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An integrative study of Cyperaceae:
focused on expressions of floral
MADS-box genes and the structural
evolution of chloroplast genomes

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ABSTRACT

An integrative study of Cyperaceae: focused on expressions of floral MADS-box genes and the structural evolution of chloroplast genomes

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Cyperaceae is the third largest family in monocots and the seventh largest family in angiosperm containing 88 genera and ca. 5,500 species worldwide. They are well known as a material for the paper (papyrus; *Cyperus papyrus* L.) in ancient Egypt and are economically and environmentally useful plants. The family is placed in Poales and is distinguished by highly reduced flowers and complex inflorescences. However, many studies in Poales are mainly focused on Poaceae, and the comprehensive studies of Cyperaceae are insufficient. Four subjects were included in this study: 1) the MADS-box genes of *Carex dickinsii* as a representative of Cyperaceae were identified using transcriptome

analysis to understand the evolution and diversification of flowers in Cyperaceae, and their expression patterns were confirmed in each organ. 2) the genome sizes were estimated from 43 taxa of Korean *Carex*, representing 15 sections. 3) the entire chloroplast (cp) genome of *C. lupulina* as a representative of the *Carex* was determined. 4) the cp genome structure of *C. lupulina* was compared with those of related taxa to understand the evolution and diversification of the cp genomes in Cyperaceae.

Carex L., with more than 2,000 species, is the largest genus in Cyperaceae and distinguished by unisexual flowers without perianth. The pistillate flowers of *Carex* are characterized by the presence of a perigynium which is a sac-like organ surrounding the perianthless female flower and the staminate flowers consist of three or fewer stamens subtended by a scale. In this study, a total of 48 MADS-box genes [40 type II (35 MIKC^C and five MIKC*-type) and eight type I MADS-box genes] were identified in *C. dickinsii*. The MADS-box genes of *C. dickinsii* were expressed in leaves, pistillate scales, perigynia, carpels, staminate scales, and stamens. Especially, E function genes were expressed in pistillate scales, perigynia, and staminate scales, which are specialized organs in *Carex*. Therefore, these organs are considered as a part of flower in *Carex*. Considering different expression patterns of floral MADS-box genes, the evolutionary origins of pistillate scale and staminate scale are different although their morphology is identical.

The genome sizes of 43 Korean *Carex* were estimated using

flow cytometry. The number of taxa represent 24.4% of Korean *Carex*. The average genome size of *Carex* species based on current study and data from the Plant DNA C-value Database (release 7.1) is 0.47 pg (1C). The genome size of *C. cuspidate* is the largest (1C=1.64 pg), and that of *C. brownii*, *C. kobomugi*, *C. nubigena*, and *C. paxii* were identical and the smallest (1C=0.20pg). The large genomes are frequently found in the subg. *Carex*, especially in sect. *Aulocystis*, sect. *Digitatae*, sect. *Glaucæ*, sect. *Paniceae*, and sect. *Siderostictae*. The subg. *Vigneæ* had relatively small genome in which the sect. *Phleoideæ* had the smallest genome.

The complete cp genome of *C. lupulina* was sequenced based on the Nanopore platform. The cp genome of *C. lupulina* is 246,165 bp in size which is the second largest in the reported cp genomes in angiosperm (NCBI organelle DB; accessed on July 2019). The cp genome consists of LSC (99,356 bp), SSC (10,293 bp), and two inverted repeats (each 68,258 bp), and it has a total of 123 genes including 63 unique protein-coding genes, 29 unique tRNA genes, and 4 rRNA genes. To address the structural evolution of cp genomes in Cyperaceae, cp genome of *C. lupulina* was compared with previously reported cp genomes from relative taxa. Compare to the sister groups of Cyperaceae, there are tree inversions (*rps4*~part of the *accD*: 12~13 kb, *rps12*~*trnL*-*CAA*: 6~7 kb, and *ndhF*: ca. 2.2 kb), two translocations (part of the *accD*: 0.2~1.4 kb and *rps14*~*trnS*-*GGA*: 7.5~9 kb), one inverted translocation (*ndhG*~*ycf*: 5~11 kb), three gene losses (*accD*, *infA*, and *rps18*),

and one IR expansion (*ndhG~ycf1*: 10~11 kb). In *Carex*, there are one inversion (part of the *clpP~rps11*: ca. 10 kb), two translocations (*rps4~part of the clpP*: ca. 15 kb and *rps16*: ca. 1.2 kb), three inverted translocations (*psbK~atpI*: ca. 8 kb, *rps14~psaA*: ca. 5 kb, and *trnQ-UUG*: ca. 140 bp), seven gene losses (*clpP*, *rpl23*, *rpoA*, *rps3*, *ycf1*, *ycf2*, and *trnT-GGU*), and one gene duplication (*trnfM-CAU*). Autapomorphic characters of *C. lupulina* were two large inverted translocations (*rps8~petD*: ca. 30 kb and *psbA~matK*: ca. 5.2 kb), eight gene losses (*ndhD*, *petA*, *rpoC2*, *rps2*, *rps7*, *rps16*, *ycf4*, and *ycf68*), and five gene duplication (*rps14*, *trnfM-CAU*, *trnG-GCC*, *trnR-UCU*, and *trnT-AGU*). The number of repeat sequences in Cyperaceae are higher than that of Typhaceae and Eriocaulaceae. The repeats are more distributed in the LSC region than in other regions except for oligonucleotide repeats of *C. lupulina* that are frequently distributed in the IR region. Also, the repeats are frequently located in the non-coding region such as IGS (intergenic spacer region). Accumulation of repeats led to increase of size of the cp genomes in Cyperaceae. Especially in *C. lupulina*, many repeats in the IR region causes an increase in the size of the IR region, and are the main reason for the increase in the size of the cp genome. In addition, IR expansion into SSC region by the duplication of *ndhG~ ycf1* region increases the size of the cp genome in Cyperaceae. And, these repeats can be found at the borders of rearrangements in *Carex*. It seems that these repeats correlated with structural changes in *Carex*.

This study is the first report for 1) 48 floral MADS-box genes in *Carex* and their expression patterns in floral organs, 2) for genome size from 43 taxa of *Carex* in Korea, 3) for the complete cp genome of *C. lupulina*, and 4) for the structural changes in Cyperaceae. The results of this study will provide the basis for understanding the evolution and diversification of flowers in *Carex* and the structural evolution of cp genome in Cyperaceae.

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Chapter 1
Introduction

1.1 Cyperaceae

1.1.1 Background of the family

Cyperaceae are the third largest family in monocots, comprising 88 genera and c. 5,500 species in the world (Govaerts et al., 2020). As a cosmopolitan family of herbaceous plants, they have a broad range of habitats from arctic tundra to tropical forests and deserts (Bruhl, 1995; Simpson, 2011). The family is economically and environmentally useful plants. They are well known as a material for the paper (papyrus; *Cyperus papyrus* L.) in ancient Egypt and are used as materials for matting, basketry, medicine, fuel, and fodder (Govaerts et al., 2007; Simpson et al., 2011). Because some of the aquatic taxa are pollution-sensitive, these plants are recognized as indicators of environmental damage (Govaerts et al., 2007; Simpson et al., 2011).

Cyperaceae are perennial or annual herbs and are rhizomatous to stoloniferous (Dai et al., 2010). Stems are usually trigonous and solid. Leaves are alternate, usually 3-ranked, consisting of a blade and sheath that is closed (Dai et al., 2010). They are characterized by highly reduced flower and complex inflorescences. Inflorescences are paniculate, corymbose, spicate, anthelate, or capitate, and they comprise one to many spikelets (Ball et al., 2002; Dai et al., 2010). Spikelets have one to many glumaceous bracts (scales) arranged in a spiral or in 2-ranked, and each bract subtends a single flower

(Ball et al., 2002). Flowers are bisexual or unisexual without perianth or with bristles or scales (Ball et al., 2002). Stamens are one to three. Pistils are one with 2-3(-4)-carpellate and two or three stigmas (Ball et al., 2002). Fruits are trigonous or biconvex achenes (Ball et al., 2002).

Cyperaceae are included in Poales. With the traditional concept, the family is closely related to Poaceae because of their similar vegetative characters and reduced flowers. However, recent morphological and molecular phylogenetic studies revealed that Cyperaceae is a sister to Juncaceae, and they are placed in relatively distant locations in Poales (APG IV; Muasya et al., 1998; Angiosperm Phylogeny Group, 2016; Fig. 1.1).

1.1.2 Classification and molecular phylogenetic studies

Classification systems in Cyperaceae have been suggested by many researchers starting from early 19th century (Nees 1835; Kunth, 1837). However, the recognition of subgroups in the family (subfamilies and tribes) are continuously controversial (Muasya et al., 1998). Jussieu (1789) and Bentham (1883) recognized subfamilies according to whether the flowers are unisexual or hermaphrodite. Clarke (1908) and Koyama (1961) recognized subfamilies based on characters of inflorescences and flowers (Muasya et al., 1998). However, their definition of flowers and spikelets was controversial, causing the confusion in the

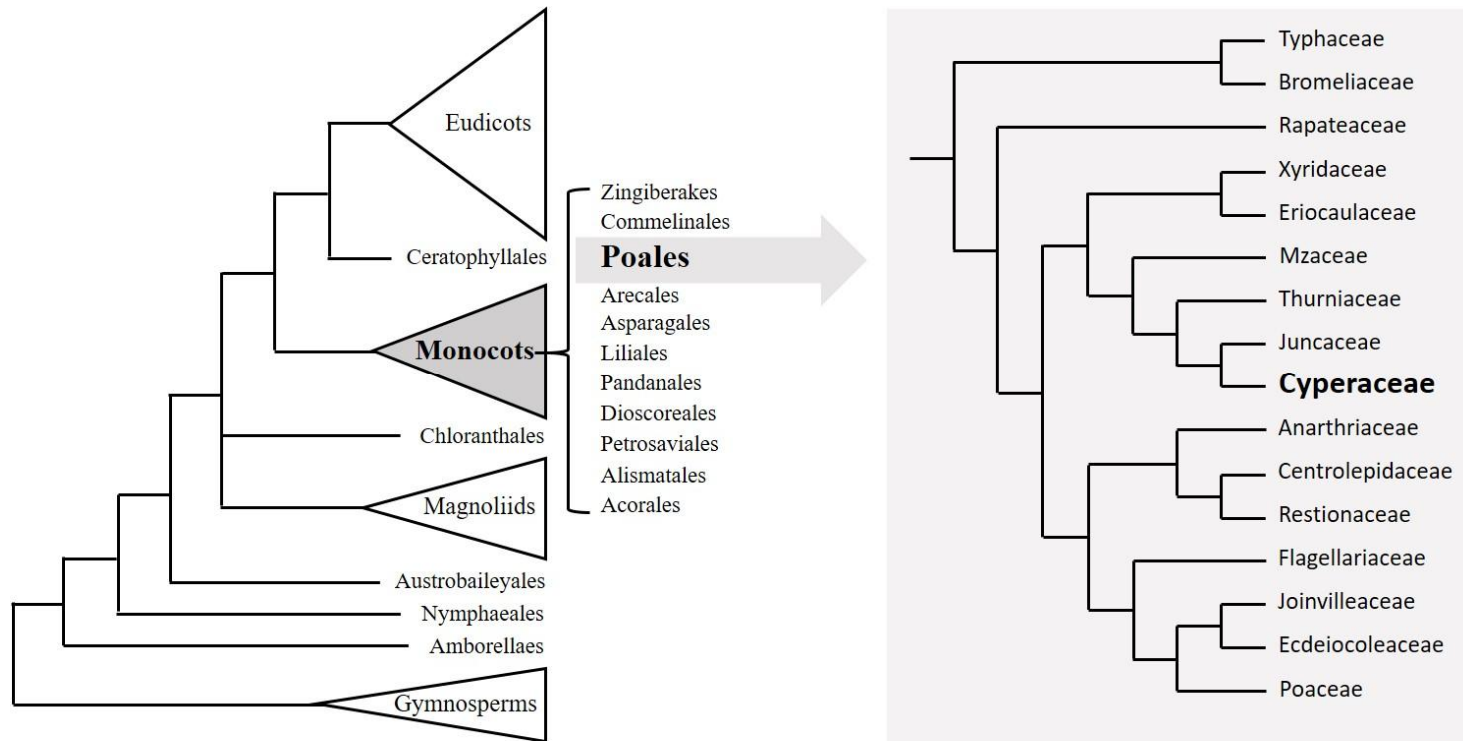


Fig. 1.1 Phylogenetic position of Cyperaceae in the angiosperm phylogenetic tree. Topologies are summarized from Stevens (2001) and Angiosperm Phylogeny Group (2016).

classification of some taxa (Muasya et al., 1998).

Later, Goetghebeur (1986) recognized four subfamilies and 17 tribes based on the morphological characters of inflorescences and embryo, and Bruhl (1995) recognized two subfamilies and 12 tribes based on morphological, anatomical, phytochemical, and physiological characters (Muasya et al., 1998; Table 1.1). In particular, Bruhl (1995) combined five tribes (Scirpeae, Fuireneae, Eleocharideae, Ficinieae, and Dulichieae) into the tribe Scirpeae, and also combined two tribes (Hypolytreae and Chrysitricheae) into the tribe Hypolytreae (Table 1.1). However, there are difficulties to understand their phylogenetic relationships and to make a classification system based on morphological data because of the reduced flowers and complex inflorescences. (Muasya et al., 1998; Semmouri et al., 2019). Recently, the analyses of molecular data is available to resolve the phylogenetic relationships in angiosperms, and they have applied in the studies of Cyperaceae.

Molecular phylogenetic studies of Cyperaceae have conducted with chloroplast (*matK*, *rbcL*, *rps16*, and *trnL-F*) and nuclear (ETS and ITS) regions (Muasya et al., 1998; Simpson et al., 2007; Muasya et al., 2009; Jung and Choi, 2012; Hinchliff and Roalson, 2013; Semmouri et al., 2019). As a result, the previous morphological classifications were incongruent with the molecular phylogenies, and the classification of Cyperaceae has revised based on data from molecular phylogeny (Muasya et al., 1998, 2009; Simpson et al., 2007). Among them, a study by Muasya et al.

Table 1.1 Classification history of Cyperaceae

Bruhl (1995) (based on morphological phylogeny)	Goetghebeur (1986) (based on morphological phylogeny)	Muasya et al. (2009) (based on molecular phylogeny)
<p>Subfamily Cyperoideae</p> <p>Tribe Abildgaardieae Tribe Arthrostylideae Tribe Cypereae Tribe Scirpeae</p>	<p>Subfamily Cyperoideae</p> <p>Tribe Abildgaardieae Tribe Arthrostylideae Tribe Cypereae Tribe Dulichieae Tribe Eleocharideae Tribe Ficinieae Tribe Fuireneae Tribe Scirpeae</p> <p>Tribe Schoeneae Tribe Rhynchosporeae</p> <p>Subfamily Sclerioideae</p> <p>Tribe Bisboeckelereae Tribe Cryptangieae Tribe Sclerieae Tribe Trilepideae</p> <p>Subfamily Caricoideae</p> <p>Tribe Cariceae</p> <p>Subfamily Mapanioideae</p> <p>Tribe Hypolytreae Tribe Chrysitricheae</p>	<p>Subfamily Cyperoideae</p> <p>Tribe Abildgaardieae Tribe Cypereae Tribe Dulichieae Tribe Eleocharideae Tribe Fuireneae Tribe Scirpeae</p> <p>Tribe Schoeneae Tribe Rhynchosporeae</p> <p>Tribe Bisboeckelereae Tribe Cryptangieae Tribe Sclerieae Tribe Trilepideae</p> <p>Tribe Cariceae</p> <p>Subfamily Mapanioideae</p> <p>Tribe Hypolytreae Tribe Chrysitricheae</p>

(2009), the most cited one, recognized to two subfamilies and 15 tribes based on *rbcL* and *trnL-F* (intron and intergenic spacer) sequences with the framework of a classification by Goetghebeur (1986) (Table 1.1). However, phylogenetic relationships within the tribe Scirpeae, Schoeneae, and Fuireneae were not resolved. Recent molecular phylogenetic studies include more taxa and more sequence data (Hinchliff and Roalson, 2013; Semmouri et al., 2019). Hinchliff and Roalson (2013) analyzed more than 1,500 species in Cyperaceae using a supermatrix data-mining methods that gathered scattered data in 23 genes. Semmouri et al. (2019) performed phylogenetic analysis of 500 species based on seven DNA regions (*rbcL*, *matK*, *ndhF*, the pseudogene *rps16*, the intergenic spacer *trnL-F*, ITS, and ETS) and embryonic morphological characters. Their result mostly supported that of Muasya et al. (2009) except some cases (Fig. 1.2).

Cyperaceae is a monophyletic group and is a sister to Juncaceae (Simpson et al., 2007; Muasya et al., 2009; Jung and Choi, 2012, Hinchliff and Roalson, 2013; Semmouri et al., 2019), and the family is divided into two clades, the subfamily Mapanioideae and Cyperoideae, in all of previous molecular phylogenetic studies (Simpson et al., 2007; Muasya et al., 2009; Jung and Choi, 2012, Hinchliff and Roalson, 2013; Semmouri et al., 2019). Within Mapanioideae, the relationship between the tribes Hypolytreae and Chrysitricheae was unclear in the studies of Muasya et al. (2009) and Hinchliff and Roalson (2013). However, Semmouri et al. (2019)

found that they are a sister to each other (Fig. 1.2A~C-i).

Within Cyperoideae, three molecular phylogenetic studies agree that the tribe Trilepideae is a sister to the rest of Cyperoideae. In Muasya et al. (2009), the next diverged group is Schoeneae 3 clade (*Cladium* clade; Fig. 1.2A-ii), and the tribe Sclerieae + Bisboeckelereae are included the tribe Schoeneae (Fig. 1.2A-iii). However, in Hinchliff and Roalson (2013), the tribe Sclerieae + Bisboeckelereae clade diverged first at the base (Fig. 1.2B-iii), and the genus *Cladium* was a sister to all other members in tribe Schoeneae (Fig. 1.2B-ii). In Semmouri et al. (2019), *Cladium* clade diverged first (Fig. 1.2C-ii), and the Sclerieae + Bisboeckelereae clade is sister to the rest of the subfamily Cyperoideae (Fig. 1.2C-iii). Although the position of *Cladium* is different in each tree, the clade is recognized as a distinct group in all of these studies (Fig. 1.2). Thus, Semmouri et al. (2019) resurrected the tribe Cladieae, which contains only *Cladium*, a previous member of the tribe Schoeneae. The position of *Carpha* and *Trianoptiles* that belongs to the tribe Schoeneae was also unclear, but recent study (Semmouri et al., 2019) proposed a new tribe (Carpheae) based on molecular phylogenetic, ecological, morphological, and embryological characters (Fig. 1.2C-v).

There are two large major clades (CDS and FAEC) within Cyperoideae and each clade is highly supported (Fig. 1.2). The first major clade is the CDS Clade (*Khaosokia* + Cariceae + Dulichieae + Scirpeae). In this clade, the tribe Dulichieae is a sister to all

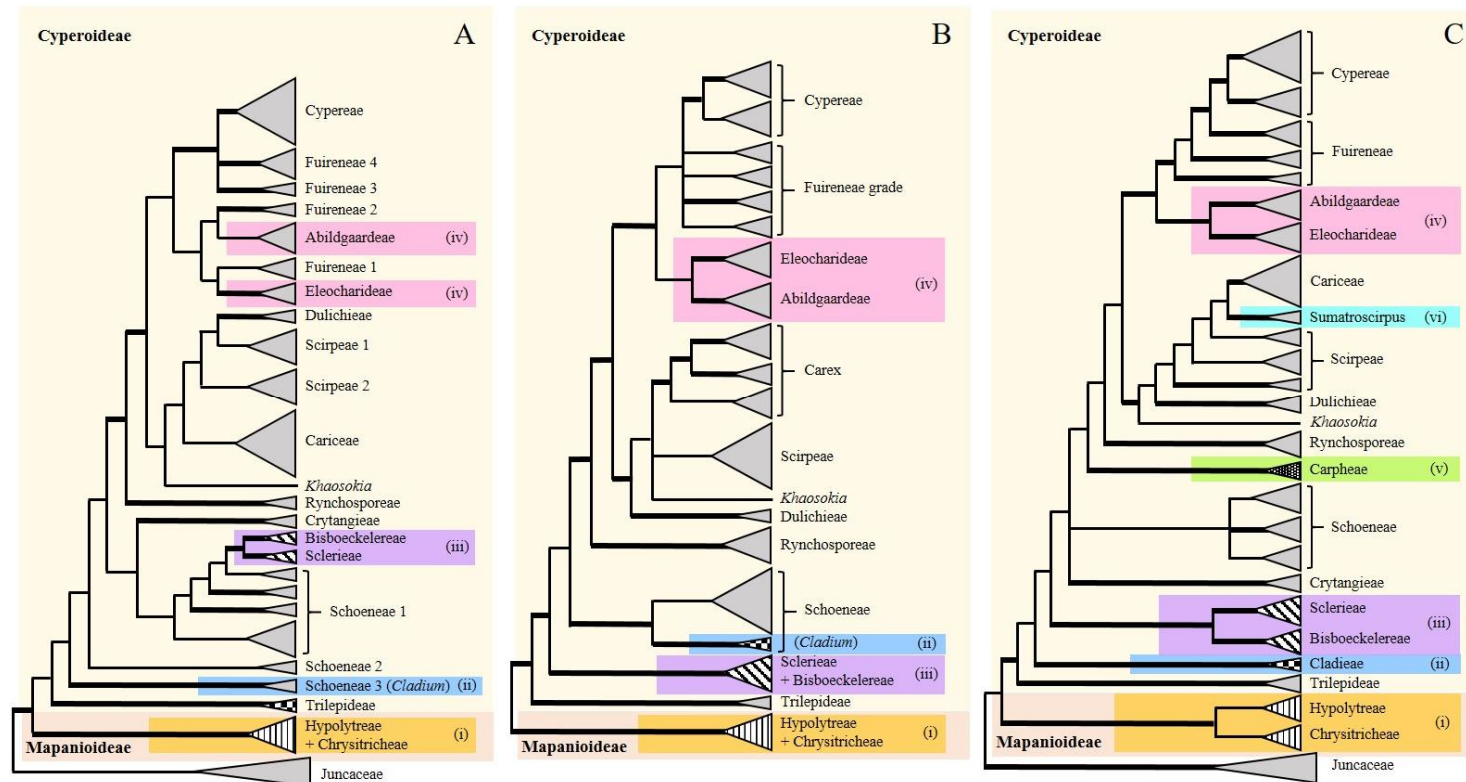


Fig. 1.2 Comparison of previous phylogenetic studies in Cyperaceae. Trees were summarized with recognized major clades. (A) Muasya et al. (2009). (B) Hinchliff and Roalson (2013). (C) Semmouri et al. (2019).

other members of tribes (Cariceae + Scirpeae). In particular, molecular phylogenetic studies in the tribe Cariceae have shown that the genera included in the Cariceae (*Cymophyllus*, *Kobresia*, *Schoenoxiphium*, and *Uncinia*) are nested within the *Carex* clade. Thus, the Global Carex Group (2015) recently transferred all species in tribe Cariceae into the genus *Carex*, which became a monophyletic group. Also, the tribe Sumatrosirpeae, which contains one genus (*Sumatrosirpus*), was included in the tribe Dulichieae, but recently recognized as a new tribe. It is a sister to the tribe Cariceae based on molecular and morphological data (Léveillé–Bourret et al., 2018). The result of Semmouri et al. (2019) strongly supported the recognition of new tribe (Fig. 1.2C–vi). The tribe Scirpeae is still divided into several clades.

The second major clade is the FAEC Clade (Fuireneae + Abildgaardieae + Eleocharideae + Cyperaea). The tribe Eleocharideae is a sister to the tribe Fuireneae I, and the tribe Abildgaardieae is a sister to the tribe Fuireneae II in Muasya et al. (2009) (Fig 1.2A–iv). However, in Hinchliff and Roalson (2013) and Semmouri et al. (2019), the Abildgaardieae + Eleocharideae clade is monophyletic, and the monophyly of each tribe is also highly supported (Fig. 1.2A~B–iv). Some as the case of *Carex*, *Eleocharis* is merged with other genera (*Websteria*, *Egleria*, and *Chillania*) and these genera forms a monophyletic clade (Eleocharideae). Within the tribe Cyperaea, the tribe is divided into two clades. However, the relationship within each clade remains

unclear.

Much data has been accumulated so far and the circumscription of genera and tribes have been revised accordingly, but the taxonomic problems of some taxa such as Fuireneae, Schoeneae, Scirpeae, Cyperaea, and *Khaosokia* still remain unclear.

1.1.3 Cyperaceae in Korea

Korean Cyperaceae have been listed up by T. H. Chung (1957), T. B. Lee (1980), Y. N. Lee (1996), and W. T. Lee (1996a, b) since Nakai (1952) reported approximately 240 species (Oh, 2006). A comprehensive morphological study of Cyperaceae was conducted by Oh (2006), and 13 genera and 226 taxa were reported in this study. Later, Oh (2007) recognized 13 genera and 246 taxa in Korea. However, these studies did not consider molecular data.

Molecular phylogenetic studies of Cyperaceae for Korean taxa have been conducted only in some taxa (*Scirpus*, *Cyperus*, and *Carex*) but still insufficient compared with those in other families (Jung and Choi, 2010; Jung et al., 2016). The first molecular phylogenetic study focused on the Korean Cyperaceae was conducted by Jung and Choi (2012). They analyzed 81 genera and 426 species of Cyperaceae including 20 genera and 140 species in Korea based on ITS, *rbcL*, and *trnL-F* (Jung and Choi, 2012). This study was confirmed that the phylogenetic positions of Korean Cyperaceae were placed in 10 tribes and 14 clades (Jung and Choi,

2012). The relationship among the major groups was consistent with the results from other studies: 1) Cyperaceae is a monophyletic group and is a sister to Juncaceae, 2) the subfamily Mapanioideae is a sister to subfamily Cyperoideae, 3) within Cyperoideae, FAEC and SDC clades were recognized and EDGs (Early Diverged Groups; tribe Schoeneae, Bisboeckelereae, Sclerieae, and Rhynchosporae) are proposed, 4) within EDGs clades, the tribe Trilepideae is a sister to the rest of the subfamily Cyperoideae, and the tribe Rhynchosporae is a sister to both FAEC and SDC clades. 5) within FAEC clade, the tribe Eleocharideae and Abildgaardieae were monophyletic and Eleocharideae is a sister to Abildgaardieae, 6) within SDC clade, the tribe Cariceae is monophyletic group (Muasya et al., 2009; Hinchliff and Roalson, 2013; Semmouri et al., 2019). However, unclear taxonomic positions of EDGs, Fuireneae, and Scirpeae are still remained (Jung and Choi, 2012).

Although Cyperaceae are the third largest family in monocots and the seventh largest family in angiosperm (Govaerts et al., 2007), the comprehensive molecular studies in Cyperaceae especially the field related to genomics are insufficient. In the other hand, many studies have been conducted especially focused on the economically and evolutionarily important plants. In this study, 1) the floral transcriptome of *C. dickinsii* was analyzed, 2) the genome size of Korean *Carex* were estimated, 3) the chloroplast genome

sequences of *C. lupulina* was completed, and 4) the chloroplast genome structure of *C. lupulina* was compared with those of related taxa. These studies will help to understand the evolution and diversification of flowers in Cyperaceae and the evolution of the chloroplast genomes in Cyperaceae.

Chapter 2

The floral transcriptome of *Carex dickinsii*

Franch. & Sav.

2.1 Introduction

2.1.1 Flowers of *Carex*

Carex L., with more than 2,000 species, is the largest genus in Cyperaceae and in the temperate regions (Global Carex Group, 2015). The genus is distributed in a broad range of habitats such as tundra, desert, and tropical forests (Global Carex Group, 2015; Lévillé–Bourret et al., 2018).

The *Carex* belongs to the tribe Cariceae, which is monophyletic and distinguished from other taxa in the Cyperaceae by unisexual flowers without perianth (Starr and Ford, 2009). The tribe was traditionally divided into *Carex* L., *Cymophyllus* Mack., *Kobresia* Willd., *Schoenoxiphium* Nees, and *Uncinia* Pers., based on characteristics (or presence/absence) of perigynium and rachilla (Starr and Ford, 2009). However, molecular phylogenetic studies revealed that *Carex* includes all other genera (Global Carex Group, 2015). Thus, the Global Carex group (2015) integrated these genera into one genus, *Carex*, and updated their scientific names based on combinations.

The flowers of Cariceae are unisexual and highly reduced. Especially, the pistillate flowers are characterized by the presence of a perigynium which is a sac-like organ surrounding a perianthless female flower (Starr and Ford, 2009; Fig. 2.1). The staminate flowers consist of three or fewer stamens subtended by a

scale (Molina et al., 2012; Fig. 2.1).

The perigynium is a unique organ of Cariceae, and its origin has received keen attention from many botanists. Kunth (1835) suggested on evolutionary interpretation of perigynium that the origin of the perigynium is prophyll which is the first single bracts of the lateral axis (Snell, 1936). Nees (1835) and Jermy & Tutin (1968) also proposed that it is derived from the fusion of two opposite bracts (Smith and Faulkner, 1976). Schleiden proposed that it is derived from perianth (Smith and Faulkner, 1976). However, many researchers supported Kunth's hypothesis and developed it (Snell, 1936). And, Kunth's hypothesis is widely accepted to date (Global Carex Group, 2015).

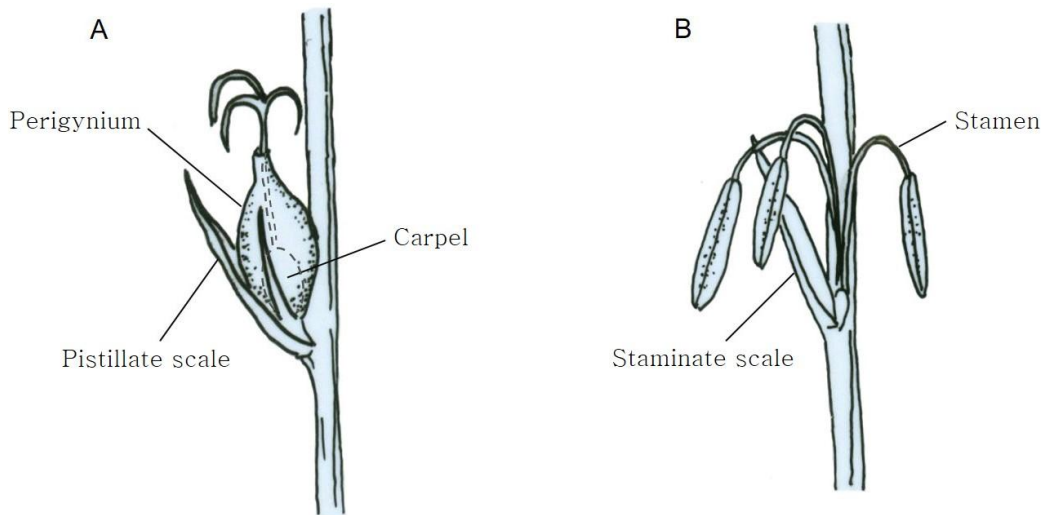


Fig. 2.1 Floral Structure of *Carex*. The pictures are redrawn from Hoshino et al. (2011). (A) Pistillate flower. (B) Staminate flower.

2.1.2 MADS–box genes

The MADS–box genes encode transcription factors containing the conserved DNA–binding MADS domain and play important roles in the development of eukaryotes (Soltis et al., 2007). These are involved in muscle development in animals and the pheromone response in yeast (Gramzow and Theissen, 2010). In plants, these genes control major aspects of the life cycle from embryo to gametophyte development (Smaczniak et al., 2012). Especially, they play the most important role in determining floral organ identity (Smaczniak et al., 2012). The name of the MADS–box is an acronym from *MINICHROMOSOME MAINTENANCE 1* (*MCM1*; *Saccharomyces cerevisiae*), *AGAMOUS* (*AG*; *Arabidopsis thaliana*), *DEFICIENS* (*DEF*; *Antirrhinum majus*), and *SERUM RESPONSE FACTOR* (*SRF*; *Homo sapiens*), that are the first discovered four genes (Norman et al., 1988; Passmore et al., 1989; Sommer et al., 1990; Yanofsky et al., 1990). The phylogenetic study of MADS–box genes in *Arabidopsis* showed that these genes were divided into five groups ($M\alpha$, $M\beta$, $M\gamma$, $M\delta$ (MIKC*), and MIKC^C) and *AGL33* (Pařenicová et al., 2003). The $M\alpha$, $M\beta$, and $M\gamma$ groups belong to the type I MADS–box genes, and the $M\delta$ (MIKC*) and MIKC^C groups belong to the type II MADS–box genes (Pařenicová et al., 2003; Fig. 2.2).

The type I MADS–box genes usually consist of one or two exons and are distinguished by a lack of the keratin–like (K) domain (De Bodt et al., 2003). They have experienced faster

birth-and-death evolution than type II genes and are involved in the development of female gametophytes, embryos, and seeds (Nam et al., 2004; Gramzow and Theissen, 2010; Masiero et al., 2011).

The type II MADS-box genes are composed of MADS (M), intervening (I), K, and C-terminal (C) domains (MIKC-type), and they consist of seven exons (Becker and Theissen, 2003; De Bodt et al., 2003). The K domain is a conserved region and consists of about 70 amino acids (Gramzow and Theissen, 2010). This domain mediates protein-protein interaction for the formation of the DNA-binding dimer and the complex of higher order (Kaufmann et

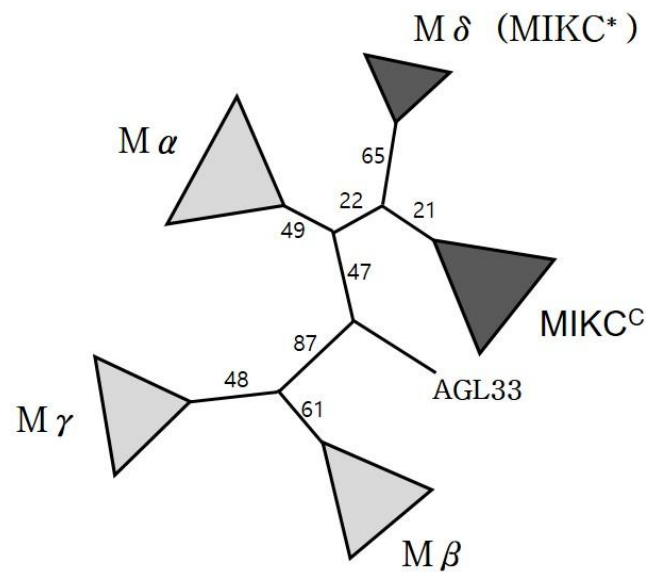


Fig. 2.2 Phylogeny of the 107 MADS-box genes in *Arabidopsis*. The tree is redrawn from Parěnicová et al. (2003). Gray is type I MADS-box genes and dark gray is type II MADS-box genes.

al., 2005; Gramzow and Theissen, 2010). The I domain is weakly conserved and consists of about 30 amino acids (Riechmann et al., 1996). This domain is located between the MADS domain and the K domain, and is involved in the selective formation of DNA-binding dimers (Riechmann et al., 1996). The C domain is the least conserved region in MIKC-type proteins with the most variable sequence and length, and is located in the C-terminal region (Becker and Theissen, 2003; Kaufmann et al., 2005). The region is involved in the transcriptional activation or the formation of multimeric protein complexes (Becker and Theissen, 2003). The type II (MIKC-type) MADS-box genes are divided into MIKC^C and MIKC* according to the phylogenetic reconstructions and exon-intron structures (Henschel et al., 2002). The MIKC^C-type genes classified into 14 subfamilies based on phylogenetic analysis: AG, AGL2 (SEP), AGL6, AGL12, AGL15, AGL17, DEF, FLC, GGM13 (B sister), GLO, SQUA, SVP/STMADS11, SOC1/TM3, and TM8 (Becker and Theissen, 2003). Members of each subfamily share similar expression patterns and highly related functions (Becker and Theissen, 2003). These genes are involved in the floral organ identity, the development of the reproductive organ, the root morphogenesis, and the leaf morphogenesis in angiosperms (Gramzow and Theissen, 2010; Smaczniak et al., 2012). The MIKC*-type genes have a longer I domain than MIKC^C-type encoded by four or five exons (Henschel et al., 2002). These genes are involved in the development of male gametophytes

(Smaczniak et al., 2012).

The determination of floral organs identities is explained by the ABCDE model which has been widely accepted (Fig. 2.3). Initially, the ABC model was proposed that A, B, and C function genes act in combination to specify different floral organs based on the homeotic mutant phenotypes in *Arabidopsis* and *Antirrhinum* (Schwarz–Sommer et al., 1990; Bowman et al., 1991; Coen and Meyerowitz, 1991). The A function genes determine sepal identity, the A and B function genes determine petal identity, the B and C function genes determine stamen identity, and the C function genes determine carpel identity (Coen and Meyerowitz, 1991). Thereafter, additional function genes were proposed. The D function genes determine ovule identity together with the C function genes, and the E function genes are required for floral organ development and floral meristem determinacy (Colombo et al., 1995; Honma and Goto, 2001). Thus, the A and E function genes specify sepal identity, the A, B, and E function genes specify petal identity, the B, C, and E function genes specify stamen identity, the C and E function genes specify carpel identity, and the C, D, and E function genes specify ovule identity (Fig. 2.3; Colombo et al., 1995; Theissen, 2001). In *Arabidopsis*, the A function genes are *APETALA1* (*AP1*) and *APETALA2* (*AP2*) (Mandel et al., 1992; Bowman et al., 1993), the B function genes are *APETALA3* (*AP3*) and *PISTILLATA* (*PI*) (Jack et al., 1992; Goto and Meyerowitz, 1994; Jack et al., 1994), the C function gene is *AGAMOUS* (*AG*)

(Yanofsky et al., 1990), the D function gene is *SEEDSTICK* (*STK*), *SHATTERPROOF1* (*SHP1*), and *SHP2*, (Favaro et al., 2003; Pinyopich et al., 2003), and the E function genes are *SEPALLATA1* (*SEP1*), *SEP2*, *SEP3*, and *SEP4* (Theissen, 2001; Ditta et al., 2004). All of these genes are MADS-box genes except for *AP2* (Theissen et al., 2000).

The molecular mechanism by which the ABCDE genes control floral organ specification is explained by the quartet model (Theissen and Saedler, 2001). The quaternary complexes composed of the ABCDE proteins. These proteins control floral organ specification by binding to the promoter region (CArG boxes) of the target DNA (Theissen and Saedler, 2001).

In this study, I addressed the following three subjects to understand the evolutionary origins of unique organs in *Carex*: 1) the MADS-box genes in *C. dickinsii* were identified using transcriptome analyses, 2) the phylogenetic analysis were performed with the MADS-box genes of *Arabidopsis*, *Amborella*, and rice to confirm their orthologies, and 3) differential expression of the MADS-box genes was confirmed in different organs.

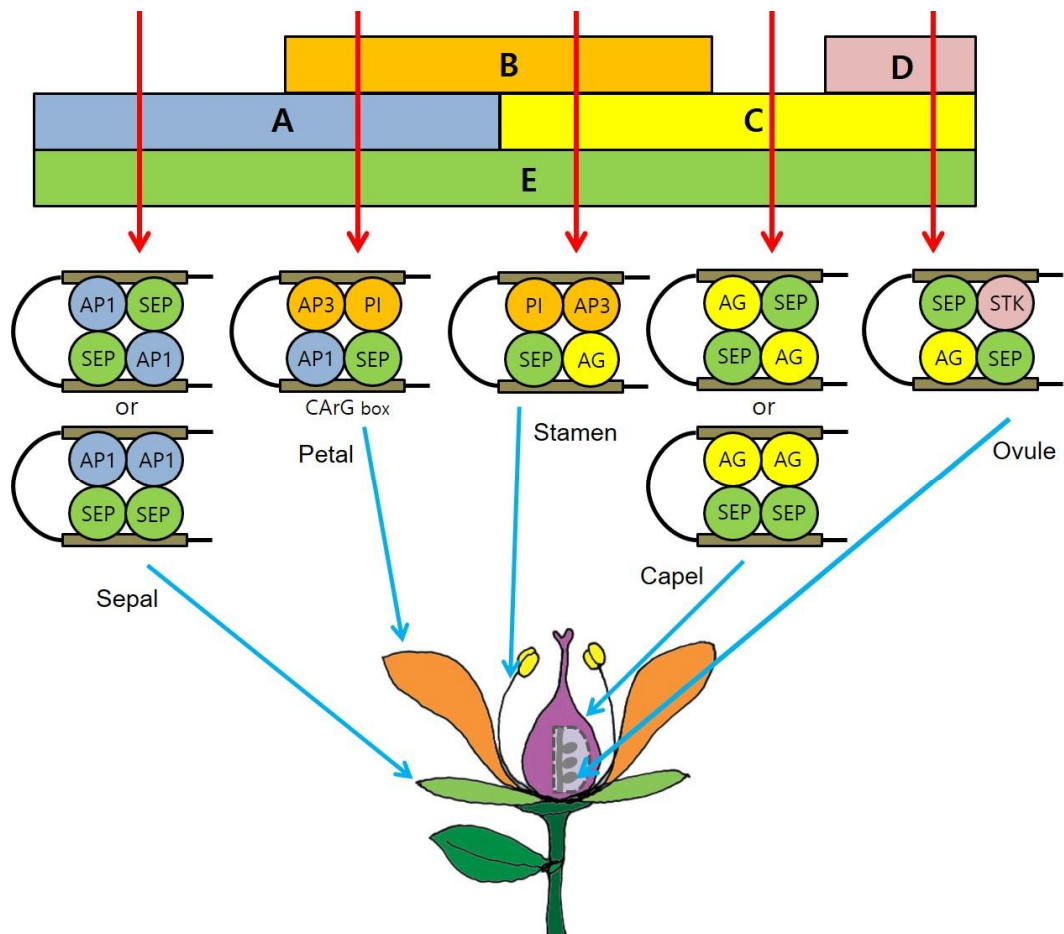


Fig. 2.3 The ABCDE model and the floral quartet model in *Arabidopsis*. The ABCDE protein complex specifies floral organ identity by binding CARG boxes in the promoter region of the target gene (Coen and Meyerowitz, 1991; Colombo et al., 1995; Tilly et al., 1998; Honma and Goto, 2001; Theissen and Saedler, 2001; Immink et al., 2010).

2.2 Materials and Methods

2.2.1 Plant material

The plant material of *C. dickinsii* Franch. & Sav. has cultivated for several years in the greenhouse of Sungshin Women's University (Fig. 2.4). The plants were collected at Hwaseong-si, Gyeonggi-do, Republic of Korea (N 37°16'14.37", E 126°55'19.17"). The voucher specimen was deposited in the herbarium of Sungshin Women's University (SWU; B. Lee 2013-01). Leaves and inflorescences of various stages were used. Female and male inflorescences were dissected into five parts: pistillate scales (F-SC), perigynia (PG), carpels (CA), staminate scales (M-SC), and stamens (ST). These samples were immediately frozen in liquid nitrogen and stored at -80°C.

2.2.2 RNA extraction and sequencing

Total RNAs were extracted using RNeasy Plant Mini kit (Qiagen, Hilden, Germany) following the manufacturer's manual. The extracted total RNAs were checked using 1.3% agarose gel electrophoresis. Sequencing libraries were constructed using TruSeq™ RNA Sample Preparation Kit v2 (Illumina, San Diego, USA) according to the manufacturer's manual. Libraries were sequenced using HiSeq 2000 sequencer (Illumina, San Diego, USA)

with TruSeq SBS Kit v3 (Illumina, San Diego, USA) as 2 x 101 bp reads. Library construction and sequencing were conducted by a commercial company (Macrogen Inc., Seoul, Korea).

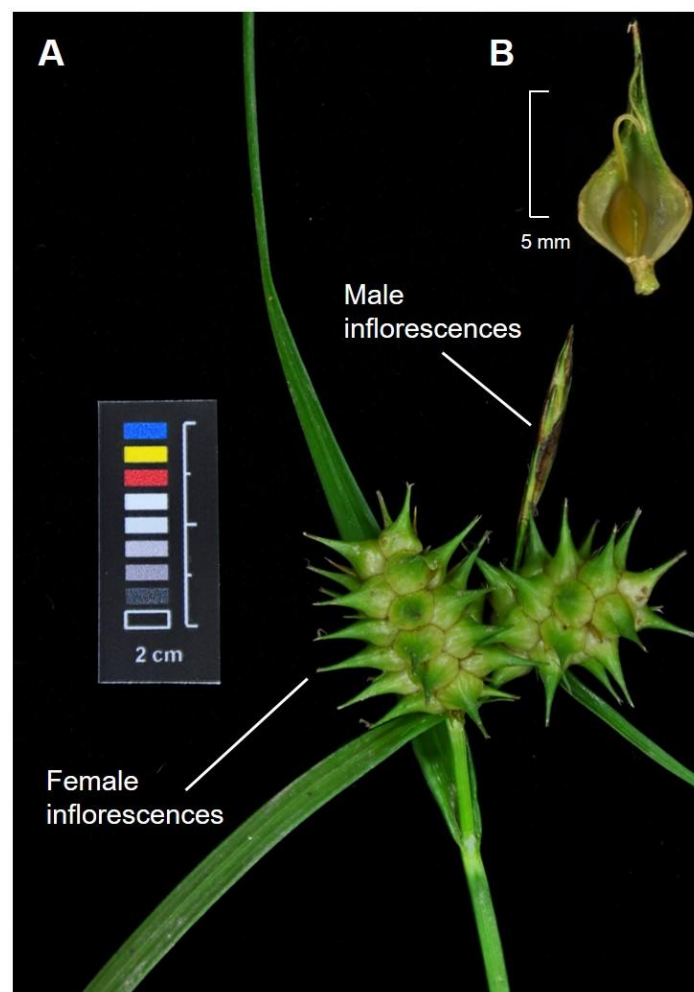


Fig 2.4 Pictures of *C. dickinsii*. (A) Male and female inflorescences. (B) Longitudinal section of perigynium.

2.2.3 *De novo* assembly and functional annotation

All of the raw reads were trimmed adapters and filtered low-quality sequence using trimmomatic (Bolger et al., 2014). The filtered raw reads were assembled using SOAPdenovo-TRANS (Xie et al., 2014). The assembled transcripts were annotated using InterProScan v. 5.18-57.0 (Jones et al., 2014). The detected MADS-box transcripts were filtered by the following process: 1) found the correct reading frame, 2) recognized initiation and stop codon compare to the MADS-box genes of *Arabidopsis*, and trimmed, 3) excluded short sequence less than 102 bp. These transcripts were considered non-assembled transcripts because its length is the same as that of raw read, 4) filtered out potential chimeric sequence during the assembly, and 5) excluded redundant transcripts and different type of MADS-box gene (SRF and MEF-type).

2.2.4 Confirmation of MADS-box genes

In order to confirm the detected MADS-box genes from transcriptome analysis, polymerase chain reactions (PCR) was performed with specific primers (Appendix 1). Prior to PCR, extracted RNAs were performed the following process: 1) contaminating DNAs were removed using DNA-freeTM kit DNase Treatment and Removal Reagents (Ambion, Austin, USA), 2)

cDNAs were synthesized from DNase treated RNAs using SuperScriptTM II Reverse Transcriptase (Invitrogen, Carlsbad, USA) with polyT primer (5'-CCG GAT CCT CTA GAG CGG CCG C(T)17-3'; Kramer et al., 1998). PCR were performed using DiaStarTMTaq DNA Polymerase (Solgent Co., Daejeon, Korea) with the following steps: 1) 95°C for 2 min, 2) 35 cycles of 95°C for 20 sec, 55 or 57°C for 40 sec, and 72°C for 2 min, and 3) 72°C for 5 min. Primers were designed based on sequences assembled from the transcriptome of *C. dickinsii* (Appendix 1). The PCR products were checked by 1.3% agarose gel electrophoresis. The target PCR bands were excised from the agarose gel and purified using ExpinTMGel SV kit (GeneAll, Seoul, Korea) according to the manufacturer's manual. Purified PCR products were cloned using the TOPclonerTM TA cloning kit (Enzymomics, Daejeon, Korea) according to the manufacturer's manual. Plasmid DNAs were checked by 1.3% agarose gel electrophoresis. The target plasmid DNAs were performed cyclic sequencing reactions using the BigDye Terminator v3.1 Cycle Sequencing Kits (Applied Biosystems, USA) and determined using a PRISM 3730xl Analyzer (Applied Biosystems, USA). The sequencing of plasmid DNAs was conducted by a commercial company (Macrogen Inc., Seoul, Korea). Sequences were aligned and edited using Sequencher ver. 4.9 (Gene Code Corporation, Ann Arbor, USA).

2.2.5 Determination of Genomic DNA sequences

In order to identify the gene structure, total genomic DNAs were extracted from fresh leaves using ExgeneTM Plant SV kit (GeneAll, Seoul, Korea) following the manufacturer's manual. Long-range PCRs were performed using DiaStarTM EF-Taq DNA Polymerase (Solgent, Daejeon, Korea) with the following steps: 1) 95°C for 2 min, 2) 40 cycles of 95°C for 20 sec, 55°C for 40 sec, and 68°C for 5~10 min, and 3) 68°C for 5~10 min. Primers were designed based on sequences assembled from transcriptome of *C. dickinsii* (Appendix 1). The PCR products were checked by 1.3% agarose gel electrophoresis and purified using ExpinTMPCR SV kit (GeneAll, Seoul, Korea) according to the manufacturer's manual. The sequencing method of PCR products was the same as that of cDNA. Sequences were aligned and edited using Sequencher v. 4.9 (Gene Code Corporation, Ann Arbor, USA).

2.2.6 Phylogenetic analysis

To confirm the orthology of MADS-box genes, a phylogenetic analysis was performed on the detected MADS-box genes in *C. dickinsii* with 108 MADS-box genes in *Arabidopsis thaliana* [The Arabidopsis Information Resource (TAIR); www.arabidopsis.org], 36 MADS-box genes in *Amborella trichopoda* (Amborella genome project, 2013), and 76 MADS-box genes in *Oryza sativa* subsp.

japonica (Goff et al., 2002). For phylogenetic analysis, the amino acid sequences of the combined data set were aligned using a module of CLUSTALW (Thompson et al., 1997) in MEGA 7 (Kumar et al., 2016) with the default option. The maximum likelihood tree was conducted using IQ-TREE v. 1.6.12 (Nguyen et al., 2015) with 1,000 ultrafast bootstrap replicates (Hoang et al., 2018) and the GTR+F+R8 nucleotide substitution model. The model was selected by ModelFinder (Kalyaanamoorthy et al., 2017).

2.2.7 Expression analyses of MADS-box genes in different organs

To investigate differential gene expression in different organs, cleaned reads were mapped to the detected MADS-box genes using Bowtie2 v. 1.2.2 with default parameters (Langmead et al., 2009). The mapped reads were calculated as FPKM (Fragment Per Kilobase of transcript per Million mapped reads) values using Cufflinks v. 2.2.1 (Trapnell et al., 2010) with default parameters. Based on the normalized FPKM values (\log_2 FPKM), the expression pattern of MADS-box genes was visualized by heatmap using Heatmapper (<http://www.heatmapper.ca/>; Babicki et al., 2016) with average linkage and euclidean measure. Previous detected genes and genes with an FPKM value of 0 were filtered out.

2.3 Results

2.3.1 Transcriptome sequencing and *de novo* assembly

To investigate differential expression of the MADS-box genes of *C. dickinsii*, libraries were constructed from the six organs (leaves, pistillate scales, perigynia, carpels, staminate scales, and stamens) and sequenced. The total number of raw reads were 399,723,766 and ranged from 61,972,118 in stamens to 74,653,200 in leaves (Table 2.1). The raw reads were filtered for adapters and low-quality sequence using trimmomatic (Bolger et al., 2014). As a result, total reads of cleaned data were 40,063,080,660 bp (Table 2.1).

The cleaned reads of six organs were *de novo* assembled independently using SOAPdenovo-Trans (Xie et al., 2014). The number of assembled transcripts were 74,279, 139,966, 94,258, 103,495, 148,021, and 296,686 for leaves, pistillate scales, perigynia, carpels, staminate scales, and stamens, respectively (Table 2.2). The highest N50 value was 2,019 bp in leaves and the lowest was 1,006 bp in stamens (Table 2.2). More detailed information was provided in Table 2.2.

Table 2.1 Statistics of transcriptome sequences

Sample	Raw reads	Raw read bases (bp)	Clean read bases (bp)
Leaves	74,653,200	7,539,973,200	7,465,304,533
Pistillate scales	64,681,126	6,532,793,726	6,492,543,809
Perigynia	63,098,052	6,372,903,252	6,329,610,406
Carpels	71,778,436	7,249,622,036	7,183,614,213
Staminate scales	63,540,834	6,417,624,234	6,377,592,153
Stamens	61,972,118	6,259,183,918	6,214,415,546
Total	399,723,766	40,372,100,366	40,063,080,660

Table 2.2 Statistics of assembled transcripts and identified genes

Sample	Statistic	Transcripts	Genes
Leaves	Total number	74,279	68,281
	Total length (bp)	56,933,548	40,974,951
	Maximum length (bp)	16,562	16,562
	Average length (bp)	766.4824244	600.0930127
	Minimum length (bp)	100	100
	GC Ratio (%)	40.92%	40.83%
	N50 (bp)	2,019	1,595
Pistillate scales	Total number	139,966	132,059
	Total length (bp)	75,970,277	55,583,383
	Maximum length (bp)	16,656	16,656
	Average length (bp)	542.7766529	420.8981061
	Minimum length (bp)	100	100
	GC Ratio (%)	41.65%	41.73%
	N50 (bp)	1,772	1,193

Perigynia	Total number	94,258	87,425
	Total length (bp)	65,080,762	47,273,452
	Maximum length (bp)	16,598	16,598
	Average length (bp)	690.4534575	540.731507
	Minimum length (bp)	100	100
	GC Ratio (%)	40.97%	40.91%
	N50 (bp)	1,914	1,458
Carpels	Total number	103,495	98,164
	Total length (bp)	61,383,249	48,521,410
	Maximum length (bp)	23,927	23,927
	Average length (bp)	593.1035219	494.2892506
	Minimum length (bp)	100	100
	GC Ratio (%)	40.62%	40.44%
	N50 (bp)	1,609	1,245
Staminate scales	Total number	148,021	139,733
	Total length (bp)	78,790,423	57,396,034
	Maximum length (bp)	17,356	17,356
	Average length (bp)	532.292195	410.75504
	Minimum length (bp)	100	100
	GC Ratio (%)	42.02%	42.27%
	N50 (bp)	1,781	1,170
Stamens	Total number	296,686	287,852
	Total length (bp)	105,228,488	84,794,933
	Maximum length (bp)	15,555	15,555
	Average length (bp)	354.6796546	294.5782312
	Minimum length (bp)	100	100
	GC Ratio (%)	44.90%	45.27%
	N50 (bp)	1,006	570

2.3.2 Identification of MADS–box genes

The prediction of the MADS domain for each organs was performed by InterProScan (Jones et al., 2014). A total of 182 transcripts, including isoforms, were detected as MADS–box gene candidates (Table 2.3). The MADS–box gene candidates were detected the most in stamens and the least in leaves (Table 2.3). Redundant transcripts and different types of MADS–box gene (SRF and MEF–type) were removed. The longest transcripts are determined as representative transcripts of the genes. As a result, a total of 48 MADS–box genes including isoforms were identified (Table 2.4). Among them, the major MADS–box genes were confirmed using Sanger sequencing (Table 2.4).

Phylogenetic analysis was performed for 1) detected 48 MADS–box genes of *C. dickinsii* in this study, 2) previously studied seven MADS–box genes of *C. dickinsii*, 3) MADS–box genes from genomes of *Arabidopsis thaliana*, *Amborella trichopoda*, and *Oryza sativa* subsp. *japonica*. The ML tree showed that all MADS–box genes of *C. dickinsii* were clustered into each subclade (MIKC^C, MIKC*, M α , M β , and M γ ; Fig. 2.5). The MIKC^C–type genes were clustered into 15 clades (Fig. 2.5). Among them, 12 clades contained MADS–box genes of all four species and well supported (83~100%): SQUA (AP1), GLO, DEF, AG, AGL2 (SEP), AGL6, AGL12, AGL17, FLC, GGM13 (B sister), STMADS11 (SVP), and TM3 (SOC1). Therefore, the phylogenetic analysis showed that the orthology of MADS–box genes in *C. dickinsii* was confirmed against

Arabidopsis MADS-box genes. OsMADS32 clade, which is a monocot-specific clade, contained MADS-box genes of *C. dickinsii* and rice (Arora et al., 2007). Whereas, the AGL15 and TM8 clades did not contain the MADS-box genes of *C. dickinsii* and rice. In MIKC*-type MADS-box genes, three MADS-box genes were clustered in P clade and two MADS-box genes were clustered in S clade. In Type I MADS-box genes, six MADS-box genes were clustered in M α clade and two MADS-box genes were clustered in M γ clade. Thus, 40 type II (35 MIKC^C and five MIKC*-type) and eight type I MADS-box genes were identified in this study (Fig. 2.5; Table 2.4). As in the previous study, the newly detected genes in this study were named based on the naming system of Kim et al. (2005), which is the combination of the scientific name and the subfamily name of the MADS-box gene (Table 2.4). In case of multiple sequences in a subfamily, numbers are followed after the combined names.

Table 2.3 Number of detected MADS-box genes in this study

Library	Number of detected MADS-box genes	Number of MADS-box genes including isoforms
Leaves	18	22
Pistillate scales	24	31
Perigynia	29	30
Carpels	30	35
Staminate scales	21	24
Stamens	33	40
Total	155	182

Table 2.4 Identified MADS-box genes in *C. dickinsii*

Type	Group	Subfamily name	Gene name	Sequence length (bp)	Confirmation of cDNA	Determination of Gene structure		
Type II	MIKC ^C	SQUA	<i>Ca.di.API.1-1</i>	837				
			<i>Ca.di.API.1-2</i> (Lee, 2014)	763				
			<i>Ca.di.API.2</i>	729	0	△		
			<i>Ca.di.API.3</i>	720				
					<i>Ca.di.API.4</i>	741		△
				DEF	<i>Ca.di.AP3</i>	687		0
			<i>Ca.di.AP3</i> (Lee, 2014)		616			
				GLO	<i>Ca.di.PI-1</i>	627	0	0
			<i>Ca.di.PI-2</i> (Lee, 2014)		608			
				AG	<i>Ca.di.AG.1-1</i>	729	0	
			<i>Ca.di.AG.1-1</i> (Lee, 2014)		710			
			<i>Ca.di.AG.1-2</i> (Lee, 2014)		710			
			<i>Ca.di.AG.1-3</i> (Lee, 2014)		710			
			<i>Ca.di.AG.2-1</i>		708	0	△	
			<i>Ca.di.AG.2-2</i>		359			
					<i>Ca.di.AG.2-3</i>	714	0	
				AGL2	<i>Ca.di.SEP.1</i>	729	0	
			<i>Ca.di.SEP.1</i> (Lee, 2014)		655			
			<i>Ca.di.SEP.2</i>		729	0	0	
			<i>Ca.di.SEP.3</i>		729	0		
					<i>Ca.di.SEP.4</i>	723		△
				AGL6	<i>Ca.di.AGL6</i>	738	0	△
				AGL12	<i>Ca.di.AGL12.1</i>	690		
			<i>Ca.di.AGL12.2</i>		696		0	
				AGL17	<i>Ca.di.AGL17.1</i>	765		0
			<i>Ca.di.AGL17.2</i>		909			
			<i>Ca.di.AGL17.3</i>		696			
				GMM13	<i>Ca.di.GMM13</i>	684	0	0

	STMADS11	<i>Ca.di.STMADS11.1</i>	675	0	
		<i>Ca.di.STMADS11.2</i>	681	0	△
	TM3	<i>Ca.di.TM3.1-1</i>	672	0	
		<i>Ca.di.TM3.1-2</i>	687	0	
		<i>Ca.di.TM3.1-3</i>	288		
		<i>Ca.di.TM3.2</i>	636		
		<i>Ca.di.TM3.3</i>	585		
	FLC	<i>Ca.di.FLC.1</i>	522	0	0
		<i>Ca.di.FLC.2</i>	597		
		<i>Ca.di.FLC.3-1</i>	597		
		<i>Ca.di.FLC.3-2</i>	222		
		<i>Ca.di.FLC.3-3</i>	639		
		<i>Ca.di.FLC.4</i>	519		△
	OsMADS32	<i>Ca.di.OsMADS32</i>	591		0
	MIKC*	P	<i>Ca.di.MIKC*.P.1</i>	312	
			<i>Ca.di.MIKC*.P.2</i>	819	0
			<i>Ca.di.MIKC*.P.3</i>	1035	
		S	<i>Ca.di.MIKC*.S.1^a</i>	291	
			<i>Ca.di.MIKC*.S.2^a</i>	604	
Type I	M α	<i>Ca.di.typeIMα.1-1</i>	522		0
		<i>Ca.di.typeIMα.1-2</i>	552		
		<i>Ca.di.typeIMα.2^a</i>	474		
		<i>Ca.di.typeIMα.3^a</i>	295		
		<i>Ca.di.typeIMα.4</i>	552		
		<i>Ca.di.typeIMα.5^a</i>	232		
	M γ	<i>Ca.di.typeIMγ.1</i>	468		0
		<i>Ca.di.typeIMγ.2</i>	366		

^a and △, Gene has incomplete sequence.

TYPE II - MIKC^C

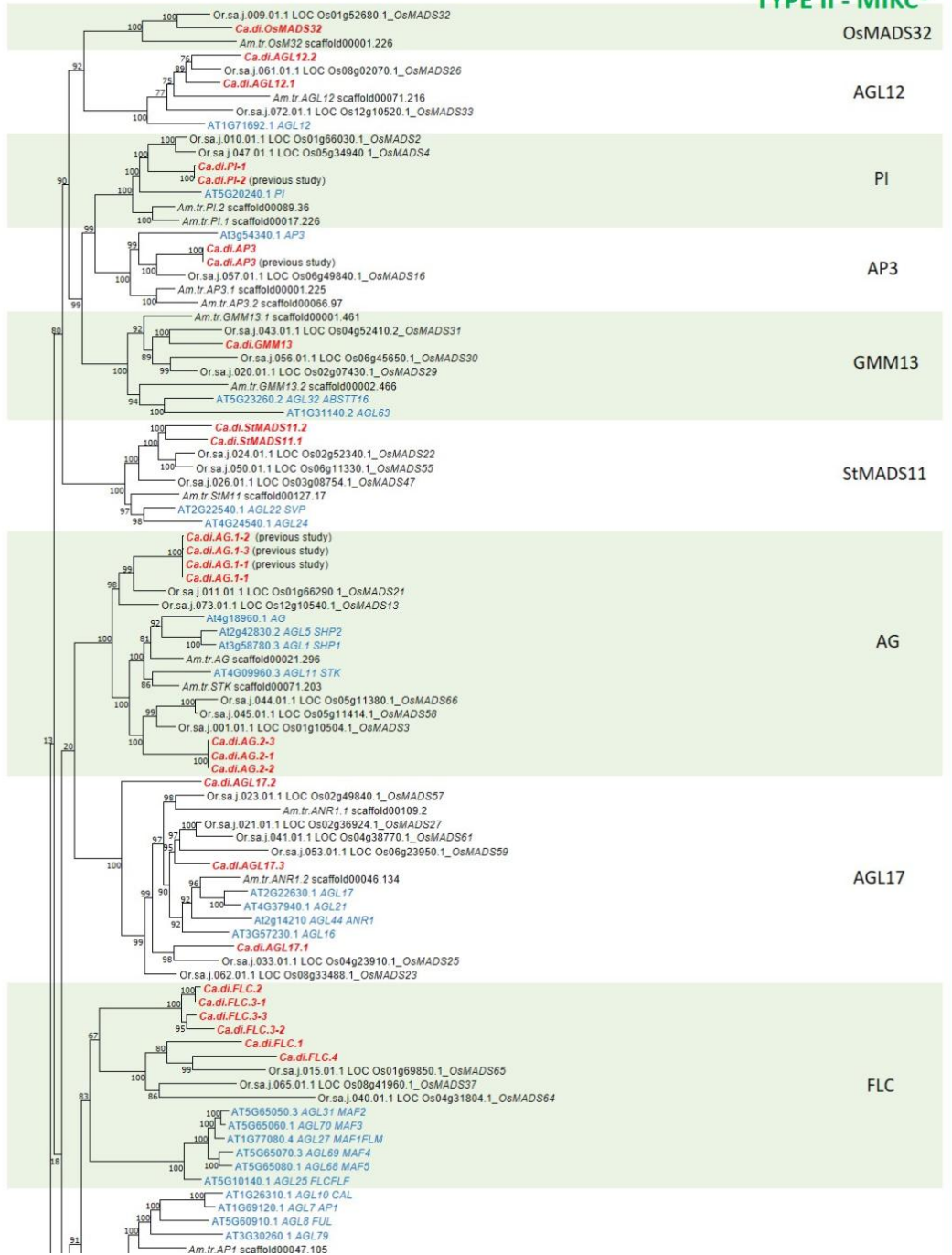


Fig. 2.5 (Continued)

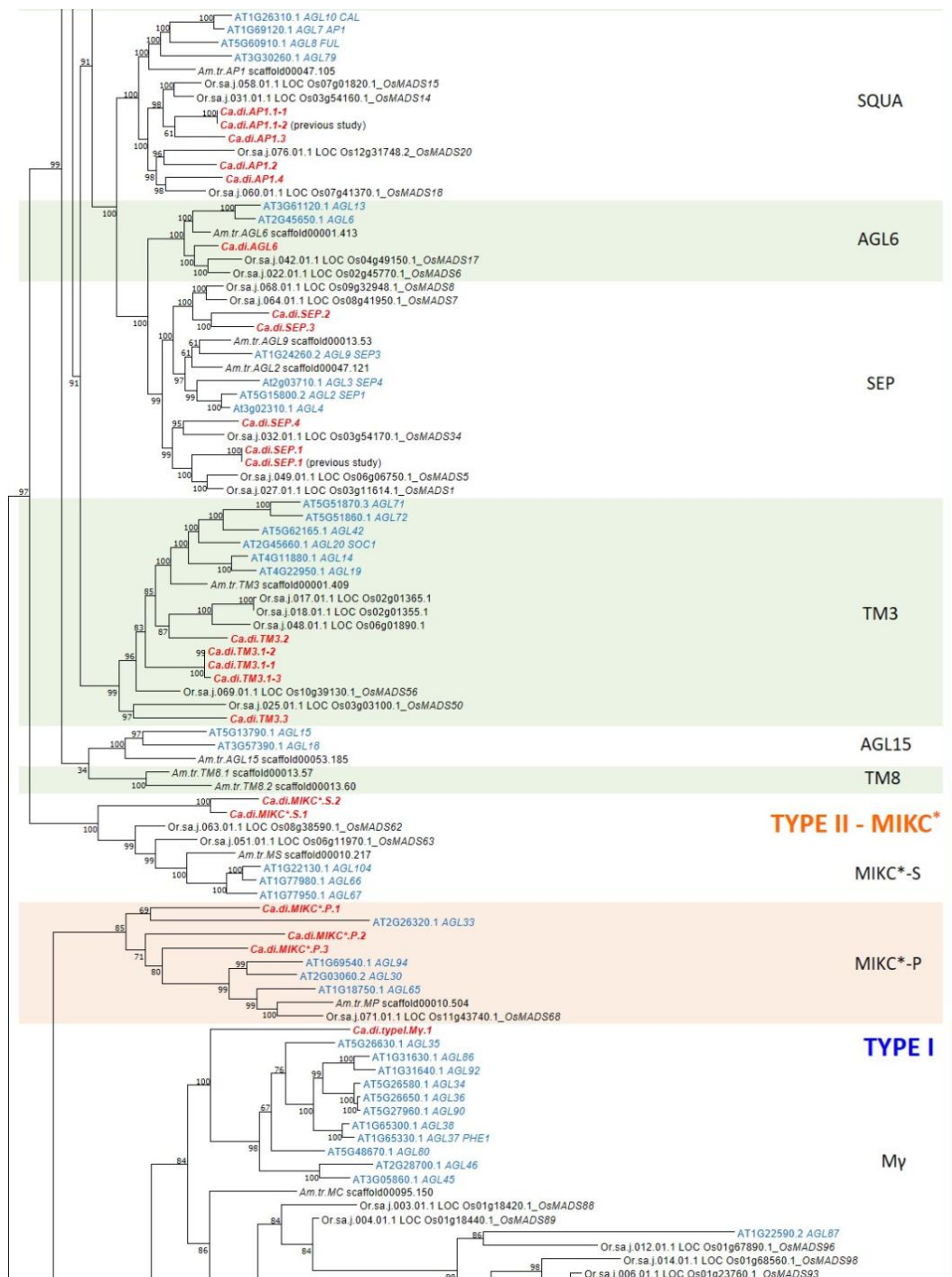


Fig. 2.5 (Continued)

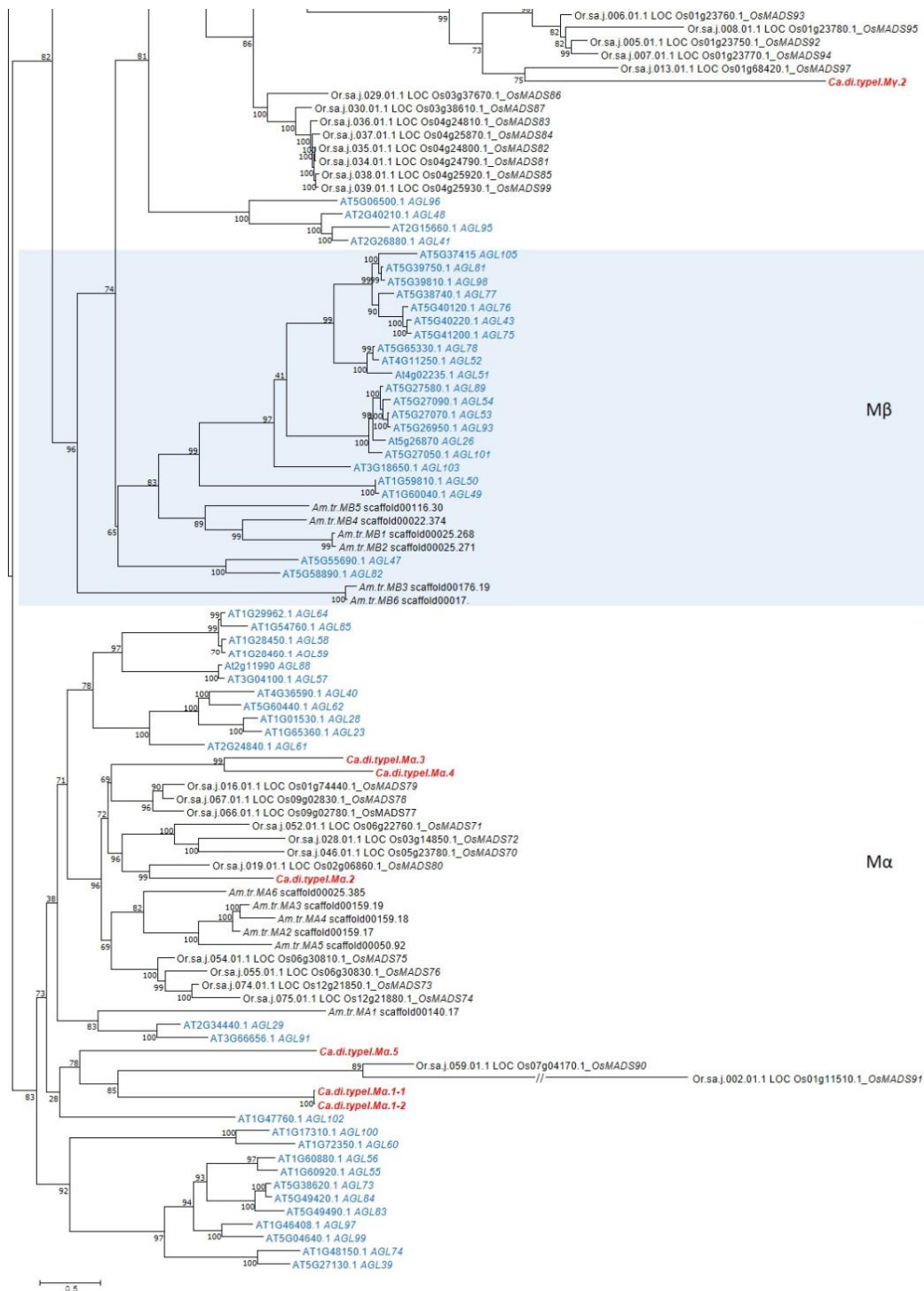


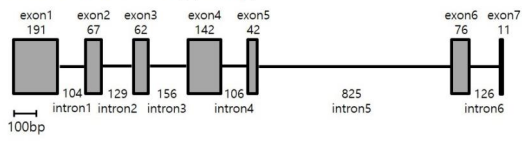
Fig. 2.5 (Continued)

Fig. 2.5 The maximum likelihood tree of MADS-box genes in *C. dickinsii* (red), *Arabidopsis* (blue), *Amborella*, and *Oryza*. Each new gene was revealed as a member of each major clade of the MADS-box family (Becker et al., 2003). Bootstrap values (>50%) by 1,000 replicates were indicated above the node in a ML tree ($-\ln L = 179473.54$).

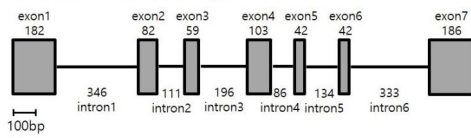
2.3.3 Gene structure

To investigate the gene structure, the major MADS-box transcripts were aligned with their genome sequence. As a result, the gene structures of 15 MADS-box genes were identified (Fig. 2.6): *Ca.di.OSMADS32*, *Ca.di.AGL12.2*, *Ca.di.PI-1*, *Ca.di.AP3*, *Ca.di.GMM13*, *Ca.di.STMADS11.2*, *Ca.di.AG.2-1*, *Ca.di.AGL17.1*, *Ca.di.FLC.1*, *Ca.di.FLC.4*, *Ca.di.AP1.2*, *Ca.di.SEP.2*, *Ca.di.SEP.4*, *Ca.di.MIKC*.P.2*, and *Ca.di.typeIM γ .1*. Among them, the full sequence of *Ca.di.STMADS11.2*, *Ca.di.AG.2-1*, *Ca.di.FLC.4*, *Ca.di.AP1.2*, and *Ca.di.SEP.2* could not be obtained, but exon-intron structure was recognized. Generally, type II MADS-box genes had more exons and were longer than type I, although only one exon-intron structure of the type I MADS-box gene was identified. *Ca.di.typeIM γ .1* belonging to the type I MADS-box gene had two exons, whereas the type II MADS-box genes had five to ten exons. In addition, the closely related genes in the phylogenetic tree had similar exon-intron structure. For example,

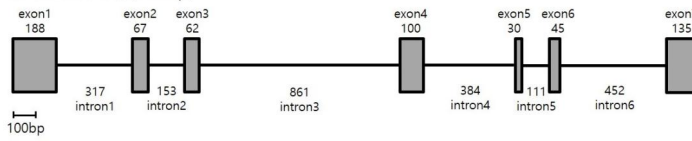
A. *Ca.di.OsMADS32* (2,037bp)



B. *Ca.di.AGL12.2* (1,902bp)



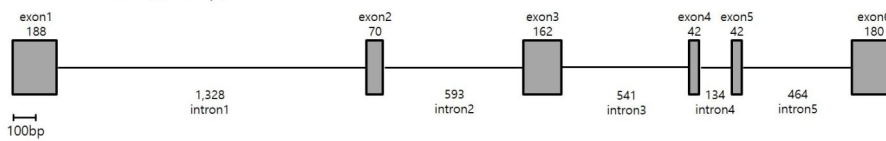
C. *Ca.di.PI-1* (2,905bp)



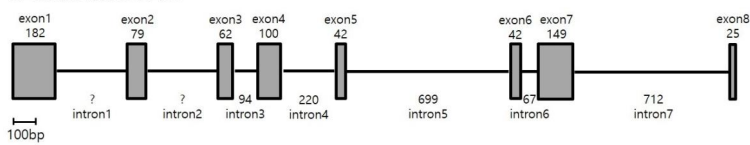
D. *Ca.di.AP3* (4,262bp)



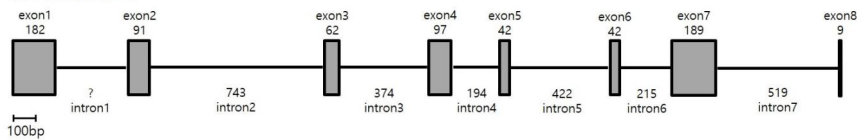
E. *Ca.di.GMM13* (3,744bp)



F. *Ca.di.STMADS11.2*



G. *Ca.di.AG.2-1*



H. *Ca.di.AGL17.1* (4,095bp)

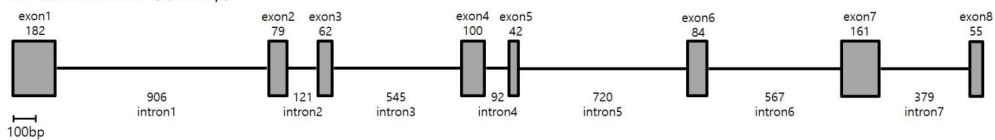


Fig. 2.6 (Continued)

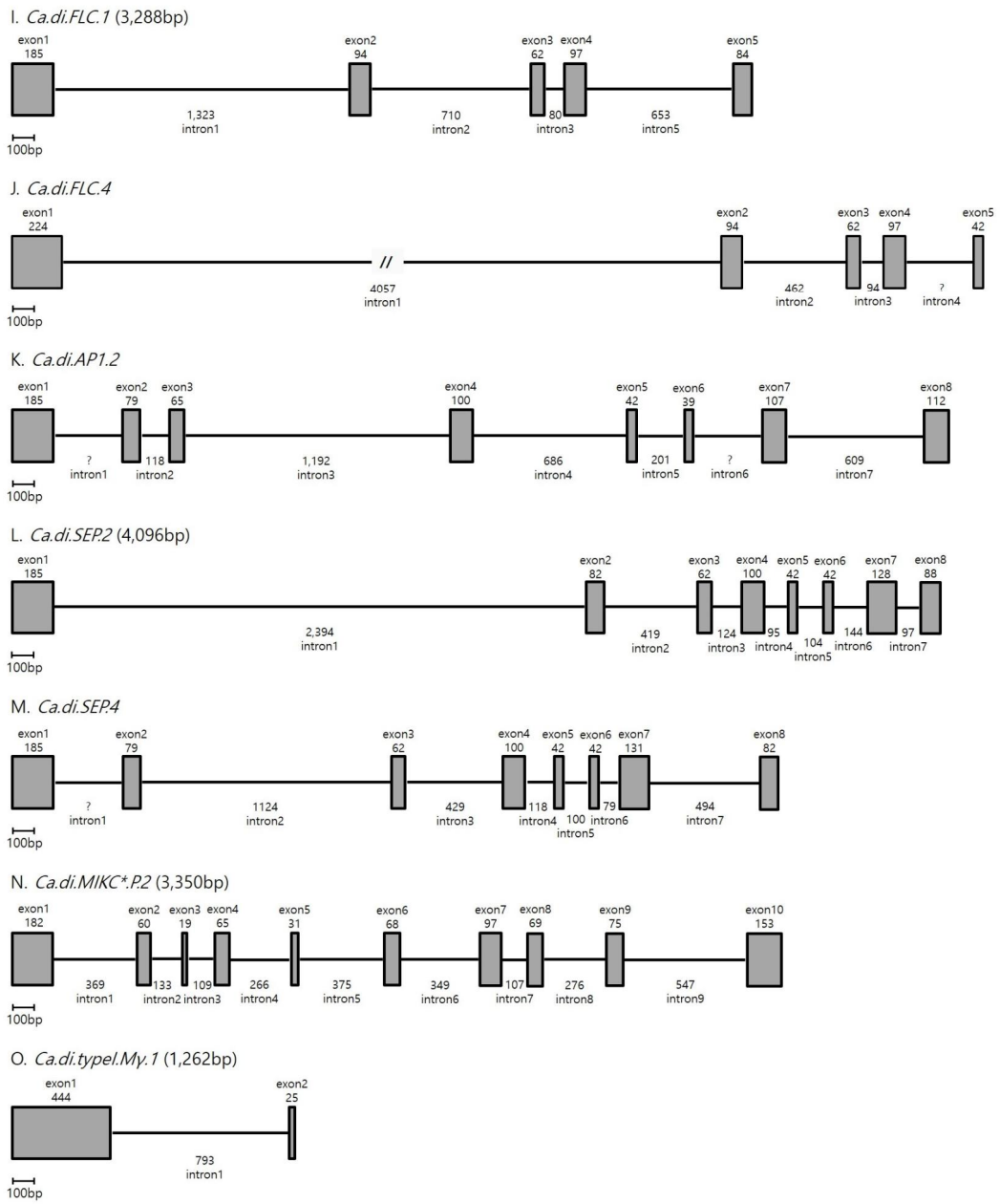


Fig. 2.6 Gene structure of MADS-box genes in *C. dickinsii*. The question marks indicate unidentified regions.

Ca.di.OSMADS32, *Ca.di.AGL12.2*, *Ca.di.PI-1*, *Ca.di.AP3*, and *Ca.di.GMM13* had seven exons except for *Ca.di.GMM13* which had six exons. *Ca.di.AG.2-1* and *Ca.di.AGL17.1* had eight exons. *Ca.di.AP1.2*, *Ca.di.SEP.2*, and *Ca.di.SEP.4* had eight exons.

2.3.4 Expression analyses of MADS-box genes

Differential expression of MADS-box genes in different organs was visualized by heatmap using Heatmapper based on the normalized FPKM (Fig. 2.7~2.9; Appendix 2 and 3).

The A-class genes, *AP1* orthologs (*Ca.di.AP1*), were widely expressed in all organs. *Ca.di.AP1.1-1* and *Ca.di.AP1.3* were highly expressed in pistillate scales, perigynia, and staminate scales. *Ca.di.AP1.2* was strongly expressed in leaves. *Ca.di.AP1.4* was highly expressed in pistillate scales and staminate scales. In the B-class genes, *AP3* ortholog (*Ca.di.AP3*) was expressed in perigynia and stamens. *PI* ortholog (*Ca.di.PI*) was highly expressed in perigynia, carpels, and stamens. In the C-class genes, *AG* orthologs (*Ca.di.AG*) were expressed in all organs except leaves and staminate scales. *Ca.di.AG.1-1* was strongly expressed in perigynia and carpels, and *Ca.di.AG.2-2* was strongly expressed in carpels and stamens. *Ca.di.AG.2-1* and *Ca.di.AG.2-3* were expressed in pistillate scales, perigynia, carpels and stamens, and more expressed in carpels and stamens. The E-class genes, *SEP* orthologs (*Ca.di.SEP*), were widely expressed all organs except

leaves. *Ca.di.SEP.1* and *Ca.di.SEP.4* were expressed higher in pistillate scales and staminate scales than other organs, whereas *Ca.di.SEP.2* and *Ca.di.SEP.3* were expressed higher in perigynia, carpels, and stamens.

In non-floral genes, *GGM13* ortholog (*Ca.di.GMM13*) was highly expressed in perigynia and carpels. *AGL6* ortholog (*Ca.di.AGL6*) was expressed in pistillate scales, perigynia, carpels, and stamens, with the lowest expression in pistillate scales. *TM3* orthologs (*Ca.di.TM3*) were expressed in most of the organs, but it was rarely expressed in perigynia and carpels. *AGL12* orthologs (*Ca.di.AGL12*) were widely expressed in all organs. *Ca.di.AGL12.1* was expressed in pistillate scales and staminate scales and *Ca.di.AGL12.2* was expressed low in most of the organs. *STMADS11* orthologs (*Ca.di.STMADS11*) were highly expressed in leaves and carpels. *FLC* orthologs (*Ca.di.FLC*) were expressed in most of the organs, but it was rarely expressed in carpels. *AGL17* orthologs (*Ca.di.AGL17*) were expressed in leaves and stamens. *Ca.di.OsMADS32* was strongly expressed in carpels. *Ca.di.MIKC*.P.2-1* was expressed low in most of the organs except carpels, and *Ca.di.MIKC*.P.4* was strongly expressed in stamens. Type I MADS-box genes were expressed in most of the organs, and *Ca.di.typeI.M α .4-1* and *Ca.di.typeI.M γ .2* were expressed only in carpels and stamens, respectively.

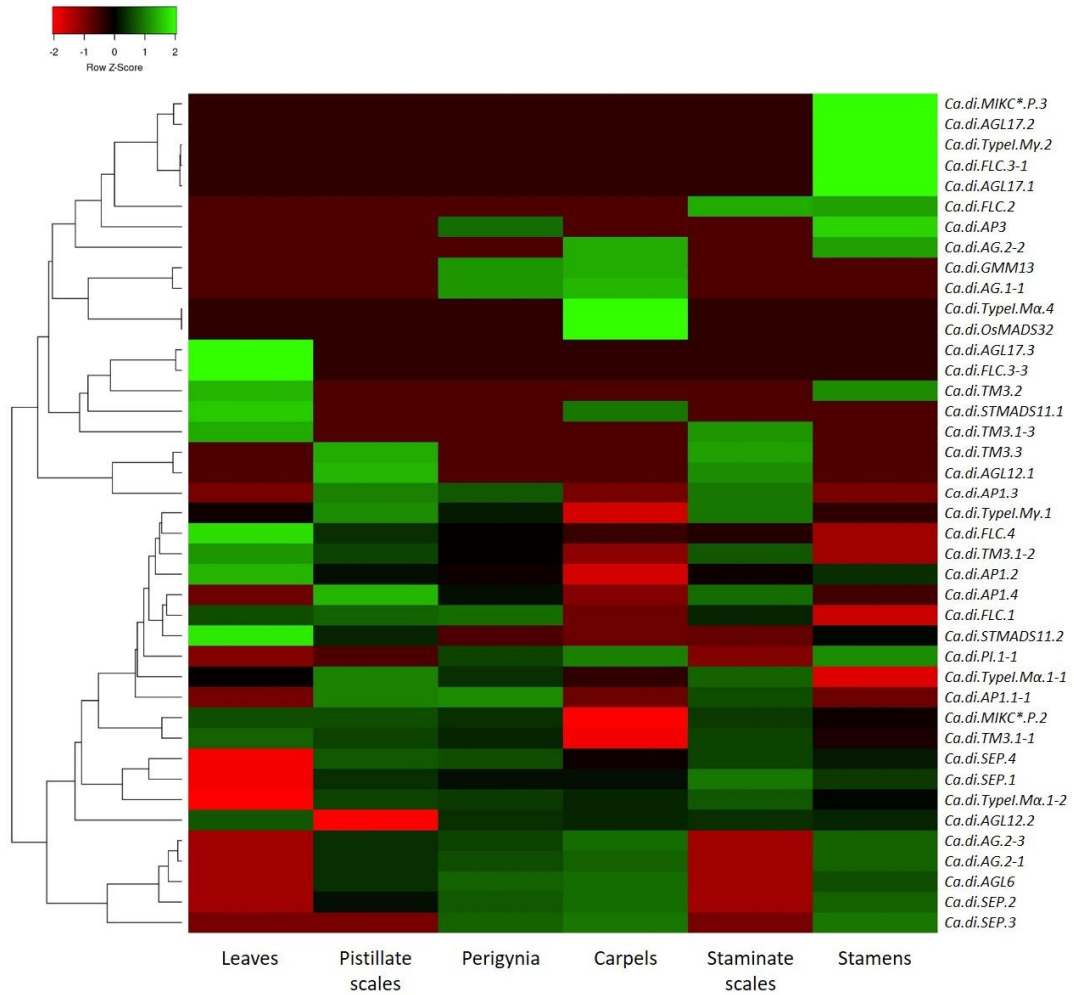


Fig. 2.7 The expression levels of the MADS-box genes in different organs. The heat map was generated based on normalized FPKM values (\log_2 FPKM).

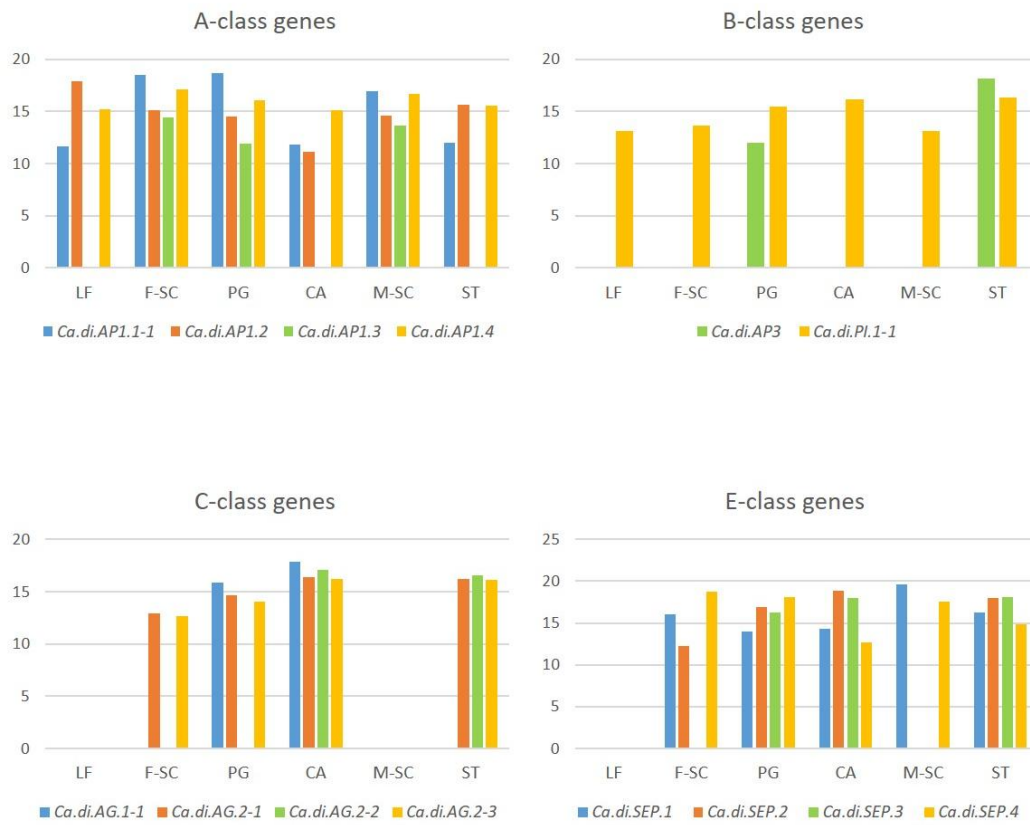


Fig. 2.8 Expression of floral genes in different organs based on normalized FPKM values (\log_2 FPKM). LF, Leaves; F-SC, Pistillate scales; PG, perigynia; CA, carpels; M-SC, staminate scales; ST, stamens.

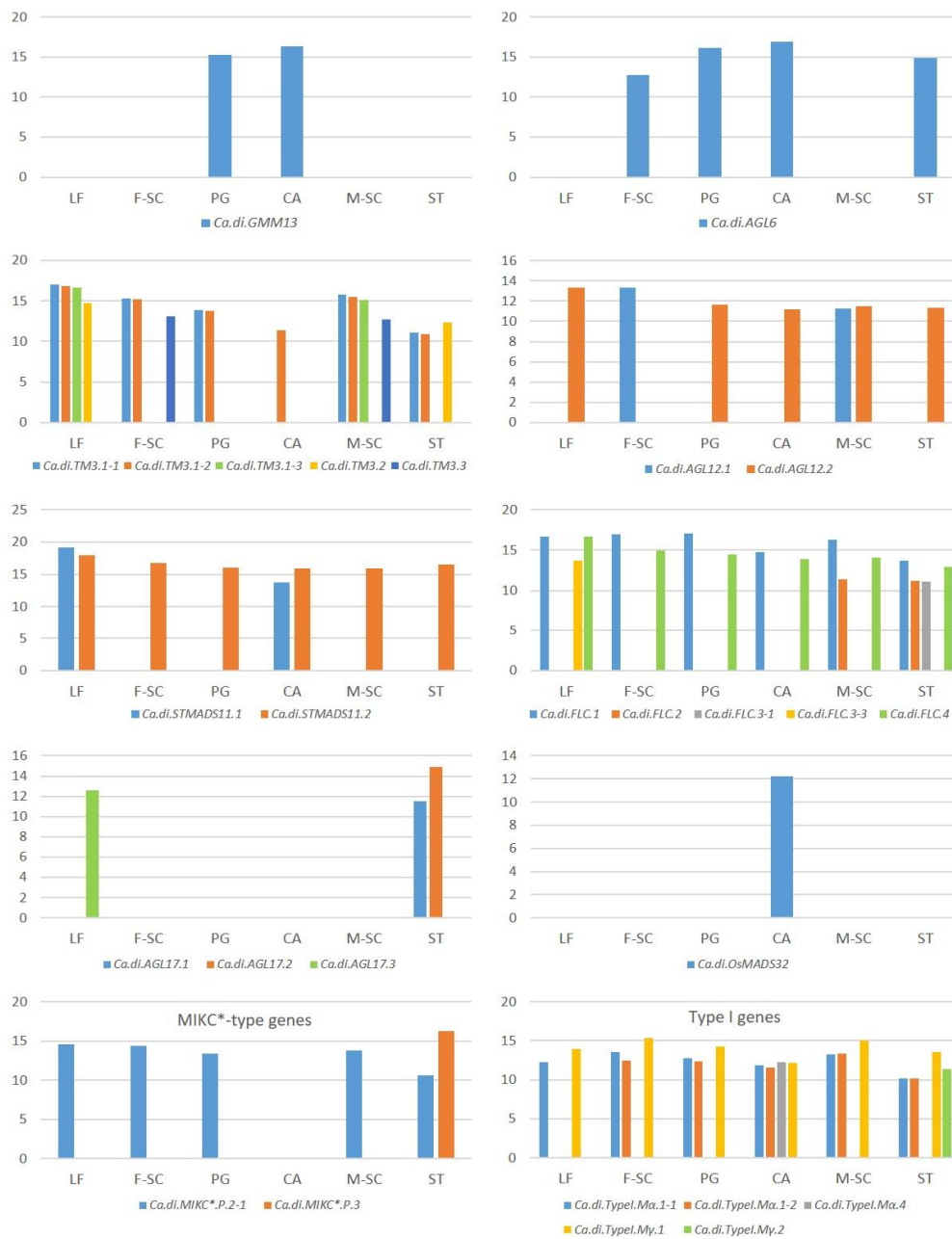


Fig. 2.9 Expression of non-floral genes in different organs based on normalized FPKM values (\log_2 FPKM). LF, Leaves; F-SC, Pistillate scales; PG, perigynia; CA, carpels; M-SC, staminate scales; ST, stamens.

2.4 Discussion

The MADS-box genes are involved in flower developments and play a crucial role in determining the floral organ identity. Many researchers have studied the evolution of flower and uncovered the homology of floral organs between model and non-model plants based on conservation of the genetic mechanisms of the MADS-box genes. In this study, to uncover the origin of the unique organ in *Carex*, transcriptome analysis was performed using *C. dickinsii*.

2.4.1 Identification and expression of MADS-box genes in *C. dickinsii*

A total of 48 MADS-box genes were identified in *C. dickinsii*, containing 40 type II (35 MIKC^C and five MIKC*-type) and eight type I MADS-box genes, and their orthologies against *Arabidopsis* genes were confirmed by phylogenetic analysis (Table 2.4; Fig. 2.5). The phylogenetic analysis showed that 1) 12 MIKC^C-type genes had already been established before separating of monocots and dicots: *SQUA*, *GLO*, *DEF*, *AG*, *AGL2*, *AGL6*, *AGL12*, *AGL17*, *FLC*, *GGM13*, *STMADS11*, and *TM3* and 2) *AGL15* and *TM8* have been lost in the MRCA of Cyperaceae and Poaceae (Gramzow and Theissen, 2015).

The MADS-box genes in *C. dickinsii* were expressed in leaves,

pistillate scales, perigynia, carpels, staminate scales, and stamens (Fig. 2.7). The A function genes were widely expressed in all organs. The B function genes were expressed in perigynia and stamens. The C function genes were expressed pistillate scales, perigynia, carpels, and stamens. The E function genes were expressed in all organs except leaves. In other words, A+C+E function genes were expressed in pistillate scales, A+B+C+E function genes were expressed in perigynia, A+C+E class genes were expressed in carpel, A+E function genes were expressed in staminate scales, and A+B+C+E class genes were expressed in stamen. The Expressions of the B, C, and E function genes were well matched only in stamen and carpel except for A function gene.

The A function has been controversial because the A function applied to *Arabidopsis* no longer applies to other angiosperms (Causier et al., 2010). For example, recessive mutants were not found in other plants except for *Arabidopsis* (Litt, 2007; Theissen et al., 2016). In addition, The A function is difficult to separate from the E function, which determines floral meristem identity, even in *Arabidopsis* (Causier et al., 2010; Theissen et al., 2016). Thus, Causier et al. (2010) redefined the A function. The redefined (A) functions are determination of floral meristem identity (the floral ground state; sepal) and activation and regulation of the B and C functions (Causier et al., 2010; Theissen et al., 2016). Furthermore, Causier et al. (2010) suggested a revised (A)BC model in which (A) function includes the E function.

The expressions of non-floral genes were also confirmed. *Ca.di.GMM13*, *Ca.di.OsMADS32*, *Ca.di.STMADS11*, and type I ($M\alpha$) gene, which are involved in the development of female reproductive organs, were expressed in carpels (Gramzow and Theissen, 2010; Smaczniak et al., 2012; Wang et al., 2015). Especially, *Ca.di.GMM13* was also expressed in perigynia. MIKC*-type genes, which control development of male gametophytes, were strongly expressed in stamens (Gramzow and Theissen, 2010). *Ca.di.AGL6*, *Ca.di.AGL12*, *Ca.di.AGL17*, *Ca.di.FLC*, and *Ca.di.TM3*, which involved in floral transition, were expressed in floral organs (Smaczniak et al., 2012).

2.4.2 Evolutionary origin of specialized organs in *Carex*

Expression patterns of MADS-box genes in *C. dickinsii* showed that (A) and E function genes are expressed in pistillate scales, perigynia, and staminate scales. Therefore, it is considered that pistillate scale, perigynium, and staminate scale are part of flowers in *Carex*.

The expression patterns of the MADS-box genes were similar in pistillate scales and staminate scales, but *Ca.di.AG*, *Ca.di.SEP.2*, and *Ca.di.AGL6* were expressed only in pistillate scale. Thus, it can be assumed that morphological characters of pistillate scales and staminate scales are similar, but evolutionary genetic mechanisms are different.

These results are partially consistent with my previous study

(unpublished). In the previous study, *Ca.di.AP1*, *Ca.di.AG*, *Ca.di.SEP*, *Ca.di.PI*, and *Ca.di.AP3* genes were identified and expression patterns of MADS-box genes were confirmed using relative-quantitative RT PCR. As a results, *Ca.di.AP1* was expressed in staminate scales, *Ca.di.AP3* and *Ca.di.PI* were expressed in stamens, and *Ca.di.SEP* were expressed in pistillate scales and staminate scales. However, the expressions of MADS-box genes were not detected in perigynia.

These studies showed that the expression patterns of *C. dickinsii* are different from that of *Arabidopsis*. Also, it is inconsistent with the widely accepted hypothesis that the origin of the perigynium is prophyll. Therefore, to clarify specific functions of floral MADS-box genes in *Carex*, detailed expression studies by in situ hybridization and phenotype complementation studies by transformation are needed.

Chapter 3

Genome size estimation of Korean *Carex*

3.1 Introduction

The amount of nuclear DNA is expressed as the genome size or C-value (Leitch and Leitch, 2013). The 'genome size' is used for the DNA content of the monoploid genome or chromosome set and the 'C (constant)-value' is used for the DNA content of the whole chromosome complement or karyotype irrespective of the degree of generative polyploidy of the organism (Greilhuber et al., 2005). However, these terms have been applied in different meanings and used ambiguously (Greilhuber et al., 2005). Thus, Greilhuber et al, (2005) proposed unified and modified terminology. The 'Holoploidy genome size (C-value)' means the DNA content of the whole chromosome complement characteristic for the organism with chromosome number n , irrespective of the degree of generative polyploidy, aneuploidies, etc. (Greilhuber et al., 2005). The 'Monoploid genome size (Cx-value)' represent the DNA content of the monoploid genome, which is one chromosome set of an organism, with chromosome base number x (Greilhuber et al., 2005).

Genome size is correlated with cell size and cell cycle time, which affects phenotypic characters such as pollen and seed size, developmental lifestyle, physiology, phenology and others (Bennett and Leitch, 2005; Greilhuber and Leitch 2013). Therefore, it is a key characteristic of organisms and one that is useful for studies of biodiversity, taxonomy, ecology, phylogeny, and population genetics

(Leitch and Bennett, 2007; Bennett and Leitch, 2011; Vrána et al., 2014). Recently, the importance of measuring genome size has been particularly emphasized in whole genome sequencing efforts, because the genome size of a taxon is directly related to the efficiency of its genome sequencing. Selecting a species having the smallest genome size in the target plant group can increase the depth of the sequencing result in next-generation sequencing (NGS) and in addition can minimize the computer memory required for genome assembly. As a preliminary step in genome research, a survey of the genome size of the targeted species and related taxa is essential.

The Plant DNA C-value Database (release 7.1; <http://data.kew.org/cvalues/>) managed by the Royal Botanic Gardens, Kew, currently contains 12,273 species comprising 10,770 angiosperms, 421 gymnosperms, 303 pteridophytes (246 ferns and fern allies and 57 lycophytes), 334 bryophytes, and 445 algae (Zonneveld et al., 2005; Leitch et al., 2019) and these numbers have grown since Bennett and Smith (1976) first published compiling lists of DNA C-values in angiosperms. The genome size of angiosperms varies enormously, with the largest genome being from *Paris japonica* (Franch. & Sav.) Franch. (Melanthiaceae) (152.23 pg; Pellicer et al., 2010) while the smallest is from *Genlisea margaretae* Hutch. (Lentibulariaceae) (0.061 pg; Fleischmann et al., 2014). Huge genome size variations in angiosperms are probably due to the polyploidization and the

replication of transposable elements (TEs) (Grover and Wendel, 2010; Kejnovsky et al., 2012; Leitch and Leitch, 2012).

The genus *Carex* is a plant group having holocentric chromosomes that might cause relatively rapid speciation (Hipp et al., 2010; Chung et al., 2012; Escudero et al., 2012). Holocentric chromosomes are characterized by a diffuse centromere that facilitates fission (agmatoploidy), fusion (symploidy), translocations, and inversion (Hipp et al., 2013). Therefore, chromosome numbers in *Carex* exhibit high diversity ranging from $n = 6$ to $n = 66$ (Tanaka, 1949; Hipp et al., 2009; Chung et al., 2016). To date, the genome size of *Carex* species has been reported for 329 accessions (292 taxa; 276 species) ranging from $1C = 0.2$ pg (*C. brownii* Tuck., *C. kobomugi* Ohwi, *C. nubigena* D.Don ex Tilloch & Taylor, and *C. paxii* Kük) to $1C = 1.64$ pg (*C. cuspidate* Bertol.) (data from the Plant DNA C-values Database; release 7.1). The number of species covered with this data corresponds to approximately 14% of reported *Carex* species worldwide.

In this study, the genome sizes of 43 *Carex* taxa distributed in the Korean peninsula were determined using flow cytometry. Although 180 *Carex* taxa have been reported in the Korean peninsula (Oh, 2007), intensive studies of their genome sizes have not yet been performed. To understand the genome size variation in each subgroup of *Carex*, the experimental data from this study were analyzed in combination with *Carex* genome size data previously reported in the Plant DNA C-values Database.

3.2 Materials and Methods

3.2.1 Plant materials

Forty-three taxa of Korean *Carex* were collected in the field and transplanted in the Sungshin Women's University, Seoul, Korea. Voucher specimens were deposited in the herbarium of the Sungshin Women's University (SWU; Table 3.1). Subgeneric and sectional classification of these taxa followed Egorova (1999) and scientific names followed a recent manual for grasses and sedges in Korea (Cho et al., 2016). Plant standards for flow cytometry have been proposed in Doležel et al. (2007). As internal reference standards, seeds of *Raphanus sativus* L. 'Saxa' (2C = 1.11 pg), *Solanum lycopersicum* L. 'Stupické polní rané' (2C = 1.96 pg), and *Glycine max* Merr. 'Polanka' (2C = 2.50 pg) were provided by Dr. Jaroslav Doležel (Laboratory of Molecular Cytogenetics and Cytometry, Institute of Experimental Botany, Olomouc, Czech Republic) and were used. Seeds were germinated and grown in the greenhouse at Sungshin Women's University and fully grown leaves were used for flow cytometry.

Table 3.1 Taxa and vouchers information

Subgenus	Section	Taxon (Korean name)	Voucher
<i>Carex</i>	<i>Siderostictae</i>	<i>C. okamotoi</i> Ohwi (지리대사초)	<i>B. Lee 2017-008</i> , <i>B. Lee 2017-029</i>
		<i>C. siderosticta</i> Hance var. <i>siderosticta</i> (대사초)	<i>B. Lee 2017-030</i> , <i>B. Lee 2017-047</i> , <i>B. Lee 2019-080</i>
		<i>C. siderosticta</i> var. <i>pilosa</i> H.Lév. ex T.Koyama (털대사초)	<i>B. Lee 2017-006</i> , <i>B. Lee 2019-081</i>
		<i>Carex</i>	<i>C. glabrescens</i> (Kük.) Ohwi (굽슬사초)
		<i>C. nakasimae</i> Ohwi (화산사초)	<i>B. Lee 2019-068</i>
	<i>Vesicariae</i>	<i>C. dickinsii</i> Franch. & Sav. (도깨비사초)	<i>S. Kim 2019-116</i> , <i>S. Kim 2019-117</i>
		<i>C. vesicaria</i> L. (새방울사초)	<i>B. Lee 2019-066</i>
	<i>Anomalae</i>	<i>C. alopecuroides</i> D.Don var. <i>alopecuroides</i> (가는흰사초)	<i>B. Lee 2017-002</i>
		<i>C. alopecuroides</i> var. <i>chlorostachya</i> C.B.Clarke (흰사초)	<i>B. Lee 2017-026</i> , <i>B. Lee 2019-060</i>
		<i>C. aphanolepis</i> Franch. & Sav. (골사초)	<i>B. Lee 2019-064</i>
	<i>C. dispalata</i> Boott ex A. Gray (삿갓사초)	<i>B. Lee 2019-072</i> , <i>B. Lee 2014-077</i>	
	<i>C. idzuroei</i> Franch. & Sav. (좁도깨비사초)	<i>B. Lee 2019-071</i>	
	<i>C. japonica</i> Thunb. (개쩌버리사초)	<i>B. Lee 2017-028</i>	
	<i>C. planiculmis</i> Kom. (그늘흰사초)	<i>B. Lee 2017-033</i> , <i>B. Lee 2017-045</i>	
	<i>C. pseudochinensis</i> H.Lév. & Vaniot (햇사초)	<i>B. Lee 2019-065</i>	
	<i>C. transversa</i> Boott (화살사초)	<i>B. Lee 2019-055</i> , <i>B. Lee 2019-058</i>	
<i>Depauperatae</i>		<i>C. kujuzana</i> Ohwi (장성사초)	<i>B. Lee 2017-016</i>
		<i>C. macroglossa</i> Franch. & Sav. (애기염주사초)	<i>B. Lee 2019-054</i>
		<i>C. pilosa</i> Scop. (털사초)	<i>B. Lee 2017-044</i>

<i>Mitratae</i>		<i>C. breviculmis</i> R.Br. (청사초)	<i>B. Lee 2019-082</i>	
		<i>C. genkaiensis</i> Ohwi (목포사초)	<i>B. Lee 2019-052</i>	
		<i>C. kamagariensis</i> K.Okamoto (큰청사초)	<i>B. Lee 2017-020</i>	
		<i>C. meridiana</i> Akiyama (갯바위청사초)	<i>B. Lee 2019-059</i>	
		<i>C. mitrata</i> Franch. var. <i>mitrata</i> (겨사초)	<i>B. Lee 2017-022</i>	
		<i>C. mitrata</i> var. <i>aristata</i> Ohwi (까락겨사초)	<i>B. Lee 2019-053</i>	
		<i>C. polyschoena</i> H.Lév. & Vaniot (가지청사초)	<i>B. Lee 2017-011</i>	
		<i>C. sabynensis</i> Less. ex Kunth (실청사초)	<i>B. Lee 2017-034</i>	
		<i>C. subebracteata</i> (Kük.) Ohwi (부리실청사초)	<i>B. Lee 2017-048</i>	
		<i>C. tristachya</i> Thunb. (만들사초)	<i>B. Lee 2019-061</i>	
	<i>Digitatae</i>		<i>C. lanceolata</i> Boott (그늘사초)	<i>B. Lee 2017-004</i>
			<i>C. macrandrolepis</i> H.Lév. & Vaniot (청피사초)	<i>B. Lee 2019-057</i>
		<i>C. pediformis</i> var. <i>pedunculata</i> Maxim. (왕그늘사초)	<i>S. Kim 2019-018</i>	
<i>Acrocystis</i>		<i>C. fusanensis</i> Ohwi (부산사초)	<i>B. Lee 2017-007</i>	
<i>Microhynchae</i>		<i>C. peiktusani</i> Kom. (백두사초)	<i>B. Lee 2017-046</i>	
<i>Kreczetoviczia</i>	<i>Praelongae</i>	<i>C. dimorpholepis</i> Steud. (이삭사초)	<i>B. Lee 2014-079</i>	
		<i>C. phacota</i> Spreng. (비늘사초)	<i>B. Lee 2017-024</i>	
<i>Vignea</i>	<i>Phleoideae</i>	<i>C. neurocarpa</i> Maxim. (괭이사초)	<i>S. Kim 2019-060</i>	
		<i>C. paxii</i> Kük. (대구사초)	<i>B. Lee 2019-073</i>	
	<i>Macrocephalae</i>	<i>C. kobomugi</i> Ohwi (통보리사초)	<i>B. Lee 2019-083</i>	
	<i>Ovales</i>	<i>C. maackii</i> Maxim. (타래사초)	<i>B. Lee 2019-067</i>	
<i>Psyllophora</i>	<i>Rarae</i>	<i>C. biwensis</i> Franch. (술잎사초)	<i>B. Lee 2017-027</i>	
		<i>C. onoei</i> Franch. & Sav. (바늘사초)	<i>B. Lee 2017-051</i>	
	<i>Circinatae</i>	<i>C. rhizopoda</i> Maxim. (뿌리대사초)	<i>B. Lee 2019-062</i>	

* Taxon names and Korean names followed Cho et al. (2016).

3.2.2 Sample preparation and flow cytometry

The genome size of each plant was estimated using flow cytometry as described in Doležel et al. (2007). Fresh leaves from a standard plant and a sample for estimation (each ca. 0.5 cm²) were co-chopped using a razor blade in a Petri dish with Otto I buffer (0.1 M citric acid plus 0.5% Tween 20; Galbraith et al., 1983; Otto, 1990). The nuclear suspension was filtered through a 30 µm nylon filter (CellTrics®, Partec GmbH, Görlitz, Germany). The filtered suspension was added to Otto II buffer (0.4 M Na₂HPO₄ • 12H₂O; Doležel and Göhde, 1995) containing 50 mg ml⁻¹ propidium iodide (PI; Sigma–Aldrich, Sigma–Aldrich, St. Louis, MO, US) and 50 mg ml⁻¹ RNaseA (Thermo Fisher Scientific Inc. Waltham, MA, USA).

Samples were analyzed on an SH800S Cell Sorter (Sony Biotechnology Inc., San Jose, CA, US). Each analysis was repeated at least three times on different days, except for *C. dispalata*, *C. mitrata* var. *mitrata*, *C. pediformis* var. *pedunculata*, *C. kobomugi*, and *C. biwensis*, which were repeated twice. At least 8,000 particles were measured in each sample, and the mean number of channels and coefficient of variation of the DNA peak (CV% = Standard deviation of the peak/mean channel number of the peak x 100) were evaluated. The final data only includes samples with a CV of less than 5% as suggested by Loureiro et al. (2007). The 2C–value was calculated based on the relative counts between G1 (growth 1 stage on the cell division) peaks from a standard plant

and from a sample for the estimation. Finally, the genome size (bp) was calculated by the equation suggested in Doležel et al. (2007):
 $1C \text{ (pg) DNA} = 0.978 \times 10^9 \text{ bp.}$

3.2.3 Statistical analysis for combined genome size data

To address genome size statistics in each subgroup in *Carex*, we added our new data to the previously reported genome size data deposited in the Plant DNA C-value Database. When a species has multiple accessions, we used an average value for statistical analyses to minimize data bias. The minimum, maximum, average, and standard deviations were calculated in each subgenus and section based on Egorova's classification system in *Carex* (Egorova, 1999).

3.3 Results

3.3.1 Genome size of Korean *Carex*

The 1C genome size of the 43 Korean *Carex* taxa were investigated in this study (Table 3.2). The flow cytometry results showed well-resolved histograms (Fig. 3.1) with 2C peaks from a target sample and a plant standard having 2.20~4.69% CV, which is within acceptable infra-specific variation limits suggested by Doležel and Bartos (2005). The measured 2C-values for Korean *Carex* range from 0.55 pg (*C. neurocarpa* Maxim.) to 2.25 pg (*C. pediformis* var. *pedunculata* Maxim.), thus making 1C-values that range from 0.28 pg (0.27 Gbp) to 1.13 pg (1.10 Gbp). The average genome size was 0.54 ± 0.19 pg (1C; Table 3.3). *C. pediformis* var. *pedunculata* Maxim. had the largest genome (1C = 1.13 pg) and *C. neurocarpa* Maxim. had the smallest genome (1C = 0.28 pg; Table 3.2). The subg. *Carex* had relatively large genome and largest range (1C = 0.37–1.13 pg) compared with other subgenera (Table 3.3). Among them, the genomes of sect. *Digitatae*, *Microrhynchae*, and *Siderostictae* was relatively large. The subg. *Vigneae* had relatively small genome compared with other subgenera (Table 3.3). Especially, the sect. *Phleoideae*, including *C. neurocarpa* Maxim., had the lowest average of 1C-value (1C = 0.28 pg).

Table 3.2 Genome size of 43 Korean *Carex*

Subgenus	Section	Taxon (Korean name) ^a	1C-value ± SD ^b (pg)	CV (%) ± SD	Genome size (Gbp)	Standard plant ^c	Previous reported 1C (pg)
<i>Carex</i>	<i>Siderostictae</i>	<i>C. okamotoi</i> Ohwi (지리대사초)	0.74 ± 0.02	3.73 ± 0.46	0.72	S	
		<i>C. siderosticta</i> Hance var. <i>siderosticta</i> (대사초)	0.77 ± 0.05	3.66 ± 1.08	0.75	R	1.2 (Nishikawa et al., 1984)
		<i>C. siderosticta</i> var. <i>pilosa</i> H.Lév. ex T.Koyama (털대사초)	0.78 ± 0.02	3.26 ± 0.58	0.76	S	0.6 (Hanson et al., unpublished)
	<i>Carex</i>	<i>C. glabrescens</i> (Kük.) Ohwi (곱슬사초)	0.44 ± 0.01	4.26 ± 0.55	0.43	R	
		<i>C. nakasimae</i> Ohwi (화산사초)	0.45 ± 0.01	3.85 ± 0.17	0.44	R	
	<i>Vesicariae</i>	<i>C. dickinsii</i> Franch. & Sav. (도깨비사초)	0.46 ± 0.03	3.33 ± 0.28	0.45	R	
		<i>C. vesicaria</i> L. (새방울사초)	0.44 ± 0.02	3.58 ± 0.11	0.43	R	0.4 (Lipnerová et al., 2012)
	<i>Anomalae</i>	<i>C. alopecuroides</i> D.Don var. <i>alopecuroides</i> (가는 흰사초)	0.42 ± 0.02	3.91 ± 0.51	0.41	R	
		<i>C. alopecuroides</i> var. <i>chlorostachya</i> C.B.Clarke (흰사초)	0.47 ± 0.03	3.56 ± 0.45	0.46	R	
		<i>C. aphanolepis</i> Franch. & Sav. (골사초)	0.42 ± 0.02	3.62 ± 0.22	0.41	R	
		<i>C. dispalata</i> Boott ex A. Gray (삿갓사초)	0.47 ± 0.00	3.41 ± 0.07	0.47	R	
		<i>C. idzuroei</i> Franch. & Sav. (좁도깨비사초)	0.52 ± 0.00	3.91 ± 0.27	0.51	S	
	<i>C. japonica</i> Thunb. (개쩌버리사초)	0.42 ± 0.02	3.86 ± 0.14	0.41	R		

	<i>C. planiculmis</i> Kom. (그늘흰사초)	0.45 ± 0.03	3.93 ± 0.11	0.44	R	
	<i>C. pseudochinensis</i> H.Lév. & Vaniot (햇사초)	0.45 ± 0.01	3.50 ± 0.33	0.44	R	
	<i>C. transversa</i> Boott (화살사초)	0.45 ± 0.02	3.46 ± 0.54	0.44	R	
<i>Depauperatae</i>	<i>C. kujuzana</i> Ohwi (장성사초)	0.64 ± 0.00	4.07 ± 0.18	0.62	S	
	<i>C. macroglossa</i> Franch. & Sav. (에기염주사초)	0.69 ± 0.00	4.02 ± 0.25	0.67	S	
	<i>C. pilosa</i> Scop. (털사초)	0.53 ± 0.00	3.83 ± 0.24	0.52	S	0.48 (Lipnerová et al., 2012)
<i>Mitratae</i>	<i>C. breviculmis</i> R.Br. (청사초)	0.51 ± 0.00	3.57 ± 0.54	0.49	S	
	<i>C. genkaiensis</i> Ohwi (목포사초)	0.60 ± 0.01	3.32 ± 0.44	0.59	S	
	<i>C. kamagariensis</i> K.Okamoto (큰청사초)	0.48 ± 0.01	3.47 ± 0.21	0.47	R	
	<i>C. meridiana</i> Akiyama (갯바위청사초)	0.52 ± 0.01	3.47 ± 0.67	0.51	S	
	<i>C. mitrata</i> Franch. var. <i>mitrata</i> (겨사초)	0.51 ± 0.01	3.40 ± 0.16	0.49	S	
	<i>C. mitrata</i> var. <i>aristata</i> Ohwi (까락겨사초)	0.49 ± 0.00	3.12 ± 0.22	0.48	R	
	<i>C. polyschoena</i> H.Lév. & Vaniot (가지청사초)	0.50 ± 0.01	3.90 ± 0.85	0.48	S	
	<i>C. sabynensis</i> Less. ex Kunth (실청사초)	0.59 ± 0.00	3.42 ± 0.82	0.57	S	
	<i>C. subbracteata</i> (Kük.) Ohwi (부리실청사초)	0.57 ± 0.01	3.86 ± 0.93	0.56	S	
	<i>C. tristachya</i> Thunb. (반들사초)	0.58 ± 0.00	3.18 ± 0.44	0.56	S	
<i>Digitatae</i>	<i>C. lanceolata</i> Boott (그늘사초)	1.10 ± 0.01	2.38 ± 0.42	1.07	G	0.87 (Lipnerová et al.,

							2012)
		<i>C. macrandrolepis</i> H.Lév. & Vaniot (청피사초)	0.54 ± 0.01	3.36 ± 0.31	0.52	S	
		<i>C. pediformis</i> var. <i>pedunculata</i> Maxim. (왕그늘사초)	1.13 ± 0.00	2.20 ± 0.21	1.10	G	
	<i>Acrocystis</i>	<i>C. fusanensis</i> Ohwi (부산사초)	0.37 ± 0.00	3.18 ± 0.45	0.36	R	
	<i>Microrhynchae</i>	<i>C. peiktusani</i> Kom. (백두사초)	1.06 ± 0.00	2.27 ± 0.24	1.04	G	
<i>Kreczetoviczia</i>	<i>Praelongae</i>	<i>C. dimorpholepis</i> Steud. (이삭사초)	0.52 ± 0.01	3.52 ± 0.71	0.50	S	
		<i>C. phacota</i> Spreng. (비늘사초)	0.49 ± 0.00	3.44 ± 0.18	0.48	S	
<i>Vigna</i>	<i>Phleoideae</i>	<i>C. neurocarpa</i> Maxim. (괘이사초)	0.28 ± 0.00	4.06 ± 0.68	0.27	R	
		<i>C. paxii</i> Kük. (대구사초)	0.29 ± 0.01	4.69 ± 0.33	0.28	R	0.2 (Nishikawa et al., 1984)
	<i>Macrocephalae</i>	<i>C. kobomugi</i> Ohwi (통보리사초)	0.35 ± 0.00	3.38 ± 0.17	0.34	R	0.2 (Nishikawa et al., 1984)
	<i>Ovales</i>	<i>C. maackii</i> Maxim. (타래사초)	0.45 ± 0.01	3.02 ± 0.39	0.44	R	
<i>Psyllophora</i>	<i>Rarae</i>	<i>C. biwensis</i> Franch. (솔잎사초)	0.51 ± 0.00	3.27 ± 0.21	0.49	S	
		<i>C. onoei</i> Franch. & Sav. (바늘사초)	0.52 ± 0.01	3.17 ± 0.49	0.50	S	
	<i>Circinatae</i>	<i>C. rhizopoda</i> Maxim. (뿌리대사초)	0.36 ± 0.02	3.57 ± 0.39	0.35	R	

^a, Taxon names and Korean names followed Cho et al. (2016)

^b, SD: standard deviation

^c, S: *Solanum lycopersicum* L. ‘Stupické polní rané’ (2C = 1.96 pg); R: *Raphanus sativus* L. ‘Saxa’ (2C = 1.11 pg); G: *Glycine max* Merr. ‘Polanka’ (2C = 2.50 pg)

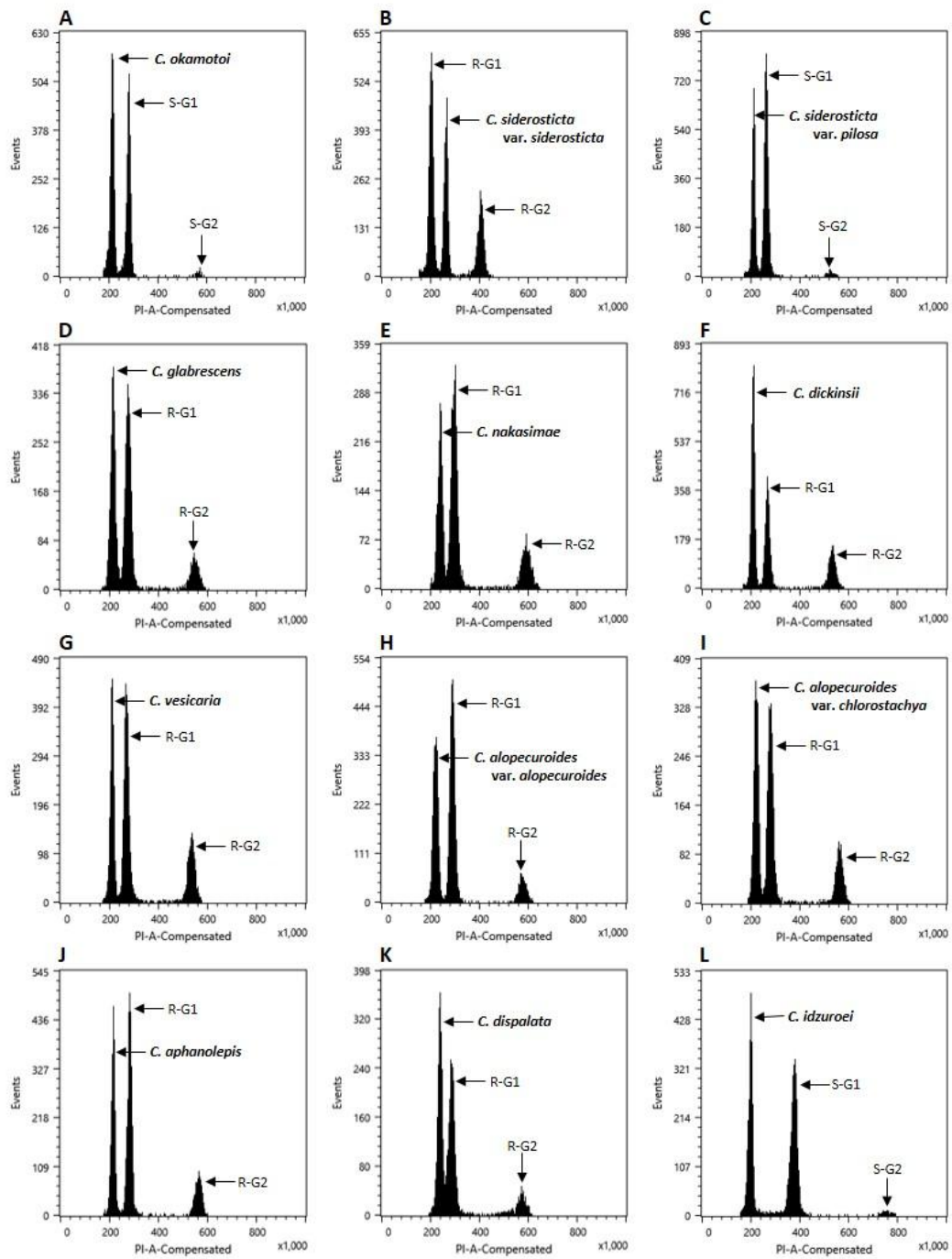


Fig. 3.1 (Continued)

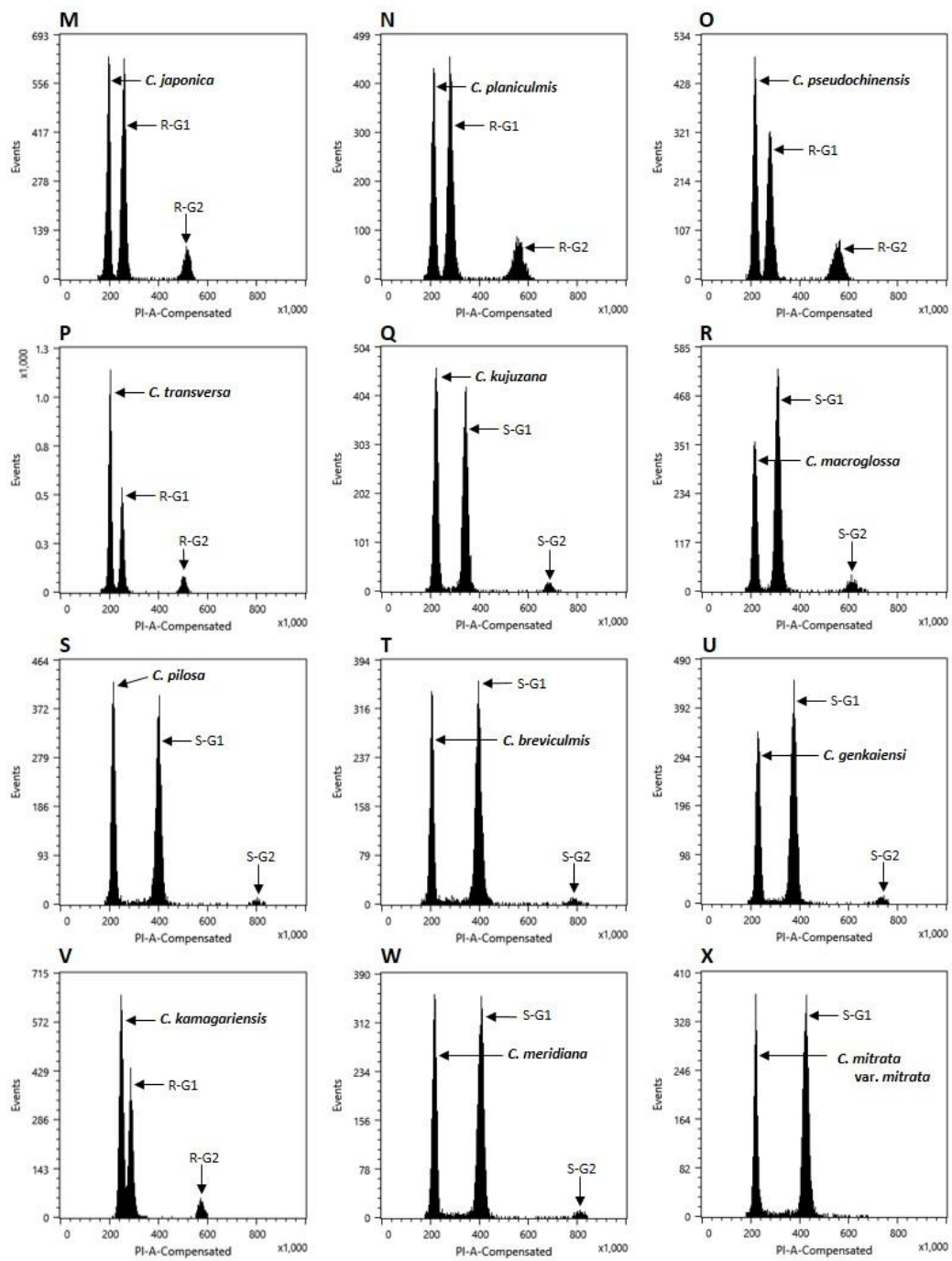


Fig. 3.1 (Continued)

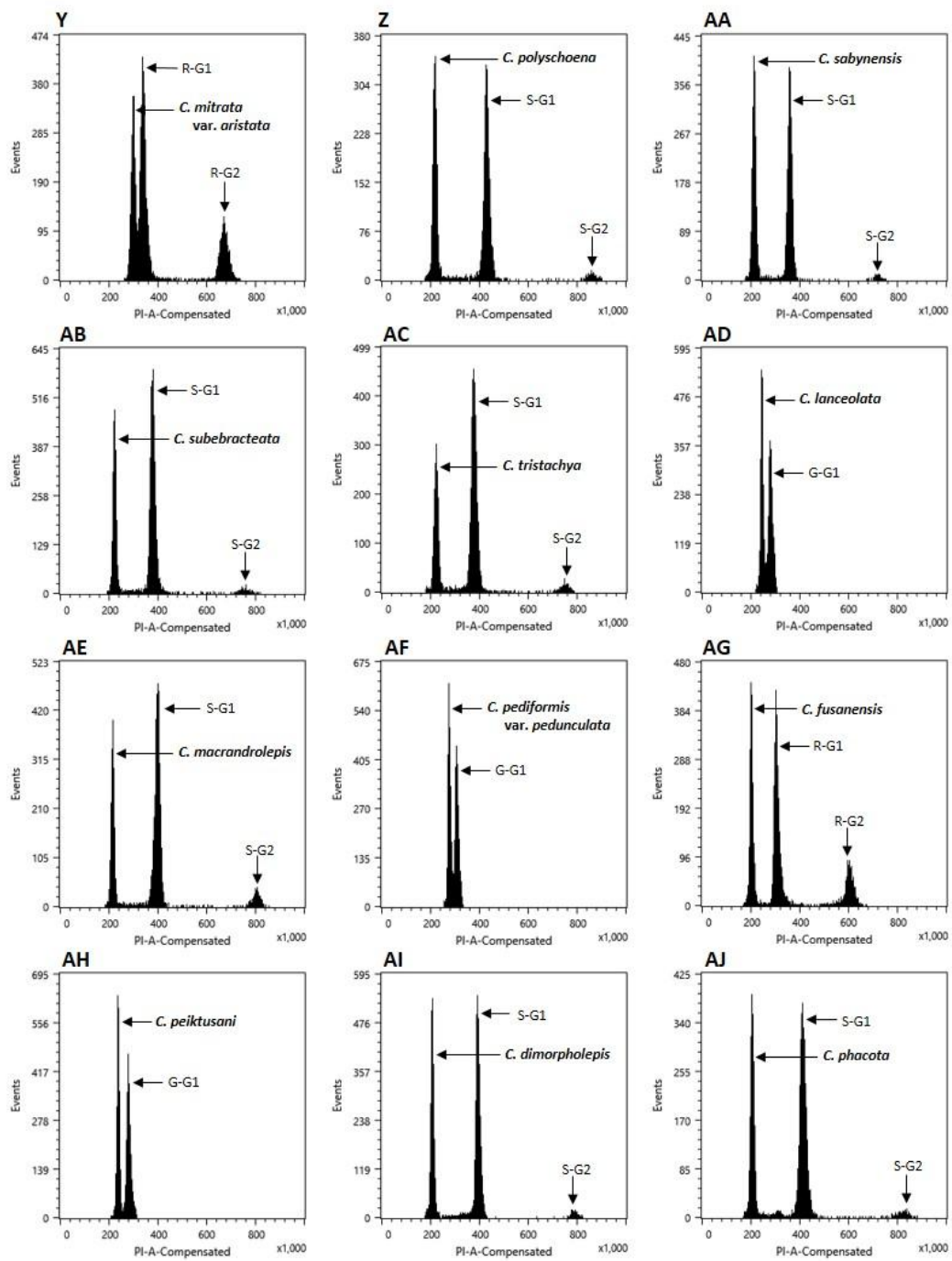


Fig. 3.1 (Continued)

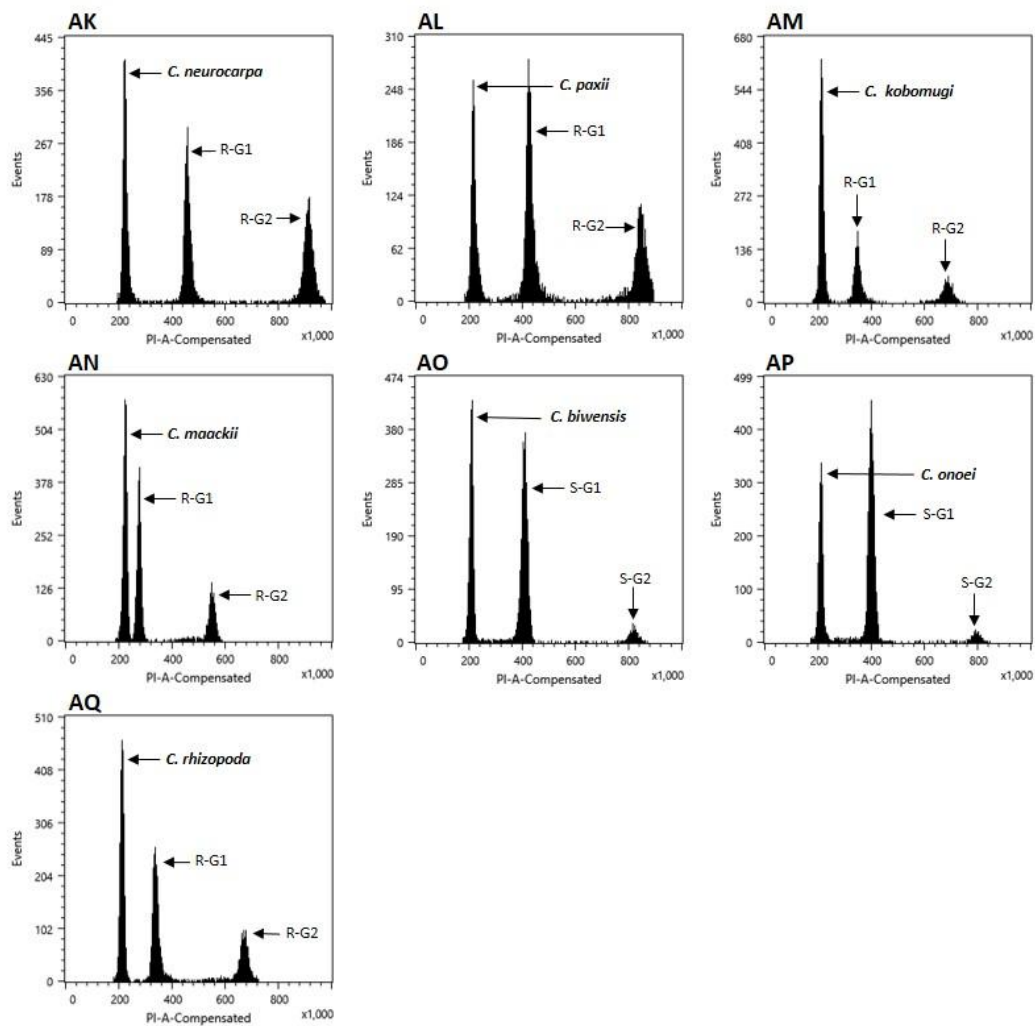


Fig. 3.1 Flow cytometry histograms showing picks of size-standard plants and targeted samples (bold). More than 8,000 count events are included in each estimation. S (*Solanum lycopersicum*), R (*Raphanus sativus*), and G (*Glycine max*) indicate standard plants. G1 and G2 after the abbreviation of standard plants indicate peaks of G1 (2C) and G2 (4C) stages of the cell cycle. (A) *C. okamotoi*,

(B) *C. siderosticta* var. *siderosticta*, (C) *C. siderosticta* var. *pilosa*, (D) *C. glabrescens*, (E) *C. nakasimae*, (F) *C. dickinsii*, (G) *C. vesicaria*, (H) *C. alopecuroides* var. *alopecuroides*, (I) *C. alopecuroides* var. *chlorostachya*, (J) *C. aphanolepis*, (K) *C. dispalata*, (L) *C. idzuroei*, (M) *C. japonica*, (N) *C. planiculmis*, (O) *C. pseudochinensis*, (P) *C. transversa*, (Q) *C. kujuzana*, (R) *C. macroglossa*, (S) *C. pilosa*, (T) *C. breviculmis*, (U) *C. genkaiensis*, (V) *C. kamagariensis*, (W) *C. meridiana*, (X) *C. mitrata* var. *mitrata*, (Y) *C. mitrata* var. *aristata*, (Z) *C. polyschoena*, (AA) *C. sabynensis*, (AB) *C. subbracteata*, (AC) *C. tristachya*, (AD) *C. lanceolata*, (AE) *C. macrandrolepis*, (AF) *C. pediformis* var. *pedunculata*, (AG) *C. fusanensis*, (AH) *C. peiktusani*, (AI) *C. dimorpholepis*, (AJ) *C. phacota*, (AK) *C. neurocarpa*, (AL) *C. paxii*, (AM) *C. kobomugi*, (AN) *C. maackii*, (AO) *C. biwensis*, (AP) *C. onoei*, and (AQ) *C. rhizopoda*.

Table 3.3 Genome size of subgroups in 43 Korean *Carex*

Subgenus	Section	No. of taxa	Min	Max	Mean	SD
<i>Carex</i>		34	0.37	1.13	0.57	0.19
	<i>Acrocystis</i>	1	0.37	0.37	0.37	–
	<i>Anomalae</i>	9	0.42	0.52	0.45	0.03
	<i>Carex</i>	2	0.44	0.45	0.45	0.01
	<i>Depauperatae</i>	3	0.53	0.69	0.62	0.08
	<i>Digitatae</i>	3	0.54	1.13	0.92	0.33
	<i>Microhynchae</i>	1	1.06	1.06	1.06	–
	<i>Mitratae</i>	10	0.48	0.60	0.53	0.04
	<i>Siderostictae</i>	3	0.74	0.78	0.76	0.02
	<i>Vesicariae</i>	2	0.44	0.46	0.45	0.01
<i>Kreczetoviczia</i>		2	0.49	0.52	0.50	0.02
	<i>Praelongae</i>	2	0.49	0.52	0.50	0.02
<i>Psyllophora</i>		3	0.36	0.52	0.46	0.09
	<i>Circinatae</i>	1	0.36	0.36	0.36	–
	<i>Rarae</i>	2	0.51	0.52	0.51	0.01
<i>Vignea</i>		4	0.28	0.45	0.35	0.08
	<i>Macrocephalae</i>	1	0.35	0.42	0.38	0.05
	<i>Ovales</i>	1	0.45	0.45	0.45	–
	<i>Phleoideae</i>	2	0.28	0.29	0.28	0.01
Total		43	0.28	1.13	0.54	0.19

3.3.2 Statistical analysis for genome size in *Carex*

372 *Carex* accesses, including 43 Korean *Carex* data and deposited data in the Plant DNA C-Value database, were identified the taxonomic position based on Egorova's classification system of *Carex* (Egorova, 1999) and performed statistical analyses in each subgroup of the *Carex*. The accessions showing unclear sectional membership were excluded, and data remained for 248 *Carex* species (Table 3.4). The final data set reveals that the average genome size of *Carex* was 0.47 ± 0.19 pg (1C; Table 3.4). *C. cuspidate* Bertol. had the largest genome (1C = 1.64 pg) and four species equally (*C. brownii* Tuck., *C. kobomugi* Ohwi, *C. nubigena* D.Don ex Tilloch & Taylor, and *C. paxii* Kük) had the smallest genome (1C = 0.20 pg). The large genomes are frequently found in the subg. *Carex* compare with other subgenera (Fig. 3.2), especially in sect. *Aulocystis*, *Digitatae*, *Glaucæ*, *Paniceae*, and *Siderostictæ*. However, genome size variations in these sections were also relatively high. The sect. *Secalinae* of the subg. *Carex* has the lowest mean value in the sectional level (1C = 0.25; Table 3.4). Also, the mean value of subg. *Vigneae* is relatively small (1C = 0.37; Table 3.4; Fig. 3.2) and is consistent with the result of Lipnerová et al. (2013).

Table 3.4 Genome size of subgroups in *Carex* reported to date including this study

Subgenus	Section	No. of taxa	Min.	Max.	Mean	SD
<i>Carex</i>		151	0.20	1.64	0.52	0.22
	<i>Acrocystis</i>	8	0.34	0.57	0.45	0.08
	<i>Albae</i>	3	0.42	0.52	0.46	0.04
	<i>Anomalae</i>	11	0.20	0.52	0.42	0.09
	<i>Aulocystis</i>	8	0.38	1.16	0.76	0.25
	<i>Carex</i>	5	0.33	0.45	0.39	0.05
	<i>Ceratocystis</i>	6	0.34	0.37	0.36	0.01
	<i>Chartoteuchium</i>	1	0.72	0.72	0.72	0.00
	<i>Chlorostachyae</i>	2	0.36	0.50	0.43	0.07
	<i>Curvulae</i>	1	0.84	0.84	0.84	0.00
	<i>Depauperatae</i>	9	0.30	0.72	0.50	0.14
	<i>Digitatae</i>	13	0.35	1.13	0.67	0.27
	<i>Glaucae</i>	3	0.30	1.64	1.00	0.55
	<i>Hallerianae</i>	1	0.48	0.48	0.48	0.00
	<i>Lamprochlaenae</i>	2	0.40	0.53	0.47	0.07
	<i>Limosae</i>	3	0.45	0.47	0.46	0.01
	<i>Microrhynchae</i>	9	0.30	1.06	0.52	0.24
	<i>Mitratae</i>	21	0.30	0.80	0.48	0.12
	<i>Paludosae</i>	3	0.41	0.43	0.42	0.01
	<i>Paniceae</i>	6	0.60	1.00	0.75	0.12
	<i>Porocystis</i>	1	0.39	0.39	0.39	0.00
	<i>Pseudocypereae</i>	2	0.36	0.45	0.41	0.04
	<i>Rhomboidales</i>	4	0.50	0.50	0.50	0.00
	<i>Rhynhocystis</i>	2	0.37	0.58	0.48	0.11
	<i>Scitae</i>	2	0.43	0.51	0.47	0.04
	<i>Secalinae</i>	2	0.24	0.25	0.25	0.01
	<i>Siderostictae</i>	6	0.60	1.20	0.80	0.19
	<i>Silvaticae</i>	3	0.34	0.60	0.44	0.11
	<i>Spirostachyae</i>	3	0.34	0.45	0.39	0.05
	<i>Tumidae</i>	3	0.30	0.41	0.36	0.05
	<i>Vesicariae</i>	8	0.37	0.46	0.41	0.03

<i>Kreczetoviczia</i>	18	0.30	0.53	0.41	0.06
<i>Phacocystis</i>	13	0.30	0.44	0.40	0.04
<i>Praelongae</i>	4	0.30	0.52	0.40	0.10
<i>Temnemis</i>	1	0.53	0.53	0.53	0.00
<i>Psyllophora</i>	16	0.30	0.62	0.41	0.10
<i>Callistachys</i>	1	0.44	0.44	0.44	0.00
<i>Capituligerae</i>	1	0.32	0.32	0.32	0.00
<i>Circinatae</i>	1	0.36	0.36	0.36	0.00
<i>Leucoglochlin</i>	2	0.30	0.38	0.34	0.04
<i>Obtusatae</i>	1	0.32	0.32	0.32	0.00
<i>Petraeae</i>	2	0.33	0.34	0.34	0.01
<i>Physoglochlin</i>	3	0.51	0.62	0.55	0.05
<i>Psyllophora</i>	2	0.32	0.40	0.36	0.04
<i>Rarae</i>	3	0.30	0.52	0.44	0.10
<i>Vignea</i>	63	0.20	0.47	0.37	0.06
<i>Ammoglochlin</i>	7	0.32	0.37	0.34	0.02
<i>Boernera</i>	1	0.30	0.30	0.30	0.00
<i>Canescentes</i>	11	0.35	0.47	0.41	0.03
<i>Cyperoideae</i>	2	0.29	0.33	0.31	0.02
<i>Dispermae</i>	1	0.43	0.43	0.43	0.00
<i>Divisae</i>	2	0.34	0.34	0.34	0.00
<i>Elongatae</i>	2	0.37	0.41	0.39	0.02
<i>Heleoglochlin</i>	4	0.36	0.43	0.40	0.03
<i>Holarrhenae</i>	3	0.36	0.43	0.39	0.03
<i>Macrocephalae</i>	2	0.20	0.35	0.27	0.07
<i>Ovales</i>	5	0.29	0.45	0.36	0.05
<i>Phaestoglochlin</i>	7	0.39	0.45	0.40	0.02
<i>Phleoideae</i>	5	0.20	0.29	0.26	0.03
<i>Physodeae</i>	1	0.33	0.33	0.33	0.00
<i>Remotae</i>	3	0.33	0.40	0.37	0.03
<i>Stellulatea</i>	2	0.38	0.42	0.40	0.02
<i>Vulpinae</i>	5	0.36	0.45	0.40	0.03
Total	248	0.20	1.64	0.47	0.19

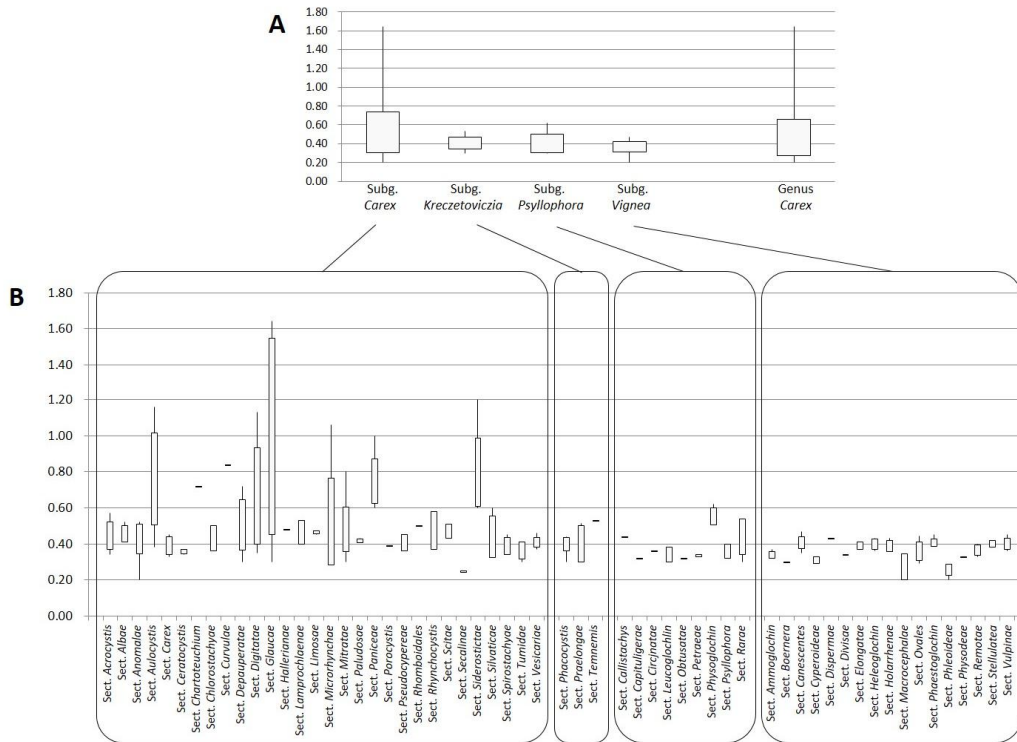


Fig. 3.2 Range of genome size variations (1C value) in each subgenus (A) and section (B) in *Carex*. Boxes indicate the range of standard deviations and ends of bars indicate the maximum and the minimum values. The number of species included in each subgenus and section is in Table 3.4.

3.4 Discussion

In this study, the genome sizes of 43 Korean *Carex* taxa were estimated using flow cytometry. It is about 24.4% of *Carex* taxa distributed in the Korean peninsula. The genome size of subg. *Carex* was relatively large and the subg. *Vignea* was relatively small compared with other subgenera. Especially, the sect. *Phleoideae*, belonging to subg. *Vignea*, had the smallest genome. These results are consistent with the Plant DNA C-Value Database updated with our data.

Among them, seven taxa in our estimation overlapped with data in the Plant DNA C-values Database, and their 1C-values were slightly different (Table 3.2). First of all, the possibility of sample misidentification cannot be excluded. However, the major contribution to differences result from different methodologies related to measurement technique, reference standard, staining dye, chemical interference, etc. (as discussed in Lipnerová et al., 2013; Wang et al., 2016; Yan et al., 2016). *C. siderosticta* var. *siderosticta*, *C. siderosticta* var. *pilosa* H. Lév. ex T.Koyama, *C. paxii* Kük., and *C. kobomugi* Ohwi, were estimated by Feulgen microdensitometry in the previous estimations, while this study was estimated by flow cytometry with PI (Leitch et al., 2019; Nishikawa et al., 1984). Although *C. vesicaria* L., *C. pilosa* Scop., and *C. lanceolata* Boott were estimated using *S. lycopersicum* L. ‘Stupické polní rané’ (1C = 0.87 pg), *C. acutiformis* Ehrh. (1C = 0.41 pg),

and *Oryza sativa* subsp. *japonica* ‘Nipponbare’ (1C = 0.40 pg) as standard plants in the previous study (Lipnerová et al., 2013), this study was estimated using *R. sativus* L. ‘Saxa’ (2C = 1.11 pg), *S. lycopersicum* L. ‘Stupické polní rané’ (2C = 1.96 pg), and *G. max* Merr. ‘Polanka’ (2C = 2.50 pg). These plant standards were calibrated using human male leukocytes (2C = 7.0 pg) which was overestimated compared with modern sequencing data (Doležel and Greilhuber, 2010; Lipnerová et al., 2013).

This study is the first to report genome size data from 43 taxa of *Carex* distributed in the Korean peninsula (Fig. 3.1; Table 3.2). These results provide a 10.7% increase in data at the species level, against the existing genome size data for *Carex* (292 taxa; 276 species; data from the Plant DNA C-Value Database). This data will form the basis for understanding the phylogeny and evolution of *Carex* as well as genetic studies on Korean endemic species. In addition, this data will be useful information for future intensive genome sequencing projects in *Carex*.

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Chapter 4

Structural evolution of the chloroplast genomes in Cyperaceae

4.1 Introduction

Chloroplasts play an important role in photosynthesis as well as the synthesis of amino acids, nucleotides, fatty acid, starch, phytohormones, and vitamins (Sugiura, 1992; Daniell et al., 2016). The chloroplast genome of land plants typically ranges in size from 120 to 160 kb and have a quadripartite structure consisting of a large single copy (LSC) and a small single copy (SSC) separated by two copies of inverted repeat (IRa and IRb) regions (Mower and Vickrey, 2018). The genome usually contains about 80 protein-coding genes, 30 tRNAs, and four rRNAs (Mower and Vickrey, 2018). The chloroplast genomes of land plants are highly conserved in structure, gene content, and gene organization (Daniell et al., 2016; Mower and Vickrey, 2018). However, several unrelated lineages have experienced rearrangements, including inversion, expansion and contraction of IR, gene loss, intron loss, gene duplication, and gene order change (Mower and Vickrey, 2018; Rabah et al., 2019). For example, large inversion is found in Euphyllophytes (35 Kb) and subfamily Papilionoideae (Fabaceae; 50 kb) (Raubeson and Jansen, 1992; Doyle et al., 1996). About 3.3 kb inversion (*trnG-GCC~trnT-GGU*) and an inverted *trnD-GUC* gene are found in all ferns (Wolf et al., 2003; Gao et al., 2009; Gao et al., 2011). Besides, IR loss is found in Fabaceae and Cactaceae (Cai et al., 2008; Sanderson et al., 2015), and IR expansion and contraction are found in Geraniaceae, Trochodendraceae, Lauraceae,

and *Plantago* (Sun et al., 2013; Weng et al., 2014; Zhu et al., 2016; Song et al., 2017). Thus, these rearrangements can become synapomorphies for their groups and diagnostic characters (Mower and Vickrey, 2018; Henriquez et al., 2020). Also, these genomic events are a major factors affecting the size of the chloroplast genome (Mower and Vickrey, 2018).

The accumulation of the complete chloroplast genome sequence has been accelerated by the introduction of next generation sequencing (NGS) technique such as Illumina sequencing to the field of organelle genomes. Some genomes have complex structural changes, including short duplications compared to the reference genome, but only partial assembly was possible with short reads of NGS. Especially, the complete chloroplast genome of *Carex* species has rarely been determined to date because of their complicated structural changes in the genus. As the first complete chloroplast genome in *Carex*, *C. siderosticta* is extremely large (195 kb) and has many short internal repeats (>100 bps) (unpublished). In comparison with *Typha*, one of the basal-group taxa in Poales, there are rearrangements including six large inversions, three translocations, ten gene losses, and one gene duplication (*trnfM-CAU*). Thus, the chloroplast genome of *C. siderosticta* was completed by re-sequencing the entire genomic region using the Sanger method in our lab (unpublished).

The third-generation sequencing (TGS) platforms, including Nanopore sequencing (Oxford Nanopore Technologies, Oxford, UK),

have many advantages such as 1) increase in read length, 2) reduction of sequencing time, and 3) reduction or elimination of sequencing biases introduced by PCR amplification (Lu et al., 2016). Especially, long-read sequencing may resolve complex sequence-structure such as a problem on repetitive regions (Michael et al., 2018).

Thus, in this study, the chloroplast genome of *Carex lupulina* as another chloroplast genome in *Carex* was sequenced based on Nanopore sequencing (Oxford Nanopore Technologies, Oxford, UK). In addition, genomic rearrangements including expansion and contraction of IR, gene and intron loss, gene duplication, and gene order change were investigated compared with the chloroplast genome of *Typha latifolia*, *Eriocaulon buergerianum*, *Hypolytrum nemorum*, and *Carex siderosticta*.

4.2 Materials and Methods

4.2.1 Plant material

Carex lupulina Muhl. ex Willd is included in subgenus *Carex* and section *Lupulinae* of *Carex*. *C. lupulina* was obtained from Dr. Erick H. Roalson (School of Biological Sciences, Washington State University, Pullman, Washington, USA) and grown in the greenhouse at Sungshin Women's University. The voucher specimen was deposited in the herbarium of Sungshin Women's University (SWU, SWU0029655).

4.2.2 DNA extraction and Nanopore sequencing

Total genomic DNA was extracted from fresh leaves using Exgene™ Plant SV DNA extraction kit (GeneAll, Seoul, Korea) according to the manufacturer's instructions. Libraries were prepared using the ONT 1D Ligation Sequencing Kit (SQK-LSK108; ONT, Oxford, UK) according to the manufacturer's instructions. Sequencing was performed with a GridION X5 sequencer and then base-called using Guppy v. 2.2.7 (ONT, Oxford, UK). Adapter sequences and chimeric reads from long-reads were trimmed using Porechop v. 0.2.3 (<https://github.com/rrwick/Porechop>). The library construction and sequencing were performed by Phyzen Co. Ltd. (Seongnam, Korea).

4.2.3 *De novo* assembly, error correction, and annotation

Total trimmed reads were assembled using SMARTdenovo (<https://github.com/ruanjue/smarddenovo>). Since there were 454 NGS data (Roche, Branford, USA) of the same sample received from Dr. Erick H. Roalson, these reads were used for the error correction of assembled sequences. The raw 454 data were trimmed using “CLC quality trim” in the CLC Assembly Cell Package v. 4.21 (CLC Inc., Aarhus, Denmark). Trimmed 454 reads were mapped to the assembled contig for error correction using “clc_ref_assemble” tool in the CLC Assembly Cell Package v. 4.21 (CLC Inc., Aarhus, Denmark). Gene annotation was performed using GeSeq (Tillich et al., 2017) and a circular map of the chloroplast genome was created using OrganellarGenomeDRAW v. 1.3.1 (OGDRAW; Greiner et al., 2019).

4.2.4 Genome rearrangement analysis

Whole genome alignment was performed to examine the rearrangement of the chloroplast genome in *C. lupulina* and related taxa using progressiveMAUVE v. 1.1.1 (Darling et al., 2010) in Geneious Prime v. 2020.02. The genome sequence of *Typha latifolia* (NC_013823, Typhaceae), *Eriocaulon buergerianum* (NC_042211, Eriocaulaceae), *Hypolytrum nemorum* (NC_036036, Cyperaceae), and *Carex siderosticta* (NC_027250, Cyperaceae) were downloaded

from NCBI database. A copy of IR was removed from the chloroplast genome prior to the alignment. The conserved segments called Locally Collinear Blocks (LCBs) were identified by the MAUVE alignment and manually numbered based on *T. latifolia* as a reference (Fig. 4.2; Appendix 1). Also, pairwise dot plot analysis embedded in UGENE v. 1.32 (Okonechnikov et al., 2012) was performed with minimum repeat length of 100 bp and repeat identity 75%. For the comparison of gene organization, the Web-based MultiPipMaker program (Schwartz et al., 2000) was performed with annotation of *T. latifolia* as a reference.

4.2.5 Repeat analyses

The online REPuter program (Kurtz et al., 2001) was used to identify for forward, palindromic, reverse, and complement oligonucleotide repeats with the minimum repeat size of 30 bp and sequence identity 90% (Hamming distance of 3). A copy of IR was removed from the chloroplast genome to avoid redundancy. Redundant repeats, which were entirely contained within other repeats, were removed. Tandem repeats were identified using the online program Tandem Repeats Finder v. 4.09 with default settings (Benson, 1999). Simple sequence repeats (SSRs) were detected using the MISA-web (Beier et al., 2017). The parameters were set to eight for mononucleotide repeats, five for dinucleotide repeats, three for trinucleotide, tetranucleotide, pentanucleotide, or

hexanucleotide repeats.

4.2.6 Phylogenetic analysis

Sixty protein-coding genes from the chloroplast genome of *C. lupulina* and related taxa in Poales were used for phylogenetic analysis (Appendix 2 and 3). These sequences were aligned using MAFFT v. 7.45 (Kato and Standley, 2013) and then concatenated using AMAS v. 0.98 (Borowiec, 2016). The maximum likelihood tree was conducted using IQ-TREE v. 1.6.12 (Nguyen et al., 2015) with 1,000 ultrafast bootstrap replicates (Hoang et al., 2018) and the GTR+F+I+G4 nucleotide substitution model. The substitution model was selected by ModelFinder (Kalyaanamoorthy et al., 2017).

4.3 Results

4.3.1 Nanopore sequencing

The complete chloroplast genome of *C. lupulina* was sequenced using the Oxford Nanopore sequencer and error corrected by Roche 454 sequencing data. About 4.8 Gb of long-read data from the Nanopore platform were obtained and comprised 2,357,429 reads with an average length of 2,051 bp (Table 4.1). Also, about 458 Mb of 454 data comprising 1,176,965 reads were used.

Table 4.1 Statistical summary of the Nanopore sequencing

	Raw data	Trimmed data
Total read number	2,357,429	2,349,820
Total read bases	4,835,887,871	4,746,461,100
Min length (bp)	5	1
Max length (bp)	154,174	154,129
Average length (bp)	2,051	2,020
N50 (bp)	5,535	5,634

4.3.2 Chloroplast genome organization of *C. lupulina*

The assembled chloroplast genome of *C. lupulina* was 246,165 bp in size. The chloroplast genome had a typical quadripartite structure consisting of LSC (99,356 bp), SSC (10,293 bp), and two inverted repeats (each 68,258 bp) (Fig. 4.1). Overall GC content of the chloroplast genome was 33.8%. The GC contents of LSC, SSC, and IR regions were 32.1%, 26.9%, and 35.5%, respectively. The genome had a total of 123 genes that included 63 unique protein-coding genes, 29 unique tRNA genes, and four rRNA genes. Among them, eight protein-coding genes, eight tRNA gene, and four rRNA genes were duplicated in the IR (Fig. 4.1; Table 4.2). Eight protein-coding genes (*atpF*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl16*, *rpl2*, and *rpoC1*) and six tRNA genes (*trnA-UGC*, *trnG-GCC*, *trnI-GAU*, *trnK-UUU*, *trnL-UAA*, and *trnV-UAC*) had a single intron, and *ycf3* gene had two introns (Table 4.2). The *rps12* gene was found to be trans-spliced with the 5' end exon located in the LSC region and the duplicated 3' end exon located in the IR region.

Among the chloroplast genome in *C. lupulina* and related taxa, *C. lupulina* has the largest chloroplast genome and *E. buergerianum* has the smallest chloroplast genome (Table 4.3). Overall, the chloroplast genomes in Cyperaceae were larger than the others. The total number of genes is the highest in *H. nemorum* and the least in *C. lupulina* (Table 4.3). Within the Cyperaceae, the chloroplast genomes in *Carex* were large in size and contained fewer genes than the others (Table 4.3).



Fig 4.1 Gene map of the chloroplast genome in *C. lupulina*. Red arrows indicate the inverted repeats (IR). Two orange areas indicate gene-free long intergenic regions in IRs.

Table 4.2 Genes in the chloroplast genome in *C. lupulina*

Category	Genes group	Gene name
Photosynthesis	Photosystem I	<i>psaA, psaB, psaC, psaI, psaJ</i>
	Photosystem II	<i>psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ</i>
	Cytochrome b/f complex	<i>petB^a, petD^a, petG, petL, petN</i>
	ATP synthase	<i>atpA, atpB, atpE, atpF^a, atpH, atpI</i>
	NADH -dehydrogenase	<i>ndhA^a(×2), ndhB^a(×2), ndhC, ndhE, ndhF, ndhG (×2), ndhH, ndhI (×2), ndhJ, ndhK</i>
	Large subunit of Rubisco	<i>rbcL</i>
Protein synthesis and DNA replication genes	Transfer RNAs	<i>trnA-UGC^a(×2), trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnM-CAU (×2), trnG-GCC (×2), trnH-GUG (×2), trnI-CAU (×2), trnI-GAU^a (×2), trnK-UUU^a, trnL-CAA (×2), trnL-UAA^a, trnM-CAU, trnN-GUU (×2), trnP-UGG, trnQ-UUG, trnR-ACG (×2), trnR-UCU (×2), trnS-GCU, trnS-GGA, trnS-UGA, trnT-AGU (×2), trnT-UGU (×2), trnV-GAC, trnV-UAC^a, trnW-CCA, trnY-GUA</i>
		Ribosomal RNAs
	Ribosomal protein small subunit	<i>rps11, rps12^c, rps14 (×2), rps15 (×2), rps19 (×2), rps4, rps8</i>
	Ribosomal protein large subunit	<i>rpl14, rpl16^a, rpl2^a (×2), rpl20, rpl22, rpl32, rpl33, rpl36</i>
	Subunit of RNA polymerase	<i>rpoB, rpoC1^a</i>
Miscellaneous group	Maturase	<i>matK</i>
	Envelope membrane protein	<i>cemA</i>
	Cytochrome c biogenesis	<i>ccsA</i>
Unknown	Hypothetical genes	<i>ycf3^b</i>

^a, Gene containing one intron

^b, Gene containing two introns

^c, Gene divided into two independent transcription units

Table 4.3 Statistical summary of the chloroplast genomes of *C. lupulina* and related taxa

	<i>Typha latifolia</i> (Typhaceae)	<i>Eriocaulon buergerianum</i> (Eriocaulaceae)	<i>Hypolytrum nemorum</i> (Cyperaceae)	<i>Carex siderosticta</i> (Cyperaceae)	<i>Carex lupulina</i> (Cyperaceae)
Genbank accession no.	NC013823	NC042211	NC036036	NC027250	in this study
Genome Size (bp)	161,572	151,434	180,648	195,251	246,165
LSC length (bp)	89,140	81,534	95,644	102,460	99,356
SSC length (bp)	19,652	17,114	8,150	8,981	10,293
IR length (bp)	26,390	26,393	38,427	41,905	68,258
Total number of genes	131	133	137	127	123
Number of genes duplicated in IR	19	21	25	22	22
Number of genes with introns	18	14	18	18	16
GC content (%)	36.6	35.7	34.9	34.1	33.8

4.3.3 Comparison of the chloroplast genome structure in *C. lupulina* and related taxa

The chloroplast genome structure in *C. lupulina* was compared with related taxa using progressiveMAUVE alignment and pairwise dot plots (Fig. 4.2 and 4.3). Only one structural change was observed between Typhaceae and Eriocaulaceae (Fig. 4.2. LCB 5; Fig. 4.3A. a). However, there were many major structural changes during the diversification of Cyperaceae (Fig. 4.2 and 4.3). *H. nemorum*, *C. siderosticta*, and *C. lupulina* shared six regions of rearrangement: 1) 12~13 kb inversion including *rps4* through part of the *accD* detected only in *Typha* and *Eriocaulon* (Fig. 4.2. LCB 10 and 11; Fig. 4.3B. b), 2) 6~7 kb inversion including *rps12* through *trnL-CAA* (Fig. 4.2. LCB 19; Fig. 4.3B. c), 3) about 2.2 kb inversion including *ndhF* (Fig. 4.2. LCB 21; Fig. 4.3B. d), 4) 0.2~1.4 kb translocation including part of the *accD* which was detected only in *Typha* and *Eriocaulon* (Fig. 4.2. LCB 12; Fig. 4.3B. e), 5) 7.5~9 kb translocation including *rps14* through *trnS-GGA* (Fig. 4.2. LCB 8 and 9; Fig. 4.3B. f), and 6) 5~11 kb inverted translocation including *ndhG* through *ycf1* (Fig. 4.2. LCB 23 and 24; Fig. 4.3B. g). In addition, IR expansion was found in Cyperaceae (Fig. 4.3B. g).

Within Cyperaceae, *Carex* was characterized by six regions of rearrangement: 1) about 10 kb inversion including part of the *clpP* through *rps11* (Fig. 4.2. LCB 14 and 15; Fig. 4.3C. h), 2) about 15 kb translocation including *rps4* through part of the *clpP* (Fig. 4.2. LCB 10 and 13; Fig. 4.3C. i), 3) about 1.2 kb translocation

including *rps16* (Fig. 4.2. LCB 2; Fig. 4.3C. j), 4) about 8 kb inverted translocation including *psbK* through *atpI* (Fig. 4.2. LCB 4, 5, and 6; Fig. 4.3C. k), 5) about 5 kb inverted translocation including *rps14* through *psaA* (Fig. 4.2. LCB 8; Fig. 4.3C. l), and 6) about 140 bp inverted translocation including *trnQ-UUG* (Fig. 4.2. LCB 3; Fig. 4.3C. m). In *Hypolytrum*, about 1.2 kb inversion including part of the *accD* was found (Fig. 4.2. LCB 12, Fig. 4.3B. e).

Within *Carex*, about 7 kb insertion (Fig. 4.3C. n) was found in *C. siderosticta*. In *C. lupulina*, two inverted translocations were present comparison with *C. siderosticta* (Fig 4.2. and 4.3D). Especially, the first was a larger inverted translocation (about 30 kb) in LSC (Fig. 4.3D. o). The second inverted translocation was about 5 kb in size and included *psbA*, *trnK-UUU*, and *matK* (Fig. 4.2. LCB 1; Fig. 34.D. p). In addition, insertion and short repeats were found in *C. lupulina* (Fig. 4.3D. q~s). Especially, many short repeats were present in the IR region of *C. lupulina* (Fig. 4.3E).



Fig. 4.2 Whole genome alignment of *C. lupulina* and related taxa. The homologous regions (LCB) were identified by progressiveMAUVE alignment based on the chloroplast genome of *T. latifolia* as a reference. A copy of IR was removed from the genome prior to the alignment. Blocks below the center line indicate the inverted regions compare to the reference.

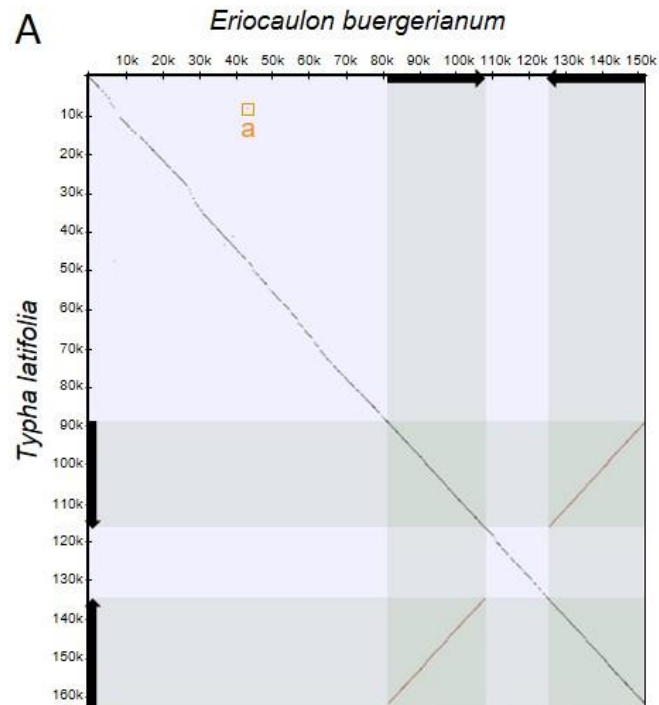


Fig. 4.3 Pairwise dot plots of *C. lupulina* and related taxa (minimum repeat length of 100 bp and repeat identity 75%). Red lines indicate inversions. Lowercase alphabet indicate major structural changes. Dot plots (A) between Typhaceae and Eriocaulaceae, (B) between Typhaceae and Cyperaceae, (C) between *Hypolytrum* and *Carex*, (D) between *C. siderosticta* and *C. lupulina*, and (E) between *C. lupulina* and *C. lupulina*. Orange indicates structural changes in Eriocaulaceae, blue indicates structural changes in Cyperaceae, green indicates structural changes in *Carex*, purple indicates structural changes in *C. siderosticta*, and black indicates structural changes in *C. lupulina*.

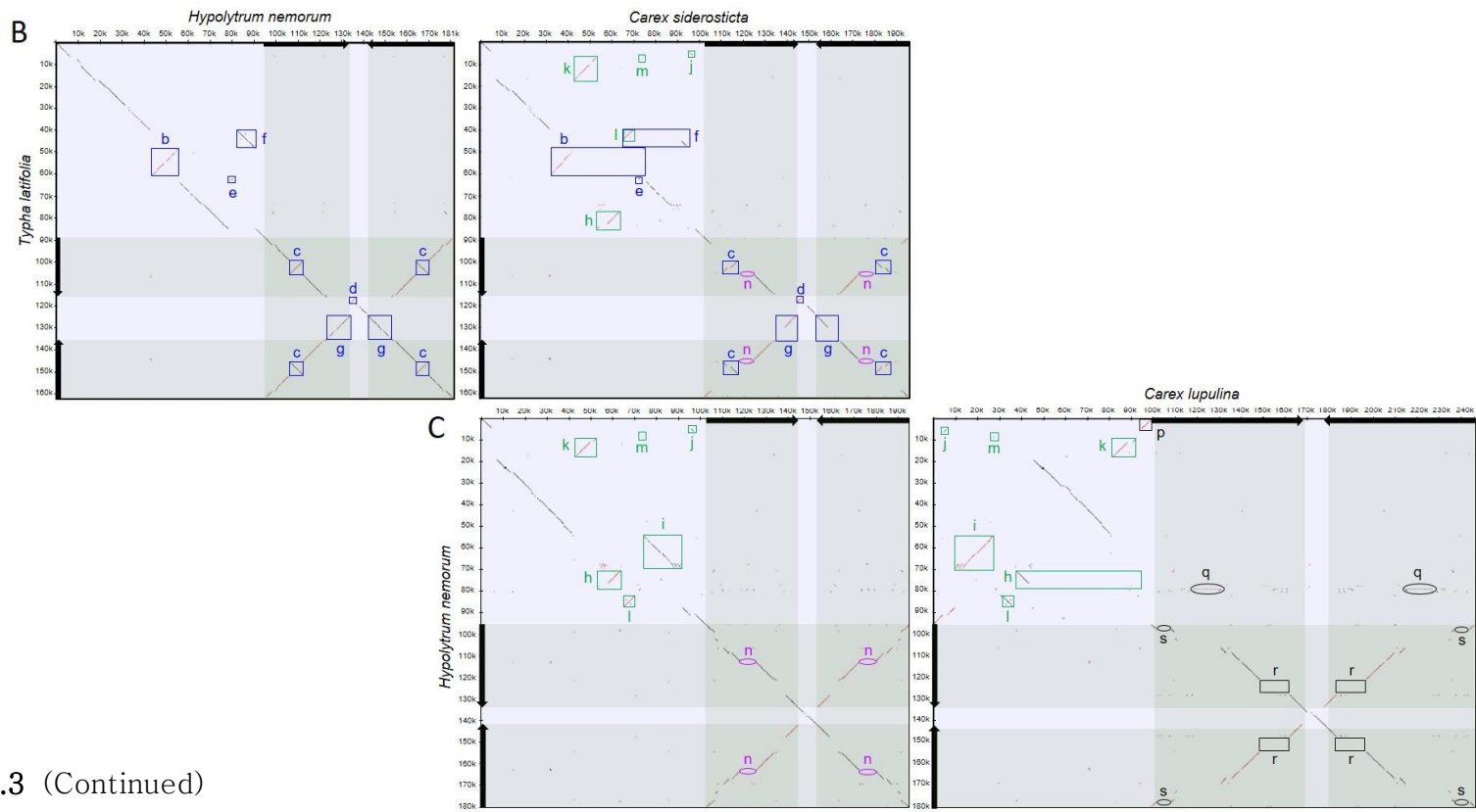


Fig. 4.3 (Continued)

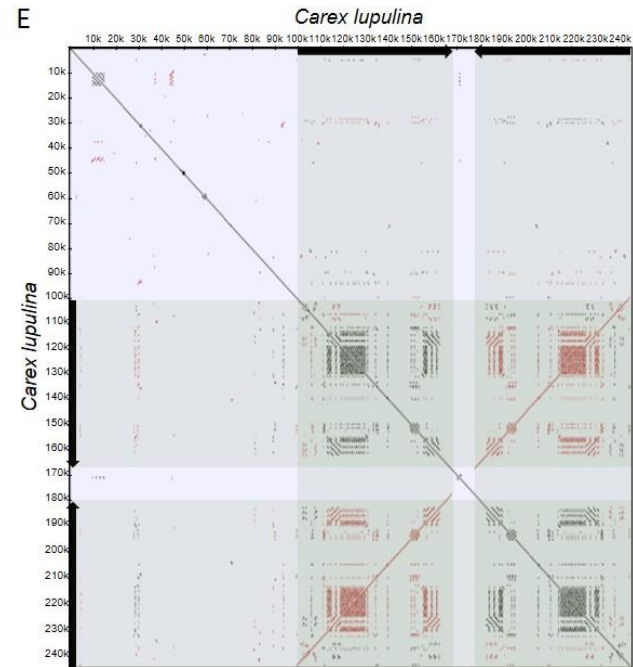
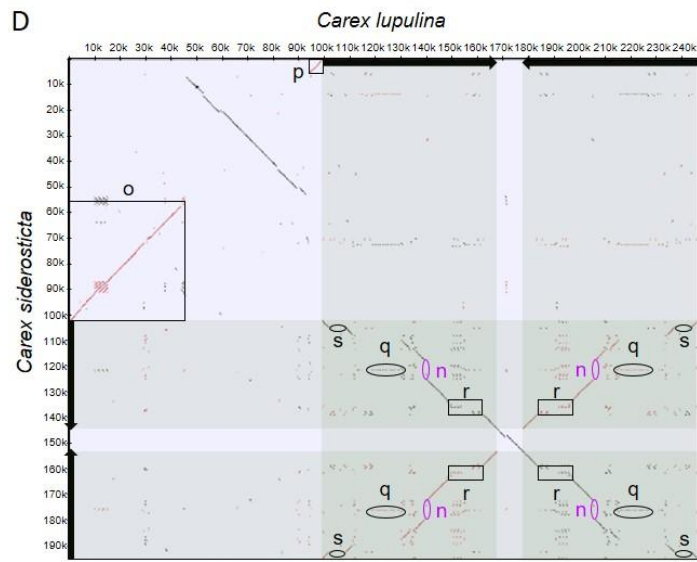


Fig. 4.3 (Continued)

4.3.4 Comparison of gene content in *C. lupulina* and related taxa

Compared to other genomes, *C. lupulina* with 123 genes had the lowest total number of genes (Table 4.3). *C. lupulina* lacked or pseudogenized nineteen genes (17 protein-coding genes and two tRNA genes) and had two *rps14*, *trnfM-CAU*, *trnG-GCC*, *trnR-UCU*, and *trnT-AGU* genes (Table 4.2). Among them, eight protein-coding genes (*ndhD*, *petA*, *rpoC2*, *rps2*, *rps7*, *rps16*, *ycf4*, and *ycf68*) were pseudogenes because they contained multiple internal stop codons. The *accD*, *clpP*, *infA*, *rpoA*, *rps18*, and *ycf2* genes were detected as partial sequences with low identity (<50%) compared with *T. latifolia* which was a basal group of Poales, and other parts were fragmented or not detected. The *rps3* gene (55.4%) and *rpl23* gene (63.5%) showed low identity compared with *T. latifolia*, and *ycf1* gene was not detected in the chloroplast genome of *C. lupulina*. The tRNAs were annotated using tRNAscan-SE, but *trnG-UCC* and *trnT-GGU* were not detected in the chloroplast genome of *C. lupulina*.

Compared with the chloroplast genome of related taxa, *accD*, *infA*, and *rps18* genes were absent from Cyperaceae (Fig. 4.4). Within Cyperaceae, *clpP*, *rpl23*, *rpoA*, *rps3*, *ycf1*, *ycf2*, and *trnT-GGU* genes were absent from *Carex* (Fig. 4.4). Thus, it is speculated that loss of *accD*, *infA*, and *rps18* genes and loss of *clpP*, *rpl23*, *rpoA*, *rps3*, *ycf1*, *ycf2*, and *trnT-GGU* genes were the synapomorphic character of Cyperaceae and *Carex*, respectively.

Besides, the duplication of *trnfM-CAU* gene was shared by *C. siderosticta* and *C. lupulina*.

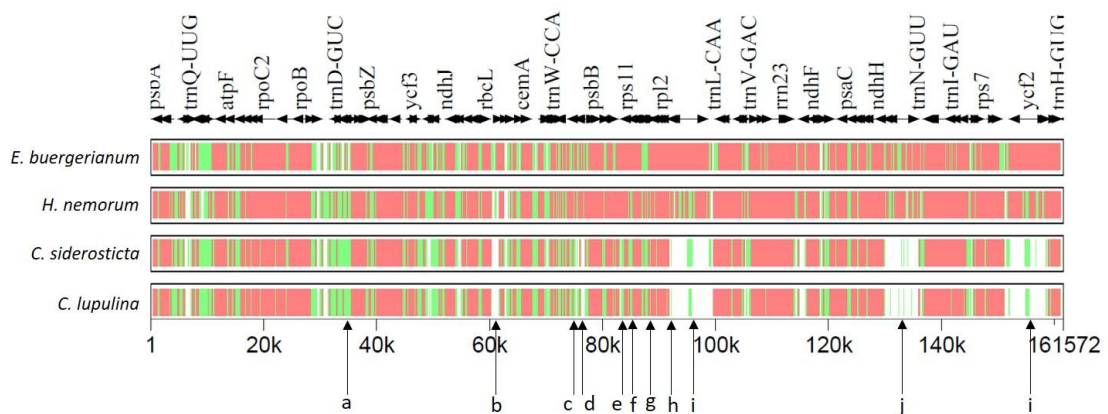


Fig. 4.4 MultiPipMaker analysis of *C. lupulina* and related taxa. The sequence similarity of the chloroplast genome was identified by the multiple alignments using *T. latifolia* as a reference. Levels of similarity were represented by red (75–100%), green (50–75%), and white (<50%). The gene losses were indicated by arrows. a. *trnT-GGU*, b. *accD*, c. *rps18*, d. *clpP*, e. *rpoA*, f. *infA*, g. *rps3*, h. *rpl23*, i. *ycf2*, j. *ycf1*.

4.3.5 IR expansion and contraction

In most angiosperms, IR has been expanded twice, resulting in 3'–*rps12*, *rps7*, *ndhB*, *trnL-CAA*, *ycf2*, *trnI-CAU*, *rpl23*, and *rpl2* moved from LSC to IR (Wicke et al., 2011). In addition, the IR expansion in monocots occurred more progressively than in non-monocot angiosperms. As a result, the IR of monocots additionally contained the *trnH-rps19* gene cluster located in the LSC region of non-monocot angiosperms (Wang et al., 2008).

To investigate IR expansion and contraction of Cyperaceae, IR boundaries of *C. lupulina* and related taxa were compared (Fig. 4.5). *T. latifolia* had the shortest IR region (26,390 bp) and *C. lupulina* had the longest IR region (68,258 bp). Especially, the length of the IR region of *T. latifolia* and *E. buergerianum* was similar, but the length of Cyperaceae was long and varied from 38,427 to 68,258 bp.

At the IR/LSC border (JLA and JLB), all taxa showed that IR region included *rps19* and *trnH*, although *rps19* of *C. lupulina* spanned LSC and IR region (Fig. 4.5). Thus, it is consistent with previous studies that the IR region of the monocots is expanded by including *trnH* and *rps19* located in the LSC region of non-monocots. (Wang et al 2008).

At the IR/SSC border (JSA and JSB), JSB of *T. latifolia* and *E. buergerianum* was located between *trnN-GUU* and *ndhF*, and JSA was located in *ycf1* (Fig. 4.5). Whereas, in Cyperaceae, JSB was located between *ndhG* and *ndhF*, and JSA was located between

ndhE and *ndhG*. In other words, *ndhG*, *ndhI*, *ndhA*, *ndhH*, *rps15*, and *ycf1* were contained in SSC region of *T. latifolia* and *E. buergerianum*. However, these genes were contained in the IR region of Cyperaceae. Thus, the IR region of Cyperaceae was expanded by duplication of *ndhG-ycf1* genes, and about 10–11 kb expansion of the IR region is characteristic of Cyperaceae. It can also be seen in Figure 4.3B. g.

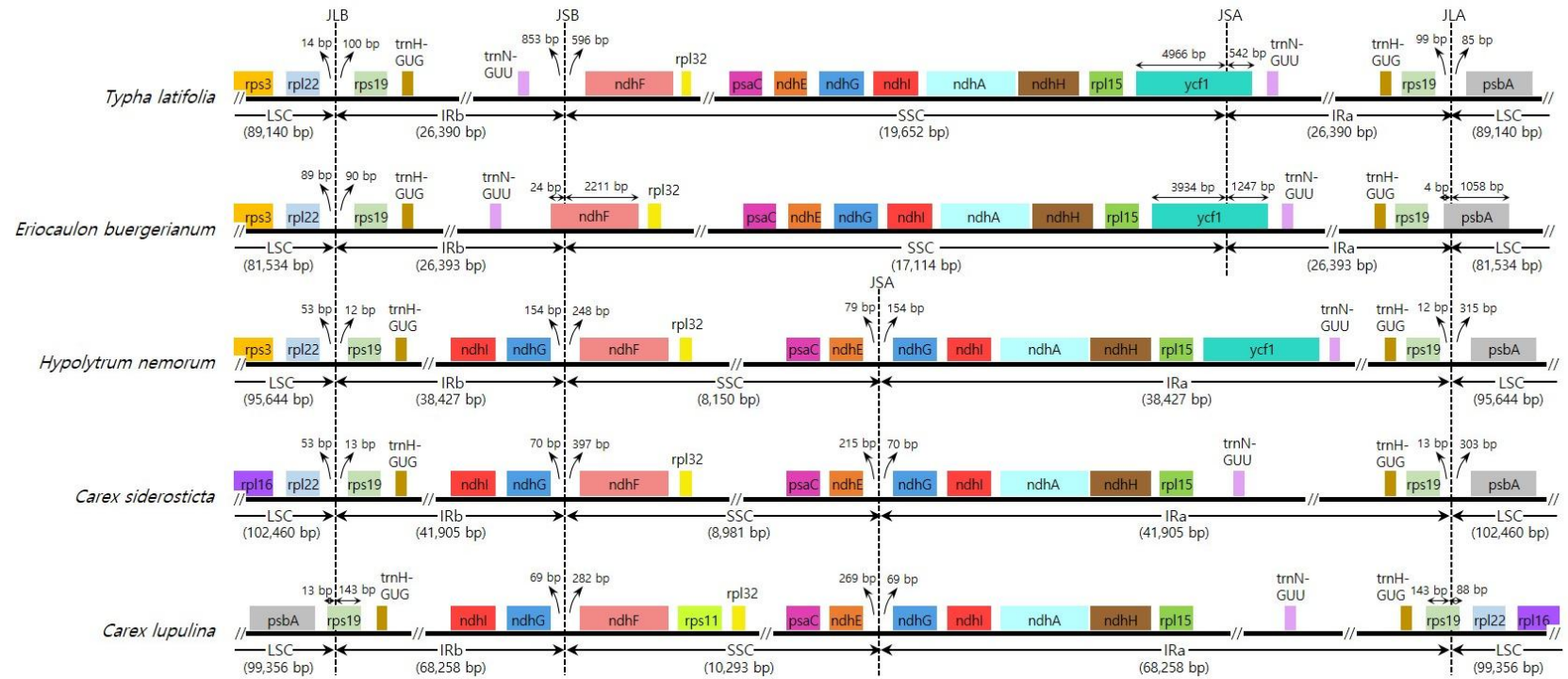


Fig. 4.5 Comparison of IR borders in *C. lupulina* and related taxa. The genes of the chloroplast genomes were represented by colored boxes. JLB, junction between LSC and IRb; JLA, junction between LSC and IRa; JSB, junction between SSC and IRb; JSA, junction between SSC and IRa.

4.3.6 Repetitive sequence

Oligonucleotide repeats were found in the chloroplast genome of *C. lupulina* and related taxa using REPuter. The details of repeats information such as repeats type, length, location and region were provided in Appendix 4.4.

The number of oligonucleotide repeats in Cyperaceae was significantly higher than that in *T. latifolia* and *E. buergerianum* (Fig. 4.6A). Especially, *C. lupulina* had the most oligonucleotide repeats with a total of 1,939 repeats, including 1,544 forward, 389 palindromic, 5 complement, and 1 reverse repeats. The most common repeat lengths were 30~39 bp (33.1~94.5%) (Fig. 4.6B). The length of repeat in Cyperaceae varied from 30 to 1,544 bp, whereas that in *T. latifolia* and *E. buergerianum* ranged from 30 to 59 bp except for a repeat with 540 bp long in Typhaceae. Especially, repeat sequences with >600 bp were only found in *Carex* (Fig. 4.6B). The repeats of *T. latifolia*, *H. nemorum*, and *C. siderosticta* were more distributed in the LSC region than in other regions, whereas most of repeats of *C. lupulina* were located in IR region (69.6%) (Fig. 4.6C). Overall, most of the repeat sequences were located in the intergenic spacer regions (IGS; 63.7~95.5%) except for *E. buergerianum* which many repeats located in the coding region (52.9%) (Fig. 4.6D).

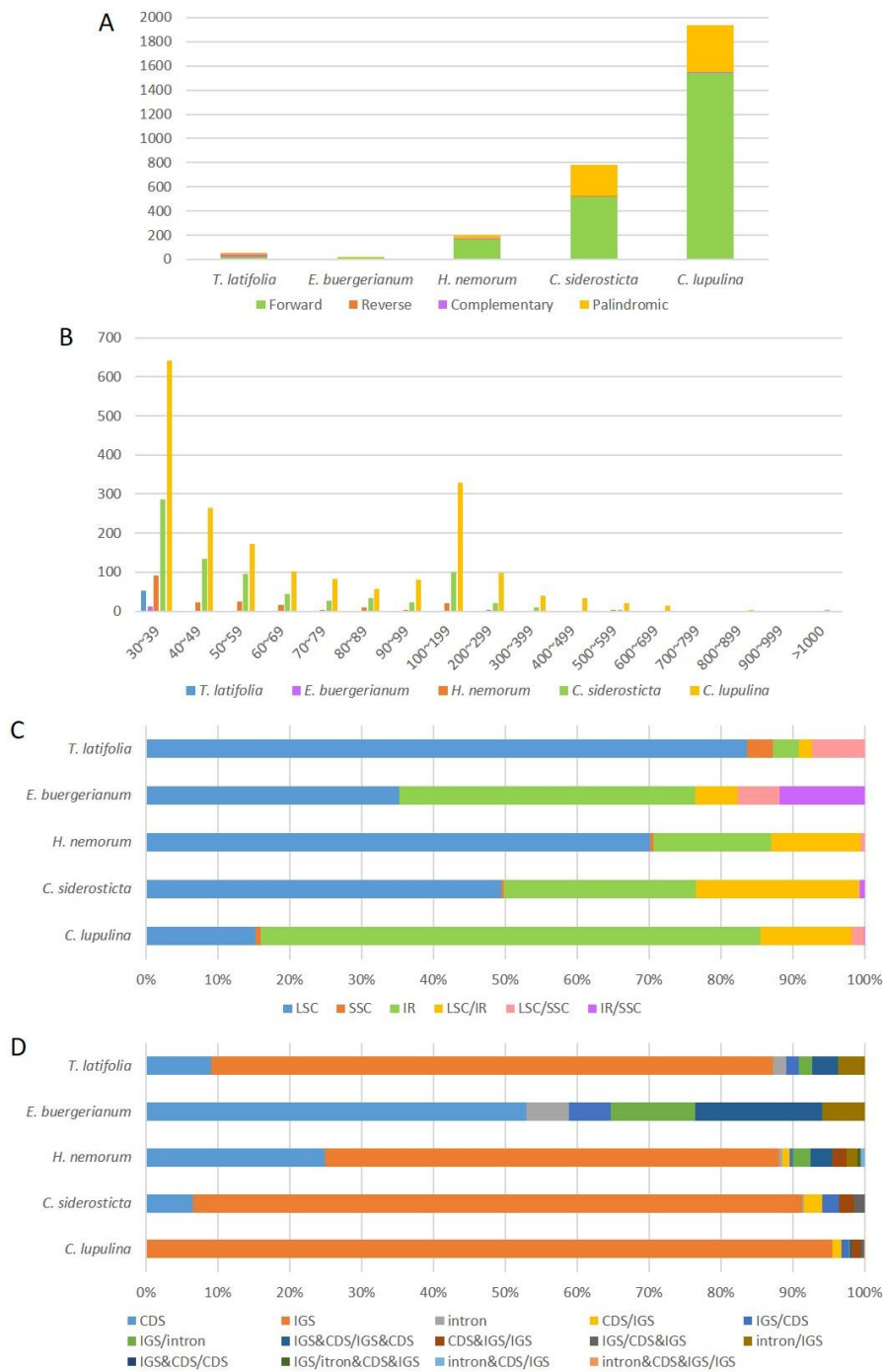


Fig. 4.6 (Continued)

Fig. 4.6. Oligonucleotide repeats in the chloroplast genomes of *C. lupulina* and related taxa. (A) show type and numbers of repeats. F: forward repeats, P: palindromic repeats, R: reverse repeats, C: complementary repeats. (B) show the size of repeats, i.e. 30–39 represent the numbers of repeats in the range of 30 and 39 bp. (C) show location of repeats. i.e. LSC indicates that repeats pairs are located in LSC. The LSC/IR indicates that one repeat copy is located in LSC and another in IR. (D) show region of repeats. i.e. CDS represents that repeats pairs is detected in CDS. The CDS/IGS represents that one repeat copy is detected in CDS and another in IGS. CDS: coding sequence regions, IGS: intergenic spacer regions, Intron: intragenic regions.

The tandem repeats were identified using the Tandem Repeats Finder and provided in Appendix 4.5. *C. lupulina* had the most tandem repeats (169), whereas *E. buergerianum* had the least (Fig. 4.7A). Most of the tandem repeats ranged from 9 to 24 bp (63.7~100%), and Cyperaceae had long repeats (>100 bp) (Fig. 4.7B). These repeats were more detected in the LSC region than in other regions (Fig. 4.7C). Also, repeats were mostly detected in non-coding regions such as IGS (68.6~93.5%) and intron (0.7~5.3%) (Fig. 4.7D).

The SSRs were identified using the MISA-web program and

provided in Appendix 4.6. The total number of SSRs in Cyperaceae was more than that in *T. latifolia* and *E. buergerianum* (Fig. 4.8A). Especially, *C. siderosticta* had the highest total number of SSRs (Fig. 4.8A). The mononucleotide SSRs was the most abundant, followed by trinucleotide except for *E. buergerianum* (Fig. 4.8A). In *E. buergerianum*, trinucleotide (45%) was more abundant than mononucleotide (38%; Fig. 4.8A). All genome showed that A/T ($\geq 96\%$) and AT/AT ($\geq 86\%$) motifs were the most abundant in mononucleotide and dinucleotide, respectively (Fig. 4.8B). In the trinucleotide SSRs, AAT/ATT motif was the most abundant in Typhaceae and Eriocaulaceae, whereas AAG/CTT motif was the most abundant in Cyperaceae (Fig. 4.8B). The SSRs of the five taxa genomes were most frequently found in the LSC region (51–65%; Fig. 4.8C). The next most frequently found region was IR region in Cyperaceae, but SSC in Typhaceae (Fig. 4.8C). Most of SSRs were located in the non-coding region (63.7~95.5%) except for *E. buergerianum* which had many repeats in the coding region (52.9%).

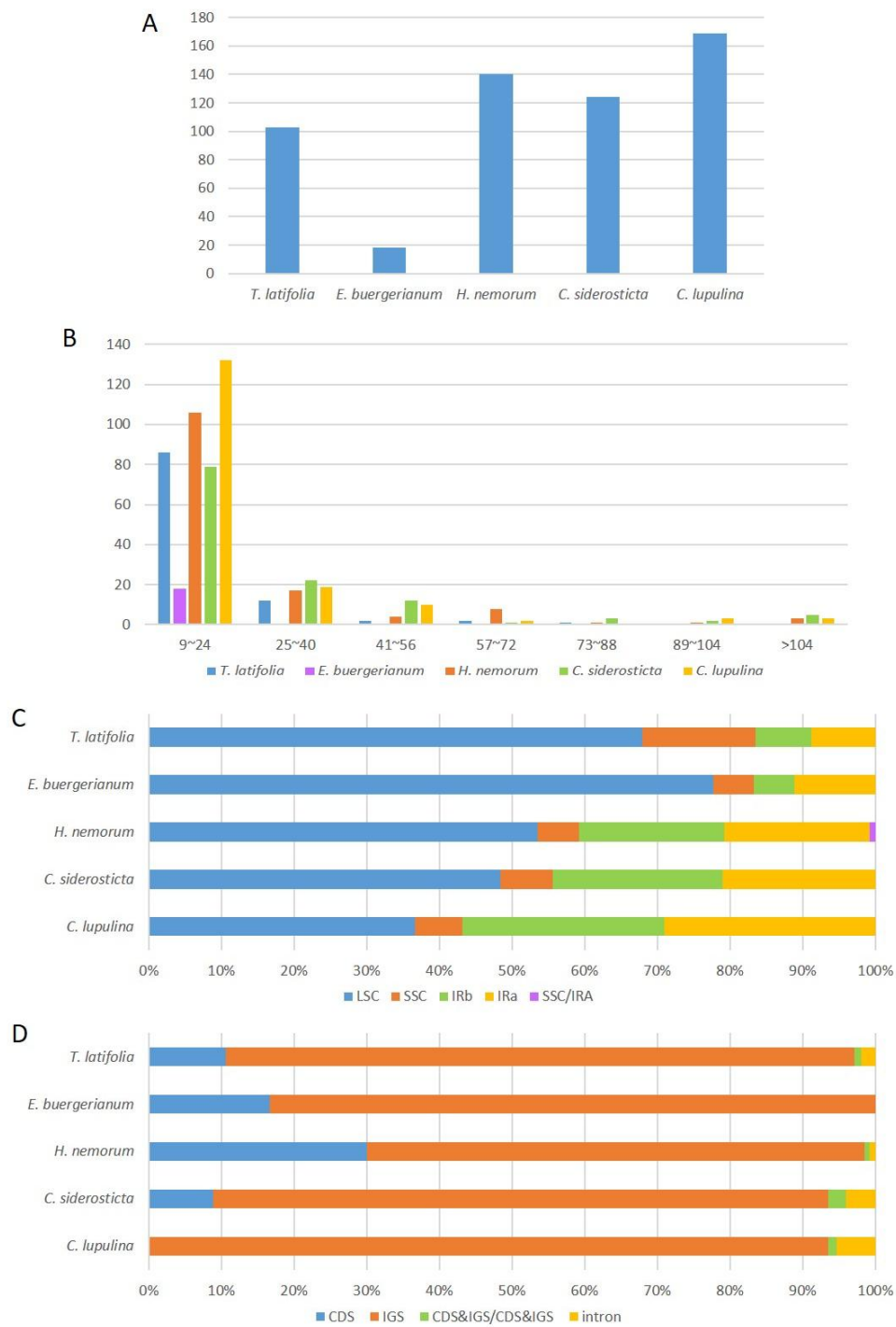


Fig. 4.7 (Continued)

Fig. 4.7 Tandem repeats in the chloroplast genomes of *C. lupulina* and related taxa. (A) show numbers of repeats. (B) show the size of repeats, (C) show location of repeats. i.e. LSC indicates that repeats pairs are located in LSC. The SSC/IRa indicates that one repeat copy is located in SSC and another in IRa. (D) show region of repeats. i.e. CDS represents that repeats pairs is detected in CDS. The CDS&IGS represents that repeats pairs is detected in CDS through IGS. CDS: coding sequence regions, IGS: intergenic spacer regions, Intron: intragenic regions.

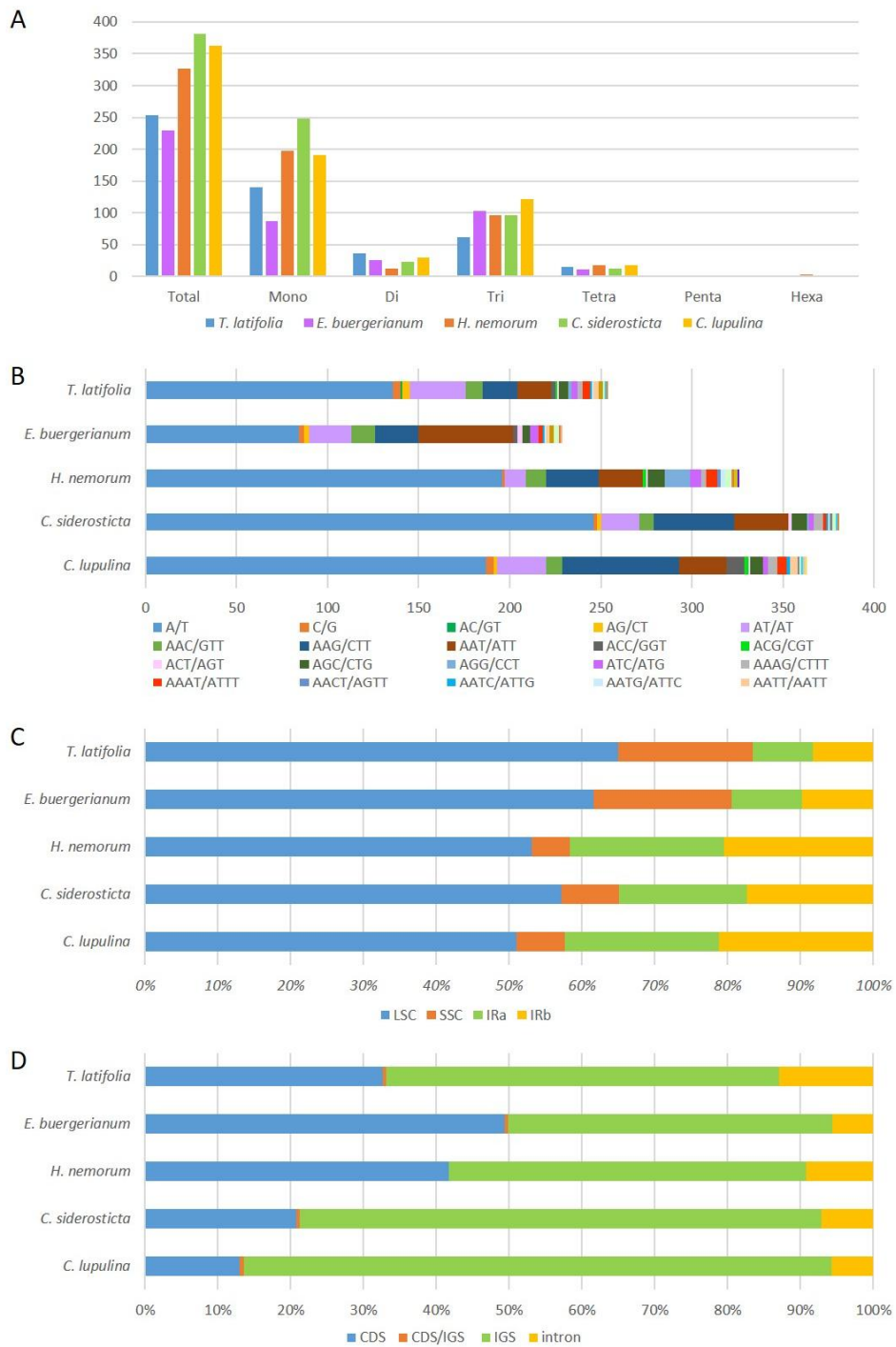


Fig. 4.8 (Continued)

Fig. 4.8 SSRs in the chloroplast genomes of *C. lupulina* and related taxa. (A) show type and numbers of repeats. (B) Frequency of identified SSR motifs in different repeat class types. (C) show location of repeats. (D) show region of repeats. i.e. CDS represents that repeats pairs are detected in CDS. CDS: coding sequence regions, IGS: intergenic spacer regions, Intron: intragenic regions.

4.4 Discussion

4.4.1 Chloroplast genome in Cyperaceae

In this study, the chloroplast genome in *C. lupulina* was sequenced using Nanopore sequencing. The chloroplast genome of *C. lupulina* is 246,165 bp in size, which is the second largest in the reported chloroplast genomes in angiosperm (NCBI organelle DB; searched on July 2019). The genome has 123 genes containing 63 unique protein-coding genes, 29 unique tRNA genes, and 4 rRNA genes.

To understand the structural evolution of chloroplast genome in Cyperaceae, the chloroplast genome in *C. lupulina* was compared with related taxa in Poales. The size of chloroplast genomes in Cyperaceae are larger than Typhaceae and Eriocaulaceae, and the chloroplast genomes in *Carex* are the largest. In addition, the chloroplast genomes in Cyperaceae can be found genomic rearrangements such as structure change, gene order change, gene loss, and IR expansion. The genomic rearrangement events were plotted on the phylogenetic tree which was generated using 60 protein-coding genes from the chloroplast genomes in *C. lupulina* and related taxa (Fig. 4.9). With accelerated transformation (ACCTRAN), the major apomorphic changes for each group of taxa were indicated on each node. Cyperaceae share six genomic structure changes, gene loss (*accD*, *infA*, and *rps18*), and 10–11 kb IR expansion. It can be assumed that

the genomic rearrangement events occurred in the early evolution of Cyperaceae. In *Carex*, six genomic structure changes, gene loss (*clpP*, *rpl23*, *rpoA*, *rps3*, *ycf1*, *ycf2*, and *trnT-GGU*), and duplication of *trnfM-CAU* gene are shared.

The chloroplast genome of *C. lupulina* has striking features compared with the chloroplast genomes of other taxa. First, as mentioned above, the size of the chloroplast genome is very large. Second, additional structural changes have occurred. A large inverted translocation (about 30 kb), 5.2 kb inverted translocation and insertions are found. Third, there are many short repeats in the IR region. Fourth, additional pseudogenization have occurred: *ndhD*, *petA*, *rpoC2*, *rps2*, *rps7*, *rps16*, *ycf4*, and *ycf68*. Fifth, additional gene duplications have occurred: *rps14*, *trnfM-CAU*, *trnG-GCC*, *trnR-UCU*, and *trnT-AGU*.

Recently, the chloroplast genome sequences in Cyperaceae were updated in NCBI. The chloroplast genomes of *Eleocharis* and *Cyperus* were reported. Fig. 4.10 represents the IR borders in Cyperaceae updated with new genome data. The IR/LSC border (JLA and JLB) of *Eleocharis* is located in *rpl16*, and the IR/LSC border of *Cyperus* is located between *rpl16* and *rpl22*. Namely, *rpl22* and *rps3* are contained in the IR region of *Eleocharis*, and *rpl22* is contained in the IR region of *Cyperus*. However, these genes are contained in the LSC region of other taxa. Thus, Fig. 4.10 shows that the IR regions of *Eleocharis* and *Cyperus* are further expanded to the LSC region.

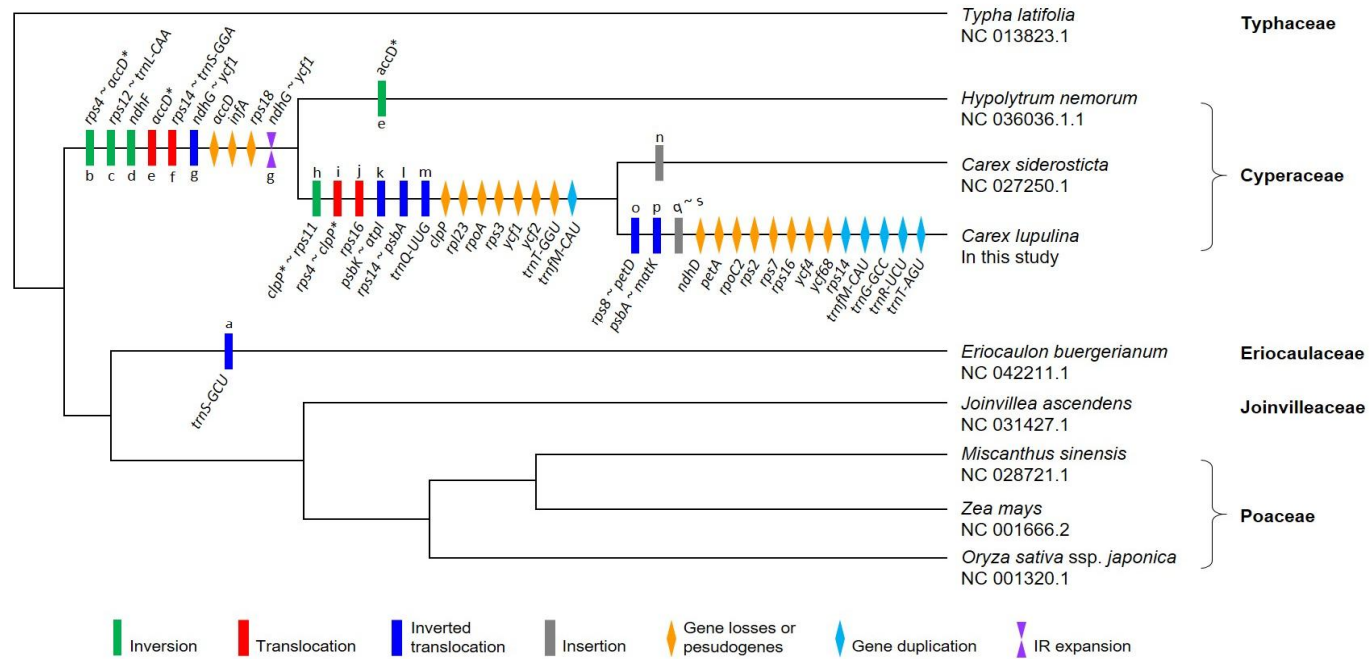


Fig. 4.9 Phylogenetic distribution of rearrangements of the chloroplast genome in Cyperaceae. Rearrangements were plotted on the ML tree of *C. lupulina* and related taxa based on 60 protein-coding genes. With ACCTRAN optimization, rearrangements of the chloroplast genome in Cyperaceae are indicated on each node. Lower case letters correspond to structural changes indicated in Fig. 4.3. The asterisk indicates a part of the gene.

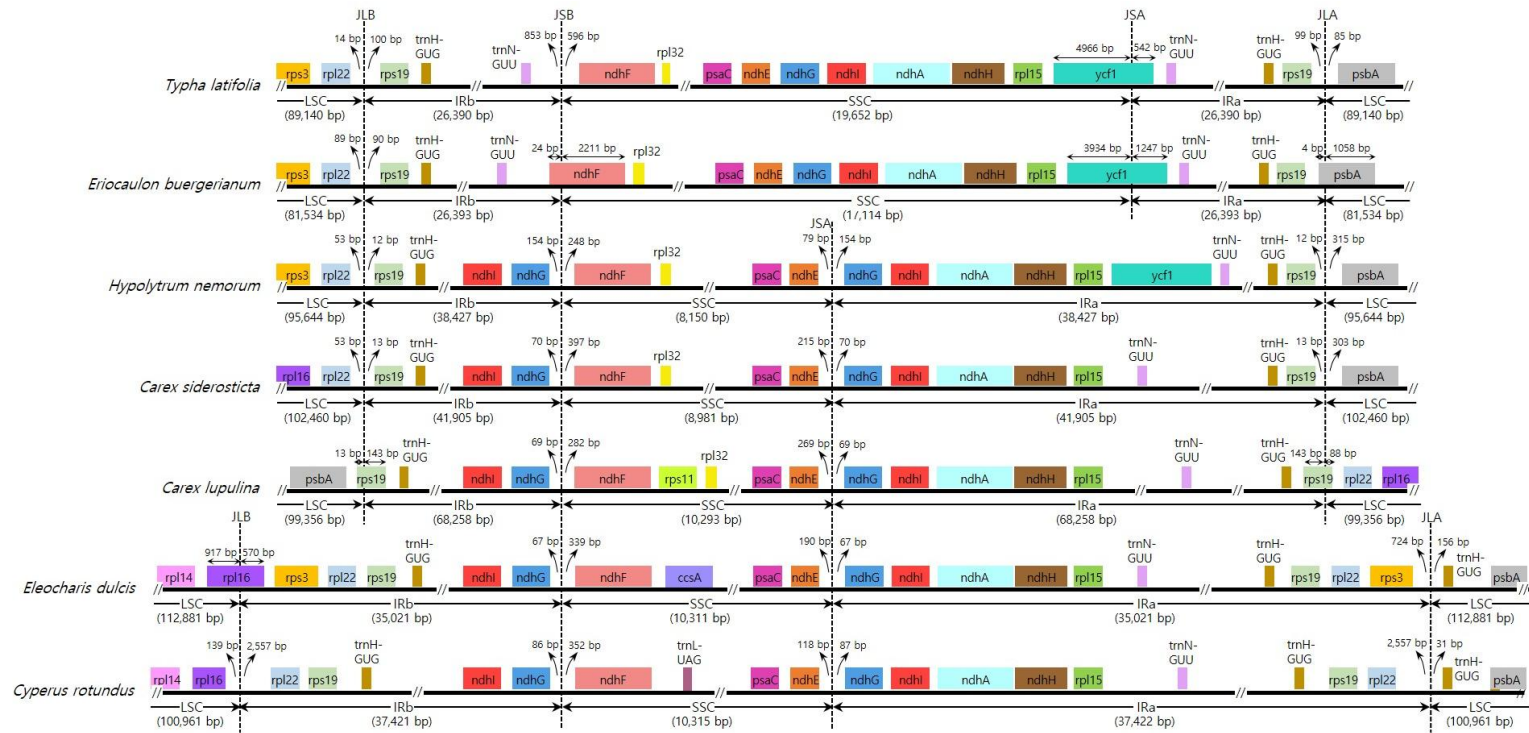


Fig. 4.10 Comparison of IR borders in Cyperaceae. The genes of the chloroplast genomes were represented by colored boxes. JLB, junction between LSC and IRb; JLA, junction between LSC and IRa; JSB, junction between SSC and IRb; JSA, junction between SSC and IRa.

4.4.2 Repetitive sequences and genomic rearrangements

The number of repetitive sequences in Cyperaceae are higher than that of Typhaceae and Eriocaulaceae. The repeats are more distributed in the LSC region than in other regions except for oligonucleotide repeats of *C. lupulina* which are more distributed in the IR region. Also, the repeats are more located in the non-coding regions such as IGS. Therefore, many repeats led to increase of the size of chloroplast genomes in Cyperaceae. Especially, in *C. lupulina*, many repeats are found in the IR region, which causes an increase in the size of the IR region. Thus, many repeats in the IR region are the main reason for the increase in the size of the chloroplast genome in *C. lupulina*. In addition, IR expansion into SSC by the duplication *ndhG-ycf1* increases the size of the chloroplast genome in Cyperaceae.

Many repeats are located in endpoints of rearrangements in *Carex*. Especially, these are found at endpoints of large inversion in *C. lupulina*. This result agrees with previous studies that repetitive DNA has been found in highly rearranged chloroplast genomes and facilitate inversions (Weng et al., 2014). Besides, inversion and IR expansion/contraction are known as the main mechanisms of gene order change (Jansen and Ruhlman, 2012). Therefore, it is considered that IR expansion and structural change cause gene order changes in Cyperaceae and *Carex*.

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ABSTRACT IN KOREAN

적 요

이 보 라

생물학과

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사초과(Cyperaceae)는 단자엽식물 중에서 세 번째로 크고, 피자식물 중에서 일곱 번째로 큰 분류군으로 88속, 약 5,500여 종이 전 세계적으로 분포한다. 사초과 식물은 고대 이집트 시대에 사용했던 종이(파피루스; *Cyperus papyrus* L.)의 재료로 잘 알려져 있으며, 경제적, 환경적으로 유용한 식물이다. 사초과는 벼목(Poales)에 속하며 매우 축소되고 복잡한 화서를 갖는 것이 다른 분류군과 크게 구분된다. 하지만 벼목에 대한 많은 연구들은 벼과(Poaceae)에 집중되어 왔고, 사초과에 대한 종합적인 연구는 아직 부족한 실정이다. 본 연구에서는 1) 사초과 식물의 꽃의 진화와 다양성을 이해하기 위해 사초과의 대표적인 식물로 도깨비사초(*Carex dickinsii*)의 전사체 분석을 통하여 MADS-box 유전자를 검출하였고, 각 기관에서 발현양상을 확인하였으며, 2) 우리나라 사초속 15개의 절(section)에 속하는 43 분류군의 유전체 크기를 측정하였고, 3) 대표적인 사초과 식물로서 *C. lupulina*의 엽록체 유전체를 완성하였으며, 4) *C. lupulina*의 엽록체 유전체의 구조를 계통적으로 가까운 분류군들의 엽록체 유전체들과 비교하여 사초과 식물의 엽록체 유전체들의 진화와 다양성을 이해하고자 하였다.

사초과에서 가장 큰 속인 사초속(*Carex* L.)은 전 세계적으로 약 2,000여종이 분포하고, 꽃은 단성화이며 화피가 없다. 사초속 식물의 암꽃은 심피를 둘러싸고 있는 과포가 있는 것이 특징이며, 수꽃은 두 개 또는 세 개의 수술과 인편으로 구성되어 있다. 본 연구에서는 도깨비사초에서 48개의 MADS-box 유전자[40 type II (35 MIKC^C, 5 MIKC*-type), 8 type I MADS-box 유전자]를 검출하였다. 그리고 이 MADS-box 유전자들은 잎, 암꽃 인편, 과포, 심피, 수꽃 인편, 수술에서 발현하는 것을 확인하였다. 특히, E 기능유전자가 사초속 식물의 독특한 기관인 암꽃 인편, 과포, 수꽃 인편에서 발현됨을 확인하였다. 따라서, 이 기관들은 사초속 식물의 꽃의 한 부분이라고 추론할 수 있었다. 또한 암꽃 인편과 수꽃 인편은 형태적으로 유사하지만 MADS-box 유전자들의 발현양상의 차이에 의해 이들의 진화적인 기원은 다르다고 판단할 수 있다.

우리나라 사초속 43 분류군의 유전체 크기를 유세포분석기를 이용하여 측정하였으며, 이는 우리나라 사초속 식물의 24.4%를 포함한다. 본 연구의 결과와 Plant DNA C-value Database (release 7.1)를 포함한 사초속의 평균 유전체 크기는 0.47 pg (1C)이며, *C. cuspidate*의 유전체 크기는 1.64 pg (1C)로 가장 크고, *C. brownii*, *C. kobomugi*, *C. nubigena*, *C. paxii*의 유전체 크기는 서로 같으며 0.20 pg (1C)로 가장 작았다. *Carex*아속의 유전체 크기가 큰 편이며, 특히 *Aulocystis*절, *Digitatae*절, *Glaucæ*절, *Paniceae*절, *Siderostictae*절의 유전체 크기가 큰 편이다. 반면에, *Vigneae*아속의 유전체 크기는 작은 편이며, *Phleoideae*절의 유전체 크기가 가장 작았다.

Nanopore platform의 염기서열 분석을 통해 *C. lupulina*의 엽록체 유전체를 완성하였다. *C. lupulina* 엽록체 유전체의 크기는 246,165 bp로 지금까지 보고된 피자식물의 엽록체 유전체들 중에서 두 번째로

크다(NCBI organelle DB; 2019년 7월 접속 정보). 이 엽록체 유전체는 LSC (99,356 bp), SSC (10,293 bp)와 한 쌍의 IR (각각 68,258 bp)로 구성되어 있으며, 123개의 유전자(63개의 단일 단백질 암호화 유전자, 29개의 단일 tRNA 유전자, 4개의 rRNA 유전자)를 포함하고 있다. 사초과 식물의 엽록체 유전체의 구조 진화를 파악하기 위해 계통적으로 가까운 분류군들의 이미 보고된 엽록체 유전체들과 비교하였다. 사초과 식물의 자매군에 비해 사초과 식물의 엽록체 유전체는 세 곳의 역위(*rps4~accD*의 일부: 12~13 kb, *rps12~trnL-CAA*: 6~7 kb, *ndhF*: 약 2.2 kb), 두 곳의 전위(*accD*의 일부: 0.2~1.4 kb, *rps14~trnS-GGA*: 7.5~9 kb), 한 곳의 역전위(*ndhG~ycf1*: 5~11 kb)가 일어나며, 세 개의 유전자(*accD*, *infA*, *rps18*)의 결실과 IR 확장(*ndhG~ycf1*: 10~11 kb)을 확인하였다. 사초속 식물의 엽록체 유전체에서는 한 곳의 역위(*clpP*의 일부~*rps11*: 약 10 kb), 두 곳의 전위(*rps4~clpP*의 일부: 약 15 kb, *rps16*: 약 1.2 kb), 세 곳의 역전위(*psbK~atpI*: 약 8 kb, *rps14~psaA*: 약 5 kb, *trnQ-UUG*: 약 140 bp)가 일어나며, 일곱 개의 유전자(*clpP*, *rpl23*, *rpoA*, *rps3*, *ycf1*, *ycf2*, *trnT-GGU*)의 결실과 *trnfM-CAU*의 복제를 확인하였다. *C. lupulina*의 자가과생형질로 엽록체 유전체에서 두 번의 큰 역전위(약 30 kb: *rps8~petD*, 약 5.2 kb: *psbA~matK*)가 일어나며, 여덟 개의 유전자(*ndhD*, *petA*, *rpoC2*, *rps2*, *rps7*, *rps16*, *ycf4*, *ycf68*)의 결실과 5개의 유전자(*rps14*, *trnfM-CAU*, *trnG-GCC*, *trnR-UCU*, *trnT-AGU*)의 복제를 확인하였다. 사초과 식물의 엽록체 유전체는 부들과와 곡정초과보다 많은 반복서열이 존재하며, 이 반복서열들은 다른 구역보다 LSC 구역에 많이 분포하는데, *C. lupulina*에서는 IR 구역에 집중적으로 분포한다. 또한 많은 반복서열은 대부분 유전자들 사이지역(IGS: intergenic spacer region)과 같은 비암호화구역에서

확인된다, 이러한 반복서열의 축적은 사초과 식물의 엽록체 유전체 크기의 확장에 영향을 주는데, 특히 *C. lupulina*의 IR 구역에서의 많은 반복서열은 *C. lupulina*의 엽록체 유전체의 IR을 확장시키고, 이는 엽록체 유전체 크기가 커지는데 주요 원인으로 작용하였다. 게다가 *ndhG-ycf1* 구간의 복제로 인한 IR 확장 또한 사초과 식물의 엽록체 유전체의 크기를 확장시키는 요인이 되었다. 이들 반복서열들은 사초속 식물의 엽록체 유전체의 재배열이 일어나는 주변에서 많이 발견되는데, 이는 반복서열들이 엽록체 유전체의 구조 변화와 관련이 있을 것으로 생각된다.

본 연구는 1) 사초속 식물에서의 48개의 꽃 발생 관여 MADS-box 유전자와 꽃 기관에서의 발현양상, 2) 우리나라의 사초속 43 분류군의 유전체 크기, 3) 완성된 *C. lupulina*의 엽록체 유전체, 4) 사초과 식물의 엽록체 유전체의 구조 변화에 대해 처음으로 보고하였다. 본 연구의 결과들은 사초과 식물의 꽃과 엽록체 유전체의 진화와 다양성을 이해하는데 기초가 될 것이다.

APPENDICES FOR CHAPTER 2

Appendix 1. Primers used in this study

Appendix 2. FPKM of MADS-box genes in different organs

Appendix 3. Normalized FPKM (\log_2 FPKM) of MADS-box genes in
different organs

Appendix 1. Primers used in this study

Primer name	Primer sequence (5'-3')	Usage
Ca.di.AP1_F-1	GCAAACCAAACCAAGACC	C, G
Ca.di.AP1_F-2	CCTACAGTGTTTTTTTACAAAATT	G
Ca.di.AP1_F-3	TGGATAAGATTTTGGACCG	G
Ca.di.AP1_F-4	ATTACAGAACAACCCGTGC	G
Ca.di.AP1_F-5	GGTCAATTAGAGATTATGTGAAGA	G
Ca.di.AP1_R-1	TGTACAGTTTGCTTTCAATTAGA	C, G
Ca.di.AP1_R-2	ATGCCTTTTTGACCCTCTAT	G
Ca.di.AP1_R-3	AGTGTGCTGTTGCCTCCA	G
Ca.di.AP1_R-4	TGGTAAGCAGTGGCATGA	G
Ca.di.AP1_R-5	GTGCAGGATGACCCTCTG	G
Ca.di.AP3_F-1	AACACCTACACCTCAACTAAAGA	C, G
Ca.di.AP3_R-1	CTTAAAGGAAAACAAAAACATAGA	C, G
Ca.di.AP3_R-2	CATGACTTCTTTTCAACGTGA	G
Ca.di.PL_F	TCTTCTCCTTCTTCTTTTGTG	C, G
Ca.di.PL_R	GCACAATCATAGCAAGTTCC	C, G
Ca.di.AG.1_F	GCAGGAAGAAGGAAGGAAC	C
Ca.di.AG.1_R	CACACACAGCAGCAAGAGAT	C
Ca.di.AG.2_F-1	CCCCTTCATCATCATCCTA	C, G
Ca.di.AG.2_F-2	TGGCACTCATAATCTTCTCG	G
Ca.di.AG.2_R-1	GATTACCAACAACGCTTCC	C, G
Ca.di.AG.2_R-2	GGCCTTTCTCGTAATTGG	G
Ca.di.AG.2_R-3	TGTCAAGGCTGTCTCCAAT	G
Ca.di.AG.2_R-4	GCTCTTAAAGCAGGTGAAATT	G
Ca.di.AG.2_R-5	GACATTTTTCTTTCACACCA	G
Ca.di.AGL2.1_F	GAGAGAGGTAGAGGGGAGAA	C
Ca.di.AGL2.1_R	AGCGAGCACAGAAAGACC	C
Ca.di.AGL2.2_F-1	TCCATCCCTTCTTTTCTCTA	C, G
Ca.di.AGL2.2_F-2	GGGGCTCATTATCTTCTCTC	G
Ca.di.AGL2.2_R-1	CCTTCACACACAACAAAAAT	C, G
Ca.di.AGL2.2_R-2	CAAATCTTCCAATGTGTCCA	G
Ca.di.AGL2.2_R-3	GGAGACGACTTTTGCTGG	G
Ca.di.AGL2.2_R-4	AGAATTCAATGTAGTCTGTCAA	G
Ca.di.AGL2.3_F	GAGAGAGAGAGAGAGAGAAGC	C
Ca.di.AGL2.3_R	AGCTCAAATAGAAGCAATATGTT	C
Ca.di.AGL2.4_F-1	CCTAGGTTTTCAAAGGGAAAT	C, G
Ca.di.AGL2.4_F-2	CTTAAGACATTGGAGAGGTATCA	G
Ca.di.AGL2.4_R-1	TTCGAATGCTTGTTCAACTT	C, G

Ca.di.AGL2.4_R-2	TTGTTGTAGAGAGCGTTGATC	G
Ca.di.AGL2.4_R-3	ACTTCAACTCGTGACTTCAAT T	G
Ca.di.AGL2.4_R-4	TCATCATTAGGAACAGCAGC	G
Ca.di.AGL6_F	AAGAGAGGAGGTTCAGATCGA	C
Ca.di.AGL6_R	AAGAGGACCAAAGGACCC	C
Ca.di.AGL12.2_F-1	CGGGACAAATTACGAGCT	C, G
Ca.di.AGL12.2_F-2	CGGCATTGATGATCAACA	G
Ca.di.AGL12.2_R-1	ACTAGGAGCAAACCTGGAAGTAA	C, G
Ca.di.AGL12.2_R-2	CCTGAAGAATTTTCATTAGCG	G
Ca.di.AGL17.1_F-1	TGTGCAAACATCCCATATATT	C, G
Ca.di.AGL17.1_F-2	ATGGGAAGAGGAAAAATATTG	G
Ca.di.AGL17.1_F-3	CATGAAAGCAATAATTGATCG	G
Ca.di.AGL17.1_F-4	TACCCGTTTTTCCCAATAAG	G
Ca.di.AGL17.1_R-1	GCAAGCTGATGGTAAGGAG	C, G
Ca.di.AGL17.1_R-2	CACGTTATGGTGTCCATTTTC	G
Ca.di.GMM13_F-1	CGTCACACACTTCTTCCATC	C, G
Ca.di.GMM13_F-2	TTTTTCCGTTTAATTTAAGCA	G
Ca.di.GMM13_F-3	TGAACCTAAACAAACTGGCTA	G
Ca.di.GMM13_R-1	TTTCCCGAGTTTCTGCTT	C, G
Ca.di.GMM13_R-2	TGTCATCATCTGCTGCTCA	G
Ca.di.GMM13_R-3	AGCTGCTGGTTTAGCAATT	G
Ca.di.OsMADS32_F-1	AATTTCCCCCTCATCTT	C, G
Ca.di.OsMADS32_F-2	AGAGATAGCTAAGGTGGAGAAGT	G
Ca.di.OsMADS32_R-1	TTAGAAAATGAGCAAACCCA	C, G
Ca.di.OsMADS32_R-2	ATTTAAGGTCCAACGCATG	G
Ca.di.STMADS11.1_F	GCACTACTACCGCTCAAGAA	C
Ca.di.STMADS11.1_R	ACTCTTGGAAGCATCATG	C
Ca.di.STMADS11.2_F-1	GATCCATTTTCGTGGCAGT	C, G
Ca.di.STMADS11.2_F-2	ATCTAATACGATCTGCAGCG	G
Ca.di.STMADS11.2_F-3	TGGAAATTAGGATTTTGTGA	G
Ca.di.STMADS11.2_F-4	ACGCTTCGCAAGTACTCTG	G
Ca.di.STMADS11.2_R-1	TTTGAAAAGTAAAAAGGAGCA	C, G
Ca.di.STMADS11.2_R-2	TCTGAGGGAAGTGTGCGGA	G
Ca.di.STMADS11.2_R-3	CGGTTGGTTCATTTCATTTT	G
Ca.di.STMADS11.2_R-4	TCGTACATTACTTGGCCTCA	G
Ca.di.TM3.1_F	ACTGGTGGAGGTTGAGCA	C
Ca.di.TM3.1_R	GCGACATTGCTTCCATCT	C
Ca.di.MADS1_F-1	CCTACTTCCACTTCTCCCC	C, G
Ca.di.MADS1_F-2	ATGTATGAAGAAGAGAGCGTGT	G

Ca.di.MADS1_F-3	ATTGACACCATATACACCCG	G
Ca.di.MADS1_R-1	CCATTCATTAGTCTCTCCCC	C, G
Ca.di.MADS1_R-2	TCTAAAAGCCTCCAATAACG	G
Ca.di.MADS1_R-3	TCTTTATCAGCGGCACCT	G
Ca.di.MADS4_F-1	TCAATCTGTCCCGTCTCG	C, G
Ca.di.MADS4_F-2	CAGAGTGTGAAGATCTGGCA	G
Ca.di.MADS4_F-3	TGCGGTGTCAGTTCATAATT	G
Ca.di.MADS4_F-4	AGGGCTGATCATGAAGATCT	G
Ca.di.MADS4_R-1	TTCTCTTCCATCCTCTTCCA	C, G
Ca.di.MADS4_R-2	TCATGCTCAGTGCATTTAGTAA	G
Ca.di.MADS4_R-3	GTTTTATTTGGACTTGGTTTCA	G
Ca.di.MADS4_R-4	TTATTGGTGTCAAGCTGTGG	G
Ca.di.P.2_F	CGCTCTTTTCTTCTCCGA	C, G
Ca.di.P.2_R-1	CATGCATAAAACTAAGATAAAAAAT	C, G
Ca.di.P.2_R-2	AAGTTGGTTCCGTTGTTC	G
Ca.di.P.2_R-3	AAGCAGGGCACACAAATT	G
Ca.di.P.2_R-4	TGAGCTGTTGAACATCGATT	G
Ca.di.M γ .1_F-1	ATTCAAGTCCAAGCATACAGAT	C, G
Ca.di.M γ .1_F-2	GGTCTTTTCAGGATGGCA	G
Ca.di.M γ .1_R	GTTTACTGGATGGAAGGGAT	C, G

* C, confirmation of cDNA; G, determination of genomic DNA

Appendix 2. FPKM of MADS-box genes in different organs

Gene name	Leaves	Pistillate scales	Perigynia	Carpels	Staminate scales	Stamens
<i>Ca.di.AP1.1-1</i>	3233.14	381934	417258	3731.12	128288	4198.79
<i>Ca.di.AP1.2</i>	237023	34644.2	22947.4	2223.76	24509.3	51430.2
<i>Ca.di.AP1.3</i>	0	22354.7	3742.38	0	12930.1	0
<i>Ca.di.AP1.4</i>	38222.7	145729	67483.3	35099.5	102912	46858.3
<i>Ca.di.AP3</i>	0	0	4177.3	0	0	292667
<i>Ca.di.PI-1</i>	8735.25	12852.3	45609.4	71202	8973.6	82700.5
<i>Ca.di.AG.1-1</i>	0	0	58403.9	234211	0	0
<i>Ca.di.AG.2-1</i>	0	7625.74	25432.3	85699.4	0	75926.3
<i>Ca.di.AG.2-2</i>	0	0	0	135955	0	95690.1
<i>Ca.di.AG.2-3</i>	0	6437.19	17285.5	74262.7	0	70040.5
<i>Ca.di.SEP.1</i>	0	67363.7	16509.3	20893.1	784996	79237.3
<i>Ca.di.SEP.2</i>	0	4910.84	120576	483845	0	251385
<i>Ca.di.SEP.3</i>	0	0	77260.4	267258	0	283093
<i>Ca.di.SEP.4</i>	0	426242	277852	6426.54	189373	29562.2
<i>Ca.di.AGL6</i>	0	7044.02	73463.5	123879	0	29781.4
<i>Ca.di.AGL12.1</i>	0	10280.8	0	0	2411.31	0
<i>Ca.di.AGL12.2</i>	10484.6	0	0	2296.56	2860.26	2635.4
<i>Ca.di.AGL17.1</i>	0	0	0	0	0	2962.66
<i>Ca.di.AGL17.2</i>	0	0	0	0	0	29625.1
<i>Ca.di.AGL17.3</i>	6255.5	0	0	0	0	0
<i>Ca.di.GMM13</i>	0	0	38768.1	84155.7	0	0
<i>Ca.di.STMADS11.1</i>	602384	0	0	13602.6	0	0
<i>Ca.di.STMADS11.2</i>	253315	112015	68925.5	60302.4	61859.5	96749.8
<i>Ca.di.TM3.1-1</i>	136935	41001.8	15344.7	0	57247.6	2222.83
<i>Ca.di.TM3.1-2</i>	115442	37014.3	14227.9	2620.09	47137.7	1905.19
<i>Ca.di.TM3.1-3</i>	100585	0	0	0	35598.9	0
<i>Ca.di.TM3.2</i>	26927.6	0	0	0	0	5051.7
<i>Ca.di.TM3.3</i>	0	8709.14	0	0	6763.44	0
<i>Ca.di.OsMADS32</i>	0	0	0	4807.08	0	0
<i>Ca.di.FLC.1</i>	104184	124433	136001	27361.5	77842.4	13200.4
<i>Ca.di.FLC.2</i>	0	0	0	0	2653.15	2309.1
<i>Ca.di.FLC.3-1</i>	0	0	0	0	0	2263.45
<i>Ca.di.FLC.3-3</i>	12828.6	0	0	0	0	0
<i>Ca.di.FLC.4</i>	102249	31243	21707.7	15031.4	17666.6	7667.34
<i>Ca.di.MIKC*.P.2</i>	17950.2	20657.2	10619.4	0	13813.8	1524.23
<i>Ca.di.MIKC*.P.3</i>	0	0	0	0	0	78140.2
<i>Ca.di.typeI.Mα.1-1</i>	4755.63	12141.6	7060.45	3673.76	9516.79	1123.2
<i>Ca.di.typeI.Mα.1-2</i>	0	5463.62	5117.78	2958.99	10451.1	1130.39
<i>Ca.di.typeI.Mα.4</i>	0	0	0	4777.87	0	0
<i>Ca.di.typeI.Mγ.1</i>	15270.1	40692.1	19357.6	4589.94	34356.7	12252.2
<i>Ca.di.typeI.Mγ.2</i>	0	0	0	0	0	2555.67

Appendix 3. Normalized FPKM (\log_2 FPKM) of MADS-box genes in different organs

Gene name	Leaves	Pistillate scales	Perigynia	Carpels	Staminate scales	Stamens
<i>Ca.di.AP1.1-1</i>	11.65872	18.54296	18.67058	11.86539	16.96903	12.03576
<i>Ca.di.AP1.2</i>	17.85467	15.08033	14.48604	11.11879	14.58104	15.65033
<i>Ca.di.AP1.3</i>	0	14.44829	11.86974	0	13.65845	0
<i>Ca.di.AP1.4</i>	15.22214	17.15293	16.04224	15.09916	16.65105	15.51602
<i>Ca.di.AP3</i>	0	0	12.02836	0	0	18.1589
<i>Ca.di.PI-1</i>	13.09263	13.64974	15.47704	16.11963	13.13147	16.33561
<i>Ca.di.AG.1-1</i>	0	0	15.83378	17.83745	0	0
<i>Ca.di.AG.2-1</i>	0	12.89666	14.63437	16.387	0	16.21231
<i>Ca.di.AG.2-2</i>	0	0	0	17.05277	0	16.54608
<i>Ca.di.AG.2-3</i>	0	12.65222	14.07727	16.18035	0	16.0959
<i>Ca.di.SEP.1</i>	0	16.03968	14.01099	14.35074	19.58233	16.27389
<i>Ca.di.SEP.2</i>	0	12.26175	16.87958	18.88419	0	17.93954
<i>Ca.di.SEP.3</i>	0	0	16.23744	18.02787	0	18.11092
<i>Ca.di.SEP.4</i>	0	18.70131	18.08396	12.64983	17.53087	14.85147
<i>Ca.di.AGL6</i>	0	12.78218	16.16474	16.91857	0	14.86212
<i>Ca.di.AGL12.1</i>	0	13.32766	0	0	11.2356	0
<i>Ca.di.AGL12.2</i>	13.35598	0	11.63102	11.16526	11.48193	11.36381
<i>Ca.di.AGL17.1</i>	0	0	0	0	0	11.53268
<i>Ca.di.AGL17.2</i>	0	0	0	0	0	14.85453
<i>Ca.di.AGL17.3</i>	12.61091	0	0	0	0	0
<i>Ca.di.GMM13</i>	0	0	15.24258	16.36077	0	0
<i>Ca.di.STMADS11.1</i>	19.20032	0	0	13.73159	0	0
<i>Ca.di.STMADS11.2</i>	17.95057	16.77333	16.07275	15.87993	15.91671	16.56197
<i>Ca.di.TM3.1-1</i>	17.06313	15.3234	13.90545	0	15.80493	11.11818
<i>Ca.di.TM3.1-2</i>	16.81681	15.1758	13.79644	11.3554	15.52459	10.89572
<i>Ca.di.TM3.1-3</i>	16.61806	0	0	0	15.11955	0
<i>Ca.di.TM3.2</i>	14.7168	0	0	0	0	12.30255
<i>Ca.di.TM3.3</i>	0	13.08831	0	0	12.72354	0
<i>Ca.di.OsMADS32</i>	0	0	0	12.23095	0	0
<i>Ca.di.FLC.1</i>	16.66877	16.92501	17.05326	14.73986	16.24827	13.68829
<i>Ca.di.FLC.2</i>	0	0	0	0	11.37349	11.17311
<i>Ca.di.FLC.3-1</i>	0	0	0	0	0	11.14431
<i>Ca.di.FLC.3-3</i>	13.64708	0	0	0	0	0
<i>Ca.di.FLC.4</i>	16.64173	14.93125	14.40592	13.87569	14.10874	12.90451
<i>Ca.di.MIKC*.P.2</i>	14.58958	14.33436	13.37441	0	13.75382	10.57386
<i>Ca.di.MIKC*.P.3</i>	0	0	0	0	0	16.25378
<i>Ca.di.typeI.Mα.1-1</i>	12.21542	13.56767	12.78554	11.84304	13.21626	10.1334
<i>Ca.di.typeI.Mα.1-2</i>	0	12.41564	12.3213	11.53089	13.35137	10.1426
<i>Ca.di.typeI.Mα.4</i>	0	0	0	12.22215	0	0
<i>Ca.di.typeI.Mγ.1</i>	13.89842	15.31246	14.24061	12.16426	15.0683	13.58075
<i>Ca.di.typeI.Mγ.2</i>	0	0	0	0	0	11.31949

APPENDICES FOR CHAPTER 4

- Appendix 1. Genes in locally collinear blocks (LCB) identified by progressiveMAUVE alignment for the chloroplast genomes of *C. lupulina* and related taxa
- Appendix 2. List of 60 protein-coding genes used for the phylogenetic analysis
- Appendix 3. List of the chloroplast genomes used for the phylogenetic analysis
- Appendix 4. List of oligonucleotide repeats in the chloroplast genome of *C. lupulina* and related taxa
- Appendix 5. List of tandem repeats in the chloroplast genome of *C. lupulina* and related taxa
- Appendix 6. Total number of perfect simple sequence repeats (SSRs) identified within the chloroplast genome of *C. lupulina* and related taxa

Appendix 1. Genes in locally collinear blocks (LCB) identified by progressiveMAUVE alignment for the chloroplast genomes of *C. lupulina* and related taxa

LCB	Genes
1	<i>psbA, trnK-UUU, matK</i>
2	Intergenic spacer region
3	<i>trnQ-UUG</i>
4	<i>psbK, psbI</i>
5	<i>trnS-GCU</i>
6	<i>trnR-UCU, atpA, atpF, atpH, atpI</i>
7	<i>rpoC1, rpoB, trnC-GCA, petN, psbM, trnD-GUC, trnY-GUA, trnE-UUC, psbD, psbC, trnS-UGA, psbZ, trnG-UCC, trnM-CAU</i>
8	<i>rps14, psaB, psaA</i>
9	<i>ycf3, trnS-GGA</i>
10	<i>rps4</i>
11	<i>trnT-UGU, trnL-UAA, trnF-GAA, ndhJ, ndhK, ndhC, trnV-UAC, trnM-CAU, atpE, atpB, rbcL, trnV-GAC</i>
12	Intergenic spacer region
13	<i>psaI, cemA, psbJ, psbL, psbF, psbE, petL, petG, trnW-CCA, trnP-UGG, psaJ, rpl33, rpl20, rps12</i>
14	<i>psbB, psbT, psbN, psbH, petB, petD</i>
15	<i>rps11</i>
16	<i>rpl36</i>
17	<i>rps8, rpl14, rpl16, rpl22, rps19</i>
18	<i>rps19, trnH-GUG, rpl2, trnI-CAU</i>
19	<i>trnL-CAA, ndhB, rps12</i>
20	<i>rrn16, trnI-GAU, trnA-UGC, rrn23, rrn4.5, rrn5, trnR-ACG, trnN-GUU</i>
21	<i>ndhF</i>
22	<i>rpl32, trnL-UAG, ccsA, psaC, ndhE</i>
23	<i>ndhG, ndhI, ndhA, ndhH, rps15</i>
24	Intergenic spacer region

* *accD, clpP, infA, ndhD, rpl23, petA, rpoA, rpoC2, rps2, rps3, rps7, rps16, rps18, rps19, ycf1, ycf2, ycf4, ycf68, trnG-GCC, trnT-GGU,* and *trnV-GAC* were not included in the LCBs because they were not present in all of the plastomes.

Appendix 2. List of 60 protein-coding genes used for the phylogenetic analysis

Gene name	Position		
<i>atpA</i>	1-1533	<i>psbI</i>	23935-24090
<i>atpB</i>	1534-3030	<i>psbJ</i>	24091-24219
<i>atpE</i>	3031-3447	<i>psbK</i>	24220-24405
<i>atpF</i>	3448-4059	<i>psbL</i>	24406-24522
<i>atpH</i>	4060-4305	<i>psbM</i>	24523-24627
<i>atpI</i>	4306-5052	<i>psbN</i>	24628-24759
<i>ccsA</i>	5053-6027	<i>psbT</i>	24760-24867
<i>cemA</i>	6028-6720	<i>psbZ</i>	24868-25056
<i>matK</i>	6721-8325	<i>rbcL</i>	25057-26505
<i>ndhC</i>	8326-8688	<i>rpl14</i>	26506-26877
<i>ndhE</i>	8689-8994	<i>rpl16</i>	26878-27315
<i>ndhF</i>	8995-11253	<i>rpl20</i>	27316-27705
<i>ndhJ</i>	11254-11745	<i>rpl22</i>	27706-28182
<i>petB</i>	11746-12450	<i>rpl32</i>	28183-28395
<i>petD</i>	12451-12945	<i>rpl33</i>	28396-28608
<i>petG</i>	12946-13059	<i>rpl36</i>	28609-28722
<i>petL</i>	13060-13155	<i>rpoB</i>	28723-31995
<i>petN</i>	13156-13245	<i>rpoC1</i>	31996-34116
<i>psaA</i>	13246-15498	<i>rps11</i>	34117-34626
<i>psaB</i>	15499-17706	<i>rps4</i>	34627-35265
<i>psaC</i>	17707-17952	<i>rps8</i>	35266-35676
<i>psaI</i>	17953-18063	<i>ycf3</i>	35677-36195
<i>psaJ</i>	18064-18198	<i>ndhA</i>	36196-37290
<i>psbA</i>	18199-19260	<i>ndhB</i>	37291-38835
<i>psbB</i>	19261-20790	<i>ndhG</i>	38836-39366
<i>psbC</i>	20791-22254	<i>ndhH</i>	39367-40554
<i>psbD</i>	22255-23334	<i>ndhI</i>	40555-41097
<i>psbE</i>	23335-23586	<i>rpl2</i>	41098-41922
<i>psbF</i>	23587-23706	<i>rps12</i>	41923-42321
<i>psbH</i>	23707-23934	<i>rps19</i>	42322-42645

Appendix 3. List of the chloroplast genomes used for the phylogenetic analysis

Family name	Taxon	GenBank accession number
Typhaceae	<i>Typha latifolia</i> L.	NC_013823
Eriocaulaceae	<i>Eriocaulon buergerianum</i> Körn.	NC_042211
Cyperaceae	<i>Hypolytrum nemorum</i> (Vahl) Spreng.	NC_036036
Cyperaceae	<i>Carex siderosticta</i> Hance	NC_027250
Cyperaceae	<i>Carex lupulina</i> Muhl. ex Willd.	this study
Joinvilleaceae	<i>Joinvillea ascendens</i> Gaudich. ex Brongn. & Gris	NC_031427
Poaceae	<i>Miscanthus sinensis</i> Andersson	NC_028721
Poaceae	<i>Zea mays</i> L.	NC_001666
Poaceae	<i>Oryza sativa</i> L.	NC_001320

Appendix 4. List of oligonucleotide repeats in the chloroplast genome of *C. lupulina* and related taxa

* *T. latifolia*

Repeat length (bp)	Repeat A start site	Repeat A location	Repeat A region	Repeat B start site	Repeat B location	Repeat B region	Repeat type		
30	3327	<i>tmk-UUU</i> intron	intron	LSC	9760	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	C
38	6148	<i>rps16-tmQ-UUG</i>	IGS	LSC	6154	<i>rps16-tmQ-UUG</i>	IGS	LSC	P
31	8396	<i>psbI-trnS-GCU/trnS-GCU</i>	IGS/CDS	LSC	38106	<i>psbC-trnS-UGA/trnS-UGA</i>	IGS/CDS	LSC	F
31	8396	<i>psbI-trnS-GCU/trnS-GCU</i>	IGS/rRNA	LSC	47765	<i>trnS-GGA/trnS-GGA-rps4</i>	rRNA/IGS	LSC	P
30	9003	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	123687	<i>psaC-ndhE</i>	IGS	SSC	C
31	9122	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9146	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	F
31	9132	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	69973	<i>psbE-petL</i>	IGS	LSC	R
37	9162	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9174	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	R
30	9163	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63479	<i>accD-psal</i>	IGS	LSC	F
31	9163	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63469	<i>accD-psal</i>	IGS	LSC	R
31	9163	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63468	<i>accD-psal</i>	IGS	LSC	P
30	9168	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9758	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	P
30	9170	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63368	<i>accD-psal</i>	IGS	LSC	C
31	9174	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9758	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	F
33	9182	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63432	<i>accD-psal</i>	IGS	LSC	P
30	9702	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9759	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	C
35	9747	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	68189	<i>petA-psbJ</i>	IGS	LSC	F
30	9762	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63453	<i>accD-psal</i>	IGS	LSC	R
30	9762	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9763	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	C
30	9762	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63452	<i>accD-psal</i>	IGS	LSC	P
32	9765	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	48841	<i>rps4-trnT-UGU</i>	IGS	LSC	C
30	9767	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63454	<i>accD-psal</i>	IGS	LSC	F
30	9767	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	48845	<i>rps4-trnT-UGU</i>	IGS	LSC	C
33	9767	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63455	<i>accD-psal</i>	IGS	LSC	C
31	9767	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	123732	<i>psaC-ndhE</i>	IGS	SSC	C
32	9767	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	123705	<i>psaC-ndhE</i>	IGS	SSC	P
32	9768	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63462	<i>accD-psal</i>	IGS	LSC	R
30	9769	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63485	<i>accD-psal</i>	IGS	LSC	C
31	9769	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	63463	<i>accD-psal</i>	IGS	LSC	P
30	9815	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9835	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	F
30	9819	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	87460	<i>rpl16</i> intron	intron	LSC	P
34	9822	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9827	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	R
30	9844	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	9866	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	F
31	9893	<i>trnS-GCU-trmG-GCC</i>	IGS	LSC	85756	<i>rps8-rpl14</i>	IGS	LSC	P
30	10948	<i>trmG-GCC</i>	CDS	LSC	39091	<i>trnG-UCC</i>	CDS	LSC	F
30	15344	<i>atpH-atpI</i>	IGS	LSC	15358	<i>atpH-atpI</i>	IGS	LSC	P
30	34303	<i>trnE-UUC-trmT-GGU</i>	IGS	LSC	118806	<i>ndhF-rpl32</i>	IGS	SSC	C
31	41320	<i>psaB</i>	CDS	LSC	43544	<i>psaA</i>	CDS	LSC	F
30	41361	<i>psaB</i>	CDS	LSC	43585	<i>psaA</i>	CDS	LSC	F
39	46259	<i>ycf3</i> intron	Intron	LSC	104411	<i>rps12-3-trnV-GAC</i>	IGS	IR	F
30	48843	<i>rps4-trnT-UGU</i>	IGS	LSC	63453	<i>accD-psal</i>	IGS	LSC	F
31	48843	<i>rps4-trnT-UGU</i>	IGS	LSC	63454	<i>accD-psal</i>	IGS	LSC	C
30	48845	<i>rps4-trnT-UGU</i>	IGS	LSC	63454	<i>accD-psal</i>	IGS	LSC	C
31	49407	<i>trnT-UGU-trmL-UAA</i>	IGS	LSC	63432	<i>accD-psal</i>	IGS	LSC	P
31	49430	<i>trnT-UGU-trmL-UAA</i>	IGS	LSC	49508	<i>trnT-UGU-trmL-UAA</i>	IGS	LSC	F
46	49433	<i>trnT-UGU-trmL-UAA</i>	IGS	LSC	49474	<i>trnT-UGU-trmL-UAA</i>	IGS	LSC	F
30	49473	<i>trnT-UGU-trmL-UAA</i>	IGS	LSC	49510	<i>trnT-UGU-trmL-UAA</i>	IGS	LSC	F
30	49495	<i>trnT-UGU-trmL-UAA</i>	IGS	LSC	63450	<i>accD-psal</i>	IGS	LSC	P
35	63448	<i>accD-psal</i>	IGS	LSC	63449	<i>accD-psal</i>	IGS	LSC	C
41	63466	<i>accD-psal</i>	IGS	LSC	63467	<i>accD-psal</i>	IGS	LSC	C
30	76580	<i>clpP</i> intron	Intron	LSC	76583	<i>clpP</i> intron	Intron	LSC	F
30	94500	<i>ycf2</i>	CDS	IR	94521	<i>ycf2</i>	CDS	IR	F
37	96900	<i>ycf2</i>	CDS	IR	96948	<i>ycf2</i>	CDS	IR	F
540	115531	<i>trnN-GUU-ndhF</i>	IGS	SSC	134642	<i>ycf1</i>	CDS	SSC	P
30	123785	<i>psaC-ndhE</i>	IGS	SSC	123804	<i>psaC-ndhE</i>	IGS	SSC	F

* F, forward repeats; P, palindromic repeats; R, reverse repeats; C, complementary repeats; CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

* *E. buergerianum*

Repeat length (bp)	Repeat A start site	Repeat A location	Repeat A region	Repeat B start site	Repeat B location	Repeat B region	Repeat type		
31	7196	<i>psbI-trnS-GGA/trnS-GGA</i>	IGS/rRNA	LSC	33918	<i>psbC-trnS-UGA/trnS-UGA</i>	IGS/rRNA	LSC	F

31	7196	<i>psbI-tms-GGA/tms-GGA</i>	IGS/tRNA	LSC	43350	<i>tms-GCU/tms-GCU-rps4</i>	tRNA/IGS	LSC	P
31	8831	<i>tms-GGA-tmR-UUCU</i>	IGS	LSC	34872	<i>tmG-UCC</i>	tRNA	LSC	F
32	33917	<i>psbC-tms-UGA/tms-UGA</i>	IGS/tRNA	LSC	43350	<i>tms-GCU/tms-GCU-rps4</i>	tRNA/IGS	LSC	P
38	36197	<i>psaB</i>	CDS	LSC	38433	<i>psaA</i>	CDS	LSC	F
30	37059	<i>psaB</i>	CDS	LSC	39283	<i>psaA</i>	CDS	LSC	F
35	41881	<i>ycf3</i> intron	Intron	LSC	117602	<i>ndhA</i> intron	Intron	SSC	F
36	41884	<i>ycf3</i> intron	Intron	LSC	96428	<i>rps12-3'-tmV-GAC</i>	IGS	IR	F
36	89203	<i>ycf2</i>	CDS	IR	89251	<i>ycf2</i>	CDS	IR	F
44	89204	<i>ycf2</i>	CDS	IR	89276	<i>ycf2</i>	CDS	IR	F
59	89216	<i>ycf2</i>	CDS	IR	89240	<i>ycf2</i>	CDS	IR	F
34	89222	<i>ycf2</i>	CDS	IR	89294	<i>ycf2</i>	CDS	IR	F
47	89222	<i>ycf2</i>	CDS	IR	89270	<i>ycf2</i>	CDS	IR	F
32	89240	<i>ycf2</i>	CDS	IR	89288	<i>ycf2</i>	CDS	IR	F
53	89240	<i>ycf2</i>	CDS	IR	89264	<i>ycf2</i>	CDS	IR	F
32	96428	<i>rps12-3'-tmV-GAC</i>	IGS	IR	117605	<i>ndhA</i> intron	Intron	SSC	F
33	96812	<i>rps12-3'-tmV-GAC</i>	IGS	IR	117960	<i>ndhA</i> intron	Intron	SSC	F

* F, forward repeats; P, palindromic repeats; R, reverse repeats; C, complementary repeats; CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

* *H. nemorum*

Repeat length (bp)	Repeat A start site	Repeat A location	Repeat A region	Repeat B start site	Repeat B location	Repeat B region	Repeat type		
30	5167	<i>rps16</i> intron	Intron	LSC	89206	<i>ycf3</i> intron	Intron	LSC	F
30	5167	<i>rps16</i> intron	Intron	LSC	107293	<i>ycf2-rps12_3'</i>	IGS	IR	P
30	6026	<i>rps16/rps16-tmQ-UUG</i>	CDS/IGS	LSC	99556	<i>tml-CAU-ycf2</i>	IGS	IR	P
32	6054	<i>rps16-tmQ-UUG</i>	IGS	LSC	99520	<i>tml-CAU-ycf2</i>	IGS	IR	P
33	6062	<i>rps16-tmQ-UUG</i>	IGS	LSC	99511	<i>tml-CAU-ycf2</i>	IGS	IR	P
58	6078	<i>rps16-tmQ-UUG</i>	IGS	LSC	99470	<i>tml-CAU-ycf2</i>	IGS	IR	P
64	6078	<i>rps16-tmQ-UUG</i>	IGS	LSC	122311	<i>tmN-GUU-ycf1</i>	IGS	IR	P
32	6133	<i>rps16-tmQ-UUG</i>	IGS	LSC	6149	<i>rps16-tmQ-UUG</i>	IGS	LSC	P
250	6346	<i>rps16-tmQ-UUG</i>	IGS	LSC	91043	<i>rpl36/rps8</i>	IGS	LSC	F
130	6464	<i>rps16-tmQ-UUG</i>	IGS	LSC	55783	<i>rps4-psa1</i>	IGS	LSC	P
82	6600	<i>rps16-tmQ-UUG</i>	IGS	LSC	91306	<i>rpl36/rps8</i>	IGS	LSC	F
50	6645	<i>rps16-tmQ-UUG</i>	IGS	LSC	91351	<i>rpl36/rps8</i>	IGS	LSC	F
45	6667	<i>rps16-tmQ-UUG</i>	IGS	LSC	91373	<i>rpl36/rps8</i>	IGS	LSC	F
60	6684	<i>rps16-tmQ-UUG</i>	IGS	LSC	91390	<i>rpl36/rps8</i>	IGS	LSC	F
53	6696	<i>rps16-tmQ-UUG</i>	IGS	LSC	91402	<i>rpl36/rps8</i>	IGS	LSC	F
51	6698	<i>rps16-tmQ-UUG</i>	IGS	LSC	55732	<i>rps4-psa1</i>	IGS	LSC	P
51	6714	<i>rps16-tmQ-UUG</i>	IGS	LSC	91420	<i>rpl36/rps8</i>	IGS	LSC	F
51	6714	<i>rps16-tmQ-UUG</i>	IGS	LSC	55716	<i>rps4-psa1</i>	IGS	LSC	P
31	6799	<i>rps16-tmQ-UUG</i>	IGS	LSC	91499	<i>rpl36/rps8</i>	IGS	LSC	F
31	6996	<i>rps16-tmQ-UUG</i>	IGS	LSC	7113	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
32	7028	<i>rps16-tmQ-UUG</i>	IGS	LSC	7133	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
34	7053	<i>rps16-tmQ-UUG</i>	IGS	LSC	42938	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	F
34	7053	<i>rps16-tmQ-UUG</i>	IGS	LSC	113126	<i>tmV-GAC-tm16</i>	IGS	IR	P
37	7296	<i>rps16-tmQ-UUG</i>	IGS	LSC	7520	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
40	7296	<i>rps16-tmQ-UUG</i>	IGS	LSC	7654	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
63	7319	<i>rps16-tmQ-UUG</i>	IGS	LSC	7422	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
47	7354	<i>rps16-tmQ-UUG</i>	IGS	LSC	7457	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
119	7479	<i>rps16-tmQ-UUG</i>	IGS	LSC	7669	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
69	7488	<i>rps16-tmQ-UUG</i>	IGS	LSC	7622	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
30	7574	<i>rps16-tmQ-UUG</i>	IGS	LSC	7804	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
65	7611	<i>rps16-tmQ-UUG</i>	IGS	LSC	7667	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
30	7766	<i>rps16-tmQ-UUG</i>	IGS	LSC	7806	<i>rps16-tmQ-UUG</i>	IGS	LSC	F
214	9095	<i>tmQ-UUG-psbK</i>	IGS	LSC	37682	<i>tmT-GGU-psbD</i>	IGS	LSC	F
31	10410	<i>psbI-tms-GCU/tms-GCU</i>	IGS/tRNA	LSC	41214	<i>psbC-tms-UGA/tms-UGA</i>	IGS/tRNA	LSC	F
31	10410	<i>psbI-tms-GCU/tms-GCU</i>	IGS/tRNA	LSC	90679	<i>tms-GGA/tms-GGA-rpl36</i>	tRNA/IGS	LSC	P
31	15826	<i>atpH-atpI</i>	IGS	LSC	18726	<i>atpI-rps2</i>	IGS	LSC	F
68	17593	<i>atpI-rps2</i>	IGS	LSC	17764	<i>atpI-rps2</i>	IGS	LSC	F
174	17595	<i>atpI-rps2</i>	IGS	LSC	18078	<i>atpI-rps2</i>	IGS	LSC	F
116	17595	<i>atpI-rps2</i>	IGS	LSC	17832	<i>atpI-rps2</i>	IGS	LSC	F
239	17709	<i>atpI-rps2</i>	IGS	LSC	17955	<i>atpI-rps2</i>	IGS	LSC	F
34	17928	<i>atpI-rps2</i>	IGS	LSC	18261	<i>atpI-rps2</i>	IGS	LSC	F
60	17955	<i>atpI-rps2</i>	IGS	LSC	18192	<i>atpI-rps2</i>	IGS	LSC	F
30	18289	<i>atpI-rps2</i>	IGS	LSC	80763	<i>rps11-rps14</i>	IGS	LSC	F
37	18296	<i>atpI-rps2</i>	IGS	LSC	80707	<i>rps11-rps14</i>	IGS	LSC	F
30	18304	<i>atpI-rps2</i>	IGS	LSC	80715	<i>rps11-rps14</i>	IGS	LSC	F
31	18842	<i>atpI-rps2</i>	IGS	LSC	18890	<i>atpI-rps2</i>	IGS	LSC	F
68	18931	<i>atpI-rps2</i>	IGS	LSC	82184	<i>rps11-rps14</i>	IGS	LSC	F
72	19119	<i>atpI-rps2</i>	IGS	LSC	81387	<i>rps11-rps14</i>	IGS	LSC	F
87	19133	<i>atpI-rps2</i>	IGS	LSC	81401	<i>rps11-rps14</i>	IGS	LSC	F
30	19193	<i>atpI-rps2</i>	IGS	LSC	81461	<i>rps11-rps14</i>	IGS	LSC	F
53	22588	<i>rpoC2</i>	CDS	LSC	22984	<i>rpoC2</i>	CDS	LSC	F

30	22612	<i>rpoC2</i>	CDS	LSC	22780	<i>rpoC2</i>	CDS	LSC	F
37	22612	<i>rpoC2</i>	CDS	LSC	22870	<i>rpoC2</i>	CDS	LSC	F
31	22623	<i>rpoC2</i>	CDS	LSC	22791	<i>rpoC2</i>	CDS	LSC	F
35	22623	<i>rpoC2</i>	CDS	LSC	22881	<i>rpoC2</i>	CDS	LSC	F
57	22623	<i>rpoC2</i>	CDS	LSC	22971	<i>rpoC2</i>	CDS	LSC	F
46	22643	<i>rpoC2</i>	CDS	LSC	22991	<i>rpoC2</i>	CDS	LSC	F
30	22660	<i>rpoC2</i>	CDS	LSC	22780	<i>rpoC2</i>	CDS	LSC	F
37	22660	<i>rpoC2</i>	CDS	LSC	22870	<i>rpoC2</i>	CDS	LSC	F
66	22671	<i>rpoC2</i>	CDS	LSC	22971	<i>rpoC2</i>	CDS	LSC	F
31	22671	<i>rpoC2</i>	CDS	LSC	22791	<i>rpoC2</i>	CDS	LSC	F
35	22671	<i>rpoC2</i>	CDS	LSC	22881	<i>rpoC2</i>	CDS	LSC	F
55	22691	<i>rpoC2</i>	CDS	LSC	22991	<i>rpoC2</i>	CDS	LSC	F
52	22749	<i>rpoC2</i>	CDS	LSC	23022	<i>rpoC2</i>	CDS	LSC	F
65	22757	<i>rpoC2</i>	CDS	LSC	22937	<i>rpoC2</i>	CDS	LSC	F
92	22757	<i>rpoC2</i>	CDS	LSC	22892	<i>rpoC2</i>	CDS	LSC	F
190	22767	<i>rpoC2</i>	CDS	LSC	22812	<i>rpoC2</i>	CDS	LSC	F
43	22767	<i>rpoC2</i>	CDS	LSC	23040	<i>rpoC2</i>	CDS	LSC	F
45	22810	<i>rpoC2</i>	CDS	LSC	23038	<i>rpoC2</i>	CDS	LSC	F
50	22850	<i>rpoC2</i>	CDS	LSC	23033	<i>rpoC2</i>	CDS	LSC	F
54	22891	<i>rpoC2</i>	CDS	LSC	23029	<i>rpoC2</i>	CDS	LSC	F
54	22936	<i>rpoC2</i>	CDS	LSC	23029	<i>rpoC2</i>	CDS	LSC	F
31	22975	<i>rpoC2</i>	CDS	LSC	23023	<i>rpoC2</i>	CDS	LSC	F
89	34666	<i>psbM-tmD-GUC</i>	IGS	LSC	81284	<i>rps11-rps14</i>	IGS	LSC	F
69	34690	<i>psbM-tmD-GUC</i>	IGS	LSC	81308	<i>rps11-rps14</i>	IGS	LSC	F
33	41209	<i>psbC-tms-UGA/tms-UGA</i>	IGS/tRNA	LSC	90682	<i>tms-GGA/tms-GGA-rpl36</i>	tRNA/IGS	LSC	P
30	42339	<i>trnG-GCC-trmM-CAU</i>	IGS	LSC	42340	<i>trnG-GCC-trmM-CAU</i>	IGS	LSC	R
37	42340	<i>trnG-GCC-trmM-CAU</i>	IGS	LSC	42342	<i>trnG-GCC-trmM-CAU</i>	IGS	LSC	F
30	42340	<i>trnG-GCC-trmM-CAU</i>	IGS	LSC	42341	<i>trnG-GCC-trmM-CAU</i>	IGS	LSC	R
38	42340	<i>trnG-GCC-trmM-CAU</i>	IGS	LSC	42341	<i>trnG-GCC-trmM-CAU</i>	IGS	LSC	C
565	42644	<i>trnM-CAU/trmM-CAU-tmV-GAC/tmV-GAC</i>	tRNA/IGS/tRNA	LSC	112889	<i>tmV-GAC/tmV-GAC-rm16/rm16</i>	tRNA/IGS/tRNA	IR	P
510	42742	<i>trnM-CAU-tmV-GAC/tmV-GAC/tmV-GAC-rbcL</i>	IGS/tRNA/IGS	LSC	112846	<i>tmL-CAA-tmV-GAC/tmV-GAC/tmV-GAC-rm16</i>	IGS/tRNA/IGS	IR	P
183	43252	<i>tmV-GAC-rbcL</i>	IGS	LSC	112654	<i>tmL-CAA-tmV-GAC</i>	IGS	IR	P
55	47722	<i>atpE-tmM-CAU</i>	IGS	LSC	56009	<i>rps4-psaI</i>	IGS	LSC	F
30	47750	<i>atpE-tmM-CAU</i>	IGS	LSC	56037	<i>rps4-psaI</i>	IGS	LSC	F
36	47762	<i>atpE-tmM-CAU</i>	IGS	LSC	56055	<i>rps4-psaI</i>	IGS	LSC	P
40	47822	<i>trnM-CAU</i>	tRNA	LSC	56094	<i>rps4-psaI</i>	IGS	LSC	F
31	47862	<i>trnM-CAU/trmM-CAU-tmV-UAC</i>	tRNA/IGS	LSC	56150	<i>rps4-psaI</i>	IGS	LSC	F
38	47893	<i>trnM-CAU-tmV-UAC</i>	IGS	LSC	56160	<i>rps4-psaI</i>	IGS	LSC	F
34	49271	<i>tmV-UAC-ndhC</i>	IGS	LSC	49272	<i>tmV-UAC-ndhC</i>	IGS	LSC	C
35	53691	<i>trnL-UAA-tmT-UGU</i>	IGS	LSC	62423	<i>psbE-petL</i>	IGS	LSC	P
100	53725	<i>trnL-UAA-tmT-UGU</i>	IGS	LSC	62339	<i>psbE-petL</i>	IGS	LSC	P
99	55684	<i>rps4-psaI</i>	IGS	LSC	91404	<i>rpl36-rps8</i>	IGS	LSC	P
130	55783	<i>rps4-psaI</i>	IGS	LSC	91161	<i>rpl36-rps8</i>	IGS	LSC	P
32	57809	<i>ycf4-cemA</i>	IGS	LSC	136194	<i>ndhF</i>	CDS	SSC	C
125	65609	<i>rpl33-rpl20</i>	IGS	LSC	99150	<i>tmL-CAU-ycf2</i>	IGS	IR	F
165	65609	<i>rpl33-rpl20</i>	IGS	LSC	121797	<i>tmN-GUU-ycf1</i>	IGS	IR	F
108	65666	<i>rpl33-rpl20</i>	IGS	LSC	121919	<i>tmN-GUU-ycf1</i>	IGS	IR	F
103	65696	<i>rpl33-rpl20</i>	IGS	LSC	121949	<i>tmN-GUU-ycf1</i>	IGS	IR	F
124	65731	<i>rpl33-rpl20</i>	IGS	LSC	99207	<i>tmL-CAU-ycf2</i>	IGS	IR	F
68	65731	<i>rpl33-rpl20</i>	IGS	LSC	121854	<i>tmN-GUU-ycf1</i>	IGS	IR	F
94	65761	<i>rpl33-rpl20</i>	IGS	LSC	122079	<i>tmN-GUU-ycf1</i>	IGS	IR	F
83	65780	<i>rpl33-rpl20</i>	IGS	LSC	99256	<i>tmL-CAU-ycf2</i>	IGS	IR	F
33	66121	<i>rpl33-rpl20</i>	IGS	LSC	66139	<i>rpl33-rpl20</i>	IGS	LSC	F
39	66124	<i>rpl33-rpl20</i>	IGS	LSC	66133	<i>rpl33-rpl20</i>	IGS	LSC	F
32	66441	<i>rpl33-rpl20</i>	IGS	LSC	66495	<i>rpl33-rpl20</i>	IGS	LSC	F
42	66458	<i>rpl33-rpl20</i>	IGS	LSC	66512	<i>rpl33-rpl20</i>	IGS	LSC	F
30	66460	<i>rpl33-rpl20</i>	IGS	LSC	66595	<i>rpl33-rpl20</i>	IGS	LSC	F
37	66460	<i>rpl33-rpl20</i>	IGS	LSC	66541	<i>rpl33-rpl20</i>	IGS	LSC	F
31	66476	<i>rpl33-rpl20</i>	IGS	LSC	66908	<i>rpl33-rpl20</i>	IGS	LSC	F
37	66514	<i>rpl33-rpl20</i>	IGS	LSC	66541	<i>rpl33-rpl20</i>	IGS	LSC	F
75	66530	<i>rpl33-rpl20</i>	IGS	LSC	66584	<i>rpl33-rpl20</i>	IGS	LSC	F
48	66557	<i>rpl33-rpl20</i>	IGS	LSC	66881	<i>rpl33-rpl20</i>	IGS	LSC	F
30	66561	<i>rpl33-rpl20</i>	IGS	LSC	66696	<i>rpl33-rpl20</i>	IGS	LSC	F
41	66561	<i>rpl33-rpl20</i>	IGS	LSC	66642	<i>rpl33-rpl20</i>	IGS	LSC	F
44	66561	<i>rpl33-rpl20</i>	IGS	LSC	66777	<i>rpl33-rpl20</i>	IGS	LSC	F
37	66568	<i>rpl33-rpl20</i>	IGS	LSC	66865	<i>rpl33-rpl20</i>	IGS	LSC	F
32	66576	<i>rpl33-rpl20</i>	IGS	LSC	66792	<i>rpl33-rpl20</i>	IGS	LSC	F
82	66611	<i>rpl33-rpl20</i>	IGS	LSC	66773	<i>rpl33-rpl20</i>	IGS	LSC	F
30	66611	<i>rpl33-rpl20</i>	IGS	LSC	66908	<i>rpl33-rpl20</i>	IGS	LSC	F
34	66611	<i>rpl33-rpl20</i>	IGS	LSC	66692	<i>rpl33-rpl20</i>	IGS	LSC	F
37	66611	<i>rpl33-rpl20</i>	IGS	LSC	66638	<i>rpl33-rpl20</i>	IGS	LSC	F
54	66611	<i>rpl33-rpl20</i>	IGS	LSC	66881	<i>rpl33-rpl20</i>	IGS	LSC	F
57	66626	<i>rpl33-rpl20</i>	IGS	LSC	66869	<i>rpl33-rpl20</i>	IGS	LSC	F
32	66636	<i>rpl33-rpl20</i>	IGS	LSC	66906	<i>rpl33-rpl20</i>	IGS	LSC	F
39	66636	<i>rpl33-rpl20</i>	IGS	LSC	66771	<i>rpl33-rpl20</i>	IGS	LSC	F
42	66636	<i>rpl33-rpl20</i>	IGS	LSC	66690	<i>rpl33-rpl20</i>	IGS	LSC	F
33	66642	<i>rpl33-rpl20</i>	IGS	LSC	66858	<i>rpl33-rpl20</i>	IGS	LSC	F
47	66673	<i>rpl33-rpl20</i>	IGS	LSC	66754	<i>rpl33-rpl20</i>	IGS	LSC	F
40	66680	<i>rpl33-rpl20</i>	IGS	LSC	66788	<i>rpl33-rpl20</i>	IGS	LSC	F
32	66687	<i>rpl33-rpl20</i>	IGS	LSC	66903	<i>rpl33-rpl20</i>	IGS	LSC	F
33	66714	<i>rpl33-rpl20</i>	IGS	LSC	66741	<i>rpl33-rpl20</i>	IGS	LSC	F

58	66733	<i>rpl33-rpl20</i>	IGS	LSC	66841	<i>rpl33-rpl20</i>	IGS	LSC	F
33	66741	<i>rpl33-rpl20</i>	IGS	LSC	66822	<i>rpl33-rpl20</i>	IGS	LSC	F
49	66761	<i>rpl33-rpl20</i>	IGS	LSC	66788	<i>rpl33-rpl20</i>	IGS	LSC	F
59	66768	<i>rpl33-rpl20</i>	IGS	LSC	66876	<i>rpl33-rpl20</i>	IGS	LSC	F
45	66792	<i>rpl33-rpl20</i>	IGS	LSC	66873	<i>rpl33-rpl20</i>	IGS	LSC	F
33	66804	<i>rpl33-rpl20</i>	IGS	LSC	66858	<i>rpl33-rpl20</i>	IGS	LSC	F
43	66865	<i>rpl33-rpl20</i>	IGS	LSC	66892	<i>rpl33-rpl20</i>	IGS	LSC	F
33	70107	<i>clpP</i> intron	Intron	LSC	99334	<i>trnI-CAU-yef2</i>	IGS	IR	P
170	70369	<i>clpP</i> intron/ <i>cloP</i>	Intron/CDS	LSC	98961	<i>trnI-CAU-yef2</i>	IGS	IR	P
157	70545	<i>clpP/clpP-psbB</i>	CDS/IGS	LSC	98806	<i>trnI-CAU-yef2</i>	IGS	IR	P
39	70701	<i>clpP-psbB</i>	IGS	LSC	121437	<i>trnN-GUU-yef1</i>	IGS	IR	P
524	70701	<i>clpP-psbB/psbB</i>	IGS/CDS	LSC	98318	<i>trnI-CAU-yef2</i>	IGS	IR	P
31	71199	<i>psbB</i>	CDS	LSC	98313	<i>trnI-CAU-yef2</i>	IGS	IR	P
34	76605	<i>petD-rpoA</i>	IGS	LSC	76650	<i>petD-rpoA</i>	IGS	LSC	P
30	78336	<i>rps11</i>	CDS	LSC	78384	<i>rps11</i>	CDS	LSC	F
47	79628	<i>rps11-rps14</i>	IGS	LSC	79637	<i>rps11-rps14</i>	IGS	LSC	F
35	79730	<i>rps11-rps14</i>	IGS	LSC	79739	<i>rps11-rps14</i>	IGS	LSC	F
30	79739	<i>rps11-rps14</i>	IGS	LSC	79748	<i>rps11-rps14</i>	IGS	LSC	F
80	79940	<i>rps11-rps14</i>	IGS	LSC	80030	<i>rps11-rps14</i>	IGS	LSC	F
40	79940	<i>rps11-rps14</i>	IGS	LSC	79970	<i>rps11-rps14</i>	IGS	LSC	F
50	79940	<i>rps11-rps14</i>	IGS	LSC	80000	<i>rps11-rps14</i>	IGS	LSC	F
53	79940	<i>rps11-rps14</i>	IGS	LSC	80060	<i>rps11-rps14</i>	IGS	LSC	F
64	79951	<i>rps11-rps14</i>	IGS	LSC	80011	<i>rps11-rps14</i>	IGS	LSC	F
49	79961	<i>rps11-rps14</i>	IGS	LSC	79991	<i>rps11-rps14</i>	IGS	LSC	F
92	79991	<i>rps11-rps14</i>	IGS	LSC	80021	<i>rps11-rps14</i>	IGS	LSC	F
54	79991	<i>rps11-rps14</i>	IGS	LSC	80051	<i>rps11-rps14</i>	IGS	LSC	F
39	80011	<i>rps11-rps14</i>	IGS	LSC	80071	<i>rps11-rps14</i>	IGS	LSC	F
30	80700	<i>rps11-rps14</i>	IGS	LSC	80763	<i>rps11-rps14</i>	IGS	LSC	F
34	81554	<i>rps11-rps14</i>	IGS	LSC	93651	<i>rpl16</i> intron	intron	LSC	F
30	81563	<i>rps11-rps14</i>	IGS	LSC	93660	<i>rpl16</i> intron	intron	LSC	F
45	81588	<i>rps11-rps14</i>	IGS	LSC	93672	<i>rpl16</i> intron	intron	LSC	F
68	81612	<i>rps11-rps14</i>	IGS	LSC	93696	<i>rpl16</i> intron	intron	LSC	F
136	81683	<i>rps11-rps14</i>	IGS	LSC	93760	<i>rpl16</i> intron	intron	LSC	F
116	81726	<i>rps11-rps14</i>	IGS	LSC	93803	<i>rpl16</i> intron/ <i>rpl16/rpl16-rps3</i>	Intron/CDS/IGS	LSC	F
38	89200	<i>yef3</i> intron	Intron	LSC	107291	<i>yef2-rps12_3'</i>	IGS	IR	P
353	98803	<i>trnI-CAU-yef2</i>	IGS	IR	121437	<i>trnN-GUU-yef1</i>	IGS	IR	F
149	99126	<i>trnI-CAU-yef2</i>	IGS	IR	121773	<i>trnN-GUU-yef1</i>	IGS	IR	F
263	99207	<i>trnI-CAU-yef2</i>	IGS	IR	122049	<i>trnN-GUU-yef1</i>	IGS	IR	F
68	99207	<i>trnI-CAU-yef2</i>	IGS	IR	121919	<i>trnN-GUU-yef1</i>	IGS	IR	F
156	99470	<i>trnI-CAU-yef2</i>	IGS	IR	122317	<i>trnN-GUU-yef1</i>	IGS	IR	F
60	99606	<i>trnI-CAU-yef2/yef2</i>	IGS/CDS	IR	122467	<i>trnN-GUU-yef1/yef1</i>	IGS/CDS	IR	F
58	105445	<i>yef2</i>	CDS	IR	105490	<i>yef2</i>	CDS	IR	F
86	105460	<i>yef2</i>	CDS	IR	105490	<i>yef2</i>	CDS	IR	F
31	105475	<i>yef2</i>	CDS	IR	105550	<i>yef2</i>	CDS	IR	F
71	105490	<i>yef2</i>	CDS	IR	105505	<i>yef2</i>	CDS	IR	F
31	105505	<i>yef2</i>	CDS	IR	105550	<i>yef2</i>	CDS	IR	F
33	108458	<i>rps7</i>	CDS	IR	108465	<i>rps7</i>	CDS	IR	R
35	121310	<i>trnN-GUU-yef1</i>	IGS	IR	121354	<i>trnN-GUU-yef1</i>	IGS	IR	F
33	124139	<i>yef1</i>	CDS	IR	124145	<i>yef1</i>	CDS	IR	R
30	124152	<i>yef1</i>	CDS	IR	124153	<i>yef1</i>	CDS	IR	R
31	124589	<i>yef1</i>	CDS	IR	124628	<i>yef1</i>	CDS	IR	F
42	126853	<i>yef1</i>	CDS	IR	126937	<i>yef1</i>	CDS	IR	F
89	126854	<i>yef1</i>	CDS	IR	126866	<i>yef1</i>	CDS	IR	F
35	126854	<i>yef1</i>	CDS	IR	126950	<i>yef1</i>	CDS	IR	F
53	126866	<i>yef1</i>	CDS	IR	126914	<i>yef1</i>	CDS	IR	F
89	126872	<i>yef1</i>	CDS	IR	126884	<i>yef1</i>	CDS	IR	F
41	126920	<i>yef1</i>	CDS	IR	126956	<i>yef1</i>	CDS	IR	F
62	126926	<i>yef1</i>	CDS	IR	126950	<i>yef1</i>	CDS	IR	F
56	126944	<i>yef1</i>	CDS	IR	126968	<i>yef1</i>	CDS	IR	F
86	126950	<i>yef1</i>	CDS	IR	126962	<i>yef1</i>	CDS	IR	F
30	127242	<i>yef1</i>	CDS	IR	127362	<i>yef1</i>	CDS	IR	F
133	127244	<i>yef1</i>	CDS	IR	127259	<i>yef1</i>	CDS	IR	F
30	128036	<i>yef1</i>	CDS	IR	128081	<i>yef1</i>	CDS	IR	F
59	128037	<i>yef1</i>	CDS	IR	128052	<i>yef1</i>	CDS	IR	F
30	128037	<i>yef1</i>	CDS	IR	128139	<i>yef1</i>	CDS	IR	F
37	128045	<i>yef1</i>	CDS	IR	128132	<i>yef1</i>	CDS	IR	F
37	128060	<i>yef1</i>	CDS	IR	128132	<i>yef1</i>	CDS	IR	F
36	128075	<i>yef1</i>	CDS	IR	128132	<i>yef1</i>	CDS	IR	F
30	142168	<i>ndhE-ndhG</i>	IGS	SSC	142190	<i>ndhE-ndhG</i>	IGS	SSC	F

* F, forward repeats; P, palindromic repeats; R, reverse repeats; C, complementary repeats; CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

* *C. siderosticta*

Repeat length (bp)	Repeat A start site	Repeat A location	Repeat A region	Repeat B start site	Repeat B location	Repeat B region	Repeat type		
35	1447	<i>psbA-tmK-UUU</i>	IGS	LSC	1625	<i>psbA-tmK-UUU</i>	IGS	LSC	F
32	1502	<i>psbA-tmK-UUU</i>	IGS	LSC	1625	<i>psbA-tmK-UUU</i>	IGS	LSC	F
90	4658	<i>tmK-UUU-rps2</i>	IGS	LSC	122031	<i>tml-CAA-rm16</i>	IGS	IR	P
30	4723	<i>tmK-UUU-rps2</i>	IGS	LSC	122026	<i>tml-CAA-rm16</i>	IGS	IR	P
47	4820	<i>tmK-UUU-rps2</i>	IGS	LSC	6634	<i>tmK-UUU-rps2</i>	IGS	LSC	F
219	4849	<i>tmK-UUU-rps2</i>	IGS	LSC	6679	<i>tmK-UUU-rps2</i>	IGS	LSC	F
30	4872	<i>tmK-UUU-rps2</i>	IGS	LSC	6718	<i>tmK-UUU-rps2</i>	IGS	LSC	P
32	4887	<i>tmK-UUU-rps2</i>	IGS	LSC	6701	<i>tmK-UUU-rps2</i>	IGS	LSC	P
32	5083	<i>tmK-UUU-rps2</i>	IGS	LSC	53203	<i>psbK-rps11</i>	IGS	LSC	P
42	5171	<i>tmK-UUU-rps2</i>	IGS	LSC	118961	<i>tml-CAA-rm16</i>	IGS	IR	P
34	5287	<i>tmK-UUU-rps2</i>	IGS	LSC	118844	<i>tml-CAA-rm16</i>	IGS	IR	P
37	5287	<i>tmK-UUU-rps2</i>	IGS	LSC	135383	<i>tmN-GUU-rps15</i>	IGS	IR	P
32	5295	<i>tmK-UUU-rps2</i>	IGS	LSC	135380	<i>tmN-GUU-rps15</i>	IGS	IR	P
36	5365	<i>tmK-UUU-rps2</i>	IGS	LSC	138279	<i>tmN-GUU-rps15</i>	IGS	IR	P
34	5461	<i>tmK-UUU-rps2</i>	IGS	LSC	5909	<i>tmK-UUU-rps2</i>	IGS	LSC	F
34	5461	<i>tmK-UUU-rps2</i>	IGS	LSC	138291	<i>tmN-GUU-rps15</i>	IGS	IR	P
33	5501	<i>tmK-UUU-rps2</i>	IGS	LSC	138300	<i>tmN-GUU-rps15</i>	IGS	IR	P
32	5537	<i>tmK-UUU-rps2</i>	IGS	LSC	138265	<i>tmN-GUU-rps15</i>	IGS	IR	P
33	5548	<i>tmK-UUU-rps2</i>	IGS	LSC	138253	<i>tmN-GUU-rps15</i>	IGS	IR	P
34	5551	<i>tmK-UUU-rps2</i>	IGS	LSC	14187	<i>rpoC2-rpoC1</i>	IGS	LSC	F
43	5624	<i>tmK-UUU-rps2</i>	IGS	LSC	14259	<i>rpoC2-rpoC1</i>	IGS	LSC	F
56	5624	<i>tmK-UUU-rps2</i>	IGS	LSC	138155	<i>tmN-GUU-rps15</i>	IGS	IR	P
34	5646	<i>tmK-UUU-rps2</i>	IGS	LSC	14281	<i>rpoC2-rpoC1</i>	IGS	LSC	F
39	5646	<i>tmK-UUU-rps2</i>	IGS	LSC	138150	<i>tmN-GUU-rps15</i>	IGS	IR	P
37	5654	<i>tmK-UUU-rps2</i>	IGS	LSC	14289	<i>rpoC2-rpoC1</i>	IGS	LSC	F
39	5670	<i>tmK-UUU-rps2</i>	IGS	LSC	14305	<i>rpoC2-rpoC1</i>	IGS	LSC	F
30	5670	<i>tmK-UUU-rps2</i>	IGS	LSC	138135	<i>tmN-GUU-rps15</i>	IGS	IR	P
39	5681	<i>tmK-UUU-rps2</i>	IGS	LSC	105148	<i>rpl2-tml-CAU</i>	IGS	IR	F
59	5681	<i>tmK-UUU-rps2</i>	IGS	LSC	14316	<i>rpoC2-rpoC1</i>	IGS	LSC	F
55	5681	<i>tmK-UUU-rps2</i>	IGS	LSC	138099	<i>tmN-GUU-rps15</i>	IGS	IR	P
31	5693	<i>tmK-UUU-rps2</i>	IGS	LSC	105160	<i>rpl2-tml-CAU</i>	IGS	IR	F
54	5693	<i>tmK-UUU-rps2</i>	IGS	LSC	14328	<i>rpoC2-rpoC1</i>	IGS	LSC	F
43	5704	<i>tmK-UUU-rps2</i>	IGS	LSC	138088	<i>tmN-GUU-rps15</i>	IGS	IR	P
36	5728	<i>tmK-UUU-rps2</i>	IGS	LSC	14345	<i>rpoC2-rpoC1</i>	IGS	LSC	F
36	5728	<i>tmK-UUU-rps2</i>	IGS	LSC	138089	<i>tmN-GUU-rps15</i>	IGS	IR	P
92	5754	<i>tmK-UUU-rps2</i>	IGS	LSC	137989	<i>tmN-GUU-rps15</i>	IGS	IR	P
86	5837	<i>tmK-UUU-rps2</i>	IGS	LSC	137903	<i>tmN-GUU-rps15</i>	IGS	IR	P
131	5923	<i>tmK-UUU-rps2</i>	IGS	LSC	137711	<i>tmN-GUU-rps15</i>	IGS	IR	P
31	6026	<i>tmK-UUU-rps2</i>	IGS	LSC	137708	<i>tmN-GUU-rps15</i>	IGS	IR	P
48	6055	<i>tmK-UUU-rps2</i>	IGS	LSC	8521	<i>rpoC2</i>	CDS	LSC	F
30	6094	<i>tmK-UUU-rps2</i>	IGS	LSC	8807	<i>rpoC2</i>	CDS	LSC	F
41	6590	<i>tmK-UUU-rps2</i>	IGS	LSC	7980	<i>rps2-rpoC2</i>	IGS	LSC	F
50	6897	<i>tmK-UUU-rps2</i>	IGS	LSC	122302	<i>tml-CAA-rm16</i>	IGS	IR	P
45	6917	<i>tmK-UUU-rps2</i>	IGS	LSC	52469	<i>psbK-rps11</i>	IGS	LSC	P
48	6936	<i>tmK-UUU-rps2</i>	IGS	LSC	122265	<i>tml-CAA-rm16</i>	IGS	IR	P
51	6949	<i>tmK-UUU-rps2</i>	IGS	LSC	122249	<i>tml-CAA-rm16</i>	IGS	IR	P
43	6975	<i>tmK-UUU-rps2</i>	IGS	LSC	122231	<i>tml-CAA-rm16</i>	IGS	IR	P
41	6985	<i>tmK-UUU-rps2</i>	IGS	LSC	122223	<i>tml-CAA-rm16</i>	IGS	IR	P
31	7001	<i>tmK-UUU-rps2</i>	IGS	LSC	122217	<i>tml-CAA-rm16</i>	IGS	IR	P
74	7043	<i>tmK-UUU-rps2</i>	IGS	LSC	122128	<i>tml-CAA-rm16</i>	IGS	IR	P
40	10502	<i>rpoC2</i>	CDS	LSC	11138	<i>rpoC2</i>	CDS	LSC	F
43	10507	<i>rpoC2</i>	CDS	LSC	10555	<i>rpoC2</i>	CDS	LSC	F
30	10515	<i>rpoC2</i>	CDS	LSC	11151	<i>rpoC2</i>	CDS	LSC	F
32	10516	<i>rpoC2</i>	CDS	LSC	10657	<i>rpoC2</i>	CDS	LSC	F
30	10518	<i>rpoC2</i>	CDS	LSC	11199	<i>rpoC2</i>	CDS	LSC	F
36	10518	<i>rpoC2</i>	CDS	LSC	10611	<i>rpoC2</i>	CDS	LSC	F
41	10519	<i>rpoC2</i>	CDS	LSC	10567	<i>rpoC2</i>	CDS	LSC	F
41	10520	<i>rpoC2</i>	CDS	LSC	10847	<i>rpoC2</i>	CDS	LSC	F
43	10520	<i>rpoC2</i>	CDS	LSC	10799	<i>rpoC2</i>	CDS	LSC	F
32	10529	<i>rpoC2</i>	CDS	LSC	10622	<i>rpoC2</i>	CDS	LSC	F
39	10540	<i>rpoC2</i>	CDS	LSC	10867	<i>rpoC2</i>	CDS	LSC	F
37	10550	<i>rpoC2</i>	CDS	LSC	10829	<i>rpoC2</i>	CDS	LSC	F
35	10555	<i>rpoC2</i>	CDS	LSC	10648	<i>rpoC2</i>	CDS	LSC	F
40	10568	<i>rpoC2</i>	CDS	LSC	10847	<i>rpoC2</i>	CDS	LSC	F
32	10580	<i>rpoC2</i>	CDS	LSC	10625	<i>rpoC2</i>	CDS	LSC	F
35	10600	<i>rpoC2</i>	CDS	LSC	11188	<i>rpoC2</i>	CDS	LSC	F
31	10610	<i>rpoC2</i>	CDS	LSC	11198	<i>rpoC2</i>	CDS	LSC	F
30	10611	<i>rpoC2</i>	CDS	LSC	11154	<i>rpoC2</i>	CDS	LSC	F
41	10613	<i>rpoC2</i>	CDS	LSC	10799	<i>rpoC2</i>	CDS	LSC	F
32	10625	<i>rpoC2</i>	CDS	LSC	10811	<i>rpoC2</i>	CDS	LSC	F
51	10625	<i>rpoC2</i>	CDS	LSC	10859	<i>rpoC2</i>	CDS	LSC	F
35	10632	<i>rpoC2</i>	CDS	LSC	10725	<i>rpoC2</i>	CDS	LSC	F
49	10633	<i>rpoC2</i>	CDS	LSC	10867	<i>rpoC2</i>	CDS	LSC	F
38	10655	<i>rpoC2</i>	CDS	LSC	10748	<i>rpoC2</i>	CDS	LSC	F
41	10660	<i>rpoC2</i>	CDS	LSC	10987	<i>rpoC2</i>	CDS	LSC	F

31	10670	<i>rpoC2</i>	CDS	LSC	10763	<i>rpoC2</i>	CDS	LSC	F
40	10677	<i>rpoC2</i>	CDS	LSC	11004	<i>rpoC2</i>	CDS	LSC	F
40	10705	<i>rpoC2</i>	CDS	LSC	11032	<i>rpoC2</i>	CDS	LSC	F
31	10719	<i>rpoC2</i>	CDS	LSC	10953	<i>rpoC2</i>	CDS	LSC	F
34	10728	<i>rpoC2</i>	CDS	LSC	10962	<i>rpoC2</i>	CDS	LSC	F
31	10729	<i>rpoC2</i>	CDS	LSC	10870	<i>rpoC2</i>	CDS	LSC	F
33	10736	<i>rpoC2</i>	CDS	LSC	10970	<i>rpoC2</i>	CDS	LSC	F
32	10753	<i>rpoC2</i>	CDS	LSC	11155	<i>rpoC2</i>	CDS	LSC	F
45	10753	<i>rpoC2</i>	CDS	LSC	10987	<i>rpoC2</i>	CDS	LSC	F
51	10763	<i>rpoC2</i>	CDS	LSC	10997	<i>rpoC2</i>	CDS	LSC	F
58	10763	<i>rpoC2</i>	CDS	LSC	11165	<i>rpoC2</i>	CDS	LSC	F
37	10777	<i>rpoC2</i>	CDS	LSC	10918	<i>rpoC2</i>	CDS	LSC	F
30	10787	<i>rpoC2</i>	CDS	LSC	10928	<i>rpoC2</i>	CDS	LSC	F
34	10787	<i>rpoC2</i>	CDS	LSC	11021	<i>rpoC2</i>	CDS	LSC	F
40	10787	<i>rpoC2</i>	CDS	LSC	11189	<i>rpoC2</i>	CDS	LSC	F
30	10799	<i>rpoC2</i>	CDS	LSC	11201	<i>rpoC2</i>	CDS	LSC	F
32	10808	<i>rpoC2</i>	CDS	LSC	10856	<i>rpoC2</i>	CDS	LSC	F
32	10870	<i>rpoC2</i>	CDS	LSC	11056	<i>rpoC2</i>	CDS	LSC	F
44	10892	<i>rpoC2</i>	CDS	LSC	10985	<i>rpoC2</i>	CDS	LSC	F
33	10918	<i>rpoC2</i>	CDS	LSC	11179	<i>rpoC2</i>	CDS	LSC	F
43	10918	<i>rpoC2</i>	CDS	LSC	11011	<i>rpoC2</i>	CDS	LSC	F
39	10940	<i>rpoC2</i>	CDS	LSC	11033	<i>rpoC2</i>	CDS	LSC	F
32	10987	<i>rpoC2</i>	CDS	LSC	11155	<i>rpoC2</i>	CDS	LSC	F
57	11004	<i>rpoC2</i>	CDS	LSC	11172	<i>rpoC2</i>	CDS	LSC	F
30	11154	<i>rpoC2</i>	CDS	LSC	11199	<i>rpoC2</i>	CDS	LSC	F
33	13362	<i>rpoC2-rpoC1</i>	IGS	LSC	102901	<i>rps19-tmH-GUG</i>	IGS	IR	F
36	13362	<i>rpoC2-rpoC1</i>	IGS	LSC	108248	<i>tnl-CAU-rps12_3'</i>	IGS	IR	P
33	13362	<i>rpoC2-rpoC1</i>	IGS	LSC	70825	<i>rps14-tmQ-UUG</i>	IGS	LSC	P
60	13717	<i>rpoC2-rpoC1</i>	IGS	LSC	104529	<i>rpl2/rpl2-tmI-CAU</i>	CDS/IGS	IR	F
52	13775	<i>rpoC2-rpoC1</i>	IGS	LSC	104597	<i>rpl2-tmI-CAU</i>	IGS	IR	F
528	13827	<i>rpoC2-rpoC1</i>	IGS	LSC	104659	<i>rpl2-tmI-CAU</i>	IGS	IR	F
31	14154	<i>rpoC2-rpoC1</i>	IGS	LSC	138285	<i>tmN-GUU-rps15</i>	IGS	IR	P
61	14187	<i>rpoC2-rpoC1</i>	IGS	LSC	138222	<i>tmN-GUU-rps15</i>	IGS	IR	P
82	14206	<i>rpoC2-rpoC1</i>	IGS	LSC	138182	<i>tmN-GUU-rps15</i>	IGS	IR	P
96	14224	<i>rpoC2-rpoC1</i>	IGS	LSC	138150	<i>tmN-GUU-rps15</i>	IGS	IR	P
89	14237	<i>rpoC2-rpoC1</i>	IGS	LSC	138144	<i>tmN-GUU-rps15</i>	IGS	IR	P
46	14289	<i>rpoC2-rpoC1</i>	IGS	LSC	138135	<i>tmN-GUU-rps15</i>	IGS	IR	P
43	14328	<i>rpoC2-rpoC1</i>	IGS	LSC	138099	<i>tmN-GUU-rps15</i>	IGS	IR	P
49	14339	<i>rpoC2-rpoC1</i>	IGS	LSC	138082	<i>tmN-GUU-rps15</i>	IGS	IR	P
30	14371	<i>rpoC2-rpoC1</i>	IGS	LSC	138060	<i>tmN-GUU-rps15</i>	IGS	IR	P
55	14401	<i>rpoC2-rpoC1</i>	IGS	LSC	125481	<i>rm16</i>	rRNA	IR	P
102	14405	<i>rpoC2-rpoC1</i>	IGS	LSC	31559	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	F
115	14428	<i>rpoC2-rpoC1</i>	IGS	LSC	31582	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	F
30	14428	<i>rpoC2-rpoC1</i>	IGS	LSC	125479	<i>rm16</i>	rRNA	IR	P
88	14455	<i>rpoC2-rpoC1</i>	IGS	LSC	125385	<i>tml-CAA-rm16/rm16</i>	IGS/rRNA	IR	P
49	21225	<i>rpoB-tmC-GCA</i>	IGS	LSC	43504	<i>atpI</i>	CDS	LSC	P
60	21233	<i>rpoB-tmC-GCA</i>	IGS	LSC	43485	<i>atpI</i>	CDS	LSC	P
53	21244	<i>rpoB-tmC-GCA</i>	IGS	LSC	43481	<i>atpI</i>	CDS	LSC	P
69	21257	<i>rpoB-tmC-GCA</i>	IGS	LSC	43452	<i>atpI</i>	CDS	LSC	P
62	21275	<i>rpoB-tmC-GCA</i>	IGS	LSC	43441	<i>atpI</i>	CDS	LSC	P
35	21345	<i>rpoB-tmC-GCA</i>	IGS	LSC	43402	<i>tmT-UGU-atpI/atpI</i>	IGS/CDS	LSC	P
31	26411	<i>tmE-UUC-psbD</i>	IGS	LSC	52505	<i>psbK-rps11</i>	IGS	LSC	P
33	26430	<i>tmE-UUC-psbD</i>	IGS	LSC	122302	<i>tml-CAA-rm16</i>	IGS	IR	P
30	26454	<i>tmE-UUC-psbD</i>	IGS	LSC	52463	<i>psbK-rps11</i>	IGS	LSC	P
72	31235	<i>tmM-CAU-tmM-CAU</i>	IGS	LSC	125628	<i>rm16</i>	rRNA	IR	P
156	31391	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	125544	<i>rm16</i>	rRNA	IR	P
155	31403	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	125533	<i>rm16</i>	rRNA	IR	P
190	31418	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	125483	<i>rm16</i>	rRNA	IR	P
157	31609	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	125316	<i>tml-CAA-rm16/rm16</i>	IGS/rRNA	IR	P
113	31765	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	125203	<i>tml-CAA-rm16</i>	IGS	IR	P
41	36445	<i>tmM-CAU</i>	tRNA	LSC	75577	<i>rps4-psaI</i>	IGS	LSC	F
50	36470	<i>tmM-CAU/tmM-CAU-tmV-UAC</i>	tRNA/IGS	LSC	75602	<i>rps4-psaI</i>	IGS	LSC	F
37	36489	<i>tmM-CAU/tmM-CAU-tmV-UAC</i>	tRNA/IGS	LSC	75621	<i>rps4-psaI</i>	IGS	LSC	F
34	42284	<i>tmT-UGU-atpI</i>	IGS	LSC	85281	<i>rpl33-rpl20</i>	IGS	LSC	F
77	42528	<i>tmT-UGU-atpI</i>	IGS	LSC	51728	<i>psbI-psbK</i>	IGS	LSC	P
30	42602	<i>tmT-UGU-atpI</i>	IGS	LSC	51707	<i>psbI-psbK</i>	IGS	LSC	P
31	42625	<i>tmT-UGU-atpI</i>	IGS	LSC	106334	<i>tnl-CAU-rps12_3'</i>	IGS	IR	F
50	42650	<i>tmT-UGU-atpI</i>	IGS	LSC	106358	<i>tnl-CAU-rps12_3'</i>	IGS	IR	F
41	42769	<i>tmT-UGU-atpI</i>	IGS	LSC	55042	<i>rps11-petD</i>	IGS	LSC	F
41	42769	<i>tmT-UGU-atpI</i>	IGS	LSC	87314	<i>rpl20-rps12_5'</i>	IGS	LSC	P
34	43785	<i>atpI</i>	CDS	LSC	133524	<i>tmR-ACG-tmN-GUU</i>	IGS	IR	P
84	43810	<i>atpI</i>	CDS	LSC	133449	<i>tmR-ACG-tmN-GUU</i>	IGS	IR	P
173	43822	<i>atpI</i>	CDS	LSC	133348	<i>tmR-ACG-tmN-GUU</i>	IGS	IR	P
50	44178	<i>atpI-atpH</i>	IGS	LSC	91679	<i>rps12_5'-ycf3</i>	IGS	LSC	P
44	44252	<i>atpI-atpH</i>	IGS	LSC	64264	<i>psbB-psaA</i>	IGS	LSC	F
87	44424	<i>atpI-atpH</i>	IGS	LSC	64431	<i>psbB-psaA</i>	IGS	LSC	F
32	44495	<i>atpI-atpH</i>	IGS	LSC	85313	<i>rpl33-rpl20</i>	IGS	LSC	C
79	48683	<i>atpA-tmR-UCU/tmR-UCU</i>	IGS/tRNA	LSC	64113	<i>psbB-psaA</i>	IGS	LSC	F
49	48722	<i>atpA-tmR-UCU/tmR-UCU</i>	IGS/tRNA	LSC	64152	<i>psbB-psaA</i>	IGS	LSC	F
68	48740	<i>tmR-UCU/tmR-UCU-tmG-GCC</i>	tRNA/IGS	LSC	64170	<i>psbB-psaA</i>	IGS	LSC	F
53	48763	<i>tmR-UCU/tmR-UCU-tmG-GCC</i>	tRNA/IGS	LSC	64193	<i>psbB-psaA</i>	IGS	LSC	F

32	50816	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC	50849	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC	P
30	51266	<i>tmS-GCU</i>	tRNA	LSC	94623	<i>tmS-GGA</i>	tRNA	LSC	F
35	52469	<i>psbK-rps11</i>	IGS	LSC	122287	<i>tml-CAA-rrn16</i>	IGS	IR	F
30	52484	<i>psbK-rps11</i>	IGS	LSC	122302	<i>tml-CAA-rrn16</i>	IGS	IR	F
41	52903	<i>psbK-rps11</i>	IGS	LSC	72136	<i>rps14-trnQ-UUG</i>	IGS	LSC	F
40	52904	<i>psbK-rps11</i>	IGS	LSC	110171	<i>tmf-CAU-rps12_3'</i>	IGS	IR	F
39	52905	<i>psbK-rps11</i>	IGS	LSC	110010	<i>tmf-CAU-rps12_3'</i>	IGS	IR	F
38	52906	<i>psbK-rps11</i>	IGS	LSC	118432	<i>tml-CAA-rrn16</i>	IGS	IR	F
32	52912	<i>psbK-rps11</i>	IGS	LSC	110152	<i>tmf-CAU-rps12_3'</i>	IGS	IR	F
31	52913	<i>psbK-rps11</i>	IGS	LSC	72110	<i>rps14-trnQ-UUG</i>	IGS	LSC	F
30	52915	<i>psbK-rps11</i>	IGS	LSC	118441	<i>tml-CAA-rrn16</i>	IGS	IR	F
75	52968	<i>psbK-rps11</i>	IGS	LSC	118103	<i>tml-CAA-rrn16</i>	IGS	IR	F
34	52985	<i>psbK-rps11</i>	IGS	LSC	71038	<i>rps14-trnQ-UUG</i>	IGS	LSC	F
31	52985	<i>psbK-rps11</i>	IGS	LSC	109675	<i>tmf-CAU-rps12_3'</i>	IGS	IR	F
57	53315	<i>psbK-rps11</i>	IGS	LSC	117967	<i>tml-CAA-rrn16</i>	IGS	IR	F
114	53960	<i>rps11-petD</i>	IGS	LSC	56519	<i>rps11-petD</i>	IGS	LSC	F
233	53960	<i>rps11-petD</i>	IGS	LSC	55240	<i>rps11-petD</i>	IGS	LSC	F
148	53960	<i>rps11-petD</i>	IGS	LSC	121674	<i>tml-CAA-rrn16</i>	IGS	IR	F
233	53960	<i>rps11-petD</i>	IGS	LSC	89500	<i>rpl20-rps12_5'</i>	IGS	LSC	P
1544	53960	<i>rps11-petD</i>	IGS	LSC	86893	<i>rpl20-rps12_5'</i>	IGS	LSC	P
112	54048	<i>rps11-petD</i>	IGS	LSC	121762	<i>tml-CAA-rrn16</i>	IGS	IR	F
136	54057	<i>rps11-petD</i>	IGS	LSC	91105	<i>rps12_5'-ycf3</i>	IGS	LSC	P
132	54061	<i>rps11-petD</i>	IGS	LSC	121775	<i>tml-CAA-rrn16</i>	IGS	IR	F
118	54075	<i>rps11-petD</i>	IGS	LSC	56632	<i>rps11-petD</i>	IGS	LSC	F
34	54125	<i>rps11-petD</i>	IGS	LSC	82468	<i>psbE-petL</i>	IGS	LSC	P
1140	54200	<i>rps11-petD</i>	IGS	LSC	55479	<i>rps11-petD</i>	IGS	LSC	F
61	54200	<i>rps11-petD</i>	IGS	LSC	91038	<i>rps12_5'-ycf3</i>	IGS	LSC	P
81	54200	<i>rps11-petD</i>	IGS	LSC	89413	<i>rpl20-rps12_5'</i>	IGS	LSC	P
37	54304	<i>rps11-petD</i>	IGS	LSC	89353	<i>rpl20-rps12_5'</i>	IGS	LSC	P
37	54312	<i>rps11-petD</i>	IGS	LSC	89345	<i>rpl20-rps12_5'</i>	IGS	LSC	P
62	54312	<i>rps11-petD</i>	IGS	LSC	90907	<i>rps12_5'-ycf3</i>	IGS	LSC	P
58	54322	<i>rps11-petD</i>	IGS	LSC	89314	<i>rpl20-rps12_5'</i>	IGS	LSC	P
32	54342	<i>rps11-petD</i>	IGS	LSC	91482	<i>rps12_5'-ycf3</i>	IGS	LSC	P
30	54350	<i>rps11-petD</i>	IGS	LSC	90901	<i>rps12_5'-ycf3</i>	IGS	LSC	P
51	54350	<i>rps11-petD</i>	IGS	LSC	89293	<i>rpl20-rps12_5'</i>	IGS	LSC	P
50	54383	<i>rps11-petD</i>	IGS	LSC	89261	<i>rpl20-rps12_5'</i>	IGS	LSC	P
44	54385	<i>rps11-petD</i>	IGS	LSC	90852	<i>rps12_5'-ycf3</i>	IGS	LSC	P
42	54397	<i>rps11-petD</i>	IGS	LSC	90842	<i>rps12_5'-ycf3</i>	IGS	LSC	P
37	54402	<i>rps11-petD</i>	IGS	LSC	89255	<i>rpl20-rps12_5'</i>	IGS	LSC	P
36	54415	<i>rps11-petD</i>	IGS	LSC	90830	<i>rps12_5'-ycf3</i>	IGS	LSC	P
30	54469	<i>rps11-petD</i>	IGS	LSC	89207	<i>rpl20-rps12_5'</i>	IGS	LSC	P
46	54503	<i>rps11-petD</i>	IGS	LSC	89157	<i>rpl20-rps12_5'</i>	IGS	LSC	P
48	54551	<i>rps11-petD</i>	IGS	LSC	90694	<i>rps12_5'-ycf3</i>	IGS	LSC	P
38	54561	<i>rps11-petD</i>	IGS	LSC	89107	<i>rpl20-rps12_5'</i>	IGS	LSC	P
56	54561	<i>rps11-petD</i>	IGS	LSC	90676	<i>rps12_5'-ycf3</i>	IGS	LSC	P
62	54572	<i>rps11-petD</i>	IGS	LSC	89072	<i>rpl20-rps12_5'</i>	IGS	LSC	P
54	54582	<i>rps11-petD</i>	IGS	LSC	90657	<i>rps12_5'-ycf3</i>	IGS	LSC	P
34	54583	<i>rps11-petD</i>	IGS	LSC	63690	<i>psbB-psaA</i>	IGS	LSC	F
40	54601	<i>rps11-petD</i>	IGS	LSC	63708	<i>psbB-psaA</i>	IGS	LSC	F
40	54601	<i>rps11-petD</i>	IGS	LSC	90652	<i>rps12_5'-ycf3</i>	IGS	LSC	P
42	54601	<i>rps11-petD</i>	IGS	LSC	89063	<i>rpl20-rps12_5'</i>	IGS	LSC	P
30	54647	<i>rps11-petD</i>	IGS	LSC	63754	<i>psbB-psaA</i>	IGS	LSC	F
72	54703	<i>rps11-petD</i>	IGS	LSC	63824	<i>psbB-psaA</i>	IGS	LSC	F
101	54703	<i>rps11-petD</i>	IGS	LSC	90483	<i>rps12_5'-ycf3</i>	IGS	LSC	P
96	54713	<i>rps11-petD</i>	IGS	LSC	90478	<i>rps12_5'-ycf3</i>	IGS	LSC	P
83	54725	<i>rps11-petD</i>	IGS	LSC	88874	<i>rpl20-rps12_5'</i>	IGS	LSC	P
128	54725	<i>rps11-petD</i>	IGS	LSC	90434	<i>rps12_5'-ycf3</i>	IGS	LSC	P
36	54760	<i>rps11-petD</i>	IGS	LSC	63881	<i>psbB-psaA</i>	IGS	LSC	F
108	54778	<i>rps11-petD</i>	IGS	LSC	90401	<i>rps12_5'-ycf3</i>	IGS	LSC	P
72	54779	<i>rps11-petD</i>	IGS	LSC	63900	<i>psbB-psaA</i>	IGS	LSC	F
55	54802	<i>rps11-petD</i>	IGS	LSC	88819	<i>rpl20-rps12_5'</i>	IGS	LSC	P
53	54810	<i>rps11-petD</i>	IGS	LSC	88813	<i>rpl20-rps12_5'</i>	IGS	LSC	P
33	54847	<i>rps11-petD</i>	IGS	LSC	88796	<i>rpl20-rps12_5'</i>	IGS	LSC	P
47	54858	<i>rps11-petD</i>	IGS	LSC	63979	<i>psbB-psaA</i>	IGS	LSC	F
61	54886	<i>rps11-petD</i>	IGS	LSC	88726	<i>rpl20-rps12_5'</i>	IGS	LSC	P
110	54895	<i>rps11-petD</i>	IGS	LSC	90278	<i>rps12_5'-ycf3</i>	IGS	LSC	P
312	54895	<i>rps11-petD</i>	IGS	LSC	88466	<i>rpl20-rps12_5'</i>	IGS	LSC	P
62	54909	<i>rps11-petD</i>	IGS	LSC	64030	<i>psbB-psaA</i>	IGS	LSC	F
50	54927	<i>rps11-petD</i>	IGS	LSC	87420	<i>rpl20-rps12_5'</i>	IGS	LSC	F
50	54927	<i>rps11-petD</i>	IGS	LSC	54927	<i>rps11-petD</i>	IGS	LSC	P
44	54933	<i>rps11-petD</i>	IGS	LSC	64054	<i>psbB-psaA</i>	IGS	LSC	F
31	54948	<i>rps11-petD</i>	IGS	LSC	64069	<i>psbB-psaA</i>	IGS	LSC	F
93	54999	<i>rps11-petD</i>	IGS	LSC	90187	<i>rps12_5'/rps12_5'-ycf3</i>	CDS/IGS	LSC	P
89	55004	<i>rps11-petD</i>	IGS	LSC	57552	<i>rps11-petD</i>	IGS	LSC	F
39	55084	<i>rps11-petD</i>	IGS	LSC	90155	<i>rps12_5'</i>	CDS	LSC	P
218	55122	<i>rps11-petD</i>	IGS	LSC	121556	<i>tml-CAA-rrn16</i>	IGS	IR	F
51	55122	<i>rps11-petD</i>	IGS	LSC	89800	<i>rpl20-rps12_5'</i>	IGS	LSC	P
91	55140	<i>rps11-petD</i>	IGS	LSC	89742	<i>rpl20-rps12_5'</i>	IGS	LSC	P
338	55152	<i>rps11-petD</i>	IGS	LSC	89483	<i>rpl20-rps12_5'</i>	IGS	LSC	P
346	55174	<i>rps11-petD</i>	IGS	LSC	89453	<i>rpl20-rps12_5'</i>	IGS	LSC	P
267	55206	<i>rps11-petD</i>	IGS	LSC	88204	<i>rpl20-rps12_5'</i>	IGS	LSC	P

170	55207	<i>rps11-petD</i>	IGS	LSC	121641	<i>tml-CAA-rm16</i>	IGS	IR	F
340	55207	<i>rps11-petD</i>	IGS	LSC	89426	<i>rpl20-rps12_5'</i>	IGS	LSC	P
156	55232	<i>rps11-petD</i>	IGS	LSC	121666	<i>tml-CAA-rm16</i>	IGS	IR	F
328	55232	<i>rps11-petD</i>	IGS	LSC	89413	<i>rpl20-rps12_5'</i>	IGS	LSC	P
112	55328	<i>rps11-petD</i>	IGS	LSC	121762	<i>tml-CAA-rm16</i>	IGS	IR	F
203	55337	<i>rps11-petD</i>	IGS	LSC	91038	<i>rps12_5'-ycf3</i>	IGS	LSC	P
133	55341	<i>rps11-petD</i>	IGS	LSC	121775	<i>tml-CAA-rm16</i>	IGS	IR	F
119	55355	<i>rps11-petD</i>	IGS	LSC	56632	<i>rps11-petD</i>	IGS	LSC	F
115	55389	<i>rps11-petD</i>	IGS	LSC	56666	<i>rps11-petD</i>	IGS	LSC	F
34	55405	<i>rps11-petD</i>	IGS	LSC	82468	<i>psbE-petL</i>	IGS	LSC	P
30	55475	<i>rps11-petD</i>	IGS	LSC	56752	<i>rps11-petD</i>	IGS	LSC	F
1140	55479	<i>rps11-petD</i>	IGS	LSC	87057	<i>rpl20-rps12_5'</i>	IGS	LSC	P
37	55583	<i>rps11-petD</i>	IGS	LSC	89353	<i>rpl20-rps12_5'</i>	IGS	LSC	P
37	55591	<i>rps11-petD</i>	IGS	LSC	89345	<i>rpl20-rps12_5'</i>	IGS	LSC	P
62	55591	<i>rps11-petD</i>	IGS	LSC	90907	<i>rps12_5'-ycf3</i>	IGS	LSC	P
58	55601	<i>rps11-petD</i>	IGS	LSC	89314	<i>rpl20-rps12_5'</i>	IGS	LSC	P
32	55621	<i>rps11-petD</i>	IGS	LSC	91482	<i>rps12_5'-ycf3</i>	IGS	LSC	P
30	55629	<i>rps11-petD</i>	IGS	LSC	90901	<i>rps12_5'-ycf3</i>	IGS	LSC	P
51	55629	<i>rps11-petD</i>	IGS	LSC	89293	<i>rpl20-rps12_5'</i>	IGS	LSC	P
50	55662	<i>rps11-petD</i>	IGS	LSC	89261	<i>rpl20-rps12_5'</i>	IGS	LSC	P
44	55664	<i>rps11-petD</i>	IGS	LSC	90852	<i>rps12_5'-ycf3</i>	IGS	LSC	P
42	55676	<i>rps11-petD</i>	IGS	LSC	90842	<i>rps12_5'-ycf3</i>	IGS	LSC	P
37	55681	<i>rps11-petD</i>	IGS	LSC	89255	<i>rpl20-rps12_5'</i>	IGS	LSC	P
36	55694	<i>rps11-petD</i>	IGS	LSC	90830	<i>rps12_5'-ycf3</i>	IGS	LSC	P
30	55748	<i>rps11-petD</i>	IGS	LSC	89207	<i>rpl20-rps12_5'</i>	IGS	LSC	P
46	55782	<i>rps11-petD</i>	IGS	LSC	89157	<i>rpl20-rps12_5'</i>	IGS	LSC	P
48	55830	<i>rps11-petD</i>	IGS	LSC	90694	<i>rps12_5'-ycf3</i>	IGS	LSC	P
38	55840	<i>rps11-petD</i>	IGS	LSC	89107	<i>rpl20-rps12_5'</i>	IGS	LSC	P
56	55840	<i>rps11-petD</i>	IGS	LSC	90676	<i>rps12_5'-ycf3</i>	IGS	LSC	P
62	55851	<i>rps11-petD</i>	IGS	LSC	89072	<i>rpl20-rps12_5'</i>	IGS	LSC	P
54	55861	<i>rps11-petD</i>	IGS	LSC	90657	<i>rps12_5'-ycf3</i>	IGS	LSC	P
34	55862	<i>rps11-petD</i>	IGS	LSC	63690	<i>psbB-psaA</i>	IGS	LSC	F
40	55880	<i>rps11-petD</i>	IGS	LSC	63708	<i>psbB-psaA</i>	IGS	LSC	F
40	55880	<i>rps11-petD</i>	IGS	LSC	90652	<i>rps12_5'-ycf3</i>	IGS	LSC	P
42	55880	<i>rps11-petD</i>	IGS	LSC	89063	<i>rpl20-rps12_5'</i>	IGS	LSC	P
30	55926	<i>rps11-petD</i>	IGS	LSC	63754	<i>psbB-psaA</i>	IGS	LSC	F
72	55982	<i>rps11-petD</i>	IGS	LSC	63824	<i>psbB-psaA</i>	IGS	LSC	F
101	55982	<i>rps11-petD</i>	IGS	LSC	90483	<i>rps12_5'-ycf3</i>	IGS	LSC	P
96	55992	<i>rps11-petD</i>	IGS	LSC	90478	<i>rps12_5'-ycf3</i>	IGS	LSC	P
83	56004	<i>rps11-petD</i>	IGS	LSC	88874	<i>rpl20-rps12_5'</i>	IGS	LSC	P
128	56004	<i>rps11-petD</i>	IGS	LSC	90434	<i>rps12_5'-ycf3</i>	IGS	LSC	P
36	56039	<i>rps11-petD</i>	IGS	LSC	63881	<i>psbB-psaA</i>	IGS	LSC	F
108	56057	<i>rps11-petD</i>	IGS	LSC	90401	<i>rps12_5'-ycf3</i>	IGS	LSC	P
72	56058	<i>rps11-petD</i>	IGS	LSC	63900	<i>psbB-psaA</i>	IGS	LSC	F
55	56081	<i>rps11-petD</i>	IGS	LSC	88819	<i>rpl20-rps12_5'</i>	IGS	LSC	P
53	56089	<i>rps11-petD</i>	IGS	LSC	88813	<i>rpl20-rps12_5'</i>	IGS	LSC	P
33	56126	<i>rps11-petD</i>	IGS	LSC	88796	<i>rpl20-rps12_5'</i>	IGS	LSC	P
47	56137	<i>rps11-petD</i>	IGS	LSC	63979	<i>psbB-psaA</i>	IGS	LSC	F
61	56165	<i>rps11-petD</i>	IGS	LSC	88726	<i>rpl20-rps12_5'</i>	IGS	LSC	P
110	56174	<i>rps11-petD</i>	IGS	LSC	90278	<i>rps12_5'-ycf3</i>	IGS	LSC	P
312	56174	<i>rps11-petD</i>	IGS	LSC	88466	<i>rpl20-rps12_5'</i>	IGS	LSC	P
62	56188	<i>rps11-petD</i>	IGS	LSC	64030	<i>psbB-psaA</i>	IGS	LSC	F
50	56206	<i>rps11-petD</i>	IGS	LSC	87420	<i>rpl20-rps12_5'</i>	IGS	LSC	F
50	56206	<i>rps11-petD</i>	IGS	LSC	56206	<i>rps11-petD</i>	IGS	LSC	P
44	56212	<i>rps11-petD</i>	IGS	LSC	64054	<i>psbB-psaA</i>	IGS	LSC	F
31	56227	<i>rps11-petD</i>	IGS	LSC	64069	<i>psbB-psaA</i>	IGS	LSC	F
93	56278	<i>rps11-petD</i>	IGS	LSC	90187	<i>rps12_5'/rps12_5'-ycf3</i>	CDS/IGS	LSC	P
89	56283	<i>rps11-petD</i>	IGS	LSC	57552	<i>rps11-petD</i>	IGS	LSC	F
39	56363	<i>rps11-petD</i>	IGS	LSC	90155	<i>rps12_5'</i>	CDS	LSC	P
232	56401	<i>rps11-petD</i>	IGS	LSC	121556	<i>tml-CAA-rm16</i>	IGS	IR	F
51	56401	<i>rps11-petD</i>	IGS	LSC	89800	<i>rpl20-rps12_5'</i>	IGS	LSC	P
91	56419	<i>rps11-petD</i>	IGS	LSC	89742	<i>rpl20-rps12_5'</i>	IGS	LSC	P
188	56431	<i>rps11-petD</i>	IGS	LSC	89633	<i>rpl20-rps12_5'</i>	IGS	LSC	P
180	56453	<i>rps11-petD</i>	IGS	LSC	89619	<i>rpl20-rps12_5'</i>	IGS	LSC	P
148	56485	<i>rps11-petD</i>	IGS	LSC	88323	<i>rpl20-rps12_5'</i>	IGS	LSC	P
30	56607	<i>rps11-petD</i>	IGS	LSC	121762	<i>tml-CAA-rm16</i>	IGS	IR	F
201	56632	<i>rps11-petD</i>	IGS	LSC	121789	<i>tml-CAA-rm16</i>	IGS	IR	F
118	56632	<i>rps11-petD</i>	IGS	LSC	88204	<i>rpl20-rps12_5'</i>	IGS	LSC	P
119	56632	<i>rps11-petD</i>	IGS	LSC	86923	<i>rpl20-rps12_5'</i>	IGS	LSC	P
101	56666	<i>rps11-petD</i>	IGS	LSC	89483	<i>rpl20-rps12_5'</i>	IGS	LSC	P
115	56666	<i>rps11-petD</i>	IGS	LSC	91074	<i>rps12_5'-ycf3</i>	IGS	LSC	P
116	56666	<i>rps11-petD</i>	IGS	LSC	86892	<i>rpl20-rps12_5'</i>	IGS	LSC	P
34	56682	<i>rps11-petD</i>	IGS	LSC	82468	<i>psbE-petL</i>	IGS	LSC	P
63	56718	<i>rps11-petD</i>	IGS	LSC	89469	<i>rpl20-rps12_5'</i>	IGS	LSC	P
30	56752	<i>rps11-petD</i>	IGS	LSC	89468	<i>rpl20-rps12_5'</i>	IGS	LSC	P
43	56755	<i>rps11-petD</i>	IGS	LSC	86876	<i>rpl20-rps12_5'</i>	IGS	LSC	P
42	56885	<i>rps11-petD</i>	IGS	LSC	57167	<i>rps11-petD</i>	IGS	LSC	F
33	56899	<i>rps11-petD</i>	IGS	LSC	57181	<i>rps11-petD</i>	IGS	LSC	F
89	57552	<i>rps11-petD</i>	IGS	LSC	87304	<i>rpl20-rps12_5'</i>	IGS	LSC	P
80	57560	<i>rps11-petD</i>	IGS	LSC	90187	<i>rps12_5'/rps12_5'-ycf3</i>	CDS/IGS	LSC	P
30	57811	<i>rps11-petD/petD</i>	IGS/CDS	LSC	94397	<i>ycf3-trnS-GGA</i>	IGS	LSC	P

33	59278	<i>petD-petB/petB</i>	IGS/CDS	LSC	82383	<i>psbE-petL</i>	IGS	LSC	P
86	59403	<i>petB</i>	CDS	LSC	82234	<i>psbE-petL</i>	IGS	LSC	P
57	59474	<i>petB</i>	CDS	LSC	82192	<i>psbE-petL</i>	IGS	LSC	P
51	59490	<i>petB</i>	CDS	LSC	82182	<i>psbE-petL</i>	IGS	LSC	P
46	59552	<i>petB</i>	CDS	LSC	82133	<i>psbE-petL</i>	IGS	LSC	P
57	59619	<i>petB</i>	CDS	LSC	82067	<i>psbE-petL</i>	IGS	LSC	P
35	59696	<i>petB</i>	CDS	LSC	82024	<i>psbE-petL</i>	IGS	LSC	P
48	59712	<i>petB</i>	CDS	LSC	81995	<i>psbE-petL</i>	IGS	LSC	P
72	59727	<i>petB</i>	CDS	LSC	81956	<i>psbE-petL</i>	IGS	LSC	P
35	59968	<i>petB</i> intron	Intron	LSC	93104	<i>ycf3</i> intron	Intron	LSC	F
30	61183	<i>psbH-psbN</i>	IGS	LSC	137183	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	63090	<i>psbB</i>	CDS	LSC	105548	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
46	63133	<i>psbB</i>	CDS	LSC	105582	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
104	63198	<i>psbB/psbB-psaA</i>	CDS/IGS	LSC	105656	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
46	63267	<i>psbB-psaA</i>	IGS	LSC	105725	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
30	63284	<i>psbB-psaA</i>	IGS	LSC	105742	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
193	63353	<i>psbB-psaA</i>	IGS	LSC	105823	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
34	63539	<i>psbB-psaA</i>	IGS	LSC	106013	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
31	63577	<i>psbB-psaA</i>	IGS	LSC	91813	<i>rps12_5-ycf3</i>	IGS	LSC	P
36	63600	<i>psbB-psaA</i>	IGS	LSC	91789	<i>rps12_5-ycf3</i>	IGS	LSC	P
30	63642	<i>psbB-psaA</i>	IGS	LSC	91779	<i>rps12_5-ycf3</i>	IGS	LSC	P
93	63685	<i>psbB-psaA</i>	IGS	LSC	90622	<i>rps12_5-ycf3</i>	IGS	LSC	P
34	63690	<i>psbB-psaA</i>	IGS	LSC	87780	<i>rpl20-rps12_5'</i>	IGS	LSC	P
51	63690	<i>psbB-psaA</i>	IGS	LSC	89072	<i>rpl20-rps12_5'</i>	IGS	LSC	P
40	63708	<i>psbB-psaA</i>	IGS	LSC	87756	<i>rpl20-rps12_5'</i>	IGS	LSC	P
70	63727	<i>psbB-psaA</i>	IGS	LSC	90603	<i>rps12_5-ycf3</i>	IGS	LSC	P
30	63754	<i>psbB-psaA</i>	IGS	LSC	87720	<i>rpl20-rps12_5'</i>	IGS	LSC	P
32	63772	<i>psbB-psaA</i>	IGS	LSC	89009	<i>rpl20-rps12_5'</i>	IGS	LSC	P
102	63815	<i>psbB-psaA</i>	IGS	LSC	90491	<i>rps12_5-ycf3</i>	IGS	LSC	P
72	63824	<i>psbB-psaA</i>	IGS	LSC	87622	<i>rpl20-rps12_5'</i>	IGS	LSC	P
74	63843	<i>psbB-psaA</i>	IGS	LSC	88886	<i>rpl20-rps12_5'</i>	IGS	LSC	P
36	63881	<i>psbB-psaA</i>	IGS	LSC	87601	<i>rpl20-rps12_5'</i>	IGS	LSC	P
44	63881	<i>psbB-psaA</i>	IGS	LSC	90483	<i>rps12_5-ycf3</i>	IGS	LSC	P
30	63897	<i>psbB-psaA</i>	IGS	LSC	88876	<i>rpl20-rps12_5'</i>	IGS	LSC	P
72	63900	<i>psbB-psaA</i>	IGS	LSC	87546	<i>rpl20-rps12_5'</i>	IGS	LSC	P
60	63918	<i>psbB-psaA</i>	IGS	LSC	90430	<i>rps12_5-ycf3</i>	IGS	LSC	P
78	63923	<i>psbB-psaA</i>	IGS	LSC	88796	<i>rpl20-rps12_5'</i>	IGS	LSC	P
79	63928	<i>psbB-psaA</i>	IGS	LSC	90401	<i>rps12_5-ycf3</i>	IGS	LSC	P
47	63979	<i>psbB-psaA</i>	IGS	LSC	87492	<i>rpl20-rps12_5'</i>	IGS	LSC	P
46	64007	<i>psbB-psaA</i>	IGS	LSC	88741	<i>rpl20-rps12_5'</i>	IGS	LSC	P
62	64030	<i>psbB-psaA</i>	IGS	LSC	87426	<i>rpl20-rps12_5'</i>	IGS	LSC	P
30	64032	<i>psbB-psaA</i>	IGS	LSC	91723	<i>rps12_5-ycf3</i>	IGS	LSC	P
50	64048	<i>psbB-psaA</i>	IGS	LSC	64048	<i>psbB-psaA</i>	IGS	LSC	P
44	64054	<i>psbB-psaA</i>	IGS	LSC	87420	<i>rpl20-rps12_5'</i>	IGS	LSC	P
31	64069	<i>psbB-psaA</i>	IGS	LSC	87418	<i>rpl20-rps12_5'</i>	IGS	LSC	P
30	64070	<i>psbB-psaA</i>	IGS	LSC	88694	<i>rpl20-rps12_5'</i>	IGS	LSC	P
45	69972	<i>rps14</i>	CDS	LSC	114069	<i>rps7-ndhB</i>	IGS	IR	F
130	70104	<i>rps14-tmQ-UUG</i>	IGS	LSC	114117	<i>rps7-ndhB</i>	IGS	IR	F
64	70364	<i>rps14-tmQ-UUG</i>	IGS	LSC	102819	<i>rps19-trmH-GUG</i>	IGS	IR	P
45	70374	<i>rps14-tmQ-UUG</i>	IGS	LSC	119209	<i>tml-CAA-rm16</i>	IGS	IR	F
54	70374	<i>rps14-tmQ-UUG</i>	IGS	LSC	135742	<i>tmN-GUU-rps15</i>	IGS	IR	F
66	70438	<i>rps14-tmQ-UUG</i>	IGS	LSC	112896	<i>rps7-ndhB</i>	IGS	IR	F
66	70438	<i>rps14-tmQ-UUG</i>	IGS	LSC	102707	<i>rps19-trmH-GUG</i>	IGS	IR	P
135	70500	<i>rps14-tmQ-UUG</i>	IGS	LSC	139009	<i>tmN-GUU-rps15/rps15</i>	IGS/CDS	IR	F
31	70663	<i>rps14-tmQ-UUG</i>	IGS	LSC	119146	<i>tml-CAA-rm16</i>	IGS	IR	F
58	70822	<i>rps14-tmQ-UUG</i>	IGS	LSC	102879	<i>rps19-trmH-GUG</i>	IGS	IR	P
65	70825	<i>rps14-tmQ-UUG</i>	IGS	LSC	108251	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
36	71030	<i>rps14-tmQ-UUG</i>	IGS	LSC	109667	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
34	71030	<i>rps14-tmQ-UUG</i>	IGS	LSC	123776	<i>tml-CAA-rm16</i>	IGS	IR	F
36	71030	<i>rps14-tmQ-UUG</i>	IGS	LSC	137146	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	71030	<i>rps14-tmQ-UUG</i>	IGS	LSC	137598	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	71034	<i>rps14-tmQ-UUG</i>	IGS	LSC	108334	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
34	71038	<i>rps14-tmQ-UUG</i>	IGS	LSC	118120	<i>tml-CAA-rm16</i>	IGS	IR	F
31	71078	<i>rps14-tmQ-UUG</i>	IGS	LSC	108370	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
36	71078	<i>rps14-tmQ-UUG</i>	IGS	LSC	137186	<i>tmN-GUU-rps15</i>	IGS	IR	F
276	71461	<i>rps14-tmQ-UUG</i>	IGS	LSC	109185	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
122	71731	<i>rps14-tmQ-UUG</i>	IGS	LSC	109453	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
37	71782	<i>rps14-tmQ-UUG</i>	IGS	LSC	113044	<i>rps7-ndhB</i>	IGS	IR	F
164	71806	<i>rps14-tmQ-UUG</i>	IGS	LSC	113068	<i>rps7-ndhB</i>	IGS	IR	F
240	71823	<i>rps14-tmQ-UUG</i>	IGS	LSC	113085	<i>rps7-ndhB</i>	IGS	IR	F
262	71823	<i>rps14-tmQ-UUG</i>	IGS	LSC	120733	<i>tml-CAA-rm16</i>	IGS	IR	F
73	71839	<i>rps14-tmQ-UUG</i>	IGS	LSC	119268	<i>tml-CAA-rm16</i>	IGS	IR	F
31	71881	<i>rps14-tmQ-UUG</i>	IGS	LSC	113141	<i>rps7-ndhB</i>	IGS	IR	R
35	71932	<i>rps14-tmQ-UUG</i>	IGS	LSC	119337	<i>tml-CAA-rm16</i>	IGS	IR	F
122	71971	<i>rps14-tmQ-UUG</i>	IGS	LSC	120881	<i>tml-CAA-rm16</i>	IGS	IR	F
104	71999	<i>rps14-tmQ-UUG</i>	IGS	LSC	120909	<i>tml-CAA-rm16</i>	IGS	IR	F
46	72017	<i>rps14-tmQ-UUG</i>	IGS	LSC	119416	<i>tml-CAA-rm16</i>	IGS	IR	F
83	72094	<i>rps14-tmQ-UUG</i>	IGS	LSC	109966	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
31	72110	<i>rps14-tmQ-UUG</i>	IGS	LSC	72146	<i>rps14-tmQ-UUG</i>	IGS	LSC	F
41	72112	<i>rps14-tmQ-UUG</i>	IGS	LSC	110128	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
47	72112	<i>rps14-tmQ-UUG</i>	IGS	LSC	110182	<i>tml-CAU-rps12_3'</i>	IGS	IR	F

65	72112	<i>rps14-tmQ-UUG</i>	IGS	LSC	110020	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
32	72112	<i>rps14-tmQ-UUG</i>	IGS	LSC	124177	<i>tml-CAA-rm16</i>	IGS	IR	F
43	72112	<i>rps14-tmQ-UUG</i>	IGS	LSC	118441	<i>tml-CAA-rm16</i>	IGS	IR	F
57	72112	<i>rps14-tmQ-UUG</i>	IGS	LSC	124195	<i>tml-CAA-rm16</i>	IGS	IR	F
30	72114	<i>rps14-tmQ-UUG</i>	IGS	LSC	72899	<i>rps14-tmQ-UUG</i>	IGS	LSC	F
59	72114	<i>rps14-tmQ-UUG</i>	IGS	LSC	118407	<i>tml-CAA-rm16</i>	IGS	IR	F
49	72128	<i>rps14-tmQ-UUG</i>	IGS	LSC	124175	<i>tml-CAA-rm16</i>	IGS	IR	F
32	72130	<i>rps14-tmQ-UUG</i>	IGS	LSC	124168	<i>tml-CAA-rm16</i>	IGS	IR	F
40	72137	<i>rps14-tmQ-UUG</i>	IGS	LSC	110171	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
38	72139	<i>rps14-tmQ-UUG</i>	IGS	LSC	118432	<i>tml-CAA-rm16</i>	IGS	IR	F
32	72145	<i>rps14-tmQ-UUG</i>	IGS	LSC	110152	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
31	72146	<i>rps14-tmQ-UUG</i>	IGS	LSC	72895	<i>rps14-tmQ-UUG</i>	IGS	LSC	F
30	72148	<i>rps14-tmQ-UUG</i>	IGS	LSC	118441	<i>tml-CAA-rm16</i>	IGS	IR	F
30	72621	<i>rps14-tmQ-UUG</i>	IGS	LSC	138908	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	72628	<i>rps14-tmQ-UUG</i>	IGS	LSC	121284	<i>tml-CAA-rm16</i>	IGS	IR	F
34	72639	<i>rps14-tmQ-UUG</i>	IGS	LSC	110468	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
30	72658	<i>rps14-tmQ-UUG</i>	IGS	LSC	110487	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
30	72875	<i>rps14-tmQ-UUG</i>	IGS	LSC	109944	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
48	72875	<i>rps14-tmQ-UUG</i>	IGS	LSC	118383	<i>tml-CAA-rm16</i>	IGS	IR	F
46	72883	<i>rps14-tmQ-UUG</i>	IGS	LSC	118391	<i>tml-CAA-rm16</i>	IGS	IR	F
34	72895	<i>rps14-tmQ-UUG</i>	IGS	LSC	110018	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
30	72899	<i>rps14-tmQ-UUG</i>	IGS	LSC	109986	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
31	73859	<i>tmQ-UUG-rps4</i>	IGS	LSC	147434	<i>ndhF-rpl32</i>	IGS	SSC	F
31	74348	<i>rps4</i>	CDS	LSC	101657	<i>rpl16-rpl22</i>	IGS	LSC	C
30	74349	<i>rps4</i>	CDS	LSC	101649	<i>rpl16-rpl22</i>	IGS	LSC	C
34	82468	<i>psbE-petL</i>	IGS	LSC	86958	<i>rpl20-rps12_5'</i>	IGS	LSC	F
34	82468	<i>psbE-petL</i>	IGS	LSC	121839	<i>tml-CAA-rm16</i>	IGS	IR	P
31	82476	<i>psbE-petL</i>	IGS	LSC	86966	<i>rpl20-rps12_5'</i>	IGS	LSC	F
31	82476	<i>psbE-petL</i>	IGS	LSC	121834	<i>tml-CAA-rm16</i>	IGS	IR	P
55	84369	<i>psaI</i>	CDS	LSC	133565	<i>tmR-ACG-trmN-GUU</i>	IGS	IR	F
34	84397	<i>psaI</i>	CDS	LSC	133593	<i>tmR-ACG-trmN-GUU</i>	IGS	IR	F
33	84434	<i>psaI</i>	CDS	LSC	133620	<i>tmR-ACG-trmN-GUU</i>	IGS	IR	F
90	84476	<i>psaI/psaI-rpl33</i>	CDS/IGS	LSC	133651	<i>tmR-ACG-trmN-GUU</i>	IGS	IR	F
43	84569	<i>psaI-rpl33</i>	IGS	LSC	133753	<i>tmR-ACG-trmN-GUU</i>	IGS	IR	F
43	84590	<i>psaI-rpl33</i>	IGS	LSC	133774	<i>tmR-ACG-trmN-GUU</i>	IGS	IR	F
34	84606	<i>psaI-rpl33</i>	IGS	LSC	133790	<i>tmR-ACG-trmN-GUU</i>	IGS	IR	F
67	84634	<i>psaI-rpl33</i>	IGS	LSC	133819	<i>tmR-ACG-trmN-GUU</i>	IGS	IR	F
33	85481	<i>rpl33-rpl20</i>	IGS	LSC	85505	<i>rpl33-rpl20</i>	IGS	LSC	F
36	85500	<i>rpl33-rpl20</i>	IGS	LSC	85524	<i>rpl33-rpl20</i>	IGS	LSC	F
42	86026	<i>rpl33-rpl20</i>	IGS	LSC	86104	<i>rpl33-rpl20</i>	IGS	LSC	F
30	86066	<i>rpl33-rpl20</i>	IGS	LSC	86156	<i>rpl33-rpl20</i>	IGS	LSC	F
43	86876	<i>rpl20-rps12_5'</i>	IGS	LSC	121912	<i>tml-CAA-rm16</i>	IGS	IR	P
116	86892	<i>rpl20-rps12_5'</i>	IGS	LSC	121823	<i>tml-CAA-rm16</i>	IGS	IR	P
330	86893	<i>rpl20-rps12_5'</i>	IGS	LSC	89469	<i>rpl20-rps12_5'</i>	IGS	LSC	F
167	86893	<i>rpl20-rps12_5'</i>	IGS	LSC	91074	<i>rps12_5'-ycf3</i>	IGS	LSC	F
338	86907	<i>rpl20-rps12_5'</i>	IGS	LSC	89483	<i>rpl20-rps12_5'</i>	IGS	LSC	F
133	86923	<i>rpl20-rps12_5'</i>	IGS	LSC	121775	<i>tml-CAA-rm16</i>	IGS	IR	P
267	86924	<i>rpl20-rps12_5'</i>	IGS	LSC	88204	<i>rpl20-rps12_5'</i>	IGS	LSC	F
112	86957	<i>rpl20-rps12_5'</i>	IGS	LSC	121762	<i>tml-CAA-rm16</i>	IGS	IR	P
156	87009	<i>rpl20-rps12_5'</i>	IGS	LSC	121666	<i>tml-CAA-rm16</i>	IGS	IR	P
170	87020	<i>rpl20-rps12_5'</i>	IGS	LSC	121641	<i>tml-CAA-rm16</i>	IGS	IR	P
218	87057	<i>rpl20-rps12_5'</i>	IGS	LSC	121556	<i>tml-CAA-rm16</i>	IGS	IR	P
91	87166	<i>rpl20-rps12_5'</i>	IGS	LSC	89742	<i>rpl20-rps12_5'</i>	IGS	LSC	F
312	87190	<i>rpl20-rps12_5'</i>	IGS	LSC	88466	<i>rpl20-rps12_5'</i>	IGS	LSC	F
51	87224	<i>rpl20-rps12_5'</i>	IGS	LSC	89800	<i>rpl20-rps12_5'</i>	IGS	LSC	F
30	87246	<i>rpl20-rps12_5'</i>	IGS	LSC	89822	<i>rpl20-rps12_5'</i>	IGS	LSC	F
39	87274	<i>rpl20-rps12_5'</i>	IGS	LSC	90155	<i>rps12_5'</i>	CDS	LSC	F
93	87305	<i>rpl20-rps12_5'</i>	IGS	LSC	90187	<i>rps12_5'/rps12_5'-ycf3</i>	CDS/IGS	LSC	F
110	87392	<i>rpl20-rps12_5'</i>	IGS	LSC	90278	<i>rps12_5'-ycf3</i>	IGS	LSC	F
61	87450	<i>rpl20-rps12_5'</i>	IGS	LSC	88726	<i>rpl20-rps12_5'</i>	IGS	LSC	F
108	87511	<i>rpl20-rps12_5'</i>	IGS	LSC	90401	<i>rps12_5'-ycf3</i>	IGS	LSC	F
33	87517	<i>rpl20-rps12_5'</i>	IGS	LSC	88796	<i>rpl20-rps12_5'</i>	IGS	LSC	F
55	87540	<i>rpl20-rps12_5'</i>	IGS	LSC	88819	<i>rpl20-rps12_5'</i>	IGS	LSC	F
128	87544	<i>rpl20-rps12_5'</i>	IGS	LSC	90434	<i>rps12_5'-ycf3</i>	IGS	LSC	F
83	87589	<i>rpl20-rps12_5'</i>	IGS	LSC	88874	<i>rpl20-rps12_5'</i>	IGS	LSC	F
101	87593	<i>rpl20-rps12_5'</i>	IGS	LSC	90483	<i>rps12_5'-ycf3</i>	IGS	LSC	F
60	87620	<i>rpl20-rps12_5'</i>	IGS	LSC	88905	<i>rpl20-rps12_5'</i>	IGS	LSC	F
46	87638	<i>rpl20-rps12_5'</i>	IGS	LSC	88923	<i>rpl20-rps12_5'</i>	IGS	LSC	F
54	87761	<i>rpl20-rps12_5'</i>	IGS	LSC	90657	<i>rps12_5'-ycf3</i>	IGS	LSC	F
62	87763	<i>rpl20-rps12_5'</i>	IGS	LSC	89072	<i>rpl20-rps12_5'</i>	IGS	LSC	F
56	87780	<i>rpl20-rps12_5'</i>	IGS	LSC	90676	<i>rps12_5'-ycf3</i>	IGS	LSC	F
38	87798	<i>rpl20-rps12_5'</i>	IGS	LSC	89107	<i>rpl20-rps12_5'</i>	IGS	LSC	F
48	87798	<i>rpl20-rps12_5'</i>	IGS	LSC	90694	<i>rps12_5'-ycf3</i>	IGS	LSC	F
46	87848	<i>rpl20-rps12_5'</i>	IGS	LSC	89157	<i>rpl20-rps12_5'</i>	IGS	LSC	F
30	87898	<i>rpl20-rps12_5'</i>	IGS	LSC	89207	<i>rpl20-rps12_5'</i>	IGS	LSC	F
36	87946	<i>rpl20-rps12_5'</i>	IGS	LSC	90830	<i>rps12_5'-ycf3</i>	IGS	LSC	F
42	87958	<i>rpl20-rps12_5'</i>	IGS	LSC	90842	<i>rps12_5'-ycf3</i>	IGS	LSC	F
50	87964	<i>rpl20-rps12_5'</i>	IGS	LSC	89261	<i>rpl20-rps12_5'</i>	IGS	LSC	F
44	87968	<i>rpl20-rps12_5'</i>	IGS	LSC	90852	<i>rps12_5'-ycf3</i>	IGS	LSC	F
38	87984	<i>rpl20-rps12_5'</i>	IGS	LSC	89281	<i>rpl20-rps12_5'</i>	IGS	LSC	F
30	87984	<i>rpl20-rps12_5'</i>	IGS	LSC	90868	<i>rps12_5'-ycf3</i>	IGS	LSC	F

51	87996	<i>rpl20-rps12_5'</i>	IGS	LSC	89293	<i>rpl20-rps12_5'</i>	IGS	LSC	F
58	88017	<i>rpl20-rps12_5'</i>	IGS	LSC	89314	<i>rpl20-rps12_5'</i>	IGS	LSC	F
32	88023	<i>rpl20-rps12_5'</i>	IGS	LSC	91482	<i>rps12_5'-ycf3</i>	IGS	LSC	F
62	88023	<i>rpl20-rps12_5'</i>	IGS	LSC	90907	<i>rps12_5'-ycf3</i>	IGS	LSC	F
37	88048	<i>rpl20-rps12_5'</i>	IGS	LSC	89345	<i>rpl20-rps12_5'</i>	IGS	LSC	F
42	88048	<i>rpl20-rps12_5'</i>	IGS	LSC	90932	<i>rps12_5'-ycf3</i>	IGS	LSC	F
37	88056	<i>rpl20-rps12_5'</i>	IGS	LSC	89353	<i>rpl20-rps12_5'</i>	IGS	LSC	F
81	88116	<i>rpl20-rps12_5'</i>	IGS	LSC	89413	<i>rpl20-rps12_5'</i>	IGS	LSC	F
61	88136	<i>rpl20-rps12_5'</i>	IGS	LSC	91038	<i>rps12_5'-ycf3</i>	IGS	LSC	F
266	88204	<i>rpl20-rps12_5'</i>	IGS	LSC	89500	<i>rpl20-rps12_5'</i>	IGS	LSC	F
136	88204	<i>rpl20-rps12_5'</i>	IGS	LSC	91105	<i>rps12_5'-ycf3</i>	IGS	LSC	F
132	88204	<i>rpl20-rps12_5'</i>	IGS	LSC	121775	<i>tml-CAA-rm16</i>	IGS	IR	P
112	88237	<i>rpl20-rps12_5'</i>	IGS	LSC	121762	<i>tml-CAA-rm16</i>	IGS	IR	P
156	88289	<i>rpl20-rps12_5'</i>	IGS	LSC	121666	<i>tml-CAA-rm16</i>	IGS	IR	P
170	88300	<i>rpl20-rps12_5'</i>	IGS	LSC	121641	<i>tml-CAA-rm16</i>	IGS	IR	P
31	88446	<i>rpl20-rps12_5'</i>	IGS	LSC	89742	<i>rpl20-rps12_5'</i>	IGS	LSC	F
31	88446	<i>rpl20-rps12_5'</i>	IGS	LSC	121634	<i>tml-CAA-rm16</i>	IGS	IR	P
66	88467	<i>rpl20-rps12_5'</i>	IGS	LSC	89767	<i>rpl20-rps12_5'</i>	IGS	LSC	F
84	88467	<i>rpl20-rps12_5'</i>	IGS	LSC	121556	<i>tml-CAA-rm16</i>	IGS	IR	P
51	88500	<i>rpl20-rps12_5'</i>	IGS	LSC	89800	<i>rpl20-rps12_5'</i>	IGS	LSC	F
30	88522	<i>rpl20-rps12_5'</i>	IGS	LSC	89822	<i>rpl20-rps12_5'</i>	IGS	LSC	F
39	88550	<i>rpl20-rps12_5'</i>	IGS	LSC	90155	<i>rps12_5'</i>	CDS	LSC	F
93	88581	<i>rpl20-rps12_5'</i>	IGS	LSC	90187	<i>rps12_5'/rps12_5'-ycf3</i>	CDS/IGS	LSC	F
130	88668	<i>rpl20-rps12_5'</i>	IGS	LSC	90278	<i>rps12_5'-ycf3</i>	IGS	LSC	F
46	88825	<i>rpl20-rps12_5'</i>	IGS	LSC	90436	<i>rps12_5'-ycf3</i>	IGS	LSC	F
87	88878	<i>rpl20-rps12_5'</i>	IGS	LSC	90483	<i>rps12_5'-ycf3</i>	IGS	LSC	F
86	88893	<i>rpl20-rps12_5'</i>	IGS	LSC	90498	<i>rps12_5'-ycf3</i>	IGS	LSC	F
34	88961	<i>rpl20-rps12_5'</i>	IGS	LSC	90566	<i>rps12_5'-ycf3</i>	IGS	LSC	F
48	88993	<i>rpl20-rps12_5'</i>	IGS	LSC	90580	<i>rps12_5'-ycf3</i>	IGS	LSC	F
36	89016	<i>rpl20-rps12_5'</i>	IGS	LSC	90603	<i>rps12_5'-ycf3</i>	IGS	LSC	F
62	89072	<i>rpl20-rps12_5'</i>	IGS	LSC	90659	<i>rps12_5'-ycf3</i>	IGS	LSC	F
30	89138	<i>rpl20-rps12_5'</i>	IGS	LSC	90725	<i>rps12_5'-ycf3</i>	IGS	LSC	F
36	89211	<i>rpl20-rps12_5'</i>	IGS	LSC	90798	<i>rps12_5'-ycf3</i>	IGS	LSC	F
45	89252	<i>rpl20-rps12_5'</i>	IGS	LSC	90839	<i>rps12_5'-ycf3</i>	IGS	LSC	F
51	89265	<i>rpl20-rps12_5'</i>	IGS	LSC	90852	<i>rps12_5'-ycf3</i>	IGS	LSC	F
55	89297	<i>rpl20-rps12_5'</i>	IGS	LSC	91459	<i>rps12_5'-ycf3</i>	IGS	LSC	F
73	89298	<i>rpl20-rps12_5'</i>	IGS	LSC	90885	<i>rps12_5'-ycf3</i>	IGS	LSC	F
70	89317	<i>rpl20-rps12_5'</i>	IGS	LSC	90904	<i>rps12_5'-ycf3</i>	IGS	LSC	F
42	89353	<i>rpl20-rps12_5'</i>	IGS	LSC	90940	<i>rps12_5'-ycf3</i>	IGS	LSC	F
37	89363	<i>rpl20-rps12_5'</i>	IGS	LSC	91516	<i>rps12_5'-ycf3</i>	IGS	LSC	F
203	89433	<i>rpl20-rps12_5'</i>	IGS	LSC	91038	<i>rps12_5'-ycf3</i>	IGS	LSC	F
63	89469	<i>rpl20-rps12_5'</i>	IGS	LSC	121875	<i>tml-CAA-rm16</i>	IGS	IR	P
101	89483	<i>rpl20-rps12_5'</i>	IGS	LSC	121823	<i>tml-CAA-rm16</i>	IGS	IR	P
133	89499	<i>rpl20-rps12_5'</i>	IGS	LSC	121775	<i>tml-CAA-rm16</i>	IGS	IR	P
112	89533	<i>rpl20-rps12_5'</i>	IGS	LSC	121762	<i>tml-CAA-rm16</i>	IGS	IR	P
214	89585	<i>rpl20-rps12_5'</i>	IGS	LSC	121608	<i>tml-CAA-rm16</i>	IGS	IR	P
225	89596	<i>rpl20-rps12_5'</i>	IGS	LSC	121586	<i>tml-CAA-rm16</i>	IGS	IR	P
200	89633	<i>rpl20-rps12_5'</i>	IGS	LSC	121574	<i>tml-CAA-rm16</i>	IGS	IR	P
55	89800	<i>rpl20-rps12_5'</i>	IGS	LSC	121552	<i>tml-CAA-rm16</i>	IGS	IR	P
43	89822	<i>rpl20-rps12_5'</i>	IGS	LSC	121542	<i>tml-CAA-rm16</i>	IGS	IR	P
110	89835	<i>rpl20-rps12_5'</i>	IGS	LSC	121462	<i>tml-CAA-rm16</i>	IGS	IR	P
51	90888	<i>rps12_5'-ycf3</i>	IGS	LSC	91463	<i>rps12_5'-ycf3</i>	IGS	LSC	F
40	90950	<i>rps12_5'-ycf3</i>	IGS	LSC	91516	<i>rps12_5'-ycf3</i>	IGS	LSC	F
115	91074	<i>rps12_5'-ycf3</i>	IGS	LSC	121823	<i>tml-CAA-rm16</i>	IGS	IR	P
133	91104	<i>rps12_5'-ycf3</i>	IGS	LSC	121775	<i>tml-CAA-rm16</i>	IGS	IR	P
47	91228	<i>rps12_5'-ycf3</i>	IGS	LSC	91411	<i>rps12_5'-ycf3</i>	IGS	LSC	F
156	91228	<i>rps12_5'-ycf3</i>	IGS	LSC	91289	<i>rps12_5'-ycf3</i>	IGS	LSC	F
129	94870	<i>rpl36/rpl36-rps16</i>	CDS/IGS	LSC	97616	<i>rps16-rps8</i>	IGS	LSC	F
80	94924	<i>rpl36/rpl36-rps16</i>	CDS/IGS	LSC	97670	<i>rps16-rps8</i>	IGS	LSC	F
31	94998	<i>rpl36-rps16</i>	IGS	LSC	98032	<i>rps16-rps8</i>	IGS	LSC	F
54	95239	<i>rpl36-rps16</i>	IGS	LSC	97296	<i>rps16-rps8</i>	IGS	LSC	F
61	95239	<i>rpl36-rps16</i>	IGS	LSC	96977	<i>rps16-rps8</i>	IGS	LSC	F
44	95256	<i>rpl36-rps16</i>	IGS	LSC	97313	<i>rps16-rps8</i>	IGS	LSC	F
103	95256	<i>rpl36-rps16</i>	IGS	LSC	96994	<i>rps16-rps8</i>	IGS	LSC	F
80	95265	<i>rpl36-rps16</i>	IGS	LSC	97322	<i>rps16-rps8</i>	IGS	LSC	F
112	95265	<i>rpl36-rps16</i>	IGS	LSC	97003	<i>rps16-rps8</i>	IGS	LSC	F
67	95287	<i>rpl36-rps16</i>	IGS	LSC	97344	<i>rps16-rps8</i>	IGS	LSC	F
101	95301	<i>rpl36-rps16</i>	IGS	LSC	97039	<i>rps16-rps8</i>	IGS	LSC	F
54	95360	<i>rpl36-rps16</i>	IGS	LSC	97098	<i>rps16-rps8</i>	IGS	LSC	F
54	95365	<i>rpl36-rps16</i>	IGS	LSC	97422	<i>rps16-rps8</i>	IGS	LSC	F
41	95378	<i>rpl36-rps16</i>	IGS	LSC	97116	<i>rps16-rps8</i>	IGS	LSC	F
45	95395	<i>rpl36-rps16</i>	IGS	LSC	97133	<i>rps16-rps8</i>	IGS	LSC	F
37	95403	<i>rpl36-rps16</i>	IGS	LSC	97460	<i>rps16-rps8</i>	IGS	LSC	F
39	95415	<i>rpl36-rps16</i>	IGS	LSC	97472	<i>rps16-rps8</i>	IGS	LSC	F
34	95420	<i>rpl36-rps16</i>	IGS	LSC	97158	<i>rps16-rps8</i>	IGS	LSC	F
34	96934	<i>rps16-rps8</i>	IGS	LSC	97572	<i>rps16-rps8</i>	IGS	LSC	F
158	96934	<i>rps16-rps8</i>	IGS	LSC	97253	<i>rps16-rps8</i>	IGS	LSC	F
82	97103	<i>rps16-rps8</i>	IGS	LSC	97422	<i>rps16-rps8</i>	IGS	LSC	F
76	97116	<i>rps16-rps8</i>	IGS	LSC	97435	<i>rps16-rps8</i>	IGS	LSC	F
59	97163	<i>rps16-rps8</i>	IGS	LSC	97482	<i>rps16-rps8</i>	IGS	LSC	F
88	97193	<i>rps16-rps8</i>	IGS	LSC	97512	<i>rps16-rps8</i>	IGS	LSC	F

59	97228	<i>rps16--rps8</i>	IGS	LSC	97547	<i>rps16-rps8</i>	IGS	LSC	F
30	97808	<i>rps16-rps8</i>	IGS	LSC	121260	<i>tml-CAA-rm16</i>	IGS	IR	P
31	98891	<i>rpl16</i> intron	Intron	LSC	99912	<i>rpl16</i> intron	Intron	LSC	F
33	101649	<i>rpl16-rpl22</i>	IGS	LSC	101658	<i>rpl16-rpl22</i>	IGS	LSC	F
34	101654	<i>rpl16-rpl22</i>	IGS	LSC	101667	<i>rpl16-rpl22</i>	IGS	LSC	R
30	101658	<i>rpl16-rpl22</i>	IGS	LSC	101661	<i>rpl16-rpl22</i>	IGS	LSC	F
140	102648	<i>rps19/rps19-tmH-GUG</i>	CDS/AGS	IR	112881	<i>rps7-ndhB</i>	IGS	IR	P
134	102654	<i>rps19/rps19-tmH-GUG</i>	CDS/AGS	IR	135827	<i>tmN-GUU-rps15</i>	IGS	IR	P
33	102759	<i>rps19-tmH-GUG</i>	IGS	IR	135808	<i>tmN-GUU-rps15</i>	IGS	IR	P
39	102761	<i>rps19-tmH-GUG</i>	IGS	IR	120517	<i>tml-CAA-rm16</i>	IGS	IR	P
35	102765	<i>rps19-tmH-GUG</i>	IGS	IR	112869	<i>rps7-ndhB</i>	IGS	IR	P
76	102765	<i>rps19-tmH-GUG</i>	IGS	IR	135774	<i>tmN-GUU-rps15</i>	IGS	IR	P
78	102795	<i>rps19-tmH-GUG</i>	IGS	IR	135742	<i>tmN-GUU-rps15</i>	IGS	IR	P
45	102828	<i>rps19-tmH-GUG</i>	IGS	IR	119209	<i>tml-CAA-rm16</i>	IGS	IR	P
55	102879	<i>rps19-tmH-GUG</i>	IGS	IR	108251	<i>tml-CAU-rps12_3'</i>	IGS	IR	P
31	104986	<i>rpl2-tml-CAU</i>	IGS	IR	138285	<i>tmN-GUU-rps15</i>	IGS	IR	P
61	105019	<i>rpl2-tml-CAU</i>	IGS	IR	138222	<i>tmN-GUU-rps15</i>	IGS	IR	P
82	105038	<i>rpl2-tml-CAU</i>	IGS	IR	138182	<i>tmN-GUU-rps15</i>	IGS	IR	P
96	105056	<i>rpl2-tml-CAU</i>	IGS	IR	138150	<i>tmN-GUU-rps15</i>	IGS	IR	P
89	105069	<i>rpl2-tml-CAU</i>	IGS	IR	138144	<i>tmN-GUU-rps15</i>	IGS	IR	P
46	105121	<i>rpl2-tml-CAU</i>	IGS	IR	138135	<i>tmN-GUU-rps15</i>	IGS	IR	P
34	106044	<i>tml-CAU-rps12_3</i>	IGS	IR	134611	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	107832	<i>tml-CAU-rps12_3</i>	IGS	IR	110619	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
193	107917	<i>tml-CAU-rps12_3</i>	IGS	IR	110647	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
537	107917	<i>tml-CAU-rps12_3</i>	IGS	IR	123363	<i>tml-CAA-rm16</i>	IGS	IR	F
134	108108	<i>tml-CAU-rps12_3</i>	IGS	IR	110847	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
69	108108	<i>tml-CAU-rps12_3</i>	IGS	IR	125004	<i>tml-CAA-rm16</i>	IGS	IR	F
38	108191	<i>tml-CAU-rps12_3</i>	IGS	IR	125086	<i>tml-CAA-rm16</i>	IGS	IR	F
31	108220	<i>tml-CAU-rps12_3</i>	IGS	IR	110959	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
190	108234	<i>tml-CAU-rps12_3</i>	IGS	IR	109571	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
160	108241	<i>tml-CAU-rps12_3</i>	IGS	IR	137057	<i>tmN-GUU-rps15</i>	IGS	IR	F
33	108620	<i>tml-CAU-rps12_3</i>	IGS	IR	121204	<i>tml-CAA-rm16</i>	IGS	IR	F
33	108679	<i>tml-CAU-rps12_3</i>	IGS	IR	136224	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	108715	<i>tml-CAU-rps12_3</i>	IGS	IR	138880	<i>tmN-GUU-rps15</i>	IGS	IR	F
48	108715	<i>tml-CAU-rps12_3</i>	IGS	IR	136259	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	108762	<i>tml-CAU-rps12_3</i>	IGS	IR	125133	<i>tml-CAA-rm16</i>	IGS	IR	F
740	108763	<i>tml-CAU-rps12_3</i>	IGS	IR	136316	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	108799	<i>tml-CAU-rps12_3</i>	IGS	IR	125170	<i>tml-CAA-rm16</i>	IGS	IR	F
58	108993	<i>tml-CAU-rps12_3</i>	IGS	IR	122654	<i>tml-CAA-rm16</i>	IGS	IR	F
60	109481	<i>tml-CAU-rps12_3</i>	IGS	IR	113021	<i>rps7-ndhB</i>	IGS	IR	F
41	109528	<i>tml-CAU-rps12_3</i>	IGS	IR	113068	<i>rps7-ndhB</i>	IGS	IR	F
30	109545	<i>tml-CAU-rps12_3</i>	IGS	IR	113085	<i>rps7-ndhB</i>	IGS	IR	F
190	109571	<i>tml-CAU-rps12_3</i>	IGS	IR	123680	<i>tml-CAA-rm16</i>	IGS	IR	F
160	109578	<i>tml-CAU-rps12_3</i>	IGS	IR	137057	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	109675	<i>tml-CAU-rps12_3</i>	IGS	IR	118120	<i>tml-CAA-rm16</i>	IGS	IR	F
58	109793	<i>tml-CAU-rps12_3</i>	IGS	IR	123896	<i>tml-CAA-rm16</i>	IGS	IR	F
82	109807	<i>tml-CAU-rps12_3</i>	IGS	IR	118246	<i>tml-CAA-rm16</i>	IGS	IR	F
80	109815	<i>tml-CAU-rps12_3</i>	IGS	IR	118254	<i>tml-CAA-rm16</i>	IGS	IR	F
75	109827	<i>tml-CAU-rps12_3</i>	IGS	IR	118266	<i>tml-CAA-rm16</i>	IGS	IR	F
246	109860	<i>tml-CAU-rps12_3</i>	IGS	IR	123954	<i>tml-CAA-rm16</i>	IGS	IR	F
50	109866	<i>tml-CAU-rps12_3</i>	IGS	IR	118305	<i>tml-CAA-rm16</i>	IGS	IR	F
41	109896	<i>tml-CAU-rps12_3</i>	IGS	IR	118335	<i>tml-CAA-rm16</i>	IGS	IR	F
54	109917	<i>tml-CAU-rps12_3</i>	IGS	IR	118356	<i>tml-CAA-rm16</i>	IGS	IR	F
42	109939	<i>tml-CAU-rps12_3</i>	IGS	IR	118378	<i>tml-CAA-rm16</i>	IGS	IR	F
32	109984	<i>tml-CAU-rps12_3</i>	IGS	IR	110155	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
47	109984	<i>tml-CAU-rps12_3</i>	IGS	IR	110182	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
89	109984	<i>tml-CAU-rps12_3</i>	IGS	IR	110020	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
104	109984	<i>tml-CAU-rps12_3</i>	IGS	IR	110056	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
43	109984	<i>tml-CAU-rps12_3</i>	IGS	IR	118441	<i>tml-CAA-rm16</i>	IGS	IR	F
53	109984	<i>tml-CAU-rps12_3</i>	IGS	IR	124195	<i>tml-CAA-rm16</i>	IGS	IR	F
68	109984	<i>tml-CAU-rps12_3</i>	IGS	IR	124114	<i>tml-CAA-rm16</i>	IGS	IR	F
51	109990	<i>tml-CAU-rps12_3</i>	IGS	IR	118411	<i>tml-CAA-rm16</i>	IGS	IR	F
97	110000	<i>tml-CAU-rps12_3</i>	IGS	IR	124256	<i>tml-CAA-rm16</i>	IGS	IR	F
55	110006	<i>tml-CAU-rps12_3</i>	IGS	IR	110114	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
57	110010	<i>tml-CAU-rps12_3</i>	IGS	IR	110172	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
96	110010	<i>tml-CAU-rps12_3</i>	IGS	IR	110082	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
114	110010	<i>tml-CAU-rps12_3</i>	IGS	IR	110046	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
60	110010	<i>tml-CAU-rps12_3</i>	IGS	IR	124140	<i>tml-CAA-rm16</i>	IGS	IR	F
41	110011	<i>tml-CAU-rps12_3</i>	IGS	IR	118432	<i>tml-CAA-rm16</i>	IGS	IR	F
35	110017	<i>tml-CAU-rps12_3</i>	IGS	IR	110152	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
50	110017	<i>tml-CAU-rps12_3</i>	IGS	IR	124336	<i>tml-CAA-rm16</i>	IGS	IR	F
89	110020	<i>tml-CAU-rps12_3</i>	IGS	IR	124078	<i>tml-CAA-rm16</i>	IGS	IR	F
47	110026	<i>tml-CAU-rps12_3</i>	IGS	IR	118411	<i>tml-CAA-rm16</i>	IGS	IR	F
95	110038	<i>tml-CAU-rps12_3</i>	IGS	IR	110074	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
31	110038	<i>tml-CAU-rps12_3</i>	IGS	IR	124330	<i>tml-CAA-rm16</i>	IGS	IR	F
35	110042	<i>tml-CAU-rps12_3</i>	IGS	IR	118427	<i>tml-CAA-rm16</i>	IGS	IR	F
81	110043	<i>tml-CAU-rps12_3</i>	IGS	IR	124182	<i>tml-CAA-rm16</i>	IGS	IR	F
90	110043	<i>tml-CAU-rps12_3</i>	IGS	IR	124263	<i>tml-CAA-rm16</i>	IGS	IR	F
58	110045	<i>tml-CAU-rps12_3</i>	IGS	IR	110171	<i>tml-CAU-rps12_3'</i>	IGS	IR	F
87	110046	<i>tml-CAU-rps12_3</i>	IGS	IR	124104	<i>tml-CAA-rm16</i>	IGS	IR	F
50	110053	<i>tml-CAU-rps12_3</i>	IGS	IR	124336	<i>tml-CAA-rm16</i>	IGS	IR	F

32	110056	<i>tmi-CAU-rps12_3</i>	IGS	IR	118441	<i>tmi-CAA-rm16</i>	IGS	IR	F
113	110056	<i>tmi-CAU-rps12_3</i>	IGS	IR	124078	<i>tmi-CAA-rm16</i>	IGS	IR	F
30	110074	<i>tmi-CAU-rps12_3</i>	IGS	IR	110200	<i>tmi-CAU-rps12_3'</i>	IGS	IR	F
68	110074	<i>tmi-CAU-rps12_3</i>	IGS	IR	124132	<i>tmi-CAA-rm16</i>	IGS	IR	F
99	110079	<i>tmi-CAU-rps12_3</i>	IGS	IR	124182	<i>tmi-CAA-rm16</i>	IGS	IR	F
117	110079	<i>tmi-CAU-rps12_3</i>	IGS	IR	124263	<i>tmi-CAA-rm16</i>	IGS	IR	F
58	110081	<i>tmi-CAU-rps12_3</i>	IGS	IR	110171	<i>tmi-CAU-rps12_3'</i>	IGS	IR	F
105	110082	<i>tmi-CAU-rps12_3</i>	IGS	IR	124104	<i>tmi-CAA-rm16</i>	IGS	IR	F
41	110083	<i>tmi-CAU-rps12_3</i>	IGS	IR	118432	<i>tmi-CAA-rm16</i>	IGS	IR	F
35	110089	<i>tmi-CAU-rps12_3</i>	IGS	IR	110152	<i>tmi-CAU-rps12_3'</i>	IGS	IR	F
50	110089	<i>tmi-CAU-rps12_3</i>	IGS	IR	124336	<i>tmi-CAA-rm16</i>	IGS	IR	F
47	110098	<i>tmi-CAU-rps12_3</i>	IGS	IR	118411	<i>tmi-CAA-rm16</i>	IGS	IR	F
79	110108	<i>tmi-CAU-rps12_3</i>	IGS	IR	124211	<i>tmi-CAA-rm16</i>	IGS	IR	F
32	110110	<i>tmi-CAU-rps12_3</i>	IGS	IR	110146	<i>tmi-CAU-rps12_3'</i>	IGS	IR	F
35	110114	<i>tmi-CAU-rps12_3</i>	IGS	IR	118427	<i>tmi-CAA-rm16</i>	IGS	IR	F
52	110117	<i>tmi-CAU-rps12_3</i>	IGS	IR	110171	<i>tmi-CAU-rps12_3'</i>	IGS	IR	F
32	110128	<i>tmi-CAU-rps12_3</i>	IGS	IR	118441	<i>tmi-CAA-rm16</i>	IGS	IR	F
44	110152	<i>tmi-CAU-rps12_3</i>	IGS	IR	110179	<i>tmi-CAU-rps12_3'</i>	IGS	IR	F
32	110155	<i>tmi-CAU-rps12_3</i>	IGS	IR	118441	<i>tmi-CAA-rm16</i>	IGS	IR	F
43	110160	<i>tmi-CAU-rps12_3</i>	IGS	IR	124173	<i>tmi-CAA-rm16</i>	IGS	IR	F
69	110160	<i>tmi-CAU-rps12_3</i>	IGS	IR	124254	<i>tmi-CAA-rm16</i>	IGS	IR	F
31	110162	<i>tmi-CAU-rps12_3</i>	IGS	IR	110198	<i>tmi-CAU-rps12_3'</i>	IGS	IR	F
52	110171	<i>tmi-CAU-rps12_3</i>	IGS	IR	124139	<i>tmi-CAA-rm16</i>	IGS	IR	F
58	110171	<i>tmi-CAU-rps12_3</i>	IGS	IR	124184	<i>tmi-CAA-rm16</i>	IGS	IR	F
57	110172	<i>tmi-CAU-rps12_3</i>	IGS	IR	124104	<i>tmi-CAA-rm16</i>	IGS	IR	F
41	110173	<i>tmi-CAU-rps12_3</i>	IGS	IR	118432	<i>tmi-CAA-rm16</i>	IGS	IR	F
35	110179	<i>tmi-CAU-rps12_3</i>	IGS	IR	124174	<i>tmi-CAA-rm16</i>	IGS	IR	F
737	110179	<i>tmi-CAU-rps12_3</i>	IGS	IR	124336	<i>tmi-CAA-rm16</i>	IGS	IR	F
43	110182	<i>tmi-CAU-rps12_3</i>	IGS	IR	118441	<i>tmi-CAA-rm16</i>	IGS	IR	F
47	110182	<i>tmi-CAU-rps12_3</i>	IGS	IR	124078	<i>tmi-CAA-rm16</i>	IGS	IR	F
45	110184	<i>tmi-CAU-rps12_3</i>	IGS	IR	118407	<i>tmi-CAA-rm16</i>	IGS	IR	F
31	110198	<i>tmi-CAU-rps12_3</i>	IGS	IR	124175	<i>tmi-CAA-rm16</i>	IGS	IR	F
41	110421	<i>tmi-CAU-rps12_3</i>	IGS	IR	122993	<i>tmi-CAA-rm16</i>	IGS	IR	F
30	110472	<i>tmi-CAU-rps12_3</i>	IGS	IR	121299	<i>tmi-CAA-rm16</i>	IGS	IR	F
30	110487	<i>tmi-CAU-rps12_3</i>	IGS	IR	121314	<i>tmi-CAA-rm16</i>	IGS	IR	F
324	110516	<i>tmi-CAU-rps12_3</i>	IGS	IR	123232	<i>tmi-CAA-rm16</i>	IGS	IR	F
134	110847	<i>tmi-CAU-rps12_3</i>	IGS	IR	123554	<i>tmi-CAA-rm16</i>	IGS	IR	F
38	110930	<i>tmi-CAU-rps12_3</i>	IGS	IR	125086	<i>tmi-CAA-rm16</i>	IGS	IR	F
31	110959	<i>tmi-CAU-rps12_3</i>	IGS	IR	123666	<i>tmi-CAA-rm16</i>	IGS	IR	F
537	112788	<i>rps7-ndh8</i>	IGS	IR	120436	<i>tmi-CAA-rm16</i>	IGS	IR	F
82	112788	<i>rps7-ndh8</i>	IGS	IR	114248	<i>rps7-ndh8/ndh8</i>	IGS/CDS	IR	F
146	112869	<i>rps7-ndh8</i>	IGS	IR	135815	<i>tmiN-GUU-rps15</i>	IGS	IR	F
30	113015	<i>rps7-ndh8</i>	IGS	IR	137028	<i>tmiN-GUU-rps15</i>	IGS	IR	F
73	113101	<i>rps7-ndh8</i>	IGS	IR	119268	<i>tmi-CAA-rm16</i>	IGS	IR	F
31	113143	<i>rps7-ndh8</i>	IGS	IR	119308	<i>tmi-CAA-rm16</i>	IGS	IR	R
35	113194	<i>rps7-ndh8</i>	IGS	IR	119337	<i>tmi-CAA-rm16</i>	IGS	IR	F
654	113279	<i>rps7-ndh8</i>	IGS	IR	119416	<i>tmi-CAA-rm16</i>	IGS	IR	F
37	113517	<i>rps7-ndh8</i>	IGS	IR	134815	<i>tmiN-GUU-rps15</i>	IGS	IR	F
91	113517	<i>rps7-ndh8</i>	IGS	IR	136031	<i>tmiN-GUU-rps15</i>	IGS	IR	F
103	113605	<i>rps7-ndh8</i>	IGS	IR	136128	<i>tmiN-GUU-rps15</i>	IGS	IR	F
38	113670	<i>rps7-ndh8</i>	IGS	IR	138814	<i>tmiN-GUU-rps15</i>	IGS	IR	F
30	113803	<i>rps7-ndh8</i>	IGS	IR	113905	<i>rps7-ndh8</i>	IGS	IR	F
79	113803	<i>rps7-ndh8</i>	IGS	IR	113854	<i>rps7-ndh8</i>	IGS	IR	F
521	113809	<i>rps7-ndh8/ndh8</i>	IGS/CDS	IR	119997	<i>tmi-CAA-rm16</i>	IGS	IR	F
30	113905	<i>rps7-ndh8</i>	IGS	IR	119940	<i>tmi-CAA-rm16</i>	IGS	IR	F
31	118120	<i>tmi-CAA-rm16</i>	IGS	IR	137154	<i>tmiN-GUU-rps15</i>	IGS	IR	F
44	118246	<i>tmi-CAA-rm16</i>	IGS	IR	123910	<i>tmi-CAA-rm16</i>	IGS	IR	F
50	118305	<i>tmi-CAA-rm16</i>	IGS	IR	123960	<i>tmi-CAA-rm16</i>	IGS	IR	F
41	118335	<i>tmi-CAA-rm16</i>	IGS	IR	123990	<i>tmi-CAA-rm16</i>	IGS	IR	F
54	118356	<i>tmi-CAA-rm16</i>	IGS	IR	124011	<i>tmi-CAA-rm16</i>	IGS	IR	F
42	118378	<i>tmi-CAA-rm16</i>	IGS	IR	124033	<i>tmi-CAA-rm16</i>	IGS	IR	F
30	118407	<i>tmi-CAA-rm16</i>	IGS	IR	118443	<i>tmi-CAA-rm16</i>	IGS	IR	F
41	118411	<i>tmi-CAA-rm16</i>	IGS	IR	124345	<i>tmi-CAA-rm16</i>	IGS	IR	F
47	118411	<i>tmi-CAA-rm16</i>	IGS	IR	124120	<i>tmi-CAA-rm16</i>	IGS	IR	F
51	118411	<i>tmi-CAA-rm16</i>	IGS	IR	124084	<i>tmi-CAA-rm16</i>	IGS	IR	F
35	118421	<i>tmi-CAA-rm16</i>	IGS	IR	124175	<i>tmi-CAA-rm16</i>	IGS	IR	F
37	118421	<i>tmi-CAA-rm16</i>	IGS	IR	124211	<i>tmi-CAA-rm16</i>	IGS	IR	F
35	118427	<i>tmi-CAA-rm16</i>	IGS	IR	124136	<i>tmi-CAA-rm16</i>	IGS	IR	F
41	118432	<i>tmi-CAA-rm16</i>	IGS	IR	124105	<i>tmi-CAA-rm16</i>	IGS	IR	F
41	118432	<i>tmi-CAA-rm16</i>	IGS	IR	124267	<i>tmi-CAA-rm16</i>	IGS	IR	F
32	118441	<i>tmi-CAA-rm16</i>	IGS	IR	124150	<i>tmi-CAA-rm16</i>	IGS	IR	F
43	118441	<i>tmi-CAA-rm16</i>	IGS	IR	124078	<i>tmi-CAA-rm16</i>	IGS	IR	F
38	118592	<i>tmi-CAA-rm16</i>	IGS	IR	118893	<i>tmi-CAA-rm16</i>	IGS	IR	F
31	118788	<i>tmi-CAA-rm16</i>	IGS	IR	135322	<i>tmiN-GUU-rps15</i>	IGS	IR	F
43	118844	<i>tmi-CAA-rm16</i>	IGS	IR	135386	<i>tmiN-GUU-rps15</i>	IGS	IR	F
43	118974	<i>tmi-CAA-rm16</i>	IGS	IR	135516	<i>tmiN-GUU-rps15</i>	IGS	IR	F
31	119026	<i>tmi-CAA-rm16</i>	IGS	IR	135559	<i>tmiN-GUU-rps15</i>	IGS	IR	F
48	119063	<i>tmi-CAA-rm16</i>	IGS	IR	135596	<i>tmiN-GUU-rps15</i>	IGS	IR	F
135	119119	<i>tmi-CAA-rm16</i>	IGS	IR	135652	<i>tmiN-GUU-rps15</i>	IGS	IR	F
30	119227	<i>tmi-CAA-rm16</i>	IGS	IR	135760	<i>tmiN-GUU-rps15</i>	IGS	IR	F
73	119268	<i>tmi-CAA-rm16</i>	IGS	IR	120749	<i>tmi-CAA-rm16</i>	IGS	IR	F

31	119310	<i>tml-CAA-mm16</i>	IGS	IR	120789	<i>tml-CAA-mm16</i>	IGS	IR	R
35	119337	<i>tml-CAA-mm16</i>	IGS	IR	120842	<i>tml-CAA-mm16</i>	IGS	IR	F
46	119416	<i>tml-CAA-mm16</i>	IGS	IR	120927	<i>tml-CAA-mm16</i>	IGS	IR	F
37	119654	<i>tml-CAA-mm16</i>	IGS	IR	134815	<i>tmN-GUU-rps15</i>	IGS	IR	F
91	119654	<i>tml-CAA-mm16</i>	IGS	IR	136031	<i>tmN-GUU-rps15</i>	IGS	IR	F
103	119742	<i>tml-CAA-mm16</i>	IGS	IR	136128	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	119807	<i>tml-CAA-mm16</i>	IGS	IR	138814	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	119940	<i>tml-CAA-mm16</i>	IGS	IR	120093	<i>tml-CAA-mm16</i>	IGS	IR	F
130	119940	<i>tml-CAA-mm16</i>	IGS	IR	119991	<i>tml-CAA-mm16</i>	IGS	IR	F
146	120517	<i>tml-CAA-mm16</i>	IGS	IR	135815	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	120525	<i>tml-CAA-mm16</i>	IGS	IR	135808	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	120663	<i>tml-CAA-mm16</i>	IGS	IR	137028	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	121299	<i>tml-CAA-mm16</i>	IGS	IR	124629	<i>tml-CAA-mm16</i>	IGS	IR	F
30	121314	<i>tml-CAA-mm16</i>	IGS	IR	124644	<i>tml-CAA-mm16</i>	IGS	IR	F
58	121974	<i>tml-CAA-mm16</i>	IGS	IR	146920	<i>ndhF</i>	CDS	SSC	F
31	122463	<i>tml-CAA-mm16</i>	IGS	IR	122624	<i>tml-CAA-mm16</i>	IGS	IR	F
117	122463	<i>tml-CAA-mm16</i>	IGS	IR	122486	<i>tml-CAA-mm16</i>	IGS	IR	F
44	122473	<i>tml-CAA-mm16</i>	IGS	IR	122611	<i>tml-CAA-mm16</i>	IGS	IR	F
44	122496	<i>tml-CAA-mm16</i>	IGS	IR	122611	<i>tml-CAA-mm16</i>	IGS	IR	F
44	122519	<i>tml-CAA-mm16</i>	IGS	IR	122611	<i>tml-CAA-mm16</i>	IGS	IR	F
44	122542	<i>tml-CAA-mm16</i>	IGS	IR	122611	<i>tml-CAA-mm16</i>	IGS	IR	F
38	122565	<i>tml-CAA-mm16</i>	IGS	IR	122611	<i>tml-CAA-mm16</i>	IGS	IR	F
58	122654	<i>tml-CAA-mm16</i>	IGS	IR	136546	<i>tmN-GUU-rps15</i>	IGS	IR	F
41	122993	<i>tml-CAA-mm16</i>	IGS	IR	124578	<i>tml-CAA-mm16</i>	IGS	IR	F
324	123232	<i>tml-CAA-mm16</i>	IGS	IR	124673	<i>tml-CAA-mm16</i>	IGS	IR	F
69	123554	<i>tml-CAA-mm16</i>	IGS	IR	125004	<i>tml-CAA-mm16</i>	IGS	IR	F
38	123637	<i>tml-CAA-mm16</i>	IGS	IR	125086	<i>tml-CAA-mm16</i>	IGS	IR	F
160	123687	<i>tml-CAA-mm16</i>	IGS	IR	137057	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	124078	<i>tml-CAA-mm16</i>	IGS	IR	124231	<i>tml-CAA-mm16</i>	IGS	IR	F
47	124078	<i>tml-CAA-mm16</i>	IGS	IR	124339	<i>tml-CAA-mm16</i>	IGS	IR	F
53	124078	<i>tml-CAA-mm16</i>	IGS	IR	124195	<i>tml-CAA-mm16</i>	IGS	IR	F
68	124078	<i>tml-CAA-mm16</i>	IGS	IR	124114	<i>tml-CAA-mm16</i>	IGS	IR	F
97	124094	<i>tml-CAA-mm16</i>	IGS	IR	124256	<i>tml-CAA-mm16</i>	IGS	IR	F
60	124104	<i>tml-CAA-mm16</i>	IGS	IR	124140	<i>tml-CAA-mm16</i>	IGS	IR	F
168	124104	<i>tml-CAA-mm16</i>	IGS	IR	124185	<i>tml-CAA-mm16</i>	IGS	IR	F
50	124111	<i>tml-CAA-mm16</i>	IGS	IR	124336	<i>tml-CAA-mm16</i>	IGS	IR	F
31	124132	<i>tml-CAA-mm16</i>	IGS	IR	124330	<i>tml-CAA-mm16</i>	IGS	IR	F
54	124137	<i>tml-CAA-mm16</i>	IGS	IR	124182	<i>tml-CAA-mm16</i>	IGS	IR	F
35	124147	<i>tml-CAA-mm16</i>	IGS	IR	124336	<i>tml-CAA-mm16</i>	IGS	IR	F
31	124175	<i>tml-CAA-mm16</i>	IGS	IR	124355	<i>tml-CAA-mm16</i>	IGS	IR	F
50	124192	<i>tml-CAA-mm16</i>	IGS	IR	124336	<i>tml-CAA-mm16</i>	IGS	IR	F
31	124213	<i>tml-CAA-mm16</i>	IGS	IR	124330	<i>tml-CAA-mm16</i>	IGS	IR	F
63	124218	<i>tml-CAA-mm16</i>	IGS	IR	124263	<i>tml-CAA-mm16</i>	IGS	IR	F
35	124228	<i>tml-CAA-mm16</i>	IGS	IR	124336	<i>tml-CAA-mm16</i>	IGS	IR	F
31	124256	<i>tml-CAA-mm16</i>	IGS	IR	124355	<i>tml-CAA-mm16</i>	IGS	IR	F
54	124263	<i>tml-CAA-mm16</i>	IGS	IR	124299	<i>tml-CAA-mm16</i>	IGS	IR	F
50	124273	<i>tml-CAA-mm16</i>	IGS	IR	124336	<i>tml-CAA-mm16</i>	IGS	IR	F
31	124294	<i>tml-CAA-mm16</i>	IGS	IR	124330	<i>tml-CAA-mm16</i>	IGS	IR	F
35	124309	<i>tml-CAA-mm16</i>	IGS	IR	124336	<i>tml-CAA-mm16</i>	IGS	IR	F
42	125121	<i>tml-CAA-mm16</i>	IGS	IR	136303	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	125170	<i>tml-CAA-mm16</i>	IGS	IR	136352	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	132675	<i>rm5-tmR-ACG</i>	IGS	IR	132675	<i>rm5-tmR-ACG</i>	IGS	IR	P
31	132899	<i>rm5-tmR-ACG</i>	IGS	IR	149258	<i>tml-UAG-ccsA</i>	IGS	SSC	F
37	132899	<i>rm5-tmR-ACG</i>	IGS	IR	148503	<i>tml-UAG-ccsA</i>	IGS	SSC	F
33	132909	<i>rm5-tmR-ACG</i>	IGS	IR	148513	<i>tml-UAG-ccsA</i>	IGS	SSC	F
30	132912	<i>rm5-tmR-ACG</i>	IGS	IR	149271	<i>tml-UAG-ccsA</i>	IGS	SSC	F
123	134724	<i>tmN-GUU-rps15</i>	IGS	IR	135940	<i>tmN-GUU-rps15</i>	IGS	IR	F
100	136193	<i>tmN-GUU-rps15</i>	IGS	IR	138814	<i>tmN-GUU-rps15</i>	IGS	IR	F
226	137042	<i>tmN-GUU-rps15</i>	IGS	IR	137494	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	148485	<i>tml-UAG/tml-UAG-ccsA</i>	tRNA/IGS	SSC	149240	<i>tml-UAG-ccsA</i>	IGS	SSC	F
49	148497	<i>tml-UAG/tml-UAG-ccsA</i>	tRNA/IGS	SSC	149252	<i>tml-UAG-ccsA</i>	IGS	SSC	F
50	150370	<i>ccsA-ndhD</i>	IGS	SSC	150370	<i>ccsA-ndhD</i>	IGS	SSC	P

* F, forward repeats; P, palindromic repeats; R, reverse repeats; C, complementary repeats; CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

* *C. lupulina*

Repeat length (bp)	Repeat A start site	Repeat A location	Repeat A region	Repeat B start site	Repeat B location	Repeat B region	Repeat type		
59	25	<i>rps19</i>	CDS	LSC	135560	<i>rps12-3'-ndhB</i>	IGS	IR	F
44	77	<i>rps19-rps19-rpl22</i>	CDS/IGS	LSC	135611	<i>rps12-3'-ndhB</i>	IGS	IR	F
30	2462	<i>rps16</i>	CDS	LSC	60056	<i>rpoB-trnC-GCA</i>	IGS	LSC	P
30	2476	<i>rps16</i>	CDS	LSC	59127	<i>rpoB-trnC-GCA</i>	IGS	LSC	P
31	2506	<i>rps16</i>	CDS	LSC	59982	<i>rpoB-trnC-GCA</i>	IGS	LSC	P

30	2509	<i>rps16</i>	CDS	LSC	59088	<i>rpoB-tmC-GCA</i>	IGS	LSC	P
30	2549	<i>rps16</i>	CDS	LSC	59048	<i>rpoB-tmC-GCA</i>	IGS	LSC	P
47	2721	<i>rps16</i>	CDS	LSC	58847	<i>rpoB-tmC-GCA</i>	IGS	LSC	P
48	2721	<i>rps16</i>	CDS	LSC	59716	<i>rpoB-tmC-GCA</i>	IGS	LSC	P
33	2736	<i>rps16</i>	CDS	LSC	58717	<i>rpoB-tmC-GCA</i>	IGS	LSC	P
35	2776	<i>rps16</i>	CDS	LSC	58804	<i>rpoB-tmC-GCA</i>	IGS	LSC	P
30	2785	<i>rps16</i>	CDS	LSC	58800	<i>rpoB-tmC-GCA</i>	IGS	LSC	P
32	4177	<i>rps8-rpl36</i>	IGS	LSC	6604	<i>rps8-rpl36</i>	IGS	LSC	F
45	4431	<i>rps8-rpl36</i>	IGS	LSC	99682	<i>rps19-tmH-GUG</i>	IGS	IR	P
40	4436	<i>rps8-rpl36</i>	IGS	LSC	150678	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	4436	<i>rps8-rpl36</i>	IGS	LSC	134655	<i>rps12-3'-ndhB</i>	IGS	IR	F
38	4438	<i>rps8-rpl36</i>	IGS	LSC	111871	<i>tml-CAU-rps12-3'</i>	IGS	IR	F
33	4443	<i>rps8-rpl36</i>	IGS	LSC	29697	<i>tmQ-UUG-rps14</i>	IGS	LSC	P
37	4654	<i>rps8-rpl36</i>	IGS	LSC	113951	<i>tml-CAU-rps12-3'</i>	IGS	IR	F
31	4660	<i>rps8-rpl36</i>	IGS	LSC	119492	<i>tml-CAU-rps12-3'</i>	IGS	IR	F
32	4714	<i>rps8-rpl36</i>	IGS	LSC	114011	<i>tml-CAU-rps12-3'</i>	IGS	IR	F
33	5691	<i>rps8-rpl36/rps16</i>	IGS	LSC	41309	<i>petB intron</i>	Intron	LSC	F
46	5984	<i>rps8-rpl36</i>	IGS	LSC	114134	<i>tml-CAU-rps12-3'</i>	IGS	IR	F
30	6003	<i>rps8-rpl36</i>	IGS	LSC	119712	<i>tml-CAU-rps12-3'</i>	IGS	IR	F
30	6973	<i>rpl36-tmS-GGA/tmS-GGA</i>	IGS/tRNA	LSC	91108	<i>tmS-GCU</i>	tm	LSC	P
35	8482	<i>ycf3 intron</i>	Intron	LSC	41312	<i>petB intron</i>	Intron	LSC	F
260	9459	<i>ycf3 intron/ycf3/ycf3-rps12</i>	Intron/CDS/IGS	LSC	45175	<i>petD-rpoC1</i>	IGS	LSC	P
56	9713	<i>ycf3-rps12</i>	IGS	LSC	45120	<i>petD-rpoC1</i>	IGS	LSC	P
41	9747	<i>ycf3-rps12</i>	IGS	LSC	45079	<i>petD-rpoC1</i>	IGS	LSC	P
67	9783	<i>ycf3-rps12</i>	IGS	LSC	45018	<i>petD-rpoC1</i>	IGS	LSC	P
30	9822	<i>ycf3-rps12</i>	IGS	LSC	37687	<i>tmR-UUCU-psbB</i>	IGS	LSC	P
32	9849	<i>ycf3-rps12</i>	IGS	LSC	44993	<i>petD-rpoC1</i>	IGS	LSC	P
193	9875	<i>ycf3-rps12</i>	IGS	LSC	44807	<i>petD-rpoC1</i>	IGS	LSC	P
178	9891	<i>ycf3-rps12</i>	IGS	LSC	14760	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
177	9891	<i>ycf3-rps12</i>	IGS	LSC	11548	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
318	9897	<i>ycf3-rps12</i>	IGS	LSC	13146	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
47	9943	<i>ycf3-rps12</i>	IGS	LSC	171288	<i>rps11-rpl32</i>	IGS	SSC	F
34	9955	<i>ycf3-rps12</i>	IGS	LSC	19233	<i>petL-psbE</i>	IGS	LSC	F
40	10000	<i>ycf3-rps12</i>	IGS	LSC	171340	<i>rps11-rpl32</i>	IGS	SSC	F
45	10010	<i>ycf3-rps12</i>	IGS	LSC	171350	<i>rps11-rpl32</i>	IGS	SSC	F
37	10028	<i>ycf3-rps12</i>	IGS	LSC	171368	<i>rps11-rpl32</i>	IGS	SSC	F
62	10207	<i>ycf3-rps12</i>	IGS	LSC	11819	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
144	10207	<i>ycf3-rps12</i>	IGS	LSC	44574	<i>petD-rpoC1</i>	IGS	LSC	P
47	10222	<i>ycf3-rps12</i>	IGS	LSC	13471	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
41	10245	<i>ycf3-rps12</i>	IGS	LSC	13494	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
34	10245	<i>ycf3-rps12</i>	IGS	LSC	11857	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
32	10276	<i>ycf3-rps12</i>	IGS	LSC	13525	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
31	10292	<i>ycf3-rps12</i>	IGS	LSC	13541	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
104	10296	<i>ycf3-rps12</i>	IGS	LSC	44525	<i>petD-rpoC1</i>	IGS	LSC	P
37	10297	<i>ycf3-rps12</i>	IGS	LSC	11909	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
35	10310	<i>ycf3-rps12</i>	IGS	LSC	11922	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
97	10353	<i>ycf3-rps12</i>	IGS	LSC	44475	<i>petD-rpoC1</i>	IGS	LSC	P
111	10401	<i>ycf3-rps12</i>	IGS	LSC	44413	<i>petD-rpoC1</i>	IGS	LSC	P
103	10421	<i>ycf3-rps12</i>	IGS	LSC	44401	<i>petD-rpoC1</i>	IGS	LSC	P
312	10458	<i>ycf3-rps12</i>	IGS	LSC	13695	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
47	10477	<i>ycf3-rps12</i>	IGS	LSC	12083	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
31	10483	<i>ycf3-rps12</i>	IGS	LSC	37619	<i>tmR-UUCU-psbB</i>	IGS	LSC	P
88	10607	<i>ycf3-rps12</i>	IGS	LSC	37444	<i>tmR-UUCU-psbB</i>	IGS	LSC	P
46	10608	<i>ycf3-rps12</i>	IGS	LSC	12221	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
144	10608	<i>ycf3-rps12</i>	IGS	LSC	44178	<i>petD-rpoC1</i>	IGS	LSC	P
72	10617	<i>ycf3-rps12</i>	IGS	LSC	12230	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
50	10643	<i>ycf3-rps12</i>	IGS	LSC	12256	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
47	10655	<i>ycf3-rps12</i>	IGS	LSC	37437	<i>tmR-UUCU-psbB</i>	IGS	LSC	P
33	10675	<i>ycf3-rps12</i>	IGS	LSC	12288	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
53	10676	<i>ycf3-rps12</i>	IGS	LSC	37410	<i>tmR-UUCU-psbB</i>	IGS	LSC	P
47	10705	<i>ycf3-rps12</i>	IGS	LSC	12324	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
49	10707	<i>ycf3-rps12</i>	IGS	LSC	37383	<i>tmR-UUCU-psbB</i>	IGS	LSC	P
100	10765	<i>ycf3-rps12</i>	IGS	LSC	14003	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
31	10765	<i>ycf3-rps12</i>	IGS	LSC	12384	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
85	10765	<i>ycf3-rps12</i>	IGS	LSC	44079	<i>petD-rpoC1</i>	IGS	LSC	P
53	10811	<i>ycf3-rps12</i>	IGS	LSC	12436	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
41	10811	<i>ycf3-rps12</i>	IGS	LSC	37283	<i>tmR-UUCU-psbB</i>	IGS	LSC	P
50	10811	<i>ycf3-rps12</i>	IGS	LSC	37232	<i>tmR-UUCU-psbB</i>	IGS	LSC	P
41	10823	<i>ycf3-rps12</i>	IGS	LSC	12457	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	P
305	10863	<i>ycf3-rps12/rps12/rps12-rpl20</i>	IGS/CDS/IGS	LSC	14093	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
32	10863	<i>ycf3-rps12</i>	IGS	LSC	12480	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
32	10863	<i>ycf3-rps12</i>	IGS	LSC	44034	<i>petD-rpoC1</i>	IGS	LSC	P
315	10873	<i>ycf3-rps12/rps12/rps12-rpl20</i>	IGS/CDS/IGS	LSC	14103	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
55	10907	<i>ycf3-rps12/rps12</i>	IGS/CDS	LSC	12514	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
55	10907	<i>ycf3-rps12/rps12</i>	IGS/CDS	LSC	43977	<i>petD-rpoC1</i>	IGS	LSC	P
58	10962	<i>rps12 CDS_5'</i>	CDS	LSC	12570	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
55	10962	<i>rps12 CDS_5'</i>	CDS	LSC	43920	<i>petD-rpoC1</i>	IGS	LSC	P
114	11048	<i>rps12 CDS_5'/rps12 CDS_5'-rpl20</i>	CDS/IGS	LSC	12640	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
134	11048	<i>rps12 CDS_5'/rps12-rpl20</i>	CDS/IGS	LSC	43771	<i>petD-rpoC1</i>	IGS	LSC	P
164	11071	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	12663	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
206	11081	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	12673	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F

221	11104	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	12696	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
176	11163	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	12755	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
206	11188	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14411	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
42	11190	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	43729	<i>petD-rpoC1</i>	IGS	LSC	P
273	11196	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14419	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
166	11236	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	12828	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
259	11288	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	12880	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
399	11326	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	12918	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
143	11326	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14549	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
62	11459	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171151	<i>rps11-rpl32</i>	IGS	SSC	F
54	11472	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171164	<i>rps11-rpl32</i>	IGS	SSC	F
246	11479	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14691	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
39	11496	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171188	<i>rps11-rpl32</i>	IGS	SSC	F
51	11518	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171210	<i>rps11-rpl32</i>	IGS	SSC	F
177	11548	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44807	<i>petD-rpoC1</i>	IGS	LSC	P
47	11600	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171288	<i>rps11-rpl32</i>	IGS	SSC	F
34	11612	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	19233	<i>petL-psbE</i>	IGS	LSC	F
41	11656	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171339	<i>rps11-rpl32</i>	IGS	SSC	F
45	11667	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171350	<i>rps11-rpl32</i>	IGS	SSC	F
37	11685	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171368	<i>rps11-rpl32</i>	IGS	SSC	F
121	11735	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44681	<i>petD-rpoC1</i>	IGS	LSC	P
112	11769	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44656	<i>petD-rpoC1</i>	IGS	LSC	P
62	11829	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13466	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
34	11857	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44646	<i>petD-rpoC1</i>	IGS	LSC	P
42	11893	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13530	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
37	11909	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44591	<i>petD-rpoC1</i>	IGS	LSC	P
35	11922	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44580	<i>petD-rpoC1</i>	IGS	LSC	P
32	11954	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13585	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
34	12035	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13666	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
53	12077	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13708	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
58	12077	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44396	<i>petD-rpoC1</i>	IGS	LSC	P
36	12089	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37614	<i>tmR-UCU-psbB</i>	IGS	LSC	P
50	12094	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44387	<i>petD-rpoC1</i>	IGS	LSC	P
46	12221	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13845	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
34	12221	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44288	<i>petD-rpoC1</i>	IGS	LSC	P
64	12221	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37467	<i>tmR-UCU-psbB</i>	IGS	LSC	P
72	12230	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13854	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
72	12230	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44241	<i>petD-rpoC1</i>	IGS	LSC	P
66	12240	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44237	<i>petD-rpoC1</i>	IGS	LSC	P
50	12256	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13880	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
46	12256	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37450	<i>tmR-UCU-psbB</i>	IGS	LSC	P
65	12256	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44222	<i>petD-rpoC1</i>	IGS	LSC	P
33	12288	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13912	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
30	12289	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37433	<i>tmR-UCU-psbB</i>	IGS	LSC	F
47	12324	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	13942	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	P
47	12324	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44178	<i>petD-rpoC1</i>	IGS	LSC	P
45	12326	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37387	<i>tmR-UCU-psbB</i>	IGS	LSC	P
32	12383	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14002	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
32	12383	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44133	<i>petD-rpoC1</i>	IGS	LSC	P
61	12407	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37292	<i>tmR-UCU-psbB</i>	IGS	LSC	P
50	12427	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37283	<i>tmR-UCU-psbB</i>	IGS	LSC	P
76	12436	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14049	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
41	12436	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37241	<i>tmR-UCU-psbB</i>	IGS	LSC	P
43	12436	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44075	<i>petD-rpoC1</i>	IGS	LSC	P
35	12447	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	12464	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	P
32	12448	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37280	<i>tmR-UCU-psbB</i>	IGS	LSC	P
34	12448	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	37236	<i>tmR-UCU-psbB</i>	IGS	LSC	P
41	12457	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14061	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	P
100	12470	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	43976	<i>petD-rpoC1</i>	IGS	LSC	P
32	12483	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14096	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
55	12514	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14137	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
126	12569	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	43850	<i>petD-rpoC1</i>	IGS	LSC	P
58	12570	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14192	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
154	12600	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	43791	<i>petD-rpoC1</i>	IGS	LSC	P
148	12626	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	43771	<i>petD-rpoC1</i>	IGS	LSC	P
105	12640	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14278	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
91	12663	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14301	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
87	12673	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14311	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
84	12696	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14334	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
151	12780	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14411	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
42	12782	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	43729	<i>petD-rpoC1</i>	IGS	LSC	P
198	12788	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14419	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
129	12932	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14563	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
62	13051	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171151	<i>rps11-rpl32</i>	IGS	SSC	F
54	13064	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171164	<i>rps11-rpl32</i>	IGS	SSC	F
68	13071	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14691	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
39	13088	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171188	<i>rps11-rpl32</i>	IGS	SSC	F
229	13089	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	14709	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	F
47	13114	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171214	<i>rps11-rpl32</i>	IGS	SSC	F
178	13139	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	44807	<i>petD-rpoC1</i>	IGS	LSC	P
47	13192	<i>rps12 CDS_5'-rpl20</i>	IGS	LSC	171288	<i>rps11-rpl32</i>	IGS	SSC	F

34	13204	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	19233	<i>petL-psbE</i>	IGS	LSC	F
41	13248	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171339	<i>rps11-rpl32</i>	IGS	SSC	F
45	13259	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171350	<i>rps11-rpl32</i>	IGS	SSC	F
37	13277	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171368	<i>rps11-rpl32</i>	IGS	SSC	F
47	13471	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	44656	<i>petD-rpoC1</i>	IGS	LSC	P
41	13494	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	44639	<i>petD-rpoC1</i>	IGS	LSC	P
30	13675	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	37664	<i>tmR-UCU-psbB</i>	IGS	LSC	P
42	13682	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	44438	<i>petD-rpoC1</i>	IGS	LSC	P
66	13695	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	44401	<i>petD-rpoC1</i>	IGS	LSC	P
31	13720	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	37619	<i>tmR-UCU-psbB</i>	IGS	LSC	P
88	13844	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	37444	<i>tmR-UCU-psbB</i>	IGS	LSC	P
144	13845	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	44178	<i>petD-rpoC1</i>	IGS	LSC	P
47	13892	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	37437	<i>tmR-UCU-psbB</i>	IGS	LSC	P
53	13913	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	37410	<i>tmR-UCU-psbB</i>	IGS	LSC	P
49	13944	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	37383	<i>tmR-UCU-psbB</i>	IGS	LSC	P
89	13999	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	44079	<i>petD-rpoC1</i>	IGS	LSC	P
41	14049	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	37283	<i>tmR-UCU-psbB</i>	IGS	LSC	P
50	14049	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	37232	<i>tmR-UCU-psbB</i>	IGS	LSC	P
41	14061	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	14070	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	P
42	14083	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	44034	<i>petD-rpoC1</i>	IGS	LSC	P
55	14137	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	43977	<i>petD-rpoC1</i>	IGS	LSC	P
55	14192	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	43920	<i>petD-rpoC1</i>	IGS	LSC	P
105	14278	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	43800	<i>petD-rpoC1</i>	IGS	LSC	P
97	14301	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	43785	<i>petD-rpoC1</i>	IGS	LSC	P
101	14311	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	43771	<i>petD-rpoC1</i>	IGS	LSC	P
32	14384	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	43767	<i>petD-rpoC1</i>	IGS	LSC	P
42	14413	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	43729	<i>petD-rpoC1</i>	IGS	LSC	P
42	14691	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171171	<i>rps11-rpl32</i>	IGS	SSC	F
39	14742	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171222	<i>rps11-rpl32</i>	IGS	SSC	F
177	14760	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	44807	<i>petD-rpoC1</i>	IGS	LSC	P
47	14812	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171288	<i>rps11-rpl32</i>	IGS	SSC	F
34	14824	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	19233	<i>petL-psbE</i>	IGS	LSC	F
41	14868	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171339	<i>rps11-rpl32</i>	IGS	SSC	F
45	14879	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171350	<i>rps11-rpl32</i>	IGS	SSC	F
37	14897	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171368	<i>rps11-rpl32</i>	IGS	SSC	F
30	14910	<i>rps12_CDS_5'-rpl20</i>	IGS	LSC	171381	<i>rps11-rpl32</i>	IGS	SSC	F
30	15648	<i>rpl20-rpl33</i>	IGS	LSC	15724	<i>rpl20-rpl33</i>	IGS	LSC	F
31	16391	<i>rpl20-rpl33</i>	IGS	LSC	105319	<i>rpl2-tmT-UGU</i>	IGS	IR	F
30	16391	<i>rpl20-rpl33</i>	IGS	LSC	105321	<i>rpl2-tmT-UGU</i>	IGS	IR	F
31	16391	<i>rpl20-rpl33</i>	IGS	LSC	105318	<i>rpl2-tmT-UGU</i>	IGS	IR	C
36	16396	<i>rpl20-rpl33</i>	IGS	LSC	105313	<i>rpl2-tmT-UGU</i>	IGS	IR	R
30	16396	<i>rpl20-rpl33</i>	IGS	LSC	105325	<i>rpl2-tmT-UGU</i>	IGS	IR	C
35	16397	<i>rpl20-rpl33</i>	IGS	LSC	105316	<i>rpl2-tmT-UGU</i>	IGS	IR	P
34	19233	<i>petL-psbE</i>	IGS	LSC	44886	<i>petD-rpoC1</i>	IGS	LSC	P
33	19319	<i>petL-psbE</i>	IGS	LSC	42004	<i>petB/petB-petD</i>	CDS/IGS	LSC	P
82	19412	<i>petL-psbE</i>	IGS	LSC	41830	<i>petB</i>	CDS	LSC	P
42	19480	<i>petL-psbE</i>	IGS	LSC	41802	<i>petB</i>	CDS	LSC	P
39	19499	<i>petL-psbE</i>	IGS	LSC	41786	<i>petB</i>	CDS	LSC	P
31	19553	<i>petL-psbE</i>	IGS	LSC	41732	<i>petB</i>	CDS	LSC	P
61	19608	<i>petL-psbE</i>	IGS	LSC	41635	<i>petB</i>	CDS	LSC	P
56	19618	<i>petL-psbE</i>	IGS	LSC	41630	<i>petB</i>	CDS	LSC	P
42	19688	<i>petL-psbE</i>	IGS	LSC	41555	<i>petB</i>	CDS	LSC	P
30	19734	<i>petL-psbE</i>	IGS	LSC	41522	<i>petB</i>	CDS	LSC	P
50	26029	<i>psaI-rps4</i>	IGS	LSC	75830	<i>tmM-CAU/trmM-CAU-tmV-UAC</i>	tm/IGS	LSC	P
33	26886	<i>rps4</i>	CDS	LSC	60097	<i>rpoB-trnC-GCA</i>	IGS	LSC	F
33	26954	<i>rps4-tmQ-UUG</i>	IGS	LSC	105115	<i>rpl2-tmT-UGU</i>	IGS	IR	F
30	26955	<i>rps4-tmQ-UUG</i>	IGS	LSC	60173	<i>rpoB-trnC-GCA</i>	IGS	LSC	F
81	26976	<i>rps4-tmQ-UUG</i>	IGS	LSC	60202	<i>rpoB-trnC-GCA</i>	IGS	LSC	F
81	27049	<i>rps4-tmQ-UUG</i>	IGS	LSC	60276	<i>rpoB-trnC-GCA</i>	IGS	LSC	F
30	27098	<i>rps4-tmQ-UUG</i>	IGS	LSC	105238	<i>rpl2-tmT-UGU</i>	IGS	IR	F
44	27126	<i>rps4-tmQ-UUG</i>	IGS	LSC	60346	<i>rpoB-trnC-GCA</i>	IGS	LSC	F
30	27160	<i>rps4-tmQ-UUG</i>	IGS	LSC	60386	<i>rpoB-trnC-GCA</i>	IGS	LSC	F
57	27177	<i>rps4-tmQ-UUG</i>	IGS	LSC	60414	<i>rpoB-trnC-GCA</i>	IGS	LSC	F
31	27857	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	106703	<i>tmT-UGU-tmI-CAU</i>	IGS	IR	F
31	27857	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	111468	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
174	28443	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	113027	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
58	28443	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	89098	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC	P
60	28488	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	116561	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
72	28488	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	118803	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
101	28488	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	114273	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
129	28488	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	130627	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
36	28581	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	112111	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
99	28651	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	112889	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
111	28651	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	130485	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
102	28660	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	155120	<i>tmN-GUU-rps15</i>	IGS	IR	P
83	28679	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	112877	<i>tmI-CAU-rps12-3'</i>	IGS	IR	P
30	28716	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	81629	<i>tmT-AGU-atpI</i>	IGS	LSC	P
34	28993	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	154560	<i>tmN-GUU-rps15</i>	IGS	IR	P
180	29027	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	154384	<i>tmN-GUU-rps15</i>	IGS	IR	P
34	29034	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	45688	<i>petD-rpoC1</i>	IGS	LSC	F
62	29068	<i>tmQ-UUG tRNA-rps14</i>	IGS	LSC	45733	<i>petD-rpoC1</i>	IGS	LSC	F

46	29093	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	45758	<i>petD-rpoC1</i>	IGS	LSC	F
156	29093	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	154342	<i>tmN-GUU-rps15</i>	IGS	IR	P
30	29116	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	107060	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
49	29156	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	107091	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
33	29172	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	104388	<i>rpl2-tmT-UGU</i>	IGS	IR	F
34	29220	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	103297	<i>rpl2-tmT-UGU</i>	IGS	IR	F
31	29232	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	104448	<i>rpl2-tmT-UGU</i>	IGS	IR	F
43	29274	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	103351	<i>rpl2-tmT-UGU</i>	IGS	IR	F
42	29386	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	115866	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
56	29386	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	158085	<i>tmN-GUU-rps15</i>	IGS	IR	P
34	29394	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	103457	<i>rpl2-tmT-UGU</i>	IGS	IR	F
41	29453	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	103515	<i>rpl2-tmT-UGU</i>	IGS	IR	F
41	29453	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	115801	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
39	29688	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	99673	<i>rps19-tmH-GUG</i>	IGS	IR	F
42	29688	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	111876	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
59	29688	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	134645	<i>rps12-3'-ndhB</i>	IGS	IR	P
109	29688	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	150618	<i>tmN-GUU-rps15</i>	IGS	IR	P
110	29688	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	151938	<i>tmN-GUU-rps15</i>	IGS	IR	P
100	29698	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	134594	<i>rps12-3'-ndhB</i>	IGS	IR	P
93	29717	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	151926	<i>tmN-GUU-rps15</i>	IGS	IR	P
121	29717	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	153221	<i>tmN-GUU-rps15</i>	IGS	IR	P
163	29717	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	134512	<i>rps12-3'-ndhB</i>	IGS	IR	P
316	29731	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	134345	<i>rps12-3'-ndhB</i>	IGS	IR	P
307	29740	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	130982	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
90	29748	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	111769	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
32	29806	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	150579	<i>tmN-GUU-rps15</i>	IGS	IR	P
43	29836	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	131150	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
42	29836	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	94043	<i>psbK-tmK-UUU</i>	IGS	LSC	F
185	29862	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	93875	<i>psbK-tmK-UUU</i>	IGS	LSC	P
30	30018	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	93874	<i>psbK-tmK-UUU</i>	IGS	LSC	P
110	30047	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	130864	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
231	30047	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	93636	<i>psbK-tmK-UUU</i>	IGS	LSC	P
30	30073	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	111264	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
42	30099	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	106066	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
42	30099	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	150032	<i>tmN-GUU-rps15</i>	IGS	IR	P
50	30099	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	114481	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
66	30099	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	111197	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
69	30099	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	139597	<i>tmL-CAA-m16</i>	IGS	IR	P
38	30103	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	152662	<i>tmN-GUU-rps15</i>	IGS	IR	P
46	30103	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	113279	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
54	30103	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	89226	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC	P
36	30119	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	150018	<i>tmN-GUU-rps15</i>	IGS	IR	P
38	30119	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	113271	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
49	30119	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	130853	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
42	30119	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	89222	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC	P
41	30124	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	106091	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
37	30131	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	114462	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
39	30168	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	111155	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
49	30173	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	139307	<i>tmL-CAA-m16</i>	IGS	IR	P
31	30175	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	149951	<i>tmN-GUU-rps15</i>	IGS	IR	P
31	30176	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	106144	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
30	30178	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	152582	<i>tmN-GUU-rps15</i>	IGS	IR	P
38	30179	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	139273	<i>tmL-CAA-m16</i>	IGS	IR	P
46	30184	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	139221	<i>tmL-CAA-m16</i>	IGS	IR	P
38	30200	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	106172	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
30	30200	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	111128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
38	30200	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	134142	<i>rps12-3'-ndhB</i>	IGS	IR	P
30	30248	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	106217	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
250	30275	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	93396	<i>psbK-tmK-UUU</i>	IGS	LSC	P
70	30284	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	106235	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
70	30284	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	111036	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
30	30360	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	117914	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
48	30366	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	160114	<i>tmN-GUU-rps15</i>	IGS	IR	P
47	30384	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	102346	<i>rpl2-tmT-UGU</i>	IGS	IR	F
45	30384	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	107620	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
47	30384	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	115621	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
46	30385	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	160097	<i>tmN-GUU-rps15</i>	IGS	IR	P
35	30396	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	157856	<i>tmN-GUU-rps15</i>	IGS	IR	P
115	30410	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	93396	<i>psbK-tmK-UUU</i>	IGS	LSC	P
52	30473	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	99502	<i>rps19-tmH-GUG</i>	IGS	IR	F
36	30473	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	149531	<i>tmN-GUU-rps15</i>	IGS	IR	P
52	30473	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	150825	<i>tmN-GUU-rps15</i>	IGS	IR	P
51	30474	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	135348	<i>rps12-3'-ndhB</i>	IGS	IR	P
34	30491	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	93396	<i>psbK-tmK-UUU</i>	IGS	LSC	P
31	30499	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	93391	<i>psbK-tmK-UUU</i>	IGS	LSC	P
49	30539	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	93352	<i>psbK-tmK-UUU</i>	IGS	LSC	P
33	30553	<i>trmQ-UUG tRNA-rps14</i>	IGS	LSC	31214	<i>rps14-rps14</i>	IGS	LSC	F
109	30557	<i>trmQ-UUG-rps14/rps14</i>	IGS/CDS	LSC	135653	<i>rps12-3'-ndhB</i>	IGS	IR	P
123	30565	<i>trmQ-UUG-rps14/rps14</i>	IGS/CDS	LSC	93252	<i>psbK-tmK-UUU</i>	IGS	LSC	P
318	30576	<i>trmQ-UUG-rps14/rps14</i>	IGS/CDS	LSC	31247	<i>rps14-rps14/rps14</i>	IGS/CDS	LSC	F
179	30697	<i>rps14</i>	CDS	LSC	93063	<i>psbK-tmK-UUU</i>	IGS	LSC	P

153	30738	<i>rps14</i>	CDS	LSC	93048	<i>psbK-tmK-UUU</i>	IGS	LSC	P
55	30843	<i>rps14</i>	CDS	LSC	93041	<i>psbK-tmK-UUU</i>	IGS	LSC	P
30	30878	<i>rps14</i>	CDS	LSC	93031	<i>psbK-tmK-UUU</i>	IGS	LSC	P
30	30900	<i>rps14/rps14~rps14</i>	CDS/IGS	LSC	93008	<i>psbK-tmK-UUU</i>	IGS	LSC	P
55	30920	<i>rps14-rps14</i>	IGS	LSC	134700	<i>rps12-3'-ndhB</i>	IGS	IR	P
54	30921	<i>rps14-rps14</i>	IGS	LSC	111914	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
36	30929	<i>rps14-rps14</i>	IGS	LSC	135249	<i>rps12-3'-ndhB</i>	IGS	IR	P
37	30938	<i>rps14-rps14</i>	IGS	LSC	99640	<i>rps19-tmH-GUG</i>	IGS	IR	F
33	30942	<i>rps14-rps14</i>	IGS	LSC	150723	<i>tmN-GUU-rps15</i>	IGS	IR	P
30	30948	<i>rps14-rps14</i>	IGS	LSC	111911	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
120	31102	<i>rps14-rps14</i>	IGS	LSC	135757	<i>rps12-3'-ndhB</i>	IGS	IR	P
33	31214	<i>rps14-rps14</i>	IGS	LSC	93354	<i>psbK-tmK-UUU</i>	IGS	LSC	P
33	31218	<i>rps14-rps14</i>	IGS	LSC	135729	<i>rps12-3'-ndhB</i>	IGS	IR	P
90	31247	<i>tmQ-UUG~rps14/rps14</i>	IGS/CDS	LSC	135653	<i>rps12-3'-ndhB</i>	IGS	IR	P
112	31247	<i>tmQ-UUG~rps14/rps14</i>	IGS/CDS	LSC	93252	<i>psbK-tmK-UUU</i>	IGS	LSC	P
179	31368	<i>rps14</i>	CDS	LSC	93063	<i>psbK-tmK-UUU</i>	IGS	LSC	P
151	31409	<i>rps14</i>	CDS	LSC	93050	<i>psbK-tmK-UUU</i>	IGS	LSC	P
62	36813	<i>psaA-tmR-UCU</i>	IGS	LSC	101902	<i>rpl2-tmT-UGU</i>	IGS	IR	F
62	36813	<i>psaA-tmR-UCU</i>	IGS	LSC	82826	<i>atpI-atpH</i>	IGS	LSC	P
32	36858	<i>psaA-tmR-UCU</i>	IGS	LSC	101947	<i>rpl2-tmT-UGU</i>	IGS	IR	F
32	36858	<i>psaA-tmR-UCU</i>	IGS	LSC	82811	<i>atpI-atpH</i>	IGS	LSC	P
35	36922	<i>psaA-tmR-UCU</i>	IGS	LSC	102008	<i>rpl2-tmT-UGU</i>	IGS	IR	F
31	36922	<i>psaA-tmR-UCU</i>	IGS	LSC	82750	<i>atpI-atpH</i>	IGS	LSC	P
44	37016	<i>psaA-tmR-UCU</i>	IGS	LSC	82629	<i>atpI-atpH</i>	IGS	LSC	P
59	37078	<i>psaA-tmR-UCU/tmR-UCU</i>	IGS/tm	LSC	87370	<i>tmR-UCU/tmR-UCU-tmG-GCC</i>	tm/IGS	LSC	P
32	37137	<i>tmR-UCU/tmR-UCU~psbB</i>	tm/IGS	LSC	87342	<i>atpA-tmR-UCU/tmR-UCU</i>	IGS/tm	LSC	P
31	37177	<i>tmR-UCU-psbB</i>	IGS	LSC	87303	<i>atpA-tmR-UCU</i>	IGS	LSC	P
32	37250	<i>tmR-UCU-psbB</i>	IGS	LSC	44086	<i>petD-rpoC1</i>	IGS	LSC	F
64	37399	<i>tmR-UCU-psbB</i>	IGS	LSC	44190	<i>petD-rpoC1</i>	IGS	LSC	F
94	37437	<i>tmR-UCU-psbB</i>	IGS	LSC	44228	<i>petD-rpoC1</i>	IGS	LSC	F
72	37467	<i>tmR-UCU-psbB</i>	IGS	LSC	44258	<i>petD-rpoC1</i>	IGS	LSC	F
32	37513	<i>tmR-UCU-psbB</i>	IGS	LSC	44304	<i>petD-rpoC1</i>	IGS	LSC	F
31	37619	<i>tmR-UCU-psbB</i>	IGS	LSC	44411	<i>petD-rpoC1</i>	IGS	LSC	F
69	37766	<i>tmR-UCU-psbB</i>	IGS	LSC	109283	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
165	37834	<i>tmR-UCU-psbB</i>	IGS	LSC	109109	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
35	38050	<i>tmR-UCU-psbB</i>	IGS/CDS	LSC	109014	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
61	38067	<i>tmR-UCU-psbB</i>	IGS/CDS	LSC	108971	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
48	38087	<i>psbB</i>	CDS	LSC	108964	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
46	38154	<i>psbB</i>	CDS	LSC	108890	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
31	38212	<i>psbB</i>	CDS	LSC	108856	<i>tml-CAU-rps12-3'</i>	IGS	IR	P
45	44820	<i>petD-rpoC1</i>	IGS	LSC	171350	<i>rps11-rpl32</i>	IGS	SSC	P
41	44835	<i>petD-rpoC1</i>	IGS	LSC	171339	<i>rps11-rpl32</i>	IGS	SSC	P
30	44850	<i>petD-rpoC1</i>	IGS	LSC	171335	<i>rps11-rpl32</i>	IGS	SSC	P
47	44885	<i>petD-rpoC1</i>	IGS	LSC	171288	<i>rps11-rpl32</i>	IGS	SSC	P
35	44901	<i>petD-rpoC1</i>	IGS	LSC	171284	<i>rps11-rpl32</i>	IGS	SSC	P
47	45536	<i>petD-rpoC1</i>	IGS	LSC	106886	<i>tmT-UGU-tml-CAU</i>	IGS	IR	F
41	45553	<i>petD-rpoC1</i>	IGS	LSC	106903	<i>tmT-UGU-tml-CAU</i>	IGS	IR	F
77	45587	<i>petD-rpoC1</i>	IGS	LSC	106937	<i>tmT-UGU-tml-CAU</i>	IGS	IR	F
32	45638	<i>petD-rpoC1</i>	IGS	LSC	106988	<i>tmT-UGU-tml-CAU</i>	IGS	IR	F
34	45698	<i>petD-rpoC1</i>	IGS	LSC	154523	<i>tmN-GUU-rps15</i>	IGS	IR	P
83	45733	<i>petD-rpoC1</i>	IGS	LSC	154440	<i>tmN-GUU-rps15</i>	IGS	IR	P
35	45816	<i>petD-rpoC1</i>	IGS	LSC	102038	<i>rpl2-tmT-UGU</i>	IGS	IR	F
40	49424	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49565	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
32	49438	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49579	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	49440	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50314	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
156	49465	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49558	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
109	49465	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49651	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
89	49465	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49744	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
36	49465	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49837	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
39	49489	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49861	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
237	49503	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49596	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
71	49503	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49782	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
39	49503	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49875	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	49516	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50129	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
60	49530	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49809	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
42	49534	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50147	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
48	49542	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49915	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	49547	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50160	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
39	49555	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49834	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
33	49561	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49882	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
185	49575	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49688	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
46	49575	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49854	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
31	49582	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50270	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
33	49590	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50110	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
44	49591	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49870	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
31	49592	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50280	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	49609	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50129	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
153	49623	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49716	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
40	49627	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50147	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
48	49635	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49915	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	49640	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50160	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F

39	49648	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49834	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
60	49668	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49854	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
31	49675	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50270	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
31	49683	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50110	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
40	49720	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50147	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
48	49728	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49915	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	49733	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50160	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
39	49741	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49834	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
60	49761	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49854	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
31	49768	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50270	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
31	49776	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50110	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
40	49813	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50147	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
60	49821	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	49915	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
31	49861	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50270	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	49870	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50111	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	49871	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50280	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
32	49915	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50155	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
31	50102	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50270	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
44	50119	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50287	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
41	50135	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50303	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
30	50269	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	50314	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC	F
569	58170	<i>rpoB-IGS</i>	CDS/IGS	LSC	59169	<i>rpoB-trmC-GCA</i>	IGS	LSC	F
32	58178	<i>rpoB-trmC-GCA</i>	IGS	LSC	58847	<i>rpoB-trmC-GCA</i>	IGS	LSC	F
89	58847	<i>rpoB-trmC-GCA</i>	IGS	LSC	59717	<i>rpoB-trmC-GCA</i>	IGS	LSC	F
61	58880	<i>rpoB-trmC-GCA</i>	IGS	LSC	59750	<i>rpoB-trmC-GCA</i>	IGS	LSC	F
54	58899	<i>rpoB-trmC-GCA</i>	IGS	LSC	59769	<i>rpoB-trmC-GCA</i>	IGS	LSC	F
84	58957	<i>rpoB-trmC-GCA</i>	IGS	LSC	59833	<i>rpoB-trmC-GCA</i>	IGS	LSC	F
106	58982	<i>rpoB-trmC-GCA</i>	IGS	LSC	59858	<i>rpoB-trmC-GCA</i>	IGS	LSC	F
48	59070	<i>rpoB-trmC-GCA</i>	IGS	LSC	59962	<i>rpoB-trmC-GCA</i>	IGS	LSC	F
30	60173	<i>rpoB-trmC-GCA</i>	IGS	LSC	105116	<i>rpl2-tmT-UGU</i>	IGS	IR	F
30	60325	<i>rpoB-trmC-GCA</i>	IGS	LSC	105238	<i>rpl2-tmT-UGU</i>	IGS	IR	F
61	60783	<i>rpoB-trmC-GCA</i>	IGS	LSC	81866	<i>atpI</i>	CDS	LSC	P
104	60791	<i>rpoB-trmC-GCA</i>	IGS	LSC	81815	<i>atpI</i>	CDS	LSC	P
35	60908	<i>rpoB-trmC-GCA</i>	IGS	LSC	81776	<i>tmTAGU-atp/atpI</i>	IGS/CDS	LSC	P
31	63466	<i>psbM-trmD-GUC</i>	IGS	LSC	105299	<i>rpl2-tmT-UGU</i>	IGS	IR	C
31	63468	<i>psbM-trmD-GUC</i>	IGS	LSC	105314	<i>rpl2-tmT-UGU</i>	IGS	IR	P
31	65824	<i>tmT-AGU-psbD</i>	IGS	LSC	92309	<i>psbK-tmK-UUU</i>	IGS	LSC	P
41	65832	<i>tmT-AGU-psbD</i>	IGS	LSC	92291	<i>psbK-tmK-UUU</i>	IGS	LSC	P
30	65844	<i>tmT-AGU-psbD</i>	IGS	LSC	92290	<i>psbK-tmK-UUU</i>	IGS	LSC	P
69	70659	<i>tmM-CAU-tmM-CAU</i>	IGS	LSC	140497	<i>rm16</i>	rm	IR	P
182	70805	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	140384	<i>rm16</i>	rm	IR	P
209	70987	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	140166	<i>IGS-rm16</i>	IGS/rm	IR	P
205	70996	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	140161	<i>IGS-rm16</i>	IGS/rm	IR	P
95	71196	<i>tmM-CAU-tmV-GAC</i>	IGS	LSC	140077	<i>tmL-CAA-rm16</i>	IGS	IR	P
102	80722	<i>tmL-UAA-tmT-AGU</i>	IGS	LSC	105407	<i>rpl2-tmT-UGU</i>	IGS	IR	F
31	80818	<i>tmL-UAA-tmT-AGU</i>	IGS	LSC	105506	<i>rpl2-tmT-UGU</i>	IGS	IR	F
59	80836	<i>tmL-UAA-tmT-AGU</i>	IGS	LSC	105523	<i>rpl2-tmT-UGU</i>	IGS	IR	F
68	80895	<i>tmL-UAA-tmT-AGU</i>	IGS	LSC	105581	<i>rpl2-tmT-UGU</i>	IGS	IR	F
123	80962	<i>tmL-UAA-tmT-AGU/tmT-AGU/tmT-AGU~atpI</i>	IGS/trn/IGS	LSC	105839	<i>rpl2-tmT-UGU/trnT-UGU/tmT-UGU-trnI-CAU</i>	IGS/trn/IGS	IR	F
63	81084	<i>tmT-AGU-atpI</i>	IGS	LSC	130094	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
54	81093	<i>tmT-AGU-atpI</i>	IGS	LSC	107449	<i>tmT-UGU-tmI-CAU</i>	IGS	IR	P
50	81097	<i>tmT-AGU-atpI</i>	IGS	LSC	89457	<i>tmG-GCC-trmS-GCU</i>	IGS	LSC	F
112	81119	<i>tmT-AGU-atpI</i>	IGS	LSC	114967	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
94	81137	<i>tmT-AGU-atpI</i>	IGS	LSC	159457	<i>tmN-GUU-rps15</i>	IGS	IR	F
40	81250	<i>tmT-AGU-atpI</i>	IGS	LSC	107251	<i>tmT-UGU-tmI-CAU</i>	IGS	IR	P
35	81261	<i>tmT-AGU-atpI</i>	IGS	LSC	107245	<i>tmT-UGU-tmI-CAU</i>	IGS	IR	P
30	81629	<i>tmT-AGU-atpI</i>	IGS	LSC	112893	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
47	82749	<i>atpI-atpH</i>	IGS	LSC	101993	<i>rpl2-tmT-UGU</i>	IGS	IR	P
226	82797	<i>atpI-atpH</i>	IGS	LSC	101767	<i>rpl2-tmT-UGU</i>	IGS	IR	P
30	82907	<i>atpI-atpH</i>	IGS	LSC	101842	<i>rpl2-tmT-UGU</i>	IGS	IR	F
30	82907	<i>atpI-atpH</i>	IGS	LSC	82918	<i>atpI-atpH</i>	IGS	LSC	P
30	82918	<i>atpI-atpH</i>	IGS	LSC	101853	<i>rpl2-tmT-UGU</i>	IGS	IR	F
109	83017	<i>atpI-atpH</i>	IGS	LSC	101665	<i>rpl2-tmT-UGU</i>	IGS	IR	P
116	83126	<i>atpI-atpH</i>	IGS	LSC	101561	<i>rpl2-tmT-UGU</i>	IGS	IR	P
62	83242	<i>atpI-atpH</i>	IGS	LSC	108016	<i>tmI-UGU-tmI-CAU</i>	IGS	IR	P
204	83242	<i>atpI-atpH</i>	IGS	LSC	101347	<i>rpl2-tmT-UGU</i>	IGS	IR	P
84	83307	<i>atpI-atpH</i>	IGS	LSC	107933	<i>tmT-UGU-tmI-CAU</i>	IGS	IR	P
50	83357	<i>atpI-atpH</i>	IGS	LSC	120229	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
48	83359	<i>atpI-atpH</i>	IGS	LSC	114706	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
46	83361	<i>atpI-atpH</i>	IGS	LSC	113504	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
34	83419	<i>atpI-atpH</i>	IGS	LSC	113552	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
30	83423	<i>atpI-atpH</i>	IGS	LSC	161468	<i>tmN-GUU-rps15</i>	IGS	IR	F
61	83462	<i>atpI-atpH</i>	IGS	LSC	112195	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
53	83481	<i>atpI-atpH</i>	IGS	LSC	112214	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
107	83531	<i>atpI-atpH/atpH</i>	IGS/CDS	LSC	112262	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
99	83547	<i>atpI-atpH/atpH</i>	IGS/CDS	LSC	89277	<i>tmG-GCC-trmS-GCU</i>	IGS	LSC	F
95	83548	<i>atpI-atpH/atpH</i>	IGS/CDS	LSC	112279	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
106	89106	<i>tmG-GCC-trmS-GCU</i>	IGS	LSC	113151	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
106	89126	<i>tmG-GCC-trmS-GCU</i>	IGS	LSC	113171	<i>tmI-CAU-rps12-3'</i>	IGS	IR	F
101	89126	<i>tmG-GCC-trmS-GCU</i>	IGS	LSC	155414	<i>tmN-GUU-rps15</i>	IGS	IR	F

93	89134	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	130771	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	89152	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	114402	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
96	89190	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	120982	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
90	89190	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	123033	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
51	89190	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	113235	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
37	89190	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	114436	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
73	89213	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	113258	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
64	89222	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	128179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
35	89222	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	93753	<i>psbK-trnK-UUU</i>	IGS	LSC	F
58	89222	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	106070	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
58	89228	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	152648	<i>tmN-GUU-rps15</i>	IGS	IR	F
52	89228	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	150018	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	89253	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	111232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	89253	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	106067	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
95	89278	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	112279	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	89381	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	112373	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	89425	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	112419	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	89450	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	112438	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
77	89463	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	130113	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
63	89463	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	107430	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
39	89468	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	114956	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
33	89468	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	159429	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	89494	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	107416	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
56	89503	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	130198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
41	89503	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	130153	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
42	89510	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	112477	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
35	89517	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	130167	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	89523	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	112490	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
33	89546	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	130205	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
130	89992	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	133325	<i>rps12-3'-ndhB</i>	IGS	IR	F
45	89992	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	112045	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
69	90086	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	133419	<i>rps12-3'-ndhB</i>	IGS	IR	F
115	90159	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	133500	<i>rps12-3'-ndhB</i>	IGS	IR	F
36	90159	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	149916	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	90220	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	133561	<i>rps12-3'-ndhB</i>	IGS	IR	F
148	90237	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	133578	<i>rps12-3'-ndhB</i>	IGS	IR	F
39	90561	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	106789	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
32	90712	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	90745	<i>tmG-GCC-tms-GCU</i>	IGS	LSC	P
36	92941	<i>psbK-tmK-UUU</i>	IGS	LSC	170674	<i>ndhF-rps11/ps11</i>	IGS/CDS	SSC	F
44	92956	<i>psbK-tmK-UUU</i>	IGS	LSC	170689	<i>rps11</i>	CDS	SSC	F
32	92993	<i>psbK-tmK-UUU</i>	IGS	LSC	135270	<i>rps12-3'-ndhB</i>	IGS	IR	F
30	92996	<i>psbK-tmK-UUU</i>	IGS	LSC	152074	<i>tmN-GUU-rps15</i>	IGS	IR	F
103	93274	<i>psbK-tmK-UUU</i>	IGS	LSC	135653	<i>rps12-3'-ndhB</i>	IGS	IR	F
43	93340	<i>psbK-tmK-UUU</i>	IGS	LSC	135719	<i>rps12-3'-ndhB</i>	IGS	IR	F
53	93395	<i>psbK-tmK-UUU</i>	IGS	LSC	150824	<i>tmN-GUU-rps15</i>	IGS	IR	F
52	93395	<i>psbK-tmK-UUU</i>	IGS	LSC	135347	<i>rps12-3'-ndhB</i>	IGS	IR	F
53	93395	<i>psbK-tmK-UUU</i>	IGS	LSC	99502	<i>rps19-tmH-GUG</i>	IGS	IR	P
36	93412	<i>psbK-tmK-UUU</i>	IGS	LSC	149531	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	93421	<i>psbK-tmK-UUU</i>	IGS	LSC	149540	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	93492	<i>psbK-tmK-UUU</i>	IGS	LSC	107620	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
48	93507	<i>psbK-tmK-UUU</i>	IGS	LSC	160114	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	93507	<i>psbK-tmK-UUU</i>	IGS	LSC	115638	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	93507	<i>psbK-tmK-UUU</i>	IGS	LSC	102346	<i>rpl2-tmT-UGU</i>	IGS	IR	P
30	93531	<i>psbK-tmK-UUU</i>	IGS	LSC	117914	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
70	93567	<i>psbK-tmK-UUU</i>	IGS	LSC	111036	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
70	93567	<i>psbK-tmK-UUU</i>	IGS	LSC	106235	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
30	93637	<i>psbK-tmK-UUU</i>	IGS	LSC	106216	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
38	93676	<i>psbK-tmK-UUU</i>	IGS	LSC	134142	<i>rps12-3'-ndhB</i>	IGS	IR	F
38	93676	<i>psbK-tmK-UUU</i>	IGS	LSC	106172	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
46	93684	<i>psbK-tmK-UUU</i>	IGS	LSC	139221	<i>tmi-L-CAA-rm16</i>	IGS	IR	F
30	93684	<i>psbK-tmK-UUU</i>	IGS	LSC	111128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	93692	<i>psbK-tmK-UUU</i>	IGS	LSC	139307	<i>tmi-L-CAA-rm16</i>	IGS	IR	F
38	93692	<i>psbK-tmK-UUU</i>	IGS	LSC	139268	<i>tmi-L-CAA-rm16</i>	IGS	IR	F
38	93697	<i>psbK-tmK-UUU</i>	IGS	LSC	139234	<i>tmi-L-CAA-rm16</i>	IGS	IR	F
39	93707	<i>psbK-tmK-UUU</i>	IGS	LSC	111155	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	93707	<i>psbK-tmK-UUU</i>	IGS	LSC	139517	<i>tmi-L-CAA-rm16</i>	IGS	IR	F
31	93707	<i>psbK-tmK-UUU</i>	IGS	LSC	106144	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
31	93708	<i>psbK-tmK-UUU</i>	IGS	LSC	149951	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	93708	<i>psbK-tmK-UUU</i>	IGS	LSC	152584	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	93709	<i>psbK-tmK-UUU</i>	IGS	LSC	139246	<i>tmi-L-CAA-rm16</i>	IGS	IR	F
42	93746	<i>psbK-tmK-UUU</i>	IGS	LSC	130853	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
37	93746	<i>psbK-tmK-UUU</i>	IGS	LSC	114462	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	93749	<i>psbK-tmK-UUU</i>	IGS	LSC	111197	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	93749	<i>psbK-tmK-UUU</i>	IGS	LSC	106093	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	P
131	93773	<i>psbK-tmK-UUU</i>	IGS	LSC	134243	<i>rps12-3'-ndhB</i>	IGS	IR	F
42	93773	<i>psbK-tmK-UUU</i>	IGS	LSC	111221	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	93783	<i>psbK-tmK-UUU</i>	IGS	LSC	150042	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	93784	<i>psbK-tmK-UUU</i>	IGS	LSC	114500	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
270	93790	<i>psbK-tmK-UUU</i>	IGS	LSC	130897	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	93811	<i>psbK-tmK-UUU</i>	IGS	LSC	111264	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
42	94043	<i>psbK-tmK-UUU</i>	IGS	LSC	131151	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P

32	94133	<i>psbK-tmK-UUU</i>	IGS	LSC	116385	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	94553	<i>psbK-tmK-UUU</i>	IGS	LSC	104008	<i>rpl2-tmT-UGU</i>	IGS	IR	P
32	97942	<i>matK-psbA</i>	IGS	LSC	98056	<i>matK-psbA</i>	IGS	LSC	F
109	99358	<i>rps19</i>	CDS	IR	135431	<i>rps12-3'-ndhB</i>	IGS	IR	P
184	99389	<i>rps19/rps19-tmH-GUG</i>	CDS/AGS	IR	153453	<i>tmiN-GUU-rps15</i>	IGS	IR	P
40	99432	<i>rps19</i>	CDS	IR	134941	<i>rps12-3'-ndhB</i>	IGS	IR	P
30	99472	<i>rps19/rps19-tmH-GUG</i>	CDS/AGS	IR	135399	<i>rps12-3'-ndhB</i>	IGS	IR	P
80	99493	<i>rps19/rps19-tmH-GUG</i>	CDS/AGS	IR	135329	<i>rps12-3'-ndhB</i>	IGS	IR	P
42	99496	<i>rps19/rps19-tmH-GUG</i>	CDS/AGS	IR	149531	<i>tmiN-GUU-rps15</i>	IGS	IR	P
71	99496	<i>rps19/rps19-tmH-GUG</i>	CDS/AGS	IR	150812	<i>tmiN-GUU-rps15</i>	IGS	IR	P
77	99496	<i>rps19/rps19-tmH-GUG</i>	CDS/AGS	IR	152130	<i>tmiN-GUU-rps15</i>	IGS	IR	P
42	99575	<i>rps19-tmH-GUG</i>	IGS	IR	152101	<i>tmiN-GUU-rps15</i>	IGS	IR	P
36	99581	<i>rps19-tmH-GUG</i>	IGS	IR	135300	<i>rps12-3'-ndhB</i>	IGS	IR	P
30	99616	<i>rps19-tmH-GUG</i>	IGS	IR	152071	<i>tmiN-GUU-rps15</i>	IGS	IR	P
45	99616	<i>rps19-tmH-GUG</i>	IGS	IR	135255	<i>rps12-3'-ndhB</i>	IGS	IR	P
40	99627	<i>rps19-tmH-GUG</i>	IGS	IR	135249	<i>rps12-3'-ndhB</i>	IGS	IR	P
79	99643	<i>rps19-tmH-GUG</i>	IGS	IR	150678	<i>tmiN-GUU-rps15</i>	IGS	IR	P
70	99650	<i>rps19-tmH-GUG</i>	IGS	IR	111871	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
72	99650	<i>rps19-tmH-GUG</i>	IGS	IR	134655	<i>rps12-3'-ndhB</i>	IGS	IR	P
35	99660	<i>rps19-tmH-GUG</i>	IGS	IR	113750	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
38	101330	<i>rpl2-tmt-UGU</i>	IGS	IR	161470	<i>tmiN-GUU-rps15</i>	IGS	IR	P
43	101331	<i>rpl2-tmt-UGU</i>	IGS	IR	113552	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
36	101338	<i>rpl2-tmt-UGU</i>	IGS	IR	114756	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
46	101386	<i>rpl2-tmt-UGU</i>	IGS	IR	113504	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
48	101386	<i>rpl2-tmt-UGU</i>	IGS	IR	114706	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
84	101402	<i>rpl2-tmt-UGU</i>	IGS	IR	107933	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
77	101489	<i>rpl2-tmt-UGU</i>	IGS	IR	108016	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
51	101566	<i>rpl2-tmt-UGU</i>	IGS	IR	112144	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
30	101842	<i>rpl2-tmt-UGU</i>	IGS	IR	101853	<i>rpl2-tmT-UGU</i>	IGS	IR	P
105	102323	<i>rpl2-tmt-UGU</i>	IGS	IR	103666	<i>rpl2-tmT-UGU</i>	IGS	IR	F
74	102323	<i>rpl2-tmt-UGU</i>	IGS	IR	107597	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
74	102323	<i>rpl2-tmt-UGU</i>	IGS	IR	115617	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
108	102326	<i>rpl2-tmt-UGU</i>	IGS	IR	117831	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
95	102339	<i>rpl2-tmt-UGU</i>	IGS	IR	103682	<i>rpl2-tmT-UGU</i>	IGS	IR	F
102	102339	<i>rpl2-tmt-UGU</i>	IGS	IR	117824	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
94	102347	<i>rpl2-tmt-UGU</i>	IGS	IR	160049	<i>tmiN-GUU-rps15</i>	IGS	IR	P
83	102358	<i>rpl2-tmt-UGU</i>	IGS	IR	157808	<i>tmiN-GUU-rps15</i>	IGS	IR	P
74	102367	<i>rpl2-tmt-UGU</i>	IGS	IR	103710	<i>rpl2-tmT-UGU</i>	IGS	IR	F
48	102393	<i>rpl2-tmt-UGU</i>	IGS	IR	107666	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
48	102393	<i>rpl2-tmt-UGU</i>	IGS	IR	115574	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
117	102434	<i>rpl2-tmt-UGU</i>	IGS	IR	107701	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
67	102435	<i>rpl2-tmt-UGU</i>	IGS	IR	103772	<i>rpl2-tmT-UGU</i>	IGS	IR	F
32	102449	<i>rpl2-tmt-UGU</i>	IGS	IR	157767	<i>tmiN-GUU-rps15</i>	IGS	IR	P
75	102449	<i>rpl2-tmt-UGU</i>	IGS	IR	115491	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
42	102482	<i>rpl2-tmt-UGU</i>	IGS	IR	157725	<i>tmiN-GUU-rps15</i>	IGS	IR	P
39	102485	<i>rpl2-tmt-UGU</i>	IGS	IR	103822	<i>rpl2-tmT-UGU</i>	IGS	IR	P
44	102507	<i>rpl2-tmt-UGU</i>	IGS	IR	103844	<i>rpl2-tmT-UGU</i>	IGS	IR	F
105	102550	<i>rpl2-tmt-UGU</i>	IGS	IR	116303	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
62	102569	<i>rpl2-tmt-UGU</i>	IGS	IR	108322	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
74	102581	<i>rpl2-tmt-UGU</i>	IGS	IR	108334	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
34	102641	<i>rpl2-tmt-UGU</i>	IGS	IR	116303	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	102641	<i>rpl2-tmt-UGU</i>	IGS	IR	108378	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	P
36	102666	<i>rpl2-tmt-UGU</i>	IGS	IR	108418	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
123	102666	<i>rpl2-tmt-UGU</i>	IGS	IR	116172	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
40	102776	<i>rpl2-tmt-UGU</i>	IGS	IR	116172	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
71	102803	<i>rpl2-tmt-UGU</i>	IGS	IR	116141	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
67	103297	<i>rpl2-tmt-UGU</i>	IGS	IR	107146	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
55	103309	<i>rpl2-tmt-UGU</i>	IGS	IR	104448	<i>rpl2-tmT-UGU</i>	IGS	IR	F
34	103367	<i>rpl2-tmt-UGU</i>	IGS	IR	107216	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
34	103457	<i>rpl2-tmt-UGU</i>	IGS	IR	158099	<i>tmiN-GUU-rps15</i>	IGS	IR	P
206	103457	<i>rpl2-tmt-UGU</i>	IGS	IR	117947	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
278	103462	<i>rpl2-tmt-UGU</i>	IGS	IR	115617	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
198	103485	<i>rpl2-tmt-UGU</i>	IGS	IR	157906	<i>tmiN-GUU-rps15</i>	IGS	IR	P
34	103583	<i>rpl2-tmt-UGU</i>	IGS	IR	162461	<i>rps15</i>	CDS	IR	P
47	103616	<i>rpl2-tmt-UGU</i>	IGS	IR	162406	<i>rps15</i>	CDS	IR	P
79	103661	<i>rpl2-tmt-UGU</i>	IGS	IR	107592	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
124	103669	<i>rpl2-tmt-UGU</i>	IGS	IR	117815	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
103	103690	<i>rpl2-tmt-UGU</i>	IGS	IR	160040	<i>tmiN-GUU-rps15</i>	IGS	IR	P
92	103701	<i>rpl2-tmt-UGU</i>	IGS	IR	157799	<i>tmiN-GUU-rps15</i>	IGS	IR	P
103	103736	<i>rpl2-tmt-UGU</i>	IGS	IR	107666	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
57	103736	<i>rpl2-tmt-UGU</i>	IGS	IR	115565	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
32	103786	<i>rpl2-tmt-UGU</i>	IGS	IR	157767	<i>tmiN-GUU-rps15</i>	IGS	IR	P
53	103786	<i>rpl2-tmt-UGU</i>	IGS	IR	115513	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
39	103822	<i>rpl2-tmt-UGU</i>	IGS	IR	115491	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	103822	<i>rpl2-tmt-UGU</i>	IGS	IR	107752	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	P
85	103844	<i>rpl2-tmt-UGU</i>	IGS	IR	107774	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
57	103872	<i>rpl2-tmt-UGU</i>	IGS	IR	118770	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
45	103884	<i>rpl2-tmt-UGU</i>	IGS	IR	116518	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
32	103896	<i>rpl2-tmt-UGU</i>	IGS	IR	133493	<i>rps12-3'-ndhB</i>	IGS	IR	P
44	103928	<i>rpl2-tmt-UGU</i>	IGS	IR	107854	<i>tmt-UGU-tmi-CAU</i>	IGS	IR	F
44	103928	<i>rpl2-tmt-UGU</i>	IGS	IR	116479	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P

30	103946	<i>rpl2-tmT-UGU</i>	IGS	IR	116475	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
32	104107	<i>rpl2-tmT-UGU</i>	IGS	IR	106841	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
37	104275	<i>rpl2-tmT-UGU</i>	IGS	IR	107003	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
35	104298	<i>rpl2-tmT-UGU</i>	IGS	IR	107026	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
31	104323	<i>rpl2-tmT-UGU</i>	IGS	IR	107051	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
30	104358	<i>rpl2-tmT-UGU</i>	IGS	IR	107086	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
34	104388	<i>rpl2-tmT-UGU</i>	IGS	IR	107107	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
33	104388	<i>rpl2-tmT-UGU</i>	IGS	IR	154386	<i>tmN-GUU-rps15</i>	IGS	IR	P
31	104399	<i>rpl2-tmT-UGU</i>	IGS	IR	154377	<i>tmN-GUU-rps15</i>	IGS	IR	P
56	104448	<i>rpl2-tmT-UGU</i>	IGS	IR	107158	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
65	104464	<i>rpl2-tmT-UGU</i>	IGS	IR	107174	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
41	104493	<i>rpl2-tmT-UGU</i>	IGS	IR	107203	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
30	104505	<i>rpl2-tmT-UGU</i>	IGS	IR	107215	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	F
45	105305	<i>rpl2-tmT-UGU</i>	IGS	IR	105306	<i>rpl2-tmT-UGU</i>	IGS	IR	C
30	105323	<i>rpl2-tmT-UGU</i>	IGS	IR	105325	<i>rpl2-tmT-UGU</i>	IGS	IR	F
30	105323	<i>rpl2-tmT-UGU</i>	IGS	IR	105324	<i>rpl2-tmT-UGU</i>	IGS	IR	C
35	105976	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	113383	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
101	105989	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	139642	<i>tmiL-CAA-rm16</i>	IGS	IR	P
34	106008	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	111291	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
101	106008	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	139623	<i>tmiL-CAA-rm16</i>	IGS	IR	P
30	106014	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	P
60	106014	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
35	106018	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	P
56	106018	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
79	106018	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	114500	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
72	106036	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	114489	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
96	106036	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	139600	<i>tmiL-CAA-rm16</i>	IGS	IR	P
32	106042	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	P
67	106042	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	151340	<i>tmN-GUU-rps15</i>	IGS	IR	P
108	106042	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	111179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
64	106045	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	150031	<i>tmN-GUU-rps15</i>	IGS	IR	P
48	106060	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	155531	<i>tmN-GUU-rps15</i>	IGS	IR	P
42	106066	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	130880	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
84	106066	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	134201	<i>rps12-3'-ndhB</i>	IGS	IR	P
38	106070	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	113287	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
39	106070	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	152661	<i>tmN-GUU-rps15</i>	IGS	IR	P
31	106091	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	150018	<i>tmN-GUU-rps15</i>	IGS	IR	P
41	106091	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	130856	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
33	106141	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	152584	<i>tmN-GUU-rps15</i>	IGS	IR	P
30	106143	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	139519	<i>tmiL-CAA-rm16</i>	IGS	IR	P
30	106144	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	151260	<i>tmN-GUU-rps15</i>	IGS	IR	P
31	106144	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	139322	<i>tmiL-CAA-rm16</i>	IGS	IR	P
58	106144	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	111128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
78	106144	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	134130	<i>rps12-3'-ndhB</i>	IGS	IR	P
30	106145	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	149950	<i>tmN-GUU-rps15</i>	IGS	IR	P
30	106172	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	139221	<i>tmiL-CAA-rm16</i>	IGS	IR	P
113	106234	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	134014	<i>rps12-3'-ndhB</i>	IGS	IR	P
213	106239	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	110889	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
58	106454	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	110835	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
35	106455	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	111718	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
146	106494	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	151692	<i>tmN-GUU-rps15</i>	IGS	IR	P
175	106494	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	150343	<i>tmN-GUU-rps15</i>	IGS	IR	P
204	106494	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	111504	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
267	106522	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	139809	<i>tmiL-CAA-rm16</i>	IGS	IR	P
127	106561	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	152966	<i>tmN-GUU-rps15</i>	IGS	IR	P
137	106561	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	150314	<i>tmN-GUU-rps15</i>	IGS	IR	P
228	106561	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	111413	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
30	106632	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	151671	<i>tmN-GUU-rps15</i>	IGS	IR	P
33	106655	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	151646	<i>tmN-GUU-rps15</i>	IGS	IR	P
118	106671	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	150223	<i>tmN-GUU-rps15</i>	IGS	IR	P
111	106678	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	151545	<i>tmN-GUU-rps15</i>	IGS	IR	P
30	107060	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	154445	<i>tmN-GUU-rps15</i>	IGS	IR	P
53	107091	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	154382	<i>tmN-GUU-rps15</i>	IGS	IR	P
40	107415	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	130196	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
47	107415	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	130144	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
30	107416	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	112477	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
73	107430	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	130103	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
30	107454	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	114960	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
131	107592	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	115565	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
71	107600	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	117868	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
50	107621	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	160093	<i>tmN-GUU-rps15</i>	IGS	IR	P
39	107632	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	157852	<i>tmN-GUU-rps15</i>	IGS	IR	P
57	107666	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	117815	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
32	107716	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	157767	<i>tmN-GUU-rps15</i>	IGS	IR	P
67	107716	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	115499	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
60	107731	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	115491	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
42	107749	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	157725	<i>tmN-GUU-rps15</i>	IGS	IR	P
131	107802	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	118696	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
119	107814	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	116444	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
32	107826	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	133493	<i>rps12-3'-ndhB</i>	IGS	IR	P
30	107933	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	113504	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P

30	107933	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	155745	<i>tmN-GUU-rps15</i>	IGS	IR	P
32	107933	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	114706	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
34	107933	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	120229	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
31	108289	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	116391	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
62	108322	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	116327	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
78	108334	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	116299	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
45	108409	<i>tmT-UGU-tmi-CAU</i>	IGS	IR	116259	<i>tmi-CAU-rps12-3'</i>	IGS	IR	P
35	110857	<i>tmi-CAU-rps12-3'</i>	IGS	IR	111718	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
115	110994	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134014	<i>rps12-3'-ndhB</i>	IGS	IR	F
33	111101	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134122	<i>rps12-3'-ndhB</i>	IGS	IR	F
32	111126	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139219	<i>tmi-CAA-rm16</i>	IGS	IR	F
135	111128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134150	<i>rps12-3'-ndhB</i>	IGS	IR	F
34	111155	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139322	<i>tmi-CAA-rm16</i>	IGS	IR	F
31	111156	<i>tmi-CAU-rps12-3'</i>	IGS	IR	149951	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	111156	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152584	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	111157	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139246	<i>tmi-CAA-rm16</i>	IGS	IR	F
90	111197	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139600	<i>tmi-CAA-rm16</i>	IGS	IR	F
66	111197	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130856	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
34	111197	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114465	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	111201	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113267	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
173	111207	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151327	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	111207	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150018	<i>tmN-GUU-rps15</i>	IGS	IR	F
52	111207	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152648	<i>tmN-GUU-rps15</i>	IGS	IR	F
74	111213	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114481	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
56	111213	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155523	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	111213	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113279	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
96	111219	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150030	<i>tmN-GUU-rps15</i>	IGS	IR	F
89	111231	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150042	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	111231	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152672	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	111232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113298	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
125	111255	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	111255	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	111264	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130918	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
63	111285	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150096	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	111289	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121097	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
46	111291	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113352	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
58	111341	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114601	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
52	111341	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139736	<i>tmi-CAA-rm16</i>	IGS	IR	F
458	111343	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150153	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	111343	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113399	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	111343	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161313	<i>tmN-GUU-rps15</i>	IGS	IR	F
55	111344	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
38	111344	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
158	111366	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151498	<i>tmN-GUU-rps15</i>	IGS	IR	F
192	111412	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139808	<i>tmi-CAA-rm16</i>	IGS	IR	F
355	111504	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152956	<i>tmN-GUU-rps15</i>	IGS	IR	F
176	111504	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139900	<i>tmi-CAA-rm16</i>	IGS	IR	F
43	111504	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151636	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	111542	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151673	<i>tmN-GUU-rps15</i>	IGS	IR	F
239	111562	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151692	<i>tmN-GUU-rps15</i>	IGS	IR	F
90	111769	<i>tmi-CAU-rps12-3'</i>	IGS	IR	131191	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
62	111797	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151926	<i>tmN-GUU-rps15</i>	IGS	IR	F
49	111810	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150618	<i>tmN-GUU-rps15</i>	IGS	IR	F
93	111875	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134661	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	111875	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150684	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	111896	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113750	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	111920	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113788	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
128	111962	<i>tmi-CAU-rps12-3'</i>	IGS	IR	133242	<i>rps12-3'-ndhB</i>	IGS	IR	F
101	111962	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134747	<i>rps12-3'-ndhB</i>	IGS	IR	F
93	111962	<i>tmi-CAU-rps12-3'</i>	IGS	IR	135015	<i>rps12-3'-ndhB</i>	IGS	IR	F
127	111963	<i>tmi-CAU-rps12-3'</i>	IGS	IR	149659	<i>tmN-GUU-rps15</i>	IGS	IR	F
75	111986	<i>tmi-CAU-rps12-3'</i>	IGS	IR	135039	<i>rps12-3'-ndhB</i>	IGS	IR	F
30	112032	<i>tmi-CAU-rps12-3'</i>	IGS	IR	135085	<i>rps12-3'-ndhB</i>	IGS	IR	F
57	112090	<i>tmi-CAU-rps12-3'</i>	IGS	IR	113006	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
38	112109	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130625	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
40	112467	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130195	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	112467	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130240	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
42	112477	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130205	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
35	112484	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130167	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	112490	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130218	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
501	112771	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155014	<i>tmN-GUU-rps15</i>	IGS	IR	F
240	112771	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130379	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
132	112886	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130494	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
131	113025	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130625	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	113055	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114273	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
72	113084	<i>tmi-CAU-rps12-3'</i>	IGS	IR	118803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
60	113096	<i>tmi-CAU-rps12-3'</i>	IGS	IR	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
93	113179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130771	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	113197	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114402	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
148	113231	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120978	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
128	113231	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161147	<i>tmN-GUU-rps15</i>	IGS	IR	F

94	113231	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123029	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
41	113231	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114432	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
112	113267	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
58	113267	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114469	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	113267	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139604	<i>tmi-CAA-rm16</i>	IGS	IR	F
65	113287	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmiN-GUU-rps15</i>	IGS	IR	F
30	113298	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134254	<i>rps12-3'-ndhB</i>	IGS	IR	F
284	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120049	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
266	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	116770	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
85	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114523	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
84	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123119	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
72	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139658	<i>tmi-CAA-rm16</i>	IGS	IR	F
59	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156759	<i>tmiN-GUU-rps15</i>	IGS	IR	F
32	113320	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150066	<i>tmiN-GUU-rps15</i>	IGS	IR	F
38	113341	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmiN-GUU-rps15</i>	IGS	IR	F
31	113350	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmiN-GUU-rps15</i>	IGS	IR	F
46	113352	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmiN-GUU-rps15</i>	IGS	IR	F
31	113367	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmiN-GUU-rps15</i>	IGS	IR	F
30	113374	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121120	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
487	113375	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155616	<i>tmiN-GUU-rps15</i>	IGS	IR	F
229	113375	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
211	113375	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159053	<i>tmiN-GUU-rps15</i>	IGS	IR	F
176	113375	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156813	<i>tmiN-GUU-rps15</i>	IGS	IR	F
63	113375	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161289	<i>tmiN-GUU-rps15</i>	IGS	IR	F
57	113398	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150152	<i>tmiN-GUU-rps15</i>	IGS	IR	F
205	113399	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
187	113399	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114603	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
50	113399	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139738	<i>tmi-CAA-rm16</i>	IGS	IR	F
37	113399	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151463	<i>tmiN-GUU-rps15</i>	IGS	IR	F
204	113400	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
38	113400	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	113423	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmiN-GUU-rps15</i>	IGS	IR	F
169	113435	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
122	113435	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmiN-GUU-rps15</i>	IGS	IR	F
100	113504	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119209	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
91	113504	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114708	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
46	113549	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmiN-GUU-rps15</i>	IGS	IR	F
45	113558	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114762	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
41	113558	<i>tmi-CAU-rps12-3'</i>	IGS	IR	117008	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
117	113639	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157080	<i>tmiN-GUU-rps15</i>	IGS	IR	F
103	113639	<i>tmi-CAU-rps12-3'</i>	IGS	IR	114847	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
75	113639	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161555	<i>tmiN-GUU-rps15</i>	IGS	IR	F
44	113712	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161627	<i>tmiN-GUU-rps15</i>	IGS	IR	F
35	113750	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150705	<i>tmiN-GUU-rps15</i>	IGS	IR	F
311	113774	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122371	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
149	113774	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119309	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
139	113774	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129539	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
82	113774	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120333	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	113788	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134706	<i>rps12-3'-ndhB</i>	IGS	IR	F
138	113790	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119325	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
133	113790	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129555	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
123	113790	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120349	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
419	113808	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122405	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
115	113808	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120367	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
888	113817	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124466	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
656	113817	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122414	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
111	113817	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120376	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
114	113856	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156095	<i>tmiN-GUU-rps15</i>	IGS	IR	F
36	113934	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120493	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	113941	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125624	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	113941	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123569	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	113944	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119479	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
235	113967	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156205	<i>tmiN-GUU-rps15</i>	IGS	IR	F
45	113972	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120528	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	113973	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119508	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	113997	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119532	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
56	114032	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119567	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
613	114092	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
516	114092	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126780	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
381	114092	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120638	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
292	114092	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123708	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
152	114092	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121656	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
111	114092	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119617	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
102	114092	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125763	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
89	114092	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129846	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	114151	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119710	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
411	114197	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119723	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
45	114197	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
275	114198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmiN-GUU-rps15</i>	IGS	IR	F
172	114212	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
533	114228	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124877	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F

31	114242	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
517	114244	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121807	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
134	114273	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	114273	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmi-GUU-rps15</i>	IGS	IR	F
490	114302	<i>tmi-CAU-rps12-3'</i>	IGS	IR	118803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
225	114302	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmiN-GUU-rps15</i>	IGS	IR	F
171	114302	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161017	<i>tmiN-GUU-rps15</i>	IGS	IR	F
294	114314	<i>tmi-CAU-rps12-3'</i>	IGS	IR	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
444	114348	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121911	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
408	114384	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	114384	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
406	114386	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	114402	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	114432	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmiN-GUU-rps15</i>	IGS	IR	F
99	114432	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	114450	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-rm16</i>	IGS	IR	F
138	114469	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
113	114469	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmiN-GUU-rps15</i>	IGS	IR	F
58	114469	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121014	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
98	114481	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-rm16</i>	IGS	IR	F
50	114481	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	114489	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmiN-GUU-rps15</i>	IGS	IR	F
63	114489	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmiN-GUU-rps15</i>	IGS	IR	F
38	114489	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmiN-GUU-rps15</i>	IGS	IR	F
95	114500	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-rm16</i>	IGS	IR	F
30	114500	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmiN-GUU-rps15</i>	IGS	IR	F
59	114523	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	114523	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmiN-GUU-rps15</i>	IGS	IR	F
32	114523	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmiN-GUU-rps15</i>	IGS	IR	F
38	114544	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmiN-GUU-rps15</i>	IGS	IR	F
31	114553	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmiN-GUU-rps15</i>	IGS	IR	F
46	114555	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmiN-GUU-rps15</i>	IGS	IR	F
31	114570	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmiN-GUU-rps15</i>	IGS	IR	F
31	114578	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121121	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	114578	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
40	114586	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139721	<i>tmi-CAA-rm16</i>	IGS	IR	F
57	114596	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139731	<i>tmi-CAA-rm16</i>	IGS	IR	F
39	114601	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151461	<i>tmiN-GUU-rps15</i>	IGS	IR	F
348	114603	<i>tmi-CAU-rps12-3'</i>	IGS	IR	116849	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
347	114603	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159077	<i>tmiN-GUU-rps15</i>	IGS	IR	F
189	114603	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
187	114603	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155640	<i>tmiN-GUU-rps15</i>	IGS	IR	F
152	114603	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156837	<i>tmiN-GUU-rps15</i>	IGS	IR	F
56	114603	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150153	<i>tmiN-GUU-rps15</i>	IGS	IR	F
39	114603	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161313	<i>tmiN-GUU-rps15</i>	IGS	IR	F
188	114604	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
38	114604	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	114627	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmiN-GUU-rps15</i>	IGS	IR	F
153	114639	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
123	114639	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmiN-GUU-rps15</i>	IGS	IR	F
86	114706	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125355	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
91	114708	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155745	<i>tmiN-GUU-rps15</i>	IGS	IR	F
197	114753	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmiN-GUU-rps15</i>	IGS	IR	F
162	114760	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161468	<i>tmiN-GUU-rps15</i>	IGS	IR	F
45	114762	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119263	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
103	114847	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155880	<i>tmiN-GUU-rps15</i>	IGS	IR	F
30	114920	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161627	<i>tmiN-GUU-rps15</i>	IGS	IR	F
202	114945	<i>tmi-CAU-rps12-3'</i>	IGS	IR	117192	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
201	114946	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157178	<i>tmiN-GUU-rps15</i>	IGS	IR	F
43	114946	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159419	<i>tmiN-GUU-rps15</i>	IGS	IR	F
35	114960	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130122	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
501	114985	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159457	<i>tmiN-GUU-rps15</i>	IGS	IR	F
343	115143	<i>tmi-CAU-rps12-3'</i>	IGS	IR	117389	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
136	115486	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159961	<i>tmiN-GUU-rps15</i>	IGS	IR	F
84	115486	<i>tmi-CAU-rps12-3'</i>	IGS	IR	117735	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
47	115486	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157720	<i>tmiN-GUU-rps15</i>	IGS	IR	F
36	115534	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157767	<i>tmiN-GUU-rps15</i>	IGS	IR	F
57	115565	<i>tmi-CAU-rps12-3'</i>	IGS	IR	117815	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
71	115617	<i>tmi-CAU-rps12-3'</i>	IGS	IR	117868	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
50	115617	<i>tmi-CAU-rps12-3'</i>	IGS	IR	160093	<i>tmiN-GUU-rps15</i>	IGS	IR	F
39	115617	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157852	<i>tmiN-GUU-rps15</i>	IGS	IR	F
198	115674	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157906	<i>tmiN-GUU-rps15</i>	IGS	IR	F
342	115694	<i>tmi-CAU-rps12-3'</i>	IGS	IR	117947	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
340	115694	<i>tmi-CAU-rps12-3'</i>	IGS	IR	160169	<i>tmiN-GUU-rps15</i>	IGS	IR	F
47	115694	<i>tmi-CAU-rps12-3'</i>	IGS	IR	162406	<i>rps15</i>	CDS	IR	F
34	115740	<i>tmi-CAU-rps12-3'</i>	IGS	IR	162461	<i>rps15</i>	CDS	IR	F
170	115866	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158099	<i>tmiN-GUU-rps15</i>	IGS	IR	F
533	116030	<i>tmi-CAU-rps12-3'</i>	IGS	IR	118282	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	116030	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158262	<i>tmiN-GUU-rps15</i>	IGS	IR	F
40	116051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158278	<i>tmiN-GUU-rps15</i>	IGS	IR	F
38	116053	<i>tmi-CAU-rps12-3'</i>	IGS	IR	160518	<i>tmiN-GUU-rps15</i>	IGS	IR	F

477	116086	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158314	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	116519	<i>tmi-CAU-rps12-3'</i>	IGS	IR	133493	<i>rps12-3'-ndhB</i>	IGS	IR	F
477	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119840	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
294	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	118815	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
213	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158791	<i>tmN-GUU-rps15</i>	IGS	IR	F
159	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120860	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
93	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130696	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
70	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123930	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
60	116561	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155339	<i>tmN-GUU-rps15</i>	IGS	IR	F
224	116631	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	116631	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
222	116633	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	116649	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	116679	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	116679	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	116697	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-m16</i>	IGS	IR	F
138	116716	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
113	116716	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	116716	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121014	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
98	116728	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-m16</i>	IGS	IR	F
50	116728	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	116736	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	116736	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	116736	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	116747	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-m16</i>	IGS	IR	F
30	116747	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	116770	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	116770	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	116770	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	116791	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	116800	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	116802	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	116817	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	116824	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121120	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
371	116825	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159053	<i>tmN-GUU-rps15</i>	IGS	IR	F
213	116825	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
211	116825	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155616	<i>tmN-GUU-rps15</i>	IGS	IR	F
176	116825	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156813	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	116825	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161289	<i>tmN-GUU-rps15</i>	IGS	IR	F
57	116848	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150152	<i>tmN-GUU-rps15</i>	IGS	IR	F
189	116849	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
50	116849	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139738	<i>tmi-CAA-m16</i>	IGS	IR	F
37	116849	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151463	<i>tmN-GUU-rps15</i>	IGS	IR	F
188	116850	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
38	116850	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	116873	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
153	116885	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
123	116885	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
91	116954	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155745	<i>tmN-GUU-rps15</i>	IGS	IR	F
197	116999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
162	117006	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161468	<i>tmN-GUU-rps15</i>	IGS	IR	F
41	117008	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155799	<i>tmN-GUU-rps15</i>	IGS	IR	F
103	117093	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155880	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	117166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161627	<i>tmN-GUU-rps15</i>	IGS	IR	F
589	117193	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157178	<i>tmN-GUU-rps15</i>	IGS	IR	F
43	117193	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159419	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	117207	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130122	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
162	117232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159457	<i>tmN-GUU-rps15</i>	IGS	IR	F
605	117389	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161848	<i>tmN-GUU-rps15/rps15</i>	IGS/CDS	IR	F
430	117389	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159615	<i>tmN-GUU-rps15</i>	IGS	IR	F
124	117783	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157767	<i>tmN-GUU-rps15</i>	IGS	IR	F
103	117815	<i>tmi-CAU-rps12-3'</i>	IGS	IR	160040	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	117910	<i>tmi-CAU-rps12-3'</i>	IGS	IR	160134	<i>tmN-GUU-rps15</i>	IGS	IR	F
351	117936	<i>tmi-CAU-rps12-3'</i>	IGS	IR	160158	<i>tmN-GUU-rps15</i>	IGS	IR	F
178	117947	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157926	<i>tmN-GUU-rps15</i>	IGS	IR	F
34	117993	<i>tmi-CAU-rps12-3'</i>	IGS	IR	162461	<i>rps15</i>	CDS	IR	F
189	118119	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158099	<i>tmN-GUU-rps15</i>	IGS	IR	F
40	118303	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158278	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	118305	<i>tmi-CAU-rps12-3'</i>	IGS	IR	160518	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	118314	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158289	<i>tmN-GUU-rps15</i>	IGS	IR	F
690	118338	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158314	<i>tmN-GUU-rps15</i>	IGS	IR	F
636	118338	<i>tmi-CAU-rps12-3'</i>	IGS	IR	160552	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	118771	<i>tmi-CAU-rps12-3'</i>	IGS	IR	133493	<i>rps12-3'-ndhB</i>	IGS	IR	F
306	118803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119828	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
171	118803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120848	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	118803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130684	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
82	118803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123918	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
72	118803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155327	<i>tmN-GUU-rps15</i>	IGS	IR	F
649	118809	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121871	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
639	118809	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129039	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
582	118809	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124957	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F

573	118885	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	118885	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
504	118887	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	118903	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	118933	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	118933	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	118951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-rm16</i>	IGS	IR	F
138	118970	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
113	118970	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	118970	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121014	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
98	118982	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-rm16</i>	IGS	IR	F
50	118982	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndh8</i>	IGS	IR	F
66	118990	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	118990	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	118990	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	119001	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-rm16</i>	IGS	IR	F
30	119001	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	119024	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	119024	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	119024	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	119045	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	119054	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	119056	<i>tmi-CAU-rps12-3'</i>	IGS	IR	153411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	119071	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	119079	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121121	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	119079	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
40	119087	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139721	<i>tmi-CAA-rm16</i>	IGS	IR	F
57	119097	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139731	<i>tmi-CAA-rm16</i>	IGS	IR	F
39	119102	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151461	<i>tmN-GUU-rps15</i>	IGS	IR	F
624	119104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127290	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
401	119104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
189	119104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159077	<i>tmN-GUU-rps15</i>	IGS	IR	F
187	119104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155640	<i>tmN-GUU-rps15</i>	IGS	IR	F
152	119104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156837	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	119104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150153	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	119104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161313	<i>tmN-GUU-rps15</i>	IGS	IR	F
401	119105	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
38	119105	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	119128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
588	119140	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
122	119140	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
299	119207	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125355	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
100	119209	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155745	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	119254	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	119263	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	119263	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
88	119309	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	119391	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156095	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	119469	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156173	<i>tmN-GUU-rps15</i>	IGS	IR	F
49	119479	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122541	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
226	119502	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126665	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
204	119502	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129731	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
77	119502	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125649	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
220	119508	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120529	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	119508	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122570	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	119532	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122594	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
56	119567	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156270	<i>tmN-GUU-rps15</i>	IGS	IR	F
53	119567	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122629	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	119576	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125722	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
111	119617	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122689	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
110	119617	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	119676	<i>tmi-CAU-rps12-3'</i>	IGS	IR	119710	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
62	119706	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129934	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	119710	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120697	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	119712	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129907	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
806	119723	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126885	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
411	119723	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124846	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
276	119723	<i>tmi-CAU-rps12-3'</i>	IGS	IR	120743	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
187	119723	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123813	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
47	119723	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121761	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
275	119724	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
172	119738	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	119768	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
364	119770	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121807	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
134	119799	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	119799	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
225	119828	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
171	119828	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161017	<i>tmN-GUU-rps15</i>	IGS	IR	F
224	119910	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	119910	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
222	119912	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F

31	119928	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	119958	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	119958	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	119976	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-m16</i>	IGS	IR	F
138	119995	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
113	119995	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	119995	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121014	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
98	120007	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-m16</i>	IGS	IR	F
50	120007	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	120015	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	120015	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	120015	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	120026	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-m16</i>	IGS	IR	F
30	120026	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	120049	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	120049	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	120049	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	120070	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	120079	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	120081	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	120096	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	120103	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121120	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
425	120104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
229	120104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155616	<i>tmN-GUU-rps15</i>	IGS	IR	F
213	120104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159053	<i>tmN-GUU-rps15</i>	IGS	IR	F
176	120104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156813	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	120104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161289	<i>tmN-GUU-rps15</i>	IGS	IR	F
57	120127	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150152	<i>tmN-GUU-rps15</i>	IGS	IR	F
401	120128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125252	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
359	120128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
50	120128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139738	<i>tmi-CAA-m16</i>	IGS	IR	F
37	120128	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151463	<i>tmN-GUU-rps15</i>	IGS	IR	F
400	120129	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
38	120129	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	120152	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
365	120164	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
122	120164	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	120278	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	120287	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	120287	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	120333	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	120349	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156031	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	120416	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156096	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	120493	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122531	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
405	120525	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123595	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
45	120528	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122569	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
490	120529	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126671	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
401	120529	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127694	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
261	120529	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121547	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
198	120529	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129737	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
71	120529	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	120553	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122594	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
53	120588	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122629	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	120597	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125722	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
434	120638	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122689	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
381	120638	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124741	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
110	120638	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	120743	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
328	120744	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
172	120758	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	120788	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
229	120790	<i>tmi-CAU-rps12-3'</i>	IGS	IR	121807	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
134	120819	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	120819	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
258	120848	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161017	<i>tmN-GUU-rps15</i>	IGS	IR	F
171	120848	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
89	120930	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
87	120932	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	120948	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
41	120978	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
136	121014	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
58	121014	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129200	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
58	121014	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122032	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	121014	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139604	<i>tmi-CAA-m16</i>	IGS	IR	F
46	121026	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
65	121034	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	121034	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	121045	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134254	<i>rps12-3'-ndhB</i>	IGS	IR	F
83	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156759	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122086	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
56	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139658	<i>tmi-CAA-m16</i>	IGS	IR	F

32	121067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150066	<i>tmN-GUU-rps15</i>	IGS	IR	F
62	121088	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	121097	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151409	<i>tmN-GUU-rps15</i>	IGS	IR	F
43	121107	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161275	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	121120	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127265	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
62	121121	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123174	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	121121	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122141	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
156	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161314	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122167	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
36	121145	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151464	<i>tmN-GUU-rps15</i>	IGS	IR	F
629	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127326	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
366	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123233	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
323	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122202	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
169	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155676	<i>tmN-GUU-rps15</i>	IGS	IR	F
153	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159113	<i>tmN-GUU-rps15</i>	IGS	IR	F
116	121179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156873	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	121293	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	121302	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	121302	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	121348	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	121364	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156031	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	121431	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156096	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	121508	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156173	<i>tmN-GUU-rps15</i>	IGS	IR	F
49	121518	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122541	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
267	121541	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126665	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
204	121541	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129731	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
77	121541	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125649	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
261	121547	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123599	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	121547	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122570	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	121571	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122594	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
56	121606	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156270	<i>tmN-GUU-rps15</i>	IGS	IR	F
53	121606	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122629	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	121615	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125722	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
152	121656	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122689	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
110	121656	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	121761	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
46	121762	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	121776	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	121806	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130006	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
703	121807	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128975	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
646	121807	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124893	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
364	121807	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126932	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
229	121807	<i>tmi-CAU-rps12-3'</i>	IGS	IR	122841	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
140	121807	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123860	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
126	121836	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	121836	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
109	121861	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130680	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
225	121865	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
171	121865	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161017	<i>tmN-GUU-rps15</i>	IGS	IR	F
1123	121947	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	121947	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
504	121949	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	121965	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	121995	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	121995	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	122013	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-m16</i>	IGS	IR	F
138	122032	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
113	122032	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	122032	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	122044	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-m16</i>	IGS	IR	F
50	122044	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	122052	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	122052	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	122052	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	122063	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-m16</i>	IGS	IR	F
30	122063	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	122086	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	122086	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	122086	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	122107	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	122116	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	122118	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	122133	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	122141	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
40	122149	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139721	<i>tmi-CAA-m16</i>	IGS	IR	F
57	122159	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139731	<i>tmi-CAA-m16</i>	IGS	IR	F
39	122164	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151461	<i>tmN-GUU-rps15</i>	IGS	IR	F
359	122166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127290	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
205	122166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155640	<i>tmN-GUU-rps15</i>	IGS	IR	F
189	122166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159077	<i>tmN-GUU-rps15</i>	IGS	IR	F
152	122166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156837	<i>tmN-GUU-rps15</i>	IGS	IR	F

56	122166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150153	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	122166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161313	<i>tmN-GUU-rps15</i>	IGS	IR	F
358	122167	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	122190	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	122202	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	122316	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	122325	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	122325	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
88	122371	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
114	122453	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156095	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	122454	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125540	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	122538	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125624	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	122538	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123569	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	122541	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127665	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
235	122564	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156205	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	122569	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123598	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	122570	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	122594	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123623	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
53	122629	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123658	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
381	122689	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126780	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
292	122689	<i>tmi-CAU-rps12-3'</i>	IGS	IR	123708	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
102	122689	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125763	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
89	122689	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129846	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
45	122794	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
383	122795	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
172	122809	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	122839	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
134	122870	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	122870	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
224	122899	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161017	<i>tmN-GUU-rps15</i>	IGS	IR	F
171	122899	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
89	122981	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
87	122983	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	122999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
41	123029	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
138	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124084	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
68	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155511	<i>tmN-GUU-rps15</i>	IGS	IR	F
62	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130860	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
58	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	123065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139604	<i>tmi-CAA-m16</i>	IGS	IR	F
98	123077	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-m16</i>	IGS	IR	F
50	123077	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndh8</i>	IGS	IR	F
66	123085	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	123085	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	123085	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	123096	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-m16</i>	IGS	IR	F
30	123096	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	123119	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	123119	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	123119	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	123140	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	123149	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	123151	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	123166	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	123173	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128285	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
401	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125253	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
358	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124219	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
204	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155641	<i>tmN-GUU-rps15</i>	IGS	IR	F
188	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159078	<i>tmN-GUU-rps15</i>	IGS	IR	F
151	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156838	<i>tmN-GUU-rps15</i>	IGS	IR	F
55	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150154	<i>tmN-GUU-rps15</i>	IGS	IR	F
49	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139739	<i>tmi-CAA-m16</i>	IGS	IR	F
38	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161314	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	123198	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151464	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	123233	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	123347	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	123356	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	123356	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	123402	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	123418	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156031	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	123485	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156096	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	123562	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156173	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	123569	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124590	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
203	123594	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129732	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
76	123594	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125650	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
45	123598	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124621	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
543	123599	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127694	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
401	123599	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126671	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	123623	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124646	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
56	123658	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156270	<i>tmN-GUU-rps15</i>	IGS	IR	F
53	123658	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124681	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F

143	123667	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125722	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
292	123708	<i>tmi-CAU-rps12-3'</i>	IGS	IR	124741	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
110	123708	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	123813	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
186	123814	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
172	123828	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	123858	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
111	123889	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	123889	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	123918	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
563	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129115	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
506	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125033	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
224	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127072	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
143	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158861	<i>tmN-GUU-rps15</i>	IGS	IR	F
89	123999	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156621	<i>tmN-GUU-rps15</i>	IGS	IR	F
504	124001	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	124017	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	124047	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	124047	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	124065	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmL-CAA-m16</i>	IGS	IR	F
113	124084	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	124084	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	124096	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmL-CAA-m16</i>	IGS	IR	F
50	124096	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	124104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	124104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	124104	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	124115	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmL-CAA-m16</i>	IGS	IR	F
30	124115	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	124138	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	124138	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	124138	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	124159	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	124168	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	124170	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	124185	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	124193	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
40	124201	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139721	<i>tmL-CAA-m16</i>	IGS	IR	F
57	124211	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139731	<i>tmL-CAA-m16</i>	IGS	IR	F
39	124216	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151461	<i>tmN-GUU-rps15</i>	IGS	IR	F
359	124218	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127290	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
205	124218	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155640	<i>tmN-GUU-rps15</i>	IGS	IR	F
189	124218	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159077	<i>tmN-GUU-rps15</i>	IGS	IR	F
152	124218	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156837	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	124218	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150153	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	124218	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161313	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	124242	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	124254	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	124368	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	124377	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	124377	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
88	124423	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
114	124505	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156095	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	124506	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125540	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	124590	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125624	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	124593	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127665	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
235	124616	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156205	<i>tmN-GUU-rps15</i>	IGS	IR	F
44	124622	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
32	124646	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125679	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
53	124681	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126730	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
43	124691	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125723	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
798	124741	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
516	124741	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126780	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
292	124741	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
102	124741	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125763	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
89	124741	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129846	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
45	124846	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
275	124847	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
172	124861	<i>tmi-CAU-rps12-3'</i>	IGS	IR	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	124891	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
134	124922	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	124922	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
225	124951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
171	124951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161017	<i>tmN-GUU-rps15</i>	IGS	IR	F
143	125033	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
691	125035	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	125051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	125081	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	125081	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	125099	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmL-CAA-m16</i>	IGS	IR	F
113	125118	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F

58	125118	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	125130	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-m16</i>	IGS	IR	F
50	125130	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	125138	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	125138	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	125138	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	125149	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-m16</i>	IGS	IR	F
30	125149	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	125172	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	125172	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	125172	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	125193	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	125202	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	125204	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	125219	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	125227	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
40	125235	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139721	<i>tmi-CAA-m16</i>	IGS	IR	F
57	125245	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139731	<i>tmi-CAA-m16</i>	IGS	IR	F
39	125250	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151461	<i>tmN-GUU-rps15</i>	IGS	IR	F
402	125252	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127290	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
205	125252	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155640	<i>tmN-GUU-rps15</i>	IGS	IR	F
189	125252	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159077	<i>tmN-GUU-rps15</i>	IGS	IR	F
152	125252	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156837	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	125252	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150153	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	125252	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161313	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	125276	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	125288	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	125402	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	125411	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	125411	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	125457	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	125473	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156031	<i>tmN-GUU-rps15</i>	IGS	IR	F
186	125540	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129622	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
71	125540	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156096	<i>tmN-GUU-rps15</i>	IGS	IR	F
48	125627	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156183	<i>tmN-GUU-rps15</i>	IGS	IR	F
77	125649	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127688	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	125655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156211	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	125679	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156235	<i>tmN-GUU-rps15</i>	IGS	IR	F
143	125722	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126739	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
130	125722	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129805	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
46	125723	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156280	<i>tmN-GUU-rps15</i>	IGS	IR	F
102	125763	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
172	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	126900	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
30	125879	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129966	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	125909	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
111	125940	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	125940	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	125969	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
504	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129117	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
222	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127074	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
141	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128096	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
87	126051	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156623	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	126067	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	126097	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	126097	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	126115	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-m16</i>	IGS	IR	F
113	126134	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	126134	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	126146	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-m16</i>	IGS	IR	F
50	126146	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	126154	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	126154	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	126154	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	126165	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-m16</i>	IGS	IR	F
30	126165	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	126188	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	126188	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	126188	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	126209	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	126218	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	126220	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	126235	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	126243	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
40	126251	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139721	<i>tmi-CAA-m16</i>	IGS	IR	F
57	126261	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139731	<i>tmi-CAA-m16</i>	IGS	IR	F
39	126266	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151461	<i>tmN-GUU-rps15</i>	IGS	IR	F
402	126268	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127290	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
205	126268	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155640	<i>tmN-GUU-rps15</i>	IGS	IR	F
189	126268	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159077	<i>tmN-GUU-rps15</i>	IGS	IR	F
152	126268	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156837	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	126268	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150153	<i>tmN-GUU-rps15</i>	IGS	IR	F

39	126268	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161313	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	126292	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	126304	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	126418	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	126427	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	126427	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	126473	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	126489	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156031	<i>tmN-GUU-rps15</i>	IGS	IR	F
313	126556	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129622	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
71	126556	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156096	<i>tmN-GUU-rps15</i>	IGS	IR	F
48	126643	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156183	<i>tmN-GUU-rps15</i>	IGS	IR	F
631	126665	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128708	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
407	126665	<i>tmi-CAU-rps12-3'</i>	IGS	IR	127688	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	126671	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156211	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	126695	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156235	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	126730	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156270	<i>tmN-GUU-rps15</i>	IGS	IR	F
110	126780	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	126885	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
275	126886	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	126930	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
134	126961	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	126961	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
225	126990	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
171	126990	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161017	<i>tmN-GUU-rps15</i>	IGS	IR	F
143	127072	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
31	127090	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	127120	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	127120	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	127138	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-m16</i>	IGS	IR	F
113	127157	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	127157	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	127169	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-m16</i>	IGS	IR	F
50	127169	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	127177	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	127177	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	127177	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	127188	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-m16</i>	IGS	IR	F
30	127188	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	127211	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
39	127211	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	127211	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	127232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	127241	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	127243	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	127258	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
829	127266	<i>tmi-CAU-rps12-3'</i>	IGS	IR	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
229	127266	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155616	<i>tmN-GUU-rps15</i>	IGS	IR	F
213	127266	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159053	<i>tmN-GUU-rps15</i>	IGS	IR	F
176	127266	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156813	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	127266	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161289	<i>tmN-GUU-rps15</i>	IGS	IR	F
57	127289	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150152	<i>tmN-GUU-rps15</i>	IGS	IR	F
402	127290	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129334	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
50	127290	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139738	<i>tmi-CAA-m16</i>	IGS	IR	F
37	127290	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151463	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	127326	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	127440	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	127449	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	127449	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	127495	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	127511	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156031	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	127578	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156096	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	127655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156173	<i>tmN-GUU-rps15</i>	IGS	IR	F
204	127688	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129731	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	127694	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156211	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	127718	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156235	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	127753	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156270	<i>tmN-GUU-rps15</i>	IGS	IR	F
110	127803	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	127908	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
186	127909	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	127953	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
111	127984	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	127984	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	128013	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
405	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158861	<i>tmN-GUU-rps15</i>	IGS	IR	F
143	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129115	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
89	128094	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156621	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	128112	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
95	128142	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	128160	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-m16</i>	IGS	IR	F
92	128179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	128179	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F

46	128191	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
65	128199	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	128199	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	128210	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134254	<i>rps12-3'-ndhB</i>	IGS	IR	F
230	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156759	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129254	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
56	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139658	<i>tmi-CAA-m16</i>	IGS	IR	F
32	128232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150066	<i>tmN-GUU-rps15</i>	IGS	IR	F
262	128253	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	128262	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151409	<i>tmN-GUU-rps15</i>	IGS	IR	F
77	128272	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161275	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	128286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129309	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
57	128309	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150152	<i>tmN-GUU-rps15</i>	IGS	IR	F
402	128310	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129334	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
50	128310	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139738	<i>tmi-CAA-m16</i>	IGS	IR	F
37	128310	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151463	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	128334	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	128346	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	128460	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	128469	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	128469	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	128515	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	128531	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156031	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	128598	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156096	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	128675	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156173	<i>tmN-GUU-rps15</i>	IGS	IR	F
204	128708	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129731	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	128714	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156211	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	128738	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156235	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	128773	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156270	<i>tmN-GUU-rps15</i>	IGS	IR	F
110	128823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	128928	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129951	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
275	128929	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	128973	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
134	129004	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
101	129004	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155298	<i>tmN-GUU-rps15</i>	IGS	IR	F
225	129033	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
171	129033	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161017	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	129133	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
105	129163	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155474	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	129163	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
49	129181	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmi-CAA-m16</i>	IGS	IR	F
113	129200	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	129200	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	129212	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139616	<i>tmi-CAA-m16</i>	IGS	IR	F
50	129212	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134235	<i>rps12-3'-ndhB</i>	IGS	IR	F
66	129220	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151341	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	129220	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	129220	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	129231	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139635	<i>tmi-CAA-m16</i>	IGS	IR	F
30	129231	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	129254	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158999	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	129254	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	129254	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	129275	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	129284	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150100	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	129286	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	129301	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	129309	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155616	<i>tmN-GUU-rps15</i>	IGS	IR	F
40	129317	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139721	<i>tmi-CAA-m16</i>	IGS	IR	F
57	129327	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139731	<i>tmi-CAA-m16</i>	IGS	IR	F
39	129332	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151461	<i>tmN-GUU-rps15</i>	IGS	IR	F
205	129334	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155640	<i>tmN-GUU-rps15</i>	IGS	IR	F
189	129334	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159077	<i>tmN-GUU-rps15</i>	IGS	IR	F
152	129334	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156837	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	129334	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150153	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	129334	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161313	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	129358	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151499	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	129370	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	129484	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	129493	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	129493	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161470	<i>tmN-GUU-rps15</i>	IGS	IR	F
88	129539	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156015	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	129621	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156095	<i>tmN-GUU-rps15</i>	IGS	IR	F
48	129709	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156183	<i>tmN-GUU-rps15</i>	IGS	IR	F
44	129737	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156211	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	129761	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156235	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	129796	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156270	<i>tmN-GUU-rps15</i>	IGS	IR	F
89	129846	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156330	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	129907	<i>tmi-CAU-rps12-3'</i>	IGS	IR	129940	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
44	129952	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156435	<i>tmN-GUU-rps15</i>	IGS	IR	F
589	129973	<i>tmi-CAU-rps12-3'</i>	IGS	IR	154608	<i>tmN-GUU-rps15</i>	IGS	IR	F

31	130005	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156479	<i>tmN-GUU-rps15</i>	IGS	IR	F
33	130118	<i>tmi-CAU-rps12-3'</i>	IGS	IR	159429	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	130122	<i>tmi-CAU-rps12-3'</i>	IGS	IR	157192	<i>tmN-GUU-rps15</i>	IGS	IR	F
68	130151	<i>tmi-CAU-rps12-3'</i>	IGS	IR	130196	<i>tmi-CAU-rps12-3'</i>	IGS	IR	F
68	130196	<i>tmi-CAU-rps12-3'</i>	IGS	IR	154786	<i>tmN-GUU-rps15</i>	IGS	IR	F
294	130332	<i>tmi-CAU-rps12-3'</i>	IGS	IR	154967	<i>tmN-GUU-rps15</i>	IGS	IR	F
131	130625	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155268	<i>tmN-GUU-rps15</i>	IGS	IR	F
134	130655	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156510	<i>tmN-GUU-rps15</i>	IGS	IR	F
105	130684	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
99	130771	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155422	<i>tmN-GUU-rps15</i>	IGS	IR	F
97	130782	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155433	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	130789	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156639	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	158909	<i>tmN-GUU-rps15</i>	IGS	IR	F
41	130823	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156669	<i>tmN-GUU-rps15</i>	IGS	IR	F
81	130841	<i>tmi-CAU-rps12-3'</i>	IGS	IR	139585	<i>tmL-CAA-rm16</i>	IGS	IR	F
72	130850	<i>tmi-CAU-rps12-3'</i>	IGS	IR	155501	<i>tmN-GUU-rps15</i>	IGS	IR	F
425	130856	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134219	<i>rps12-3'-ndhB</i>	IGS	IR	F
62	130860	<i>tmi-CAU-rps12-3'</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	130860	<i>tmi-CAU-rps12-3'</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
409	130880	<i>tmi-CAU-rps12-3'</i>	IGS	IR	134243	<i>rps12-3'-ndhB</i>	IGS	IR	F
42	130880	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150032	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	130880	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152662	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	130891	<i>tmi-CAU-rps12-3'</i>	IGS	IR	152673	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	130918	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150075	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	131191	<i>tmi-CAU-rps12-3'</i>	IGS	IR	153221	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	131191	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151899	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	131191	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150579	<i>tmN-GUU-rps15</i>	IGS	IR	F
70	131219	<i>tmi-CAU-rps12-3'</i>	IGS	IR	151926	<i>tmN-GUU-rps15</i>	IGS	IR	F
57	131232	<i>tmi-CAU-rps12-3'</i>	IGS	IR	150618	<i>tmN-GUU-rps15</i>	IGS	IR	F
53	133065	<i>rps12-3'-ndhB</i>	IGS	IR	135878	<i>rps12-3'-ndhB</i>	IGS	IR	F
111	133170	<i>rps12-3'-ndhB</i>	IGS	IR	150895	<i>tmN-GUU-rps15</i>	IGS	IR	F
64	133170	<i>rps12-3'-ndhB</i>	IGS	IR	149585	<i>tmN-GUU-rps15</i>	IGS	IR	F
357	133179	<i>rps12-3'-ndhB</i>	IGS	IR	150904	<i>tmN-GUU-rps15</i>	IGS	IR	F
309	133227	<i>rps12-3'-ndhB</i>	IGS	IR	149643	<i>tmN-GUU-rps15</i>	IGS	IR	F
94	133241	<i>rps12-3'-ndhB</i>	IGS	IR	135014	<i>rps12-3'-ndhB</i>	IGS	IR	F
101	133242	<i>rps12-3'-ndhB</i>	IGS	IR	134747	<i>rps12-3'-ndhB</i>	IGS	IR	F
75	133266	<i>rps12-3'-ndhB</i>	IGS	IR	135039	<i>rps12-3'-ndhB</i>	IGS	IR	F
30	133312	<i>rps12-3'-ndhB</i>	IGS	IR	135085	<i>rps12-3'-ndhB</i>	IGS	IR	F
32	133493	<i>rps12-3'-ndhB</i>	IGS	IR	158747	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	134150	<i>rps12-3'-ndhB</i>	IGS	IR	139221	<i>tmL-CAA-rm16</i>	IGS	IR	F
34	134177	<i>rps12-3'-ndhB</i>	IGS	IR	139322	<i>tmL-CAA-rm16</i>	IGS	IR	F
31	134178	<i>rps12-3'-ndhB</i>	IGS	IR	149951	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	134178	<i>rps12-3'-ndhB</i>	IGS	IR	152584	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	134179	<i>rps12-3'-ndhB</i>	IGS	IR	139246	<i>tmL-CAA-rm16</i>	IGS	IR	F
66	134219	<i>rps12-3'-ndhB</i>	IGS	IR	139600	<i>tmL-CAA-rm16</i>	IGS	IR	F
56	134229	<i>rps12-3'-ndhB</i>	IGS	IR	150018	<i>tmN-GUU-rps15</i>	IGS	IR	F
52	134229	<i>rps12-3'-ndhB</i>	IGS	IR	152648	<i>tmN-GUU-rps15</i>	IGS	IR	F
50	134235	<i>rps12-3'-ndhB</i>	IGS	IR	155523	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	134235	<i>rps12-3'-ndhB</i>	IGS	IR	158958	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	134253	<i>rps12-3'-ndhB</i>	IGS	IR	152672	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	134254	<i>rps12-3'-ndhB</i>	IGS	IR	158977	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	134281	<i>rps12-3'-ndhB</i>	IGS	IR	150075	<i>tmN-GUU-rps15</i>	IGS	IR	F
173	134554	<i>rps12-3'-ndhB</i>	IGS	IR	153221	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	134554	<i>rps12-3'-ndhB</i>	IGS	IR	150579	<i>tmN-GUU-rps15</i>	IGS	IR	F
145	134582	<i>rps12-3'-ndhB</i>	IGS	IR	151926	<i>tmN-GUU-rps15</i>	IGS	IR	F
132	134595	<i>rps12-3'-ndhB</i>	IGS	IR	150618	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	134706	<i>rps12-3'-ndhB</i>	IGS	IR	156029	<i>tmN-GUU-rps15</i>	IGS	IR	F
93	134747	<i>rps12-3'-ndhB</i>	IGS	IR	135015	<i>rps12-3'-ndhB</i>	IGS	IR	F
100	134748	<i>rps12-3'-ndhB</i>	IGS	IR	149659	<i>tmN-GUU-rps15</i>	IGS	IR	F
75	134771	<i>rps12-3'-ndhB</i>	IGS	IR	135039	<i>rps12-3'-ndhB</i>	IGS	IR	F
30	134817	<i>rps12-3'-ndhB</i>	IGS	IR	135085	<i>rps12-3'-ndhB</i>	IGS	IR	F
40	134941	<i>rps12-3'-ndhB</i>	IGS	IR	153554	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	134946	<i>rps12-3'-ndhB</i>	IGS	IR	135429	<i>rps12-3'-ndhB</i>	IGS	IR	F
44	135000	<i>rps12-3'-ndhB</i>	IGS	IR	149643	<i>tmN-GUU-rps15</i>	IGS	IR	F
68	135016	<i>rps12-3'-ndhB</i>	IGS	IR	149659	<i>tmN-GUU-rps15</i>	IGS	IR	F
69	135039	<i>rps12-3'-ndhB</i>	IGS	IR	149682	<i>tmN-GUU-rps15</i>	IGS	IR	F
59	135055	<i>rps12-3'-ndhB</i>	IGS	IR	149698	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	135085	<i>rps12-3'-ndhB</i>	IGS	IR	149728	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	135272	<i>rps12-3'-ndhB</i>	IGS	IR	152073	<i>tmN-GUU-rps15</i>	IGS	IR	F
60	135283	<i>rps12-3'-ndhB</i>	IGS	IR	152084	<i>tmN-GUU-rps15</i>	IGS	IR	F
34	135288	<i>rps12-3'-ndhB</i>	IGS	IR	150767	<i>tmN-GUU-rps15</i>	IGS	IR	F
91	135308	<i>rps12-3'-ndhB</i>	IGS	IR	152109	<i>tmN-GUU-rps15</i>	IGS	IR	F
85	135324	<i>rps12-3'-ndhB</i>	IGS	IR	153448	<i>tmN-GUU-rps15</i>	IGS	IR	F
82	135324	<i>rps12-3'-ndhB</i>	IGS	IR	152125	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	135335	<i>rps12-3'-ndhB</i>	IGS	IR	150812	<i>tmN-GUU-rps15</i>	IGS	IR	F
42	135364	<i>rps12-3'-ndhB</i>	IGS	IR	149531	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	135399	<i>rps12-3'-ndhB</i>	IGS	IR	153524	<i>tmN-GUU-rps15</i>	IGS	IR	F
78	135429	<i>rps12-3'-ndhB</i>	IGS	IR	153559	<i>tmN-GUU-rps15</i>	IGS	IR	F
92	139229	<i>tmL-CAA-rm16</i>	IGS	IR	139268	<i>tmL-CAA-rm16</i>	IGS	IR	F
30	139246	<i>tmL-CAA-rm16</i>	IGS	IR	149952	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	139285	<i>tmL-CAA-rm16</i>	IGS	IR	149952	<i>tmN-GUU-rps15</i>	IGS	IR	F

31	139323	<i>tml-CAA-rm16</i>	IGS	IR	149951	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	139363	<i>tml-CAA-rm16</i>	IGS	IR	149952	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	139401	<i>tml-CAA-rm16</i>	IGS	IR	149951	<i>tmN-GUU-rps15</i>	IGS	IR	F
75	139402	<i>tml-CAA-rm16</i>	IGS	IR	139441	<i>tml-CAA-rm16</i>	IGS	IR	F
68	139441	<i>tml-CAA-rm16</i>	IGS	IR	139480	<i>tml-CAA-rm16</i>	IGS	IR	F
30	139441	<i>tml-CAA-rm16</i>	IGS	IR	149952	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	139479	<i>tml-CAA-rm16</i>	IGS	IR	149951	<i>tmN-GUU-rps15</i>	IGS	IR	F
49	139585	<i>tml-CAA-rm16</i>	IGS	IR	158927	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	139585	<i>tml-CAA-rm16</i>	IGS	IR	155492	<i>tmN-GUU-rps15</i>	IGS	IR	F
40	139594	<i>tml-CAA-rm16</i>	IGS	IR	155501	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	139604	<i>tml-CAA-rm16</i>	IGS	IR	156705	<i>tmN-GUU-rps15</i>	IGS	IR	F
80	139610	<i>tml-CAA-rm16</i>	IGS	IR	151327	<i>tmN-GUU-rps15</i>	IGS	IR	F
77	139610	<i>tml-CAA-rm16</i>	IGS	IR	150018	<i>tmN-GUU-rps15</i>	IGS	IR	F
52	139610	<i>tml-CAA-rm16</i>	IGS	IR	152648	<i>tmN-GUU-rps15</i>	IGS	IR	F
98	139616	<i>tml-CAA-rm16</i>	IGS	IR	156717	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	139616	<i>tml-CAA-rm16</i>	IGS	IR	155523	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	139616	<i>tml-CAA-rm16</i>	IGS	IR	158958	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	139634	<i>tml-CAA-rm16</i>	IGS	IR	152672	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	139635	<i>tml-CAA-rm16</i>	IGS	IR	158977	<i>tmN-GUU-rps15</i>	IGS	IR	F
56	139658	<i>tml-CAA-rm16</i>	IGS	IR	158999	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	139658	<i>tml-CAA-rm16</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	139658	<i>tml-CAA-rm16</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	139679	<i>tml-CAA-rm16</i>	IGS	IR	155583	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	139690	<i>tml-CAA-rm16</i>	IGS	IR	151411	<i>tmN-GUU-rps15</i>	IGS	IR	F
40	139690	<i>tml-CAA-rm16</i>	IGS	IR	150102	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	139705	<i>tml-CAA-rm16</i>	IGS	IR	150117	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	139736	<i>tml-CAA-rm16</i>	IGS	IR	151461	<i>tmN-GUU-rps15</i>	IGS	IR	F
50	139738	<i>tml-CAA-rm16</i>	IGS	IR	150153	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	139738	<i>tml-CAA-rm16</i>	IGS	IR	161313	<i>tmN-GUU-rps15</i>	IGS	IR	F
119	139808	<i>tml-CAA-rm16</i>	IGS	IR	150222	<i>tmN-GUU-rps15</i>	IGS	IR	F
112	139808	<i>tml-CAA-rm16</i>	IGS	IR	151544	<i>tmN-GUU-rps15</i>	IGS	IR	F
100	139900	<i>tml-CAA-rm16</i>	IGS	IR	150314	<i>tmN-GUU-rps15</i>	IGS	IR	F
90	139910	<i>tml-CAA-rm16</i>	IGS	IR	152966	<i>tmN-GUU-rps15</i>	IGS	IR	F
33	139910	<i>tml-CAA-rm16</i>	IGS	IR	151646	<i>tmN-GUU-rps15</i>	IGS	IR	F
147	139929	<i>tml-CAA-rm16</i>	IGS	IR	150343	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	139938	<i>tml-CAA-rm16</i>	IGS	IR	151673	<i>tmN-GUU-rps15</i>	IGS	IR	F
118	139958	<i>tml-CAA-rm16</i>	IGS	IR	151692	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	147811	<i>rm5-tmR-ACG</i>	IGS	IR	173710	<i>tml-UAG-ccaA</i>	IGS	SSC	F
117	149531	<i>tmN-GUU-rps15</i>	IGS	IR	150841	<i>tmN-GUU-rps15</i>	IGS	IR	F
42	149531	<i>tmN-GUU-rps15</i>	IGS	IR	153488	<i>tmN-GUU-rps15</i>	IGS	IR	F
483	149643	<i>tmN-GUU-rps15</i>	IGS	IR	150952	<i>tmN-GUU-rps15</i>	IGS	IR	F
336	149643	<i>tmN-GUU-rps15</i>	IGS	IR	152276	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	149909	<i>tmN-GUU-rps15</i>	IGS	IR	158747	<i>tmN-GUU-rps15</i>	IGS	IR	F
157	149974	<i>tmN-GUU-rps15</i>	IGS	IR	151283	<i>tmN-GUU-rps15</i>	IGS	IR	F
75	149995	<i>tmN-GUU-rps15</i>	IGS	IR	152625	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	150032	<i>tmN-GUU-rps15</i>	IGS	IR	156725	<i>tmN-GUU-rps15</i>	IGS	IR	F
48	150032	<i>tmN-GUU-rps15</i>	IGS	IR	155531	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	150032	<i>tmN-GUU-rps15</i>	IGS	IR	158966	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	150043	<i>tmN-GUU-rps15</i>	IGS	IR	158977	<i>tmN-GUU-rps15</i>	IGS	IR	F
65	150066	<i>tmN-GUU-rps15</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	150066	<i>tmN-GUU-rps15</i>	IGS	IR	158999	<i>tmN-GUU-rps15</i>	IGS	IR	F
63	150096	<i>tmN-GUU-rps15</i>	IGS	IR	151405	<i>tmN-GUU-rps15</i>	IGS	IR	F
57	150152	<i>tmN-GUU-rps15</i>	IGS	IR	155639	<i>tmN-GUU-rps15</i>	IGS	IR	F
40	150152	<i>tmN-GUU-rps15</i>	IGS	IR	161312	<i>tmN-GUU-rps15</i>	IGS	IR	F
37	150153	<i>tmN-GUU-rps15</i>	IGS	IR	151463	<i>tmN-GUU-rps15</i>	IGS	IR	F
435	150176	<i>tmN-GUU-rps15</i>	IGS	IR	152818	<i>tmN-GUU-rps15</i>	IGS	IR	F
181	150176	<i>tmN-GUU-rps15</i>	IGS	IR	151498	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	150352	<i>tmN-GUU-rps15</i>	IGS	IR	151673	<i>tmN-GUU-rps15</i>	IGS	IR	F
251	150372	<i>tmN-GUU-rps15</i>	IGS	IR	151692	<i>tmN-GUU-rps15</i>	IGS	IR	F
155	150618	<i>tmN-GUU-rps15</i>	IGS	IR	151939	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	150705	<i>tmN-GUU-rps15</i>	IGS	IR	155991	<i>tmN-GUU-rps15</i>	IGS	IR	F
34	150767	<i>tmN-GUU-rps15</i>	IGS	IR	152089	<i>tmN-GUU-rps15</i>	IGS	IR	F
476	150812	<i>tmN-GUU-rps15</i>	IGS	IR	152136	<i>tmN-GUU-rps15</i>	IGS	IR	F
71	150812	<i>tmN-GUU-rps15</i>	IGS	IR	153459	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	151218	<i>tmN-GUU-rps15</i>	IGS	IR	158747	<i>tmN-GUU-rps15</i>	IGS	IR	F
75	151304	<i>tmN-GUU-rps15</i>	IGS	IR	152625	<i>tmN-GUU-rps15</i>	IGS	IR	F
66	151341	<i>tmN-GUU-rps15</i>	IGS	IR	156725	<i>tmN-GUU-rps15</i>	IGS	IR	F
48	151341	<i>tmN-GUU-rps15</i>	IGS	IR	155531	<i>tmN-GUU-rps15</i>	IGS	IR	F
38	151341	<i>tmN-GUU-rps15</i>	IGS	IR	158966	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	151352	<i>tmN-GUU-rps15</i>	IGS	IR	158977	<i>tmN-GUU-rps15</i>	IGS	IR	F
304	151375	<i>tmN-GUU-rps15</i>	IGS	IR	152695	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	151375	<i>tmN-GUU-rps15</i>	IGS	IR	158999	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	151409	<i>tmN-GUU-rps15</i>	IGS	IR	155592	<i>tmN-GUU-rps15</i>	IGS	IR	F
37	151463	<i>tmN-GUU-rps15</i>	IGS	IR	155640	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	151499	<i>tmN-GUU-rps15</i>	IGS	IR	155664	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	151673	<i>tmN-GUU-rps15</i>	IGS	IR	152994	<i>tmN-GUU-rps15</i>	IGS	IR	F
239	151692	<i>tmN-GUU-rps15</i>	IGS	IR	153014	<i>tmN-GUU-rps15</i>	IGS	IR	F
281	151926	<i>tmN-GUU-rps15</i>	IGS	IR	153249	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	152026	<i>tmN-GUU-rps15</i>	IGS	IR	155991	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	152542	<i>tmN-GUU-rps15</i>	IGS	IR	158747	<i>tmN-GUU-rps15</i>	IGS	IR	F
65	152662	<i>tmN-GUU-rps15</i>	IGS	IR	158966	<i>tmN-GUU-rps15</i>	IGS	IR	F

38	152662	<i>tmN-GUU-rps15</i>	IGS	IR	155531	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	152673	<i>tmN-GUU-rps15</i>	IGS	IR	155542	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	152695	<i>tmN-GUU-rps15</i>	IGS	IR	156759	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	152729	<i>tmN-GUU-rps15</i>	IGS	IR	155592	<i>tmN-GUU-rps15</i>	IGS	IR	F
37	152783	<i>tmN-GUU-rps15</i>	IGS	IR	155640	<i>tmN-GUU-rps15</i>	IGS	IR	F
32	152819	<i>tmN-GUU-rps15</i>	IGS	IR	155664	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	153349	<i>tmN-GUU-rps15</i>	IGS	IR	155991	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	154640	<i>tmN-GUU-rps15</i>	IGS	IR	156479	<i>tmN-GUU-rps15</i>	IGS	IR	F
33	154753	<i>tmN-GUU-rps15</i>	IGS	IR	159429	<i>tmN-GUU-rps15</i>	IGS	IR	F
35	154757	<i>tmN-GUU-rps15</i>	IGS	IR	157192	<i>tmN-GUU-rps15</i>	IGS	IR	F
101	155298	<i>tmN-GUU-rps15</i>	IGS	IR	156510	<i>tmN-GUU-rps15</i>	IGS	IR	F
72	155327	<i>tmN-GUU-rps15</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
31	155440	<i>tmN-GUU-rps15</i>	IGS	IR	156639	<i>tmN-GUU-rps15</i>	IGS	IR	F
95	155474	<i>tmN-GUU-rps15</i>	IGS	IR	158909	<i>tmN-GUU-rps15</i>	IGS	IR	F
41	155474	<i>tmN-GUU-rps15</i>	IGS	IR	156669	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	155511	<i>tmN-GUU-rps15</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
244	155583	<i>tmN-GUU-rps15</i>	IGS	IR	159020	<i>tmN-GUU-rps15</i>	IGS	IR	F
209	155583	<i>tmN-GUU-rps15</i>	IGS	IR	156780	<i>tmN-GUU-rps15</i>	IGS	IR	F
77	155602	<i>tmN-GUU-rps15</i>	IGS	IR	161275	<i>tmN-GUU-rps15</i>	IGS	IR	F
122	155676	<i>tmN-GUU-rps15</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
91	155745	<i>tmN-GUU-rps15</i>	IGS	IR	159182	<i>tmN-GUU-rps15</i>	IGS	IR	F
46	155790	<i>tmN-GUU-rps15</i>	IGS	IR	156986	<i>tmN-GUU-rps15</i>	IGS	IR	F
45	155799	<i>tmN-GUU-rps15</i>	IGS	IR	156995	<i>tmN-GUU-rps15</i>	IGS	IR	F
41	155799	<i>tmN-GUU-rps15</i>	IGS	IR	159236	<i>tmN-GUU-rps15</i>	IGS	IR	F
117	155880	<i>tmN-GUU-rps15</i>	IGS	IR	157080	<i>tmN-GUU-rps15</i>	IGS	IR	F
75	155880	<i>tmN-GUU-rps15</i>	IGS	IR	161555	<i>tmN-GUU-rps15</i>	IGS	IR	F
44	155953	<i>tmN-GUU-rps15</i>	IGS	IR	161627	<i>tmN-GUU-rps15</i>	IGS	IR	F
224	156539	<i>tmN-GUU-rps15</i>	IGS	IR	161017	<i>tmN-GUU-rps15</i>	IGS	IR	F
171	156539	<i>tmN-GUU-rps15</i>	IGS	IR	158779	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	156705	<i>tmN-GUU-rps15</i>	IGS	IR	158946	<i>tmN-GUU-rps15</i>	IGS	IR	F
230	156759	<i>tmN-GUU-rps15</i>	IGS	IR	158999	<i>tmN-GUU-rps15</i>	IGS	IR	F
39	156759	<i>tmN-GUU-rps15</i>	IGS	IR	161236	<i>tmN-GUU-rps15</i>	IGS	IR	F
77	156799	<i>tmN-GUU-rps15</i>	IGS	IR	161275	<i>tmN-GUU-rps15</i>	IGS	IR	F
163	156873	<i>tmN-GUU-rps15</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
235	156986	<i>tmN-GUU-rps15</i>	IGS	IR	159227	<i>tmN-GUU-rps15</i>	IGS	IR	F
162	156993	<i>tmN-GUU-rps15</i>	IGS	IR	161468	<i>tmN-GUU-rps15</i>	IGS	IR	F
68	157153	<i>tmN-GUU-rps15</i>	IGS	IR	161627	<i>tmN-GUU-rps15</i>	IGS	IR	F
162	157217	<i>tmN-GUU-rps15</i>	IGS	IR	159457	<i>tmN-GUU-rps15</i>	IGS	IR	F
393	157374	<i>tmN-GUU-rps15</i>	IGS	IR	159615	<i>tmN-GUU-rps15</i>	IGS	IR	F
124	157767	<i>tmN-GUU-rps15</i>	IGS	IR	162242	<i>tmN-GUU-rps15</i>	IGS	IR	F
36	157767	<i>tmN-GUU-rps15</i>	IGS	IR	160009	<i>tmN-GUU-rps15</i>	IGS	IR	F
92	157799	<i>tmN-GUU-rps15</i>	IGS	IR	160040	<i>tmN-GUU-rps15</i>	IGS	IR	F
34	157896	<i>tmN-GUU-rps15</i>	IGS	IR	160138	<i>tmN-GUU-rps15</i>	IGS	IR	F
178	157926	<i>tmN-GUU-rps15</i>	IGS	IR	160169	<i>tmN-GUU-rps15</i>	IGS	IR	F
47	157926	<i>tmN-GUU-rps15</i>	IGS	IR	162406	<i>rps15</i>	CDS	IR	F
34	157972	<i>tmN-GUU-rps15</i>	IGS	IR	162461	<i>rps15</i>	CDS	IR	F
168	158099	<i>tmN-GUU-rps15</i>	IGS	IR	160341	<i>tmN-GUU-rps15</i>	IGS	IR	F
670	158280	<i>tmN-GUU-rps15</i>	IGS	IR	160518	<i>tmN-GUU-rps15</i>	IGS	IR	F
92	158946	<i>tmN-GUU-rps15</i>	IGS	IR	161183	<i>tmN-GUU-rps15</i>	IGS	IR	F
77	159039	<i>tmN-GUU-rps15</i>	IGS	IR	161275	<i>tmN-GUU-rps15</i>	IGS	IR	F
123	159113	<i>tmN-GUU-rps15</i>	IGS	IR	161348	<i>tmN-GUU-rps15</i>	IGS	IR	F
162	159234	<i>tmN-GUU-rps15</i>	IGS	IR	161468	<i>tmN-GUU-rps15</i>	IGS	IR	F
651	159394	<i>tmN-GUU-rps15</i>	IGS	IR	161627	<i>tmN-GUU-rps15</i>	IGS	IR	F
103	160040	<i>tmN-GUU-rps15</i>	IGS	IR	162274	<i>tmN-GUU-rps15</i>	IGS	IR	F
30	160134	<i>tmN-GUU-rps15</i>	IGS	IR	162369	<i>tmN-GUU-rps15</i>	IGS	IR	F
58	160158	<i>tmN-GUU-rps15</i>	IGS	IR	162395	<i>tmN-GUU-rps15/rps15</i>	IGS/CDS	IR	F
34	160215	<i>tmN-GUU-rps15</i>	IGS	IR	162461	<i>rps15</i>	CDS	IR	F
36	170051	<i>ndhF-IGS</i>	CDS/IGS	SSC	171431	<i>rps11-rpl32</i>	IGS	SSC	F
37	170070	<i>ndhF-IGS</i>	CDS/IGS	SSC	171450	<i>rps11-rpl32</i>	IGS	SSC	F
117	170089	<i>ndhF-rps11</i>	IGS	SSC	171469	<i>rps11-rpl32</i>	IGS	SSC	F
64	170211	<i>ndhF-rps11</i>	IGS	SSC	171579	<i>rps11-rpl32</i>	IGS	SSC	F
33	170274	<i>ndhF-rps11</i>	IGS	SSC	171641	<i>rps11-rpl32</i>	IGS	SSC	F
52	170301	<i>ndhF-rps11</i>	IGS	SSC	171669	<i>rps11-rpl32</i>	IGS	SSC	F
37	170330	<i>ndhF-rps11</i>	IGS	SSC	171719	<i>rps11-rpl32</i>	IGS	SSC	F
39	170364	<i>ndhF-rps11</i>	IGS	SSC	171748	<i>rps11-rpl32</i>	IGS	SSC	F
37	170392	<i>ndhF-rps11</i>	IGS	SSC	171770	<i>rps11-rpl32</i>	IGS	SSC	F
32	170444	<i>ndhF-rps11</i>	IGS	SSC	171826	<i>rps11-rpl32</i>	IGS	SSC	F
128	170468	<i>ndhF-rps11</i>	IGS	SSC	171857	<i>rps11-rpl32</i>	IGS	SSC	F
42	170609	<i>ndhF-rps11</i>	IGS	SSC	171994	<i>rps11-rpl32</i>	IGS	SSC	F
31	170641	<i>ndhF-rps11</i>	IGS	SSC	172024	<i>rps11-rpl32</i>	IGS	SSC	F
30	177276	<i>psaC-ndhE</i>	IGS	SSC	177303	<i>psaC-ndhE</i>	IGS	SSC	F

* F, forward repeats; P, palindromic repeats; R, reverse repeats; C, complementary repeats; CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

Appendix 5. List of tandem repeats in the chloroplast genome of *C. lupulina* and related taxa

* *T. latifolia*

Indices	Repeat number	Size (bp)	Location	Region
5445 - 5469	1.9	13	<i>rps16</i> intron	intron LSC
6496 - 6524	2.1	14	<i>rps16-trnQ-UUG</i>	IGS LSC
8728 - 8758	2.1	15	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
8740 - 8796	2.2	26	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
8754 - 8796	3.2	14	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
8799 - 8840	2.1	20	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
8840 - 8866	2.1	13	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
8953 - 9005	5.2	11	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
8953 - 9020	2.4	30	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
8971 - 9013	2.2	21	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
8990 - 9033	2.7	15	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9094 - 9155	3.6	17	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9106 - 9225	5.4	23	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9123 - 9222	4.1	24	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9139 - 9226	13.3	7	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9711 - 9786	6.6	11	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9711 - 9889	11.9	15	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9712 - 9882	3	58	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9768 - 9896	6.2	20	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9783 - 9896	5.2	22	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
9787 - 9909	7.1	14	<i>tmS-GCU-trnG-GCC</i>	IGS LSC
15370 - 15424	2.9	19	<i>atpH-atpI</i>	IGS LSC
15382 - 15411	2.3	13	<i>atpH-atpI</i>	IGS LSC
15402 - 15444	2	22	<i>atpH-atpI</i>	IGS LSC
15407 - 15504	2.3	45	<i>atpH-atpI</i>	IGS LSC
15428 - 15480	2.8	19	<i>atpH-atpI</i>	IGS LSC
15462 - 15531	2	36	<i>atpH-atpI</i>	IGS LSC
15599 - 15633	2.1	17	<i>atpH-atpI</i>	IGS LSC
17914 - 17943	2.1	15	<i>rpoC2</i>	CDS LSC
22201 - 22230	2.1	14	<i>rpoC2-rpoC1/rpoC1</i>	IGS&CDS LSC
32140 - 32170	2.1	15	<i>psbM-trnD-GUC</i>	IGS LSC
33203 - 33243	2.3	18	<i>tmD-GUC-trnY-GUA</i>	IGS LSC
33731 - 33778	1.9	26	<i>tmE-UUC-trnT-GGU</i>	IGS LSC
34285 - 34344	7.8	8	<i>tmE-UUC-trnT-GGU</i>	IGS LSC
34304 - 34341	4.6	8	<i>tmE-UUC-trnT-GGU</i>	IGS LSC
34304 - 34341	2.3	17	<i>tmE-UUC-trnT-GGU</i>	IGS LSC
38916 - 38954	2.1	19	<i>psbZ-trnG-UCC</i>	IGS LSC
48822 - 48865	3.2	13	<i>rps4-trnT-UGU</i>	IGS LSC
48831 - 48887	3.3	17	<i>rps4-trnT-UGU</i>	IGS LSC
48861 - 48897	2.6	14	<i>rps4-trnT-UGU</i>	IGS LSC
48979 - 49018	2.7	15	<i>rps4-trnT-UGU</i>	IGS LSC
49374 - 49539	7.8	22	<i>tmT-UGU-trnL-UAA</i>	IGS LSC
49417 - 49539	3.2	41	<i>tmT-UGU-trnL-UAA</i>	IGS LSC
49434 - 49533	3.8	26	<i>tmT-UGU-trnL-UAA</i>	IGS LSC
51627 - 51655	2.6	11	<i>tmF-GAA-ndhI</i>	IGS LSC
51707 - 51757	2	25	<i>tmF-GAA-ndhI</i>	IGS LSC
54260 - 54297	2.6	14	<i>ndhC-trnV-UAC</i>	IGS LSC
54387 - 54415	2.1	14	<i>ndhC-trnV-UAC</i>	IGS LSC
54451 - 54485	2.1	17	<i>ndhC-trnV-UAC</i>	IGS LSC
55971 - 56002	2.1	15	<i>tmM-CAU-atpE</i>	IGS LSC
56018 - 56046	2.3	12	<i>tmM-CAU-atpE</i>	IGS LSC
60405 - 60434	3.2	9	<i>rbcL-accD</i>	IGS LSC
61622 - 61654	2.2	15	<i>accD</i>	CDS LSC
63044 - 63084	2.6	16	<i>accD-psaI</i>	IGS LSC
63081 - 63140	2.2	27	<i>accD-psaI</i>	IGS LSC
63306 - 63507	15.5	13	<i>accD-psaI</i>	IGS LSC

63343 - 63392	2.9	17	<i>accD~psaI</i>	IGS	LSC
63366 - 63508	3.5	38	<i>accD~psaI</i>	IGS	LSC
66394 - 66420	1.9	14	<i>cemA~petA</i>	IGS	LSC
67536 - 67570	1.9	18	<i>petA~psbI</i>	IGS	LSC
68189 - 68228	2	20	<i>petA~psbI</i>	IGS	LSC
69908 - 69941	2.2	15	<i>psbE~petL</i>	IGS	LSC
69966 - 69998	2.1	16	<i>psbE~petL</i>	IGS	LSC
69969 - 70008	4.8	9	<i>psbE~petL</i>	IGS	LSC
72086 - 72127	2	21	<i>psaJ~rpl33</i>	IGS	LSC
72429 - 72468	2.5	16	<i>psaJ~rpl33</i>	IGS	LSC
72434 - 72475	2.9	16	<i>psaJ~rpl33</i>	IGS	LSC
73097 - 73140	2.1	21	<i>rps18</i>	CDS	LSC
85770 - 85814	3	15	<i>rps8~rpl14</i>	IGS	LSC
87492 - 87521	2	15	<i>rpl16</i> intron	intron	LSC
94459 - 94541	3.8	21	<i>ycf2</i>	CDS	IRb
94480 - 94548	3.3	21	<i>ycf2</i>	CDS	IRb
96898 - 96988	5.6	15	<i>ycf2</i>	CDS	IRb
96905 - 96981	3.2	24	<i>ycf2</i>	CDS	IRb
99119 - 99164	2.1	22	<i>ycf2~trnL-CAA</i>	IGS	IRb
99953 - 100003	2	25	<i>trnL-CAA~ndhB</i>	IGS	IRb
105184 - 105208	2.1	12	<i>rps12-3'~tmV-GAC</i>	IGS	IRb
105502 - 105546	3.5	14	<i>rps12-3'~tmV-GAC</i>	IGS	IRb
118604 - 118630	2.1	13	<i>ndhF~rpl32</i>	IGS	SSC
118884 - 118916	1.9	18	<i>ndhF~rpl32</i>	IGS	SSC
118923 - 118968	2.8	18	<i>ndhF~rpl32</i>	IGS	SSC
119568 - 119595	2	14	<i>rpl32~trnL-UAG</i>	IGS	SSC
123324 - 123361	2.1	18	<i>psaC~ndhE</i>	IGS	SSC
123634 - 123671	2	19	<i>psaC~ndhE</i>	IGS	SSC
123657 - 123809	2.1	70	<i>psaC~ndhE</i>	IGS	SSC
123658 - 123835	12.1	15	<i>psaC~ndhE</i>	IGS	SSC
123674 - 123842	14.4	12	<i>psaC~ndhE</i>	IGS	SSC
123676 - 123822	1.9	78	<i>psaC~ndhE</i>	IGS	SSC
123686 - 123921	23.1	11	<i>psaC~ndhE</i>	IGS	SSC
123687 - 123856	9.1	19	<i>psaC~ndhE</i>	IGS	SSC
123857 - 123924	2.5	28	<i>psaC~ndhE</i>	IGS	SSC
130057 - 130096	2	20	<i>rps15~ycf1</i>	IGS	SSC
130166 - 130206	2.9	15	<i>rps15~ycf1</i>	IGS	SSC
130170 - 130214	1.9	23	<i>rps15~ycf1</i>	IGS	SSC

* CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

* *E. buergerianum*

Indices	Repeat number	Size (bp)	Location	Region	
5770 - 5813	3.2	13	<i>rps16~tmQ-UUG</i>	IGS	LSC
13148 - 13173	2.2	12	<i>atpH~atpI</i>	IGS	LSC
15205 - 15260	3.4	16	<i>atpI~rps2</i>	IGS	LSC
15212 - 15261	3.7	14	<i>atpI~rps2</i>	IGS	LSC
27191 - 27248	3.7	16	<i>rpoB~trnC-GCA</i>	IGS	LSC
55492 - 55534	2	21	<i>accD</i>	CDS	LSC
56894 - 56937	2.9	14	<i>accD~psaI</i>	IGS	LSC
56897 - 56925	2.1	14	<i>accD~psaI</i>	IGS	LSC
57011 - 57062	2.6	20	<i>accD~psaI</i>	IGS	LSC
58493 - 58525	3.4	10	<i>ycf4~cemA</i>	IGS	LSC
58493 - 58531	3	13	<i>ycf4~cemA</i>	IGS	LSC
58501 - 58531	1.9	16	<i>ycf4~cemA</i>	IGS	LSC
65188 - 65214	1.9	14	<i>rpl33~rps18</i>	IGS	LSC
77325 - 77353	2.4	12	<i>rpl36~infA</i>	IGS	LSC
89204 - 89328	5.2	24	<i>ycf2</i>	CDS	IRb
116020 - 116054	2.6	13	<i>ndhG~ndhI</i>	IGS	SSC

* CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

* *H. nemorum*

Indices	Repeat number	Size (bp)	Location	Region
6192 - 6221	2	15	<i>rps16~tmQ-UUG</i>	IGS LSC
6942 - 6981	2	20	<i>rps16~tmQ-UUG</i>	IGS LSC
7612 - 7747	2.4	56	<i>rps16~tmQ-UUG</i>	IGS LSC
7811 - 7862	2.4	22	<i>rps16~tmQ-UUG</i>	IGS LSC
8120 - 8248	2	66	<i>rps16~tmQ-UUG</i>	IGS LSC
8168 - 8211	2.3	18	<i>rps16~tmQ-UUG</i>	IGS LSC
8173 - 8236	1.9	33	<i>rps16~tmQ-UUG</i>	IGS LSC
8220 - 8311	2.8	33	<i>rps16~tmQ-UUG</i>	IGS LSC
9881 - 9926	2.6	18	<i>psbK~psbI</i>	IGS LSC
10553 - 10587	2.1	17	<i>tmS-GCU~tmG-UCC</i>	IGS LSC
15414 - 15439	2	13	<i>atpF~atpH</i>	IGS LSC
17596 - 18252	2.7	246	<i>atpI~rps2</i>	IGS LSC
17767 - 17898	2	66	<i>atpI~rps2</i>	IGS LSC
18013 - 18144	2	66	<i>atpI~rps2</i>	IGS LSC
18843 - 18916	3.1	24	<i>atpI~rps2</i>	IGS LSC
22589 - 22738	3.1	48	<i>rpoC2</i>	CDS LSC
22717 - 22778	2.3	27	<i>rpoC2</i>	CDS LSC
22731 - 22786	2.1	27	<i>rpoC2</i>	CDS LSC
22758 - 23083	7.2	45	<i>rpoC2</i>	CDS LSC
31320 - 31355	2.1	17	<i>rpoB~trnC-GCA</i>	IGS LSC
31804 - 31841	2	19	<i>rpoB~trnC-GCA</i>	IGS LSC
31950 - 31980	2.1	15	<i>rpoB~trnC-GCA</i>	IGS LSC
32142 - 32177	2	18	<i>rpoB~trnC-GCA</i>	IGS LSC
35452 - 35497	2.1	22	<i>psbM~tmD-GUC</i>	IGS LSC
35551 - 35598	3	16	<i>psbM~tmD-GUC</i>	IGS LSC
36335 - 36376	1.9	22	<i>tmY-GUA~tmE-UUC</i>	IGS LSC
36593 - 36633	3.2	13	<i>tmE-UUC~tmT-GGU</i>	IGS LSC
37086 - 37115	2	15	<i>tmE-UUC~tmT-GGU</i>	IGS LSC
42314 - 42379	6	12	<i>tmG-GCC~tmfM-CAU</i>	IGS LSC
45108 - 45134	1.9	14	<i>rbcl~atpB</i>	IGS LSC
45212 - 45243	2	16	<i>rbcl~atpB</i>	IGS LSC
45549 - 45573	1.9	13	<i>rbcl~atpB</i>	IGS LSC
47873 - 47914	2	21	<i>tmM-CAU/trnM-CAU~tmV-UAC</i>	trn&IGS LSC
49272 - 49306	3.2	11	<i>tmV-UAC~ndhC</i>	IGS LSC
49401 - 49427	2.1	13	<i>tmV-UAC~ndhC</i>	IGS LSC
49601 - 49637	1.9	19	<i>tmV-UAC~ndhC</i>	IGS LSC
49693 - 49730	1.9	20	<i>tmV-UAC~ndhC</i>	IGS LSC
53713 - 53741	1.9	15	<i>tmL-UAA~tmT-UGU</i>	IGS LSC
53839 - 53879	2.4	17	<i>tmL-UAA~tmT-UGU</i>	IGS LSC
54038 - 54082	1.9	23	<i>tmL-UAA~tmT-UGU</i>	IGS LSC
54071 - 54112	2.5	17	<i>tmL-UAA~tmT-UGU</i>	IGS LSC
61029 - 61057	2.1	14	<i>petA~psbJ</i>	IGS LSC
62690 - 62723	2.7	13	<i>psbE~petL</i>	IGS LSC
62713 - 62742	2.1	15	<i>psbE~petL</i>	IGS LSC
64105 - 64135	2.1	15	<i>tmW-CCA~tmP-UGG</i>	IGS LSC
64406 - 64433	2	14	<i>tmP-UGG~psaI</i>	IGS LSC
65107 - 65169	2.6	22	<i>psaI~rpl33</i>	IGS LSC
65667 - 65799	2	65	<i>rpl33~rpl20</i>	IGS LSC
65868 - 65939	2.7	27	<i>rpl33~rpl20</i>	IGS LSC
65964 - 66020	2.7	21	<i>rpl33~rpl20</i>	IGS LSC
66115 - 66172	6.3	9	<i>rpl33~rpl20</i>	IGS LSC
66115 - 66168	2.9	18	<i>rpl33~rpl20</i>	IGS LSC
66442 - 66527	3.2	27	<i>rpl33~rpl20</i>	IGS LSC
66442 - 66608	3.1	54	<i>rpl33~rpl20</i>	IGS LSC
66481 - 66935	16.9	27	<i>rpl33~rpl20</i>	IGS LSC
66531 - 66918	4.8	81	<i>rpl33~rpl20</i>	IGS LSC
66562 - 66935	3.5	108	<i>rpl33~rpl20</i>	IGS LSC
66621 - 66670	3.6	15	<i>rpl33~rpl20</i>	IGS LSC
66783 - 66832	3.5	15	<i>rpl33~rpl20</i>	IGS LSC
70667 - 70737	2	35	<i>clpP~psbB</i>	IGS LSC
73734 - 73769	2.2	17	<i>petB</i> intron	intron LSC

78337 - 78410	3.1	24	<i>rps11</i>	CDS	LSC
78462 - 78515	2	27	<i>rps11~rps14</i>	IGS	LSC
78884 - 78915	2	16	<i>rps11~rps14</i>	IGS	LSC
79629 - 79778	16.7	9	<i>rps11~rps14</i>	IGS	LSC
79629 - 79778	8.3	18	<i>rps11~rps14</i>	IGS	LSC
79821 - 79889	2.6	27	<i>rps11~rps14</i>	IGS	LSC
79941 - 80110	5.7	30	<i>rps11~rps14</i>	IGS	LSC
79941 - 80110	1.9	90	<i>rps11~rps14</i>	IGS	LSC
81145 - 81180	2.5	13	<i>rps11~rps14</i>	IGS	LSC
81366 - 81402	2.1	18	<i>rps11~rps14</i>	IGS	LSC
81576 - 81601	2	13	<i>rps11~rps14</i>	IGS	LSC
82712 - 82753	2.1	20	<i>rps14~psaB</i>	IGS	LSC
87653 - 87687	2.2	16	<i>psaA~ycf3</i>	IGS	LSC
90245 - 90277	2.1	16	<i>ycf3~tms-GGA</i>	IGS	LSC
95660 - 95701	2	21	<i>rps19</i>	CDS	IRb
95934 - 96005	4	18	<i>rps19~tmH-GUG</i>	IGS	IRb
98280 - 98321	1.9	22	<i>tml-CAU~ycf2</i>	IGS	IRb
101748 - 101822	2.8	27	<i>ycf2</i>	CDS	IRb
102343 - 102376	2.8	12	<i>ycf2</i>	CDS	IRb
102406 - 102525	2	60	<i>ycf2</i>	CDS	IRb
102417 - 102510	3.2	29	<i>ycf2</i>	CDS	IRb
104079 - 104109	2.1	15	<i>ycf2</i>	CDS	IRb
105394 - 105576	12.2	15	<i>ycf2</i>	CDS	IRb
106289 - 106315	2.1	13	<i>ycf2~rps12_3'</i>	IGS	IRb
107139 - 107163	2.1	12	<i>ycf2~rps12_3'</i>	IGS	IRb
108466 - 108496	3.4	9	<i>rps7</i>	CDS	IRb
120962 - 121005	2.2	20	<i>tmr-ACG~trnN-GUU</i>	IGS	IRb
121763 - 121803	3.2	13	<i>trnN-GUU~ycf1</i>	IGS	IRb
121855 - 122117	4	65	<i>trnN-GUU~ycf1</i>	IGS	IRb
122287 - 122328	2.2	19	<i>trnN-GUU~ycf1</i>	IGS	IRb
122453 - 122509	2.7	21	<i>trnN-GUU~ycf1</i>	IGS	IRb
123362 - 123415	2	27	<i>ycf1</i>	CDS	IRb
123702 - 123746	2.1	21	<i>ycf1</i>	CDS	IRb
123709 - 123761	2.7	21	<i>ycf1</i>	CDS	IRb
123712 - 123761	5.2	9	<i>ycf1</i>	CDS	IRb
124146 - 124182	4.1	9	<i>ycf1</i>	CDS	IRb
126706 - 126750	2.1	21	<i>ycf1</i>	CDS	IRb
126855 - 127051	16.4	12	<i>ycf1</i>	CDS	IRb
127079 - 127120	2	21	<i>ycf1</i>	CDS	IRb
127245 - 127392	9.9	15	<i>ycf1</i>	CDS	IRb
128038 - 128169	8	15	<i>ycf1</i>	CDS	IRb
128091 - 128153	3	21	<i>ycf1</i>	CDS	IRb
136625 - 136667	2.5	18	<i>ndhF~rpl32</i>	IGS	SSC
136689 - 136721	2.1	16	<i>ndhF~rpl32</i>	IGS	SSC
137156 - 137215	4.8	13	<i>rpl32~tml-UAG</i>	IGS	SSC
137169 - 137213	2	23	<i>rpl32~tml-UAG</i>	IGS	SSC
137421 - 137461	2.7	15	<i>rpl32~tml-UAG</i>	IGS	SSC
137697 - 137740	2.8	17	<i>rpl32~tml-UAG</i>	IGS	SSC
137906 - 137945	2	20	<i>rpl32~tml-UAG</i>	IGS	SSC
142169 - 142213	2	22	<i>ndhE~ndhG</i>	IGS	SSC
142217 - 142249	2.2	15	<i>ndhE~ndhG</i>	IGS	SSC/IRa

* CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

* *C. siderosticta*

Indices	Repeat number	Size (bp)	Location	Region
250 - 291	2.9	15	<i>rps19~psbA</i>	IGS LSC
1424 - 1534	2	55	<i>psbA~tmK-UUU</i>	IGS LSC
2008 - 2044	2.4	16	<i>tmK-UUU</i> intron	intron LSC
2088 - 2114	2.1	13	<i>tmK-UUU</i> intron	intron LSC
5706 - 5758	2.9	18	<i>tmK-UUU~rps2</i>	IGS LSC

6396 - 6428	2.2	15	<i>tmk-UUU~rps2</i>	IGS	LSC
6430 - 6501	2	36	<i>tmk-UUU~rps2</i>	IGS	LSC
6664 - 6697	2.1	16	<i>tmk-UUU~rps2</i>	IGS	LSC
7164 - 7214	2	25	<i>tmk-UUU~rps2/rps2</i>	IGS/CDS	LSC
9771 - 9816	1.9	24	<i>rpoC2</i>	CDS	LSC
10503 - 10916	8.8	48	<i>rpoC2</i>	CDS	LSC
10503 - 10888	4.1	93	<i>rpoC2</i>	CDS	LSC
10519 - 11029	3.7	141	<i>rpoC2</i>	CDS	LSC
10568 - 11088	2.2	234	<i>rpoC2</i>	CDS	LSC
10626 - 11073	1.9	234	<i>rpoC2</i>	CDS	LSC
10678 - 11073	8.5	48	<i>rpoC2</i>	CDS	LSC
10848 - 11120	2.9	93	<i>rpoC2</i>	CDS	LSC
11092 - 11147	2.1	27	<i>rpoC2</i>	CDS	LSC
11129 - 11229	2.2	45	<i>rpoC2</i>	CDS	LSC
14547 - 14574	2	14	<i>rpoC2~rpoC1/rpoC1</i>	IGS/CDS	LSC
20758 - 20786	2	15	<i>rpoB~rpoB</i>	IGS	LSC
21423 - 21454	2	16	<i>rpoB~rpoB</i>	IGS	LSC
23187 - 23215	2.2	13	<i>psbM~tmD-GUC</i>	IGS	LSC
23907 - 23951	4	11	<i>psbM~tmD-GUC</i>	IGS	LSC
23907 - 23951	2	23	<i>psbM~tmD-GUC</i>	IGS	LSC
24924 - 24967	1.9	23	<i>tmY-GUA~tmE-UUC</i>	IGS	LSC
25894 - 25942	2.9	17	<i>tmE-UUC~psbD</i>	IGS	LSC
25936 - 25990	2	29	<i>tmE-UUC~psbD</i>	IGS	LSC
26819 - 26881	2.4	26	<i>tmE-UUC~psbD</i>	IGS	LSC
30420 - 30459	2	20	<i>tmS-UGA~psbZ</i>	IGS	LSC
31150 - 31463	2	156	<i>tmG-UCC~trnM-CAU/trnM-CAU/trnM-CAU~trnM-CAU/trnM-CAU/trnM-CAU~tmV-GAC</i>	IGS/CDS/IGS/CDS/IGS	LSC
32240 - 32292	2.8	17	<i>tmV-GAC~rbcl</i>	IGS	LSC
32244 - 32276	2	17	<i>tmV-GAC~rbcl</i>	IGS	LSC
34056 - 34082	1.9	14	<i>rbcl~atpB</i>	IGS	LSC
37613 - 37673	2	30	<i>tmV-UAC~ndhC</i>	IGS	LSC
41480 - 41535	1.9	29	<i>tmL-UAA~tmT-UGU</i>	IGS	LSC
41760 - 41793	2	17	<i>tmL-UAA~tmT-UGU</i>	IGS	LSC
44502 - 44548	2.9	16	<i>atpI~atpH</i>	IGS	LSC
45600 - 45677	2.2	36	<i>atpF</i>	CDS	LSC
50895 - 50936	2	21	<i>tmG-GCC~tmS-GCU</i>	IGS	LSC
51020 - 51069	3.9	14	<i>tmG-GCC~tmS-GCU</i>	IGS	LSC
51024 - 51074	2.1	24	<i>tmG-GCC~tmS-GCU</i>	IGS	LSC
52904 - 52944	2.3	18	<i>psbK~rps11</i>	IGS	LSC
53052 - 53116	2	33	<i>psbK~rps11</i>	IGS	LSC
57799 - 57829	1.9	16	<i>rps11~petD</i>	IGS	LSC
70088 - 70117	1.9	16	<i>rps14~tmQ-UUG</i>	IGS	LSC
72104 - 72177	8.2	9	<i>rps14~tmQ-UUG</i>	IGS	LSC
72113 - 72177	3.6	18	<i>rps14~tmQ-UUG</i>	IGS	LSC
82946 - 82970	1.9	13	<i>psbE~petL</i>	IGS	LSC
84057 - 84081	2.1	12	<i>tmP-UGG~psaJ</i>	IGS	LSC
84058 - 84119	3	20	<i>tmP-UGG~psaJ</i>	IGS	LSC
84084 - 84125	2.1	20	<i>tmP-UGG~psaJ</i>	IGS	LSC
85455 - 85566	4.5	24	<i>rpl33~rpl20</i>	IGS	LSC
88976 - 89013	2.1	18	<i>rpl20~rps12</i>	IGS	LSC
91229 - 91472	4	61	<i>rps12_5'~ycf3</i>	IGS	LSC
93300 - 93351	2	26	<i>ycf3</i> intron	intron	LSC
96935 - 97606	2.1	319	<i>rps16~rps8</i>	IGS	LSC
99892 - 99933	2	21	<i>rpl16</i> intron	intron	LSC
99972 - 100009	2	19	<i>rpl16</i> intron	intron	LSC
101577 - 101621	3	15	<i>rpl16~rpl22</i>	IGS	LSC
102761 - 102807	3.1	15	<i>rps19~tmH-GUG</i>	IGS	IRb
106905 - 106947	2.9	15	<i>tml-CAU~rps12_3'</i>	IGS	IRb
107072 - 107107	2	18	<i>tml-CAU~rps12_3'</i>	IGS	IRb
109831 - 109888	2.1	27	<i>tml-CAU~rps12_3'</i>	IGS	IRb
109976 - 110229	9.4	27	<i>tml-CAU~rps12_3'</i>	IGS	IRb
109985 - 110229	13.6	18	<i>tml-CAU~rps12_3'</i>	IGS	IRb
109985 - 110214	6.4	36	<i>tml-CAU~rps12_3'</i>	IGS	IRb
112870 - 112908	2.6	15	<i>rps7~ndhB</i>	IGS	IRb
113783 - 113824	2	21	<i>rps7~ndhB</i>	IGS	IRb
113804 - 113933	2.5	51	<i>rps7~ndhB</i>	IGS	IRb

116722 - 116747	2	13	<i>ndhB~tmL-CAA</i>	IGS	IRb
118270 - 118327	2.1	27	<i>tmL-CAA~rm16</i>	IGS	IRb
118412 - 118484	4.1	18	<i>tmL-CAA~rm16</i>	IGS	IRb
118412 - 118484	2	36	<i>tmL-CAA~rm16</i>	IGS	IRb
119309 - 119360	2.5	21	<i>tmL-CAA~rm16</i>	IGS	IRb
119920 - 119961	2	21	<i>tmL-CAA~rm16</i>	IGS	IRb
119941 - 120121	3.5	51	<i>tmL-CAA~rm16</i>	IGS	IRb
120518 - 120556	2.6	15	<i>tmL-CAA~rm16</i>	IGS	IRb
122464 - 122655	8.3	23	<i>tmL-CAA~rm16</i>	IGS	IRb
124079 - 124386	17.1	18	<i>tmL-CAA~rm16</i>	IGS	IRb
124079 - 124386	8.1	36	<i>tmL-CAA~rm16</i>	IGS	IRb
124079 - 124380	6.7	45	<i>tmL-CAA~rm16</i>	IGS	IRb
124079 - 124386	3.8	81	<i>tmL-CAA~rm16</i>	IGS	IRb
124095 - 124371	3.4	81	<i>tmL-CAA~rm16</i>	IGS	IRb
124105 - 124326	5.3	45	<i>tmL-CAA~rm16</i>	IGS	IRb
134560 - 134597	2.1	18	<i>tmN-GUU~rps15</i>	IGS	IRb
135813 - 135856	2.9	15	<i>tmN-GUU~rps15</i>	IGS	IRb
138072 - 138098	3	9	<i>tmN-GUU~rps15</i>	IGS	IRb
143661 - 143687	2.1	13	<i>ndhI~ndhG</i>	IGS	IRb
144649 - 144695	2.3	21	<i>ndhG~ndhF</i>	IGS	SSC
147023 - 147059	2.1	17	<i>ndhF~rpl32</i>	IGS	SSC
147137 - 147174	2.1	18	<i>ndhF~rpl32</i>	IGS	SSC
147179 - 147210	2	16	<i>ndhF~rpl32</i>	IGS	SSC
147865 - 147893	2.1	14	<i>rpl32~tmL-UAG</i>	IGS	SSC
148061 - 148096	3.2	11	<i>rpl32~tmL-UAG</i>	IGS	SSC
148957 - 149013	1.9	30	<i>tmL-UAG~ccsA</i>	IGS	SSC
153180 - 153213	2.3	15	<i>ndhE~ndhG</i>	IGS	SSC
153310 - 153340	2.2	14	<i>ndhE~ndhG</i>	IGS	SSC

* CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

* *C. lupulina*

Indices	Repeat number	Size (bp)	Location	Region	
753 - 783	2.1	15	<i>rpl22-rpl16</i>	IGS	LSC
860 - 904	1.9	23	<i>rpl22-rpl16</i>	IGS	LSC
3311 - 3351	2	20	<i>rpl14-rps8</i>	IGS	LSC
4731 - 4764	2.4	14	<i>rps8-rpl36</i>	IGS	LSC
5342 - 5395	1.9	28	<i>rps8-rpl36</i>	IGS	LSC
5370 - 5416	2	25	<i>rps8-rpl36</i>	IGS	LSC
7798 - 7838	2	20	<i>ycf3</i> intron	intron	LSC
8270 - 8320	1.9	26	<i>ycf3</i> intron	intron	LSC
16206 - 16258	2.2	24	<i>rpl20-rpl33</i>	IGS	LSC
16214 - 16261	2	24	<i>rpl20-rpl33</i>	IGS	LSC
16364 - 16417	2.1	26	<i>rpl20-rpl33</i>	IGS	LSC
16374 - 16432	4.1	14	<i>rpl20-rpl33</i>	IGS	LSC
17657 - 17681	2.1	12	<i>psaI-tmP-UGG</i>	IGS	LSC
19889 - 19921	2.5	13	<i>petL-psbE</i>	IGS	LSC
23164 - 23190	1.9	14	<i>psbI-cemA</i>	IGS	LSC
25468 - 25500	2.1	16	<i>cemA-psaI</i>	IGS	LSC
28813 - 28866	2.1	26	<i>tmQ-UUG-rps14</i>	IGS	LSC
29528 - 29575	2	24	<i>tmQ-UUG-rps14</i>	IGS	LSC
37233 - 37324	2.2	42	<i>tmR-UCU-psbB</i>	IGS	LSC
40795 - 40823	1.9	15	<i>petB</i> intron	intron	LSC
42872 - 42905	2	17	<i>petD</i> intron	intron	LSC
43496 - 43526	1.9	16	<i>petD-rpoC1</i>	IGS	LSC
45099 - 45142	2	22	<i>petD-rpoC1</i>	IGS	LSC
45919 - 45969	2	25	<i>petD-rpoC1</i>	IGS	LSC
48535 - 48580	1.9	24	<i>petD-rpoC1/rpoC2</i> gene	IGS	LSC
48686 - 48854	8	21	<i>petD-rpoC1/rpoC2</i> gene	IGS	LSC
49466 - 49975	5.5	93	<i>petD-rpoC1/rpoC2</i> gene	IGS	LSC
49942 - 50048	2.2	48	<i>petD-rpoC1/rpoC2</i> gene	IGS	LSC

49980 - 50228	2.6	99	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC
49987 - 50184	2	99	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC
50201 - 50262	2.3	27	<i>petD-rpoC1/rpoC2 gene</i>	IGS	LSC
52455 - 52482	2	14	<i>IGS-rpoC1</i>	IGS/CDS	LSC
59947 - 59980	2.1	16	<i>rpoB-tmC-GCA</i>	IGS	LSC
60005 - 60035	2.1	15	<i>rpoB-tmC-GCA</i>	IGS	LSC
61254 - 61284	2.1	15	<i>rpoB-tmC-GCA</i>	IGS	LSC
64154 - 64185	2	16	<i>tmD-GUC-tmY-GUA</i>	IGS	LSC
64374 - 64417	1.9	23	<i>tmY-GUA-tmE-UUC</i>	IGS	LSC
64647 - 64690	3.7	12	<i>tmE-UUC-tmT-AGU</i>	IGS	LSC
64647 - 64698	2.2	24	<i>tmE-UUC-tmT-AGU</i>	IGS	LSC
69839 - 69876	1.9	20	<i>tmS-UGA-psbZ</i>	IGS	LSC
70167 - 70194	2	14	<i>psbZ-tmG-GCC</i>	IGS	LSC
70583 - 70874	2	146	<i>IGS-trmM-CAU-trmM-CAU-IGS</i>	IGS-trm-trm-IGS	LSC
76868 - 76903	1.9	18	<i>tmV-UAC-ndhC</i>	IGS	LSC
76933 - 76957	2.1	12	<i>tmV-UAC-ndhC</i>	IGS	LSC
76955 - 77015	2	30	<i>tmV-UAC-ndhC</i>	IGS	LSC
79071 - 79099	2.1	14	<i>ndhJ-tmF-GAA</i>	IGS	LSC
82883 - 82924	3.4	13	<i>atpI-atpH</i>	IGS	LSC
82908 - 82950	2	21	<i>atpI-atpH</i>	IGS	LSC
84864 - 84906	2	22	<i>atpF intron</i>	intron	LSC
87278 - 87321	2	22	<i>atpA-tmR-UCU</i>	IGS	LSC
88698 - 88732	1.9	18	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC
88929 - 88981	4.7	11	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC
89073 - 89120	2.1	23	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC
89511 - 89569	3.3	18	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC
89511 - 89602	2.6	36	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC
90791 - 90832	2	21	<i>tmG-GCC-tmS-GCU</i>	IGS	LSC
94595 - 94633	2	20	<i>psbK-tmK-UUU</i>	IGS	LSC
94694 - 94725	2	16	<i>psbK-tmK-UUU</i>	IGS	LSC
96059 - 96095	2.1	18	<i>tmK-UUU intron</i>	intron	LSC
97533 - 97569	2.4	16	<i>tmK-UUU intron</i>	intron	LSC
97830 - 97880	2	26	<i>tmK-UUU-psbA</i>	IGS	LSC
97865 - 97909	3.7	12	<i>tmK-UUU-psbA</i>	IGS	LSC
101841 - 101883	2	21	<i>rpl2-tmT-UGU</i>	IGS	IRb
101845 - 101898	2.6	21	<i>rpl2-tmT-UGU</i>	IGS	IRb
101867 - 101908	3.4	13	<i>rpl2-tmT-UGU</i>	IGS	IRb
102750 - 102843	3.5	27	<i>rpl2-tmT-UGU</i>	IGS	IRb
102750 - 102845	10.7	9	<i>rpl2-tmT-UGU</i>	IGS	IRb
104601 - 104995	3.8	105	<i>rpl2-tmT-UGU</i>	IGS	IRb
104628 - 104995	7	51	<i>rpl2-tmT-UGU</i>	IGS	IRb
104636 - 104995	6.9	54	<i>rpl2-tmT-UGU</i>	IGS	IRb
107424 - 107467	2.4	18	<i>tmI-UGU-tmI-CAU</i>	IGS	IRb
109657 - 109704	2.3	20	<i>tmI-CAU-rps12</i>	IGS	IRb
110216 - 110257	2.9	15	<i>tmI-CAU-rps12</i>	IGS	IRb
110372 - 110407	2	18	<i>tmI-CAU-rps12</i>	IGS	IRb
114110 - 114153	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
116171 - 116212	4.7	9	<i>tmI-CAU-rps12</i>	IGS	IRb
118423 - 118464	4.7	9	<i>tmI-CAU-rps12</i>	IGS	IRb
119635 - 119678	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
120656 - 120699	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
121674 - 121717	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
122707 - 122750	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
123726 - 123769	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
124759 - 124802	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
125781 - 125824	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
126798 - 126841	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
127821 - 127864	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
128841 - 128884	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
129864 - 129907	2	22	<i>tmI-CAU-rps12</i>	IGS	IRb
130152 - 130264	2.5	45	<i>tmI-CAU-rps12</i>	IGS	IRb
130161 - 130263	11.5	9	<i>tmI-CAU-rps12</i>	IGS	IRb
132953 - 132978	2.9	9	<i>rps12-ndhB/rps7 gene</i>	IGS	IRb
133147 - 133176	2	15	<i>rps12-ndhB</i>	IGS	IRb
134843 - 134872	2	15	<i>rps12-ndhB</i>	IGS	IRb

135320 - 135348	1.9	15	<i>rps12-ndhB</i>	IGS	IRb
135732 - 135761	1.9	16	<i>rps12-ndhB</i>	IGS	IRb
138347 - 138372	2	13	<i>ndhB-trnL-CAA</i>	IGS	IRb
139230 - 139548	8.2	39	<i>trnL-CAA-rm16</i>	IGS	IRb
141984 - 142102	2	59	<i>rm16-trnL-GAU</i>	IGS	IRb
150002 - 150027	2.2	12	<i>trnN-GUU-rps15</i>	IGS	IRb
151311 - 151336	2.2	12	<i>trnN-GUU-rps15</i>	IGS	IRb
151487 - 151512	2.2	12	<i>trnN-GUU-rps15</i>	IGS	IRb
152632 - 152657	2.2	12	<i>trnN-GUU-rps15</i>	IGS	IRb
152807 - 152832	2.2	12	<i>trnN-GUU-rps15</i>	IGS	IRb
154787 - 154899	2.5	45	<i>trnN-GUU-rps15</i>	IGS	IRb
154796 - 154898	11.5	9	<i>trnN-GUU-rps15</i>	IGS	IRb
156348 - 156391	2	22	<i>trnN-GUU-rps15</i>	IGS	IRb
158399 - 158440	4.7	9	<i>trnN-GUU-rps15</i>	IGS	IRb
160637 - 160678	4.7	9	<i>trnN-GUU-rps15</i>	IGS	IRb
164560 - 164585	2	13	<i>ndhA</i> intron	intron	IRb
170152 - 170188	2.1	18	<i>ndhF-rps11</i>	IGS	SSC
170270 - 170306	2.1	17	<i>ndhF-rps11</i>	IGS	SSC
171532 - 171568	2.1	18	<i>rps11-rpl32</i>	IGS	SSC
171638 - 171673	2.1	17	<i>rps11-rpl32</i>	IGS	SSC
171699 - 171742	2.1	21	<i>rps11-rpl32</i>	IGS	SSC
172763 - 172824	3.1	20	<i>rpl32-trnL-UAG</i>	IGS	SSC
175025 - 175070	2.3	20	<i>ccsA-psaC/IGS-ndhD</i>	IGS/IGS-CDS	SSC
177277 - 177331	2	27	<i>psaC-ndhE</i>	IGS	SSC
177672 - 177697	2	13	<i>ndhE-ndhG</i>	IGS	SSC
177741 - 177770	2.4	12	<i>ndhE-ndhG</i>	IGS	SSC
177843 - 177872	2.1	14	<i>ndhE-ndhG</i>	IGS	SSC

* CDS, coding sequence regions; IGS, intergenic spacer regions; Intron, intragenic regions

Appendix 6. Total number of perfect simple sequence repeats (SSRs) identified within the chloroplast genome of *C. lupulina* and related taxa

* *T. latifolia*

Repeats	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	total
A/T	-	-	-	-	-	63	35	13	8	7	4	3	-	1	-	2	136
C/G	-	-	-	-	-	2	2	-	-	-	-	-	-	-	-	-	4
AC/GT	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
AG/CT	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	4
AT/AT	-	-	15	9	5	1	1	-	-	-	-	-	-	-	-	-	31
AAC/GTT	9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9
AAG/CTT	18	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	19
AAT/ATT	15	3	-	1	-	-	-	-	-	-	-	-	-	-	-	-	19
ACC/GGT	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
ACG/CGT	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
ACT/AGT	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
AGC/CTG	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
AGG/CCT	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
ATC/ATG	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
AAAG/CTTT	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
AAAT/ATTT	3	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4
AATC/ATTG	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
AATG/ATTC	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
AATT/AATT	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
ACCT/AGGT	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
AGAT/ATCT	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
AAAA/ATTTT	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
AATAT/ATATT	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1

* *E. buergerianum*

Repeats	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	total
A/T	-	-	-	-	-	48	20	5	4	2	2	1	-	1	-	-	1	84
C/G	-	-	-	-	-	1	-	-	-	2	-	-	-	-	-	-	-	3
AG/CT	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
AT/AT	-	-	15	4	2	2	-	-	-	-	-	-	-	-	-	-	-	23
AAC/GTT	12	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	13
AAG/CTT	23	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	24
AAT/ATT	41	10	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	52
ACC/GGT	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
ACT/AGT	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
AGC/CTG	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4
ATC/ATG	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5

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