGCCGATTA
 CBS238.68 --ATACTGAT---AAATACGTTCTGC--TTCAA-TAG-GA--CAA-GGACGGCGATGGTGAGTGCGACCGTC-TGCCGATTA
 AL1642 AACACTAAT---GGATGCTTTTTCCCGGGAAA-TAG-GA--CAA-GGATGGCGATGGTGAGTGCGATCGTA-CTCGGGCT
 AL1644 AACACTAAT---GGATGCTTTTTCCCGGGAAA-TAG-GA--CAA-GGATGGCGATGGTGAGTGCGATCGTA-CTCGGGCT
 AL1878 AACACTAAT---GGATGCTTTTTCCCGGGAAA-TAG-GA--CAA-GGATGGCGATGGTGAGTGCGATCGTA-CTCGGGCT
 NRRL3447 AACACTAAT---GGATGCTTTTTCCCGGGAAA-TAG-GA--CAA-GGATGGCGATGGTGAGTGCGATCGTA-CTCGGGCT
 AL1643 AACACTAAT---GGATGCTTTTTCCCGGGAAA-TAG-GA--CAAAGGATGGCGATGGTGAGTGCGATCGTA-CTCGGGCT
 CBS347.51 AATACTAAT---GGATATTCGT-----CATAA-TAG-GA--CAA-GGATGGCGATGGTGAGTGCGACCGTT-ACCGAGAT
 CBS336.48 AATACTGAT---GCATATTCGT-----CATAA-TAG-GA--CAA-GGATGGCGATGGTGAGTGCGACCGTT-ACCGAGAT
 CBS110644 AATACTAAT---GCATATTCGT-----CATAA-TAG-GA--CAA-GGATGGCGATGGTGAGTGCGACCGTT-ACCGAGAT
 CBS136.22 AATACTAAT---GGATATTCGT-----CATAA-TAA-GGACAAA-GGATGGCGATGGTGAGTGCGACCGTT-ACCGAGAT
 NRRL705 TAGACTGACCAAGGCCGTTTTCCCGCTTGTGAACAG-GA--CAA-GGATGGCGATGGTGCGTGCAGTCTTT-CCCGGTAG

[161 171 181 191 201 211 221 231]
 [| | | | | | |]
 DAOM239918 TTT--AAATTCCCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239919 TTT--AAATTCCCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA

KAS2601 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS3183 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239917 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239927 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239920 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239928 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239925 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS3186 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS3193 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS2630 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239924 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239929 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS3189 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS3187 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS3190 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239926 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS2606 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239921 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239922 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS2612 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS2615 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS3191 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 KAS2596 TTT--AAATT-CCATG--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 NRRL2074 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 NRRL32583 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239930 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239931 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239932 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239913 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 DAOM239912 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 CBS229.60 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 CBS238.68 TTT--AAATT-CCATA--CCGACTGGAGTAAACCCACTGAG-----AGAACCGAATAACTGA
 AL1642 CGA--TAATTT-CAAGATCCGATTATGTCCTCTTGACCGAG-----TGAA-CAAATCACTGA
 AL1644 CGA--TAATTT-CAAGATCCGATTATGTCCTCTTGACCGAG-----TGAA-CAAATCACTGA
 AL1878 CGA--TAATTT-CAAGATCCGATTATGTCCTCTTGACCGAG-----TGAA-CAAATCACTGA
 NRRL3447 CGA--TAATTT-CAAGATCCGATTATGTCCTCTTGACCGAG-----TGAA-CAAATCACTGA
 AL1643 CGA--TAATTT-CAAGATCCGATTATGTCCTCTTGACCGAG-----TGAA-CAAATCACTGA
 CBS347.51 CTG-----CGGA--CCAATATTACGCC--ATTGAA-----AGGA-TAAATAACTGA
 CBS336.48 CTG-----CGGA--CCAATATTACGCC--ATTGAA-----AGGA-TAAATAACTGA
 CBS110644 CTG-----CGGA--CCAATATTACGCC--ATTGAA-----AGGA-TAAATAACTGA
 CBS136.22 CTG-----CGGA--CCAATATTACGCC--ATTGAA-----AGGA-TAAATAACTGA
 NRRL705 CTG-----CGGA--CCAATATTACGCC--ATTGAA-----AGGA-TAAATAACTGA

	241	251	261	271	281	291	301	311
[								
[								
DAOM239918	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239919	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS2601	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS3183	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239917	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239927	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239920	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239928	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239925	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS3186	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS3193	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS2630	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239924	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239929	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS3189	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS3187	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS3190	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239926	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS2606	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239921	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
DAOM239922	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS2612	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS2615	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS3191	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
KAS2596	GACCGATCGATCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							
NRRL2074	GATCGATTAACTCT-ATAGGA-C-AAATCACCACCAAGGAGCT-GGGCACTGTCATGCGCTCCCTCGGCCAGAACCCCTCC							

	321	331	341	351	361	371	381	391
DAOM239918	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239919	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS2601	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS3183	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239917	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239927	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239920	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239928	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239925	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS3186	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS3193	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS2630	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239924	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239929	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS3189	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS3187	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS3190	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239926	GAGTCCGAGC	-TTCAGGACATGAGCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS2606	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239921	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGACGA	----	T				
DAOM239922	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS2612	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS2615	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS3191	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
KAS2596	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
NRRL2074	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
NRRL32583	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239930	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239931	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239932	GAGTCCGAGC	-TTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA	----	T				
DAOM239913	GAGTCCGAGC	-TTCAGGACATGATTAACGAAGTCGATGCCGACAACAACGGTACCATTGACTTCCCTGGTACGA	----	T				
DAOM239912	GAGTCCGAGC	-TTCAGGACATGATTAACGAAGTCGATGCCGACAACAACGGTACCATTGACTTCCCTGGTACGA	----	T				
CBS229.60	GAGTCTGAGC	-TTCAGGATATGATTAACGAGGTCGATGCCGACAACAACGGTACCATTGACTTCCCTGGTACGAGTTTCT						
CBS238.68	GAGTCTGAGC	-TTCAGGATATGATTAACGAGGTCGATGCCGACAACAACGGTACCATTGACTTCCCTGGTACGAGTTTCT						
AL1642	GAGTCTGAGC	-TGCAGGATATGATCAACGAGGTCGCCCGGATAATAACCGTACCATTGACTTCCCTGGTACGC	----	T				
AL1644	GAGTCTGAGC	-TGCAGGATATGATCAACGAGGTCGCCCGGATAATAACCGTACCATTGACTTCCCTGGTACGC	----	T				
AL1878	GAGTCTGAGC	-TGCAGGATATGATCAACGAGGTCGCCCGGATAATAACCGTACCATTGACTTCCCTGGTACGC	----	T				
NRRL3447	GAGTCTGAGC	-TGCAGGATATGATCAACGAGGTCGCCCGGATAATAACCGTACCATTGACTTCCCTGGTACGC	----	T				
AL1643	GAGTCTGAGC	-TGCAGGATATGATCAACGAGGTCGCCCGGATAATAACCGTACCATTGACTTCCCTGGTACGC	----	T				
CBS347.51	GAGTCTGAGC	-TGCAGGACATGATTAACGAGGTTGACGCTGACAACAACGGCACCATTGATTTCCTGGTACGC	----	T				
CBS336.48	GAGTCTGAGC	-TGCAGGACATGATTAACGAGGTTGACGCTGACAACAACGGCACCATTGATTTCCTGGTACGA	----	C				
CBS110644	GAGTCTGAGC	-TGCAGGACATGATTAACGAGGTTGACGCTGACAACAACGGCACCATTGATTTCCTGGTACGA	----	C				
CBS136.22	GAGTCTGAGC	-TGCAGGACATGATTAACGAGGTTGACGCTGACAACAACGGCACCATTGATTTCCTGGTACGC	----	T				
NRRL705	GAGTCCGAGC	-TGCAGG						

	401	411	421	431	441	451	461	471
[								
DAOM239918	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA							
DAOM239919	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA							
KAS2601	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA							

KAS3183	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239917	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239927	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239920	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239928	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239925	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS3186	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS3193	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS2630	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239924	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239929	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS3189	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS3187	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS3190	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239926	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS2606	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239921	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
DAOM239922	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS2612	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS2615	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS3191	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
KAS2596	TTCCCTTCCGATCG---GACCCCCTGCTC-----CCTCCGGATAGATGTTAA-----CG-TGCGG--CACAGA
NRRL2074	TTCCCTTCCACTCGAATGACCCCGTGCTTCGTA CTGCTTCCGGACATATGTTAA-----CA-TGCGG--CACAGA
NRRL32583	TTCCCTTCCACTCGAATGACCCCGTGCTTCGTA CTGCTTCCGGACATATGTTAA-----CA-TGCGG--CACAGA
DAOM239930	TTCCCTTCCACTCGAATGACCCCGTGCTTCGTA CTGCTTCCGGACATATGTTAA-----CA-TGCGG--CACAGA
DAOM239931	TTCCCTTCCACTCGAATGACCCCGTGCTTCGTA CTGCTTCCGGGACATATGTTAAG-----CA-TGCGG--CACAGA
DAOM239932	TTCCCTTCCACTCGAATGACCCCGTGCTTCGTA CTGCTTCCGGGACATATGTTAA-----CA-TGCGG--CACAGA
DAOM239913	TTCCCTTCCACTCGAATCATCC-----CGTCTAGTCTCCGGACATATGTTAA-----CA-TGCGA--CACAGA
DAOM239912	TTCCCTTCCACTCGAATCATCC-----CGTCTAGTCTCCGGACATATGTTAA-----CA-TGCGA--CACAGA
CBS229.60	CTTTCTTCCACCCGAA-----ATGCCCCATACTCGCCATTCCGCATATATTGA-----CA-GACGGCACACAGA
CBS238.68	CTTTCTTCCACCCGAA-----ATGCCCCATACTCGCCATTCCGCATATATTGA-----CA-GACGGCACACAGA
AL1642	CTCCCTCCCCCTCCGAATGA-----TGATCTCAAGCCCCGAGAAGACTGATATTGA-----CATTGCGA--CACAGA
AL1644	CTCCCTCCCCCTCCGAATGA-----TGATCTCAAGCCCCGAGAAGACTGATATTGA-----CATTGCGA--CACAGA
AL1878	CTCCCTCCCCCTCCGAATGA-----TGATCTCAAGCCCCGAGAAGACTGATATTGA-----CATTGCGA--CACAGA
NRRL3447	CTCCCTCCCCCTCCGAATGA-----TGATCTCAAGCCCCGAGAAGACTGATATTGA-----CATTGCGA--CACAGA
AL1643	CTCCCTCCCCCTCCGAATGA-----TGATCTCAAGCCCCGAGAAGACTGATATTGA-----CATTGCGA--CACAGA
CBS347.51	CCCTATGTCTCTCGACGGAC---TCGACTTTATTTTCTTTTCGACACGATATTGA-----CA-CCCTT--CGCAGA
CBS336.48	CTCTATGTCTCTCGACGAAC---TCGATTTTATCTCCTTTTCGGATCAGTATTGA-----CA-CCCTT--TGCAGA
CBS110644	CCCTATGTCTCTCGACGAGC---TCGATTTATCTCCTTTTCGGATCAGTATTGA-----CA-CCCTT--TGCGA
CBS136.22	CCCTATGTCTCTCGACGGAC---TCGACTTTATTTCTCTTTTCGGACGACATTGA-----TA-CCCTT--TGCAGA
NRRL705	TGGAATCGCTTGGCAGTCTGCTGTGGCTCTTTTCTCCCTTTAGACCAAGACTGATTGCTTTTCTGT--TGCGGC--TGACGA

	481	491	501	511	521	531	541	551
DAOM239918	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCA	-----						
DAOM239919	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGATC							
KAS2601	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
KAS3183	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
DAOM239917	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
DAOM239927	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
DAOM239920	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
DAOM239928	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
DAOM239925	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
KAS3186	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
KAS3193	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
KAS2630	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGATC							
DAOM239924	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGATC							
DAOM239929	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
KAS3189	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGATC							
KAS3187	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
KAS3190	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
DAOM239926	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGATC							
KAS2606	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
DAOM239921	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTCGACC							
DAOM239922	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGCCGAGTTCCAGGAGGCCTTCAAGGTTTTCGATC							
KAS2612	GTTCTCTGACCATGATGGACCGTAAGATGAAGGACACCGACTCCGAGGCCGAGTTCCAGGAGGCCTTCAAGGTTTTCGATC							
KAS2615	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCAGGAGGCCTTCAAGG-TTTCGATC							
KAS3191	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTC-----							
KAS2596	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTTCGACC							
NRRL2074	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTTCGACC							
NRRL32583	GTTCTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGTTTTTCGACC							

DAOM239930 GTTCCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCCTTCAAGGTTTTCGACC
 DAOM239931 GTTCCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCCTTCAAGGTTTTCGACC
 DAOM239932 GTTCCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCCTTCAAGGTTTTCGACC
 DAOM239913 GTTCCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCATTCAAGGTTTTCGACC
 DAOM239912 GTTCCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCATTCAAGGTTTTCGACC
 CBS229.60 GTTCCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCATTCAAGGTCTTCGACC
 CBS238.68 GTTCCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCATTCAAGGTCTTCGACC
 AL1642 GTTCCTTACCATGATGGCACGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCCTTCAAGGTGTTTCGACC
 AL1644 GTTCCTTACCATGATGGCACGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCCTTCAAGGTGTTTCGACC
 AL1878 GTTCCTTACCATGATGGCACGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCCTTCAAGGTGTTTCGACC
 NRRL3447 GTTCCTTACCATGATGGCACGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCCTTCAAGGTGTTTCGACC
 AL1643 GTTCCTTACCATGATGGCACGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTAGGCCTTCAAGGTGTTTCGACC
 CBS347.51 GTTTCTTACCATGATGGCCCGTAAGATGAAGGATACCGACTCCGAGGAGGAGATCCGCGAGGCATTCAAGGTGTTTCGATC
 CBS336.48 GTTTCTTACCATGATGGCCCGTAAGATGAAGGATACCGACTCCGAGGAGGAGATCCGCGAGGCATTCAAGGTGTTTCGATC
 CBS110644 GTTCCTTACCATGATGGCCCGTAAGATGAAGGATACCGACTCCGAGGAGGAGATCCGCGAGGCATTCAAGGTGTTTCGATC
 CBS136.22 GTTCCTTACCATGATGGCCCGTAAGATGAAGGATACCGACTCCGAGGAGGAGATCCGCGAGGCATTCAAGGTGTTTCGATC
 NRRL705 GTTCCTTACCATGATGGCCCGCAAGATGAAGGACACCGACTCAGAGGAGGAGATCCGGGAGGCCTTCAAGGTGTTTCGACC

	561	571	581	591	601	
[						]
DAOM239918	-----					
DAOM239919	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCC-----					
KAS2601	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
KAS3183	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239917	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239927	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239920	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239928	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239925	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
KAS3186	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
KAS3193	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
KAS2630	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239924	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239929	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTRATGACC					
KAS3189	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
KAS3187	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATG---					
KAS3190	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239926	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACG-----					
KAS2606	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239921	GCGAC-ACAACGGTTTCATTTCCGCCGCCGAGCTGC-----					
DAOM239922	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGT-----					
KAS2612	GCGACAACAACGGTTTCATTTCCG-----					
KAS2615	GCGACAACAACGT-----					
KAS3191	-----					
KAS2596	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACG-----					
NRRL2074	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
NRRL32583	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239930	GCGACAATAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239931	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239932	GCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC					
DAOM239913	GTGACAACAACGGTTTCATTTCCGCCGCTGAGCTGCGCCACGTCATGACC					
DAOM239912	GTGACAACAACGGTTTCATTTCCGCCGCTGAGCTGCGCCACGTCATGACC					
CBS229.60	GCGACAACAACGGTTTCATCTCCGCTGCCGAGCTGCGCCACGTCATGACC					
CBS238.68	GCGACAACAACGGTTTCATCTCCGCTGCCGAGCTGCGCCACGTCATGACC					
AL1642	GCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACC					
AL1644	GCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACC					
AL1878	GCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACC					
NRRL3447	GCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACC					
AL1643	GCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACC					
CBS347.51	GCGATAACAACGGATTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACC					
CBS336.48	GCGATAACAACGGATTTCATCTCCGCCGCCGAACTACGCCACGTCATGACC					
CBS110644	GCGATAACAACGGATTTCATCTCCGCCGCCGAACTGCGCCATGTCATGACC					
CBS136.22	GCGATAACAACGGATTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACC					
NRRL705	GCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACC					

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KAS3191	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACGTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
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DAOM239917	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
DAOM239922	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
DAOM239925	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
DAOM239943	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAT								
KAS347953	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
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DAOM239940	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
DAOM239945	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
DAOM239946	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
DAOM239939	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CCGGGGTCAAAT-----CTTCAATTG-GTGAAC								
NRRL2074	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATCAATTG-TTGAAC								
NRRL32583	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATCAATTG-TTGAAC								
DAOM239930	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATCAATTG-TTGAAC								
DAOM239931	TGGTGCCGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATCAATTG-TTGAAC								
DAOM239932	TGGTGCCGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATCAATTG-TTGAAC								
CBS25855	GGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATCAATTG-TTGAAC								
CBS12865	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATCAATTG-TTGAAC								
CBS11889	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----CATCAATTG-TTGAAC								
DAOM239912	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----TATCAATTG-TTGAAC								
DAOM239913	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTTCGGTCAAAT-----TATCAATTG-TTGAAC								
CBS24865	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--TTTGGGTCAAAT-----CTTCAATTG-TTGAAC								
DAOM239934	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--TTTGGGTCAAAT-----CATCAATTG-TTGAAC								
DAOM239935	TGGTGCCGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--TTTGGGTCAAAT-----CATCAATTG-TTGAAC								
DAOM239936	TGGTGCCGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--TTTGGGTCAAAT-----CATCAATTG-TTGAAC								
DAOM239933	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--TTTGGGTCAAAT-----CATCAATTG-TTGAAC								
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DAOM239938	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTGGGGTCAAAT-----CATCAGTTG-TTGAAC								
DAOM239937	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTGGGGTCAAAT-----CATCAGTTG-TTGAAC								
KAS3469	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC--CTGGGGTCAAAT-----CATCAATTG-TTGAAC								
CBS229.60	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCGACCTTAC--CTTGCCCTCAGGT-----AGTCAATTG-TTGAAC								
CBS238.68	CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCGACCTTAC--CTTGCCCTCAGGT-----AGTCAATTG-TTGAAC								
KAS3463	CGGTGCTGCTTTCTGGTACGTGTTTCCA-CCAC-----CTCAACC-----CATCAATTG-TTGGCT								
CBS238.68	CGGTGCTGCTTTCTGGTACGTGTTTCCA-CCAC-----CTCAACC-----CATCAATTG-TTGGCT								
KAS3464	CGGTGCTGCTTTCTGGTACGTGTTTCCA-CCAC-----CTCAACC-----CATCAATTG-TTGGCT								
KAS3466	CGGTGCTGCTTTCTGGTACGTGTTTCCA-CCAC-----CTCAACC-----CATCAATTG-TTGGCT								
KAS3465	CGGTGCTGCTTTCTGGTACGTGTTTCCA-CCCTC-----CTCAAAC-----CATCAATTG-TTGGCT								
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 DAOM239919 CAGGAA-----CC---TTTGACTGACGTGAATGATAGGCAGAACATTGCTAGCGAGCATGGCCTCGATGGCGAGGGC
 DAOM239917 CAGGAA-----CC---TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCTCGATGGCGAGGGC
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 KAS347953 CAGGAA-----CC---TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
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 NRRL32583 CAGGAC-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
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 DAOM239931 CAGGAC-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
 DAOM239932 CAGGAC-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
 CBS25855 CAAGAG-----CC---TTTACTGACTTCAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
 CBS12865 CAAGAG-----CC---TTTACTGACTTCAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
 CBS11889 CAAGAG-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
 DAOM239912 CAGGAC-----CT---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGTCTCGACGGCGAGGGC
 DAOM239913 CAGGAC-----CT---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGTCTCGACGGCGAGGGC
 CBS24865 AAGAAC-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGTCTCGACGGCGAGGGC
 DAOM239934 CACGAG-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
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 DAOM239933 CACGAG-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
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 DAOM239915 TAGGAG-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
 DAOM239938 CAAGAG-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
 DAOM239937 CAAGAG-----CC---TTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGC
 KAS3469 CAGGAA-----CC---ATATGCTAACCT-ACTTCCAGGCAGAACATTGCTAGCGAGCATGGCCTCGATGGCGAGGGC
 CBS229.60 CAGGAG-----CC---TTATGCTAACCT-ACTTCCAGGCAGAACATTGCTAGTGAGCATGGCCTTGATGGCGAGGGC
 CBS238.68 CAGGAG-----CC---TTATGCTAACCT-ACTTCCAGGCAGAACATTGCTAGTGAGCATGGCCTTGATGGCGAGGGC
 KAS3463 CTTCAA-----GCTTCTTTTACTAAC-TACCTCTTAGGCAGAACATTGCCAGTGAGCACGGCCTCGATGGCGATGGC
 CBS238.68 CTTCAA-----GCTTCTTTTACTAAC-TACCTCTTAGGCAGAACATTGCCAGTGAGCACGGCCTCGATGGCGATGGC
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 NRRL3391 --A-AA-----CC-TTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCACGGTCTCGATGGCGATGGA
 AL1878 --A-AA-----CC-TTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCACGGTCTCGATGGCGATGGA
 AL1644 --A-AA-----CC-TTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCACGGTCTCGATGGCGATGGA
 AL1642 --A-AA-----CC-TTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCACGGTCTCGATGGCGATGGA
 AL1643 --A-AA-----CC-TTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCACGGTCTCGATGGCGATGGA
 CBS136.22 CTTGAG-----ACA---TTTTACTGAC-TACTTCCAGGCAGAACATTGCCCTCCGAGCACGGCCTCGATGGCGAAGGA
 CBS347.51 ATTGAG-----ACA---TTTTACTGAC-TACTTCCAGGCAGAACATTGCCCTCCGAGCACGGCCTCGATGGCGAAGGA
 CBS336.48 CTTGGA-----ACA---ATTACTGAC-TACTTCCAGGCAGAACATTGCCCTCCGAGCATGGCCTCGATGGCGAAGGA
 CBS110644 CTTGAG-----ACA---TTTTACTGAC-TACTTCCAGGCAGAACATTGCCCTCCGAGCACGGCCTCGATGGCGAAGGA
 CBS42665 CCATTG-----AAACTTTTTTACTAAC-TACCTTATAGGCAGAACATTGCCCTCCGAGCACGGTCTCGATGGCGATGGA
 KAS2818 CCATTG-----AAACTTTTTTACTAAC-TACCTTATAGGCAGAACATTGCCCTCCGAGCACGGTCTCGATGGTGATGGA
 NRRL705 ---TCAACAGATACTGACTCG-----AACTACAGGCAGACCATTGCTGGTGAGCACGGCCTTGATGGCGATGGC

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KAS3191	CAGTAAGT-----				ATCAATT-TACGGGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239926	CAGTAAGT-----				ATCAATT-TACGGGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239919	CAGTAAGT-----				ATCAATT-TACGGGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239917	CAGTAAGT-----				ATCAATT-TACGGGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239922	CAGTAAGT-----				ATCAATT-TACGGGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239925	CAGTAAGT-----				ATCAATT-TACGGGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239943	CAGTAAGT-----				ATCAATT-TACGCGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
KAS347953	CAGTAAGT-----				ATCAATT-TGCGTGAATTGGGTGATA---		GGAGAAT-GGCGGTCT		
DAOM239941	CAGTAAGT-----				ATCAATT-TACGCGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239942	CAGTAAGT-----				ATCAATT-TACGCGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239944	CAGTAAGT-----				ATCAATT-TACGCGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239940	CAGTAAGT-----				ATCAATT-TACGCGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239945	CAGTAAGT-----				ATCAATT-TACGCGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		
DAOM239946	CAGTAAGT-----				ATCAATT-TACGCGGAATTGGGTGATA---		TGAGAAT-GGCGGTCT		

DAOM239939 CAGTAAGT-----ATCAATT-TACGCGGAATTGGGTGATA---TGAGAAT-GGCGGTCT
 NRRL2074 CAGTAAGT-----ATCCATT-CGGTTGGAATTGAGTGATA---TGAGAAT-GGCGGTCT
 NRRL32583 CAGTAAGT-----ATCCATT-CAGTTGGAATTGAGTGATA---TGAGAAT-GGCGGTCT
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 CBS12865 CAGTAAGT-----ATCAATT-TGGTTGGAATTGAGTGATA---TG-GAAT-GGCGGTCT
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 CBS24865 CAGTAAGT-----ATCGAAT-TGGTTGGCATTGGGTGATA---TGAGAAT-GGCGGTCT
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 DAOM239937 CAGTAAGT-----ATCAACA-TGGTTGGAATTGGCTGATA---GGAGAAT-GGCGGTCT
 KAS3469 ATGTAAGT-----ATCAATT-TGGTTGGAATTGGACTGATA---TGAGAAT-GGCGGTCT
 CBS229.60 CAGTAAGT-----ATCAATA-CGAGTGGGATTGGGTGATG---TGAGAAT-GGCGGTCT
 CBS238.68 CAGTAAGT-----ATCAATA-CGAGTGGGATTGGGTGATG---TGAGAAT-GGCGGTCT
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 AL1643 CAGTAAGT-----CTCGATCATCGACTCGATTGAATGAAGTGGTGGGAAT-GGCGGTCT
 CBS136.22 CAGTGAGT-----ATCAATA-TTAATGGAATTGAGTGACGAG-TAGGAAT-GGCGGTCT
 CBS347.51 CAGTGAGT-----ATCGATA-TTAATGGAATTGAGTGACGAG-TAGGAAT-GGCGGTCT
 CBS336.48 CAGTGAGT-----ATCGATA-TTAATGGAATTGAGTGACGAG-TAGGAAT-GGCGGTCT
 CBS110644 CAGTGAGT-----ATCAATA-TTAATGGAATTGAGTGACGAG-TAGGAAT-GGCGGTCT
 CBS42665 CAGTAAGT-----TCTTTGATTTCGAGTCGATTGGTATATATGGTGGGAAT-GGCGGTCT
 KAS2818 CAGTAAGT-----TCTTTGATTTCGAGTCGATTGGTATATATGGTGGGAAT-GGCGGTCT
 NRRL705 CAGTAAGTCTCTTCGATACCCTTGATACCTCT-----C-GACACGGAA-TGGCGGTCT

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KAS3191	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239926	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239919	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239917	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239922	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239925	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239943	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
KAS347953	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
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DAOM239944	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239940	GATA----	TTTTTCTTTAGCTTCAC-	TGTCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239945	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239946	GATA----	TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
DAOM239939	GATA----	TTTTTCTTTAGCTTCAC-	TGTCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG					
NRRL2074	GACATTTTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
NRRL32583	GATA-----TTTTTCTTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
DAOM239930	GATA-TTTTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
DAOM239931	GATA-TTTTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
DAOM239932	GATA-TTTTTTTTCCCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
CBS25855	GATA--TTTTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
CBS12865	GATA-TTTTTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
CBS11889	GATA-TTTTTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
DAOM239912	GATA-----TTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
DAOM239913	GATA-----TTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
CBS24865	GATA-----TTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
DAOM239934	GATATTTTTTTTCTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						
DAOM239935	GATA--TTTTTTTCTTAGCTTCAC-	TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAG						

	321	331	341	351	361	371	381	391
[								
KAS3191	-----	-----	TGTGG-AATCAACACTCCAA-AC	TCGTCA----	ACCACATCTAATACAATGGT-T	TTTCA---		
DAOM239926	-----	-----	TGTGG-AATCAACACTCCAA-AC	TCGTCA----	ACCACATCTAATACAATGGG-T	TTTCA---		
DAOM239919	-----	-----	TGTGG-AATCAACACTCCAA-AC	TCGTCA----	ACCACATCTAATACAATGGG-T	TTTCA---		
DAOM239917	-----	-----	TGTGG-AATCAACACTCCAA-AC	TCGTCA----	ACCACATCTAATACAATGGT-T	TTTCA---		
DAOM239922	-----	-----	TGTGG-AATCAACACTCCAA-AC	TCGTCA----	ACCACATCTAATACAATGGG-T	TTTCA---		
DAOM239925	-----	-----	TGTGG-AATCAACACTCCAA-AC	TCGTCA----	ACCACATCTAATACAATGGT-T	TTTCA---		
DAOM239943	-----	-----	TGTGG-AATCAACACTCGAT-AC	TCGTCA----	ACCTCATCTAATACAATGGT-T	TTTCA---		
KAS347953	-----	-----	TGTGG-AATCGACACTCGAT-AC	TCGTCA----	ACCTCATCTAATATAATGGT-T	TTTCA---		
DAOM239941	-----	-----	TGTGG-AATCGACACTCGAT-AC	CCCGTCA----	ACCTCATCTAATATAATGGT-T	TTTCA---		
DAOM239942	-----	-----	TGTGG-AATCGACACTCGAT-AC	TCGTCA----	ACCTCATCTAATACAATGGT-T	TTTCA---		
DAOM239944	-----	-----	TGTGG-AATCAACTCTCGAT-C	CTCGTCA----	ACCTCATCTAACACAATGGT-T	TTTCA---		
DAOM239940	-----	-----	TGTGG-AATCAACACTCGAT-AC	TCGTCA----	ACCTCATCTAATACAATGGT-T	TTTCA---		
DAOM239945	-----	-----	TGTGG-AATCAACACTCGAT-AT	TCGTCA----	ACCTCATCTAATACAATGGT-T	TTTCA---		
DAOM239946	-----	-----	TGTGG-AATCAACACTCGAT-AC	TCGTCA----	ACCTCATCTAATACAATGGT-T	TTTCA---		
DAOM239939	-----	-----	TGTGG-AATCAACACTCGAT-AC	TCGTCA----	ACCTCATCTAATACAATGGT-T	TTTCA---		
NRRL2074	-----	-----	TGTGG-AATCGATACTCGAT-AC	CTGCCA----	ACCCCGTCTAATATAATGGA-T	TTTCA---		
NRRL32583	-----	-----	TGTGG-AATCGATACTCCAT-AC	CTGCCA----	ACCCCGTCTAATATAATGGA-T	TTTCA---		
DAOM239930	-----	-----	TGTGG-AATCGATACTCCAT-AC	CTGCCA----	ACCCCGTCTAATATAATGGA-T	TTTCA---		
DAOM239931	-----	-----	TGTGG-AATCGATACTCGAT-AC	CTGCCA----	ACCACGTCTAATATAATGGA-T	TTTCA---		
DAOM239932	-----	-----	TGTGG-AATCGATACTCGAT-AC	CTGCCA----	ACCACGTCTAATATAATGGA-T	TTTCA---		
CBS25855	-----	-----	TGTGC-AATCGACACTCGAT-AC	CTGTCA----	ACCCCGTCTAATATAATGGA-T	TCTCA---		
CBS12865	-----	-----	TGTGC-AATCGACACTCGAT-AC	CTGTCA----	GCCCCGTCTAATAGATGGA-T	TCTCA---		
CBS11889	-----	-----	TGTGC-AATCGACACTCGATAAC	CTGTCA----	ACCCCGTCTAATATAATGGA-T	TCTCA---		
DAOM239912	-----	-----	TGTGGAAACCGACACTCGAT-AC	CTTTCA----	AACACGTCTAACATGATGCA-T	CTTCA---		
DAOM239913	-----	-----	TGTGGAAACCGACACTCGAT-AC	CTTTCA----	AACACGTCTAACATGATGCA-T	CTTCA---		
CBS24865	-----	-----	TGTGG-AATCGACACTCGAT-AT	CTTTCA----	AACCCGTCTAACACATGAA-T	TCTTTA---		
DAOM239934	-----	-----	TGTGG-AATCGACACTCGATACT	CTGGAC----	ACCCCGTCTAATATAATGGA-T	TTTCT---		
DAOM239935	-----	-----	TGTGG-AATCGACACTCGATACT	CTGAAC----	ACCCCGTCTAATATACTGGA-T	TTTCT---		
DAOM239936	-----	-----	TGTGG-AATCGACACTCGATACT	CTGAAC----	ACCCCGTCTAATATACTGGA-T	TTTCT---		
DAOM239933	-----	-----	TGTGG-AATCGACACTCGATACT	CTGAAC----	ACCCCGTCTAATATACTGGA-T	TTTCT---		
DAOM239914	-----	-----	CGTGA-AATCTACACTCGAT-AC	CATTCA----	CTCCCATCTAATATATTTGA-T	TCTTT---		
DAOM239915	-----	-----	CGTGA-AATCTACACTCGAT-AC	CATTCA----	CTCCCATCTAATATATTTGA-T	TCTTT---		
DAOM239938	-----	-----	TGTGG-AATTTACACTCGAT-AC	CCCTTCAGACCCCCCGTCTA	ATATGATGGATTCTTTT---			
DAOM239937	-----	-----	TGTGG-AATTTACACTCGAT-AC	CCCTTCAGACCCCCCGTCTA	ATATGATGGATTCTTTT---			
KAS3469	-----	-----	CGTGGAAACCCACTCTCGAT-C	CTTTCA----	ACCTGTCTAATATTTATGGA-T	TTTCA---		
CBS229.60	-----	-----	TGTGG-AATCGATAACCGTA-AC	GTTTAA----	ACCTCGTCTAATACAATGGA-T	TTTCA---		
CBS238.68	-----	-----	TGTGG-AATCGATAACCGTA-AC	GTTTAA----	ACCTCGTCTAATACAATGGA-T	TTTCA---		
KAS3463	-----	-----	TATGA-CATTGATATATTGA-AT	AATTCG----	ACCTGTCTAATATTTTGATT-T	TCA---		
CBS238.68	-----	-----	TATGA-CATTGATATATTGA-AT	AATTCG----	ACCTGTCTAATATTTTGATT-T	TCA---		
KAS3464	-----	-----	TATGA-CATTGATATATTGA-AT	AATTCG----	ACCTGTCTAATATTTTGATT-T	TCA---		
KAS3466	-----	-----	TATGA-CATTGATATATTGA-AT	AATTCG----	ACCTGTCTAATATTTTGATT-T	TCA---		
KAS3465	-----	-----	TATGA-CATTGATATATTGA-AT	AATTCG----	ACCTGTCTAATATTTTGATT-T	TCA---		

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NRRL3391 -----TGTGG-CATTGATATCCCGA-GTCACTCG---AACACGGCTAATATGTCGGGTTTTTTA---
AL1878 -----TGTGG-CATTGATATCCCGA-GTCACTCG---AACACGGCTAATATGTCGGGTTTTTTA---
AL1644 -----TGTGG-CATTGATATCCCGA-GTCACTCG---AACACGGCTAATATGTCGGGTTTTTTA---
AL1642 -----TGTGG-CATTGATATCCCGA-GTCACTCG---AACACGGCTAATATGTCGGGTTTTTTA---
AL1643 -----TGTGG-CATTGATATCCCGA-GTCACTCG---AACACGGCTAATATGTCGGGTTTTTTA---
CBS136.22 -----TGTGG-AATCAATACTCACAATACATTTCG---ACTCCGCCTAATATGATGGAAA--TTA---
CBS347.51 -----TGTGG-AATCAATACTCACAATACATTTCG---ACTCCGCCTAATATGATGGAAA--TTA---
CBS336.48 -----TGTGG-AATCCATACTCACAATACATTTCG---AATTCACCTAATAGGATTGAAA--TTA---
CBS110644 -----TGTGG-AATCATTACTCACAATACATTTCG---ACTCCGCCTAATATGCTTGAAA--TTCG---
CBS42665 -----TGTGG-AATTGATCCTCGA-GCCATTTCG---ATATTGGCTAATAT-TTGGATTGTTTA---
KAS2818 -----TGTGG-AATTGATCCTCGA-GCCATTTCG---ATATTGGCTAATAT-TTGGATTGTTTA---
NRRL705 TGGCGTGTCATCCAACGAA-----GAAACACCAGAATTA---AGTCTAACCCATGGATGTTTTGTTTAT---

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KAS3191 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239926 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239919 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239917 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239922 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239925 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239943 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
KAS347953 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239941 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239942 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239944 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239940 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239945 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239946 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239939 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
NRRL2074 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
NRRL32583 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239930 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239931 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239932 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS25855 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS12865 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS11889 ---TAGGCCTCTGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239912 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239913 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS24865 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239934 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239935 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239936 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239933 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
DAOM239914 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
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DAOM239937 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
KAS3469 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS229.60 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS238.68 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
KAS3463 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS238.68 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
KAS3464 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
KAS3466 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
KAS3465 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
NRRL3391 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTAGTCGATCTGGAGCCTGGTACCATGGACGCTGTCCGTGC
AL1878 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTAGTCGATCTGGAGCCTGGTACCATGGACGCTGTCCGTGC
AL1644 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTAGTCGATCTGGAGCCTGGTACCATGGACGCTGTCCGTGC
AL1642 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTAGTCGATCTGGAGCCTGGTACCATGGACGCTGTCCGTGC
AL1643 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTAGTCGATCTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS136.22 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTTGTGCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS347.51 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTTGTGCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS336.48 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTTGTGCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS110644 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTTGTGCGACTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
CBS42665 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGATTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
KAS2818 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGATTTGGAGCCTGGTACCATGGACGCTGTCCGTGC
NRRL705 ---TAGGCCAGCGGTGACCGTTACGTTCCCCGTGCCGTCCTGGTCGATCTGGAGCCTGGTACCATGGACGCTGTCCGTGC

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DAOM239946 ACTAC
 DAOM239939 ACTAC
 NRRL2074 ACTAC
 NRRL32583 ACTAC
 DAOM239930 ACTAC
 DAOM239931 ACTAC
 DAOM239932 ACTAC
 CBS25855 ACTAC
 CBS12865 ACTAC
 CBS11889 ACTAC
 DAOM239912 ACTAC
 DAOM239913 ACTAC
 CBS24865 ACTAC
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 DAOM239937 ACTAC
 KAS3469 ACTAC
 CBS229.60 ACTAC
 CBS238.68 ACTAC
 KAS3463 ACTAC
 CBS238.68 ACTAC
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 KAS3466 ACTAC
 KAS3465 ACTAC
 NRRL3391 ACTAC
 AL1878 ACTAC
 AL1644 ACTAC
 AL1642 ACTAC
 AL1643 ACTAC
 CBS136.22 ACTAC
 CBS347.51 ACTAC
 CBS336.48 ACTAC
 CBS110644 ACTAC
 CBS42665 ACTAC
 KAS2818 ACTAC
 NRRL705 ACTAC

Multiple ITS Sequence Alignment

	1	11	21	31	41	51	61	71	
[									]
[									]
KAS3191	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239926	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239919	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239925	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239922	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239917	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239943	-----CCTCTG-----	G	-	T	-----CACCTCCCACCCGTGTTA-TTATACCTTGGTGCCTTCGGCAGG				
KAS3479	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239941	-----AGAGAGGGCCCTCTG-----	G	-	T	-----CACCTCCCACCCGTGTTA-TTATACCTTGGTGCCTTCGGCAGG				
DAOM239942	-----AGTGAGGG-----TCT-----	G	-	T	-----CACCTCCCACCCGTGTTA-TTATACCTTGGTGCCTTCGGCAGG				
DAOM239944	-----CCTCTG-----	G	-	T	-----CACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG				
DAOM239940	C	A	T	T	A	C	G	A	AAGAGGGGCCCTCCTGGGCCTCTGGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239945	-----GCCTCTG-----	G	-	T	-----ACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG				
DAOM239946	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239939	C	A	T	T	A	C	G	A	AAGAGGGGCCCTCCTGGGCCTCTGGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
NRRL32583	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
NRRL2074	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239930	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239931	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
DAOM239932	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
CBS25855	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
CBS12865	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG
CBS118889	C	A	T	T	A	C	T	G	-----GGTCCAACCTCCCACCCGTGTTA-TTGTACCTTGGTGCCTTCGGCAGG

DAOM239913 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGTGTGCTTCGGCAGG
 DAOM239912 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGTGTGCTTCGGCAGG
 CBS24865 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 DAOM239934 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 DAOM239935 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 DAOM239936 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 DAOM239933 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 DAOM239915 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGTGTGCTTCGGCAGG
 DAOM239914 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGTGTGCTTCGGCAGG
 DAOM239938 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 DAOM239937 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 KAS3469 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTAATTGTACCTTGTGTGCTTCGGCAGG
 CBS229.60 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 CBS23865 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 KAS3463 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 CBS238.68 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 KAS3464 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 KAS3466 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 KAS3465 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
 NRRL3391 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTCTC-TTGTACCATGTGTGCTTCGGCAGG
 AL1878 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTCTC-TTGTACCATGTGTGCTTCGGCAGG
 AL1644 CATTACTG--AGTGAGGGCCCTCTG-----T-CAACCTCCCACCCGTGTCTC-TTGTACCATGTGTGCTTCGGCAGG
 AL1642 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTCTC-TTGTACCATGTGTGCTTCGGCAGG
 AL1643 CATTACTG--AGTGAGGGCCCTCTG-----ACCTCCCACCCGTGTCTC-TTGTACCATGTGTGCTTCGGCAGG
 CBS136.22 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGTGTGCTTCGGCAGG
 CBS347.51 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGTGTGCTTCGGCAGG
 CBS336.48 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGTGTGCTTCGGCAGG
 CBS110644 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGTGTGCTTCGGCAGG
 CBS42665 CATTACTG--AGTGAGGGCCCTCTG-----GTCCAACCTCCCACCCGTGTCTA-TTGTACCATGTGTGCTTCGGCAGG
 DAOM239916 CATTACTG--AGTGAGGGCCCTCTG-----GTCCAACCTCCCACCCGTGTCTA-TTGTACCATGTGTGCTTCGGCAGG
 NRRL705 CATTACCG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TCGTACCTTGTGTGCTTCGGCAGG

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KAS3191	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-TGCCCC	GGGGCC	CGCGCT
DAOM239926	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239919	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239925	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239922	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239917	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239943	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
KAS3479	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
DAOM239941	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239942	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
DAOM239944	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCTCC	GGGGCC	CGCGCT
DAOM239940	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
DAOM239945	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
DAOM239946	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
DAOM239939	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
NRRL32583	CCCGCC	-TTACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
NRRL2074	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239930	CCCGCC	-TTACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239931	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239932	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
CBS25855	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
CBS12865	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
CBS118889	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239913	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
DAOM239912	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
CBS24865	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239934	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239935	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239936	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239933	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239915	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239914	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239938	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
DAOM239937	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCT	-GCCCC	GGGGCC	CGCGCT
KAS3469	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTTT	-GCCCC	GGGGCC	CGCGCT
CBS229.60	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT
CBS23865	CCCGCC	-TCACG	GCCGCC	-GGGGGG	GCTTCC	-GCCCC	GGGGCC	CGCGCT

[illegible]

[illegible]


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CBS23865  GGCCGGC-GCCT--GCCGACA---CCCATCAACC---CTTCTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
KAS3463   GGCCGGC-GCCT--GCCGACC---CTCATCATCC---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
CBS238.68 GGCCGGC-GCCT--GCCGACC---CTCATCATCC---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
KAS3464   GGCCGGC-GCCT--GCCGACC---CTCATCATCC---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
KAS3466   GGCCGGC-GCCT--GCCGACC---CTCATCATCC---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
KAS3465   GGCCGGC-GCCT--GCCGACC---CTCATCATCC---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
NRRL3391  GGCCGGC-GCTG--GCCGACC---CTCCAACCCCA---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
AL1878    GGCCGGC-GCTG--GCCGACC---CTCCAACCCCA---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
AL1644    GGCCGGC-GCTG--GCCGACC---CTCCAACCCCA---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
AL1642    GGCCGGC-GCTG--GCCGACC---CTCCAACCCCA---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
AL1643    GGTCGGC-GCTG--GCCGACC---CTCCAACCCCA---TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
CBS136.22 GGCCGGC-GCCTTAGCCGACG-----ACACAATCTTTTTTTTCAGGTTGACCTCGGATCAGGTAGG-----
CBS347.51 GGCCGGC-GCCTTAGCCGACG-----ACACAATC-TTTTTTTTCAGGTTGACCTCGGATCAGGTAGG-----
CBS336.48 GGCCGGC-GCCTTAGCCGACG-----ACACAATC-TTTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
CBS110644 GGCCGGC-GCCTTAGCCGACG-----ACACAATC-TTTTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
CBS42665  GGCCGGC-GCCT--GTCGACC---CCCAATCTAT----TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
DAOM239916 GGCCGGC-GCCT--GTCGACC---CCCAATCTAT----TTTTTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA
NRRL705   GGCCGGC-GCCC--GCCGGCGACCCCATCAATC-----TTTCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAA

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[          561          571          ]
[          |          |          ]

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KAS3191    CTTAAGCATATCAA
DAOM239926 CTTAAGCATATCAA
DAOM239919 CTTAAGCATATCAA
DAOM239925 CTTAAGCATATCAA
DAOM239922 CTTAAGCATATCAA
DAOM239917 CTTAAGCATATCAA
DAOM239943 CTTAAGCATATCAA
KAS3479    CTTAAGCATATCAA
DAOM239941 -----
DAOM239942 CTTAAGCATATCAA
DAOM239944 CTTAAGCATATCAA
DAOM239940 CTTAAGCATATCAA
DAOM239945 CTTAAGCATATCAA
DAOM239946 CTTAAGCATATCAA
DAOM239939 CTTAAGCATATCAA
NRRL32583  CTTAAGCATATCAA
NRRL2074   CTTAAGCATATCAA
DAOM239930 CTTAAGCATATCAA
DAOM239931 CTTAAGCATATCAA
DAOM239932 CTTAAGCATATCAA
CBS25855   CTTAAGCATATCAA
CBS12865   CTTAAGCATATCAA
CBS118889  CTTAAGCATATCAA
DAOM239913 CTTAAGCATATCAA
DAOM239912 CTTAAGCATATCAA
CBS24865   CTTAAGCATATCAA
DAOM239934 CTTAAGCATATCAA
DAOM239935 CTTAAGCATATCAA
DAOM239936 CTTAAGCATATCAA
DAOM239933 CTTAAGCATATCAA
DAOM239915 -----
DAOM239914 CTTAAGCATATCAA
DAOM239938 CTTAAGCATATCAA
DAOM239937 CTTAAGCATATCAA
KAS3469    CTTAAGCATATCAA
CBS229.60  CTTAAGCATATCAA
CBS23865   CTTAAGCATATCAA
KAS3463    CTTAAGCATATCAA
CBS238.68  CTTAAGCATATCAA
KAS3464    CTTAAGCATATCAA
KAS3466    CTTAAGCATATCAA
KAS3465    CTTAAGCATATCAA
NRRL3391   CTTAAGCATATCAA
AL1878     CTTAAGCATATCAA
AL1644     CTTA-----
AL1642     CTTAAGCATATCAA
AL1643     CTTAAGCATATCAA
CBS136.22  -----
CBS347.51  -----
CBS336.48  CTTAAGCATATCAA

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CBS110644 CTTAAGCATATCAA
 CBS42665 CTTAAGCATATCAA
 DAOM239916 CTTAAGCATATCAA
 NRRL705 CTTAAGCATATCAA

Multiple *Cox1* Sequence Alignment

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
KAS3191  --GATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239926 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239919 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239917 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239922 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239925 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239943 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
KAS3479  GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239941 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239942 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239944 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239940 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239945 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239946 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239939 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
NRRL2074 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
NRRL32583 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239930 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239931 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239932 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS25848  GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS12865  -TGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS118889 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239912 --GATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239913 --GATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
CBS24865  -----TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239934 --GATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239935 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239936 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239933 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239914 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239915 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGA
DAOM239938 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGGTTAATAGGT
DAOM239937 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGGTTAATAGGT
KAS3469  GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGAAC-CTGTATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
CBS229.60 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGGTTAATAGGG
CBS238.68 GTGATTTTATC-TTCAAATGCT-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGGTTAATAGGG
KAS3463  GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGT
CBS238.68 -----TTTTT-TTTTATGCA-AAAGAAA-TTGGTAC-ATTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGT
KAS3464  GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGT
KAS3466  GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATACCTAATGTTTTCATTATTTTCAGGATTAATAGGT
KAS3465  GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
NRRL3391 GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
AL1878  GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
AL1644  GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
AL1642  GTGATTTTATC-TTCTAATGCAAAAGATATTGGTAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
AL1643  GTGATTTTATC-TTCTAATGCA-AAAGATA-TTGGTAC-ATTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
CBS136.22 GTGATTTTATC-TTCAAATGCG-AAAGATA-TAGGTAC-TCTTTATTTAATGTTTTCATTATTTTCAGGGTTAATAGGT
CBS347.51 GTGATTTTATC-TTCAAATGCG-AAAGATA-TAGGTAC-TCTTTATTTAATGTTTTCATTATTTTCAGGGTTAATAGGT
CBS336.48 GTGATTTTATC-TTCAAATGCG-AAAGATA-TAGGTAC-TCTTTATTTAATGTTTTCATTATTTTCAGGGTTAATAGGT
CBS110644 GTGATTTTATC-TTCAAATGCG-AAAGATA-TAGGTAC-TCTTTATTTAATGTTTTCATTATTTTCAGGGTTAATAGGT
BS42665  GTGATTTTATC-TTCTAACGCA-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
DAOM239916 GTGATTTTATC-TTCTAATGCA-AAAGATA-TAGGTAC-ACTATATTTAATGTTTTCATTATTTTCAGGATTAATAGGT
NRRL705  GTGATTTTATC-TTCTAATGCT-AAAGATA-TTGGTAC-TCTATACCTAATGTTTTCATTATTTTCAGGGTTAATAGGA

[      81      91     101     111     121     131     141     151     ]
[      |      |      |      |      |      |      |      |      ]
KAS3191  ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCAGGAGTACAATATATATCAGATAATCAATTATATAAT
DAOM239926 ACAGCATTTTCAGTATTAAT-AAGATTAGAAT-TATCAGGTCAGGAGTACAATATATATCAGATAATCAATTATATAAT

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	161	171	181	191	201	211	221	231
KAS3191	AGTATAATAACAGCA	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239926	AGTATAATAACAGCA	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239919	AGTATAATAACAGCA	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239917	AGTATAATAACAGCA	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239922	AGTATAATAACAGCA	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239925	AGTATAATAACAGCA	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239943	AGTATAATAACAGCT	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
KAS3479	AGTATAATAACAGCT	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239941	AGTATAATAACAGCT	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239942	AGTATAATTACAGCA	--CACGCAATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239944	AGTATAATAACAGCT	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239940	AGTATAATAACAGCT	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239945	AGTATAATAACAGCT	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239946	AGTATAATAACAGCT	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
DAOM239939	AGTATAATAACAGCT	--CACGCTATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					
NRRL2074	AGTATAATTACAGCA	--CACGCAATATTAATGATATTCTTCATGGTAATG	--CCTGCATTAATCGGAGGTTTTGGTAATTT					

AL1644 AGTTTATT-TTTATTCATATTCTCAGCAAT-AATAGAAAATGGA--GCAGGAACAGGATGAACATTATATCCACCATTAT
 AL1642 AGTTTATT-TTTATTCATATTCTCAGCAAT-AATAGAAAATGGA--GCAGGAACAGGATGAACATTATATCCACCATTAT
 AL1643 AGTTTATT-TTTATTCATATTCTCAGCAAT-AATAGAAAATGGA--GCAGGAACAGGATGAACATTATATCCACCATTAT
 CBS136.22 AGTTTATT-TTTATTCATATTCTCAGCAAT-AATAGAAAATGGT--GCAGGAACAGGATGAACATTATATCCACCATTAT
 CBS347.51 AGTTTATT-TTTATTCATATTCTCAGCAAT-AATAGAAAATGGT--GCAGGAACAGGATGAACATTATATCCACCATTAT
 CBS336.48 AGTTTATT-TTTATTCATATTCTCAGCAAT-AATAGAAAATGGT--GCAGGAACAGGATGAACATTATATCCACCATTAT
 CBS110644 AGTTTATT-TTTATTCATATTCTCAGCAAT-AATAGAAAATGGT--GCAGGAACAGGATGAACATTATATCCACCATTAT
 CBS42665 AGTTTATT-TTTATTTATATTCTCAGCAAT-AATAGAAAATGGA--GCAGGAACAGGTTGAACATTATATCCACCATTGT
 DAOM239916 AGTTTATT-TTTATTTATATTCTCAGCAAT-AATAGAAAATGGA--GCAGGAACAGGTTGAACATTATATCCACCATTGT
 NRRL705 AGTTTATT-TTTATTTATATTCTCAGCAAC-AATAGAGAATGGA--GCAGGTACAGGATGAACATTATACCCACCATTAG

[	401	411	421	431	441	451	461	471	]
[									]
KAS3191	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239926	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239919	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239917	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239922	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239925	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239943	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
KAS3479	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239941	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239942	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239944	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239940	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239945	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239946	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239939	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
NRRL2074	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
NRRL32583	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239930	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239931	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239932	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS25848	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS12865	CTGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS118889	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239912	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239913	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
CBS24865	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239934	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239935	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239936	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239933	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239914	CAGGTATACAATCT-CATAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239915	CAGGTATACAATCT-CATAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239938	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239937	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
KAS3469	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGATTACATTTAAGTGGTATAAGTAGTATGT								
CBS229.60	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS238.68	CAGGTATACAATCT-CACAGTGGACC-TAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
KAS3463	CAGGAATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGCTTACATTTAAGTGGTATAAGTAGTATGT								
CBS238.68	CAGGAATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGCTTACATTTAAGTGGTATAAGTAGTATGT								
KAS3464	CAGGAATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGCTTACATTTAAGTGGTATAAGTAGTATGT								
KAS3466	CAGGAATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGCTTACATTTAAGTGGTATAAGTAGTATGT								
KAS3465	CAGGAATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGCTTACATTTAAGTGGTATAAGTAGTATGT								
NRRL3391	CAGGAATACAATCT-CACAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
AL1878	CAGGAATACAATCT-CACAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
AL1644	CAGGAATACAATCT-CACAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
AL1642	CAGGAATACAATCT-CACAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
AL1643	CAGGAATACAATCT-CACAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS136.22	CAGGTATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS347.51	CAGGTATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS336.48	CAGGTATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS110644	CAGGTATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
CBS42665	CAGGAATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
DAOM239916	CAGGAATACAATCT-CATAGTGGACC-AAGTGTAGATTAGCTATATTGGTTTACATTTAAGTGGTATAAGTAGTATGT								
NRRL705	CAGGTATACAATCT-CACAGTGGACC-AAGTGTAGATTAGCTATTTTGGTTTACACTTGAAGTGGTATAAGTAGTATGT								

[	481	491	501	511	521	531	541	551	]
[									]
KAS3191	TA-GGTGCTATTAATTTT-ATAACAATATATTAA---ATATGAGAAGTCCAGGTATACGTTTACATAAATTAGCTTTAT								

	561	571	581	591	601	
[						]
KAS3191	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239926	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239919	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239917	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239922	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239925	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATT---					
DAOM239943	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
KAS3479	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239941	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239942	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239944	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239940	TTG-G-ATGA-GCTGT-TATTA-TAACAGC-----					
DAOM239945	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT					
DAOM239946	TTG-G-ATGA-GCTGT-TATTA-TAACAGC-----					
DAOM239939	TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATT---					

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NRRL2074      TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
NRRL32583     TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
DAOM239930    TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
DAOM239931    TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
DAOM239932    TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
CBS25848      TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
CBS12865      TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
CBS118889     TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
DAOM239912    TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
DAOM239913    TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
CBS24865      TTG-G-ATGA-GCTGT-TATAA-TAACAGCTG--TATTATTATT
DAOM239934    TTTGGGATGA-GCTGT-TATTAATAACAGGC-----
DAOM239935    TTG-G-ATGA-GCTGT-TATAA-TAACAGATG--TATTATTATT
DAOM239936    TTG-G-ATGA-GCTGT-TATAA-TAACAGCTG--TATTATTATT
DAOM239933    TTG-G-ATGA-GCTGT-TATAA-TAACAGCTG--TATTATTATT
DAOM239914    TTG-G-ATGA-GCTGT-TATAA-TAACAGCTG--TATTATTATT
DAOM239915    TTG-G-ATGA-GCTGT-TATAA-TAACAGCTG--TATTATTATT
DAOM239938    TTG-G-ATGA-GCTGT-TATAA-TAACAGCTG--TATTATTATT
DAOM239937    TTG-G-ATGA-GCTGT-TATAA-TAACAGCTG--TATTATTATT
KAS3469       TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
CBS229.60     TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
CBS238.68     TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
KAS3463       TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
CBS238.68     TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
KAS3464       TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
KAS3466       TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
KAS3465       TTG-G-ATGA-GCTGT-TATTA-TAACAGCTG--TATTATTATT
NRRL3391      TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT
AL1878        TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT
AL1644        TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT
AL1642        TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT
AL1643        TTG-G-TTGA-GCTGT-AATAA-TTACAGCTG--TATTATTATT
CBS136.22     TTG-G-ATGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT
CBS347.51     TTG-G-ATGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT
CBS336.48     TTG-G-ATGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT
CBS110644     TTG-G-ATGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT
CBS42665      TTG-G-TTGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT
DAOM239916    TTG-G-TTGA-GCTGT-AATAA-TAACAGCTG--TATTATTATT
NRRL705       TTG-G-ATGA-GCTGT-AGTTA-TTACAGCTG--TATTATTATT

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Multiple *TEF1-α* Sequence Alignment

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
KAS3191    TCGG-CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
DAOM239926 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC-
DAOM239919 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC-
DAOM239917 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
DAOM239922 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCAACGCTCC-
DAOM239925 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
DAOM239943 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
KAS3479    -----CGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACT-----CGCTCC-
DAOM239941 T--G-CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACT-----CGCTCC-
DAOM239942 -----CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
DAOM239944 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
DAOM239940 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
DAOM239945 TC-GCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACT-----CGCTCC-
DAOM239946 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
DAOM239939 -----CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACTCCATCGCTCC-
NRRL2074   TCG-CCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAATCCCCTCGCTCC-
NRRL32583   TCG-CCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAATCCCCTCGCTCC-
DAOM239930 TCGG-CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAATCCCCTCGCTCC-
DAOM239931 TCGG-CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATCCCCTCGCTCC-
DAOM239932 -----CGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATCCCCTCGCTCC-
CBS25855    -----CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAAT-CCATCGCTCC-
CBS12865    TCGG-CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAAT-CCATCGCTCC-
CBS118889   TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTTCC-----AC--CAAT-CCATCGCTCC-
DAOM239912 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACC-CAATTCATCGATCC-

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DAOM239913 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACC-CAATTCATCGATCC-
 CBS24865 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCC-----AC--CAATTCATCGATCC-
 DAOM239934 T-G--CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATCCATCGATCC-
 DAOM239935 T-GG-CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATCCATCGATCC-
 DAOM239936 T-G-CCACGTCGATTCCGGCAAGTCCACCACCACCGGTAAAGCTCTC-----AC--CAATCCATCGATCC-
 DAOM239933 T-G--CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATCCATCGCTCCT-
 DAOM239914 TCG-CCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATTCATCGCTCC-
 DAOM239915 TCG--CCCCTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATTCATCGCTCC-
 DAOM239938 --GGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATTCATCGCTCCT-
 DAOM239937 T-GG-CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----AC--CAATTCATCGCTCCT-
 KAS3469 T-GG-CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTC-----ACC-AAGACCCATCGATCTT-
 CBS229.60 TAGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCCCGC-----CAATCCATCGATCC-
 CBS238.68 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCCCGC-----CAATCCATCGATCC-
 KAS3463 ACGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTTCAACCTCCTCCC-----CCCCCA---CCTTTCC-
 CBS238.68 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTTCAACCTCCTCCC-----CCCCCA---CCTTTCC-
 KAS3464 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTTCAACCTCCTCCC-----CCCCCA---CCTTTCC-
 KAS3466 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTTCAACCTCCTCCC-----CCCCCA---CCTTTCC-
 KAS3465 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTTCAACCTCCTCCC-----CCTTCCC-
 NRRL3391 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCTA-
 AL1878 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCTT-----ACATCCCTCTA-
 AL1644 -C-GCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCTA-
 AL1642 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCTA-
 AL1643 ----CACGTCGATTCCGGCAAGTCCACCACCACCGGT-AAGCTCCT-----ACATCCCTCTA-
 CBS347.51 ----CCACGTCGATTCCGGCAAGTCCACCACCACCTGGTAAAGTTCAACC--TTAACACCTTCCCGATTAGGTAGCCATG-
 CBS336.48 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCTGGT-AAGTTATTCAATCTTCACACCTTCCCGATTAGGTAGCCATG-
 CBS136.22 TCGGCCACGTCGATT-CCGGCAAGTCCACCACCACCTGGT-AAGTTTCAACC--TTCACACCTTCCCTGATTAGGTAGCCATG-
 CBS110644 TCGGCCACGTCGATTCCGGCAAGTCCACCACCACCTGGT-AAGTTATTAAATCTTCACACCTTCCCGTTAGGTAGCATG-
 NRRL705 TCGGCCTCGTCGATTCCGGCAAGTCCACCACCACCTGGT-AAGCACCCCTCCTCCATCCGTCCTCGCTCGCCATCGA-

	81	91	101	111	121	131	141	151	
[									]
[									]
KAS3191	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239926	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239919	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239917	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239922	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239925	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239943	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
KAS3479	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239941	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239942	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239944	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239940	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239945	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239946	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239939	TTCTCTCACTTCCATCGAACAACAT----	GACTGATTATCAATGCAGGTCACTTGATCTACAAGTGCGGTGGTATCGAC							
NRRL2074	TGCCTCACATCTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
NRRL32583	TGCCTCACATCTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239930	TGCCTCACATCTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239931	TGCCTCACATCTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239932	TGCCTCACATCTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
CBS25855	TTCCCTACATCTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
CBS12865	TTCCCTACATCTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
CBS118889	TTCCCTACATCTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239912	TTCTCT-ATTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239913	TTCTCT-ATTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
CBS24865	TTCTCTTTTCCATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239934	TTCTCT-----CAATTGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239935	TTCTCT-----CAATTGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239936	TTCTCT-----CAATTGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239933	TTCTCT-----CAATTGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239914	TTCTCT-----CTATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239915	TTCTCT-----CTATCGAACAACAT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239938	TTCTCTTTTCTTCTATCGAACAACATGT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
DAOM239937	TTCTCTTTTCTTCTATCGAACAACATGT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
KAS3469	TTCTCT-----ATATCGAACAACATGT----	GACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
CBS229.60	--TCTCTCTATACCGAACAACCC-----	AACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
CBS238.68	TTCTCTACTCATACCGAACAACCC-----	AACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
KAS3463	ATT-----CCATCGAACAACAG-----	AACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
CBS238.68	ATT-----CCATCGAACAACAG-----	AACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							
KAS3464	ATT-----CCATCGAACAACAG-----	AACTGATTATCAATAGGACACTTGATCTACAAGTGCGGTGGTATCGAC							

KAS3466 ATT-----CCATCGAACAACAG-----AAGTATTGATCAATTTAGGTCACCTGATCTACAAGTGTGGTGGTATCGAC
 KAS3465 ATC-----CCATCGAACAAC-----AAGTATTGATCAATTTAGGTCACCTGATCTACAAGTGTGGTGGTATCGAC
 NRRL3391 CCTTCCCATTCATCGAATAATAT-----AGCTGATTGATCAATTTAGGTCACCTGATCTACAAGTGTGGTGGTATCGAC
 AL1878 CCTTCCCATTCATCGAATAATAT-----AGCTGATTGATCAATTTAGGTCACCTGATCTACAAGTGTGGTGGTATCGAC
 AL1644 CCTTCCCATTCATCGAATAATAT-----AGCTGATTGATCAATTTAGGTCACCTGATCTACAAGTGTGGTGGTATCGAC
 AL1642 CCTTCCCATTCATCGAATAATAT-----AGCTGATTGATCAATTTAGGTCACCTGATCTACAAGTGTGGTGGTATCGAC
 AL1643 CCTTCCCATTCATCGAATAATAT-----AGCTGATTGATCAATTTAGGTCACCTGATCTACAAGTGTGGTGGTATCGAC
 CBS347.51 GT-----AAGTAAACAAGCATAACAGGTCACCTGATCTACAAGTGTGGTGGTATTGAC
 CBS336.48 GT-----AAGTAAACAAGCATAACAGGTCACCTGATCTACAAGTGTGGTGGTATTGAC
 CBS136.22 GGT-----AAGTAAACAAGCATAACAGGTCACCTGATCTACAAGTGTGGTGGTATTGAC
 CBS110644 GT-----AAGTAAACAAGCATAACAGGTCACCTGATCTACAAGTGTGGTGGTATTGAC
 NRRL705 GGTTCATCCTTCATCCGAATGACAAAATACTGATTCTCCCGA-CAGGTCACCTGATCTACAAGTGCAGTGGTATCGAC

[	161	171	181	191	201	211	221	231	]
[									]

KAS3191 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239926 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239919 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239917 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239922 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239925 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239943 TCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3479 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239941 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239942 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239944 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239940 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239945 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239946 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239939 TCTCGTACCATCGAGAAGTTCGAGA-----
 NRRL2074 TCTCGTACCATCGAGAAGTTCGAGA-----
 NRRL32583 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239930 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239931 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239932 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS25855 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS12865 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS118889 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239912 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239913 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS24865 TCTCGTACCATTGAGAAGTTCGAGA-----
 DAOM239934 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239935 ACTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239936 ACTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239933 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239914 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239915 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239938 TCTCGTACCATCGAGAAGTTCGAGA-----
 DAOM239937 TCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3469 ACTCGTACCATCGAGAAGTTCGAGA-----
 CBS229.60 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS238.68 TCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3463 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS238.68 TCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3464 TCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3466 TCTCGTACCATCGAGAAGTTCGAGA-----
 KAS3465 TCTCGTACCATCGAGAAGTTCGAGA-----
 NRRL3391 TCTCGTACCATCGAGAAGTTCGAGA-----
 AL1878 TCTCGTACCATCGAGAAGTTCGAGA-----
 AL1644 TCTCGTACCATCGAGAAGTTCGAGA-----
 AL1642 TCTCGTACCATCGAGAAGTTCGAGA-----
 AL1643 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS347.51 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS336.48 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS136.22 TCTCGTACCATCGAGAAGTTCGAGA-----
 CBS110644 TCTCGTACCATCGAGAAGTTCGAGA-----
 NRRL705 TCTCGTACCATCGAGAAGTTCGAGAAGGTACGGAATCACAATTTTACTGCCCCCTCCTTGAGTGGGGTGGGGTCGTTCT

[	241	251	261	271	281	291	301	311	]
[									]

KAS3191 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTTCGCA-CC

DAOM239926 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239919 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239917 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239922 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239925 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCG-CC
 DAOM239943 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCACCC
 KAS3479 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239941 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239942 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239944 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239940 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239945 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239946 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239939 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 NRRL2074 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA--C
 NRRL32583 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA--C
 DAOM239930 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA--C
 DAOM239931 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA--C
 DAOM239932 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA--C
 CBS25855 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 CBS12865 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGATCGCA-CC
 CBS118889 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 DAOM239912 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCACCA
 DAOM239913 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCACCA
 CBS24865 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCACGA
 DAOM239934 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGTTTGCA-CC
 DAOM239935 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGTTTGCC-CC
 DAOM239936 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGTTTGCC-CC
 DAOM239933 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGTTTGCC-CC
 DAOM239914 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CT
 DAOM239915 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CT
 DAOM239938 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCT-TC
 DAOM239937 -----AGGAGGCTGCTGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCT-TC
 KAS3469 -----AGGAGGCTGCCGAGCTCGGCAAGGGTTCCTTCAAGGTACGGTCGCA-CC
 CBS229.60 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCAAGGTACGGTCCCA-TG
 CBS238.68 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCAAGGTACGGTCCCA-TG
 KAS3463 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 CBS238.68 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 KAS3464 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 KAS3466 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 KAS3465 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 NRRL3391 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 AL1878 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 AL1644 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 AL1642 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 AL1643 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 CBS347.51 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 CBS336.48 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 CBS136.22 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 CBS110644 -----AGGAGGCTGCTGAGCTCGGTAAGGGTTCCTTCA-----
 NRRL705 CTCGCCTTGGAACATTGTGCTAACCCCTCACAGGAAGCCGTGAGCTCGGCAAGGGTTCCTTCA-----

[	321	331	341	351	361	371	381	391	]
[									]

KAS3191 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTGTAGTACGCTTGGGTTCTTGA
 DAOM239926 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGA
 DAOM239919 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGA
 DAOM239917 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTGTAGTACGCTTGGGTTCTTGA
 DAOM239922 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGA
 DAOM239925 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGA
 DAOM239943 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTATAGTACGCTTGGGTTCTTGA
 KAS3479 CCACAACCAATGTG-----AAAATTCTGAAGTGGGTC---AACTGACATCTGTCTTATAGTACGCTTGGGTTCTTGA
 DAOM239941 CCACAACCAATGTG-----AAAATTCTGAAGTGGGTC---AACTGACATCTGTCTTATAGTACGCTTGGGTTCTTGA
 DAOM239942 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTGTATAGTACGCTTGGGTTCTTGA
 DAOM239944 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTGTATAGTACGCTTGGGTTCTTGA
 DAOM239940 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTGTATAGTACGCTTGGGTTCTTGA
 DAOM239945 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGA
 DAOM239946 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTGTATAGTACGCTTGGGTTCTTGA
 DAOM239939 CCACAACCCATGTG-----AAAATTCTGAAGTGGGTC---AACTAACATCTGTCTGTATAGTACGCTTGGGTTCTTGA
 NRRL2074 CACAACACTCAAAGTG--AAAAATTTTCAAAGTGATCAGCGAACTAACATCT--ACAATAGTACGCTTGGGTTCTTGA
 NRRL32583 CACAACACTCAAAGTG--AAAAATTTTCAAAGTGATCAGCGAACTAACATCT--ACAATAGTACGCTTGGGTTCTTGA

DAOM239930 CACAACACTCCAAGTG--AAAAAATTTTCAAAGTGGATCAGCGAACTAACATCC--ACAATAGTACGCTTGGGTTCTTGA
 DAOM239931 CACAACACCCCAAGTGAAAAAATTTTCAAAGTGGATCAGTCAACTAACATCT--ACAATAGTACGCTTGGGTTCTTGA
 DAOM239932 CACAACACCCCAAGTGAAAAAATTTTCAAAGTGGATCAGTCAACTAACATCT--ACAATAGTACGCTTGGGTTCTTGA
 CBS25855 -----AAGTG--AAAATTTTCAAAGTGGATCAAGCAACTAACATCT--TCAATAGTACGCTTGGGTTCTTGA
 CBS12865 -----AAGTG--AAAAAATTTTCAAAGTGGATCAATCAACTAACATTT--TCAATAGTACGCTTGGGTTCTTGA
 CBS118889 -----AAGTG--AAAAAATCTTCAAAGTGGATCAATCAACTAACATCT--TCAATAGTACGCTTGGGTTCTTGA
 DAOM239912 TTACAAATTTTCAC-----AAGTCTCTTAAAGTGGATC-----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTGA
 DAOM239913 TTACAAATTTTCAC-----AAGTCTCTTAAAGTGGATC-----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTGA
 CBS24865 TAACAAATCTGAA-----ATCTCTTCGAAGTGGATC-----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTGA
 DAOM239934 ATATAACAGAAAAA-----AAATCTGTGATGCGGATC-----AACTAACATCT--CCCCACAGTACGCTTGGGTTCTTGA
 DAOM239935 ATATAACAGAAAAAGA-----AAACCTGTGATGCGGATC-----AACTAACATCT--CCCCACAGTACGCTTGGGTTCTTGA
 DAOM239936 ATATAACAGAAAAAGA-----AAACCTGTGATGCGGATC-----AACTAACATCT--CCCCACAGTACGCTTGGGTTCTTGA
 DAOM239933 ATATAACAGAAAAA-A-----AAATCTGTGATGCGGATC-----AACTAACATCT--CCCCACAGTACGCTTGGGTTCTTGA
 DAOM239914 GCACAAATACAACCTG-----AAATCTGTGATGCGGATC-----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTGA
 DAOM239915 GCACAAATACAACCTG-----AAATCTGTGATGCGGATC-----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTGA
 DAOM239938 ATACCAACACAATCTG-----AATTCTCTGAATGGATC-----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTGA
 DAOM239937 ATACCAACACAATCTG-----AATTCTCTGAATGGATC-----AACTAACATCT--CCAATAGTACGCTTGGGTTCTTGA
 KAS3469 AGATACATACTACCTG-----AAGTGGATC-----GACTAACATCC--TCAATAGTACGCTTGGGTTCTTGA
 CBS229.60 AACTATATCTTACACACTCAATATGAAGCAACTAACATT-----CGCATTAGTACGCTTGGGTTCTTGA
 CBS238.68 AACTATCTCTTACACACTCAATAAGAAGCAACTAACATT-----CGCATTAGTACGCTTGGGTTCTTGA
 KAS3463 -----AGTACGCTTGGGTTCTTGA
 CBS238.68 -----AGTACGCTTGGGTTCTTGA
 KAS3464 -----AGTACGCTTGGGTTCTTGA
 KAS3466 -----AGTACGCTTGGGTTCTTGA
 KAS3465 -----AGTACGCTTGGGTTCTTGA
 NRRL3391 -----AGTACGCTTGGGTTCTTGA
 AL1878 -----AGTACGCTTGGGTTCTTGA
 AL1644 -----AGTACGCTTGGGTTCTTGA
 AL1642 -----AGTACGCTTGGGTTCTTGA
 AL1643 -----AGTACGCTTGGGTTCTTGA
 CBS347.51 -----AGTACGCTTGGGTTCTTGA
 CBS336.48 -----AGTACGCTTGGGTTCTTGA
 CBS136.22 -----AGTACGCTTGGGTTCTTGA
 CBS110644 -----AGTACGCTTGGGTTCTTGA
 NRRL705 -----AGTACGCTTGGGTTCTTGA

	401	411	421	431	441	451	461	471
[								
[								
KAS3191	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239926	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239919	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239917	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239922	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239925	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239943	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
KAS3479	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239941	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239942	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239944	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239940	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239945	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239946	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239939	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
NRRL2074	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
NRRL32583	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239930	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239931	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239932	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
CBS25855	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
CBS12865	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
CBS118889	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239912	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239913	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
CBS24865	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239934	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239935	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239936	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239933	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239914	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239915	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							
DAOM239938	CAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACCATCGACATTGCCCTCTGGAAGTTCCAGACTGCCAAGTATGAGGTCA							

CBS136.22 ACCGTCATC-----
CBS110644 CCGTCATC-----
NRRL705 CCGTCATTGGTAAGAATTATCCC-ACCCACCATCTTCTCCCATCCATCATGGACTCTCTGACTGACTCTTC--CTCCTC

[illegible]

	641	651	661	671	681	691	701	711
KAS3191	GCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCCCTTCTGGCTTTTACCCT							
DAOM239926	GCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCCCTTCTGGCTTTTACCCT							
DAOM239919	GCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCCCTTCTGGCTTTTACCCT							
DAOM239917	GCCTCCGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCCCTTCTGGCTTTTACCCT							
DAOM239922	GCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCCCTTCTGGCTTTTACCCT							
DAOM239925	GCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCCCTTCTGGCTTTTACCCT							
DAOM239943	GCCTCCGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCTCTTCTGGCTTTTACCCT							
KAS3479	GCCTCCGGWACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCTCTTCTGGCTTTTACCCT							
DAOM239941	GCCTCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCTCTTCTGGCTTTTACCCT							
DAOM239942	GCCTCCGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCAGCTCTTCTGGCTTTTACCCT							

DAOM239934 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTTGCTAATGCCTTGATATTACGTA
 DAOM239935 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTTGCTAATGCCTTGATATTACGTA
 DAOM239936 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTTGCTAATGCCTTGATATTACGTA
 DAOM239933 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTTGCTAATGCCTTGATATTACGTA
 DAOM239914 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTAAAGTCTACAATGCCTTTATGTCACGCT
 DAOM239915 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTAAAGTCTACAATGCCTTTATGTCACGCT
 DAOM239938 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTAAAGTCTACAATGTCTTTGTGTCACACT
 DAOM239937 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTAAAGTCTACAATGTCTTTGTGTCACACT
 KAS3469 CGGTGTCCGTCAGCTGATCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTCGTGATTACAATACCTTACGATA
 CBS229.60 TGGTGTCCGCCAGCTGATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
 CBS238.68 CGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
 KAS3463 TGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGACGGACACCTGCAAGT-----
 CBS238.68 TGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGACACCTGCAAGT-----
 KAS3464 TGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGACACCTGCAAGT-----
 KAS3466 TGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGACACCTGCAAGT-----
 KAS3465 TGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
 NRRL3391 CGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
 AL1878 CGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
 AL1644 CGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
 AL1642 CGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
 AL1643 CGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGATACTTGCAAGT-----
 CBS347.51 CGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT-----
 CBS336.48 CGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT-----
 CBS136.22 TCGGTGTCCGCCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGCAAGT-----
 CBS110644 CGGTGTCCGCCAGCTCATCGTTGCCCTGAACAAGATGGACACTTGCAAGT-----
 NRRL705 CGGTGTCCGTCAGCTCATTGTTGCCCTGAACAAGATGGACACTTGCAAGT-----

	801	811	821	831	841	851	861	871	
[									]
[									]
KAS3191	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239926	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239919	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239917	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239922	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239925	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239943	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
KAS3479	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239941	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239942	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239944	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239940	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239945	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239946	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
DAOM239939	-----	-----	-----	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG		
NRRL2074	ATC-----	-----	-----	CCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTG					
NRRL32583	ATC-----	-----	-----	CCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTG					
DAOM239930	ATC-----	-----	-----	CCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTG					
DAOM239931	ATC-----	-----	-----	CCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTG					
DAOM239932	ATC-----	-----	-----	CCAGAAACAATTGACTAACAACCCCAACAGGAGCGAGGACCGTTACAACGAGATTG					
CBS25855	TTAACTT-----	-----	-----	GGTTACTAATACTATCAACAGGAGCGAGGACCGTTACAACGAGATTG					
CBS12865	TTAACTT-----	-----	-----	GCTTACTAATACTATCAACAGGAGCGAGGACCGTTACAACGAGATTG					
CBS118889	CTTAACT-----	-----	-----	TTGTTACTAATACTATCAACAGGAGCGAGGACCGTTACAACGAGATTG					
DAOM239912	-----	-----	-----	TCAACCAACAAATACTAATTACCTAAACAGGAGCGAGGACCGTTACAACGAGATTG					
DAOM239913	-----	-----	-----	TCAACCAACAAATACTAATTACCTAAACAGGAGCGAGGACCGTTACAACGAGATTG					
CBS24865	-----	-----	-----	TCAAGCAACACTTACTAAGTAAACAGGAGCGAGGACCGTTACAACGAGATTG					
DAOM239934	ATCTTTG-GGATTATGTAATAAATAAACCACCATCTACTAACCATCTATACAGGTCCGAGGACCGTTACAACGAGATTG								
DAOM239935	ATCTTCG-GGATTATGTAATATATTACCCAACCATCTACTAACCATCTATACAGGTCCGAGGACCGTTACAACGAGATTG								
DAOM239936	ATCTTCG-GGATTATGTAATATATTACCCAACCATCTACTAACCATCTATACAGGTCCGAGGACCGTTACAACGAGATTG								
DAOM239933	ATCTTTG-GGATTATGTAATAAATAAACCACCATCTACTAACCATCTATACAGGTCCGAGGACCGTTACAACGAGATTG								
DAOM239914	TTATATC-----	ACGTGATGTATCCGCCCAACATATACTAACCATCTATACAGGTCCGAGGACCGTTACAACGAGATTG							
DAOM239915	TTATATC-----	ACGTGATGTATCCGCCCAACATATACTAACCATCTATACAGGTCCGAGGACCGTTACAACGAGATTG							
DAOM239938	TTGTGCTTTCTGTGACAGTGATCCCCACCAACATATACTAACCATCTATACAGGTCCGAGGACCGTTACAACGAGATTG								
DAOM239937	TTGTGCTTTCTGTGACAGTGATCCCCACCAACATATACTAACCATCTATACAGGTCCGAGGACCGTTACAACGAGATTG								
KAS3469	GCTCATC-GTCAC-----	-----	-----	GTGACATCGCGAACTAATCTTCTATACAGGTCCGAGGACCGTTACAACGAGATTG					
CBS229.60	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG					
CBS238.68	-----	-----	-----	GGAGCGAGGACCGTTACAACGAGATTG					
KAS3463	-----	-----	-----	GGGCTGAGGAGCGTTACAACGAGATTG					
CBS238.68	-----	-----	-----	GGGCTGAGGAGCGTTACAACGAGATTG					
KAS3464	-----	-----	-----	GGGCTGAGGAGCGTTACAACGAGATTG					
KAS3466	-----	-----	-----	GGGCTGAGGAGCGTTACAACGAGATTG					
KAS3465	-----	-----	-----	GGGCTGAGGAGCGTTACAACGAGATTG					

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NRRL3391 -----GGGCTGAGGAGCGTTACAACGAGATTG
AL1878 -----GGGCTGAGGAGCGTTACAACGAGATTG
AL1644 -----GGGCTGAGGAGCGTTACAACGAGATTG
AL1642 -----GGGCTGAGGAGCGTTACAACGAGATTG
AL1643 -----GGGCTGAGGAGCGTTACAACGAGATTG
CBS347.51 -----GGTCCGAGGACCGTTACAACGAGATTG
CBS336.48 -----GGTCCGAGGACCGTTACAACGAGATTG
CBS136.22 -----GGTCCGAGGACCGTTACAACGAGATTG
CBS110644 -----GGTCCGAGGACCGTTACAACGAGATTG
NRRL705 -----GGTCTGAGGACCGCTACAACGAGATCG

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[      881      891      901      911      921      931      941      951      ]
[      |      |      |      |      |      |      |      |      ]
KAS3191  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239926 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239919 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239917 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239922 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239925 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239943 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCCACCATCTCCGG-TTCAA
KAS3479  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239941 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
DAOM239942 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
DAOM239944 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
DAOM239940 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
DAOM239945 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239946 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239939 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
NRRL2074 TCAAGGAGACCTCCAACCTTCATCAAGAAGGCCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
NRRL32583 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239930 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
DAOM239931 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
DAOM239932 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
CBS25855 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
CBS12865 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
CBS118889 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239912 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
DAOM239913 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAA
CBS24865 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTAC-----AA
DAOM239934 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGCTTCAA
DAOM239935 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGCTTCAA
DAOM239936 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-CTCAA
DAOM239933 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTCAA
DAOM239914 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTCAA
DAOM239915 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTCAA
DAOM239938 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
DAOM239937 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAA
KAS3469  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTCAA
CBS229.60 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGCTTCAA
CBS238.68 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGCTTCAA
KAS3463  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGGGTGTCCCTTCGTTC-CCATCTCCGGTTTCAA
CBS238.68 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGGGTGTCCCTTCGTTC-CCATCTCCGG-TTCAA
KAS3464  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGGGTGTCCCTTCGTTC-CCATCTCCGG-TTCAA
KAS3466  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGGGT-TCCCTTCGTTC-CCATCTCCGG-TTCAA
KAS3465  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGGGTGTCCCTTCGTTC-CCATCTCCGG-TTCAA
NRRL3391 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAA
AL1878  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAA
AL1644  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAA
AL1642  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAA
AL1643  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAA
CBS347.51 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTTC-CTATCTCCGGTTTCAA
CBS336.48 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTTC-CTATCTCCGGTTTCAA
CBS136.22 ATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTTCCTATCTCCGGTTTCAAC-GGTGACAACATGCTCGAGC
CBS110644 TCAAGGAGACCTCCAACCTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTTC-CCATCTCCGGTTTCAA
NRRL705  TCAAGGAGACCTCCAACCTTCATCAAGAAGGTTGGCTACAACCCCAAGACCGTTCCCTTCGTTC-CCATCTCCGGCTTCAA

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[      961      971      981      991      1001      ]
[      |      |      |      |      |      ]
KAS3191  C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTTGGTACAAGG
DAOM239926 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTTGGTACAAGG
DAOM239919 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTTGGTACAAGG

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DAOM239917 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 DAOM239922 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 DAOM239925 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 DAOM239943 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAG-
 KAS3479 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 DAOM239941 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 DAOM239942 C-GGTGACAACATGCTTGAGGCCTCCCCC-----
 DAOM239944 C-GGTGACAACAT-----
 DAOM239940 C-GGTGACAACATGCT-----
 DAOM239945 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTAC-AGG
 DAOM239946 C-GGTGACAACATGCTTGAGGCCTCCCCCAACTGCCCTGGTACAAGG
 DAOM239939 C-GGTGACAACATGCTTGAGG-----
 NRRL2074 C-GGTGACAACATGCTTGAGGCCCCCCCC-AACTGCCCT-----
 NRRL32583 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACA--G
 DAOM239930 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACA-GG
 DAOM239931 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTG-CCCTGGTACA-GG
 DAOM239932 C-GGTGACAACATGC-TGAGT-CCCCC-----
 CBS25855 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 CBS12865 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACA-GG
 CBS118889 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGC
 DAOM239912 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 DAOM239913 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 CBS24865 C-----
 DAOM239934 C-GGTGACAACATGCTTGAGGCCTCCCCC--ACTGCCCTGG-ACAAGG
 DAOM239935 C-GGTGACAACATGCTTGAGGCCTCCCC--ACTGCCCTGGTACA-GG
 DAOM239936 C-GGTGACAACATGCTTGAGGCCTCCCC--ACTGCCCTGG-ACA-G-
 DAOM239933 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACA-GG
 DAOM239914 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTAAA-GG
 DAOM239915 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGG-ACA-GG
 DAOM239938 C-GGTGACAACATGCT-GAGGCCTCCCCC-AACTGCCCTGGTACA-G-
 DAOM239937 C-GGTGACAACATGCTTGAGGCCTCCCC--ACTG-CCCTGGTACA-G-
 KAS3469 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACA-G-
 CBS229.60 C-GGTGACAACATGCTTGAGGCCTCCACC-AACTGCCCTGGTACAAGG
 CBS238.68 C-GGTGACAACATGCTTGAGGCCTCCACCAACTGCCCTGGTACAAGG
 KAS3463 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGG-----
 CBS238.68 C-GGCGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 KAS3464 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACA-GG
 KAS3466 C-GGTGACAACATGCT-GAGGCCTCCCCC-AACTGCCCTGG-ACAAG-
 KAS3465 C-GGTGACAACATGCTTGAGGCCTCCCCC-AACTGCCCTGGTACAAGG
 NRRL3391 C-GGTGACAACATGCTGGAGCCCTCCTCC-AACTGCCCTGGTACAAG-
 AL1878 C-GGTGACAACATGCTGGAGCCCTCCTCC-AACTGCCCTGGTACAAG-
 AL1644 C-GGTGACAACATGCTGGAGCCCTCCTCC-AACTGCCCTGGTACAAGG
 AL1642 C-GGTGACAACATGCTGGAGCCCTCCTCC-AACTGCCCTGGTACAAG-
 AL1643 C-GGTGACAACATGCTGGAGCCCTCCTCC-AACTGCCCTGGTACAAGG
 CBS347.51 C-GGTGACAACATGCTCGAGCCCTCCCCCT-AACTGCCCTGGTACAAGG
 CBS336.48 C-GGTGACAACATGCTCGAGCCCTCCCCCT-AACTGCCCTGGTACAAGG
 CBS136.22 CCTCCCCCT-AACTGCCCTGGTACAAGG-----
 CBS110644 C-GGTGACAACATGCTCGAGCCCTCCCCCT-AACTGCCCTGGTACAAGG
 NRRL705 C-GGTGACAACATGCTCGAGCCCTCCCCC-AACTGCCCTGGTACA--G

Multiple CaM Sequence Alignment

	1	11	21	31	41	51	61	71	
[									]
[									]
KAS3191	CCTTCTCCCT	-C-TTTGTAAGT	--ACTCCA-A-CACGTCGATTG	-----	GAAGATCT	-GTA	ACT-GGATTT	-GATG	
DAOM239926	CCTTCTCCCT	-C-TTTGTAAGT	--ACTCCA-A-CACGTCGATTG	-----	GAAGATCT	-GTA	ACT-GGATTT	-GATG	
DAOM239919	-----	-----	ACTCCA-A-CACGTCGATTG	-----	GAAGATCT	-GTA	ACT-GGATTT	-GATG	
DAOM239917	CCTTCTCCCT	-C-TTTGTAAGT	--ACTCCA-A-CACGTCGATTG	-----	GAAGATCT	-GTA	ACT-GGATTT	-AATG	
DAOM239922	CCTTCTCCCT	-C-TTCGTAAGT	--ACTCCA-A-CACGTCGATTG	-----	GAAGATCT	-GTA	ACT-GGATTT	-CGATG	
DAOM239925	CCTTCTCCCT	-C-TTTGTAAGT	--ACTCCA-A-CACGTCGATTG	-----	GAAGATCT	-GTA	ACT-GGATTT	-AATG	
DAOM239943	CCTTCTCCCT	-C-TTTGTAAGT	--GCTCC-A-CGCGTCGATTG	-----	GAAGATTT	-GTA	ACT-GGATTT	-AATG	
KAS3479	CCTTCTCCCT	-C-TTTGTAAGT	--ACTCCC-A-CGCGTCGATTG	-----	AAACCCCTC	-GTG	ACT-GGATTT	-AATG	
DAOM239941	CCTTCTCCCT	-C-TTTGTAAGT	--ACTCCC-A-CGCGTCGATTG	-----	GAAGATCT	-GTG	GCC-GAATTT	-AATG	
DAOM239942	CCTTCTCCCT	-C-TTTGTAAGT	--GCTCCC-A-CGCGTCGATTG	-----	GAAGATTT	-GTA	ACT-GGATTT	-AATG	
DAOM239944	CCTTCTCCCT	-C-TTTGTAAGT	--ACTCCC-A-CGCGTCGATTG	-----	GAAGATCT	-GTG	ATC-GAATTT	-AATG	
DAOM239940	CCTTCTCCCT	-C-TTTGTAAGT	--GCTCCC-A-CGCGTCGATTG	-----	GAAGATTT	-GTA	ACT-GGATTT	-AATG	
DAOM239945	CCTTCTCCCT	-C-TTGTAAAGT	--ACTCCC---CCCGTCGATTG	-----	GAAGATGCTAGGCC	-GAG	TTT-AATT		
DAOM239946	-----	T-C-TTGTAAAGT	--GCTACCG--CGCGTCGATTG	-----	GAGATT---	TG	TACT-GGATTT	-AAT-	

DAOM239939 CCTTCTCCCT-C-TTTGTAAGT--GCTCCC-A-CGCGTCGATTG-----GAAGATTT-GTAACT-GGATTT-AATG
 NRRL2074 -----C-TTTGTAAGT--ACTTCC-A-CGCGTCGATTG-----AAACCCCTC-GTGACT-GGATTT-AATG
 NRRL32583 CCTTCTCCCT-C-TTTGTAAGT--ACTCCC-A-CGCGTCGATTG-----AAACCCCTC-GTGACT-GGATTT-AATG
 DAOM239931 CCTTCTCCCTC-TTTGTAAGT--ACTCTC-A-CGCGTCGATTG-----AAACCCCTC-GTGACT-GGATTT-AATG
 DSOM239932 -----TCCCTCT-TTTGTAAGTAAATTCTC-A-CGCGTCGATTG-----AA-CCCTCGGTGTCT-GGATTT-AATG
 DAOM239930 CCTTCTCCCT-C-TTTGTAAGT--ACTCCC-A-CGCGTCGATTG-----AAACCCCTC-GTGACT-GGATTT-AATG
 CBS25855 CTTTCCCTC-----TTGTAAGT--ACTCCT-A-CGCGTCGATTG-----AAACCCCTC-GTGGTT-GGATTT-AATG
 CBS12865 -----GTAAGT--ACTCCT-A-CGCGTCGATTG-----AAACCCCTC-GAGGTT-GGATTT-AATG
 CBS118889 CCTTCTCCCT-C-TTTGTAAGT--ACTCCT-A-CGCGTCGATTG-----AAACCCCTC-GTGACT-GGATTT-AATG
 DAOM239912 -CTTCTCCCT-C-TTTGTAAGT--GCCCC-A-CGCGTCGATTG-----AAGACTC---ACT-GGATTT-AATG
 DAOM239913 CCTTCTCCCT-C-TTTGTAAGT--GCCCC-A-CGCGTCGATTG-----GAAGACTC-GTGACT-GGATTT-AATG
 CBS24865 CCTTCTCCCT-C-TTTGTAAGT--GCTCCC-A-CGCGTCGATTG-----AAGACC---AAATCT-GGATTT-AATG
 DAOM239934 CCTTCTCTCTC-TTTGT-AGT--AACCCC-A-CGCGTCGATTG-----GAAGTGTC-GTGACT-GGATTT-AATG
 DAOM239935 -----ACCCCC-A-CGCGTCGATTG-----GAAGTGTC-GTGACT-GGATTT-AATG
 DAOM239936 CCTTCTCCCT-C-TTTGTAAGT--ATCCCC-A-CGCGTCGATTG-----G-AGTGTC-GTGACT-GGATTT-AATG
 DAOM239933 GCCTCTCTCT-C--TTGTAAGT--ACCCCC-A-CGCGTCGATTG-----CAGTAGTC-GTGCTT-GGATTT-AATG
 DAOM239914 CCTTCTCCCT-C-TTTGTAAGT--ACCCCC-A-CGCGTCGATTG-----GAACAGTC-ATGACT-GGATTT-AATG
 DAOM239915 CCTTCTCCCT-C-TTTGTAAGT--ACCCCC-A-CGCGTCGATTG-----GGACAGTC-ATGACC-GGATTT-AATG
 CBS110644 CCTTCTCCCT-C-TTTGTAAGT--GCACCA---T-CGTGATTG-----GAAGATTC-GTGACT-GGATTT-AATG
 DAOM239937 CCTTCTCCCT-C-TTTGTAAGT--GCTC-C-A-TGCGTCGATTG-----GAAGATTC-GTGACT-GGATTT-AATG
 CBS229.60 CCTTCTCCCT-T-TTCGTAAGT--GTCCCG-A-CGTGTCGATTG-----AAGACC-C-ATGACT-GGATTT-ATA
 CBS238.68 -CTTCTCCCT-T-TTCGTAAGT--GTCCCG-A-CGTGTCGATTG-----AAGACC-C-ATGACT-GGATTT-ATA
 NRRL3447 CATTTCCCTGTTTGTGAGT--GCCCG-ATTTTCGTTGATTG-----GAAAAAAAAGCGTCG-CCTGGAATC-AACA
 AL1878 CATTTCCCT-G-TTTGTGAGT--GCCG-G-ATTTTCGTTGATTG-----G-AAAAAAAAGCGTCG-CCTGGAATC-AACA
 AL1644 CATTTCCCT-G-TTTGTGAGT--GCCG-G-ATTTTCGTTGATTG-----G-AAAAAAAAGCGTCG-CCTGGAATC-AACA
 AL1642 CATTTCCCT-G-TTTGTGAGT--GCCG-G-ATTTTCGTTGATTG-----G-AAAAAAAAGCGTCG-CCTGGAATC-AACA
 AL1643 CATTTCCCTGTTTGTGAGT--GCCCG-ATTTTCGTTGATTG-----GAAAAAAAAGCGTCG-CCTGGAATC-AACA
 CBS136.22 -----AGT---CTTC-GA-TCTTTC--ATT-----AATGCCGT-GGTTC-AAAATTC-AATA
 CBS347.51 CCTTCTCCTT-G-TTTGTAAGT--TCTTC-GA-TCTTTCATTG-----AATGCCGT-GGTTC-AAAATTC-AATA
 CBS336.48 CCTTCTCCTT-G-TTTGTAAGT--TTATA-GA-TCTTTCATTG-----CATACTGT-GTTTTCAAATTC-AATA
 CBS110644 CCTTCTCCTT-G-TTTGTAAGT--TCATA-GA-TCTTTCATTG-----GATACTGT-GTTTT-AAAATTC-AATA
 CBS42665 CCTTCTCCCT-G-TTTGTGAGT--ATTCT--A-TTCGTTGATTG-----AGAAAGAAAAGAGTTGCCTAGAAACC-AAGA
 DAOM239916 CCTTCTCCCT-G-TTTGTGAGT--ATTCT--ATTCCGTTGATTGTGAAAAGAAAAAAATGTTGCCTAGAAACC-AAGA
 NRRL705 CCTTCTCCT--G--TTGTGAGT--GCCTCAGA-CGCGTCGATTG-----ACAACTCCTCGATCGGAAAACAGTAGA

	81	91	101	111	121	131	141	151	
[									]
[									]
KAS3191	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239926	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239919	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239917	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239922	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239925	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239943	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
KAS3479	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239941	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239942	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239944	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239940	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGACCGTCGGCGA	---	T			
DAOM239945	GAGATGGATATCG	-----TTCTG--CGG-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGAACGTCGGCGA	---	T			
DAOM239946	CTGATGGATATGTCTCCGTCTCC	-----GGC-GACAGAGA-CAA-GGATAGTT	---	GATGGTTAGTGCGAACGTCGGCGA	---	T			
DAOM239939	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGC	---	GATGGTTAGTGCGAACGTCGGCGA	---	T			
NRRL2074	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	T			
NRRL32583	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	T			
DAOM239931	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	TT			
DSOM239932	CTGAAGGATATGT	-----TCTCC--GGC-AATAGAGA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	TT			
DAOM239930	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---				
CBS25855	CTGATGGATATGT	-----TCTGC--GGC-AATAG-GA-CAAGGGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	TT			
CBS12865	CTGATGGATATGT	-----TTTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	TT			
CBS118889	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	T			
DAOM239912	CTGATGGATATGT	-----TCTCC--GGC-GATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	TT			
DAOM239913	CTGATGGATATGT	-----TCTCC--GGC-GATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	TT			
CBS24865	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA	---	T			
DAOM239934	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGATTTT					
DAOM239935	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGATTTT					
DAOM239936	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGATTTT					
DAOM239933	CTGATGGATATGTC	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GAT-GTTAGTGCGAACGTCGGCCG-ATT					
DAOM239914	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGATTTT					
DAOM239915	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGATTTT					
DAOM239938	CTGATGGATATGT	-----TCTCC--GGCAAATAG-GA-CAA-GGATGGT	---	GATGGTTAGTGCGAACGTCGGCGA-TTT					
DAOM239937	CTGATGGATATGT	-----TCTCC--GGC-AATAG-GA-CAA-GG-TGGC	---	GATGGTTAGTGCGAACGTCGGCGATTTT					

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CBS229.60 CTGATAAATACGT-----TCTGC--TTC-AATAG-GA-CAA-GGACGGC---GATGGTGAGTGCGACCGCTCTGCGA---T
CBS238.68 CTGATAAATACGT-----TCTGC--TTC-AATAG-GA-CAA-GGACGGC---GATGGTGAGTGCGACCGCTCTGCGA---T
NRRL3447 CTAATGGATGCTT-----TTTCCCGGGA--AATAG-GA-CAA-GGATGGC---GATGGTGAGTGCGATCGTACTCGG---G
AL1878 CTAATGGATGCTT-----TTTCCCGGGA--AATAG-GA-CAA-GGATGGC---GATGGTGAGTGCGATCGTACTCGG---G
AL1644 CTAATGGATGCTT-----TTTCCCGGGA--AATAG-GA-CAA-GGATGGC---GATGGTGAGTGCGATCGTACTCGG---G
AL1642 CTAATGGATGCTT-----TTTCCCGGGA--AATAG-GA-CAA-GGATGGC---GATGGTGAGTGCGATCGTACTCGG---G
AL1643 CTAATGGATGCTT-----TTTCCCGGGA--AATAG-GA-CAAAGGATGGC---GATGGTGAGTGCGATCGTACTCGG---G
CBS136.22 CTAATGGATA-----TTCGT--CAT-AATAA-GGACAAAGGATGGC---GATGGTGAGTGCGACCGTTACCGA-----
CBS347.51 CTAATGGATA-----TTCGT--CAT-AATAG-GA-CAA-GGATGGC---GATGGTGAGTGCGACCGTTACCGA-----
CBS336.48 CTGATGCATA-----TTCGT--CAT-AATAG-GA-CAA-GGATGGC---GATGGTGAGTGCGACCGTTACCGA-----
CBS110644 CTAATGCCTA-----TTCGT--CAT-AATAG-GA-CAA-GGATGGC---GATGGTGAGTGCGACCGTTACCGA-----
CBS42665 CTAATGGATACTT-----TTTCCC-GGT-AACAG-GA-CAA-GGATGGC---GATGGTGAGTGCGATCGTTATCAA---G
DAOM239916 CTAATGGATACTT-----TTTCCC-GGT-AACAG-GA-CAA-GGATGGC---GATGGTGAGTGCGATCATTATCGA---G
NRRL705 CTGACCAAGGCCGTTTT-CCCGCT-TGTGAACAG-GA-CAA-GGATGGC---GATGGTGCGTGCAGTCTTTCCCGG----

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DAOM239926 TTTT-AAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239919 TTTT-AAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239917 TTTT-AAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239922 TTTT-AAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239925 TTTT-AAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239943 TTTT-GAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
KAS3479 TTT--GAAATTCCATA--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239941 TTTT-AAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
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DAOM239944 TTTT-AAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
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DAOM239946 TTTT-GAATT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
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NRRL2074 TTTT-AAATT-CCATA--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
NRRL32583 TTTT-AAATT-CCATA--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
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DSOM239932 TTTT-AAAT-CCATA--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239930 TTTTG-AAAT-CCATA--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
CBS25855 TTTT-AAAT-CC-TG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
CBS12865 TTTT-AAAT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
CBS118889 TTTT-AAAT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239912 TTTTAAAACT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
DAOM239913 TTTTAAAACT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
CBS24865 TTTT-AAAT-CCATG--C-----CGACTGGAGTAAACC-CACTG-AGAGAACCGAATAAC
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DAOM239938 TTTT-TAAT-CCATG--C-----CGACTGGAGTAAACC-CCTA-AGAGAACCGAATAAC
DAOM239937 TTTT-TAAT-CCATG--C-----CGACTGGAGTAAACC-CCTA-AGAGAACCGAATAAC
CBS229.60 TATTT-----CCAGG--C-----CGACTGTATCACCCT-TATTG-AGAGGACCGAATAAC
CBS238.68 TATTT-----CCAGG--C-----CGACTGTATCACCCT-TATTG-AGAGGACCGAATAAC
NRRL3447 CTCGA-TAATTT-CAAGATC-----CGATTATGTCTCTT-GACCG--AGTGAACAAATCAC
AL1878 CTCGA-TAATTT-CAAGATC-----CGATTATGTCTCTT-GACCG--AGTGAACAAATCAC
AL1644 CTCGA-TAATTT-CAAGATC-----CGATTATGTCTCTT-GACCG--AGTGAACAAATCAC
AL1642 CTCGA-TAATTT-CAAGATC-----CGATTATGTCTCTT-GACCG--AGTGAACAAATCAC
AL1643 CTCGA-TAATTTCAAGATC-----CGATTATGTCTCTT-GACCG--AGTGAACAAATCAC
CBS136.22 -----GATCT-GCGGA--C-----CGACT--ATCACGCCCCATTG-AAAAGGATAAATTAAC
CBS347.51 -----GATCT-GCGGA--C-----CAACT--ATTACGCC-CATTG--AAAGGATAAATAAC
CBS336.48 -----GATCT-GCGGA--C-----CGAC--ATCACGCC-CATTG--AAAGGATAAATAAC
CBS110644 -----GATCT-GCGGA--C-----CGAC--ATCACGCC-CATTG--AAAGGATAAATAAC
CBS42665 CTCGA-TGATTTGAGGA--C-----CGATTATGTCTCTT-TGTTG--AGCGAACGAAATAAC
DAOM239916 CTCGA-TGATTTGAGGA--C-----CGATTATGTCTCTT-TGTTG--AGCGAACGAAATAAC
NRRL705 -----TAGCTCGGACGCTCTTTCTTAGGAAGCAGTCTTGGGCCACTGGCACCCGCGAAGGTTTTAAAC-ACAGAATGAC

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DAOM239926 TGAG-ACCGATCGAT-CTATA-GGA-CAAATCACCACCAAGGAGCTGGGCACGTGTCATGCGCTCCCTCGGCCAGAACCCC
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 CBS347.51 TGAG-TTGGATGAAT--TATA-GGC-CAGATCACCACCAAGGAGCTGGGTACCGTTATGCGTTCTCTCGGCCAGAACCCCT
 CBS336.48 TGAG-TTGGATGAAT--TATA-GGC-CAGATCACCACCAAGGAGCTGGGTACCGTTATGCGTTCCCTCGGCCAGAACCCCT
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[	321	331	341	351	361	371	381	391	]
[									]
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DAOM239926	TCCGAGTCCGAGCTTCAGGACATGATGACCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239919	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239917	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239922	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239925	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239943	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
KAS3479	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239941	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239942	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239944	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239940	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239945	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239946	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239939	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
NRRL2074	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
NRRL32583	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAOM239931	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DSOM239932	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
DAON239930	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
CBS25855	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
CBS12865	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGACGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								
CBS118889	TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGGTACGA----								

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 CBS24865 TCCGAGTCCGAGCTTCAGGACATGATCAACGAGGTCGATGCCGACAACAACGGCACCATTGACTTCCCTGGTACGA----
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 CBS136.22 TCCGAGTCTGAGCTGCAGGACATGATTAACGAGGTTGACGCTGACAACAACGGCACCATTGATTTCCTGGTACGG----
 CBS347.51 TCCGAGTCTGAGCTGCAGGACATGATTAACGAGGTTGACGCTGACAACAACGGCACCATTGATTTCCTGGTACGG----
 CBS336.48 TCCGAGTCTGAGCTGCAGGACATGATTAACGAGGTTGACGCTGACAACAACGGCACCATTGATTTCCTGGTACGG----
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[									]
[									]
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DAOM239919	-TTTCCCTTCCGATCG-----	GA-----	CCCCCTGCTC-----	CCTCCGGATAGATGTTAA-----	CGTGCGG				
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DAOM239922	-TTTCCCTTCCGATCG-----	GA-----	CCCCCTGCTC-----	CCTCCGGATAGATGTTAA-----	CGTGCGG				
DAOM239925	-TTTCCCTTCCGATCG-----	GA-----	CCCCCTGCTC-----	CCTCCGGATAGATGTTAA-----	CGTGCGG				
DAOM239943	-TTTCCCTTCCACCCGAA----	AGG-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CGAAAGG				
KAS3479	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239941	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CGTGCGG				
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DAOM239940	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CGTGCGG				
DAOM239945	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CGTGCGG				
DAOM239946	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CGTGCGG				
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DAOM239930	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
CBS25855	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
CBS12865	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
CBS118889	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239912	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239913	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
CBS24865	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239934	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239935	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239936	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239933	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM2399914	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM2399915	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239938	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
DAOM239937	-TTTCCCTTCCACTCGAA----	TGA-----	CCCCGTGCTT-----	CCTCCGGATAGATGTTAA-----	CATGCGG				
CBS229.60	CTCTTCTTCCACTCGAA----	ATG-----	CCCCATATCT-----	GCCATTCCGCATATATTGA-----	CAGACGG				
CBS238.68	CTCTTCTTCCACTCGAA----	ATG-----	CCCCATATCT-----	GCCATTCCGCATATATTGA-----	CAGACGG				
NRRL3447	-TCTCCCTCCCTCCGAA----	TGATGATCTCAAGCC-----	CGAGAAGACTGATATTGA-----	CATTGCG					
AL1878	-TCTCCCTCCCTCCGAA----	TGATGATCTCAAGCC-----	CGAGAAGACTGATATTGA-----	CATTGCG					
AL1644	-TCTCCCTCCCTCCGAA----	TGATGATCTCAAGCC-----	CGAGAAGACTGATATTGA-----	CATTGCG					
AL1642	-TCTCCCTCCCTCCGAA----	TGATGATCTCAAGCC-----	CGAGAAGACTGATATTGA-----	CATTGCG					
AL1643	-TCTCCCTCCCTCCGAA----	TGATGATCTCAAGCC-----	CGAGAAGACTGATATTGA-----	CATTGCG					
CBS136.22	-TCCCTATGTCTCGACGGACTCGA--	CTTTTATTTT-----	CTTTCGGACAGTATTGA-----	TACCTTT					
CBS347.51	-TCCCTATGTCTCGACGGACTCGA--	CTTTTATTTT-----	CTTTCGGACAGTATTGA-----	CACCCTT					

CBS336.48 -CCTCTATGTCTCGACGAACCTCGA---TTTTATCTCC-----TTTTCGGATCAGTATTGA-----CACCTTT
 CBS110644 -CCCCATGTCTCGACGAGCTCGA---TTGTATCTTC-----CTTTCGGATCAGTATTGA-----CACCTTT
 CBS42665 -TTTCCCTCCCTCCGAA---TAA---CCCAAGCCTC-----GAAACACTCGTATTGA-----TATGTGG
 DAOM239916 -TCTCCCTACCTCCGAA---TAA---CCCAAGCCTC-----GAAACAATCGTATTGA-----TATGTGG
 NRRL705 -ATTGAATCGCTTGGCAG---TCT---GCTGTGGCTCTTTTCTCCCTTTAGACCAAGACTGATTGCTTTTCTGTGCGC

[	481	491	501	511	521	531	541	551	]
[									]

KAS3191 --CACAGAGTTCTGACCATGATGGCCCGTAAATGAAGGACACCGACTC-----
 DAOM239926 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239919 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239917 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239922 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239925 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239943 --CACAGATTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 KAS3479 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239941 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239942 --CACAGAATTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239944 --CACAGATTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239940 --CACAGAATTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239945 --CACAGAATTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239946 --CACAGAATTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239939 --CACAGATTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 NRRL2074 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 NRRL32583 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239931 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DSOM239932 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAON239930 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 CBS25855 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 CBS12865 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAG-----
 CBS118889 --CACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239912 --CACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCATTCAAGGT
 DAOM239913 --CACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCATTCAAGGT
 CBS24865 ----CAGAGTTCTTACCATGATGGCTCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239934 --TACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239935 --TACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239936 --TACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239933 --TACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239914 --CACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCCTTCAAGGT
 DAOM239915 --CACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGGGAAGCGTTCAAGGT
 DAOM239938 --TACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAAGCGTTCAAGGT
 DAOM239937 --TACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAAGCGTTCAAGGT
 CBS229.60 CACACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCATTCAAGGT
 CBS238.68 CACACAGAGTTCTGACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCATTCAAGGT
 NRRL3447 A-CACAGAGTTCTTACCATGATGGCAGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCTTTCAAGGT
 AL1878 A-CACAGAGTTCTTACCATGATGGCAGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCTTTCAAGGT
 AL1644 A-CACAGAGTTCTTACCATGATGGCAGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCTTTCAAGGT
 AL1642 A-CACAGAGTTCTTACCATGATGGCAGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCTTTCAAGGT
 AL1643 A-CACAGAGTTCTTACCATGATGGCAGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGTGAGGCTTTCAAGGT
 CBS136.22 --TGCAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGATACCGACTCCGAGGAGGAGATCCGCGAGGCATTCAAGGT
 CBS347.51 --CGCAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGATACCGACTCCGAGGAGGAGATCCGCGAGGCATTCAAGGT
 CBS336.48 --TGCAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGATACCGACTCCGAGGAGGAGATCCGCGAGGCATTCAAGGT
 CBS110644 --TGCAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGATACCGACTCCGAGGAGGAGATCCGCGAGGCATTCAAGGT
 CBS42665 A-CACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGCGAGGCCTTCAAGGT
 DAOM239916 A-CACAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCCGAGGAGGAGATCCGCGAGGCCTTCAAGGT
 NRRL705 C-TGCAGAGTTCTTACCATGATGGCCCGTAAGATGAAGGACACCGACTCAGAGGAGGAGATCCGGGAGGCCTTCAAGGT

[	561	571	581	591	601	611	]
[							]

KAS3191 -----
 DAOM239926 TTTTCGATCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACG-----
 DAOM239919 TTTTCGATCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCC-----
 DAOM239917 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
 DAOM239922 TTTTCGATCGCGACAACAACGTTTCATTTCCGCCGCCGAGCTGCGCCACGT-----
 DAOM239925 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCT-
 DAOM239943 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
 KAS3479 TTTTCGACCGCGACAATAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
 DAOM239941 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
 DAOM239942 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
 DAOM239944 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
 DAOM239940 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC

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DAOM239945 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGATCTC
DAOM239946 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DAOM239939 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
NRRL2074 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC--
NRRL32583 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DAOM239931 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DSOM239932 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DAON239930 TTTTCGACCGCGACAATAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
CBS25855 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
CBS12865 -----
CBS118889 TTTTCGACCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DAOM239912 TTTTCGACCGTGACAACAACGGTTTCATTTCCGCCGCTGAGCTGCGCCACGTGATGACC--
DAOM239913 TTTTCGACCGTGACAACAACGGTTTCATTTCCGCCGCTGAGCTGCGCCACGTCATGACCTC
CBS24865 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCTGAGCTGCGCCACGTCATGACCTC
DAOM239934 TTTTCGACCGCGACAACAACGGTTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DAOM239935 TTTTCGACCGCGACAACAACGGTTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCAC
DAOM239936 TTTTCGACCGCGACAACAACGGTTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DAOM239933 TTTTCGACCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DAOM2399914 TTTTCGATCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATG-CC--
DAOM2399915 TTTTCGATCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTTATGACCTC
DAOM239938 TTTTCGATCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATGACC--
DAOM239937 TTTTCGATCGCGACAACAACGGTTTCATTTCCGCCGCCGAGCTGCGCCACGTCATG-CC--
CBS229.60 CTTCGACCGCGACAACAACGGTTTCATCTCCGCTGCCGAGCTGCGCCACGTCATGACCTC
CBS238.68 CTTCGACCGCGACAACAACGGTTTCATCTCCGCTGCCGAGCTGCGCCACGTCATGACCTC
NRRL3447 GTTCGACCGCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
AL1878 GTTCGACCGCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
AL1644 GTTCGACCGCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
AL1642 GTTCGACCGCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
AL1643 GTTCGACCGCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
CBS136.22 GTTCGATCGCGATAACAACGGATTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTT
CBS347.51 GTTCGATCGCGATAACAACGGATTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
CBS336.48 GTTCGATCGCGATAACAACGGATTTCATCTCCGCCGCCGAACACGCCACGTCATGACCTC
CBS110644 GTTCGATCGCGATAACAACGGATTTATCTCCGCCGCCGAACACGCCATGTGTCATGACCTC
CBS42665 CTTCGACCGCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
DAOM239916 TTTTCGACCGCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC
NRRL705 GTTTGACCGCGACAACAACGGCTTCATCTCCGCCGCCGAGCTGCGCCACGTCATGACCTC

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Combined Multiple Gene Sequence Alignment

CaM was not included in the combined gene sequence alignment because it was not congruent

with the other genes, except ITS. Data partition was as follows: ITS = 1–574; *BenA* = 575–1139;

CaM = 1140–1759; *CoxI* = 1140–1744; *TEF1-α* = 1744–2752

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
KAS3191  CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239926 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239919 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239925 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239922 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239917 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239943 -----CCTCTG-----G-T--CACCTCCCACCCGTGTTTA-TTATACCTTGGTTGCTTCGGCAGG
KAS3479  CATTACTT--AGAGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239941 -----AGAGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239942 -----AGTGAGGG--TCT-----GGT--CACCTCCCACCCGTGTTTA-TTATACCTTGGTTGCTTCGGCAGG
DAO239944 -----CCTCTG-----G-T--CACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239940 CATTACAGGAAGAGGGGCTCCTGGGCTCTGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239945 -----GCCTCTG-----GGTC--ACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
DAO239946 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
KAS3480  CATTACAGGAAGAGGGGCTCCTGGGCTCTGGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
NRRL32583 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
NRRL2074 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG
KAS346110 CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA-TTGTACCTTGGTTGCTTCGGCAGG

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KAS347530	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
KAS347430	CATTACTG--AGTGAGGGCCCTCTG-----G-TC--ACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
CBS25855	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
CBS12865	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
CBS118889	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
DAOM239913	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
DAOM239912	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
CBS24865	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
DAOM239934	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
DAOM239935	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
DAOM239936	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
DAOM239933	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
DAOM239915	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
DAOM239914	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
DAO2399383	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
DAO2399373	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
CBS229.60	-----CTCCG-----G-TC--ACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
CBS23828	CATTACTG--AGTGAGGGCCCTCCG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
KAS3463	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
CBS238.68	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
KAS34641	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
KAS34663	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
KAS3465	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTATTGTACCTTGTGTGCTTCGGCAGG
NRR13391	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGCTC--TTGTACCATGTTGCTTCGGCGAG
AL1878	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTCTC--TTGTACCATGTTGCTTCGGCGAG
AL1644	CATTACTG--AGTGAGGGCCCTCTG-----T-CAACCTCCCACCCGTGTCTC--TTGTACCATGTTGCTTCGGCGAG
AL1642	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTCTC--TTGTACCATGTTGCTTCGGCGAG
AL1643	-----ACCTCCCACCCGTGTCTC--TTGTACCATGTTGCTTCGGCGAG
CBS136.22	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
CBS347.51	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
CBS336.48	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
CBS110644	CATTACTG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TTGTACCTTGTGTGCTTCGGCAGG
CBS42665	CATTACTG--AGTGAGGGCCCTCTG-----GTCCAACCTCCCACCCGTGTCTA--TTGTACCATGTTGCTTCGGCAGG
DAOM239916	CATTACTG--AGTGAGGGCCCTCTG-----GTCCAACCTCCCACCCGTGTCTA--TTGTACCATGTTGCTTCGGCAGG
NRR1705	CATTACCG--AGTGAGGGCCCTCTG-----GGTCCAACCTCCCACCCGTGTTTA--TCGTACCTTGTGTGCTTCGGCGAG

[illegible]

[illegible]

	321	331	341	351	361	371	381	391
KAS3191	CCGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCTCTTGT	----	CCCCCCCC	----	G			
DAO239926	CCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCTCTTGT	----	CCCCCCCC	----	G			
DAO239919	CCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCTCTTGT	----	CCCCCCCC	----	G			
DAO239925	CCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCTCTTGT	----	CCCCCCCC	----	G			
DAO239922	CCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCTCTTGT	----	CCCCCCCC	----	G			
DAO239917	CCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCTCTTGT	----	CCCCCCCC	----	G			
DAO239917	CCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCTCTTGT	----	CCCCCCCC	----	G			
DAO239943	CCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCTCTTGT	----	CCCCCCCC	----	G			

	561	571	581	591	601	611	621	631
KAS3191	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACGTCAC-CCGGGGTCAAAT-----CTT							
DAO239926	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239919	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239925	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239922	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239917	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239943	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
KAS3479	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239941	-----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239942	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239944	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239940	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239945	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
DAO239946	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
KAS3480	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CCGGGGTCAAAT-----CTT							
NRRL32583	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTCGGTCAAAT-----CAT							
NRRL2074	CTTAAGCATATCAACGGTGCTGCTTT-TGGTACGTGTTGCTA-CCTGACCTCAC-CTTCGGTCAAGT-----CAT							
KAS346110	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTCGGTCAAGT-----CAT							
KAS347530	CTTAAGCATATCAACGGTGCCGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTCGGTCAAAT-----CAT							
KAS347430	CTTAAGCATATCAATGGTGCCGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTCGGTCAAAT-----CAT							
CBS25855	CTTAAGCATATCAAGGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAAAC-----CAT							
CBS12865	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAAAC-----CAT							
CBS118889	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAAAC-----CAT							
DAOM239913	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGATA-CCTGACCTCAC-CTTGGGTCAAAT-----TAT							
DAOM239912	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGATA-CCTGACCTCAC-CTTGGGTCAAAT-----TAT							
DA234865	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAAAT-----CTT							
DAOM239934	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAACTCA-----CAT							
DAOM239935	CTTAAGCATATCAATGGTGCCGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAACTCA-----CAT							
DAOM239936	CTTAAGCATATCAATGGTGCCGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAACTCA-----CAT							
DAOM239933	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAACTCA-----CAT							
DAOM239915	-----CGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTTGGGTCAAAT-----CAT							
DAOM239914	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTGGGGTCAAAT-----CAT							
DAO2399383	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTGGGGTCAACT-----CAT							
DAO2399373	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCTGACCTCAC-CTGGGGTCAACT-----CAT							
CBS229.60	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCGACTTTAC-CTTGCTCAGGT-----AGT							
CBS23828	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTGCTA-CCGACTTTAC-CTTGCTCAGGT-----AGT							
KAS3463	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCA-CCAC-----CTCAACC-----CAT							
CBS238.68	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCA-CCAC-----CTCAACC-----CAT							
KAS34641	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCA-CCAC-----CTCAACC-----CAT							
KAS34663	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCA-CCAC-----CTCAACC-----CAT							
KAS3465	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCA-CCCTC-----CTCAAAC-----CAT							
NRRL33391	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCC-GCTG-----ATGAACC-----CAT							
AL1878	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCC-GCTG-----ATGAACC-----CAT							
AL1644	CTTA-----CGGTGCTGCTTTCTGGTACGTGTTTCCC-GCTG-----ATGAACC-----CAT							
AL1642	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCC-GCTG-----ATGAACC-----CAT							
AL1643	CTTAAGCATATCAACGGTGCTGCTTTCTGGTACGTGTTTCCC-GCTG-----ATGAACC-----CAT				</			

NRRL705 CTTAAGCATATCAACGGTGTGCTTTCTGGTACGTGCCACGCCCGCC--AAACTTCCCCAGCACAAAGCAAA-CCC

[641 651 661 671 681 691 701 711]

[| | | | | | |]

KAS3191 CAATTG-GTGAACCTCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239926 CAATTG-GTGAACCTCAGGAA-----CC-----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239919 CAATTG-GTGAACCTCAGGAA-----CC-----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239925 CAATTG-GTGAACCTCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239922 CAATTG-GTGAACCTCAGGAA-----CC-----TTTGACTGACGTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239917 CAATTG-GTGAACCTCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239943 CAATTG-GTGAATCCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

KAS3479 CAATTG-GTGAACCCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239941 CAATTG-GTGAACCCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239942 CAATTG-GTGAACCTCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239944 CAATTG-GTGAACCCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239940 CAATTG-GTGAATCCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGG-C

DAO239945 CAATTG-GTGAACCTCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO239946 CAATTG-GTGAATCCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

KAS3480 CAATTG-GTGAATCCAGGAA-----CC-----TTTGACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGG-C

NRRL32583 CAATTG-TTGAACCCAGGAC-----CC-----TTTTACTGACTTGAATCACAGGCAGAACATTGCTAGCGAGCATGGCC

NRRL2074 CAATTG-TTGAACCCAGGAC-----CC-----TTTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

KAS346110 CAATTG-TTGAACCCAGGAC-----CC-----TTTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO237530 CAATTG-TTGAACCCAGGAC-----CC-----TTTTACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

KAS347430 CAATTG-TTGAACCCAGGAC-----CC-----TTTTACTGACTTGAATCACAGGCAGAACATTGCTAGCGAGCATGGCC

CBS25855 CAATTG-TTGAACCCAGGAG-----CC-----TTATACTGACTTCAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

CBS12865 CAATTG-TTGAACCCAGGAG-----CC-----TTATACTGACTTCAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

CBS118889 CAATTG-TTGAACCCAGGAG-----CC-----TTATACTGACTTCAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

DAOM239913 CAATTG-TTGAGCACAGGAC-----CT-----TTATACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGTC

DAOM239912 CAATTG-TTGAGCACAGGAC-----CT-----TTATACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGTC

CBS24865 CAATTG-TTGAGCAAAGAAC-----CC-----TTATACTGACTTGGATCATAGGCAGAACATTGCTAGCGAGCATGGTC

DAOM239934 CAATTG-TTAAACCCACGAG-----CC-----TTATACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

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DAOM239933 CAATTG-TCAAACCCACGAG-----CC-----TTATACTGACTTGAATTATAGGCAGAACATTGCTAGCGAGCATGGCC

DAOM239915 CAATTG-TTGAACCTAGGAG-----CC-----TTATACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

DAOM239914 CAATTG-TTGAACCTAGGAG-----CC-----TTATACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO2399383 CAGTTG-TTGAACCCAGGAG-----CC-----TTATACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

DAO2399373 CAGTTG-TTGAACCCAGGAG-----CC-----TTATACTGACTTGAATCATAGGCAGAACATTGCTAGCGAGCATGGCC

CBS229.60 CAATTG-TTGAACCCAGGAG-----CC-----TTATGCTAACCT-ACTTCCAGGCAGAACATTGCTAGCGAGCATGGCC

CBS23828 CAATTG-TTGAACCCAGGAG-----CC-----TTATGCTAACCT-ACTTCCAGGCAGAACATTGCTAGCGAGCATGGCC

KAS3463 CAATTG-TTGGCCTCTTCAA-----GCTTTCCTTTTACTAAC-TACCTCTTAGGCAGAACATTGCCAGTGAGCAGCGGCC

CBS238.68 CAATTG-TTGGCCTCTTCAA-----GCTTTCCTTTTACTTAC-TACCTCTTAGGCAGAACATTGCCAGTGAGCAGCGGCC

KAS34641 CAATTG-TTGGCCTCTTCAA-----GCTTTCCTTTTACTTAC-TACCTCTTAGGCAGAACATTGCCAGTGAGCAGCGGCC

KAS34663 CAATTG-TTGGCCTCTTCAA-----GCTTTCCTTTTACTTAC-TACCTCTTAGGCAGAACATTGCCAGTGAGCAGCGGCC

KAS3465 CAATTG-TTAGCCTCTTCAA-----GCTTTCCTTTTACTAAC-TACCTCTTAGGCAGAACATTGCCAGTGAGCAGCGGCC

NRRL3391 CAATTG-TTGATTG--A-AA-----CC-TTTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCAGCGGC

AL1878 CAATTG-TTGATTG--A-AA-----CC-TTTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCAGCGGC

AL1644 CAATTG-TTGATTG--A-AA-----CC-TTTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCAGCGGC

AL1642 CAATTG-TTGATTG--A-AA-----CC-TTTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCAGCGGC

AL1643 CAATTG-TTGATTG--A-AA-----CC-TTTTTTTTACTGAC-TACCTTCCAGGCAGAACATTGCCCTCCGAGCAGCGGC

CBS136.22 CAATTG-TTGAACCCCTGAG-----ACA---TTTTACTGAC-TACTTCCAGGCAGAACATTGCTTCCGAGCAGCGGCC

CBS347.51 CAATTG-TTGAACCCATTGAG-----ACA---TTTTACTGAC-TACTTCCAGGCAGAACATTGCTTCCGAGCAGCGGCC

CBS336.48 CAATTG-TTGAACCCCTGGA-----ACA---ATTTACTGAC-TACTTCCAGGCAGAACATTGCTTCCGAGCATGGCC

CBS110644 CAATTG-TTGAACCCCTGAG-----ACA---TTTTACTGAC-TACTTCCAGGCAGAACATTGCTTCCGAGCAGCGGCC

CBS42665 CAAATG-TTGACACCCATTG-----AAACTTTTTTACTAAC-TACCTCTTAGGCAGAACATTGCCCTCCGAGCAGCGGC

DAOM239916 CAAATG-TTGACACCCATTG-----AAACTTTTTTACTAAC-TACCTTATAGGCAGAACATTGCCCTCCGAGCAGCGGC

NRRL705 CAATTG-CGAG-----TCAACAGATACTGACTCG-----AACTACAGGCAGACCATTGCTGGTGAGCAGCGGCC

[721 731 741 751 761 771 781 791]

[| | | | | | |]

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DAO239926 TCGATGGCGAGGGCCAGTAAGT-----ATCAATT-TACGGGGGAATTGGGTGATA---TG

DAO239919 TCGATGGCGAGGGCCAGTAAGT-----ATCAATT-TACGGGGGAATTGGGTGATA---TG

DAO239925 TCGATGGCGAGGGCCAGTAAGT-----ATCAATT-TACGGGGGAATTGGGTGATA---TG

DAO239922 TCGATGGCGAGGGCCAGTAAGT-----ATCAATT-TACGGGGGAATTGGGTGATA---TG

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DAO239940 TCGACGGCGAGGGCCAGTAAGT-----ATCAATT-TACGCGGAATTGGGTGATA---TG
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 KAS346110 TCGACGGCGAGGGCCAGTAAGT-----ATCCATT-CAGTTGGAATTGAGTGATA---TG
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 KAS347430 TCGACGGCGAGGGCCAGTAAGT-----ATCCATT-CGGTTGGAATTGAGTGATA---TG
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 CBS12865 TCGACGGCGAGGGCCAGTAAGT-----ATCAATT-TGGTTGGAATTGAGTGATA---TG
 CBS118889 TCGACGGCGAGGGCCAGTAAGT-----ATAAATT-TGGTTGGAATTGAGTGATA---TG
 DAOM239913 TCGACGGCGAGGGCCAGTAAGT-----ATCAATT-TGGTTGGAATTGGGTGATA---TG
 DAOM239912 TCGACGGCGAGGGCCAGTAAGT-----ATCAATT-TGGTTGGAATTGGGTGATA---TG
 CBS24865 TCGACGGCGAGGGCCAGTAAGT-----ATCGAAT-TGGTTGGCATTGGGTGATA---TG
 DAOM239934 TCGACGGCGAGGGCCAGTAAGT-----ATCAATT-TGGTTGGAATTGGGTGATA---TG
 DAOM239935 TCGACGGCGAGGGCCAGTAAGT-----ACCAATT-TGGTTGGAATTGGGTGATA---TG
 DAOM239936 TCGACGGCGAGGGCCAGTAAGT-----ACCAATT-TGGTTGGAATTGGGTGATA---TG
 DAOM239933 TCGACGGCGAGGGCCAGTAAGT-----ATCAATT-TGGTTGGAATTGGGTGATA---TG
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 DAOM239914 TCGACGGCGAGGGCCAGTAAGT-----ATCAATA-TGGTTGGAATTGAATGAAA---CG
 DAO2399383 TCGACGGCGAGGGCCAGTAAGT-----ATCAACA-TGGTTGGAATTGGGTGATA---GG
 DAO2399373 TCGACGGCGAGGGCCAGTAAGT-----ATCAACA-TGGTTGGAATTGGGTGATA---GG
 CBS229.60 TTGATGGCGAGGGCCAGTAAGT-----ATCAATA-CGAGTGGGATTGGGTGATG---TG
 CBS23828 TTGATGGCGAGGGCCAGTAAGT-----ATCAATA-CGAGTGGGATTGGGTGATG---TG
 KAS3463 TCGATGGCGATGGCCAGTAAGT-----TTCTCGA-TTAAGTCGATTGGGTTATGTGGTG
 CBS238.68 TCGATGGCGATGGCCAGTAAGT-----TTCTCGA-TTAAGTCGATTGGGTTATGTGGTG
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 AL1642 TCGATGGCGATGGACAGTAAGT-----CTCGATCATCGACTCGATTGAATGAAGTGGTG
 AL1643 TCGATGGCGATGGACAGTAAGT-----CTCGATCATCGACTCGATTGAATGAAGTGGTG
 CBS136.22 TCGATGGCGAAGGACAGTGAGT-----ATCAATA-TTAATGGAATTGAGTGACGAG-TA
 CBS347.51 TCGATGGCGAAGGACAGTGAGT-----ATCGATA-TTAATGGAATTGAGTGACGAG-TA
 CBS336.48 TCGATGGCGAAGGACAGTGAGT-----ATCGATA-TTAATGGAATTGAGTGACGAG-TA
 CBS110644 TCGATGGCGAAGGACAGTGAGT-----ATCAATA-TTAATGGAATTGAGTGACGAG-TA
 CBS42665 TTGATGGCGATGGACAGTAAGT-----TCTTTGATTTCGAGTCGATTGGTATATATGGTG
 DAOM239916 TCGATGGTGTATGGACAGTAAGT-----TCTTTGATTTCGAGTCGATTGGTATATATGGTG
 NRRL705 TTGATGGCGATGGCCAGTAAGTCTCTTCGATACCACTTGATACCTCT-----C-GACAC

	801	811	821	831	841	851	861	871
[								
[								
KAS3191	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239926	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239919	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239925	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239922	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239917	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGATCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239943	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
KAS3479	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239941	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239942	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239944	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239940	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGTCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239945	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
DAO239946	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
KAS3480	AGAAT-GGCGGTCTGATA----	TTTTTCTTTAGCTTCAC-TGTCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC						
NRRL32583	AGAAT-GGCGGTCTGACATTTTTTTCCCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
NRRL2074	AGAAT-GGCGGTCTGATA-TTTTTTTCCCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
KAS346110	AGAAT-GGCGGTCTGATA-TTTTTTTCCCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
KAS347530	AGAAT-GGCGGTCTGATA-TTTTTTTCCCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
KAS347430	AGAAT-GGCGGTCTGATA-TTTTTTTCCCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
CBS25855	-GAAT-GGCGGTCTGATA-TTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
CBS12865	-GAAT-GGCGGTCTGATA-TTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
CBS118889	-GAAT-GGCGGTCTGATA-TTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
DAOM239913	AGAAT-GGCGGTCTGATA-TTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
DAOM239912	AGAAT-GGCGGTCTGATA-TTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							
CBS24865	AGAAT-GGCGGTCTGATA-TTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTCTAC							

DAOM239934 AGAAT-GGCGGTCTGATA-TTTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTTTAC
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 DAOM239936 AGAAT-GGCGGTCTGATA--TTTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTTTAC
 DAOM239933 AGAAT-GGCGGTCTGATA--TTTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTTTAC
 DAOM239915 AGGAT-GGCGGTCTGATA-TTTTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTTTAC
 DAOM239914 AGGAT-GGCGGTCTGATA-TTTTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTTTAC
 DAO2399383 AGAAT-GGCGGTCTGATA--TTTTTTTTCTTAGCTTCAC-TGGCCAGTCCGACCTCCAGCTCGAGCGCATGAACGTTTAC
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 CBS229.60 AGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTTAC-TGGCCAGTCTGACCTCCAGCTCGAGCGCATGAACGTTTAC
 CBS23828 AGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTTAC-TGGCCAGTCTGACCTCCAGCTCGAGCGCATGAACGTTTAC
 KAS3463 GGAAT-GGCGGTCTGATG-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 CBS238.68 GGAAT-GGCGGTCTGATG-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
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 AL1878 GGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 AL1644 GGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 AL1642 GGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 AL1643 GGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 CBS136.22 GGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 CBS347.51 GGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 CBS336.48 GGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 CBS110644 GGAAT-GGCGGTCTGATA-----TTTTTC-TAGCTTCAC-CGGTTCCTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 CBS42665 GGAAT-GGCGGTCTGATA---TTTTTTTC-TAGCTTCAC-CGGCCAGTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 DAOM239916 GGAAT-GGCGGTCTGATA--TTTTTTTTTC-TAGCTTCAC-CGGCCAGTCCGACCTCCAGCTGGAGCGTATGAACGTTTAC
 NRRL705 GGAA-TGGCGGTCTGATA---TTTTTGGTTAGCTACAA-TGGTACCTCCGACCTTCAGCTCGAGCGCCTGAACGTTTAC

	881	891	901	911	921	931	941	951
KAS3191	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCCAA-AC			ACTCGTCA----ACCACATCTAATACAA
DAO239926	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCCAA-AC			ACTCGTCA----ACCACATCTAATACAA
DAO239919	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCCAA-AC			ACTCGTCA----ACCACATCTAATACAA
DAO239925	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCCAA-AC			ACTCGTCA----ACCACATCTAATACAA
DAO239922	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCCAA-AC			ACTCGTCA----ACCACATCTAATACAA
DAO239917	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCCAA-AC			ACTCGTCA----ACCACATCTAATACAA
DAO239943	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCGAT-AC			CTCGTCA----ACCTCATCTAATACAA
KAS3479	TTCAACCACGTAAG-----				TGTGG-AATCGACACTCGAT-AC			CTCGTCA----ACCTCATCTAATATAA
DAO239941	TTCAACCACGTAAG-----				TGTGG-AATCGACACTCGAT-AC			CTCGTCA----ACCTCATCTAATATAA
DAO239942	TTCAACCACGTAAG-----				TGTGG-AATCGACACTCGAT-AC			CTCGTCA----ACCTCATCTAATACAA
DAO239944	TTCAACCACGTAAG-----				TGTGG-AATCAACTCTCGAT-CT			CTCGTCA----ACCTCATCTAATACAA
DAO239940	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCGAT-AC			CTCGTCA----ACCTCATCTAATACAA
DAO239945	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCGAT-AT			CTCGTCA----ACCTCATCTAATACAA
DAO239946	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCGAT-AC			CTCGTCA----ACCTCATCTAATACAA
KAS3480	TTCAACCACGTAAG-----				TGTGG-AATCAACACTCGAT-AC			CTCGTCA----ACCTCATCTAATACAA
NRRL32583	TTCAACCACGTAAG-----				TGTGG-AATCGATACTCGAT-AC			CTGCGCA----ACCCCGTCTAATATAA
NRRL2074	TTCAACCACGTAAG-----				TGTGG-AATCGATACTCCAT-AC			CTGCGCA----ACCCCGTCTAATATAA
KAS346110	TTCAACCACGTAAG-----				TGTGG-AATCGATACTCCAT-AC			CTGCGCA----ACCCCGTCTAATATAA
KAS347530	TTCAACCACGTAAG-----				TGTGG-AATCGATACTCGAT-AC			CTGCGCA----ACCAGTCTAATATAA
KAS347430	TTCAACCACGTAAG-----				TGTGG-AATCGATACTCGAT-AC			CTGCGCA----ACCAGTCTAATATAA
CBS25855	TTCAACCACGTAAG-----				TGTGC-AATCGACACTCGAT-AC			CTGTCA----ACCCCGTCTAATATAA
CBS12865	TTCAACCACGTAAG-----				TGTGC-AATCGACACTCGAT-AC			CTGTCA----GCCCGTCTAATAGAA
CBS118889	TTCAACCACGTAAG-----				TGTGC-AATCGACACTCGATAAC			CTGTCA----ACCCCGTCTAATATAA
DAOM239913	TTCAACCACGTAAG-----				TGTGGAACCGACACTCGAT-AC			CTTTCA----AACAGTCTAATATGA
DAOM239912	TTCAACCACGTAAG-----				TGTGGAACCGACACTCGAT-AC			CTTTCA----AACAGTCTAATATGA
CBS24865	TTCAACCACGTAAG-----				TGTGG-AATCGACACTCGAT-AT			CTTTCA----AACCGTCTAATACAA
DAOM239934	TTCAACCACGTAAG-----				TGTGG-AATCGACACTCGATACT			CTGGAC----ACCCCGTCTAATATAA
DAOM239935	TTCAACCACGTAAG-----				TGTGG-AATCGACACTCGATACT			CTGAAC----ACCCCGTCTAATATAC
DAOM239936	TTCAACCACGTAAG-----				TGTGG-AATCGACACTCGATACT			CTGAAC----ACCCCGTCTAATATAC
DAOM239933	TTCAACCACGTAAG-----				TGTGG-AATCGACACTCGATACT			CTGAAC----ACCCCGTCTAATATAA
DAOM239915	TTCAACCACGTAAG-----				CGTGA-AATCTACACTCGAT-AC			CATTCA---CTCCCATCTAATATAT
DAOM239914	TTCAACCACGTAAG-----				CGTGA-AATCTACACTCGAT-AC			CATTCA---CTCCCATCTAATATAT
DAO2399383	TTCAACCACGTAAG-----				TGTGG-AATTTACACTCGAT-AC			CCCTTCAGACCCCGCTCTAATATGA
DAO2399373	TTCAACCACGTAAG-----				TGTGG-AATTTACACTCGAT-AC			CCCTTCAGACCCCGCTCTAATATGA
CBS229.60	TTCAACCACGTAAG-----				TGTGG-AATCGATACCCGTA-AC			GTTTTAA---ACCTCGTCTAATACAA
CBS23828	TTCAACCACGTAAG-----				TGTGG-AATCGATACCCGTA-AC			GTTTTAA---ACCTCGTCTAATACAA
KAS3463	TTCAACCACGTAAG-----				TATGA-CATTGATATATTGA-ATA			AATTCG---ACCTGTCTAATATTT
CBS238.68	TTCAACCACGTAAG-----				TATGA-CATTGATATATTGA-ATA			AATTCG---ACCTGTCTAATATTT
KAS34641	TTCAACCACGTAAG-----				TATGA-CATTGATATATTGA-ATA			AATTCG---ACCTGTCTAATATTT
KAS34663	TTCAACCACGTAAG-----				TATGA-CATTGATATATTGA-ATA			AATTCG---ACCTGTCTAATATTT
KAS3465	TTCAACCACGTAAG-----				TATGA-CATTGATATATTGA-ATA			AATTCG---ACCTGTCTAATATTC

[illegible]

[illegible]

	1121	1131	1141	1151	1161	1171	1181	1191
KAS3191	CTGGGCCAAGGGTCACTAC	--GATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239926	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239919	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239925	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239922	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239917	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239943	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
KAS3479	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239941	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239942	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239944	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239940	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239945	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
DAO239946	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		
KAS3480	CTGGGCCAAGGGTCACTACG	TGATTTTTATC	-TTCAAATGCT	-AAAGATA	-TAGGTAC	-ACTATATTTAATGTTTTCAAT		

AL1643	AGATAATCAATTATATAAATAGTATAATTACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAA
CBS136.22	AGATAATCAATTATATAAATAGTATAAATACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAA
CBS347.51	AGATAATCAATTATATAAATAGTATAAATACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAA
CBS336.48	AGATAATCAATTATATAAATAGTATAAATACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAA
CBS110644	AGATAATCAATTATATAAATAGTATAAATACAGCT--CATGCTATATTAATGATTTTTTTCATGGTTATG-CCAGCTTTAA
CBS42665	AGATAATCAATTATATAAATAGTATAAATACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAA
DAOM239916	AGATAATCAATTATATAAATAGTATAAATACAGCT--CATGCTATATTAATGATATTCTTTATGGTTATG-CCAGCATTAA
NRRL705	AGATAACCAATTATATAAATAGTATAAATACAGCT--CATGCTATAATGATGATTTTCTTTATGGTTATG-CCAGCTTTAA

	1361	1371	1381	1391	1401	1411	1421	1431
[	[	[	[	[	[	[	[	[
KAS3191	T	C	G	G	A	G	G	T
DAO239926	T	C	G	G	A	G	G	T
DAO239919	T	C	G	G	A	G	G	T
DAO239925	T	C	G	G	A	G	G	T
DAO239922	T	C	G	G	A	G	G	T
DAO239917	T	C	G	G	A	G	G	T
DAO239943	T	C	G	G	A	G	G	T
KAS3479	T	C	G	G	A	G	G	T
DAO239941	T	C	G	G	A	G	G	T
DAO239942	T	C	G	G	A	G	G	T
DAO239944	T	C	G	G	A	G	G	T
DAO239940	T	C	G	G	A	G	G	T
DAO239945	T	C	G	G	A	G	G	T
DAO239946	T	C	G	G	A	G	G	T
KAS3480	T	C	G	G	A	G	G	T
NRRL32583	T	C	G	G	A	G	G	T
NRRL2074	T	C	G	G	A	G	G	T
KAS346110	T	C	G	G	A	G	G	T
KAS347530	T	C	G	G	A	G	G	T
KAS347430	T	C	G	G	A	G	G	T
CBS25855	T	C	G	G	A	G	G	T
CBS12865	T	C	G	G	A	G	G	T
CBS118889	T	C	G	G	A	G	G	T
DAOM239913	T	A	G	G	A	G	G	T
DAOM239912	T	A	G	G	A	G	G	T
CBS24865	T	A	G	G	A	G	G	T
DAOM239934	T	A	G	G	A	G	G	T
DAOM239935	T	A	G	G	A	G	G	T
DAOM239936	T	A	G	G	A	G	G	T
DAOM239933	T	A	G	G	A	G	G	T
DAOM239915	T	A	G	G	A	G	G	T
DAOM239914	T	A	G	G	A	G	G	T
DAO2399383	T	A	G	G	A	G	G	T
DAO2399373	T	A	G	G	A	G	G	T
CBS229.60	T	A	G	G	A	G	G	T
CBS23828	T	A	G	G	A	G	G	T
KAS3463	T	A	G	G	A	G	G	T
CBS238.68	T	A	G	G	A	G	G	T
KAS34641	T	A	G	G	A	G	G	T
KAS34663	T	A	G	G	A	G	G	T
KAS3465	T	A	G	G	A	G	G	T
NRRL3391	T	T	G	G	T	G	G	T
AL1878	T	T	G	G	T	G	G	T
AL1644	T	T	G	G	T	G	G	T
AL1642	T	T	G	G	T	G	G	T
AL1643	T	T	G	G	T	G	G	T
CBS136.22	T	T	G	G	T	G	G	T
CBS347.51	T	T	G	G	T	G	G	T
CBS336.48	T	T	G	G	T	G	G	T
CBS110644	T	T	G	G	T	G	G	T
CBS42665	T	T	G	G	T	G	G	T
DAOM239916	T	T	G	G	T	G	G	T
NRRL705	T	A	G	G	T	G	G	T

	1441	1451	1461	1471	1481	1491	1501	1511
KAS3191	TTTCTGATTATTAGTGCCAAGTTTATT	TTTATTTCATATTCTCAGCAAT	AATAGAAAATGGA	--GCTGGAACAGGATGA				
DAO239926	TTTCTGATTATTAGTGCCAAGTTTATT	TTTATTTCATATTCTCAGCAAT	AATAGAAAATGGA	--GCTGGAACAGGATGA				
DAO239919	TTTCTGATTATTAGTGCCAAGTTTATT	TTTATTTCATATTCTCAGCAAT	AATAGAAAATGGA	--GCTGGAACAGGATGA				
DAO239925	TTTCTGATTATTAGTGCCAAGTTTATT	TTTATTTCATATTCTCAGCAAT	AATAGAAAATGGA	--GCTGGAACAGGATGA				

CBS229.60 AGTGGTATAAGTAGTATGTGA-GGTGCTATTAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGAATACGT
CBS23828 AGTGGTATAAGTAGTATGTGA-GGTGCTATTAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGAATACGT
KAS3463 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGTATACGT
CBS238.68 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGTATACGT
KAS34641 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGTATACGT
KAS34663 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGTATACGT
KAS3465 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGTATACGT
NRRL3391 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATTTTTAA---ATATGAGAAGTCCAGGTATACGT
AL1878 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATTTTTAA---ATATGAGAAGTCCAGGTATACGT
AL1644 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATTTTTAA---ATATGAGAAGTCCAGGTATACGT
AL1642 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATTTTTAA---ATATGAGAAGTCCAGGTATACGT
AL1643 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATTTTTAA---ATATGAGAAGTCCAGGTATACGT
CBS136.22 AGTGGTATTAGTAGTATGTGA-GGTGCTATTAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGAATACGT
CBS347.51 AGTGGTATTAGTAGTATGTGA-GGTGCTATTAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGAATACGT
CBS336.48 AGTGGTATTAGTAGTATGTGA-GGTGCTATTAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGAATACGT
CBS110644 AGTGGTATTAGTAGTATGTGA-GGTGCTATTAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGAATACGT
DS42665 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGTATACGT
DAOM239916 AGTGGTATAAGTAGTATGTGA-GGAGCTATGAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGTATACGT
NRRL705 AGTGGTATAAGTAGTATGTGA-GGTGCTATGAATTTT-ATAACAACATATTTAA---ATATGAGAAGTCCAGGTATACGT

	1681	1691	1701	1711	1721	1731	1741	1751
KAS3191								
DAO239926	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGG-CACGTCGATTCC					
DAO239919	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
DAO239925	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
DAO239922	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
DAO239917	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATT-----TCGGCCACGTCGATTCC					
DAO239943	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
KAS3479	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATT-----					
DAO239941	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTT--G-CACGTCGATTCC					
DAO239942	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATT----CACGTCGATTCC					
DAO239944	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
DAO239940	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGC-----	-----TTCGGCCACGTCGATTCC					
DAO239945	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTC-GCCACGTCGATTCC					
DAO239946	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGC-----	-----TCGGCCACGTCGATTCC					
KAS3480	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATT-----CACGTCGATTCC					
NRRL32583	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCG-CCACGTCGATTCC					
NRRL2074	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCG-CCACGTCGATTCC					
KAS346110	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGG-CACGTCGATTCC					
KAS347530	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGG-CACGTCGATTCC					
KAS347430	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATT-----CGTCGATTCC					
CBS25855	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATT----CACGTCGATTCC					
CBS12865	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGG-CACGTCGATTCC					
CBS118889	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
DAOM239913	TTACATAAGTTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATATT--TCGGCCACGTCGATTCC					
DAOM239912	TTACATAAGTTAGCTTTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
CBS24865	TTACATAAGTTAGCTTTTATTG	-G-ATGA-GCTGT-TATAA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
DAOM239934	TTACATAAAATTAGCTTTTATTTGGGATGA	-GCTGT-TATTAATAACAGGC-----	-----T-G--CACGTCGATTCC					
DAOM239935	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATAA-TAACAGATG	--TATTATTATTT--GG-CACGTCGATTCC					
DAOM239936	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATAA-TAACAGCTG	--TATTATTATTT--G-CACGTCGATTCC					
DAOM239933	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATAA-TAACAGCTG	--TATTATTATTT--G--CACGTCGATTCC					
DAOM239915	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATAA-TAACAGCTG	--TATTATTATTTTCG-CCACGTCGATTCC					
DAOM239914	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATAA-TAACAGCTG	--TATTATTATTTTCG---CCCCTCGATTCC					
DAO2399383	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATAA-TAACAGCTG	--TATTATTATT--GGCCACGTCGATTCC					
DAO2399373	TTACATAAAATTAGCTTTTATTG	-G-ATGA-GCTGT-TATAA-TAACAGCTG	--TATTATTATTT--GG-CACGTCGATTCC					
CBS229.60	TTACATAAAATTAGCATTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTAGGCCACGTCGATTCC					
CBS23828	TTACATAAAATTAGCATTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
KAS3463	TTACATAAAATTAGCGTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTAT--ACGCCACGTCGATTCC					
CBS238.68	TTACATAAAATTAGCGTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
KAS34641	TTACATAAAATTAGCGTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
KAS34663	TTACATAAAATTAGCGTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
KAS3465	TTACATAAAATTAGCGTTATTG	-G-ATGA-GCTGT-TATTA-TAACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
NRRL3391	TTACATAAAATTAGCGTTATTG	-G-TTGA-GCTGT-AATAA-TTACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
AL1878	TTACATAAAATTAGCGTTATTG	-G-TTGA-GCTGT-AATAA-TTACAGCTG	--TATTATTATTTTCGGCCACGTCGATTCC					
AL1644	TTACATAAAATTAGCGTTATTG	-G-TTGA-GCTGT-AATAA-TTACAGCTG	--TATTATTATT--C-GCCACGTCGATTCC					

	1761	1771	1781	1791	1801	1811	1821	1831
KAS3191	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
DAO239926	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCAACGCTCC-	TTCTCACTTCCATCGA	
DAO239919	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCAACGCTCC-	TTCTCACTTCCATCGA	
DAO239925	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
DAO239922	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCAACGCTCC-	TTCTCACTTCCATCGA	
DAO239917	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
DAO239943	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
KAS3479	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACT---	CGCTCC-TTCTCACTTCCATCGA	
DAO239941	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACT---	CGCTCC-TTCTCACTTCCATCGA	
DAO239942	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
DAO239944	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
DAO239940	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
DAO239945	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACT---	CGCTCC-TTCTCACTTCCATCGA	
DAO239946	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
KAS3480	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	-----	ACTCCATCGCTCC-	TTCTCACTTCCATCGA	
NRR132583	GGCAAGTCCACCACCA	CTGGT	-AAGCTCCC-	-----	AC--	CAATCCCATCGCTCC-	TGCCTCACATCTATCGA	
NRR12074	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCC-	-----	AC--	CAATCCCCCTCGCTCC-	TGCCTCACATCCATCGA	
KAS346110	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCC-	-----	AC--	CAATCCCCCTCGCTCC-	TGCCTCACATCCATCGA	
KAS347530	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATCCCATCGCTCC-	TGCCTCACATCCATCGA	
KAS347430	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATCCCATCGCTCC-	TGCCTCACATCCATCGA	
CBS25855	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCC-	-----	AC--	CAAT-CCATCGCTCC-	TTCCCTACATCCATCGA	
CBS12865	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCC-	-----	AC--	CAAT-CCATCGCTCC-	TTCCCTACATCCATCGA	
CBS118889	GGCAAGTCCACCACCA	CACCGGT	-AAGCTTCC-	-----	AC--	CAAT-CCATCGCTCC-	TTCCCTACATCCATCGA	
DAOM239913	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	ACC-	CAATTCCATCGATCC-	TTCT-ATTTCCATCGA	
DAOM239912	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	ACC-	CAATTCCATCGATCC-	TTCT-ATTTCCATCGA	
CBS24865	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCC-	-----	AC--	CAATTCCATCGATCC-	TTCTCTTTTCCATCGA	
DAOM239934	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATCCCATCGATCC-	TTCT---CAATTGA	
DAOM239935	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATCCCATCGATCC-	TTCT---CAATTGA	
DAOM239936	GGCAAGTCCACCACCA	CACCGGTAAAGCTCTC-	-----	AC--	CAATCCCATCGATCC-	TTCT---CAATTGA		
DAOM239933	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATCCCATCGATCC-	TTCT---CAATTGA	
DAOM239915	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATCCCATCGCTCC-	TTCT---CTATCGA	
DAOM239914	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATCCCATCGCTCC-	TTCT---CTATCGA	
DAO2399383	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATTCATCGCTCTCTTCTTGCTATCGA		
DAO2399373	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCTC-	-----	AC--	CAATTCATCGCTCTCTTCTTGCTATCGA		
CBS229.60	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCG-	-----	CAATCCCATCGATCC-	TTCTCTCATACCGA		
CBS23828	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCG-	-----	CAATCCCATCGATCC-	TTCTCTCATACCGA		
KAS3463	GGCAAGTCCACCACCA	CACCGGT	-AAGCTTCAACCTCCTCC-	-----	CCCCCCCCA--	CCTTTCCATT----	CCATCGA	
CBS238.68	GGCAAGTCCACCACCA	CACCGGT	-AAGCTTCAACCTCCTCC-	-----	CCCCCCCCA--	CCTTTCCATT----	CCATCGA	
KAS34641	GGCAAGTCCACCACCA	CACCGGT	-AAGCTTCAACCTCCTCC-	-----	CCCCCCCCA--	CCTTTCCATT----	CCATCGA	
KAS34663	GGCAAGTCCACCACCA	CACCGGT	-AAGCTTCAACCTCCTCC-	-----	CCCCCCCCA--	CCTTTCCATT----	CCATCGA	
KAS3465	GGCAAGTCCACCACCA	CACCGGT	-AAGCTTCAATCCCCCAA-	-----	CCCCCCCCA--	CCTTTCCATT----	CCATCGA	
NRR13391	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCT-	-----	-----	ACATCCCTCTACCTTCCCATTCATCGA		
AL1878	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCT-	-----	-----	ACATCCCTCTACCTTCCCATTCATCGA		
AL1644	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCT-	-----	-----	ACATCCCTCTACCTTCCCATTCATCGA		
AL1642	GGCAAGTCCACCACCA	CACCGGT	-AAGCTCCT-	-----	-----	ACATCCCTCTACCTTCCCATTCATCGA		
AL1643								

	1841	1851	1861	1871	1881	1891	1901	1911
KAS3191	ACAACAT	-----	GACTGATT	CATCAATGCAGGTC	CACTTGATCTACAAGT	GCGGTGGTATCGACTCTCGT	TACCATCGAGAA	
DAO239926	ACAACAT	-----	GACTGATT	CATCAATGCAGGTC	CACTTGATCTACAAGT	GCGGTGGTATCGACTCTCGT	TACCATCGAGAA	
DAO239919	ACAACAT	-----	GACTGATT	CATCAATGCAGGTC	CACTTGATCTACAAGT	GCGGTGGTATCGACTCTCGT	TACCATCGAGAA	
DAO239925	ACAACAT	-----	GACTGATT	CATCAATGCAGGTC	CACTTGATCTACAAGT	GCGGTGGTATCGACTCTCGT	TACCATCGAGAA	
DAO239922	ACAACAT	-----	GACTGATT	CATCAATGCAGGTC	CACTTGATCTACAAGT	GCGGTGGTATCGACTCTCGT	TACCATCGAGAA	
DAO239917	ACAACAT	-----	GACTGATT	CATCAATGCAGGTC	CACTTGATCTACAAGT	GCGGTGGTATCGACTCTCGT	TACCATCGAGAA	
DAO239943	ACAACAT	-----	GACTGATT	TATCAATGCAGGTC	CACTTGATCTACAAGT	GCGGTGGTATCGACTCTCGT	TACCATCGAGAA	
KAS3479	ACAACAT	-----	GACTGATC	TATCAATGCAGGTC	CACTTGATCTACAAGT	GCGGTGGTATCGACTCTCGT	TACCATCGAGAA	

[illegible]

[illegible]

	2001	2011	2021	2031	2041	2051	2061	2071
KAS3191	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239926	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239919	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239925	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239922	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239917	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCG-CCCCACAACCCATGTG---						
DAO239943	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCACCCECAACCCATGTG---						
KAS3479	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCAATGTG---						
DAO239941	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCAATGTG---						
DAO239942	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239944	-----	-AGGAGGCTGCTGARCTCSGAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239940	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239945	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
DAO239946	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
KAS3480	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CCCCACAACCCATGTG---						
NRRL32583	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGGTCGCA--CCACAACACTCAAAGTG-						
NRRL2074	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGGTCGCA--CCACAACACTCAAAGTG-						
KAS346110	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGGTCGCA--CCACAACACTCAAAGTG-						
KAS347530	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGGTCGCA--CCACAACACCCCAGTGA						
KAS347430	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGGTCGCA--CCACAACACCCCAGTGA						
CBS25855	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGGTCGCA-CC-----AAGTG-						
CBS12865	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGATCGCA-CC-----AAGTG-						
CBS118889	-----	-AGGAGGCTGCTGAGCTCGGAAAGGGTTCCCTTCAAGGTACGGTCGCA-CC-----AAGTG-						
DAOM239913	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCACATTACAATTTTCAC---						
DAOM239912	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCACATTACAATTTTCAC---						
CBS24865	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCACGATAACAATCTGAA---						
DAOM239934	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGTTTGCA-CCATATAACGAAAAA-						
DAOM239935	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGTTTGCC-CCATATAACGAAAAAGA-						
DAOM239936	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGTTTGCC-CCATATAACGAAAAAGA-						
DAOM239933	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGTTTGCC-CCATATAACGAAAAA-A-						
DAOM239915	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CTGCACAAATACAACCTG-						
DAOM239914	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCA-CTGCACAAATACAACCTG-						
DAO2399383	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCT-TCATACCAACAACATCTG-						
DAO2399373	-----	-AGGAGGCTGCTGAGCTCGGCAAGGGTTCCCTTCAAGGTACGGTCGCT-TCATACCAACAACATCTG-						
CBS229.60	-----	-AGGAGGCCGCTGAGCTCGGTAAGGGTTCCCTTCAAGGTATGAGCCCA-TGAATATATCTTACACAC						
CBS23828	-----	-AGGAGGCTGCTGAGCTCGGTAAAGGGTTCCCTTCAAGGTACGGTCCCA-TGAATATCTCTTACACAC						
KAS3463	-----	-AGGAGGCTGCTGAGCTCGGTAAGGGTTCCCTTCA-----						
CBS238.68	-----	-AGGAGGCTGCTGAGCTCGGTAAGGGTTCCCTTCA-----						

	2081	2091	2101	2111	2121	2131	2141	2151
KAS3191	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239926	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239919	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239925	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTTGTAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239922	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239917	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239943	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
KAS3479	----	AAAATTCTGAAGTGGGTC----	AACTGACATCTGTCTTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239941	----	AAAATTCTGAAGTGGGTC----	AACTGACATCTGTCTTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239942	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239944	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239940	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239945	----	AAAATTCTGAAGTGGGTC----	AACTAACATATGTCTTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAO239946	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
KAS3480	----	AAAATTCTGAAGTGGGTC----	AACTAACATCTGTCTATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
NRRL32583	-----	AAAAATTTTCAAAGTGGATCAGCGAACTAACATCT--	ACAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
NRRL2074	-----	AAAAAATTTTCAAAGTGGATCAGCGAACTAACATCC--	ACAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
KAS346110	-----	AAAAAATTTTCAAAGTGGATCAGCGAACTAACATCC--	ACAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
KAS347530	-----	AAAAAATTTTCAAAGTGGATCAGTCAACTAACATCT--	ACAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
KAS347430	-----	AAAAAATTTTCAAAGTGGATCAGTCAACTAACATCT--	ACAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
CBS25855	-----	AAAAATTTTCAAAGTGGATCAAGCAACTAACATCT--	TCAAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
CBS12865	-----	AAAAAATTTTCAAAGTGGATCAATCAACTAACATTT--	TCAAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
CBS118889	-----	AAAAAATCTTCAAAGTGGATCAATCAACTAACATCT--	TCAAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
DAOM239913	-----	AAGTCTCTTAAAGTGGATC----	AACTAACATCT--	CCAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAOM239912	-----	AAGTCTCTTAAAGTGGATC----	AACTAACATCT--	CCAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
CBS24865	-----	ATCTCTTCGAAGTGGATC----	AACTAACAACT--	CCAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAOM239934	-----	AAATCTGTGATGCGGATC----	AACTAACATCT--	CCCCACAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAOM239935	-----	AAACCTGTGATGCGGATC----	AACTAACATCT--	CCCCACAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAOM239936	-----	AAACCTGTGATGCGGATC----	AACTAACATCT--	CCCCACAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAOM239933	-----	AAATCTGTGATGCGGATC----	AACTAACATCT--	CCCCACAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAOM239915	-----	AAATCTCTGCATTGGATC----	AACTAACATCT--	CCAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAOM239914	-----	AAATCTCTGCATTGGATC----	AACTAACATCT--	CCAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAO2399383	-----	AATTCTCTGAATTGGATC----	AACTAACATCT--	CCAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
DAO2399373	-----	AATTCTCTGAATTGGATC----	AACTAACATCT--	CCAATAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC				
CBS229.60		TCAATATGAAGCAACTAACATT-----	CGCATTAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
CBS23828		TCAATAAGAAGCAACTAACATT-----	CGCATTAGTACGCTTGGGTTCTTGACAAGCTCAAGGCTGAGC					
KAS3463		-----	AGTACGCTTGGGTTCTTGACAAGCTCAAGGCCGAGC					
CBS238.68		-----	AGTACGCTTGGGTTCTTGACAAGCTCAAGGCCGAGC					
KAS34641		-----	AGTACGCTTGGGTACTTGACAAGCTCAAGGCCGAGC					
KAS34663		-----	AGTACGCTTGGGTTCTTGACAAGCTCAAGGCCGAGC					
KAS3465		-----	AGTACGCTTGGGTTCTTGACAAGCTCAAGGCCGAGC					
NRRL3391		-----	AGTACGCTTGGGTTCTTGACAAGCTCAAGGCCGAGC					
AL1878		-----	AGTACGCTTGGGTTCTTGACAAGCTCAAGGCCGAGC					
AL1644		-----	AGTACGCTTGGGTTCTTGACAAGCTCAAGGCCGAGC					
AL1642		-----	AGTACGCTTGGGTTCTTGACAAGCTCAAGGCCGAGC					
AL1643								

	2401	2411	2421	2431	2441	2451	2461	2471																																																																			
KAS3191	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	C	G	T	G	A	C	A	G	C	C	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A			
DAO239926	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	C	C	G	T	G	A	C	A	G	C	C	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A		
DAO239919	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	A	C	C	C	G	T	G	A	C	A	G	C	C	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A
DAO239925	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	A	C	C	C	G	T	G	A	C	A	G	C	C	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A
DAO239922	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	A	C	C	C	G	T	G	A	C	A	G	C	C	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A
DAO239917	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	A	C	C	C	G	T	G	A	C	A	G	C	C	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A
DAO239943	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	A	C	C	G	T	G	A	C	A	G	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A			
KAS3479	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	A	C	C	G	T	G	A	C	A	G	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	G	K	T	C	C	G	C	A	G	C	T	C	A			
DAO239941	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	A	C	C	G	T	G	A	C	A	G	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A			
DAO239942	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A	G	A	C	A	C	C	G	T	G	A	C	A	G	C	T	T	C	T	G	G	C	T	T	C	A	C	C	T	C	G	T	G	T	C	C	G	C	A	G	C	T	C	A			
DAO239944	G	T	T	C	G	A	G	G	C	T	G	G	T	A	T	C	T	C	C	A	A	G	A	T	G	G	C	C	A																																														

AL1878 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTTACCCCTCGGTGTCCGCCAGCTCA
 AL1644 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTTACCCCTCGGTGTCCGCCAGCTCA
 AL1642 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTTACCCCTCGGTGTCCGCCAGCTCA
 AL1643 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTTACCCCTCGGTGTCCGCCAGCTCA
 CBS136.22 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTTACCCCTCGGTGTCCGCCAGCTCA
 CBS347.51 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTTACCCCTCGGTGTCCGCCAGCTCA
 CBS336.48 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTTACCCCTCGGTGTCCGCCAGCTCA
 CBS110644 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTTACCCCTCGGTGTCCGCCAGCTCA
 CBS42665 NNN
 DAOM239916 NNN
 NRRL705 GTTCGAGGCTGGTATCTCCAAGGATGGCCAGACTCGTGAGCACGCTCTGCTCGCTTTACCCCTCGGTGTCCGTGAGCTCA

[	2481	2491	2501	2511	2521	2531	2541	2551	]
[									]
KAS3191	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239926	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239919	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239925	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239922	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239917	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239943	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
KAS3479	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239941	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239942	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239944	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239940	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239945	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
DAO239946	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
KAS3480	TCGTTGCCCTGAACAAGATGGAMACTTGCAAGT	-----							
NRRL32583	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTGTAACCTGTCTGACTACATGACATC	-----							
NRRL2074	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTATAACCTGCCTGACTACATGACATC	-----							
KAS346110	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTATAACCTGCCTGACTACATGACATC	-----							
KAS347530	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTGTAACCTGCCTGACTACATGACATC	-----							
KAS347430	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTGTAACCTGCCTGACTACATGACATC	-----							
CBS25855	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTAACCTCCCGGCTAGTCCAACCTTAACCT	-----							
CBS12865	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTAACCTCCCGGCTAGTCCAACCTTAACCT	-----							
CBS118889	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTTACCCTCCCTGACTAGTCCAGCTTAACCT	-----							
DAOM239913	TCGTTGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTTCTAATCCATGGCTACTTGACC	-----							
DAOM239912	TCGTTGCCCTGAACAAGATGGACACTTGCAAGTGGTACGTTTCTAATCCATGGCTACTTGACC	-----							
CBS24865	TCGTTGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTGTCTAATCCTATCTTACTTTATC	-----							
DAOM239934	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTTGCTAATGCCTTGATATTACGTAATCTTTG-GGATTATGT	-----							
DAOM239935	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTTGCTAATGCCTTGATATTACGTAATCTTTG-GGATTATGT	-----							
DAOM239936	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTTGCTAATGCCTTGATATTACGTAATCTTTG-GGATTATGT	-----							
DAOM239933	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTATGTTGCTAATGCCTTGATATTACGTAATCTTTG-GGATTATGT	-----							
DAOM239915	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTAACTCTACAATGCCTTTATGTCACGCTTTATATC-----ACGT	-----							
DAOM239914	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTAACTCTACAATGCCTTTATGTCACGCTTTATATC-----ACGT	-----							
DAO2399383	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTAACTCTACAATGTCTTTGTGTACACTTTGTGCTTTTCGTGACAC	-----							
DAO2399373	TCGTCGCCCTGAACAAGATGGACACTTGCAAGTGGTAACTCTACAATGTCTTTGTGTACACTTTGTGCTTTTCGTGACAC	-----							
CBS229.60	TCGTCGCCCTCAACAAGATGGATACTTGCAAGT	-----							
CBS23828	TCGTTGCCCTCAACAAGATGGATACTTGCAAGT	-----							
KAS3463	TCGTCGCCCTGAACAAGATGGACACCTGCAAGT	-----							
CBS238.68	TCGTCGCCCTGAACAAGATGGACACCTGCAAGT	-----							
KAS34641	TCGTCGCCCTGAACAAGATGGACACCTGCAAGT	-----							
KAS34663	TCGTCGCCCTGAACAAGATGGACACCTGCAAGT	-----							
KAS3465	TCGTCGCCCTGAACAAGATGGATACCTGCAAGT	-----							
NRRL3391	TCGTCGCCCTGAACAAGATGGATACTTGCAAGT	-----							
AL1878	TCGTCGCCCTGAACAAGATGGATACTTGCAAGT	-----							
AL1644	TCGTCGCCCTGAACAAGATGGATACTTGCAAGT	-----							
AL1642	TCGTCGCCCTGAACAAGATGGATACTTGCAAGT	-----							
AL1643	TCGTCGCCCTGAACAAGATGGATACTTGCAAGT	-----							
CBS136.22	TCGTCGCCCTGAACAAGATGGACACTTGCAAGT	-----							
CBS347.51	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
CBS336.48	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
CBS110644	TCGTTGCCCTGAACAAGATGGACACTTGCAAGT	-----							
CBS42665	NN	-----							
DAOM239916	NN	-----							
NRRL705	TTGTTGCCCTCAACAAGATGGACACCTGCAAGT	-----							

[	2561	2571	2581	2591	2601	2611	2621	2631	]
[									]
KAS3191	-----	GGAGCGAGGACCGTTACAACGAGATTGTCAAGGAGACCTCCAAC							

	2641	2651	2661	2671	2681	2691	2701	2711
KAS3191	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239926	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239919	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239925	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239922	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239917	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239943	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
KAS3479	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239941	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239942	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239944	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239940	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239945	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
DAO239946	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
KAS3480	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							
NRRL32583	TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT							

NRRL2074 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 KAS346110 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAAC-GGTGACAACATGCTT
 KAS347530 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAAC-GGTGACAACATGCTT
 KAS347430 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAAC-GGTGACAACATGC-T
 CBS25855 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 CBS12865 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 CBS118889 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 DAOM239913 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 DAOM239912 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 CBS24865 TTCATCAAGAAGGTCGGCTAC-----AAC-----
 DAOM239934 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 DAOM239935 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 DAOM239936 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-CTCAAC-GGTGACAACATGCTT
 DAOM239933 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 DAOM239915 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 DAOM239914 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 DAO2399383 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAAC-GGTGACAACATGCTT
 DAO2399373 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGG-TTCAAC-GGTGACAACATGCTT
 CBS229.60 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 CBS23828 TTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 KAS3463 TTCATCAAGAAGGTCGGCTACAACCCCAAGGTTGCCCTTCGTTC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTT
 CBS238.68 TTCATCAAGAAGGTCGGCTACAACCCCAAGGTTGCCCTTCGTTC-CCATCTCCGG-TTCAAC-GGTGACAACATGCTT
 KAS34641 TTCATCAAGAAGGTCGGCTACAACCCCAAGGTTGCCCTTCGTTC-CCATCTCCGG-TTCAAC-GGTGACAACATGCTT
 KAS34663 TTCATCAAGAAGGTCGGCTACAACCCCAAGGTTGCCCTTCGTTC-CCATCTCCGG-TTCAAC-GGTGACAACATGCTT
 KAS3465 TTCATCAAGAAGGTCGGCTACAACCCCAAGGTTGCCCTTCGTTC-CCATCTCCGG-TTCAAC-GGTGACAACATGCTT
 NRRL3391 TTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTCC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTG
 AL1878 TTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTG
 AL1644 TTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTG
 AL1642 TTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTG
 AL1643 TTCATCAAGAAGGTCGGATTCAACCCCAAGACTGTCCCTTCGTTC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTG
 CBS136.22 TTCATCAAGAAGGTCGGCTACAACCCCAAGAACGTTCCCTTCGTTC-CTATCTCCGGTTTCAAC-GGTGACAACATGCTC
 CBS347.51 TTCATCAAGAAGGTCGGCTACAACCCCAAGAACGTTCCCTTCGTTC-CTATCTCCGGTTTCAAC-GGTGACAACATGCTC
 CBS336.48 TTCATCAAGAAGGTCGGCTACAACCCCAAGAACGTTCCCTTCGTTC-CTATCTCCGGTTTCAAC-GGTGACAACATGCTC
 CBS110644 TTCATCAAGAAGGTCGGCTACAACCCCAAGAACGTTCCCTTCGTTC-CTATCTCCGGTTTCAAC-GGTGACAACATGCTC
 CBS42665 NNN
 DAOM239916 NNN
 NRRL705 TTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTTC-CCATCTCCGGTTTCAAC-GGTGACAACATGCTC

	2721	2731	2741	2751
[				]
KAS3191	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAO239926	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAO239919	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAO239925	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAO239922	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAO239917	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAO239943	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAG-	
KAS3479	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAO239941	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAO239942	GAGGCCCTCCCC	-----		
DAO239944	-----			
DAO239940	-----			
DAO239945	GAGGCCCTCCCC	-AACTGCCCC	TGGTAC-AGG	
DAO239946	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
KAS3480	GAGG	-----		
NRRL32583	GAGGCCCTCCCC	-AACTGCCCC	-----	
NRRL2074	GAGGCCCTCCCC	-AACTGCCCC	TGGTACA--G	
KAS346110	GAGGCCCTCCCC	-AACTGCCCC	TGGTACA-GG	
KAS347530	GAGGCCCTCCCC	-AACTG--CCCT	TGGTACA-GG	
KAS347430	GAGT-CCCCC	-----		
CBS25855	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
CBS12865	GAGGCCCTCCCC	-AACTGCCCC	TGGTACA-GG	
CBS118889	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGC	
DAOM239913	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
DAOM239912	GAGGCCCTCCCC	-AACTGCCCC	TGGTACAAGG	
CBS24865	-----			
DAOM239934	GAGGCCCTCCCC	--ACTGCCC	TGG-ACAAGG	
DAOM239935	GAGGCCCTCCCC	--ACTGCCC	TGGTACA-GG	
DAOM239936	GAGGCCCTCCCC	--ACTGCCCC	TGG-ACA-G-	
DAOM239933	GAGGCCCTCCCC	-AACTGCCCC	TGGTACA-GG	
DAOM239915	GAGGCCCTCCCC	-AACTGCCCC	TGGTAAA-GG	

DAOM239914 GAGGCCTCCCC-AACTGCCCCCTGG-ACA-GG
 DAO2399383 GAGGCCTCCCC-AACTGCCCCCTGGTACA-G-
 DAO2399373 GAGGCCTCCCC--AACTG-CCCTGGTACA-G-
 CBS229.60 GAGCCCTCCACC-AACTGCCCCCTGGTACAAGG
 CBS23828 GAGCCCTCCACCAACTGCCCCCTGGTACAAGG
 KAS3463 GAGCCCTCCCC-AACTGCCCCCTGG-----
 CBS238.68 GAGCCCTCCCC-AACTGCCCCCTGGTACAAGG
 KAS34641 GAGCCCTCCCC-AACTGCCCCCTGGTACA-GG
 KAS34663 GAGCCCTCCCC-AACTGCCCCCTGG-ACAAG-
 KAS3465 GAGCCCTCCCC-AACTGCCCCCTGGTACAAGG
 NRRL3391 GAGCCCTCCTCC-AACTGCCCCCTGGTACAAG-
 AL1878 GAGCCCTCCTCC-AACTGCCCCCTGGTACAAG-
 AL1644 GAGCCCTCCTCC-AACTGCCCCCTGGTACAAGG
 AL1642 GAGCCCTCCTCC-AACTGCCCCCTGGTACAAG-
 AL1643 GAGCCCTCCTCC-AACTGCCCCCTGGTACAAGG
 CBS136.22 GAGCCCTCCCCT-AACTGCCCCCTGGTACAAGG
 CBS347.51 GAGCCCTCCCCT-AACTGCCCCCTGGTACAAGG
 CBS336.48 GAGCCCTCCCCT-AACTGCCCCCTGGTACAAGG
 CBS110644 GAGCCCTCCCCT-AACTGCCCCCTGGTACAAGG
 CBS42665 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
 DAOM239916 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
 NRRL705 GAGCCCTCCCC-AACTGCCCCCTGGTACA--G

Appendix 5: Chapter 4 Multiple Sequence Alignments

Multiple *BenA* Sequence Alignment

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
DAOM239952 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM239954 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM214729 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM239950 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM213268 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM239955 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM239951 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM239948 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM239949 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
FRR2695    TGGGA-ATCCCGAGCACAACACGACAATTCCTCTATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
96M111148 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM213171 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM178627 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM208497 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
CBS30197   TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
KAS3459   TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
NRRL35183 TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
CBS83896  TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
CBS70888  TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM239953 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
CBS30097   -----CCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
FRR1268    TGGGA-ATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
DAOM226579 TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
FRR1391    TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
KAS3460    TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
CBS114222  TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
FRR1511    TGGGA-ATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
KAS3458    TGGGA-ATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
CBS46067   TGGGA-ATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
CBS34768   TGGGA-ATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
CBS102405   -----
CBS118872   -----
DAOM239957 CTGGGAATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAAAGTACTCGATATTC
FRR1058     -TGGATATCCCGAGCACAACACGACAATTCCT-CGTGTCGTGCTTCGATCTAATATGAGAACCAAAGTACTCAAGATTC
DAOM226606 TGACCTCACCTTCGGTCAAATCATCAATTGTT-GAACCAGGACCCCTT-----TACTGACTTGAATCAC
NRRL787     TGACCTCACCTTCGGTCAAATCATCAATTGTT-GAACCAGGACCCCTT-----TACTGACTTGAATCAC
DAOM215381 TGACCTCACCTTCGGTCAAATCATCAATTGTT-GAACCAGGACCCCTT-----TACTGACTTGAATCAC
CBS21930    -----
NRRL3447    -AAAACCTCCCGAGCACAACAAAGCAACCCCT-AATTGCGAGTTTCATGCAACA-----GATACTGACTCGAAGTAC

[      81      91      101     111     121     131     141     151     ]
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DAOM239954 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM214729 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM239950 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM213268 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM239955 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM239951 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM239948 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM239949 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
FRR2695    AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
96M111148 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM213171 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM178627 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM208497 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
CBS30197   AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
KAS3459   AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
NRRL35183 AGGCAAACCATTTGCTGGTGAGCAGCGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----

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CBS83896 AGGCAAACCAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTTG-----
CBS70888 AGGCAAACAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-GAACAGCTTG-----
DAOM239953 AGGCAAACCAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTCG-----
CBS30097 AGGCAAACCAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCCCG-----
FRR1268 AGGCAAACCAATTGCTGGTGAGCACGGCCTTGASGGCGATGGCCAGTAAGT-CAACAGCTCG-----
DAOM226579 AGGCAAACAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTTG-----
FRR1391 AGGCAAACAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTTG-----
KAS3460 AGGCAAACAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGC-CAACAGCTTG-----
CBS114222 AGGCAAACCAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CTACAGCTTG-----
FRR1511 AGGCAAACCAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTTG-----C
KAS3458 AGGCAAACCAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTGCAACAGCTTG-----C
CBS46067 AGGCAAACAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTTG-----C
CBS34768 AGGCAAACAATTGCTGGCGAGCACGGCCTTGAGGGCGATGGCCAGTAAGT-CAACAGCTTG-----CCCC
CBS102405 -----
CBS118872 -----
DAOM239957 AGGCAAACAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGCTTGCCCCCCCCCCCCCCCC
FRR1058 AGGCAAACCAATTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGT-CAACAGTTTG-----GCCCC
DAOM22606 AGGCAGAACATTGCTAGCGAGCATGGCCTGACGGCGAGGGCCAGTAAGT-----
NRRL787 AGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGCCAGTAAGT-----
DAOM215381 AGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGCCAGTAAGT-----
CBS21930 -GGCAGACCATCTCTGGCGAGCACGGTCTCGACAGCAACGG-----
NRRL3447 AGGCAGACCATTGCTGGTGAGCACGGCCTTGATGGCGATGGCCAGTAAGT-----

[ 161 171 181 191 201 211 221 231 ]
[ | | | | | | | ]
DAOM239952 --CCCTCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
DAOM239954 --CCCTCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
DAOM214729 --CCCTCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
DAOM239950 --CCCTCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
DAOM213268 --CCCTCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
DAOM239955 --CCCTCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
DAOM239951 --CCCTCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
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CBS30197 --CCCTCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
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CBS83896 --CCCCCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
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KAS3460 ---CCCCCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
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FRR1511 CCCCCCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
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CBS46067 CCCCCCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
CBS34768 CCCCCCCCCCACCAGTGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
CBS102405 -----TGGGTTCTTGACGACAGA-GAATGGCGGTSAGATA--TTTTTCGGTTTAGCTACAATGGTTCCCT
CBS118872 -----TCCT
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CBS21930 -----TGCTTACAATGGCAGCT
NRRL3447 --CTCTTCGATACCATTGATACCTCTCGACACG-GAATGGCGGTCTGATA--TTTTT--GGTTAGCTACAATGGTACCT

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DAOM214729 CCGACCTCCAGCTGGAGCGCATGAACGTCTACTTCACCCACGTAAGTCG-TGAAAAACGTCTTCCCAATCAAAGAAATCT
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DAOM239950	---	CCCAAACCTGAC	-CATTGA	-----	ACCGTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
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CBS30197	---	CCCAAACCTGAC	-CATTGA	-----	ACCGTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
KAS3459	---	CCCAAACCTGAT	-CATTGA	-----	AACGTTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
NRRL35183	---	CCCAAACCTGAT	-CATTGA	-----	AACGTTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
CBS83896	---	CCCAAACCTGAT	-CATTGA	-----	AACGTTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
CBS70888	---	CCCAAACCTGAT	-CATTGA	-----	AACGTTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
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KAS3460	---	CCCAAACCTGAT	GCATTGA	-----	AACGTTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
CBS114222	---	CCCAAACCTGAC	-CATTGA	-----	AACGTTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
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CBS102405	---	CCCAAACCTGAT	-CATTGA	-----	AACGTTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
CBS118872	---	CCCAAACCTGAT	-CATTGA	-----	AACGTTTCGATTTTC	CAGGC	-TAGCGG	-TGACAAGTATGTT	CCCCG
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 CBS21930 ---CCACAACGCGTC-TCTTGGTTCATACGGACCCACTGACCGCCTCTCCAGGC-TTCCGG-CAACAAGTACGTTCCCTCG
 NRRL3447 AGAATTAAGTCTAAC-CCATG-----GATGTTTTGTTTTATCAGGC-CAGCGG-TGACAAGTACGTTCCCCG

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DAOM213268	TGCCGTTCTCGTCGA-CCTGGAGCCCGGTACCATGGACGCTGT-CCGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGA							
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FRR1268	TGCCGTTCTCGTCGA-CCTGGAGCCCGGTACCATGGACGCTGT-CCGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGA							
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CBS118872	TGCCGTTCTCGTCGA-CCTGGAGCCCGGTACCATGGACGCTGT-CCGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGA							
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CBS21930	TGCCGTTCTCGTCGA-CCTGGAGCCCGGTACCATGGACGCTGT-CCGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGA							
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CBS70888	CAACTTCGTCTTTGGCCAGTCTG		
DAOM239953	CAACTTCGTCTTTGGCCAGTCTG		

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NRRL787	C	A	T	T	A	C	C	G	A	G	T	G	A	G	G	C	C	T	C	T	G	G	G	T	C	C	A	A	C	T	C	C	C	A	C	C	G	T	G	T	T	A	T	C	G	T	A	C	C	T	T	G	T	T	G	C	T	T	C	G	G	C	G	G	C	C	G	C	-	T	C	A	
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DAOM178627	C	A	T	T	A	C	C	G	A	G	T	G	A	G	G	C	C	T	C	T	G	G	G	T	C	C	A	A	C	T	C	C	C	A	C	C	C	G	T	G	T	T	A	T	C	G	T	A	C	C	T	T	G	T	T	G	C	T	T	C	G	G	C	G	G	C	C	G	C	-	T	C	A
DAOM213171	C	A	T	T	A	C	C	G	A	G	T	G	A	G	G	C	C	T	C	T	G	G	G	T	C	C	A	A	C	T	C	C	C	A	C	C	C	G	T	G	T	T	A	T	C	G	T	A	C	C	T	T	G	T	T	G	C	T	T	C	G	G	C	G	G	C	C	G	C	-	T	C	A
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DAOM239949	C	A	T	T	A	C	C	G	A	G	T	G																																																													

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 96M111148 ATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCTCG-CCCCCGCTTCCGGGGGGCGGGC
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 FRR1391 ATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCTCG-CCCCCGCTTCCGGGGGGCGGGC
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[401 411 421 431 441 451 461 471]
 [| | | | | | |]
 NRRL787 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 NRRL35183 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM178627 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM213171 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM213268 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM226577 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM214729 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM226606 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239947 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239948 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239949 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239950 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239951 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239952 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239953 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239954 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAG--CCGCCGGCGCC
 DAOM239955 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239956 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 DAOM239957 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 96M111148 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS219.30 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS300.97 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS301.97 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS336.59 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS347.68 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS358.48 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS460.67 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS708.88 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS838.96 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS102405 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 CBS118872 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 FRR1058 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 FRR1391 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 FRR1511 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 FRR2695 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 KAS3458 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 KAS3459 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 KAS3460 CCGAAAGGCAGCGCGGCACCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC
 NRRL3447 CCGAAAGGCAGCGCGGCATCGCGTCCGGTCTCGAGCGTATGGGGCTTCGTACCCGCTCTGTAGGCCCGGCCGGCGCC

[481 491 501 511 521 531 541 551]
 [| | | | | | |]
 NRRL787 CGCCGGCGAACACCATCAATCTTAACAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTTAAGCATATCAATAA
 NRRL35183 CGCCGGCGAACACCATCAATCTTAACAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTTAAGCATATCAATA-
 DAOM178627 CGCCGGCGAACACCATCAATCTTAACAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTTAAGCATATCAATAA
 DAOM213171 CGCCGGCGAACACCATCAATCTTAACAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTTAAGCATATCAATAA
 DAOM213268 CGCCGGCGAACACCATCAATCTTAACAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTTAAGCATATCAATAA

DAOM226577 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATA-
 DAOM214729 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 DAOM226606 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 DAOM239947 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 DAOM239948 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 DAOM239949 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGC-----
 DAOM239950 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 DAOM239951 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTA-----
 DAOM239952 CGCCGGCGAACACCATCAATCTTAACCAGG-TGACCTCG-----
 DAOM239953 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 DAOM239954 CGCCGGCGAACACCATCAATCTTAACCAGG-TGACCTCGGATCAGGTAG-----
 DAOM239955 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 DAOM239956 CGCCGGCGAACACCATCAATCTTAACCAGG-TGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 DAOM239957 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 96M111148 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS219.30 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS300.97 CGCCGGCGAACACCATCAATCTTAACCAGG-TGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS301.97 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS336.59 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS347.68 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS358.48 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS460.67 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS708.88 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS838.96 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS102405 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 CBS118872 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATA-
 FRR1058 CGCCGGCGAACACCATCAATCTTAACCAGG-TGACCTCGGATCAG-----
 FRR1391 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATA-
 FRR1511 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCA-TA-
 FRR2695 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 KAS3458 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 KAS3459 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 KAS3460 CGCCGGCGAACACCATCAATCTTAACCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA
 NRRL3447 CGCCGGCGACCCCATCAATCTT-TCCAGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATAA

[561]
 [|]
 NRRL787 G
 NRRL35183 G
 DAOM178627 G
 DAOM213171 G
 DAOM213268 G
 DAOM226577 -
 DAOM214729 G
 DAOM226606 G
 DAOM239947 G
 DAOM239948 G
 DAOM239949 -
 DAOM239950 G
 DAOM239951 -
 DAOM239952 -
 DAOM239953 G
 DAOM239954 -
 DAOM239955 G
 DAOM239956 G
 DAOM239957 G
 96M111148 G
 CBS219.30 -
 CBS300.97 G
 CBS301.97 G
 CBS336.59 G
 CBS347.68 G
 CBS358.48 G
 CBS460.67 G
 CBS708.88 G
 CBS838.96 G
 CBS102405 G
 CBS118872 G
 FRR1058 -
 FRR1391 -
 FRR1511 -

FRR2695 G
 KAS3458 G
 KAS3459 G
 KAS3460 G
 NRRL3447 G

Multiple *Cox1* Sequence Alignment

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      |      ]
NRRL787  -----AAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
NRRL35183 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM178627 GTGATTTT-ATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM213268 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM214729 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM213171 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM226577 -TGA-TTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAAGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM226606 -----ATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239948 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239949 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239950 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239951 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239952 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239953 GTGA-TTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239954 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239955 -----TAGG-ACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239956 GTGA-TTTTATCTTCAAATGCTAAAGATATAGG-ACATAATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
DAOM239957 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
96M111148 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS219.30 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS300.97 ---ATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS301.97 ---A-TTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS300.50 -TGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS347.68 -TGA-TTTTCTCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS358.48 -TGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS460.67 -----AGG-ACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS708.88 -TGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS838.96 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS102405 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS114222 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
CBS118872 ----TTTTT-T-TT-AAATGCTAAAG-AATAGG-ACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
FRR1058 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
FRR1391 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
FRR1511 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
FRR2695 GTGA-TTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
KAS3458 GTGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
KAS3459 -----ATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
KAS3460 -TGATTTTATCTTCAAATGCTAAAGATATAGGAACATTATATTTAATGTTTTCATTATTTTCAGGATTACTTGAACAG
NRRL3447 GTGATTTTATCTTCTAATGCTAAAGATATGGTACTCTATACTTAATGTTTTCATTATTTTCAGGGTTAATAGGAACAG

[      81      91      101      111      121      131      141      151      ]
[      |      |      |      |      |      |      |      |      ]
NRRL787  CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
NRRL35183 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM178627 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM213268 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM214729 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM213171 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM226577 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM226606 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM239948 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM239949 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM239950 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM239951 CATTTTCTGTAAGCTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM239952 CATTTTCTGTAAGCTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM239953 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM239954 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA
DAOM239955 CATTTTCTGTACTTATAAGATTAGAGCTTTCAGGTCAGGAGTACAATATATTTTCAGATAACCAATTATATAAATAGTATA

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	321	331	341	351	361	371	381	391
NRRL787	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
NRRL35183	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM178627	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM213268	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM214729	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM213171	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM226577	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM226606	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239948	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239949	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239950	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239951	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239952	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239953	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239954	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239955	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239956	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
DAOM239957	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
96M111148	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS219.30	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS300.97	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS301.97	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS300.50	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS347.68	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS358.48	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS460.67	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS708.88	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS838.96	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS102405	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS114222	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
CBS118872	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			
FRR1058	TTCTTATTTATATTCTCAGCAAC	AATAGAGAATGGAGCA	GGTACAGGATGAACATTAT	ACCCACCATTAT	CAGGTATA			


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CBS219.30  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS300.97  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS301.97  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS300.50  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS347.68  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTA--CCTTATTTGGAT--GAG
CBS358.48  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS460.67  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS708.88  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS838.96  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS102405  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS114222  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
CBS118872  TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
FRR1058    TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
FRR1391    TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
FRR1511    TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
FRR2695    TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
KAS3458    TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
KAS3459    TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
KAS3460    TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG
NRRL3447   TATGAATTTTCAT-AACAACAATATTTAAATATGAGAAGTCCAGGTATACGTTTACACAAATTAGCCTTATTTGGAT--GAG

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[          561          571          581          591 ]
[          |          |          |          | ]
NRRL787     CGTAGTTATTA-----
NRRL35183   CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM178627  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM213268  CGTAGTTATTACAGCTGTATTATTATTAT-A
DAOM214729  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM213171  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM226577  CGTAGTTATTACAGCTGTAT-----
DAOM226606  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM239948  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM239949  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM239950  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM239951  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM239952  CGTTATTATTACAGCTGTATTATTATTATTA
DAOM239953  CGTAGTTATTACAGCTGTATTATTATTA---
DAOM239954  CGTAGTTATTACAGCTGTATTATTATTAT-A
DAOM239955  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM239956  CGTAGTTATTACAGCTGTATTATTATTATTA
DAOM239957  CGTAGTTATTACAGCTGTATTATTATTATTA
96M111148   CGTAGTTATTACAGCTGTATTATTATTATTA
CBS219.30   CGTAGTTATTACAGCTGTATTATTATTA---
CBS300.97   CGTAGTTATTACAGCTGTATTATTATTATTA
CBS301.97   CGTAGTTATTACAGCTGTATTATTATTAT-A
CBS300.50   CGTAGTTATTACAG-----
CBS347.68   CGTAGTTATTACAGCTGTATTATTATTATTA
CBS358.48   CGTAGTTATTACAG-----
CBS460.67   CGTAGTTATTACAGCTGTATTATTATTAT-A
CBS708.88   CGTAGTTATTACAGCTGTATTATTATTAT-A
CBS838.96   CGTAGTTATTACAGCTGTATTATTATTAT-A
CBS102405   CGTAGTTATTACAGCTGTATTATTATTAT-A
CBS114222   CGTAGTTATTACAGCTGTATTATTATTATTA
CBS118872   CGTAGTTATTACAGCTGTATTATTATTATTA
FRR1058     CGTAGTTATTACAGCTGTATTATTATTATTA
FRR1391     CGTAGTTATTACAGCTGTATTATTATTATTA
FRR1511     CGTAGTTATTACAGCTGTATTATTATTATTA
FRR2695     CGTAGTTATTACAGCTGTATTATTATTAT-A
KAS3458     CGTAGTTATTACAGCTGTATTATTATTATTA
KAS3459     CGTAGTTATTACAGCTGTATTATTATTATTA
KAS3460     CGTAGTTATTACAGCTGTATTATTATTATTA
NRRL3447    CGTAGTTATTACAGCTGTATTATTATTATTA

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Multiple *TEF1-α* Sequence Alignment

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[          1          11          21          31          41          51          61          71          ]
[          |          |          |          |          |          |          |          ]
NRRL35183   CACGTCGA-TTCCGCAAGTCCACCACC-----

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	81	91	101	111	121	131	141	151
[								
[								]
NRR135183	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS358.48	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS336.59	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS118872	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM226579	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS102405	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
FRR1511	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS708.88	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS838.96	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
FRR1391	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
FRR2695	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM239957	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM239956	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
KAS3459	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
NRR1787	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS114222	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM226606	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS347.68	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
KAS3460	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS460.67	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGT-GTATCGACTCTCG			
DAOM178627	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM213171	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM239955	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
96M111148	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM239949	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM239950	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM239948	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM239952	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
DAOM239953	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS300.97	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			
CBS301.97	-----	-----	-----	-----	ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG			

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DAOM239954 -----ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG
KAS3458 -----ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG
CBS219.30 -----ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG
FRR1058 -----ACCGGTCACCTGATCTACAAGTGCGGTGGTATCGACTCTCG
DAOM239951 ----CCTATCCCACAATAACCACATTCTGATTTCTCCCAACAGGTCACTTGATCTACAAGTGCGGTGGTATCGACTCTCG
DAOM239947 ----CCTATCCCACAATAACCATATACTGATTTCTCCCAACAGGTCACTTGATCTACAAGTGCGGTGGTATCGACTCTCG
NRRL3441 CATCCTTCATCCGCAATGACAAAATACTGA-TTCTCCCGACAGGTCACTGATCTACAAGTGCGGTGGTATCGACTCTCG

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[ 161 171 181 191 201 211 221 231 ]
[ | | | | | | | ]
NRRL35183 TACCATCGAGAAGTTCGAGA-----
CBS358.48 TACCATCGAGAAGTTCGAGA-----
CBS336.59 TACCATCGAGAAGTTCGAGA-----
CBS118872 TACCATCGAGAAGTTCGAGA-----
DAOM226579 TACCATCGAGAAGTTCGAGA-----
CBS102405 TACCATCGAGAAGTTCGAGA-----
FRR1511 TACCATCGAGAAGTTCGAGA-----
CBS708.88 TACCATCGAGAAGTTCGAGA-----
CBS838.96 TACCATCGAGAAGTTCGAGA-----
FRR1391 TACCATCGAGAAGTTCGAGA-----
FRR2695 TACCATCGAGAAGTTCGAGA-----
DAOM239957 TACCATCGAGAAGTTCGAGA-----
DAOM239956 TACCATCGAGAAGTTCGAGA-----
KAS3459 TACCATCGAGAAGTTCGAGA-----
NRRL787 TACCATCGAGAAGTTCGAGA-----
CBS114222 TACCATCGAGAAGTTCGAGA-----
DAOM226606 TACCATCGAGAAGTTCGAGA-----
CBS347.68 TACCATCGAGAAGTTCGAGA-----
KAS3460 TACCATCGAGAAGTTCGAGA-----
CBS460.67 TACCATCGAGAAGTTCGAGA-----
DAOM178627 TACCATCGAGAAGTTCGAGA-----
DAOM213171 TACCATCGAGAAGTTCGAGA-----
DAOM239955 TACCATCGAGAAGTTCGAGA-----
96M111148 TACCATCGAGAAGTTCGAGA-----
DAOM239949 TACCATCGAGAAGTTCGAGA-----
DAOM239950 TACCATCGAGAAGTTCGAGA-----
DAOM239948 TACCATCGAGAAGTTCGAGA-----
DAOM239952 TACCATCGAGAAGTTCGAGA-----
DAOM239953 TACCATCGAGAAGTTCGAGA-----
CBS300.97 TACCATCGAGAAGTTCGAGA-----
CBS301.97 TACCATCGAGAAGTTCGAGA-----
DAOM239954 TACCATCGAGAAGTTCGAGA-----
KAS3458 TACCATCGAGAAGTTCGAGA-----
CBS219.30 TACCATCGAGAAGTTCGAGA-----
FRR1058 TACCATCGAGAAGTTCGAGA-----
DAOM239951 TACCATCGAGAAGTTCGAGA-----
DAOM239947 TACCATCGAGAAGTTCGAGA-----
NRRL3441 TACCATCGAGAAGTTCGAGAAGGTACGGAATCACAATTTTCTACTGCCCTCCTTGAGTGGGGTGGGGTCG-----TTC

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[ 241 251 261 271 281 291 301 311 ]
[ | | | | | | | ]
NRRL35183 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS358.48 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS336.59 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS118872 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM226579 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS102405 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
FRR1511 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS708.88 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS838.96 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
FRR1391 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
FRR2695 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239957 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239956 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
KAS3459 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
NRRL787 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS114222 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM226606 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS347.68 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
KAS3460 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS460.67 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----

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DAOM178627 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM213171 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239955 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
96M111148 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239949 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239950 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239948 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239952 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239953 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS300.97 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS301.97 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239954 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
KAS3458 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
CBS219.30 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
FRR1058 -----AGGAAGCCGCCGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239951 -----AGGAGGCCGCTGAGCTCGGCAAGGGTTCCTTCA-----
DAOM239947 -----AGGAGGCCGCTGAGCTCGGCAAGGGTTCCTTCA-----
NRRL3441 TCTCGCCTTGGAACATTGTGCTAACCCCTCACAGGAAGCCGCTGAGCTCGGCAAGGGTTCCTTCA-----

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[ 321 331 341 351 361 371 381 391 ]
[ | | | | | | | | ]
NRRL35183 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS358.48 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS336.59 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS118872 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM226579 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS102405 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
FRR1511 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS708.88 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS838.96 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
FRR1391 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
FRR2695 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239957 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239956 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
KAS3459 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
NRRL787 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS114222 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM226606 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS347.68 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
KAS3460 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS460.67 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM178627 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM213171 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239955 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
96M111148 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239949 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239950 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239948 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239952 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239953 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS300.97 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS301.97 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239954 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
KAS3458 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
CBS219.30 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
FRR1058 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239951 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
DAOM239947 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG
NRRL3441 -----AGTACGCCTGGGTTCTTGACAAGCTGAAGGCTGAG

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[ 401 411 421 431 441 451 461 471 ]
[ | | | | | | | | ]
NRRL35183 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC
CBS358.48 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC
CBS336.59 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC
CBS118872 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC
DAOM226579 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC
CBS102405 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC
FRR1511 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC
CBS708.88 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC
CBS838.96 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTCACCGTCATTGGTATGTC

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FRR1391 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 FRR2695 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 DAOM239957 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 DAOM239956 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 KAS3459 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCTGTCATTGGTATGTC
 NRRL787 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 CBS114222 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 DAOM226606 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 CBS347.68 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 KAS3460 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 CBS460.67 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 DAOM178627 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 DAOM213171 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 DAOM239955 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 96M111148 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 DAOM239949 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 DAOM239950 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 DAOM239948 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 DAOM239952 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 DAOM239953 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 CBS300.97 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 CBS301.97 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 DAOM239954 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTACGTC
 KAS3458 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 CBS219.30 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 FRR1058 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 DAOM239951 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 DAOM239947 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC
 NRRL3441 CGTGAGCGTGGTATCACCATCGATATCGCTCTCTGGAAGTTCCAGACCGCCAAGTATGAGGTACCGTCATTGGTATGTC

	481	491	501	511	521	531	541	551
[								
[								
NRRL35183	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS358.48	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS336.59	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS118872	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
DAOM226579	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS102405	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
FRR1511	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS708.88	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS838.96	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
FRR1391	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
FRR2695	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
DAOM239957	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
DAOM239956	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
KAS3459	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
NRRL787	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS114222	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
DAOM226606	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS347.68	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
KAS3460	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS460.67	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
DAOM178627	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
DAOM213171	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
DAOM239955	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
96M111148	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
DAOM239949	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
DAOM239950	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
DAOM239948	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
DAOM239952	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
DAOM239953	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
CBS300.97	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
CBS301.97	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
DAOM239954	TTATCT--GTCACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAATGTTCTCTC---TCAGACGCC							
KAS3458	TTATCT--GTTACC-CCTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
CBS219.30	TTCTCT--GTTACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
FRR1058	TTCTCT--GTTACC-CTTT---CCACCCGT-----CTGTC-----CAT-CGACTAACGTTCTCTC---CAGACGCC							
DAOM239951	CTAACC--ACAACCACTC---CCACACGTTGTCACCAACC-----CCT-CTAACATTATCTCCTA---CAGACGCC							
DAOM239947	CTAACC--ACAACCACTC---CCACACGTTGTCACCAACC-----CCT-CTAACATTATCTCCTA---CAGACGCC							
NRRL3441	TTATCCACCCACC-ATCT---TCTCCCAT-----CCATCATGGACTCTC-TGACTGACTCTCTCTCTCTAGACGCC							

DAOM239948 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 DAOM239952 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 DAOM239953 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 CBS300.97 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 CBS301.97 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 DAOM239954 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 KAS3458 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 CBS219.30 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 FRR1058 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTTGCCTTCACCCCTCGGTGTCCG
 DAOM239951 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACTCGTGAGCACGCTCTGCTCGCTTTCACCCCTCGGTGTCCG
 DAOM239947 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACTCGTGAGCACGCTCTGCTCGCTTTCACCCCTCGGTGTCCG
 NRRL3441 ACTGGTGAGTTCGAGGCTGGTATCTCCAAGGATGGCCAGACTCGTGAGCACGCTCTGCTCGCTTTCACCCCTCGGTGTCCG

[	721	731	741	751	761	771	781	791	]
[									]
NRRL35183	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS358.48	CCAGCTCATTGTCGCCCTGWACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS336.59	CCAGCTCATTGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS118872	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM226579	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS102405	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
FRR1511	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS708.88	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS838.96	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
FRR1391	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
FRR2695	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239957	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239956	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
KAS3459	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
NRRL787	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS114222	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM226606	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS347.68	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
KAS3460	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS460.67	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM178627	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM213171	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239955	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
96M111148	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239949	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239950	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239948	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239952	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239953	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS300.97	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS301.97	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239954	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
KAS3458	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
CBS219.30	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
FRR1058	CCAGCTCATCGTCGCCCTGAACAAGATGGACACTTGAAGTGGTCCGAGGACCGTTACAACGAGATTGTCAAGGAGACCT								
DAOM239951	TCAGCTCATTGTTGCCCTCAACAAGATGGACACCTGCAAGTGGTCCGAGGACCGCTACAACGAGATCGTCAAGGAGACCT								
DAOM239947	TCAGCTCATTGTTGCCCTCAACAAGATGGACACCTGCAAGTGGTCCGAGGACCGCTACAACGAGATCGTCAAGGAGACCT								
NRRL3441	TCAGCTCATTGTTGCCCTCAACAAGATGGACACCTGCAAGTGGTCTGAGGACCGCTACAACGAGATCGTCAAGGAGACCT								

[	801	811	821	831	841	851	861	871	]
[									]
NRRL35183	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
CBS358.48	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
CBS336.59	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
CBS118872	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
DAOM226579	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
CBS102405	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
FRR1511	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
CBS708.88	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
CBS838.96	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
FRR1391	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
FRR2695	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
DAOM239957	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
DAOM239956	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
KAS3459	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								
NRRL787	CCAATTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCTTCGTCCTCCATCTCCGGCTTCAACGGTGACAACATG								

CBS114222 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM226606 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 CBS347.68 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 KAS3460 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 CBS460.67 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM178627 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM213171 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTGT-TCGGTGACAACATG
 DAOM239955 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 96M111148 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM239949 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM239950 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM239948 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM239952 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM239953 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 CBS300.97 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 CBS301.97 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM239954 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCG-CCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 KAS3458 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 CBS219.30 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 FRR1058 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM239951 CCAACTTCATCAAGAAGGTCGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 DAOM239947 CCAACTTCATCAAGAAGGTCGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG
 NRRL3441 CCAACTTCATCAAGAAGGTTGGCTACAACCCCAAGAGCGTCCCCCTTCGTCCCCATCTCCGGCTTCAACGGTGACAACATG

	881	891	901	911
[				
[				
NRRL35183	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS358.48	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS336.59	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS118872	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM226579	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS102405	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
FRR1511	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS708.88	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS838.96	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
FRR1391	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
FRR2695	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM239957	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM239956	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
KAS3459	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
NRRL787	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS114222	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM226606	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS347.68	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
KAS3460	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS460.67	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM178627	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM213171	CTCGAGCC-TCGCC-AA-TGCC-TGG-ACA			
DAOM239955	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
96M111148	CTCGAGCCCTCCCCCAACTGCCCTTGGTAC-			
DAOM239949	CTCGAGCCCTCCCCCAACTGCCCTTGGTAC-			
DAOM239950	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM239948	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM239952	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM239953	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS300.97	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS301.97	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM239954	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
KAS3458	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
CBS219.30	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
FRR1058	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM239951	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
DAOM239947	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			
NRRL3441	CTCGAGCCCTCCCCCAACTGCCCTTGGTACA			

Multiple CaM Sequence Alignment

	1	11	21	31	41	51	61	71	
[									]
[									]
NRRL787	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGATTTTCTATC								
DAOM239956	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
KAS3458	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
NRRL35183	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
CBS708.88	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
CBS347.68	-----CCAAATGTCGAGCATTGGGACTTCCCATG								
DAOM239950	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
CBS336.59	-----C-AATGACGAGCATTGGGACTTCCCATG								
KAS3459	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
FRR1391	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
DAOM239957	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
FRR1268	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
CBS460.67	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
DAOM213171	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
CBS838.96	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
DAOM226579	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
CBS102045	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
CBS114222	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
CBS218.30	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
KAS3460	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
FRR1511	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCAAATGACGAGCATTGGGACTTCCCATG								
DAOM239948	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
FRR1058	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
DAOM213268	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
96111148	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
DAOM239955	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
DAOM239953	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
CBS300.97	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
DAOM239949	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
CBS301.97	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
DAOM239952	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
CBS219.30	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
DAOM239954	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
DAOM239951	GAAGAACAAGTTTCCGAGTACAAGGAGGCCTTCTCCTTGTTTGTGAGTGCCCCGAATGACGAGCATTGGGACTTCCCATG								
NRRL3441	-----CCGAGTACAAGGAG-CCTTCT-CCTG-TTGTGAGTGC-CTCAGACGCGTGCATTGACAATCTCCGAT								
[	81	91	101	111	121	131	141	151	]
[									]
NRRL787	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM239956	TGAAAGAGGAAATCCCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
KAS3458	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
NRRL35183	TGAAAG-GGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
CBS708.88	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
CBS347.68	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM239950	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
CBS336.59	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
KAS3459	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
FRR1391	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM239957	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
FRR1268	TGAAAGAGGAAATCCCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
CBS460.67	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM213171	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
CBS838.96	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM226579	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
CBS102045	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
CBS114222	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
CBS218.30	TGAAAGAGGAAAT-TCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
KAS3460	TGAAAGAGGAAAT-CCAAAAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
FRR1511	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM239948	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
FRR1058	TGAAAGAGGAAAT-TCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM213268	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
96111148	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM239955	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								
DAOM239953	TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTTTCCCGCGTGTAGGACAAGGATGGCG								

CBS300.97 TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTCCCGCGTGTAGGACAAGGATGGCG
 DAOM239949 TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTCCCGCGTGTAGGACAAGGATGGCG
 CBS301.97 TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTCCCGCGTGTAGGACAAGGATGGCG
 DAOM239952 TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTCCCGCGTGTAGGACAAGGATGGCG
 CBS219.30 TGAAAGAGGAAAT-TCAACAACAACATGGTAAACTAATGGGGC-T-G-TTTTTTCCCGCGTATAGGACAAGGATGGCG
 DAOM239954 TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTCCCGCGTGTAGGACAAGGATGGCG
 DAOM239951 TGAAAGAGGAAAT-CCAACAACAACATGGTAAACTAATGGGGC-T-GTTTTTTTCCCGCGTGTAGGACAAGGATGGCG
 NRRL3441 CGGGA-----AAACAGTAGACTGACCAAGGCC-GTTTTCCCGCTTGTGAACAGGACAAGGATGGCG

[	161	171	181	191	201	211	221	231	]
[									]
NRRL787	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239956	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
KAS3458	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
NRRL35183	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS708.88	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS347.68	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239950	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS336.59	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
KAS3459	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
FRR1391	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239957	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
FRR1268	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS460.67	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM213171	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS838.96	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM226579	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS102045	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS114222	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS218.30	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
KAS3460	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
FRR1511	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239948	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
FRR1058	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM213268	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
96111148	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239955	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239953	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS300.97	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239949	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS301.97	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239952	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
CBS219.30	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239954	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
DAOM239951	ATGGTGAGATTCTTCCCTCTCTCCCTCCCCCACC	GATTCTTTGTGCATGGTTGCAAGGAATCTTGACCGGAATGATGAA							
NRRL3441	ATGGTGCGTGCAGTCTTCCCGTAGCTCGG-----ACGCTCTTCTTAGGAAGCAGTCTTGGGCCACTGGC								

[	241	251	261	271	281	291	301	311	]
[									]
NRRL787	TGCTCGGGGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
DAOM239956	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
KAS3458	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
NRRL35183	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
CBS708.88	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
CBS347.68	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
DAOM239950	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
CBS336.59	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
KAS3459	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
FRR1391	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
DAOM239957	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
FRR1268	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
CBS460.67	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
DAOM213171	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
CBS838.96	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
DAOM226579	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
CBS102045	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
CBS114222	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
CBS218.30	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
KAS3460	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								
FRR1511	TGCTCGGTGCTTCCCGTAGCACAGTGGTTCGAATGGGTATAGCTGACTCGAGGGTTGCAATCAGGCCAAATCACCACCAAG								

DAOM239948 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 FRR1058 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 DAOM213268 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 96111148 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 DAOM239955 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 DAOM239953 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 CBS300.97 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
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 CBS301.97 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 DAOM239952 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 CBS219.30 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 DAOM239954 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 DAOM239951 TGCTCGGTGCTTCCCGTAGCACAGTGGTCTGAATCTGGATAGCTGACTCGAGGATTGCAATCAGGCCAAATCACCACCAAG
 NRRL3441 ACCCGCGAAGGTT-----TTAAACAGAATGACTGAGTTATATATCATCGTTAGGCCAAATCACCACCAAG

[	321	331	341	351	361	371	381	391	]
[									
NRRL787	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239956	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
KAS3458	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
NRRL35183	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS708.88	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS347.68	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239950	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS336.59	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
KAS3459	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
FRR1391	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239957	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
FRR1268	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS460.67	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM213171	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS838.96	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM226579	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS102045	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS114222	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS218.30	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
KAS3460	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
FRR1511	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239948	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
FRR1058	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM213268	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
96111148	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239955	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239953	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS300.97	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239949	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS301.97	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239952	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
CBS219.30	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239954	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
DAOM239951	GAGCTCGGTACTGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCTGAGCTGCAGGACATGATCAACGAGGTCGATGC								
NRRL3441	GAGCTCGGCACCGTCATGCGCTCGCTTGGCCAGAACCCCTCCGAGTCCGAGCTGCAGGATATGATCAACGAGGTCGATGC								

[	401	411	421	431	441	451	461	471	]
[									
NRRL787	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
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KAS3458	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
NRRL35183	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
CBS708.88	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
CBS347.68	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
DAOM239950	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
CBS336.59	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
KAS3459	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
FRR1391	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
DAOM239957	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
FRR1268	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
CBS460.67	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
DAOM213171	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
CBS838.96	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								
DAOM226579	CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTACACC--TTTTTTT								

CBS102045 CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTCACC--TTTTTT
 CBS114222 CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTCACC--TTTTTT
 CBS218.30 CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTCACC--TTTTTT
 KAS3460 CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTCACC--TTTTTT
 FRR1511 CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCGGTGTCACC--TTTTTT
 DAOM239948 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 FRR1058 CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 DAOM213268 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 96111148 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 DAOM239955 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 DAOM239953 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 CBS300.97 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 DAOM239949 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 CBS301.97 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
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 CBS219.30 CGACAACAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
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 DAOM239951 CGACAATAACGGCACCATTGACTTCCCTGGTACGCTTTTCCCTAGTACCGTATCTTGCAACCCATCGTCACC--TTTTTT
 NRRL3441 CGACAACAACGGCACCATCGACTTCCCGGTATGTATTGAAT-----CGCTTGGCAGTCTGCTGTGGCT--CTTTTT

[	481	491	501	511	521	531	541	551	]
[									]
NRRL787	TTGGGGGGGGGGT	GCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG						
DAOM239956	TT-----TGGGTGCCCTGAGCGCAGTGTAAATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
KAS3458	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
NRRL35183	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
CBS708.88	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
CBS347.68	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
DAOM239950	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
CBS336.59	TT-----TGGGTGCCCTGGGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	TCGATGATGGCCCGCAAG							
KAS3459	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
FRR1391	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
DAOM239957	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
FRR1268	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
CBS460.67	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
DAOM213171	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
CBS838.96	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
DAOM226579	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
CBS102045	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
CBS114222	TT---GGGGGGGGT	GCCCTGAGCACAGTGTGATTAATCGTGGCCCGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG						
CBS218.30	GG-----GGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
KAS3460	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
FRR1511	TT-----TGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACGATGATGGCCCGCAAG							
DAOM239948	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
FRR1058	GG-----GGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
DAOM213268	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
96111148	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
DAOM239955	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
DAOM239953	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
CBS300.97	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
DAOM239949	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
CBS301.97	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
DAOM239952	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
CBS219.30	GG-----GGGGTGCCCTGAGCGCAGTGTGATTAATTGTGGCCCGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
DAOM239954	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
DAOM239951	TT----GGGGAGTGCCCTGAGCGCAGTGTGATTAATCGTGGCCTGCACCGACAGAGTTCCCTC	CACCATGATGGCCCGCAAG							
NRRL3441	CT-----CCCTTTAGACCAAGACTGATTGCTTTTCTGTGCGCTGCAGAGTTCCCTC	CACCATGATGGCCCGCAAG							

[	561	571	581	591	601	611	621	631	]
[									]
NRRL787	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC								
DAOM239956	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC								
KAS3458	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC								
NRRL35183	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC								
CBS708.88	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGA-----								
CBS347.68	ATGAAGGACACCGATTCCGAGGAGGAGATCC-----								
DAOM239950	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGA-----								
CBS336.59	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCC-----								
KAS3459	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC								
FRR1391	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC								
DAOM239957	ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC								


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FRR1268      ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
CBS460.67    ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
DAOM213171   ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
CBS838.96    ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
DAOM226579   ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
CBS102045    ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
CBS114222    ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
CBS218.30    ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
KAS3460      ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
FRR1511      ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
DAOM239948   ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-ACAGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
FRR1058      ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
DAOM213268   ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
96111148    ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
DAOM239955   ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
DAOM239953   ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
CBS300.97    ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
DAOM239949   ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
CBS301.97    ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
DAOM239952   ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
CBS219.30    ATGAAGGACACCGATTCCGAGGAGGAGATCCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTCATTTTC
DAOM239954   ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAGGCCTTC-A-AGG-TCTTTGACCGTGATAACAACGGCTTTATTTTC
DAOM239951   ATGAAGGACACCGATTCTGAGGAGGAGATTCGTGAG--CCTC-A-----
NRRL3441     ATGAAGGACACCGACTCAGAGGAGGAGATCCGGGAGGCGTTC-A-AGG-TGTTTGACCGGACAACAACGGCTTCATCTC

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[      641      651      661      671      681      691      701      711      ]
[      |      |      |      |      |      |      |      |      ]
NRRL787    CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACG-----
DAOM239956 CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
KAS3458    CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
NRRL35183 CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS708.88  -----
CBS347.68  -----
DAOM239950 -----
CBS336.59  -----
KAS3459    CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
FRR1391    CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
DAOM239957 CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
FRR1268    CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS460.67  CGCCGCTCAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGATGATGAG-----
DAOM213171 CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS838.96  CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
DAOM226579 CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS102045  CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS114222  CGCCGCTGAGCTGCGCCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS218.30  CGCCGCTGAGCTGCGCCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGTGAGG
KAS3460    CGCCGCTGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
FRR1511    CGCCGCGGAGCTGCGCCATGTGATGACCTCGATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
DAOM239948 CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
FRR1058    CGCCGCTGAGCTGCGCCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGTGAGG
DAOM213268 CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
96111148  CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
DAOM239955 CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
DAOM239953 CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS300.97  CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
DAOM239949 CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS301.97  CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
DAOM239952 CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAGG
CBS219.30  CGCCGCTGAGCTGCGCCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGTGAGG
DAOM239954 CGCCGCTGAGCTGCGTCATGTGATGACCTCCATTGGCGAGAAGCTGACCGACGATGAGGTGGATGAGATGATCCGCGAG-
DAOM239951 -----
NRRL3441   CGCCGCGGAGCTGCGCCACGTGATGACCTCCATCGGA-----

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Multiple *BenA* Sequence Alignment for Paralogs

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[      1      11      21      31      41      51      61      71      ]
[      |      |      |      |      |      |      |      ]
DAOM239955 TGGGATATCCCGAGCACACGACAATTCTT-TATGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA

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DAOM239950 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
CBS70888 TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
NRRL35183 TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
FRR1391 TGGGATATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
FRR1268 T-GGGAATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
DAOM239952 TGGGATATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
FRR2695 T-GGGAATCCCGAGCACAACACGACAATTCCT-TATGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
CBS460.67 T-GGGAATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
CBS347.68 T-GGGAATCCCGAGCACAACACGACAATTCCT-TGTGTCGTGATTTCGATCTAATATGAGAACCAA-----ACTGA
NRRL787 TGACCTCACCTTCGGTCAAATCATCAATTGTT-----GAACCCAGGACCCCTTTTACTGA
DAOM215381 TGACCTCACCTTCGGTCAAATCATCAATTGTT-----GAACCCAGGACCCCTTTTACTGA
DAOM226606 TGACCTCACCTTCGGTCAAATCATCAATTGTT-----GAACCCAGGACCCCTTTTACTGA
CBS21930 -----
sequence3 G-----GTAACCAAATCGGTGCTGCTT-----
sequence4 -----AAATCGGTGCTGCTT-TCTGGTGAGTTGCGGATAAACAATGACACAAA---AAAACATTGCTT
sequence2 GG-----TAACCAAATCGGTGCTGCTTCTGGTAAGTTTGTGATATGGTTTTTCTTAATTTTTTGGTACCGGCT

[ 81 91 101 111 121 131 141 151 ]
[
DAOM239955 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTCG-----CCC
DAOM239950 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTCG-----CCC
CBS70888 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTTG-----CCC
NRRL35183 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTTG-----CCC
FRR1391 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTTG-----CC
FRR1268 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTCG-----CCC
DAOM239952 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTCG-----CCC
FRR2695 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTCG-----CCC
CBS460.67 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGACGGCGATGGCCAGTAAGTCAACAGCTTG---CCCCC
CBS347.68 CTCGATATTCAGGCAAACCATTTGCTGGTGAGCACGGCCTTGAGGGCGATGGCCAGTAAGTCAACAGCTTGCCCCCCCCC
NRRL787 CTTGAATCACAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGCCAGTAAGT-----
DAOM215381 CTTGAATCACAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGCCAGTAAGT-----
DAOM226606 CTTGAATCACAGGCAGAACATTGCTAGCGAGCATGGCCTCGACGGCGAGGGCCAGTAAGT-----
CBS21930 -----GGCAGACCATCTCTGGCGAGCACGGTCTCGACAGCAACGGTGT-----
sequence3 -----TCTGGCAGACCATCTCTGGCGAGCACGGTCTCGACAGCAACGGTGT-----
sequence4 AACGTTGTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCTCCGGAATGTGAGT-----
sequence2 AACGGGAAACAGGCAAACCATCTCCGGTGAACATGGCCTCGACGGCGAGGGTGTGTAAGT-----

[ 161 171 181 191 201 211 221 231 ]
[
DAOM239955 TCCCCCACCAGATGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
DAOM239950 TCCCCCACCAGATGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
CBS70888 CCCCCCACCAGACGGGATCCGGACGACAGA-AAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
NRRL35183 CCCCCCACCAGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
FRR1391 CTCCCCCACCAGATGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
FRR1268 TCCCCCACCAGATGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
DAOM239952 TCCCCCACCAGATGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
FRR2695 TCCCCCACCAGATGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
CBS460.67 CCCCCCACCAGATGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
CBS347.68 CCCCCCACCAGATGGGATCCTGACGACAGA-GAATGGCGGTCTGATA--TTTTTCGGTTTAGCTACAATGGTTCCCTCCGAC
NRRL787 -ATCCATTTCGGTTGGAATTGAGTGATATGAGAATGGCGGTCTGACATTTTTTTTCCCTTAGCTTCACTGGCCAGTCCGAC
DAOM215381 -ATCCATTTCGGTTGGAATTGAGTGATATGAGAATGGCGGTCTGACATTTTTTTTCCCTTAGCTTCACTGGCCAGTCCGAC
DAOM226606 -ATCCATTTCGGTTGGAATTGAGTGATATGAGAATGGCGGTCTGACATTTTTTTTCCCTTAGCTTCACTGGCCAGTCCGAC
CBS21930 -----CTACAATGGCAGCTCCGAG
sequence3 -----CTACAATGGCAGCTCCGAG
sequence4 -----TATAGTGATTTTCAAATTTTCGACATCCACCCTAATC-----ATTTCCAGTTACAATGGCACCTCCGAC
sequence2 -ATCATGTCTTCCCTGCTTCTGCAATTGTC-----AGTGGCTGACA--AGCGTGCGAATAGGTACACAGGTTACCTCCGAT

[ 241 251 261 271 281 291 301 311 ]
[
DAOM239955 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
DAOM239950 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
CBS70888 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
'NRRL35183 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
FRR1391 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
FRR1268 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
DAOM239952 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
FRR2695 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
CBS46067 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
CBS34768 CTCCAGCTGGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
NRRL787 CTCCAGCTCGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA
DAOM215381 CTCCAGCTCGAGCGCATGAACGTCTACTTCAACCCACGTAAGTCGTGAAAAACGCTCTTCCCAATCAAAGAAATCTCCCAAA

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DAOM226606 CTCCAGCTCGAGCGCATGAACGTCTACTTCAACCACGTAAGTGTGGAA-----TCGATACTCGATACTGCCAAC
 CBS21930 CTTTCAGCTCGAGCGCATGAGCGTTTACTTCAACGAGGTTTCGTGGCCCGAA----CTCCAAACCTTCCGAGATGTCCACAA
 sequence3 CTTTCAGCTCGAGCGCATGAGCGTTTACTTCAACGAGGTTTCGTGGCCCGAA----CTCCAAACCTTCCGAGATGTCCACAA
 sequence4 CTCCAGTTGGAGCGTATGAACGTCTACTTCAACGAGGTGCGT--GGAATCTGCCCCGCGACATTCGGAATATAC----
 sequence2 TTGCAATTGGAGCGCATGAACGTCTACTACAACGAGGTTTGTGTTTGGTCTACGTTGAACCCATATATGCAATGGCTAAA-

	[	321	331	341	351	361	371	381	391	]
	[									]
DAOM239955		CCTGACCATTGA-----	ACC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
DAOM239950		CCTGACCATTGA-----	ACC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
CBS70888		CCTGATCATTGA-----	AAC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
NRRL35183		CCTGATCATTGA-----	AAC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
FRR1391		CCTGATCATTGA-----	AAC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
FRR1268		CCTGACCATTGA-----	ACC	GTTTCGATT	TTTCCAGGCATAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG					
DAOM239952		CCTGACCATTGA-----	ACC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
FRR2695		CCTGACCATTGA-----	ACC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
CBS460.67		CCTGATCATTGA-----	AAC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
CBS347.68		CCTGATCATTGA-----	AAC	GTTTCGATT	TTTCCAGGC-	TAGCGGTGACAAGTATGTTCCCGTGCCGTTCTCG				
NRRL787		CCCGTCTAAT-----	ATA	ATGGATT	TTTCATAGGC-TTCCGGTGACCGTTACGTTCCCGTGCCGTTCTCG					
DAOM215381		CCCGTCTAAT-----	ATA	ATGGATT	TTTCATAGGC-TTCCGGTGACCGTTACGTTCCCGTGCCGTTCTCG					
DAOM226606		CCCGTCTAAT-----	ATA	ATGGATT	TTTCATAGGC-TTCCGGTGACCGTTACGTTCCCGTGCCGTTCTCG					
CBS219.30		CGCGTCTCTTGGTTT	CATACGGACCCACTGACCGCCTCTCCAGGC-TTCCGGCAACAAGTACGTTCCCGTGCCGTTCTCG							
sequence3		CGCGTCTCTTGGTTT	CATACGGACCCACTGACCGCCTCTCCAGGC-TTCCGGCAACAAGTACGTTCCCGTGCCGTTCTCG							
sequence4		-----	TCATATCGTATAGGC-TAGCGGCAACAAGTACGTTCCCGTGCCGTTCTCG							
sequence2		-----	ATAACAACGTGAATAGGT-CAACAAGAGAAATATGTTCTCGCGCGTTCTCG							

	[	401	411	421	431	441	451	461	471	]
	[									]
DAOM239955		TCGA-CCTGGAGCCCGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
DAOM239950		TCGA-CCTGGAGCCCGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
CBS70888		TCGA-CCTGGAGCCTGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
NRRL35183		TCGA-CCTGGAGCCTGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
FRR1391		TCGA-CCTGGAGCCTGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
FRR1268		TCGA-CCTGGAGCCCGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
DAOM239952		TCGACCCCTGGAGCCCGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
FRR2695		TCGA-CCTGGAGCCCGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
CBS460.67		TCGA-CCTGGAGCCTGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
CBS347.68		TCGA-CCTGGAGCCTGGTACCATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
NRRL787		TCGA-CCTGGAGCCCGGTACTATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
DAOM215381		TCGA-CCTGGAGCCCGGTACTATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
DAOM226606		TCGA-CCTGGAGCCCGGTACTATGGACGCTGTCGGTGCCGGTCCCTTTGGCAAGCTCTTCCGCCCCGACAACCTTCGTCTT								
CBS21930		TCGA-TCTTGAGCCCGGTACCATGGATGCTGTCGGTGCTGGTCTTTCGGTCAGCTTTTCCGCCCCGACAACCTTCGTTTT								
sequence3		TCGA-TCTTGAGCCCGGTACCATGGATGCTGTCGGTGCTGGTCTTTCGGTCAGCTTTTCCGCCCCGACAACCTTCGTTTT								
sequence4		TCGA-TTTTGAGCCTGGCACCATGGACGCTGTCGGTGCTGGTCTTTCGGTCAGCTCTTCCGTCCCGACAACCTTCGTCTT								
sequence2		TTGA-TCTCGAGCCCGGTACCATGGATGCCATCCGCGCTGGTCTTTCGGTGCCCTCTTCCGCCCCGACAACCTTGTTTTT								

	[	481	491	]
	[			]
DAOM239955		TGGCCAGTCTG		
DAOM239950		TGGCCAGTCTG		
CBS70888		TGGCCAGTCTG		
NRRL35183		TGGCCAGTCTG		
FRR1391		TGGCCAGTCTG		
FRR1268		TGGCCAGTCTG		
DAOM239952		TGGCCAGTCT-		
FRR2695		TGGCCAGTCTG		
CBS460.67		TGGCCAGTCTG		
CBS347.68		TGGCCAGTCTG		
NRRL787		CGGTCAGTCCG		
DAOM215381		CGGTCAGTCCG		
DAOM226606		CGGTCAGTCCG		
CBS219.30		CGGCCAGTCTG		
sequence3		CGGCCAGTCTT		
sequence4		CGGCCAGTCGG		
sequence2		CGGTCAGGCTG		