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Hidden Diversity In Aquatic Habitats: Lessons From Cryptic Species In Microscopic Invertebrates (rotifera)

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HIDDEN DIVERSITY IN AQUATIC HABITATS: LESSONS FROM CRYPTIC SPECIES IN
MICROSCOPIC INVERTEBRATES (ROTIFERA)

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HIDDEN DIVERSITY IN AQUATIC HABITATS: LESSONS FROM CRYPTIC SPECIES IN
MICROSCOPIC INVERTEBRATES (ROTIFERA)

by

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Abstract

Speciation is a continuous and adaptive process by which lineages are diverged into multiple groups, and species are the product of this process. Taxonomy is the study of relationship between organisms, classifying and naming them, and one of the taxonomical challenges is delimiting species boundaries. Species delimitation can be controversial because biologists do not agree on species concepts and approaches for defining species boundaries. One of the well-known species concepts is the Biological Species Concept that requires studying reproductive barriers among populations. Investigating strength of reproductive isolation among populations is not always practical in the wild. Therefore, many biologists have used morphological traits as an indicator of reproductive isolation and for delineating species. Yet, morphological methods are not fully effective in defining species boundaries and detecting species diversity, since some species are morphologically identical. Molecular analyses have contributed to species delimitation for morphologically indistinguishable groups (cryptic species). Species that are delimited based on molecular methods have been further tested using multiple complementary approaches (integrative taxonomy) such as ecological, behavioral and morphological differentiation especially for groups such as microorganisms that show high morphological uniformity.

Rotifers, similar to other microorganisms, have drought-resistance propagules that are efficient for long distance dispersal. Therefore, they are assumed to have high rates of gene flow among habitats even across large geographic scales. As a result of high population connectivity, little genetic variation in population structure within rotifer morphospecies is expected. Moreover, rotifers do not have a lot of recognizable morphological characteristics and there has not been enough effort to resolve the taxonomical controversies resulted from morphological

plasticity and cryptic species; morphologically similar species (cryptic species) are often not distinguished. However, high genetic structure has been reported among populations of many rotifer morphospecies suggesting they are species complexes with multiple cryptic species. Thus, rotifers are a good model organism for the application of molecular methods for species delimitation and to test the DNA based species boundaries using an integrative taxonomy. Integrating multiple approaches has been successfully used to delimit species boundaries in some rotifer species complexes such as *Epiphanes senta* and *Brachionus calicyflorus*.

In Chapters 1 and 2, I used COI gene and ITS region sequences to study genetic structure and to delimit cryptic species in a littoral rotifer morphospecies, *Euchlanis dilatata* (62 populations), and four sessile morphospecies (*Limnias melicerta* [29 populations]; *L. ceratophylli* [20 populations]; *Collotheca campanulata* [19 populations]; *C. ornata* [45 populations]). Using Bayesian species delimitation (BSD), I found seven putative cryptic species for *E. dilatata* based on the ITS region sequence analysis. Based on COI gene sequences analyzed by BSD, nine putative cryptic species within *L. melicerta*, four putative cryptic species within *L. ceratophylli*, seven putative cryptic species for *C. campanulata* and eight putative cryptic species for *C. ornata* were detected. The relationship between genetic and geographic distance was weak or lacking within the examined morphospecies. Moreover, geographic distributions of cryptic species varied from occurring in a single locality, broadly, or even overlapping suggesting that they may differ in their capabilities to disperse, colonize, and persist in new habitats. Geometric and morphometric analyses did not show significant variation in trophi (rotifer's jaws) shape and size among cryptic species of *L. melicerta* and *L. ceratophylli*. The lack of morphological variation can be a case of morphological stasis 1) through stabilizing

selection because of niche conservatism, or 2) a result of speciation mediated by ecological and/or mating signals differentiation without morphological changes.

In Chapter 3, to test the species boundaries defined by a molecular approach, I investigated reproductive isolation, variation in trophi morphology and life history characteristics among cryptic species of *E. dilatata*. Mating success rate between each cryptic species was 0-1.1%, which was lower than that of positive controls (intra-clonal: 15.6-43.9%; Chi-Square= 15.3-52.2, $p < 0.001$). SEM trophi images representing the seven cryptic species of *E. dilatata* were used for morphometric analyses. Using Discriminant analysis, 64% of individuals were correctly assigned to cryptic species (Chi-Square= 78, $p < 0.001$); trophi morphology cannot be used to distinguish *E. dilatata* cryptic species except for cryptic species A. To investigate life history characteristics of cryptic species, four treatments were used: (1) 20°C, 180 $\mu\text{S}/\text{cm}$, (2) 20°C, 1800 $\mu\text{S}/\text{cm}$, (3) 27°C, 180 $\mu\text{S}/\text{cm}$, and (4) 27°C, 1800 $\mu\text{S}/\text{cm}$. The interaction between temperature and conductivity had significant effects on generation time, net reproductive rate, and the intrinsic rate of population increase in some of the cryptic species ($p = 0.03$). All cryptic species had higher survivorship and fecundity under temperature 27°C while showing variation in response to water conductivity. My findings showed cryptic species of *E. dilatata* are reproductively isolated and they show differentiation in life history characteristics although except for one cryptic species they cannot be distinguished based on morphology. Because I provided support for the DNA taxonomy species boundaries by finding they are reproductively isolated and ecologically differentiated, I described four cryptic species of *E. dilatata* as new species. A specimen from cryptic species A was selected as neotype for *Euchlanis dilatata* because this species showed the widest geographic distribution in USA and Mexico. In Chapter 4, I used ddRAD-Seq to investigate the molecular basis of ecological adaptation and to gauge

adaptive genetic variation between two cryptic species of *E. dilatata*. I obtained 107 loci that were present in at least 40% of individuals for seven populations representing two proposed cryptic species. F_{ST} values ranged from 0-0.95 indicating there was high genetic differentiation between them. Most populations from different cryptic species showed high genetic divergence. One exception was the F_{ST} value of 0 between Cattle Tank, NM (cryptic species D) and Triangle Pond, AZ (cryptic species C). The genetic similarity between these two populations could be a result of admixture, or inefficiency of obtained loci in representing accurate amount of genetic divergence among populations of *E. dilatata*. There was no significant relationship between genetic variation at those loci and geographic distance among populations. However, in Discriminant Analysis of Principle Components, populations that were collected from similar habitats were grouped together. This indicates there could be a relationship between genetic variation and habitat features. To provide support for these results, additional samples should be included and only loci with coverage across at least 80% of individuals should be retained for downstream analysis.

Finally, in my research on cryptic species of rotifers, I was able to show that isolation by distance was not strongly related to the observed genetic variation. On the other hand, as it was shown by ddRAD-Seq analyses of *E. dilatata*, genetic divergence may be related to ecological adaptation. However, because of the low number of loci and their low coverage I was not able to find genes that could be related to ecological adaptation. Further studies focused on genomic regions with adaptive functions among rotifer cryptic species will obtain a better understanding of the ecological speciation mechanisms in rotifers.

I studied cryptic diversity within *Euchlanis dilatata* and for the first time, for four sessile morphospecies. I used DNA-based taxonomy to delimit species boundaries for morphologically

similar lineages within five rotifer morphospecies. Integrative taxonomy has been suggested for species delimitation in especially in groups with limited morphological characteristics such as microorganisms. Here, I used integrative approach for more reliable species delimitation within *Euchlanis dilatata* and I found that those cryptic species are reproductively isolated and ecologically differentiated. On the other hand, I showed that genetic diversity within each morphospecies has weak correlation with geographic isolation. This may indicate that speciation in rotifers is not necessarily caused by geographic isolation. On the other hand, genetic variation among cryptic species is potentially associated to differentiation in ecological adaptation. Therefore, cryptic species of rotifers are likely to show variation in their adaptive range resulting in genetic variation and reproductive isolation among them. This mode of speciation is not necessarily accompanied by morphological divergence.

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Introduction

During speciation events, genetically cohesive and interbreeding populations diverge into multiple distinct groups because gene flow among them becomes limited (Petersen & Hughes, 1999). Depending on the speciation mode, barriers to gene flow may be a result of complete or partial geographic isolation (allopatric and parapatric (Bush, 1975)) or reproductive isolation within the ancestral species distribution range (sympatric, (Gavrilets, 2014)). Selection is one of the important contributors to speciation because sometimes it acts against hybrids to enforce reproductive isolation. Moreover, selection is involved in adaptation and divergence among taxa (Barton, 2010). Speciation is a continuous process of divergence among lineages, and species are the product of this adaptive process (Verma et al., 2013). Accurate species delimitation contributes to a comprehensive data baseline for most biological studies. However, species delimitation can be a complicated task because biologists advocate different species concepts. This results in different conclusions about the number of species and species boundaries (De Queiroz, 2007). Over 20 species concepts have been introduced (see Mayden, 1997) and different concepts are of interest to different group of biologists. However, they all consider species as independently evolving groups (De Queiroz, 2007).

In 1942, Mayr introduced the Biological Species Concept: it defines species as a group of actually or potentially interbreeding individuals representing a cohesive gene pool that are reproductively isolated from other groups. He posited that between species, barriers to gene flow define species boundaries. The Biological Species Concept has been criticized because testing reproductive isolation is not always feasible; many biologists use the extent of morphological differentiation as an indicator of reproductive isolation (Balakrishnan, 2005; Verma et al., 2013).

The problem with using morphological characteristics is that there is a risk for using arbitrary levels of divergence for species delimitation (Mayden, 1997). Moreover, speciation does not always happen in concert with morphological changes (Bickford et al., 2007), and there may not be sufficient recognizable morphological variation among species. Therefore, relying solely on morphology to classify species can be misleading and may not always reflect the true level of species richness and biodiversity (Bickford et al., 2007; Birky, 2007; Kaya et al., 2009; Oliver et al., 2009). A growing number of studies have demonstrated that cryptic diversity is a common phenomenon in animals including mammals (Baker, 1984; Kváč et al., 2016), birds (Lohman et al., 2010; Campbell et al., 2016), lizards (Hoogmoed et al., 1992; Oliver et al., 2009; Domingos et al., 2017), fishes (Kon et al., 2007; Healey et al., 2018), amphibians (Löters et al., 2006; Funk et al., 2012; Chambers & Hebert, 2016) and a variety of invertebrates (de Vargas et al., 1999; Lee, 2000; Gómez et al., 2002; Lee & Frost, 2002; Hebert et al., 2003; Gilbert & Walsh, 2005; Chen & Hare, 2008; Schön et al., 2012; Leasi et al., 2013; Viñas et al., 2015; Khan et al., 2018). Hebert et al. (2003) suggested DNA barcoding as a tool to improve taxonomical efforts and to overcome limitations of morphology-based taxonomy in capturing species diversity. Molecular studies are now contributing to the identifying morphologically similar but genetically distinct (cryptic) species (Bickford et al., 2007; Pfenninger & Schwenk, 2007; Fontaneto et al., 2015; Proudlove & Wood, 2018).

The cytochrome *c* oxidase I (COI) mitochondrial gene and the internal transcribed spacer (ITS) nuclear region are among the mostly used molecular markers to study cryptic species. The COI gene contains conserved regions that generally are not variable within populations (Spooner, 2009). In addition, universal primers are available to amplify this gene (Folmer et al., 1994). Moreover, mitochondrial genes are haploid, thus there is no need to distinguish between

alleles of a gene prior to sequencing (Birky, 2007), making them easier to analyze. The COI gene has been suggested as an appropriate marker to delimit species of meiofauna by Tang et al. (2012) and has been used to distinguish among species across taxa (e.g., earthworms: Huang et al., 2007; copepods: Cornils & Held, 2014; daphnia: Duggan et al., 2012; rotifers: Li et al., 2010). It also has the potential to define species boundaries and to reveal cryptic species in both bdelloid and monogonont rotifers (e.g., *Brachionus plicatilis*: Mills et al., 2016; *Testudinella clypeata*: Leasi et al., 2013; *B. calyciflorus*: Li et al., 2010; *Philodina flaviceps*: Fontaneto et al., 2008). The ITS region has also been used in taxonomy and molecular phylogeny (Blouin, 2002) because it is easy to amplify due to accessibility of universal primers (White et al., 1990). Furthermore, the ITS region is highly conserved within species and shows a high degree of variation among species (Bruns et al., 1991). Thus, the ITS region has also been widely applied to discover cryptic species (e.g., Gilbert & Walsh, 2005; Miura et al., 2005; Walsh et al., 2009; Xiang et al., 2010; Ge et al., 2012; Lindner & Banik, 2011; Schön et al., 2012; Jiménez-Contreras et al., 2013; Mills et al., 2016; Papakostas et al., 2016).

Although using DNA sequences (DNA-based taxonomy) is not necessarily sufficient to define species boundaries, it can be considered an effective tool to complement traditional taxonomy (Packer et al., 2009). DNA taxonomy provides hypotheses about species that can be tested with morphological, behavioral, ecological, and mate choice studies, and to eventually describe cryptic species. Integrative taxonomy uses multiple and complementary approaches for reliable species delineation (Dayrat, 2005), especially for understudied taxa such as microorganisms. There are many examples of implementing integrative taxonomy for species delimitation in variety of taxa from plants to microorganisms (e.g., Gibbs, 2009; André et al., 2014; Darienko et al., 2015; Papakostas et al., 2016).

The amount of cryptic diversity that is overlooked by morphological approaches may be high in microorganisms as they lack easily recognizable morphological characters and therefore morphologically similar species are not distinguished. Moreover, there has not been sufficient taxonomic effort in studying them (Fontaneto et al., 2009; Kaya et al., 2009). Consequently, morphological approaches may not have enough resolution to reflect the true estimate of species richness and biodiversity patterns in microorganisms such as rotifers (Kaya et al., 2009). Therefore, microorganisms are good models for applying DNA-based taxonomy for defining species boundaries, and to examine those boundaries using an integrative approach. Integrative taxonomy has been successfully used for species delineation in several microorganisms. For instance, André et al. (2014) included geographic distribution, ecological and morphological differentiations to delimit cryptic species within 23 morphospecies of planktonic foraminifera. In another study, Darienko et al. (2015) found seven species within the algae *Coccomyxa* by integrating DNA taxonomy, morphological differentiation, and variation in population growth in response to salinity. Integrative taxonomy used in those studies provided support for the delimitation results. Moreover, in case of cryptic species with no morphological differences, DNA taxonomy that is supported by an integrative approach can be used for describing and naming new species. Describing cryptic species solely based on genetic variation was first applied to 10 cryptic species of the skipper butterfly *Astrartes fuligator* (Walch, 1775) complex (Brower, 2010). Jörger and Schrödl (2013) suggested a protocol for describing cryptic species to establish a consistent process for future work. Those guidelines have been used for describing cryptic species: e.g., for five cryptic species of the snail *Alviniconcha hessleri* Okutani & Ohta, 1988 by Johnson et al. (2015) and nine cryptic species in the amphipod *Niphargus stygius* (Schiödte, 1847) by Delić et al. (2017).

Phylum Rotifera comprises aquatic, semi-aquatic, or parasitic microscopic invertebrates that are obligatory or cyclically parthenogenetic (class Eurotatoria) or dioecious (Classes Pararotatoria and Acanthocephala) (Wallace et al., 2006). These animals are characterized by two features: an anterior ciliated organ, called the corona, and a muscular pharynx called the mastax that contains a set of jaws known as trophi (Wallace & Snell, 2010). This phylum includes about 2000 species (Segers, 2007; Wallace & Snell, 2010). Though small, rotifers are vital components of aquatic food systems as they connect microbial life to higher trophic levels (Wallace et al., 2006). Rotifers are capable of passive long-distance dispersal through their dormant stages (Wallace et al., 2006; Walsh et al., 2016). Therefore, they are often considered cosmopolitan (e.g., Rousselet, 1909; Pejler, 1977), with high rates of gene flow even among geographically distant habitats. However, there are many examples of rotifer morphospecies showing substantial genetic divergence even across small geographic scales (e.g., Schröder & Walsh, 2007; Fontaneto et al., 2008a; Walsh et al., 2009; Xiang et al., 2011). Consequently, genetically distinct cryptic species are common in rotifers for example in *Brachionus plicatilis* Müller, 1786 (Gomez & Snell, 1996; Gómez et al., 2002a; Suatoni et al., 2006; Montero-Pau et al., 2011a; Michaloudi et al., 2016), *Brachionus calyciflorus* (Gilbert & Walsh, 2005; Xiang et al., 2011; Papakostas et al., 2016), *Epiphanes senta* (Müller, 1773) (Schröder & Walsh 2007; 2010), *Testudinella clypeata* (Müller, 1786) (Leasi et al., 2013), *Polyarthra dolichoptera* Idelson, 1925 (Obertegger et al., 2014), and *Synchaeta pectinata* Ehrenberg, 1832 (Kimpel et al., 2015). Cryptic species in most taxa, including rotifers, are primarily delimited using molecular analyses (Fontaneto et al., 2015). Most cryptic species within Rotifera have remained unnamed lineages and have not been established as new species.

In rotifers, some studies have provided additional evidences to investigate variation among genetically diverged cryptic species and to test the hypothesis that they are evolutionary distinct lineages. For example, morphological variation among cryptic species have been reported and some are described based on their morphological features such as *Epiphanes hawaiiensis*, *E. ukera* and *E. chihuahuaensis* within the *E. senta* (Müller, 1773) species complex (Schröder & Walsh, 2007), *Brachionus manjavacas* Fontaneto, Giordani, Melone & Serra, 2007 (Fontaneto et al., 2007) and *B. koreanus* Hwang, Dahms, Park & Lee, 2013 (Hwang et al., 2013) in *B. plicatilis* species complex.

Ascertaining reproductive isolation among populations in their natural habitats is not always practical (Sokal, 1973). However, rotifer populations can be maintained under laboratory conditions, and mate choice experiments can examine the strength of reproductive isolation and lack of gene flow among populations and cryptic species (e.g., Schröder & Walsh, 2007). This has provided the opportunity to examine the species boundaries that are delimited by DNA taxonomy for multiple rotifer cryptic species (e.g., *B. plicatilis* species complex: Gómez et al., 1995; Rico-Martinez & Snell, 1995; Gomez & Snell, 1996; Suatoni et al., 2006; *B. calyciflorus* species complex: Xiang et al., 2011; Gilbert & Walsh, 2005; *Epiphanes senta* species complex: Schröder & Walsh, 2007; 2010). Still, reproductive isolation and its underlying mechanisms have not been studied for many rotifer cryptic species leading to gaps in our knowledge about gene flow, causes of genetic divergence, and species boundaries in rotifers.

When populations adapt to divergent environments, they potentially become reproductively isolated which could result in ecological speciation (Schluter, 2001). By incorporating the physical and chemical features of the habitat in the study of cryptic species, we can examine whether occurrence of a cryptic species is correlated to specific environmental

factors (e.g., Ortells et al., 2003; Zhang et al., 2015) and, beyond that, whether ecological differentiation could be a driver of speciation (e.g., Liu et al., 2013; Fouet et al., 2017). Moreover, investigating differentiation in ecological adaptations among cryptic species can be applied to examine the species boundaries specified by molecular methods (Rissler & Apodaca, 2007).

Ecological differentiation can be readily examined among rotifer cryptic species by studying the relationship between the occurrence of genotypes and habitat features such as water temperature and salinity (Ortells et al., 2003; Dennis & Hellberg, 2010; Tang et al., 2012; Papakostas et al., 2013; Zhang et al., 2015) or by conducting life table experiments (Wang et al., 2014; Gabaldón et al., 2015). Variation in ecological adaptation among cryptic species has not been studied for many rotifer species complexes. Furthermore, studying genetic variation that has adaptive significance can elucidate the molecular basis of ecological differentiation (Watt et al., 1983; Bailey & Bataillon, 2016). There is little known about genetic basis of ecological adaptation, and the importance of ecological speciation for rotifers cryptic species. Double digest Restriction Site Associated DNA markers (ddRAD-Seq) provide a useful tool for identifying large numbers of single nucleotide polymorphisms (SNP) for detecting loci that have been under selection (Etter et al., 2011; Andrews et al., 2016). Thus, ddRAD-Seq can be used to obtain hundreds of markers for studying population genetics of rotifers and for discovering candidate genes that could play a role in ecological adaptation. Since ecological adaptation has been reported among rotifer cryptic species (see above), rotifers can be used to examine the genetic basis of ecological differentiation and its significance in creating cryptic species.

Despite the high number of studies on rotifer cryptic species, many potential species complexes remain to be investigated. Moreover, reproductive barriers, biogeographical

distributions, ecological differentiation, and speciation processes for rotifer cryptic species are not fully investigated. Because rotifers are one of the major constituents of the aquatic communities, studying their population genetic structure and cryptic diversity will provide a framework for estimating diversity in aquatic environments, examining patterns of dispersal and gene flow, and understanding evolutionary processes underlying speciation. For this reason, I selected rotifers as the model organism to study cryptic species and speciation in aquatic microinvertebrates.

One of the understudied rotifer morphospecies is *Euchlanis dilatata* from family Euchlanidae. *Euchlanis dilatata* is a littoral rotifer and is reported from eight biogeographical regions and it is considered cosmopolitan (Segers, 2007). However, there is evidence of variation in body size related to the ploidy levels (Walsh & Zhang, 1992), and variation in ecological adaptation among different genotypes of *E. dilatata* (King, 1972). There are many examples of cryptic species in rotifers (see above). But, most studies on cryptic species have focused on planktonic and littoral groups resulting in a gap in our knowledge about cryptic species in sessile rotifers. Two poorly studied sessile taxa are the genera *Limnias* and *Collotheca*. To my knowledge, there have not been any studies on population genetic structure and cryptic species within these genera. *Limnias* includes six morphospecies (Wallace et al., 2018), from which *L. melicerta* and *L. ceratophylli* show cosmopolitan distributions (Segers, 2007). However, morphological and molecular differentiation have not been investigated within these morphospecies. Genus *Collotheca* includes 48 morphospecies (Segers, 2007; Meksuwan et al., 2013). Eleven morphospecies of *Collotheca*, including *C. campanulata* and *C. ornata*, are two widely distributed species (Segers, 2007).

I selected *E. dilatata*, *L. melicerta*, *L. ceratophylli*, *C. campanulata* and *C. ornata* morphospecies to study genetic variation in the COI gene and ITS region to detect cryptic species for two reasons: 1) Each morphospecies has multiple synonyms (Segers, 2007) indicating their taxonomic status needs to be re-evaluated. 2) They are considered cosmopolitan, and previous studies have shown cosmopolitan morphospecies can be species complexes. I hypothesized that there is substantial genetic differentiation within *E. dilatata*, *L. melicerta*, *L. ceratophylli*, *C. campanulata* and *C. ornata*, and each includes multiple cryptic species. I explored morphological variation in jaws (trophi) for cryptic species of *E. dilatata*, *L. melicerta* and *L. ceratophylli* to see whether morphological approaches are effective to identify them. Further, to examine species boundaries defined by a molecular approach, I conducted cross mating and life table experiments for cryptic species of *E. dilatata*. I hypothesized that cryptic species are reproductively isolated and ecologically differentiated. And finally, I used ddRAD-Seq for single nucleotide polymorphisms discovery to find genomic regions that may be under selection and to investigate the genetic basis of ecological adaptation in cryptic species of *E. dilatata*. My hypothesis was that there is relationship between genetic variation among cryptic species and ecological differentiation among them.

Chapter 1: Population structure and cryptic species in the cosmopolitan rotifer *Euchlanis dilatata*¹

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ABSTRACT

Determining genetic structure is fundamental to our understanding of how populations adapt and evolve. Increasingly cryptic species complexes are being discovered in zooplankton, including rotifers. We investigated genetic differentiation among 62 populations across a broad area of North America. One population was assayed for ITS and COI markers and also showed low divergence (0 and <1%, respectively). Overall, ITS sequences were less variable (0–13.4%) than COI sequences (0.0–21.9%). When sequences were used for phylogenetic analysis, we found substantial differentiation among populations and seven putative cryptic species based on Bayesian Species Delimitation (ITS: 0–5.2% genetic divergence within, and 1.0–13.4% between putative species). Cryptic lineages varied from occurring in a single locality, broadly, or even overlapping suggesting that they may differ in their capabilities to disperse, colonize, and persist in new habitats. Accordingly, *E. dilatata* can be considered a species complex, and additional species are likely to be uncovered.

INTRODUCTION

Studying population genetic structure informs our understanding of how populations evolve under evolutionary forces such as gene flow. There is a growing number of examples of small organisms that disperse passively over long distances implying that, for these taxa, gene flow can occur even among geographically distant populations. However, many of these taxa show high levels of genetic differentiation and form cryptic species complexes, even across small spatial scales within the range of their dispersal (e.g., Zeller, Reusch & Lampert, 2006; Fontaneto, Boschetti & Ricci, 2008a; Xiang *et al.*, 2011). Rotifers, a common constituent of freshwater ecosystems, possess the ability for passive, long-distance dispersal through their diapausing stages (e.g., resting eggs, xerosomes, (Dumont, 1983; Walsh, May & Wallace, 2016)). These propagules are within the size range of particles that can be transported with dust during wind events, can be dispersed by animals, or through water flow (Fontaneto, 2011). Based on the high likelihood of passive dispersal, most rotifer species are assumed to have cosmopolitan distributions. Nevertheless, application of molecular, behavioral, and morphological methods has revealed high numbers of cryptic species complexes within the phylum (e.g., *Brachionus plicatilis* Müller, 1786 [Gómez & Snell, 1996; Mills *et al.*, 2016], *Brachionus calyciflorus* Pallas, 1766 [Xiang *et al.*, 2011; Papakostas *et al.*, 2016], *Lecane bulla* (Gosse, 1851) [Walsh *et al.*, 2009], *Epiphanes senta* (Müller, 1773) [Schröder & Walsh, 2007, 2010], *Testudinella clypeata* (Müller, 1786) [Leasi *et al.*, 2013], *Polyarthra dolichoptera* Idelson, 1925 [Obertegger, Flaim & Fontaneto, 2014], *Synchaeta pectinata* Ehrenberg, 1832 [Kimpel *et al.*, 2015], and a number of bdelloid species [Fontaneto *et al.*, 2007, Fontaneto *et al.*, 2011; Xiang *et al.*, 2016]). Thus, we know that genetic differentiation is common among

populations of rotifers, not only among those that are geographically isolated but also for some within small geographic ranges (e.g., Fontaneto *et al.*, 2008b; Xiang *et al.*, 2011).

We specifically focus on *Euchlanis dilatata* Ehrenberg, 1830 because there is morphological and genetic evidence that the species is variable. *E. dilatata* has been reported from eight biogeographical regions (Segers, 2007). Across this global distribution, there are two described subspecies, *Euchlanis dilatata dilatata* Ehrenberg, 1830 and *Euchlanis dilatata lucksiana* (Hauer, 1930) (Koste, 1978), five forms and one variety (Jersabek & Leitner, 2015). These variants differ in body size (Parise, 1966; Kutikova, 1970; Koste, 1978), lorica shape (Koste & Shiel, 1989) and ecological features such as habitat association (Koste, 1978; Walsh, 1989), predation susceptibility (Walsh, 1995), egg deposition pattern and some other behaviors (Walsh, 1989). Intraspecific variation in *E. dilatata* body size likely has a genetic basis as noted by several authors (Morales-Baquerol *et al.*, 1992; Walsh & Zhang, 1992). For instance, Walsh & Zhang (1992) found extensive variation in size and among life history characteristics associated with ploidy level in an Oregon population. Moreover, King (1972) hypothesized that sequential replacement of genetically distinct populations may be responsible for ecological adaptation to seasonal variation in *E. dilatata*. Allochronic succession of genotypes has been demonstrated within the *Brachionus plicatilis* species complex. Papakostas *et al.* (2013) found that *B. plicatilis* s.s. and *B. "Austria"* (subsequently re-described as *B. asplanchnoidis* Charin, 1946; Michaloudi *et al.*, 2016) were more abundant in cold months while *B. ibericus* Ciros-Pérez *et al.*, 2001 were more abundant during warm months. Thus, it is becoming apparent that many members of cryptic species are not only genetically distant but can be ecologically specialized.

To determine broad scale (6032 km) genetic differentiation and to test for evolutionary divergent lineages, we sampled 62 populations collected from 13 states in the USA and two

states in Mexico. This study, demonstrating extensive genetic variation in *E. dilatata* populations and the existence of seven putative species, contributes to our understanding of evolutionary processes in passively dispersed zooplankton and helps us in gaining a better estimate of diversity in freshwater habitats.

METHODS

Study Sites

Plankton (64- μ m nytex mesh) and vegetation samples were collected from a variety of water sources in the USA and Mexico (Figure 1.1, Supplemental Table S1.1). *Euchlanis dilatata* were isolated and a single asexual female was used to establish a clonal lineage. Clonal lineages were cultured in modified MBL media (Stemberger, 1981) and fed the algae *Rhodomonas minuta* Skutja 1948, *Chlorella vulgaris* Berijerinck, 1890 (Culture Collection of Algae at the University of Texas at Austin [UTEX] strain 30), *Ankistrodesmus falcatus* (Corda) Ralfs, 1848 (UTEX strain 749), and/or *Chlamydomonas reinhardtii* Dangeard, 1888 (UTEX strain 90) depending upon availability.

Voucher specimens representing each population were preserved in 95% ethanol and 4% buffered formalin and deposited in the Biodiversity Collections at the University of Texas at El Paso. Water temperature, pH, dissolved oxygen, conductivity, and nutrient concentrations were measured in the field at most sites and GPS coordinates were recorded.

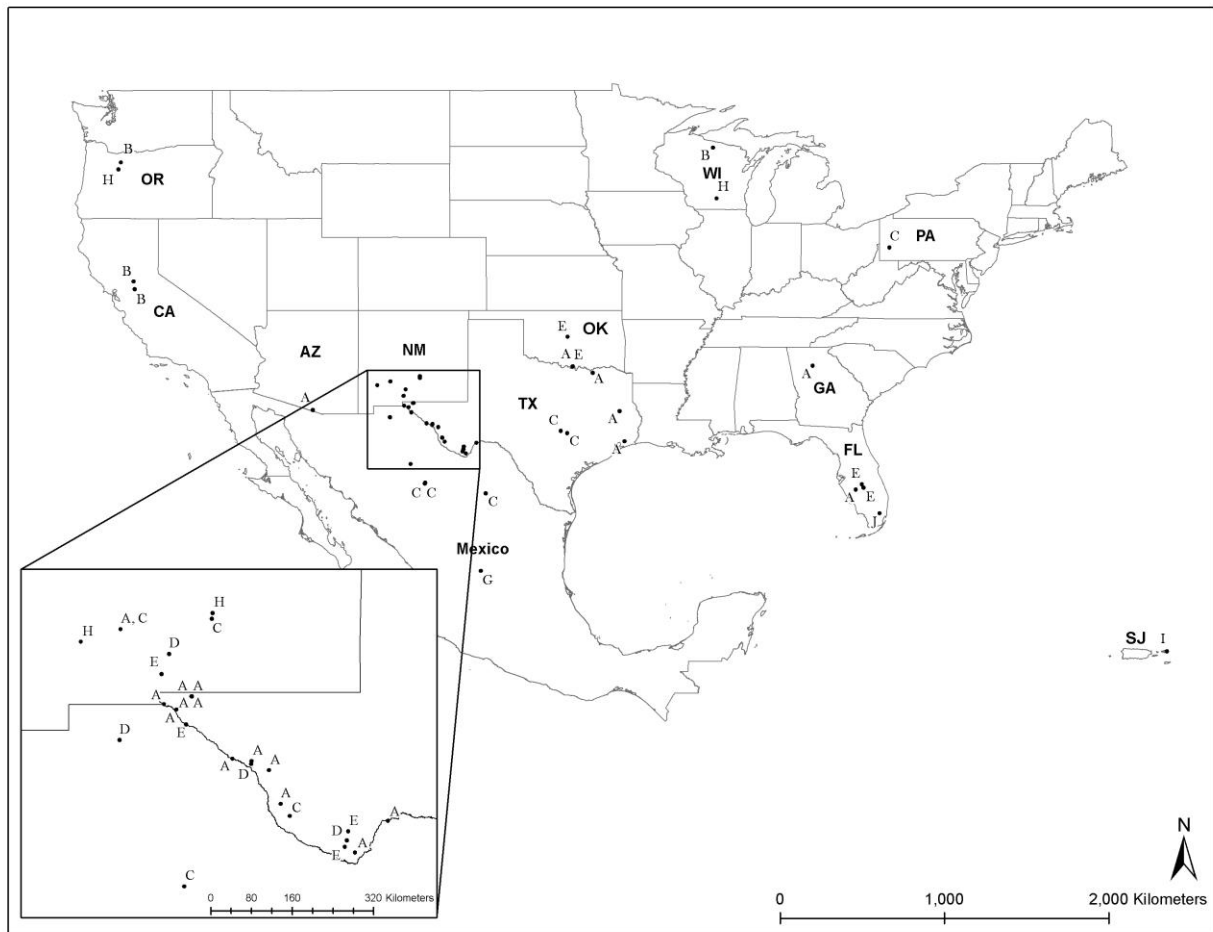


Figure 1.1. Location of sites sampled in the USA and Mexico representing geographic distribution of six putative cryptic species (A-F) within the *Euchlanis dilatata* species complex and populations included in AFLP analysis (*). Species G from Mexico is not shown.

DNA extraction

DNA was extracted from approximately 20–25 female individuals from one clonal lineage from each population using 9.5 µl lysis buffer (5 µl of proteinase K solution, 20 mg/ml and 95 µl of 1X PCR buffer (10X PCR Buffer, Invitrogen; 50mM MgCl₂)), followed by incubation at 55°C for 90 min and at 95°C for 15 min respectively. For some populations where lysis buffer did not result in successful extraction, the extraction was repeated using 1–40 clonally-derived individuals per population in 12–13 µl Chelex[®] 100 (*Bio-Rad* Laboratories, CA,

USA) followed by incubation at 100°C for 10 min. All templates were stored at –80°C for further analyses.

To determine within population variation using DNA sequences (ITS and COI), DNA was extracted from 17 clonal lineages from a population collected from the Rio Grande at Williamsburg, NM. Two isolates were collected in winter 2005 and 15 were collected in summer 2013.

Amplification

To look for patterns in diversity among populations, the internal transcribed spacer 1, 5.8S ribosomal RNA gene, and the internal transcribed spacer 2 (hereafter referred to as ITS) were amplified using the primers ITS4: 5'-TCCTCCGCTTATTGATATGC-3', ITS5: 5'-GGAAGTAAAAGTCGTAACAAGG-3' (White *et al.*, 1990), and the cytochrome *c* oxidase subunit I (COI) gene was amplified using the primers LCO1490: 5' - GGTCAACAAATCATAAAGATATTGG-3', HCO2198: 5'-TAAACT TCAGGGTGACCAAAAAATCA-3' (Folmer *et al.*, 1994).

Amplification reactions contained 5 µl of extracted DNA, 1 µl of each primer (ITS4 and ITS5 for ITS region amplification, HCO and LCO for COI gene amplification; 500 ng/ µl), 1 µl MgCl₂ (50mM), 12.5 µl HotStarTaq™ Master Mix (Qiagen), and 4.5 µl HPLC grade sterile water. Cycle conditions were initial denaturation at 94°C for 15 min, followed by 35 cycles of 94°C for 1 min, 47°C for 1 min and 72°C for 1 min, and a final extension of 72°C for 10 min on a thermocycler (Techne TC-412). If amplifications using this protocol failed, PCR optimization was carried out using Life Technologies PCR Optimizer™ kits according to the manufacturer's specifications. In these cases, each PCR reaction contained 5 µl (in lysis buffer) or 10 µl (extracted by Chelex) of genomic DNA, 1 µl of each primer (500 ng/ µl), 28 µl (where DNA

extraction was done using lysis buffer) or 23 μ l (where DNA extraction was done using Chelex100) HPLC grade sterile water, 1 to 1.5 unit GoTaq® G2 DNA Polymerase (Promega), 10 μ l 5X PCR buffer C (12.5 mM MgCl₂, pH 8.5) or 5X PCR buffer F (10 mM MgCl₂, pH 9), followed by adding 5 μ l dNTP mix (2.5 mM each of dATP, dCTP, dGTP, dTTP) to each reaction at 80°C. Reactions were run on a thermocycler (Techne TC-412) with an initial denaturation at 94°C for 1 min, followed by denaturation at 94°C for 1 min, annealing at 48°C for 2 min and extension at 72°C for 3 min in 35 cycles and a final extension at 72°C for 7 min.

Sequencing

Amplification products were examined by electrophoresis to verify their size and then purified using GENECLAN® kits (MP Biomedicals, LLC) before sequencing. Templates (2 μ l of 10–30 ng/ μ l purified DNA) and 1 μ l of each primer (50 ng/ μ l) were sent to UTEP's Genomic Analysis Core Facility to be sequenced in both directions. Sequencing was done using BigDye® Terminator v3.1 Cycle Sequencing Kits (Applied Biosystems) on an Applied Biosystems 3130xl Genetic Analyzer. Some sequences were obtained using an Applied Biosystems 3730X DNA Analyzer at the University of Arizona Genetics Core.

GenBank accession numbers are given in Table S1.1. For the ITS region, *E. deflexa* and *Limnias ceratophylli* were selected as outgroups in phylogenetic reconstructions. Additional COI gene sequences for *E. dilatata* were obtained through GenBank (Accession #: JX216599.1, JX216598.1, and DQ297773.1). For the COI gene, *Euchlanis alata* Voronkov, 1912 (Accession #: DQ079962.1) and *E. deflexa* Gosse, 1851 were included as outgroups (Table S1.1).

Genetic Diversity

Sequences were viewed and checked manually in FinchTV 1.4.0 (Geospiza, Inc., Seattle, WA, USA; <http://www.geospiza.com>). Contigs were made in CAP 3 (Huang & Madan, 1999). Sequences were aligned using MAFFT v 7 (Kato & Standley, 2013) and then checked manually in Mesquite v 3.01 (Maddison & Maddison, 2014). The same program was used to translate COI gene sequences to proteins and to check for stop codons.

In order to phase and obtain haplotypes for ITS region sequences, we used SeqPHASE web tool (Flot, 2010). To phase ITS region sequences, the ITS FASTA alignment was uploaded to the SeqPHASE online tool (<http://seqphase.mpg.de/seqphase>) following the protocol of Flot (2010). The obtained seqphase.inp file was used to run the command line, /PHASE -d1 seqphase.inp seqphase.out locally. Then, seqphase.out and seqphase.const files were used to run the second step to obtain a FASTA alignment of the phased sequences using an online tool at <http://seqphase.mpg.de/seqphase/final.html>. ITS chromatograms are available as supplementary information. DAMBE v 5 (Xia, 2013) was used to measure substitution saturation of each sequence set. Number of polymorphic sites, number of parsimony informative sites, number of haplotypes, haplotype diversity (h) and nucleotide diversity (π) were calculated using DnaSp v 5 (Librado & Rozas, 2009). The uncorrected ("p") distance matrix was calculated in PAUP* v 4.0a 152 (Swofford, 2002).

Phylogenetic analysis and cryptic species delimitation

Models for sequence evolution were TPM2uF+G for the ITS region and TPM2uF+I+G for the COI gene as specified by Jmodeltest2 (Guindon & Gascuel, 2003; Darriba *et al.*, 2012). RAxML v 8.0.0 (Stamatakis, 2014) was used to reconstruct a maximum likelihood phylogenetic tree with 1000 bootstrap replicates to evaluate node support. Bayesian analysis was run in

MrBayes v 3.2.2 (Ronquist *et al.*, 2012) for 10^7 generations with two parallel runs and a 25% burn-in.

For species delimitation, we used Bayesian Species Delimitation (BSD; Rannala & Yang, 2003; Yang & Rannala, 2010, 2014), the K/ θ method (Birky *et al.*, 2010), Automatic Barcode Gap Discovery (ABGD; Puillandre *et al.*, 2012), Generalized Mixed Yule Coalescent (GMYC; Pons *et al.*, 2006) models, and the Poisson Tree Process method (PTP; Zhang *et al.*, 2013). BSD is a multispecies, coalescent-based model that can accommodate multi-locus datasets. Posterior probabilities of species delimitation models are calculated using Reversible-Jump Markov Chain Monte Carlo (rjMCMC). BSD assumes shared polymorphism arises from ancestral polymorphism. BSD implemented in BPP v 3.1 does not require a user specified guide tree and incorporates phylogenetic uncertainty in the analysis (Yang & Rannala, 2014). The BSD analysis was run using sequences of the ITS region and COI gene separately. To apply K/ θ method, the ratio of mean genetic variation between closely related putative cryptic species (K) to mean genetic variation within putative cryptic species (θ) was calculated. According to Birky *et al.* (2010), when $K/\theta \geq 4$, putative cryptic species can be considered independently evolving lineages with a 95% level of confidence. ABGD classifies sequences into putative cryptic species based on pairwise genetic distances without any prior assumptions (Puillandre *et al.*, 2012). ABGD was run by uploading a FASTA alignment of sequences to the online tool at <http://wwwabi.snv.jussieu.fr/public/abgd/abgdweb.html>.

To run GMYC and PTP an ultrametric tree is required. Ultrametric trees for the ITS region and COI gene were constructed separately using a GTR+G model for the ITS region and GTR+I+G model for the COI sequences, an uncorrelated lognormal relaxed clock, a constant-size coalescent prior, 10,000,000 generations with sampling every 1,000 generations in BEAST v

1.8.3 (Drummond *et al.*, 2012). The effective sample size (ESS > 200) of the parameters was checked in Tracer v 1.6.0 (Rambaut *et al.*, 2013) to verify convergence. Consensus trees were calculated after discarding the first 25% of trees in TreeAnnotator v 1.8.3.

PTP is a tree-based method that uses the number of substitutions to distinguish intraspecies processes from interspecies processes. Since, substitution information is obtained based on tree branch lengths, PTP is a tree-based method. This method considers two classes of Poisson processes, speciation (higher substitution rate associated to interspecies events) and coalescent (within species events; Zhang *et al.*, 2013). PTP (<http://species.h-its.org/ptp/>) was applied to ultrametric BEAST trees for each gene region using the default settings to detect the number of entities (putative cryptic species).

GMYC is a statistical model used to find the threshold in branching rates between intraspecific (coalescent) and interspecific (diversification) processes. Single and multiple threshold GMYC analyses (Fujisawa & Barraclough, 2013) were run using the online tool at <http://species.h-its.org/gmyc/> and bGMYC (Reid & Carstens, 2012) was run in the R package {bGMYC} 1.0.2 for 100,000 iterations, with a 10,000 burn-in. In single threshold GMYC, threshold is the time before which nodes represent diversification events and after which they represent coalescence. Multiple threshold GMYC does not assume that all the diversification events are older than coalescent events and searches for alternative models (Fujisawa & Barraclough, 2013). bGMYC is a Bayesian approach that incorporates uncertainty in branch length and topology of the phylogenetic tree and also uncertainty in the model parameters using Markov Chain Monte Carlo simulation (Reid & Carstens, 2012).

The effect of the number of individuals (hereafter, sequences) on the mean pairwise genetic distance within each cryptic species was tested using the Phylogenetic Generalized Least

Squares (PGLS) model in R 3.1.1 (R Development Core Team, 2014) using the packages `{ade4}` (Dray & Dufour, 2007) and `{nlme}` 3.1 (Pinheiro *et al.*, 2016). For PGLS, a phylogenetic tree with seven taxa each representing one putative cryptic species detected by BSD analysis based on the ITS region sequences was used. For each cryptic species, the number of sequences was the explanatory variable and the mean genetic variation within cryptic species was the response variable.

To test for hybridization, we used JML 1.3.0 (Joly, 2012) to examine whether the minimum interspecies genetic distance in COI gene sequences is significantly smaller than what is predicted based on a model that does not account for hybridization (Joly, 2012). If the interspecies distance is smaller than predicted, it indicates that hybridization is also involved in explaining any discordance between species tree and mitochondrial gene (COI) tree rather than incomplete lineage sorting alone. The species tree was constructed based on ITS region by running *BEAST v 1.8.3 (Drummond *et al.*, 2012) for 60,000,000 generations, sampling every 60,000 generations. Convergence was verified by checking the effective sample size (ESS > 200) in Tracer v 1.6.0 (Rambaut *et al.*, 2013). Species were delimited based on BSD using ITS region sequences. A Birth-Death process and a piecewise constant were selected as priors for the species tree. We ran JML with an effective population size (heredity scalar) of 0.25 for the COI gene, and with a 20% burn-in period.

Isolation by Distance

Version 1.2.3 of the Geographic Distance Matrix Generator (Ersts, 2006) was used to construct a geographic distance matrix. Mantel tests were run in the R package `{ecodist}` (Goslee & Urban, 2007) with 10,000 permutations to test whether genetic variation among populations

(log transformed) is correlated to geographic distances (log transformed) (km) among populations.

Occurrence of cryptic species in Big Bend National Park, TX

Three putative cryptic species were found within Big Bend National Park, TX. To examine the relationship between occurrence of those species and selected environmental variables, weighted classical multi-dimensional scaling (WCMDS) analysis was run using R packages {*vegan* 2.3-5} (Oksanen *et al.*, 2016) and {*MASS*} (Venables & Ripley, 2002). We included habitat type in the analysis by categorizing them from temporary to permanent. Temporary habitats are ranked 1, semi-permanent habitats are ranked 2, and permanent habitats are ranked 3.

RESULTS

Genetic Diversity

We obtained 98 sequences of the ITS region and 81 partial COI gene sequences from 62 populations of *E. dilatata* that were collected in the USA and Mexico. Three additional *E. dilatata* COI sequences from MA, USA (n=1) and Veracruz, Mexico (n=2) available in GenBank were included in phylogenetic reconstructions. The COI gene and ITS region sequences were not saturated (index of substitution saturation < critical index of substitution saturation, $p < 0.001$ for both markers). The ITS region alignment included 780 bp (including insertions) with 175 polymorphic sites and 71 parsimony informative sites. The COI alignment included 634 bp with 210 parsimony informative sites and 220 polymorphic sites.

ITS region sequences consisted of 23 haplotypes with haplotype diversity of 0.81 and nucleotide diversity of 0.03, while COI gene sequences represented 54 haplotypes with a

haplotype diversity (h) of 0.95 and nucleotide diversity (π) of 0.14. A number of populations with geographic distance as great as 4000 km (e.g., from Arizona to Georgia) were classified under one haplotype based on the ITS region.

Genetic distance between *E. dilatata* and the selected outgroup taxa ranged from 22.5 to 33.9% based on the ITS region, and from 20.0 to 30.0% based on COI sequences. The uncorrected pairwise genetic distance in the ITS region was 0–13.4% and 0–3.4%, among and within populations respectively. The uncorrected pairwise genetic distance in the COI gene ranged from 0 to 21.9% among populations and from 0 to 2.5% within populations.

Phylogenetic analysis and cryptic species delimitation

Using Bayesian phylogenetic reconstruction, the COI gene provided higher resolution among closely related populations as compared to the ITS region (Figures 1.2, and 1.3). The Maximum Likelihood phylogenetic reconstruction is not presented here because of low bootstrap support of clades for both markers. Most populations occurring within clusters are not in close geographic proximity based on Bayesian analysis of both markers. The number of putative cryptic species ranged from 3 to 45 based on ITS region sequences, and from 11 to 24 based on COI gene sequences (Table 1.1, Figures 1.2 and 1.3).

Table 1. 1. The number of entities (putative cryptic species) detected using Bayesian Species Delimitation (BSD), K/ θ , Automatic Barcoding Gap Discovery (ABGD), Generalized Mixed Yule Coalescent models (single threshold, multiple threshold and Bayesian GMYC) and Poisson Tree Process (PTP) within *Euchlanis dilatata* based on ITS region and COI gene. The range of likely values for number of putative cryptic species detected by PTP, and 95% confidence intervals for single and multiple threshold GMYC are shown in parentheses.

Delimitation method	ITS region	COI gene
BSD	7	12
K/ θ	8	11
ABGD	3	12
Single threshold GMYC	9 (3-33)	14 (8-39)
Multiple threshold GMYC	45 (5-45)	22 (8-37)
Bayesian GMYC	23	22
PTP	16 (12-22)	24

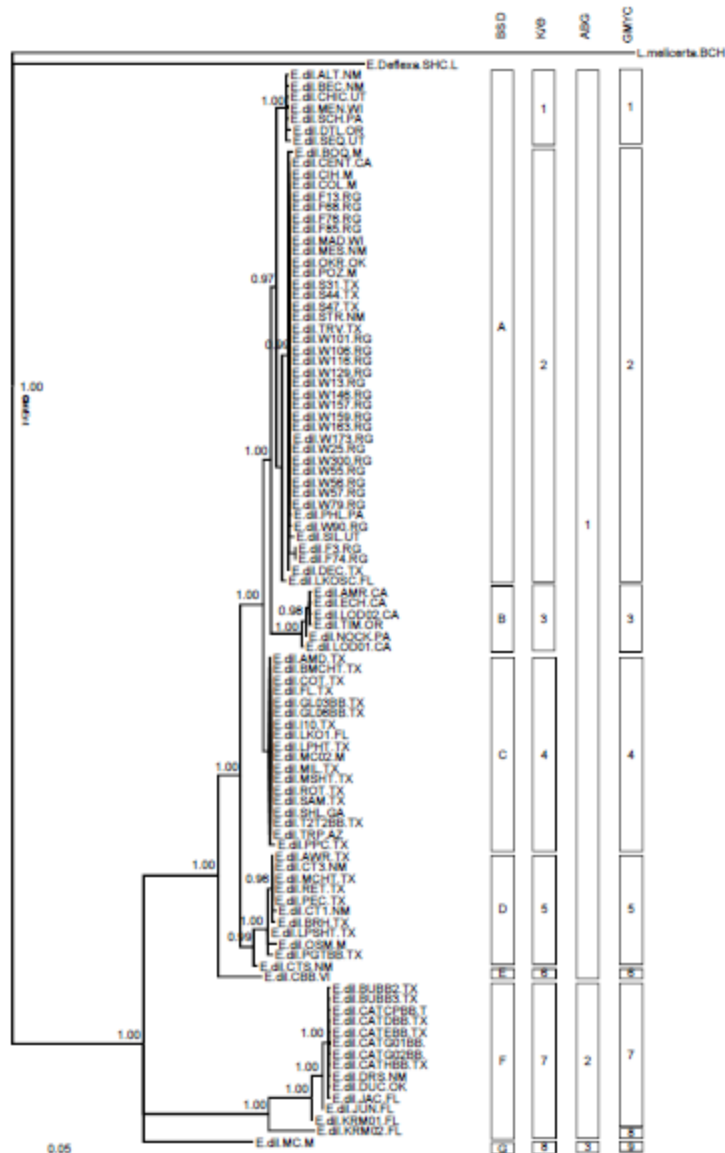


Figure 1.2. Phylogenetic relationships of 62 populations of the morphological species *Euchlanis dilatata* based on ITS region sequences, sampled from TX, NM, AZ, WI, CA, PA, GA, FL, UT, St. John, US Virgin Islands and Mexico. *Limnias melicerta* and *E. deflexa* are included as outgroups. The average branch lengths are proportional to the number of substitutions per site under a TPM2uF+G substitution model. Posterior probabilities above 0.50 from Bayesian reconstruction are shown at each node. Putative cryptic species detected using Bayesian Species Delimitation (BSD), K/θ, Automatic Barcoding Gap Discovery (ABGD), and Single Threshold Generalized Mixed Yule Coalescent models (GMYC) are shown.

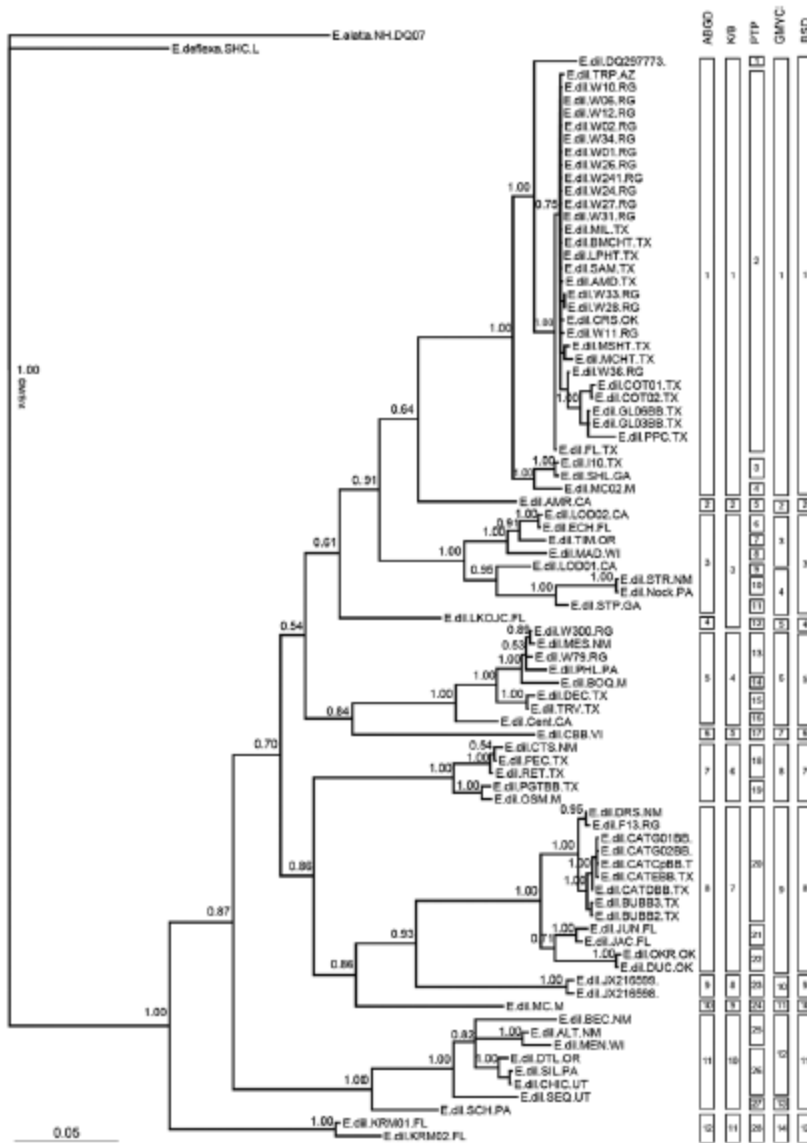


Figure 1.3. Phylogenetic relationships of 56 populations of the morphological species *Euchlanis dilatata* based on COI gene sequences, sampled from TX, NM, AZ, WI, CA, PA, GA, FL, UT, St. John, US Virgin Islands and Mexico. *E. alata* and *E. deflexa* are included as outgroups. The average branch lengths are proportional to the number of substitutions per site under a TPM2uF+I+G substitution model. Posterior probabilities above 0.50 from Bayesian reconstruction are shown at each node. Putative cryptic species detected using Bayesian Species Delimitation (BSD), K/θ, Automatic Barcoding Gap Discovery (ABGD), Single Threshold Generalized Mixed Yule Coalescent models (GMYC), and Poisson Tree Process (PTP) are shown.

The most conservative estimate of putative species was obtained using ABGD based on ITS sequences; three species were delimited with one species consisting of 85% of the

populations. Clearly, this method underestimates the number of cryptic species in *E. dilatata*. This finding is similar to the results obtained by (Papakostas *et al.*, 2016) for the rotifer *Brachionus calyciflorus* where no cryptic species were detected by ABGD. Therefore, we delimited seven entities as *E. dilatata* putative cryptic species based on the BDS analysis of ITS sequences, the next most conservative method. The genetic distance in the ITS sequences ranged from 0.0 to 5.2% within cryptic species and from 1.0 to 13.4% among cryptic species. The genetic distance in the COI gene ranged from 0.0 to 18.7% within those cryptic species and from 0.2 to 21.9% among them. There was no significant relationship between maximum pairwise genetic distance and number of individuals within each cryptic species (PGLS model, ITS region: t value= 0.42, p= 0.7; COI gene: t value= 1.18, p= 0.3).

Most putative cryptic species are represented by widely distributed genotypes (Figure 1.1). For example, species “B” that showed the largest geographic range was collected from Texas, New Mexico, Wisconsin, Oregon, Pennsylvania, Florida and Oklahoma in the USA and a site in Mexico. However, cryptic species “E” and “G” are found only in one location, a temporary pond in U.S. Virgin Island and a different site in Mexico, respectively. In a temporary habitat at Hueco Tanks State Park and Historic Site, TX, we detected two co-occurring cryptic species (species “C” and “D”; Figure 1.1).

For 24 out of 28 pairwise comparisons between the seven putative cryptic species in JML test, the interspecies genetic distance in the COI gene was not significantly smaller than expected (JML test: $p > 0.05$). Thus based on these results, hybridization is not the driver of observed discordance between gene tree and species tree. This discordance may result from incomplete lineage sorting.

Isolation by distance

We plotted log transformed genetic distance among populations of *E. dilatata* against log transformed geographic distance (km). For both ITS region and COI gene sequences, the relationship between genetic and geographic distance was significant (Mantel test: ITS: $r = 0.15$ with 95% confidence interval of 0.09-0.2, $p = 0.01$, COI: $r = 0.18$ with 95% confidence interval of 0.1-0.24, $p < 0.01$) over the collection range (approximately 6032 km from Oregon to St. John, US Virgin Islands).

To test whether there was significant pattern in smaller geographical scales, we analyzed two data subsets: one including populations from west Texas and eastern New Mexico that show a maximum geographic distance of 372 km, and one with populations from Big Bend National Park (BIBE), TX having a maximum geographic distance of 43 km among populations. In the first subset, genetic distance was not significantly correlated with geographic distance (Mantel test: $r = 0.06$ with 95% confidence interval of 0.03-0.1, $p = 0.12$) based on ITS region, while a significant correlation was detected for COI gene (Mantel test: $r = 0.3$ with 95% confidence interval of 0.15-0.35, $p = 0.01$). A similar pattern was observed in the BIBE subset, with genetic variation not correlated with geographic distance based on ITS sequences while genetic variation in the COI gene showed a significant correlation (Mantel test: ITS: $r = -0.35$, 95% confidence interval: -0.4 to -0.25, $p = 0.25$; COI: $r = 0.9$, 95% confidence interval: 0.8-0.94, $p < 0.01$).

Occurrence of cryptic species in Big Bend National Park, TX

The occurrence of cryptic species “C”, “D” and “F” in Big Bend National Park, TX was significantly correlated (WCMDs) to temperature ($r^2 = 0.66$, $p = 0.006$), conductivity ($r^2 = 0.99$, $p = 0.006$), turbidity ($r^2 = 0.81$, $p = 0.02$), nitrite ($r^2 = 0.64$, $p = 0.03$), alkalinity ($r^2 = 0.95$, $p = 0.006$), silica ($r^2 = 0.75$, $p = 0.008$), TDS ($r^2 = -0.85$, $p = 0.006$), ammonia ($r^2 = 0.86$, $p = 0.006$), elevation

($r^2 = 0.74$, $p = 0.02$), and habitat type ($r^2 = 1$, $p = 0.03$). Ranges of these environmental variables are given in Supplemental Table S1.2.

DISCUSSION

By definition it is difficult to identify cryptic species based solely on morphology, so it is expected that the number of cryptic species will be high in groups showing high morphological uniformity (Kon *et al.*, 2007). Therefore, levels of cryptic diversity may be high in microscopic organisms as there has not been sufficient taxonomic effort in many groups. Moreover, many of these taxa lack easily recognizable morphological characters. Consequently, traditional taxonomy is not likely to reflect true levels of species richness and or fully account for biodiversity patterns within rotifers and other small organisms (Fontaneto *et al.*, 2009; Kaya *et al.*, 2009). Our results support these observations as well as the prediction of King (1972) of underlying genetic variation in *Euchlanis dilatata* populations that varies both temporally and spatially. We found high levels of genetic variation in *E. dilatata* populations at both small and broad geographic scales in the USA and Mexico. By examining two molecular markers, ITS and COI sequences, seven putative cryptic species were detected by Bayesian Species Delimitation based on ITS sequences. Based on other detection methods (except ABGD), this is likely a conservative estimate of the diversity within the complex. These cryptic species varied greatly in their geographic distribution and their spatial overlap.

High genetic variation among *E. dilatata* populations was revealed based on sequences from both the ITS region and COI gene. Levels of genetic variation detected in this study were within the range of those found in other microinvertebrates. Albeit, the genetic diversity based on the ITS region was lower than that of the COI gene. This has also been found in studies of a variety of other microinvertebrate species (Tables 1.2, 1.3). The higher observed genetic

differentiation in the COI gene has been attributed to its faster rate of evolution as compared to the ITS region (Cruickshank, 2002; Vilas, Criscione & Blouin, 2005).

Discordance between gene trees and species trees can stem from hybridization, incomplete lineage sorting, gene duplication and horizontal gene transfer (Maddison, 1997). In the early stages of speciation, incomplete lineage sorting is a common reason of discordance (Tajima, 1983). In our study, incomplete lineage sorting is likely to cause discordance between gene tree and species tree meaning similar sequences in *E. dilatata* cryptic species coalesced before divergence of cryptic species. However, the possibility of undetected hybridization should not be overlooked. Although there is no objective criteria to select one of the species delimitation methods over the others (Fontaneto, Flot & Tang, 2015), we have delineated seven putative cryptic species according to BSD based on ITS region sequences. ITS has been suggested to delimit cryptic species more accurately in two rotifer species complexes, *B. plicatilis* (Mills *et al.*, 2016) and *B. calyciflorus* (Papakostas *et al.*, 2016). In addition, in our analysis BSD of ITS sequences provides a conservative yet effective method for delimiting species boundaries within *E. dilatata* complex.

Although most putative cryptic species in *E. dilatata* were represented by widely distributed genotypes, two were found in one region. Species “E” was found in a temporary beach pond on St. John, US Virgin Islands and species “G” was represented by a population from Mexico. Under-sampling can result in bias in singleton frequencies (Coddington *et al.*, 2009). Thus, it is possible that the singletons in our study have a wider geographic distribution than reported here as only a small subset of all aquatic habitats was sampled.

We found two putative cryptic species in Laguna Prieta, HTSPHS, El Paso Co., TX. A clone of *E. dilatata* collected in summer 2013 was sufficiently different from a clonal lineage

that was hatched from sediments to be classified as separate putative cryptic species “C” and “D” respectively. Coexistence of cryptic species has been reported in several other invertebrates including rotifer species complexes (Table 1.4). A more comprehensive list of co-occurring cryptic species in rotifers is provided by Gabaldón *et al.* (2016). Coexistence may be a result of adaptation to environmental conditions such as variation in tolerance to salinity as seen among cryptic species of the nematode *Rhabditis (Pellioiditis) marina* (Bastian, 1865) Andrassy, 1984 (de Meester *et al.*, 2011) or variation in optimal temperature, diet, and predator vulnerability among cryptic species of the rotifer *P. dolichoptera* (Obertegger *et al.*, 2014). Coexistence of cryptic species can also be a result of secondary sympatry following allopatric speciation as may have occurred in the *B. plicatilis* species complex (Gómez, 2005).

In addition to finding co-occurrence of cryptic species within a site, we found more than one cryptic species occur across a small geographical scale in Big Bend National Park, TX (species “C”, “D” and “F”). Those cryptic species were collected from various habitat types at different elevations and differ in their ecological features. Species “C” was found in a perennial spring-fed stream. Species “D” was collected from a temporary former cattle tank and species “F” from a permanent series of interconnected springs at higher elevation. Based on WCMDs analysis, the occurrence of species “C”, “D” and “F” was correlated to variation in conductivity, TDS, ammonia, nitrite, alkalinity, silica, elevation, turbidity, and temperature (likely not biologically significant) among habitats, and also the habitat type (temporary vs permanent). Thus, we hypothesize occurrence of these three putative cryptic species maybe explained under the ecological differentiation model suggested by McPeck (2008) where speciation occurs along an environmental gradient. This model may also apply to bdelloid rotifers where genetically distinct lineages differed in temperature tolerance and resource utilization (Birky *et al.*, 2005)

and oribatid mites with cryptic species differing in their trophic niches (Schneider *et al.*, 2004). Another potential explanation for co-occurrence of three cryptic species in Big Bend National Park may be that these cryptic species colonized their current habitats after diverging into genetically distinct entities and the observed genetic diversity is a consequence of founder events.

Further, geographic isolation has been documented in some microinvertebrate species complexes (e.g., *Philodina flaviceps* Bryce, 1906: Fontaneto *et al.*, 2008a; *B. plicatilis*: Gómez, Carvalho & Lunt, 2000; *Acartia tonsa* Dana, 1849: Chen & Hare, 2008; *Mesocyclops thermocyclopoides* Harada, 1931: Suárez-Morales, Mercado-Salas & Morales-Ramírez, 2011; *Daphnia pulex* Leydig, 1860: Cristescu *et al.*, 2012; *D. laevis* Birge, 1878: Taylor, Finston & Hebert, 1998). In our study, we found a significant but weak correlation between genetic and geographic distance, thus indicating genetic variation among *E. dilatata* populations can be partially explained by geography. The weak correlation was not surprising, given that highly divergent populations were found in close geographic proximity. Similar results have been obtained for *B. calyciflorus* (Xiang *et al.*, 2011) and some species of *Rotaria* (Fontaneto *et al.*, 2008b). Alternatively, temporal variation and habitat heterogeneity have been hypothesized as potential drivers of cryptic speciation in rotifers (Fontaneto *et al.*, 2009). These factors likely play an important role in speciation within *E. dilatata*, generating high genetic diversity in close geographic proximity. Notwithstanding, a strong positive correlation between genetic distance and geographic range was found when sites at Big Bend National Park were compared.

However, less genetic differentiation was seen within the highly connected river sites using AFLP markers. Given that the effect of geographic distance on genetic differentiation was

not consistent across the broad geographical scale of our study, it is reasonable to conclude that cryptic species within *E. dilatata* species complex may arise under various speciation scenarios.

Clearly, *E. dilatata* can be considered a species complex with higher diversity that can be identified by morphological features alone. Many of the detected cryptic species in this study displayed wide geographic distributions that can be attributed to the potential for long distance dispersal of rotifers through their diapausing stage. Yet, a few putative cryptic species were restricted to one region. This may indicate that cryptic species within *E. dilatata* have different capabilities to colonize new habitats. Variation in dispersal and colonization ability among several bdelloid species (Fontaneto & Melone, 2004) and among some species of *Lecane* (Segers, 1996) has also been hypothesized.

It is likely that additional cryptic species within the *Euchlanis dilatata* species complex will be found by analyzing other geographical regions and/or other markers. It should be noted that species delimitation methods that are solely based on molecular methods should be augmented by with other lines of evidence (Fontaneto *et al.*, 2015; Mills *et al.*, 2016). As suggested by Dayrat (2005), biodiversity should be studied using multiple and complementary perspectives.

Table 1. 2. Range of genetic divergence in ITS region and COI gene sequences of selected rotifers and other species representing major zooplankton groups. "-" indicates that data were not available.

Species	Genetic divergence in ITS region (%)	Genetic divergence in COI gene (%)	Reference(s)
<i>Brachionus plicatilis</i>	≤1.9 within clades ≥ 2.5 between clades	≤13.3 within clades ≥11.9 between clades	(Gómez et al., 2002b)
<i>B. calyciflorus</i>	4-6	0.0-13	Gilbert & Walsh, 2005; Li et al., 2010
<i>Epiphanes senta</i>	-	10.9-12.5	Schröder & Walsh, 2007
<i>Philodina flaviceps</i>	-	0-3.2 within clades 4.5-18.8 between clades	Fontaneto et al., 2008b
<i>Lecane bulla</i>	0.0-12.5	0.9-16	Walsh et al., 2009
<i>Adineta</i> spp.	-	1-23	Fontaneto et al., 2011
<i>Synchaeta</i> spp.	-	0.2–2.7 within clades 5.9–25.3 between clades	Obertegger et al., 2012
<i>Polyarthra dolichoptera</i>	-	≤4.4 within species ≥5-24 between species	Obertegger et al., 2014
<i>Testudinella clypeata</i>	-	0.16-4.5 within clades 16.7-27.7 between clades	Leasi et al., 2013
<i>Philodina flaviceps</i>	-	0-3.2 within clades 4.5-18.8 between clades	Fontaneto et al., 2008a
<i>Eucypris virens</i>	-	≤14.5	Bode et al., 2010
<i>Eurytemora affinis</i>	-	0.15-17.1	Lee & Frost, 2002
<i>Acartia tonsa</i>	32.2 between clades	13.7 between clades	Chen & Hare, 2008

<i>Chydorus sphaericus</i>	0.7-26 between clades	4.9-25.2 between clades	Belyaeva & Taylor, 2009
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Table 1. 3. Number of haplotypes of the ITS region and COI gene sequences reported for some rotifer species and representative species from other small invertebrates. “-” indicates that data are not available.

Species complex	ITS region number of sequences/number of haplotypes	COI gene number of sequences/number of haplotypes	Reference(s)
<i>Euchlanis dilatata</i>	98/23	81/54	Current study
<i>Brachionus calyciflorus</i>	661/191	888/404	Papakostas et al., 2016
<i>B. calyciflorus</i>	-	96/15	Li et al., 2010
<i>B. plicatilis</i>	55/19	57/39	Gómez et al., 2002b
<i>B. plicatilis</i>	481/45	1223/275	Mills et al., 2016
<i>Philodina flaviceps</i>	-	86/25	Fontaneto et al., 2008c
<i>Synchaeta pectinata</i>	-	174/27-30	Kimpel et al., 2015
<i>Rotaria rotatoria</i>	-	33/13	Xiang et al., 2016
<i>Acartia tonsa</i>	74/6	76/29	Chen & Hare, 2008
<i>Echiniscus testudo</i>	18/7	18/11	Jørgensen et al., 2007
<i>Chydorus sphaericus</i>	-	142/44	Belyaeva & Taylor, 2009

Table 1. 4. Co-occurrence of cryptic species reported in rotifers and other groups.

Group	Species	Reference(s)
Rotifera	<i>Brachionus plicatilis</i> complex	Ortells et al., 2003
	<i>B. plicatilis</i> and <i>B. manjavacas</i>	Gómez et al., 2000, 2007; Montero-Pau et al., 2011
	<i>B. plicatilis</i> , <i>B. ibericus</i> , and <i>B. rotundiformis</i>	Gómez & Serra, 1995; Ciroso-Pérez, Gómez & Serra, 2001
	<i>B. calyciflorus</i> species complex	Wen et al., 2016; Papakostas et al., 2016
	<i>Lecane bulla</i> species complex	Walsh et al., 2009
	<i>Testudinella clypeata</i> species complex	Leasi et al., 2013
	<i>Polyarthra dolichoptera</i> species complex	Obertegger et al., 2014
	<i>Philodina flaviceps</i> species complex	Fontaneto et al., 2008a
	<i>Adineta vaga</i>	Kaya et al., 2009
	<i>Rotaria sordida</i>	Kaya et al., 2009
Nematoda	<i>Rhabditis (Pellioiditis) marina</i> species complex	de Meester et al., 2011
Brown algae	<i>Dictyota dichotoma</i> and <i>D. cymatophila</i>	Tronholm et al., 2010
Amphipoda	<i>Hyalella</i> sp. species complex	Wellborn & Cothran, 2007
Whitefly	<i>Bemisia tabaci</i> species complex	Saleh et al., 2012
Fig Wasp	<i>Pleistodontes imperialis</i> species complex	Haine et al., 2006

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Chapter 2: Detecting cryptic species of *Limnias melicerta*, *L. ceratophylli*, *Collothea campanulata*, and *C. ornata* using molecular and morphological approaches

ABSTRACT

Microorganisms, including rotifers, are thought to be capable of long distance dispersal. Therefore, they should show little or no genetic variation in population structure due to high gene flow. Nevertheless, substantial genetic structure has been reported among populations of many microorganisms. In rotifers, genetic studies have mainly focused on planktonic taxa leaving sessile groups largely unexplored. Here, I used COI gene and ITS region sequences to study genetic structure and delimit cryptic species in four sessile morphospecies (*Limnias melicerta* [29 populations]; *L. ceratophylli* [20 populations]; *Collotheca campanulata* [19 populations]; *C. ornata* [45 populations]). Among populations of *Limnias* spp, ITS region sequences were less variable as compared to those of the COI gene (ITS; *L. melicerta*: 0-2.4% and *L. ceratophylli*: 0-5.7%; COI; *L. melicerta*: 0-22.5% and *L. ceratophylli*: 0-21.5%). Moreover, *L. melicerta* and *L. ceratophylli* were not distinguished in phylogenetic analyses based on ITS sequences. Thus, I used COI sequences for species delimitation. Bayesian Species Delimitation (BSD) detected nine putative cryptic species within *L. melicerta* and four putative cryptic species for *L. ceratophylli*. The mean genetic variation in COI gene was 0-11.4% within cryptic species of *L. melicerta*, and 0.5-0.6% within cryptic species of *L. ceratophylli*. Among cryptic species, the COI mean genetic variation ranged from 8 to 20.5% for *L. melicerta*, and from 15.1 to 21% for *L. ceratophylli*. For *Collotheca* spp., I only included COI gene in the analyses. Based on BSD, I found seven putative cryptic species in *C. campanulata* and eight putative cryptic species for *C. ornata*. Within cryptic species genetic variation in COI gene was 0.0-11.7% for *C. campanulata*, and 0.3-20.0% within *C. ornata*. Among cryptic species, the mean genetic variation was 10.8-25.2% for *C. campanulata*, and 14.6-29.0% for *C. ornata*. The correlation between geographic and genetic distance was weak or lacking; geographic isolation cannot be considered a strong driver of genetic variation. In addition, geometric and morphometric analyses of trophi (jaws) of *Limnias*

spp. did not show significant variation among cryptic species. In this study I used a conservative approach for species delimitation, yet I was able to show that species diversity in these sessile rotifer species is underestimated.

INTRODUCTION

Microorganisms are capable of long distance dispersal thus it has been suggested that they have cosmopolitan distributions with little geographic structure (Finlay, 2002; Fenchel, 2005; Mazaris et al., 2010; Teittinen & Soininen, 2015). However, biogeographical patterns have been documented for many taxa such as soil (Fierer & Jackson, 2006) and marine bacteria (Schauer et al., 2010; Marteinsson et al., 2016; Salerno et al., 2016), protists (Chao et al., 2006; Foissner et al., 2008), fungi (Gumiere et al., 2016), and rotifers (Dumont, 1983; Segers, 1996). One of the reasons that microorganisms are often considered ubiquitous is the failure to identify cryptic species (Artois et al., 2011; Guil, 2011). However, cryptic species complexes commonly occur in these taxa (e.g., Šlapeta et al., 2005; Kon et al., 2007; Lahr et al., 2014; Hahn et al., 2016).

Similar to the other microorganisms, rotifers have passive dispersal through their dormant stages (Wallace et al., 2006; Walsh et al., 2016). Thus, researchers inferred that rotifers have cosmopolitan distributions (e.g., Rousselet, 1909), and thus should show little population genetic structure due to gene flow. However, incorporating molecular tools in the study of rotifer morphospecies has provided ample evidence of cryptic species complexes and substantial genetic structure within and among rotifer populations (e.g., Fontaneto et al., 2009; Walsh et al., 2009; Obertegger et al., 2012; Kimpel et al., 2015; Mills et al., 2017). Although by definition cryptic species are not readily distinguished by morphology, subtle morphological variations have been detected among some rotifer cryptic species. For instance, size and shape of lorica varies among cryptic species of *Brachionus plicatilis* Müller, 1786 (e.g., Fu et al., 1991; Ciroso-Pérez et al., 2001; Campillo et al., 2005; Anitha & George, 2006; Hwang et al., 2013; Michaloudi et al., 2016), trophi and resting egg morphology differ in the *Epiphanes senta*

(Müller, 1773) species complex (Schröder & Walsh, 2007), and trophi size varies among populations of *Rotaria magnacalcarata* (Parsons, 1892) (Fontaneto et al., 2007b).

Almost all studies on genetic structure and cryptic species of the subclass Monogononta focused on planktonic taxa, with little attention having been paid to sessile species. Sessile rotifers of orders Collotheceae and Flosculariaceae are common in a wide assortment of aquatic habitats and attach to varied substrata (Wallace & Snell, 2010). Study of these forms is challenging as their plant substrata must be inspected to find them and several diagnostic characteristics need to be examined in live individuals (Wallace et al., 2006). Thus, they are often overlooked, which has led to gaps in my knowledge about their taxonomic diversity. Molecular tools have been applied in few phylogenetic studies that have included sessile rotifers (e.g., Sørensen & Giribet, 2006; Meksuwan et al., 2015), but these have not focused on examination of population level genetic patterns or detection of cryptic species.

One poorly studied sessile taxon is the genus *Limnias* (Flosculariidae), in which six morphospecies are currently recognized (Wallace et al., 2018): *Limnias ceratophylli* Schrank, 1803; *L. cornuella* Rousselet, 1889; *L. melicerta* Weisse, 1848, *L. myriophylli* (Tatum, 1868), *L. nymphaea* Stenroos, 1898, and *L. shiawasseensis* Kellicott, 1888. Other designations are considered to be synonyms, or species inquirenda (Segers, 2007; Segers et al., 2012). *Limnias* species are distinguished based on several characters. These include tube length and structure, colony formation, length of the ventral antennae, size of the coronal dorsal gap, and number of hardened nodules on the dorsal side of neck (Wright, 1954; Koste, 1978; Wallace et al., 2018). *Limnias melicerta* and *L. ceratophylli* are considered cosmopolitan and are each reported from seven biogeographical regions (Segers, 2007). The other four species have restricted distributions. *Limnias cornuella* has only been reported from the Palearctic (Rousselet, 1889), *L.*

myriophylli is reported from the Afrotropical and Palearctic (Segers, 2007), *L. nymphaea* from the Palearctic, and *L. shiawasseensis* from Nearctic biogeographical regions (Segers, 2007). The few available studies on this genus include the following: taxonomy (Tatem, 1868; Cubitt, 1871; Rousselet, 1889; Wright, 1954; Wallace et al., 2018), trophi descriptions (Gosse, 1856; Meksuwan et al., 2015), tube formation (Wright, 1954), tube ultrastructure of *L. melicerta* (Yang & Hochberg, 2018), post-natal development (Kutikova, 1995), phylogeny of Flosculariaceae (Meksuwan et al., 2015), ecological studies (i.e., water quality and abundance: *L. melicerta*; Bankit S, 1995; Arora & Mehra, 2003), population growth (*L. melicerta* and *L. ceratophylli*; Sarma et al., 2017), and toxicology (Upreti et al., 2012). To my knowledge, there are no published studies on genetic variation and population structure within or among species of this genus.

Taxonomic status of *Limnias* should be re-evaluated for three important reasons. (1) Koste (1978) grouped *Limnias ceratophylli*, *L. cornuella*, *L. melicerta*, *L. nymphaea* and *L. shiawasseensis* within either of the two species groups, however the original classification of Hlava (1908) has been restored by Wallace et al. (2018) resurrecting the six species noted above as valid. (2) There has been no examination of the intraspecies variation in diagnostic characters. (3) Sarma et al. (2017) suggested to uses *Limnias melicerta* and *L. ceratophylli* in toxicology bioassays. Those studies and other biological investigations can benefit from an accurate estimate of species diversity within *Limnias* genus.

Genus *Collotheca* (Flosculariidae) is another unexplored group of sessile rotifers. This genus includes 48 morphospecies (Segers, 2007; Meksuwan et al., 2013). Many *Collotheca* species have restricted distributions. Only 11 morphospecies are reported from at least four biogeographic regions (Segers, 2007). *Collotheca campanulata* (Dobie, 1849) and *C. ornata*

(Ehrenberg, 1830) are among these widely distributed morphospecies. Each of these two cosmopolitan morphospecies have multiple synonyms (two for *C. campanulata*; five for *C. ornata*: Segers (2007)). Examples of studies on *Collotheca* are shown in Table 2.1. To my knowledge, there are no published studies on genetic variation within and among species of these genera.

Table 2. 1. Representative studies on species of the genus *Collotheca*.

Study type	Reference(s)
Taxonomy	Edmondson (1948); Meksuwan et al. (2013)
Morphology of the corona	Edmondson (1959)
Mechanisms of food capture in several species including <i>C. campanulata</i> and <i>C. ornata</i>	Wright (1952)
Substrate choice in several species including <i>C. gracilipes</i> and <i>C. ornata</i>	Wallace & Edmondson (1986)
Larval development of <i>C. ornata</i>	Kutikova (1995)
Macrophyte choice for an unidentified <i>Collotheca</i> species	Duggan et al. (2001)
Ecology of an unidentified <i>Collotheca</i> species and <i>C. ornata</i>	Baião & Boavida (2000); Sendacz et al. (2006)

Here, I studied genetic structure and identified cryptic species in *Limnias melicerta*, *L. ceratophylli*, *C. campanulata* and *C. ornata* collected from habitats across the USA using partial COI gene and the ITS region sequences. I also used partial 18S rRNA sequences to study the monophyly of *L. melicerta* and *L. ceratophylli*. I selected *L. melicerta*, *L. ceratophylli*, *C. campanulata* and *C. ornata* for investigation of potential cryptic species because they each have several synonyms indicating that their taxonomic statuses may need to be re-evaluated. Moreover, they are reported to have cosmopolitan distributions, and as mentioned above, molecular tools have shown that many rotifer species with broad geographic ranges are in fact

species complexes. Therefore, I predict that cryptic species will be present within each of these morphospecies. In addition, I examined morphological variation in trophi among putative cryptic species within *L. melicerta* and *L. ceratophylli*.

METHODS

Sample collection and culture

Aquatic plant samples were collected from habitats across the USA (Supplemental Tables S2.1 - S2.4). *Limnias melicerta*, *L. ceratophylli*, *C. campanulata* and *C. ornata* were isolated by removing a piece of vegetation to which they were attached and isolating them. Clonal lineages initiated from single females were cultured in modified MBL media (Stemberger, 1981) and fed a mixture of the algae *Chlorella vulgaris* Berijerinck, 1890 (The UTEX Culture Collection of Algae at the University of Texas at Austin [UTEX] strain 30) and *Chlamydomonas reinhardtii* Dangeard, 1888 (UTEX strain 90). *L. melicerta* and *L. ceratophylli* are sessile rotifers producing tubes of hardened secretions (Wallace et al., 2006), thus I added powdered carmine (Alfa Aesar, UK) to lab cultures to provide a matrix to aid tube construction.

Voucher specimens were deposited in the UTEP Biodiversity Collections at the University of Texas at El Paso (*L. melicerta*: UTEP:Zoo: 43, 105-134, *L. ceratophylli*: UTEP:Zoo:32-42, UTEP:Zoo:52-61). Deposited specimens included approximately 10 individuals from each population preserved in 95% ethanol and 10 individuals preserved in 4% buffered formalin.

DNA extraction and gene amplification

For *Limnias* spp., DNA was extracted from one individual by adding 13 µl Chelex[®]-100 (Bio-Rad Laboratories, CA, USA) and incubating at 100°C for 10 min. DNA templates were

stored at -80°C until used for amplification. For *Collotheca* spp., DNA was extracted from approximately 3-10 clonal female individuals from each population using 9.5 µl lysis buffer (5 µl of proteinase K solution (20 mg/ml) and 95 µl of 1X PCR buffer (10X PCR Buffer, Invitrogen; 50mM MgCl₂)), followed by incubation at 55°C for 90 min and at 95°C for 15 min respectively.

An approximate 630 bp portion of the cytochrome c oxidase subunit I (COI) gene was amplified using the primers LCO1490: 5' -GGTCAACAAATCATAAAGATATTGG-3' and HCO2198: 5'-TAAACTTCAGGGTGACCAAAAAATCA-3' (Folmer et al., 1994). The entire nuclear internal transcribed spacer region (ITS) was amplified using the primers ITS4: 5'-TCCTCCGCTTATTGATATGC-3' and ITS5: 5'-GGAAGTAAAAGTCGTAACAAGG-3' (White et al., 1990). For *Limnias* spp. I also amplified 865 bp of the 18S rRNA gene using primers 3F: 5'-GTTCGATTCCGGAGAGGG-3' as modified by Giribet et al. (Giribet et al., 1996) and primer 18Sbi: 5'-CTAGAGTCTCGTTTCGTTATCGG-3' as modified by Whiting et al. (Whiting et al., 1997).

PCR reactions contained 10 µl of genomic DNA, 1 µl of each primer (500 ng/ µl), 22 µl HPLC grade sterile water, 1 µl GoTaq® G2 DNA Polymerase (Promega), 10 µl 5X PCR buffer B (10 mM MgCl₂, pH 8.5) or 5X PCR buffer A (7.5 mM MgCl₂, pH 8.5), followed by adding 5 µl dNTP mix (2.5 mM each of dATP, dCTP, dGTP, dTTP) at 80°C. PCR cycles were run on a thermocycler (TECHNE TC-412) and consisted of an initial denaturation at 94°C for 1 min, followed by denaturation at 94°C for 1 min, annealing at 48°C for 2 min and extension at 72°C for 3 min for 35 cycles, and a final extension step at 72°C for 7 min. To verify the size of amplification products I used electrophoresis, and I purified them using GENECLAN® kits (MP Biomedicals, LLC) before sequencing. Sequencing was done at UTEP's BBRC Genomic

Analysis Core Facility on an Applied Biosystems 3130xl Genetic Analyzer using BigDye Terminator v3.1 Cycle Sequencing Kits (Applied Biosystems). GenBank accession numbers for all *Limnias* spp. sequences obtained are given in Tables S2.1 (*L. melicerta*) and S2.2 (*L. ceratophylli*). Additional 18S rRNA sequences were included from GenBank (accession numbers, *L. melicerta*: KM873599.1, *L. ceratophylli*: KM873598). The COI gene sequences of *L. melicerta* (KT870155.1 and KT870154.1) and *L. ceratophylli* (KT870157) from GenBank are not included in my analyses for three reasons. 1) The COI sequence of *L. melicerta* (KT870155) is 330 bp which was much shorter than COI sequences I obtained (623 bp). 2) *L. melicerta* (KT870154) did not comprise a new distinct clade, instead it was grouped with cryptic species J (Figure S2.2). Therefore, it did not add to the species diversity found in this study. 3) The COI sequence of *L. ceratophylli* (KT870157) was classified with cryptic species M of *L. melicerta* (Figure S2.1). *Floscularia conifera* (Hudson, 1886) and *Ptygura brachiata* (Hudson, 1886) were included as outgroups in the phylogenetic analyses for COI gene and ITS region of *L. melicerta* and *L. ceratophylli*. For analysis of 18S rRNA sequences, I used *Collothea campanulata* as the outgroup (Table S2.1). I used COI gene sequences for the phylogenetic analyses of *C. campanulata* and *C. ornata* with *C. ferox* and *C. tenuilobata* as outgroups (Tables S2.3, 2.4).

Genetic diversity

FinchTV v 1.4.0 (Geospiza.com, 2014) was used to check sequences manually, especially for potential double peaks in the ITS region sequences of *L. melicerta* and *L. ceratophylli*. The ITS region alignment was uploaded to the SeqPhase online tool (<http://seqphase.mpg.de/seqphase/>) to phase the sequences as described by Flot (2010). Contigs for all sequences were made using CAP 3 (Huang & Madan, 1999) and were aligned using MAFFT v 7 (Kato & Standley, 2013). Mesquite v 3.2 (Maddison, 2017) was used to manually

check the alignments as well as to translate COI gene sequences to proteins. To measure substitution saturation I used DAMBE v 6 (Xia, 2017). Number of polymorphic sites, number of parsimony informative sites, number of haplotypes, haplotype diversity (h), and nucleotide diversity (π) were calculated using DnaSp v 5.10.01 (Librado & Rozas, 2009), and uncorrected pairwise sequences distances ("p") were calculated in Mega v 7.0 (Kumar et al., 2015). A haplotype network was constructed using the median joining method in Network v 5.0.0.1 (Bandelt et al., 1999).

Species delimitation

Models for sequence evolution for *Limnias* spp. were TPM2uF+I+G for the COI gene, TPM1uF+I for the ITS region, and JC for the 18S rRNA gene as determined using Jmodeltest2 (Guindon & Gascuel, 2003; Darriba et al., 2012) available at the CIPRES Science Gateway 3.3 (Miller et al., 2010). For *Collotheca* spp., the model for sequence evolution of the COI gene was TPM2uF+I+G. To construct the phylogenetic trees, Bayesian analysis was run for 10^7 generations with two parallel runs and a 25% burn in period using MrBayes v 3.2.6 on XSEDE high-throughput computing resources available at CIPRES Science Gateway (Miller et al., 2010). For the phylogenetic analyses implemented in BEAST and *BEAST (Drummond et al., 2012), I used the GTR+I+G model of sequence evolution for the COI gene and the GTR+I model for the ITS region. TPM2uF and TPM1uF models are not available in BEAST. However, both of these models are classified under the GTR model. Thus GTR was used in both instances.

To determine the number of evolutionary entities (putative cryptic species), I used Generalized Mixed Yule Coalescent (GMYC, Pons et al. (2006)), Poisson Tree Process (PTP, Zhang et al. (2013)), Automatic Barcoding Gap Discovery (ABGD, Puillandre et al. (2012)), *BEAST v 1.8.3 (Drummond et al., 2012) (only for *Limnias* spp.), K/ θ (Birky et al., 2010) (only

for *Collotheca* spp.) and Bayesian Species Delimitation (BSD) implemented in Bayesian Phylogenetics and Phylogeography software (BPP v 3.1, Rannala & Yang (2003); Yang & Rannala (2010, 2014)). I did not use *BEAST for *Collotheca* because this method did not yield consistent and reliable species delimitation results based on COI gene for *Limnias* (oversplitting for *L. melicerta* and underestimating diversity for *L. ceratophylli*, see Table 2.4). For *Limnias*, the genetic variation within some clades (θ) was 0, so I was not able to use K/ θ method for species delimitation.

I used BEAST v 1.8.3 (Drummond et al., 2012) to construct ultrametric trees, and *BEAST v 1.8.3 (Drummond et al., 2012) for species delimitation. Both analyses were run for the COI gene and ITS region sequences separately for 10^7 generations, with sampling every 1,000 generations. Tracer v 1.6.0 (Rambaut et al., 2013) was used to check the effective sample size (ESS>200), and to verify convergence. Consensus trees were obtained using TreeAnnotator v 1.8.3 with a 25% burn. The ultrametric trees were used for species delimitation in single threshold and multiple threshold GMYC (Fujisawa & Barraclough, 2013), Bayesian GMYC (bGMYC) (Reid & Carstens, 2012), and PTP methods. bGMYC was run using the R package *bGMYC* v 1.0.2 for 100,000 iterations with sampling every 1,000 iterations. PTP was run by uploading the ultrametric trees to the online tool available at <http://species.h-its.org/ptp/> and using default settings. ABGD delimitation was done by uploading the sequence alignment to the online tool available at www.wabi.snv.jussieu.fr/public/abgd/ and using default settings.

*BEAST v 1.8.3 (Drummond et al., 2012) was run under several assumptions regarding the number of species for both the COI gene and ITS region sequences. Only those putative species with posterior probabilities higher than 0.95 were considered as validated species in *BEAST. To run BSD, the phylogenetic tree based on Bayesian inference was used as the

guide tree, and I used the joint species delimitation and tree estimation method (unguided species delimitation) that does not rely on topology of the guide tree.

Isolation by distance

Geographic distance matrices were constructed using Geographic Distance Matrix Generator v 1.2.3 (Ersts PJ, 2006). To test the correlation between genetic variation and geographic distances (log transformed; km) among populations, mantel tests with 10,000 permutations were run using the R package *ecodist* v 1.2.9 (Goslee & Urban, 2007).

Trophi morphology

I was not able to extract trophi and obtain SEM images for *Collothea campanulata* and *C. ornata* due to the difficulty in working with the small size of their trophi. Trophi of *Limnias melicerta* and *L. ceratophylli* were prepared for scanning electron microscopy (SEM) by dissolving rotifer tissue in ~5% sodium hypochlorite, rinsing with deionized water 10-15 times, and air-drying on circular cover slips at room temperature (Segers, 1993). Trophi were coated with gold/palladium using a Gatan 682 PECS sputter coat. SEM images were obtained at 20 kV using a Hitachi S-4800 scanning electron microscope.

I used a geometric morphometric approach to study variation in the shape and size of trophi among putative cryptic species. This method uses Cartesian coordinates for a set of anatomical landmarks (Adams et al., 2004). SEM images were obtained from caudal and frontal views of the trophi. Using TPS series software (Rohlf, 2015), nine landmarks on the caudal view and 10 landmarks on the frontal view of the trophi were digitized (Figure 2.1). Configuration of landmarks were analyzed using Generalized Procrustes Analysis (Adams et al., 2004). Trophi size was calculated as Centroid Size (CS) which is the square root of the sum of squared

distances between landmarks and their centroid (Cavalcanti et al., 1999). Variation in the shape of trophi among putative cryptic species was examined using Discriminant Analysis in SPSS v 24 (IBM Corp, 2016). Because trophi centroid size was not normally distributed, variation in the size of trophi among putative cryptic species was tested using a non-parametric Kruskal-Wallis test, and between the two morphospecies using a non-parametric Man-Whitney U test implemented in SPSS v 24 (IBM Corp, 2016).

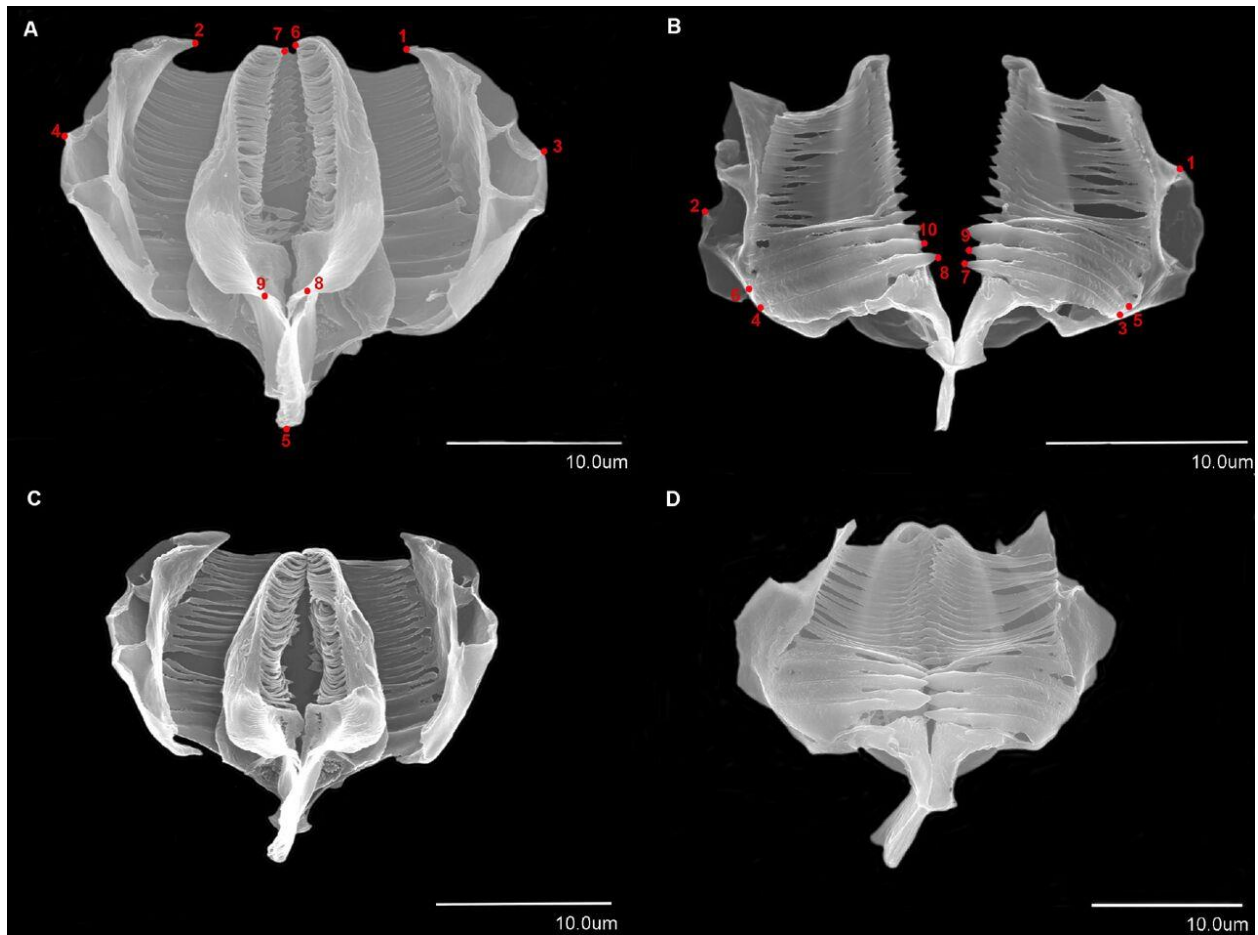


Figure 2.1. Shape of *Limnias* spp. trophi and landmarks used in the geometric morphometric analysis. A: frontal view of *Limnias ceratophylli* trophi, 1, 2: apical point of manubrium; 3, 4: midpoint of manubrium; 5: apical point of fulcrum; 6, 7: apical point of ramus; 8, 9: basal point of ramus. B: caudal view of *L. ceratophylli* trophi, 1, 2: midpoint of manubrium; 3, 4: base of first large teeth of ramus; 5, 6: base of second large teeth of ramus; 7-8: tip of first large teeth of ramus; 9, 10: tip of second large teeth of ramus. C: frontal view of *Limnias melicerta* trophi. D: caudal view of *L. melicerta* trophi.

RESULTS

Genetic diversity

Limnias melicerta and *L. ceratophylli*

For the COI gene, I obtained 69 sequences from 29 populations for *Limnias melicerta* and 24 sequences from 20 populations for *L. ceratophylli*. For the ITS region, 72 individuals

from 33 populations of *L. melicerta* and 33 individuals from 19 populations of *L. ceratophylli* were sequenced. For 18S rRNA, one sequence from a representative of 17 populations of *L. melicerta* and 18 populations of *L. ceratophylli* were acquired. Alignment length was 623 bp for the partial COI gene sequences, 763 bp for the ITS region including insertions, and 865 bp for partial 18S rRNA gene sequences. COI gene, ITS region, and 18S rRNA sequences were not saturated (index of substitution saturation < critical index of substitution saturation, $p < 0.001$). For the COI gene, haplotype diversity was 0.85 for *L. melicerta* and 0.94 for *L. ceratophylli*; nucleotide diversity was 0.13 for *L. melicerta* and 0.12 for *L. ceratophylli*. The overall genetic distance in the COI gene among populations was 0-22.5% for *L. melicerta* and 0-21.5% for *L. ceratophylli*, and the genetic distance between *L. melicerta* and *L. ceratophylli* ranged from 19.1 to 25.0%. For the ITS region, haplotype diversity was 0.64 for *L. melicerta* and 0.56 for *L. ceratophylli*, nucleotide diversity was 0.008 for *L. melicerta* and 0.015 for *L. ceratophylli*. The overall genetic distance in the ITS region among populations was 0-2.4% for *L. melicerta* and 0-5.7% for *L. ceratophylli*, and the genetic distance between *L. melicerta* and *L. ceratophylli* was 1.2-6.0%. I also found seven heterozygous individuals for the ITS region in *L. melicerta* and two in *L. ceratophylli*. Based on 18S rRNA sequences, haplotype diversity, nucleotide diversity, and genetic diversity were 0 for both *L. melicerta* and *L. ceratophylli*. The genetic distance between *L. melicerta* and *L. ceratophylli* was 0.5%. Genetic diversity measures for all markers are summarized in Table 2.2.

Table 2. 2. Inter- and intra-population genetic variation (uncorrected “p” distance), haplotype and nucleotide diversity, number of haplotypes, number of polymorphic sites for partial COI gene, ITS region, and partial 18S rRNA sequences, and the number of heterozygotes detected by phasing ITS region in *Limnias melicerta* and *L. ceratophylli*. NA = Not applicable. ND= No data.

	<i>Limnias melicerta</i>			<i>Limnias ceratophylli</i>		
	COI gene	ITS region	18S rRNA	COI gene	ITS region	18S rRNA
Inter-population genetic variation (%)	0.3-22.5	0-2.4	0	0-21.5	0-5.7	0
Intra-population genetic variation (%)	0-0.8	0	ND	0-1.9	0	ND
Number of haplotypes/ number of sequences	29/69	10/72	1/18	14/24	4/33	1/19
Haplotype diversity	0.85	0.64	0	0.94	0.56	0
Nucleotide diversity	0.13	0.008	0	0.12	0.015	0
Polymorphic sites/ number of base pairs	249/623	33/763	0/865	217/623	54/763	0/865
Heterozygous individuals (#)	NA	7	NA	NA	2	NA

Collothea campanulata* and *C. ornata

For the COI gene, I obtained 24 sequences from 21 populations for *Collothea campanulata* and 51 sequences from 45 populations for *C. ornata*. The COI gene sequences were not saturated (index of substitution saturation < critical index of substitution saturation, $p < 0.001$). The haplotype diversity was 0.94 for *C. campanulata* and 0.99 for *C. ornata*, nucleotide diversity was 0.16 for *C. campanulata* and 0.21 for *C. ornata*, the overall genetic variation was 0-30.5% for *C. campanulata* and 0-25.2% for *C. ornata*. I did not include the analyses based on ITS region for *Collothea* spp. because of issues with sequence quality and alignment. Genetic diversity measures for the COI gene are summarized in the Table 2.3.

Table 2. 3. Inter- and intra-population genetic variation (uncorrected “p” distance), haplotype and nucleotide diversity, number of haplotypes, number of polymorphic sites based on the COI gene in selected populations of *Collothea campanulata* and *C. ornata*.

	<i>Collothea campanulata</i>	<i>Collothea ornata</i>
Inter population genetic variation (%)	0-30.5	0-25.2
Number of haplotypes/ number of sequences	15/24	41/51
Haplotype diversity	0.94	0.99
Nucleotide diversity	0.16	0.21
Polymorphic sites/ number of base pairs	257/622	301/622

Species delimitation

Limnias melicerta and *L. ceratophylli*

In the two phylogenetic trees, one based on COI gene and the other based on 18S rRNA sequences, both *Limnias melicerta* and *L. ceratophylli* were monophyletic (Figures 2.2, 2.3). However, based on ITS region sequences they were paraphyletic (Figure 2.4). In the phylogenetic tree based on 18S rRNA sequences, there were only two clades with each morphospecies representing a highly supported, monophyletic clade. In addition, the separation of two morphospecies was supported by an example in my study in which *Limnias melicerta* and *L. ceratophylli* co-occurred in one lake (Moon Lake, WI), and yet, they were distinct based on COI gene and 18S rRNA. The number of detected putative cryptic species within *L. melicerta* ranged from 9-43 based on the COI gene and 2-44 based on the ITS region sequences. For *L. ceratophylli*, 2-12 putative cryptic species were detected based on COI gene, and 3-20 based on ITS region sequences (Figures 2.2, 2.4; Table 2.4). The most conservative results were nine

putative cryptic species for *L. melicerta* (BSD based on COI gene), and two putative cryptic species for *L. ceratophylli* (*BEAST based on COI gene). However, *BEAST classified a distinct clade that was represented by a population from New Mexico as part of cryptic species B, and another distinct clade represented by a population from Florida as part of species D. Those two clades were considered separate putative cryptic species by BSD (Figure 2.2). As *BEAST may have underestimated diversity within *L. ceratophylli*, I delimited cryptic species based on BSD analysis of the COI gene which was the second most conservative method for this species (Table 2.4).

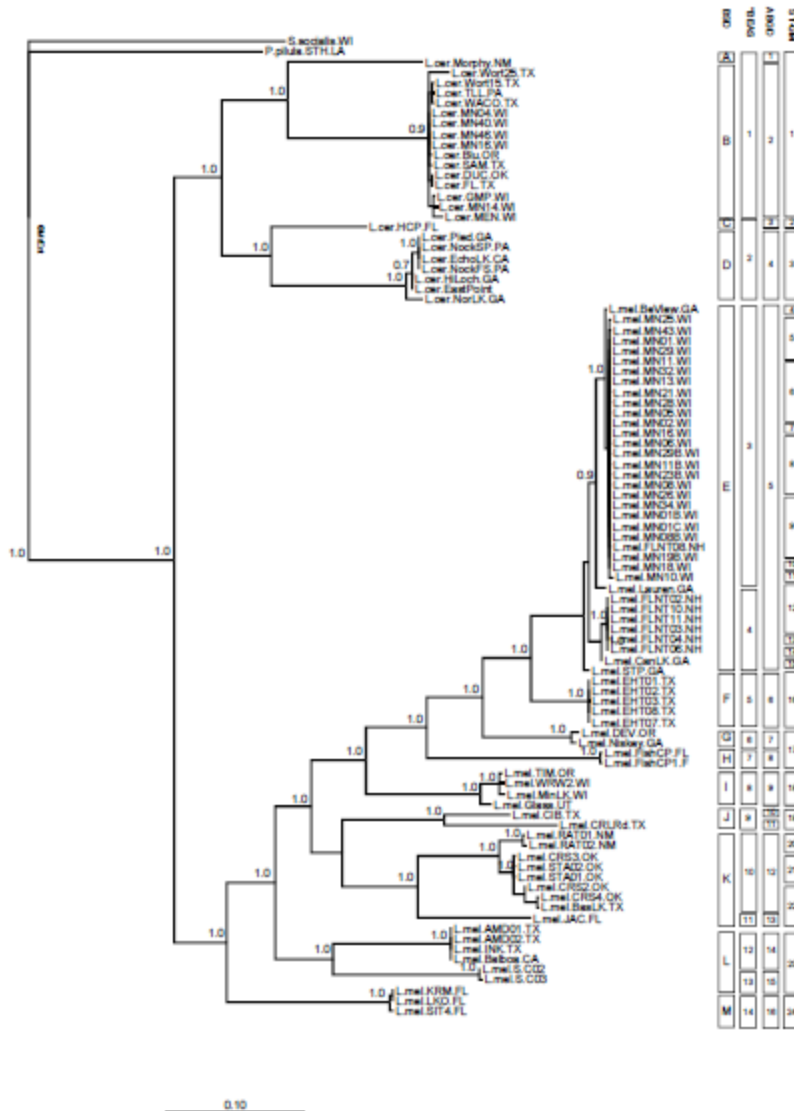


Figure 2.2. The Bayesian inference consensus phylogenetic tree based on partial COI gene sequences of 29 populations of the morphological species *Limnias melicerta* and 20 populations of *L. ceratophylli*. Average branch lengths are proportional to the number of substitutions per site under a TPM2uF+I+G substitution model. At each node posterior probabilities >0.50 are shown. Putative cryptic species detected using Bayesian Species Delimitation (BSD), Automatic Barcoding Gap Discovery (ABGD), *BEAST, and Single Threshold Generalized Mixed Yule Coalescent models (GMYC) are shown. Abbreviations as in Tables S2.1 and S2.2; independent clonal isolates are indicated by a number (e.g., 01).

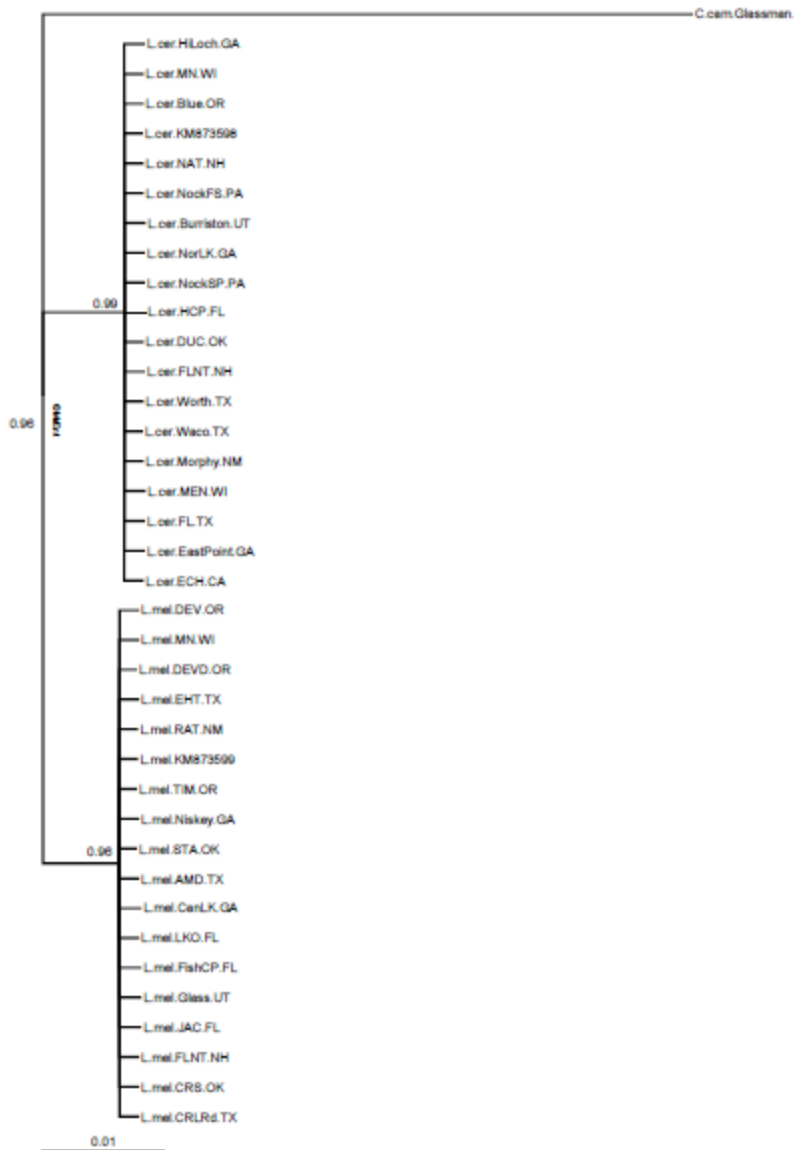


Figure 2.3. The Bayesian inference consensus phylogenetic tree based on partial 18S rRNA sequences of 17 populations of *Limnias melicerta* and 18 populations of *L. ceratophylli*. Average branch lengths are proportional to the number of substitutions per site under a JC substitution model. At each node, posterior probabilities > 0.50 are shown (Abbreviations as in Tables S2.1 and S2.2).

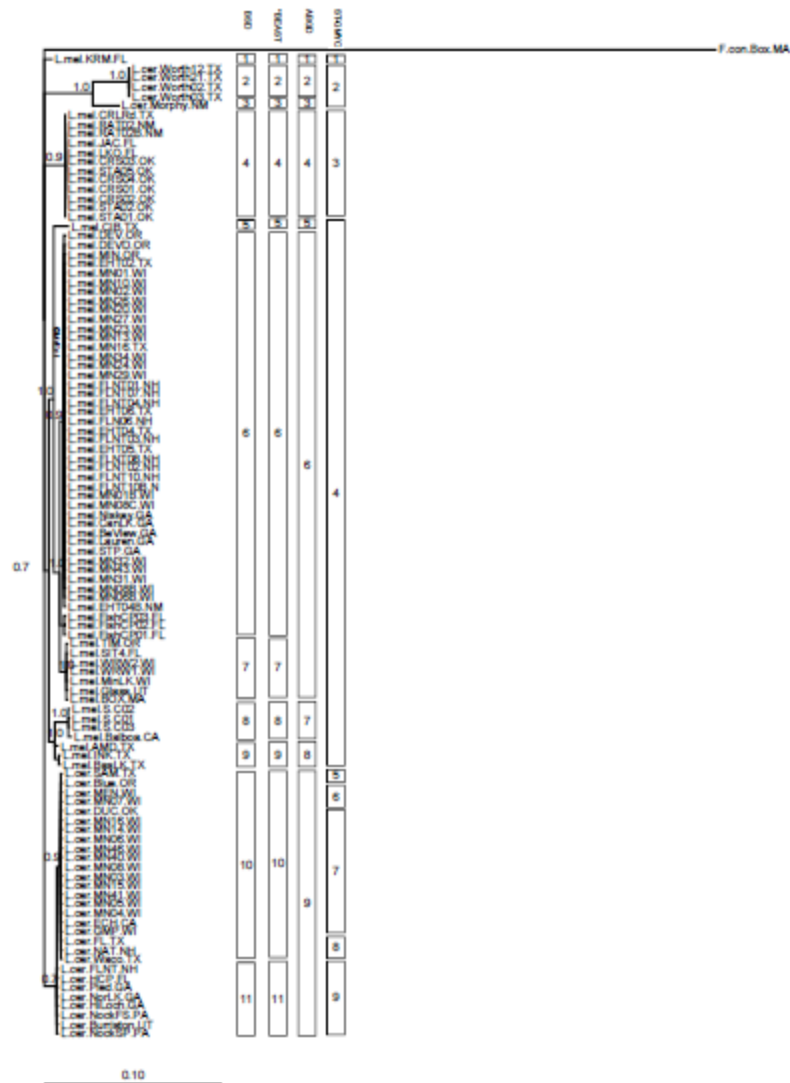


Figure 2.4. The Bayesian inference consensus phylogenetic tree based on ITS region sequences of 33 populations of *Limnias melicerta* and 19 populations of *L. ceratophylli*. Average branch lengths are proportional to the number of substitutions per site under a TPM1uF+I substitution model. Posterior probabilities >0.50 are shown at nodes. Putative cryptic species detected using Bayesian Species Delimitation (BSD), Automatic Barcoding Gap Discovery (ABGD), *BEAST, and Single Threshold Generalized Mixed Yule Coalescent models (ST-GMYC) are shown. Abbreviations as in Tables S2.1 and S2.2; independent clonal isolates are indicated by a number (e.g., 01).

Table 2. 4. Number of putative cryptic species delimited by seven methods based on partial COI gene and ITS region sequences for *Limnias melicerta* and *L. ceratophylli*. The range of likely number of putative cryptic species detected by PTP or 95% confidence intervals for single and multiple threshold GMYC are shown in parentheses.

Delimitation method	<i>Limnias melicerta</i>		<i>Limnias ceratophylli</i>	
	COI gene	ITS region	COI gene	ITS region
Single threshold GMYC	21 (2-21)	2 (1-30)	3 (1-23)	6 (1-10)
Multi threshold GMYC	43 (14-43)	44 (12-44)	10 (1-11)	8 (5-21)
bGMYC	14	7	5	3
PTP	38 (19-53)	40 (25-54)	12 (4-20)	20 (7-30)
*BEAST	12	5	2	4
BSD	9	7	4	4
ABGD	12	6	4	3

The mean genetic distance in COI gene sequences was 0-11.4% within cryptic species of *L. melicerta*, and 0.5-0.6% within cryptic species of *L. ceratophylli* (BSD of COI gene: *L. melicerta*: nine putative cryptic species, *L. ceratophylli*: four putative cryptic species). Among BSD cryptic species, the COI mean genetic distance was 8-20.5% for *L. melicerta*, and 15.1-21% for *L. ceratophylli*. For ITS region sequences, within cryptic species mean genetic distance ranged 0-1.5% for *L. melicerta* and 0.04 to 1.5% for *L. ceratophylli*. Among putative cryptic species, the ITS mean genetic distance was 0-2% for *L. melicerta*, and 0-5.3% for *L. ceratophylli*. In the haplotype networks based on COI gene sequences for both species, genotype clusters corresponded to the BSD cryptic species (Figure 2.5A: *L. melicerta*, Figure 2.5B: *L. ceratophylli*).

There was discordance between phylogenetic trees based on COI gene and ITS region sequences. For example, multiple cryptic species based on COI gene (“E”, F”, “G”, and “H”) are clustered as one lineage based on ITS region (lineage “6”). In another example, one lineage (lineage “4”) based on the ITS region is comprised of populations from multiple COI cryptic species (“J”, “K”, and “M”) (Figures 2.2, 2.4).

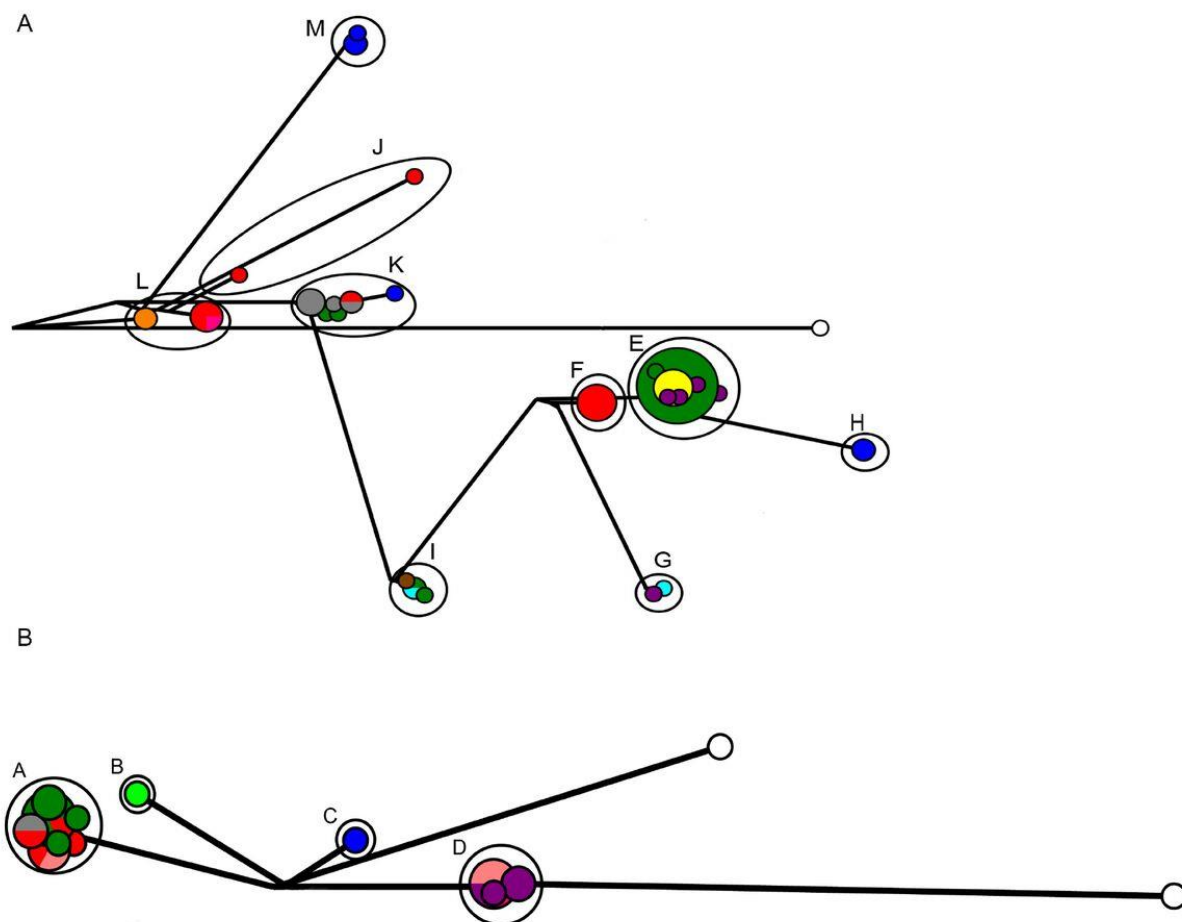


Figure 2.5. Haplotype network analysis of partial COI gene sequences of A) *Limnias melicerta* and B) *L. ceratophylli* populations as determined by the median joining method (Bandelt et al., 1999). Size of circles is proportional to the number of sequences sharing the same haplotype. Branch lengths are proportional to the number of nucleotide substitutions. Open circles and ovals on the network correspond to cryptic species detected by Bayesian Species Delimitation. Color codes are based on the collection region; Texas: red, New Mexico: light green, Georgia: purple, Oregon: light blue, Utah: Brown, Oklahoma: gray, California: pink, Florida: dark blue, Wisconsin: Dark green, New Hampshire: yellow, Carolina: Orange, Pennsylvania: salmon, outgroups: white.

Collothea campanulata and *C. ornata*

The number of detected putative cryptic species within *C. campanulata* ranged from 4-12 and for *C. ornata*, from 8 to 29 based on COI gene sequences (Figures 2.6, 2.7; Table 2.5). I

based my delimitation based on BSD results because it was the most conservative approach for *C. ornata* and the second most conservative approach for *C. campanulata*.

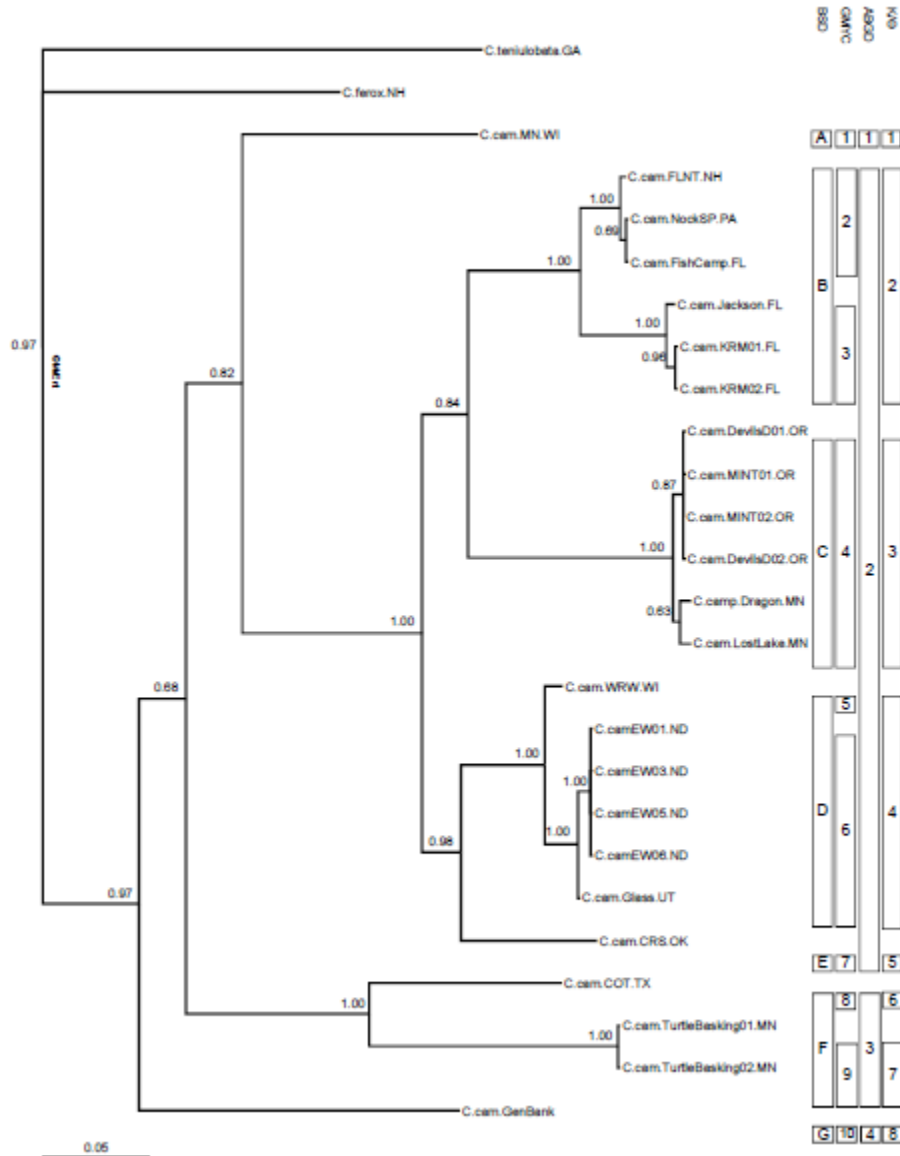


Figure 2.6. The Bayesian consensus inference phylogenetic tree based on COI gene sequences of 19 populations of the morphological species *Collothea campanulata*. Average branch lengths are proportional to the number of substitutions per site under a TPM2uF+I+G substitution model. At each node posterior probabilities >0.50 are shown. Putative cryptic species were detected using Bayesian Species Delimitation (BSD), Single Threshold Generalized Mixed Yule Coalescent models (GMYC), Automatic Barcoding Gap Discovery (ABGD) and K/Θ are shown. Abbreviations as in Tables S2.3; independent clonal isolates are indicated by a number (e.g., 01).

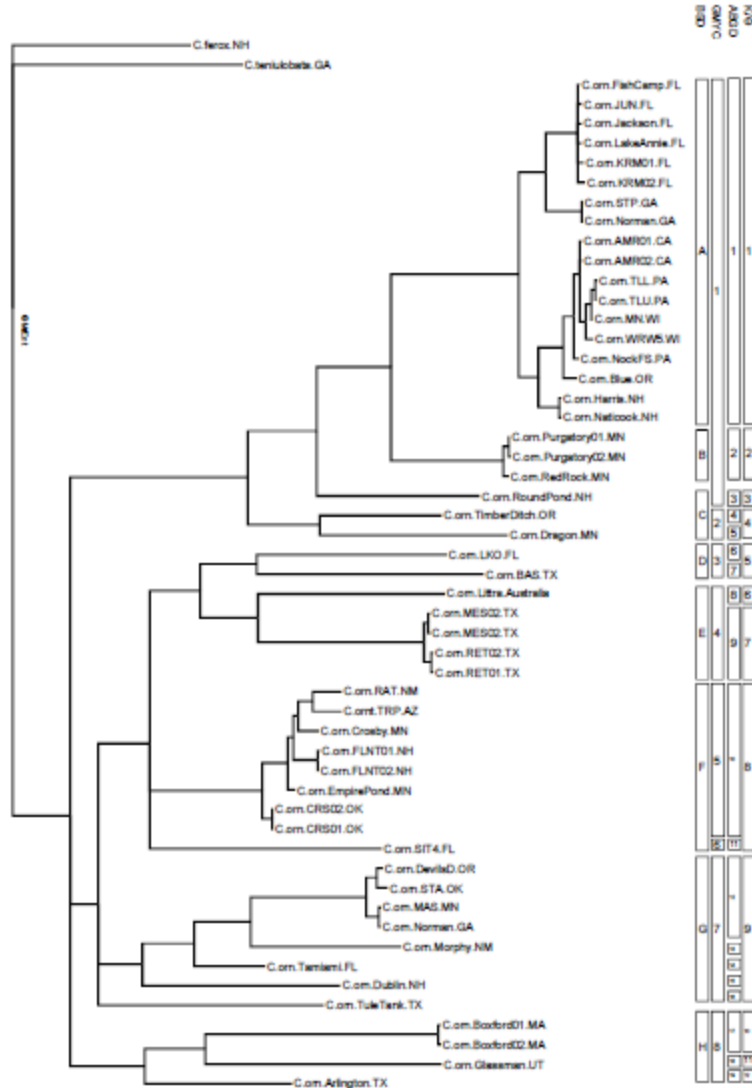


Figure 2.7. The Bayesian consensus inference phylogenetic tree based on COI gene sequences of 45 populations of the morphological species *Collotheca ornata*. Average branch lengths are proportional to the number of substitutions per site under a TPM2uF+I+G substitution model. At each node posterior probabilities >0.50 are shown. Putative cryptic species detected using Bayesian Species Delimitation (BSD), Single Threshold Generalized Mixed Yule Coalescent models (GMYC), Automatic Barcoding Gap Discovery (ABGD) and K/Θ are shown. Abbreviations as in Tables S2.4; independent clonal isolates are indicated by a number (e.g., 01).

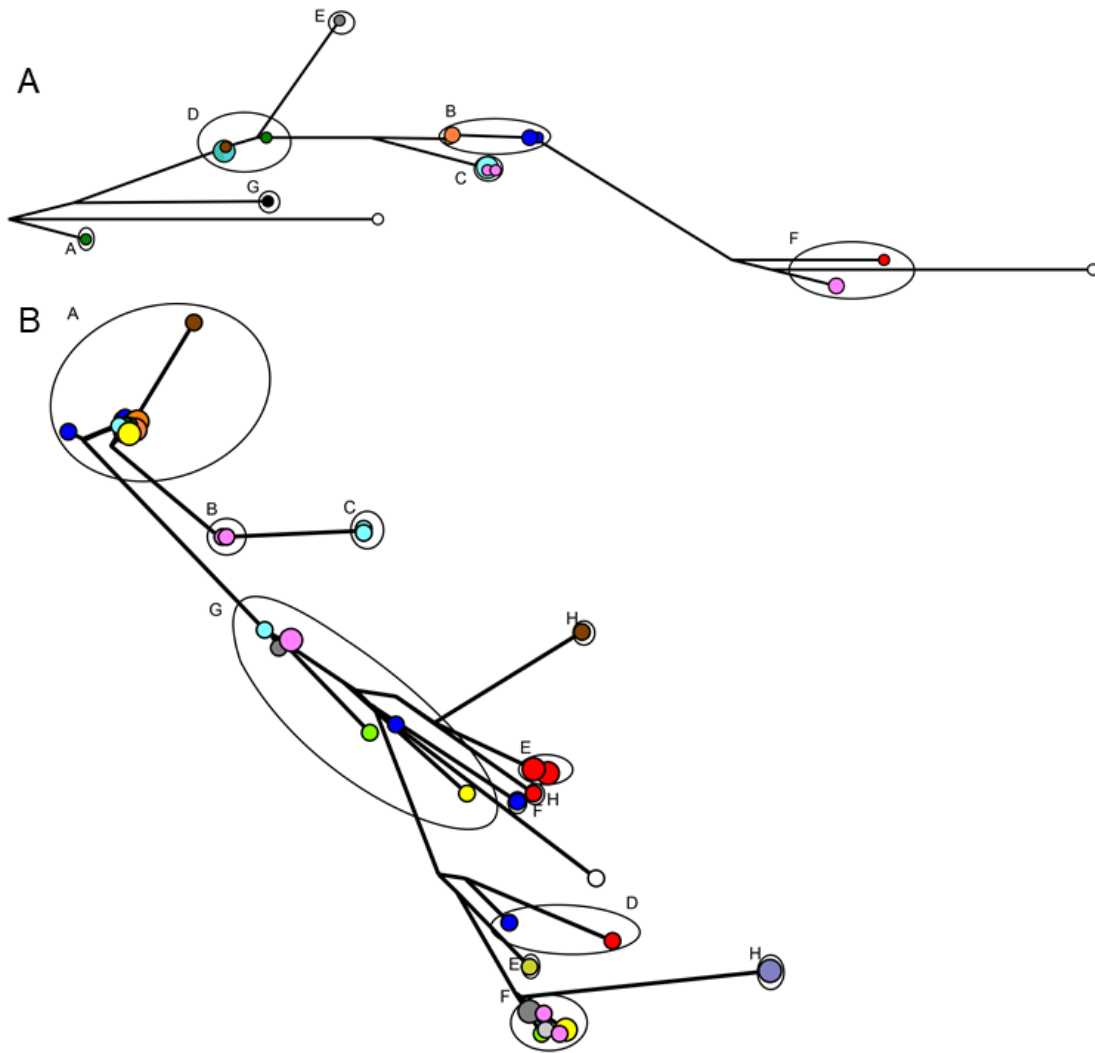


Figure 2.8. Haplotype network analysis of partial COI gene sequences of A) *Collotheca campanulata* and B) *C. ornata* populations as determined by the median joining method (Bandelt et al., 1999). Size of circles is proportional to the number of sequences sharing the same haplotype. Branch lengths are proportional to the number of nucleotide substitutions. Open ovals on the network correspond to cryptic species detected by Bayesian Species Delimitation. Color codes are based on the collection region; Texas: red, New Mexico: light green, Georgia: purple, Oregon: light blue, Utah: Brown, Oklahoma: gray, California: pink, Florida: dark blue, Wisconsin: Dark green, New Hampshire: yellow, Carolina: Orange, Pennsylvania: salmon, Minnesota: light pink, North Dakota: Aqua, Arizona: silver, Massachusetts: light purple, Australia: gold, outgroups: white.

Table 2. 5. Number of putative cryptic species delimited by six methods based on COI gene sequences for *Collothea campanulata* and *C. ornata*. The range of likely number of putative cryptic species detected by PTP or 95% confidence interval for single and multiple threshold GMYC are shown in parentheses.

	<i>Collothea campanulata</i>	<i>Collothea ornata</i>
Single threshold GMYC	10 (7-13)	8 (8-27)
Multi threshold GMYC	12 (10-14)	10 (9-27)
PTP	11 (10-13)	29 (26-32)
BSD	7	8
ABGD	4	19
K/Θ	8	12

The mean genetic variation in COI gene was 0.0-11.7% within cryptic species of *C. campanulata*, and 0.3-20.0% within cryptic species of *C. ornata* (BSD of COI gene: *C. campanulata*: seven putative cryptic species, *C. ornata*: eight putative cryptic species). Among BSD cryptic species, the COI mean genetic variation was 10.8-25.2% for *C. campanulata*, and 14.6-29.0% for *C. ornata*. In the haplotype networks based on COI gene for both species, genotype clusters corresponded to the BSD cryptic species (Figure 8A: *C. campanulata*, Figure 8B: *C. ornata*).

Isolation by distance

For *Limnias melicerta* populations, there was a significant, but weak correlation between genetic distance and log transformed geographic distance for the COI gene and ITS region sequences (Mantel test: COI: $r = 0.4$ with 95% confidence interval of 0.27-0.46, $p < 0.001$ and ITS: $r = 0.14$ with 95% confidence interval of 0.06-0.2, $p = 0.03$). For *L. ceratophylli*, genetic variation in the COI gene was significantly correlated to log transformed geographic distance (Mantel test: $r = 0.3$; 95% confidence interval of 0.27-0.4, $p = 0.001$), however this correlation

was not significant based on ITS sequences (Mantel test: $r = -0.02$; 95% confidence interval of -0.12 to 0.08, $p = 0.8$).

For *Collothea campanulata* populations, there was a significant, but weak correlation between genetic distance and log transformed geographic distance for the COI gene sequences (Mantel test: $r = 0.28$ with 95% confidence interval of 0.1-0.45, $p = 0.004$). For *C. ornata*, genetic variation in the COI gene was significantly correlated to log transformed geographic distance (Mantel test: $r = 0.13$ with 95% confidence interval of 0.08-0.2, $p = 0.01$).

Trophi morphology

As noted in the methods, the SEM images were not obtained for *Collothea campanulata* and *C. ornata*. I obtained 92 SEM images of trophi for *L. melicerta* representing seven putative cryptic species (based on COI sequences), and 60 SEM images for *L. ceratophylli* representing three putative cryptic species (based on COI sequences). Trophi images are available at <http://datarepo.bioinformatics.utep.edu/getdata?acc=468Y2C8Q43EZY9T>. No significant variation was detected between *L. melicerta* and *L. ceratophylli* in trophi shape (Discriminant Analysis: **frontal**: Wilks' Lambda = 1, chi-squared < 0.001, df = 16, $p = 1$, and **caudal**: Wilks' Lambda = 1, chi-squared = 0.001, df = 42, $p = 1$) or trophi size (**frontal**: Man-Whitney U = 911, $p = 0.76$, and **caudal**: Man-Whitney U = 298, $p = 0.77$). Trophi shape did not show significant variation among putative cryptic species of *L. melicerta* (Discriminant Analysis: **frontal**: Wilks' Lambda = 1, chi-squared = 0.001, df = 80, $p = 1$, and **caudal**: Wilks' Lambda = 1, chi-squared = 0.0, df = 70, $p = 1$) or *L. ceratophylli* (Discriminant Analysis: **frontal**: Wilks' Lambda = 1, chi-squared = 0.001, df = 12, $p = 1$, and **caudal**: Wilks' Lambda = 1, chi-squared = 0.001, df = 28, $p = 1$). There was significant variation in trophi size among putative cryptic species of *L. melicerta* (**frontal**: Kruskal-Wallis chi-squared = 12.2, $p = 0.002$, and **caudal**: Kruskal-Wallis chi-squared =

10.3, $p=0.02$). Cryptic species “D” had the smallest centroid size (frontal and caudal: 1.33) and cryptic species “E” had the largest centroid size (frontal: 4, and caudal: 5). However, the trophic size showed no significant differentiation among putative cryptic species of *L. ceratophylli* (**frontal**: Kruskal-Wallis chi-squared= 2.5, $p=0.11$, and **caudal**: Kruskal-Wallis chi-squared= 5.9, $p=0.051$).

DISCUSSION

With the advent of molecular tools, detecting cryptic species in rotifers has become common and has improved our knowledge of their diversity. Here, using two molecular markers I detected cryptic diversity within four rotifer morphospecies, *Limnias melicerta*, *L. ceratophylli*, *Collotheca campanulata* and *C. ornata*. BSD delimitation method detected nine putative cryptic species for *L. melicerta*, four putative cryptic species for *L. ceratophylli*, seven putative cryptic species for *C. campanulata* and eight cryptic species for *C. ornata* based on COI gene, a subset of these is described below.

Although the benefit of using multiple markers to detect cryptic species is accepted (Shaw, 2002; Xiao et al., 2010; Dupuis et al., 2012; Finnegan et al., 2013; Fontaneto et al., 2015), most studies of rotifers are based solely on the mitochondrial COI gene (e.g., Li et al., 2010; Obertegger et al., 2012, 2014; Leasi et al., 2013; Malekzadeh-Viayeh et al., 2014; Kimpel et al., 2015; Wen et al., 2016). In a study based on all available COI and ITS sequences of the *Brachionus plicatilis* complex by (Mills et al., 2016), the nuclear marker ITS1 was recommended over COI to obtain more conservative results within this species complex. In another study, Papakostas et al. (Papakostas et al., 2016) reported great discordance between the mitochondrial COI and nuclear ITS markers for species delimitation within the *B. calyciflorus* Pallas, 1766 complex. They argued that species delimitation based on the ITS region can better explain the

morphological variation within the complex. Similarly, the ITS region was recommended for species delimitation within *Euchlanis dilatata* (see Chapter 1) because it gave a more conservative separation as compared to the COI gene. Nuclear markers can complement mitochondrial genes for detecting cryptic species within other rotifer species complexes; this indicates the necessity of including those markers in the molecular studies of rotifers. In studies of other organisms, mitochondrial and nuclear markers are concatenated for species delimitation (e.g., the Bothriurid scorpion: Ojanguren-Affilastro et al. (2016); the copepod *Cyclops*: Krajíček et al., (2016)), or nuclear markers are used to complement species delimitations which were based on mitochondrial markers (e.g., sea spider species complex *Pallenopsis patagonica* (Hoek, 1881): Dömel et al. (2017); Madagascar's Mouse Lemurs *Microcebus* spp. species complexes: Weisrock et al., (2010)). However, I did not use concatenated dataset for species delimitation because of difference in the coalescent time between these markers (Birky et al., 1989), and specifically discordance between COI and ITS phylogenetic trees in my study. The observed discordance indicates the lack of coherence within those cryptic species for mitochondrial and nuclear markers. This could have stemmed from introgression as shown for *B. calyciflorus* by Papakostas et al. (2016) or incomplete lineage sorting as discussed for *E. dilatata* (see Chapter 1) and for *Keratella cochlearis*, *Polyarthra dolichoptera* and *Synchaeta pectinata* by (Obertegger et al., 2018). In my study, species delimitation in *Limnias* spp. based on ITS region was more conservative than COI gene. But, ITS region showed overall very low levels of variation for *Limnias* spp. populations (*L. melicerta*: $\leq 1.9\%$, *L. ceratophylli*: $\leq 5.7\%$), and failed to separate *L. melicerta* and *L. ceratophylli* in the phylogenetic analysis while they were monophyletic based on COI gene and 18S rRNA. On the other hand, mitochondrial genes can be more informative in the phylogenetic analyses of recently diverged lineages because of their

faster rate of evolution (Moore, 1995). These markers have been successfully used to delimit species in, for example, the Puerto Rican termite *Heterotermes* (Eaton et al., 2016), the copepod *Paracalanus parvus* (Claus, 1863) species complex (Cornils & Held, 2014), and within several rotifer species (e.g., *Keratella cochlearis* Gosse, 1851: Cieplinski et al. (2017); *Synchaeta pectinata* Ehrenberg, 1832: Kimpel et al. (2015); *Polyarthra dolichoptera* Idelson, 1925: Obertegger et al. (2014); *Epiphanes senta*: Schröder & Walsh (2007); *Lecane bulla* (Gosse, 1851): Walsh et al. (2009)). Therefore, despite the possibility of oversplitting, I used COI gene over ITS region sequences for species delimitation within *L. melicerta* and *L. ceratophylli* because this marker showed sufficient resolution to distinguish between these two morphospecies. For *Collotheca* spp., although I used COI gene for species delimitation, I recommend comparing the results with species delimitation based on other markers such as nuclear genes.

Populations included in this study were obtained from a wide geographic range in the USA (*L. melicerta* and *C. campanulata*: Oregon to Florida (4413 km); *L. ceratophylli*: Pennsylvania to Georgia (3839 km); *C. ornata*: Massachusetts, USA to Australia (17100 km)). Cryptic species showed varying ranges of distribution from a single habitat to several distant habitats. For example, one putative cryptic species of *L. melicerta* (species “H”) was collected only from a permanent lake in Florida, while “K” was collected from New Mexico, Oklahoma, Texas, and Florida. From four *L. ceratophylli* cryptic species, two were collected from a variety of habitats across my sampling range, species “B” from Texas, Wisconsin, Oregon, Oklahoma, Pennsylvania, and species “D” from Georgia, California, and Pennsylvania. The other two cryptic species are found in only one habitat, one from a permanent lake in New Mexico, and the other from a pond in Florida. In *C. campanulata*, cryptic species “A” was only found in a lake

from Wisconsin, and cryptic species “E” was only collected from a pond in Oklahoma. The other five cryptic species showed wider geographic ranges. Within *C. ornata*, all cryptic species were found in at least two sampling sites. However, cryptic species “A” and “E” showed the widest geographic distributions. Cryptic species “A” was represented by populations from Pennsylvania, Wisconsin, Oregon, Florida, Georgia, California, and New Hampshire. Cryptic species “E” was found in two sites in West Texas, USA and one site in Chowilla, South Australia.

The observed variation in geographic distributions of these putative cryptic species may be an artifact of under sampling. In other words, the specified geographic distributions of cryptic species in this study may expand by including samples from various biogeographical regions; and there is a possibility that each of cryptic species is in fact cosmopolitan. However, similar variation has been reported for other rotifer species complexes such as the *B. plicatilis* complex (out of 15 cryptic species, one cryptic species (SM7) was restricted to North America, SM8 to Australia, and *B. ibericus* to Europe; (Mills et al., 2016)). I observed cryptic species with small sample sizes that showed wide geographic range. Thus, cryptic species in my study probably vary in their ability for dispersal and colonizing distant habitats. For example, cryptic species “G” from *L. melicerta* represented by two clonal isolates; one found in Oregon and the other in Georgia (2726 km apart). Besides, cryptic species “E” from *C. ornata* comprised of three populations and, as mentioned above, showed the widest geographic distribution. The geographic distance between two populations in Texas, USA and the population in Australia was approximately 14000 km. Intraspecific variation in dispersal ability has been discussed for other passively dispersing taxa (see Bilton et al., 2001), which could apply to cryptic species in this study although it is highly likely that including additional samples results in observing different

distribution patterns. Including more samples may yield higher number of cryptic species without necessarily affecting the species boundaries I delimited in this study (e.g., splitting or lumping cryptic species).

In my study, genetic variation among populations based on COI gene and ITS region sequences was significantly correlated with the geographic distance, except for ITS sequences corresponding to *L. ceratophylli*. Because the correlation was weak (or lacking) between the geographic and genetic distance, geographic isolation cannot be considered a strong driver of genetic variation in the studied taxa. Similar to some other studies on other invertebrates (e.g., 18 invertebrate species: Boileau et al. (1992); *Daphnia lumholtzi* Sars, 1885: Frisch et al. (2013); *E. dilatata* Ehrenberg, 1830: Kordbach et al. (2017); *Synchaeta pectinate* Ehrenberg, 1832: Kimpel et al. (2015); *Brachionus calyciflorus*: Xiang et al. (2011)), my study populations showed high genetic differentiation across small geographic scales.

The trophi of the genus *Limnias* is malleoramate which is specific to Order Flosculariacea (Wallace & Snell, 2010). For more detailed descriptions of *Limnias* trophi see Gosse (1856), Meksuwan et al. (2015) and Wallace et al. (2018). While trophi size differed among putative cryptic species of *L. melicerta*, it did not show significant variation among putative cryptic species of *L. ceratophylli* or even between *L. melicerta* and *L. ceratophylli*. The high variability in trophi size within each morphospecies may have led to failure in detecting significant differences between them. No significant variation was found between *L. melicerta* and *L. ceratophylli*, and among putative cryptic species in trophi shape. Therefore, trophi shape cannot be used to distinguish between *L. melicerta* and *L. ceratophylli* or among their putative cryptic species. This morphological conservation and stasis in trophi morphology, despite high genetic variation among putative cryptic species (COI gene: *L. melicerta* \leq 22.5%, *L.*

ceratophylli $\leq 21.5\%$), may potentially stem from incongruence between the rates of speciation and morphological evolution (Lee & Frost, 2002). Morphological stasis in a variety of traits, has been observed in a numerous organisms (e.g., the copepod *Eurytemora affinis* (Poppe, 1880): (Lee & Frost, 2002b); the butterfly fish *Pantodon buchholzi* Peters, 1876: (Lavoué et al., 2011); two amphipods *Leucothoe ashleyae* Thomas and Klebba, 2006 and *Leucothoe kensleyi* Thomas and Klebba, 2006: (Richards et al., 2012)). Differences in trophi morphology has been shown to be connected to variation in feeding habits (see Asplanchnidae: (Salt et al., 1997)). Therefore, morphological stasis in trophi could be a result of ecological niche conservatism through similarity in the diet (including yeast (Wallace & Starkweather, 1983) and planktonic algae (Sarma et al., 2017)) of *L. melicerta* and *L. ceratophylli*. However, morphological stasis could be investigated within morphospecies of other rotifer taxa such as the genus *Floscularia*. This is because, unlike *L. melicerta* and *L. ceratophylli*, *Floscularia* spp. show interspecies variation in trophi morphology (Segers, 1997) they are likely to show variation in trophi features at the level of cryptic lineages.

Similar to other taxonomic groups, there are a variety of studies that did not record significant morphological variation among rotifer cryptic species. Based on geometric morphometric analyses of lorica and trophi features, Fontaneto et al. (2007a) suggested there are no robust morphological differences between *B. plicatilis* and *B. manjavacas*. In addition, Leasi et al. (2013) did not detect any significant variation in morphological features of the lorica or body size among seven genetically detected cryptic species within the *Testudinella clypeata* Ehrenberg, 1832 species complex. Similarly, morphological characteristics such as variation in lorica size, and absence/presence of posterior spine were not valuable in distinguishing among eight putative cryptic species of *Keratella cochlearis* (Gosse, 1851) (Cieplinski et al., 2017). In

summary, morphological features have not always been effective in distinguishing among cryptic species of rotifers.

Few studies have complemented molecular methods with other types of data to delimit species boundaries (e.g., Gilbert & Walsh, 2005; Fontaneto et al., 2007a; Schröder & Walsh, 2010; Xiang et al., 2011; Malekzadeh-Viayeh et al., 2014; Papakostas et al., 2016; Kim et al., 2017). In this study, I attempted to use a morphological characteristic and geographic isolation of genotypes to find a reliable predictor of genetic variation among putative cryptic species within *L. melicerta* and *L. ceratophylli*. However, trophi shape did not vary among cryptic species, and there was not a strong correlation between genetic and geographic distance in these species. Therefore, I did not find sufficient morphological variation or geographic isolation needed to predict the observed genetic differentiation among putative cryptic species. Past studies have focused on ecological differences between *L. melicerta* and *L. ceratophylli*. For instance, it has been shown by Sarma et al. (Sarma et al., 2017) that generation time changes in response to food (the algae *Chlorella vulgaris*) concentration for *L. ceratophylli* while there is no effect in *L. melicerta*. Although the ecological differentiation has been recorded among many rotifer cryptic species (see Gabaldón et al., 2017), to my knowledge, there is no information on ecological or behavioral variation among genetic entities of any *Limnias* species. Therefore, I recommend further studies such as examining ecological and behavioral variation to obtain more information about *Limnias* cryptic species, and mechanisms involved in their speciation.

This is the first study that shows sessile morphospecies, *L. melicerta*, *L. ceratophylli*, *C. ornata* and *C. campanulata* are species complexes. At least for *Limnias* species, COI gene sequences is more reliable for species delimitation compared to the ITS region. For all of these morphospecies, the relationship between geographic and genetic distance was weak or lacking.

This was similar to some other rotifer species complexes (see above) and indicates geographic isolation may not be a major factor in genetic divergence among rotifer population. Moreover, I did not find morphological variation in trophi among cryptic species of *L. melicerta* and *L. ceratophylli*. This could be interpreted as a case of morphological stasis. To better illuminate speciation mechanisms such as ecological speciation in sessile groups, future studies can include life table experiments to investigate ecological differentiation among cryptic species. The variation in fitness of cryptic species in response to environmental variables can be used to apply Differential Fitness Species concept. Furthermore, more comprehensive morphological analyses, mating experiments to apply Biological Species Concept, and behavior studies including patterns of metamorphosis and substrate selection will assist in examining boundaries of sessile rotifer cryptic species, and understanding speciation in rotifers

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Chapter 3: Reproductive isolation, morphological and ecological differentiation among cryptic species of *Euchlanis dilatata*, with description of four new species

ABSTRACT

Morphological approaches may not provide sufficient resolution for species delineation. I hypothesized that integrating molecular, morphological, and ecological analyses will elicit a better estimate of species diversity. Applying an integrative taxonomy approach will provide evidence to distinguish among species as well as improve our understanding of the speciation within rotifers. Seven putative cryptic species were found within *Euchlanis dilatata* based on a nuclear marker (see Chapter 1). Here, I investigated reproductive isolation, variation in trophi morphology, and life history characteristics in response to temperature and conductivity among representatives of these cryptic species. Mating success rate between each cryptic species was 0-1.1%, which was lower than that of positive controls (intra-clonal: 15.6-43.9%; Chi-Square, $p < 0.001$). SEM trophi images ($n=175$) representing individuals from the seven lineages were used for morphometric analyses. Using Discriminant Analysis, 64% of individuals were correctly assigned to cryptic species (Chi-Square= 78, $p < 0.001$). Moreover, there was a small projection on the left ramus of trophi in populations of one cryptic species (species A). To investigate life history characteristics of cryptic species, four treatments were used: (1) 20°C, 180 $\mu\text{S/cm}$, (2) 20°C, 1800 $\mu\text{S/cm}$, (3) 27°C, 180 $\mu\text{S/cm}$, and (4) 27°C, 1800 $\mu\text{S/cm}$. The interaction between temperature and conductivity had significant effects on generation time, net reproductive rate, and the intrinsic rate of population increase in some of the cryptic species ($p=0.03$). In the present study, I showed at least six cryptic species of *E. dilatata* are reproductively isolated and that they showed variation in life history characteristics. Because of high genetic variation, reproductive isolation and ecological differentiation among *E. dilatata* cryptic species, I described four of them as new species. One specimen from cryptic species A was designated as neotype of *E. dilatata*.

INTRODUCTION

Accurate species delimitation contributes to a comprehensive data baseline for most biological studies. Reliable species delineation can be obtained based on an integrative taxonomy which implements various complementary approaches (Dayrat, 2005), especially for understudied taxa such as microorganisms. Relying solely on morphology to classify species of microorganisms can be misleading and could not reflect true levels of species richness and biodiversity as there may not be sufficient detectable morphological variation among species (Kaya et al., 2009). Often, morphologically similar forms and cryptic species are lumped together taxonomically (Maddison, 1997; Finlay, 2002).

Rotifers are ubiquitous microorganisms inhabiting various aquatic habitats making them one of the major constituents of freshwater zooplankton communities (Segers, 2008; Wallace & Snell, 2010). Cryptic diversity can be high in rotifers as they lack easily recognizable morphological characters (Segers, 2008; Fontaneto et al., 2009). Cryptic species in most taxa, including rotifers, are primarily detected using molecular analyses (Fontaneto et al., 2015). Most of cryptic species within Rotifera have remained at the putative species level and have not been established as new species. Some exceptions include members of the *Epiphanes senta* (Müller, 1773) species complex. *Epiphanes hawaiiensis*, *E. ukera* and *E. chihuahuaensis* were described using cross-mating experiments, morphological, and molecular analyses (Schröder & Walsh, 2007). *Brachionus manjavacas* (Fontaneto et al., 2007a) and *B. koreanus* (Hwang et al., 2013) in *B. plicatilis* Müller, 1786 species complex were described based on molecular, and morphological analyses.

Although DNA taxonomy is not always sufficient to define species boundaries, it can be considered an effective tool to complement traditional taxonomy (Packer et al., 2009). DNA

taxonomy provides hypotheses about species that can be tested with morphological, behavioral, ecological, and mate choice studies, and to eventually describe cryptic species. Using several lines of evidence to describe cryptic species will aid in substantiating the taxonomic status of new species.

Genetic studies are only capable of indicating that cryptic species have not exchanged genetic material. However, it is not possible to determine whether they have lost the ability for such exchange (Bickford et al., 2007). Mate choice experiments can examine the strength of reproductive isolation among cryptic species (e.g., in rotifers: Gómez et al., 1995; Gilbert & Walsh, 2005; Schröder & Walsh, 2007, 2010; Wiwegweaw et al., 2009).

The life cycle of monogonont rotifers consists of sexual and asexual phases. In the asexual cycle, amictic (asexual) females lay diploid eggs that develop to amictic daughters. In response to environmental cues such as temperature, photoperiod, vitamins, and crowding, the population may shift to mixis (sexual reproduction; reviewed by Schröder, 2005). When fertilized by males, mictic (sexual) females produce diploid resting eggs; otherwise, unfertilized haploid eggs develop into males.

Although mating experiments have the potential to confirm whether genetic variation among cryptic species of monogonont rotifers is accompanied by reproductive isolation (Rico-Martinez & Snell, 1995; Schröder & Walsh, 2007), few studies have focused on examining this among rotifer cryptic species. For example, Xiang et al. (2011) carried out cross mating experiments among cryptic of *Brachionus calyciflorus* Pallas, 1766 and considered the production of resting eggs as the indicator of successful mating. Others studied pre- and post-mating reproductive isolation among cryptic species (e.g., *B. plicatilis* species complex: Gómez et al., 1995; Rico-Martinez & Snell, 1995; Gomez & Snell, 1996; Suatoni et al., 2006; *B.*

calyciflorus species complex: Gilbert & Walsh, 2005; *Epiphanes senta* species complex: Schröder & Walsh, 2007; 2010). Examining reproductive isolation and its drivers can add confidence to delimiting species boundaries and eventually describing them as new species.

Studying morphological variation is another approach that can complement results obtained through DNA taxonomy for species delineation in cryptic species complexes. For rotifers, morphological variation among cryptic species has been found in some complexes. This is illustrated in the *B. plicatilis* complex where variation in lorica size could be used to differentiate between *B. plicatilis* and *B. rotundiformis* Tschugunoff, 1921 (Fu et al., 1991). Similarly, lorica size and spine patterns vary between *B. rotundiformis* and *B. ibericus* (Ciros-Pérez et al., 2001). Hwang et al. (2013) showed that *B. koreanus* has smaller lorica with shorter distances between pair of inner and outer spines as compared to *B. plicatilis*. In *Epiphanes senta*, morphological variation in trophi and resting eggs features, along with DNA evidence and cross mating experiments, lead to the designation of new species in the complex (Schröder & Walsh, 2007; 2010). In bdelloid rotifers, Fontaneto et al., (2007) found variation in trophi size and shape within seven bdelloid morphospecies. In other studies, no robust morphological variation was found among cryptic species. For instance, Fontaneto et al. (2007) suggested there are no robust morphological differences between *B. plicatilis* and *B. manjavacas* based on geometric morphometric analyses of lorica and trophi. Leasi et al. (2013) did not detect any significant variation in morphological features of lorica and body size among cryptic species of *Testudinella clypeata* (Müller, 1786). In a study by Malekzadeh et al. (2014), there was not robust variation between *B. 'Tiscar'*, and a new lineage from Iran in the lorica morphology. Therefore, morphological analyses are not always sufficient to represent all of the diversity that is detected through molecular methods; in some cases, they could be applied to distinguish among some

rotifer cryptic species. In addition, finding morphological variation among cryptic species adds additional evidence supporting the description of new species.

Ecological niche differentiation can promote reproductive isolation, and consequently speciation (Schluter, 2001). By incorporating the physical and chemical features of the habitat in the study of cryptic species, I can examine whether occurrence of a cryptic species is correlated to specific environmental factors (e.g., Ortells et al., 2003; Dennis & Hellberg, 2010; Obertegger et al., 2012; Papakostas et al., 2013; Zhang et al., 2015) and, beyond that, whether ecological differentiation could be a driver of speciation (e.g., Liu et al., 2013; Fouet et al., 2017). Moreover, investigating ecological adaptations among cryptic species can test the species boundaries specified by molecular methods (Rissler & Apodaca, 2007). Temperature is an environmental factor that affects age-specific survivorship and reproduction rate of zooplankton, including rotifers (e.g., Galkovskaja, 1987; Ma et al., 2010; Johnston & Snell, 2016). Furthermore, variation in response to temperature has been documented among some cryptic species from a variety of protists and rotifers (e.g., 15 protist species: Rose et al., 2008; dinoflagellate: *Akashiwo sanguinea* (K. Hirasaka) species complex: Luo et al., 2017; rotifers: *B. ibericus* Ciro-Pérez, Gómez & Serra, 2001, *B. plicatilis*, and *B. rotundiformis*: Gómez et al., 1995; *Brachionus calyciflorus*: Li et al., 2010). While the relationship between conductivity and zooplankton species composition and abundance has also been well studied (e.g., Bos et al., 1996; Soto & Rios, 2006; Çelik & Ongun, 2007; Sousa et al., 2008; Walsh et al., 2008; Fatema et al., 2016; Celewicz-Goldyn & Kuczynska-Kippen, 2017), few studies have addressed the differential response to conductivity among cryptic species. Pfenninger & Nowak (2008) showed that the midge *Chironomus piger* Strenzke, 1956 can tolerate higher levels of conductivity compared to *C. riparius* (Meigen, 1804). Obertegger et al. (2014) found that the occurrence of

cryptic species in the rotifer *Polyarthra dolichoptera* Bartoš, 1951 in high-altitude lakes was related to longitude, conductivity and silica. Differential response of cryptic species to conductivity levels can contribute to ecological niche differentiation. Investigating the relationship between conductivity and the occurrence of cryptic species can provide information on their ecological variation among them.

Despite the observed reproductive isolation and variation in ecological adaptation among cryptic species of rotifers, many of them are not described. In a few studies where, cryptic species are described (as mentioned above), morphological variation has been detected among them. It seems that rotifer cryptic species are likely to be left unnamed if they are not morphologically distinguishable. However, to address cryptic diversity, these species can be described based on their diagnostic nucleotides. This method has been successfully used to describe cryptic species of other taxa (e.g., Brower, 2010; Johnson et al., 2015; Delić et al., 2017), and has been recommended for this purpose by Jörger & Schrödl (2013).

In this study, I investigated reproductive isolation, and variation in trophi morphology among *Euchlanis dilatata* cryptic species. In addition, I conducted life table experiments to examine variation in survivorship, fecundity, and population growth among five cryptic species of *E. dilatata* in response to water temperature and conductivity. Finally, I used diagnostic nucleotides in the ITS region to describe five *E. dilatata* cryptic species.

METHODS

As described in Chapter 1, ITS region and COI gene sequences from 62 populations *Euchlanis dilatata* were analyzed. Molecular species delimitation was based on ITS region sequences and seven putative cryptic species were found. Populations representing these cryptic

species were used in the following experiments and analyzed based on their availability in the lab.

Cross mating experiments

Euchlanis dilatata clonal lineages from 11 populations were used in mating experiments within and between six putative cryptic species (Table 3.1). Each clonal lineage was initiated using one asexual female. Clonal lineages were cultured in modified MBL media (Stemberger, 1981) at room temperature and were fed a mixture of the algae *Rhodomonas minuta* Skutja, 1948, *Chlorella vulgaris* Berijerinck, 1890 (Culture Collection of Algae at the University of Texas at Austin [UTEX] strain 30), and *Chlamydomonas reinhardtii* Dangeard, 1888 (UTEX strain 90).

To conduct mating experiments, female embryos and males were isolated from cultures that were mictic under lab conditions. I did not control for male age, however, slow swimming males (indicative of old age) were not used. Two female embryos and two males were used in each mating trial. Females and males obtained from the same clonal lineage (intra-clonal) were included as positive controls. For cross mating experiments (inter-clonal) females and males were obtained from different lineages. Trials were checked after 48 hrs and the success of mating (e.g., the production of resting eggs) was recorded. If the female embryos did not hatch, or the neonate produced amictic eggs, the trial was excluded from statistical analyses. Cross mating experiments were reciprocal, for example between males from lineage 1 and females from lineage 2 and vice versa. I conducted six combinations of mating experiments between putative cryptic species that were either sister groups (e.g., species A and B, Figure 1.2) or had low genetic distance ($\leq 3.2\%$ e.g., species C and D) based on the ITS region sequences. Cryptic species F showed high genetic differentiation in the ITS region compared to the other five

cryptic species (9.7-10.3%). I crossed this species with species E (genetic distance: 10.3%) and species D (genetic distance: 9.7%). I also used four inter-clonal combinations of mating experiments within cryptic species and 11 intra-clonal combinations as positive controls (Tables 3.2, 3.3). Success of each mating experiments was determined by dividing number of successful trials (e.g., fertilized resting egg produced) by the total number of trials. Inter-clonal mating success was compared to success found in positive controls. To test whether there was a significant difference in mating success between inter-clonal and intra-clonal trials, Pearson's Chi-Square test was implemented in RStudio v 1.1.383 (RStudio Team, 2016). Clonal lineages were considered to be reproductively isolated based on Chi-square tests where inter-clonal mating success rate was significantly lower than intra-clonal mating success rate.

Table 3. 1. Collection site of *Euchlanis dilatata* clonal lineages used in mating experiments, and the cryptic species to which they were assigned (Figure 1.2). Modified from Supplemental Table S1.1. Abbreviations are shown in parentheses and are used in other tables.

Origin of populations	Collection date	GPS coordinates (decimal degrees N/W)	Cryptic species
Rio Grande, Williamsburg, Sierra Co., NM (Williamsburg)	07.24.2013	33.110039/ -107.297839	A
Mescalero Lake, Otero Co., NM (Mescalero)	07.05.2013	33.2984/ -105.6886	A
Fish Pond, Nockamixon State Park, Bucks Co., PA (NockFish)	05.20.2016	40.472567/ -75.224823	B
Feather Lake Wildlife Sanctuary, El Paso Co., TX (Feather Lake)	10.10.2007	31.6890972/ -106.3052666	C
Rio Grande, American Dam, El Paso Co., TX (American Dam)	12.19.2013	31.784234/ -106.527845	C
Former cattle tank sediments, White Sands National Monument, Doña Ana Co., NM (Cattle Tank)	09.20.2006	32.67485/ -106.44345	D
Red Tank, Hudspeth Co., TX (Red Tank)	06.04.2014	30.7303083/ -104.9891083	D
Cinnamon Bay Beach pond, St. John, U.S. Virgin Islands (CBB)	05.24.2012	18.356281/ -64.752136	E
Cattail Falls, pool C', Brewster Co., TX (Cattail C')	08.08.2006	29.2731833/ -103.3361638	F

Cattail Falls, pool G, Brewster Co., TX (Cattail G)	06.23.2013	29.2731666/ -103.3361638	F
Krome pond, Miami-Dade Co., FL (Krome)	11.24.2015	25.883615/ -80.484920	F

Trophi morphology

Trophi, dorsal and ventral view, for seven putative cryptic species of *E. dilatata* were prepared for scanning electron microscopy (SEM) by dissolving rotifer tissue in ~5% sodium hypochlorite, extracting the trophi and rinsing them with deionized water approximately 15 times, and air-drying them on circular cover slips at room temperature (modified from Segers, 1993). Trophi were coated with gold/palladium using a Gatan 682 PECS sputter coater. I used a Hitachi S-4800 scanning electron microscope to obtain SEM images at 20 kV.

Images of trophi were observed and examined for features to distinguish among putative cryptic species. Length of rami, manubria, and fulcrum were measured for 175 trophi representing seven putative cryptic species (A (n=32), B (n=4), C (n=44), D (n=23), E (n=32), F (n=36), and G (n=4)) using a Zeiss Axioscope equipped with a SPOT camera and software v 5.0 (Diagnostic Instruments, Inc). Discriminant *Analysis* in SPSS v 24.0 (IBM Corp, 2016) was used to determine the percentage of individuals that were correctly assigned to cryptic species based on the size of trophi elements.

Life table experiments

Five clonal lineages representing five putative cryptic species of *E. dilatata* collected from the Rio Grande at Williamsburg, Sierra Co., NM (cryptic species A), the Rio Grande at American Dam, El Paso Co., TX (cryptic species C), a former cattle tank, White Sands National Monument, Doña Ana Co., NM (cryptic species D), a small, temporary pond at Cinnamon Bay

Beach, St. John, U.S. Virgin Islands (cryptic species E), and a pond alongside Krome Ave., Miami-Dade Co., FL (cryptic species F) were selected for life table experiments. Populations from cryptic species “B” and “G” were not available in the lab at the time of the experiments. Age-specific survivorship (l_x), fecundity (m_x), generation time (T), net reproductive rate (R_0), and the intrinsic rate of population increase (r) were examined under four conditions: (1) Low temperature, low conductivity (tc: 20°C, conductivity at 180 μ S/cm), (2) Low temperature, high conductivity (tC: 20°C, conductivity at 1800 μ S/cm), (3) High temperature, low conductivity (Tc: 27°C, conductivity at 180 μ S/cm), and (4) High temperature, high conductivity (TC: 27°C, conductivity at 1800 μ S/cm). The high values for water temperature and conductivity in these treatments were higher than what I recorded in the field for most studied populations. For the field collections where *E. dilatata* was found, the highest recorded conductivity was at Rio Grande at Williamsburg, NM (~ 1,600 uS/CM). An exception for temperature was the population from Rio Grande at Williamsburg, NM with 27.7 °C as the highest recorded value. The conductivity of modified MBL medium was 180 μ S/cm. To raise the conductivity to 1800 μ S/cm, I added 0.73 g NaCl to 1 L MBL medium. Each treatment initially consisted of four replicates of nine females. Female neonates (< 6 hrs old) were placed into nine well culture plates with 0.8 mL of modified MBL medium containing the alga *C. reinhardtii* (500,000 \pm 50,000 cell/ml), and were incubated using a 18 hrs: 6 hrs light:dark photoperiod cycle. Females were checked every 12 hrs to determine survival and the number of eggs and offspring that were produced until the death of the last individual. Offspring were removed from the culture plates as they hatched. Females were moved to new food-containing medium every 24 hrs. Mictic females, females lost during the experiment, or those that died in the first 24 hrs were excluded from the analyses. The following formulae were used to calculate age-specific survivorship (l_x),

fecundity (m_x), net reproductive rate (R_0), generation time (T), and intrinsic rate of population increase (r):

$$l_x = s_x/s_0$$

$$m_x = b_x/n_x$$

$$R_0 = \sum_{x=0}^k l_x m_x$$

$$T = \sum_{x=0}^k x l_x m_x / R_0$$

$$r = \ln(R_0)/T$$

Where x is time (day), n_x is the number of females, s_x is the number of survivors, and b_x is the number of offspring at each day.

I used a Linear Mixed-effects model in RStudio v 1.1.383 (RStudio Team, 2016) to test whether temperature, conductivity and their interaction was related to the differences in $l_x m_x$ and e_x . To determine significant differences in generation time (T), net reproductive rate (R_0), and intrinsic rate of population increase (r) among cryptic lineages I used the exact permutation test in R v 3.4.3 (R core team, 2017).

Description of new species

I described cryptic species A, B, C, D and F from the *E. dilatata* complex (Kordbacheh et al., 2017) following Jörger and Schrödl (2013). The position and character state of diagnostic nucleotides correspond to the alignment of ITS region sequences (849 bp including the insertions) in MAFFT v 7 (Katoh & Standley, 2013) (Supplemental Document S1.4) were used for species description. Following the recommendation of Jörger and Schrödl's (2013), species E and G are not described because they were represented by only one population.

RESULTS

Cross mating experiments

The intra-clonal mating success rate (positive controls) ranged from 15.6-43.9%. Within cryptic species mating success rate was 1.2-17.9% and between cryptic species success rate was 0-1.1% (Table 3.2). Within cryptic species, the probability of inter-clonal mating success was 3.5-26 times lower than intra-clonal mating success (Chi-square value= 0.04-47.4, $p < 0.001$), except for crosses between Cattail Falls pool C' and G from cryptic species "F" (Chi-Square=0.035, $df=1$, $p=0.8$). Further, resting eggs were produced in all of within cryptic species mating experiments (Table 3.2). However, it should be noted that the viability of eggs was not determined.

For intra-clonal crosses between cryptic species, the success rate was 0 for all crosses except for the cross-mating experiments between individuals from Cattail Falls pool C', TX (cryptic species F) and Cinnamon Bay Beach pond, USVI (cryptic species E). In this cross, one resting egg was produced out of 40 trials between males from cryptic species F and females from cryptic species E. However, no resting eggs were produced in 49 trials when females from cryptic species F were crossed with males from cryptic species E. The genetic variation between these cryptic species was 10.3 % in the ITS region and 13.5% in the COI gene sequences.

Based on Chi-Square test results, the probability of interbreeding between cryptic species was 14-44 times lower than the probability of inbreeding within clonal lineages (Table 2.3, 3.3). Therefore, under these experimental conditions, putative cryptic species were reproductively isolated.

Table 3. 2. Intra- and inter- clonal mating success rate (%) for populations of *Euchlanis dilatata*. Inter-clonal mating success rates between cryptic species are shown in bold. Cryptic species to which clonal lineages belong are shown in parentheses. Mating experiments included reciprocal trials. Abbreviations are the same as in Table 3.1.

Population	Population	Mating success rate (%)	Trials (n)
Williamsburg (A)	Williamsburg (A)	32.5	40
Mescalero (A)	Mescalero (A)	42.5	40
NockFish (B)	NockFish (B)	41.5	41
Feather Lake (C)	Feather Lake (C)	23.6	93
American Dam (C)	American Dam (C)	27.4	51
Red Tank (D)	Red Tank (D)	42.8	70
Cattle Tank (D)	Cattle Tank (D)	43.9	41
CBB (E)	CBB (E)	36.5	123
Cattail C' (F)	Cattail C' (F)	15.6	115
Cattail G (F)	Cattail G (F)	22.4	67
Krome (F)	Krome (F)	22.2	36
Williamsburg (A)	Mescalero (A)	1.25	80
Feather Lake (C)	American Dam (C)	6.7	89
Red Tank (D)	Cattle Tank (D)	3.2	92
Cattail C' (F)	Cattail G (F)	17.9	39
Williamsburg (A)	NockFish (B)	0	92
Feather Lake (C)	Red Tank (D)	0	83
Feather Lake (C)	CBB (E)	0	84
Red Tank (D)	CBB (E)	0	85

Red Tank (D)	Cattail G (F)	0	72
CBB (E)	Cattail C' (F)	1.1	89

Table 3. 3. Chi-Square tests used to examine whether intra-clonal mating success was significantly higher than inter-clonal mating success for both within and between cryptic species trials of *Euchlanis dilatata*. Mating experiments included reciprocal trials. Abbreviations are the same as in Table 3.1.

Clonal lineages	Cryptic species	Number of trials	Chi Square value	p value
Williamsburg vs NockFish	A vs B	92	47.5	p < 0.001
Feather Lake vs Red Tank	C vs D	83	52.2	p < 0.001
CBB vs Feather Lake	E vs C	84	41.5	p < 0.001
CBB vs Red Tank	E vs D	85	52.2	p < 0.001
Cattail C' vs CBB	F vs E	89	15.3	p < 0.001
Cattail G vs Red Tank	F vs D	72	22.5	p < 0.001
Williamsburg vs Mescalero	A vs A	80	47.4	p < 0.001
American Dam vs Feather Lake	C vs C	89	12.8	p < 0.001
Red Tank vs Cattle Tank	D vs D	92	34.1	p < 0.001
Cattail C' vs Cattail G	F vs F	39	0.04	p= 0.8

Trophi morphology

Discriminant Analysis showed that only 64% of individuals were assigned correctly to their cryptic species based on trophi measurements (Wilks' Lambda = 0.08, Chi-Square= 78, p< 0.001, Figure 3.1). Species "A" was the most distinguishable, with 83% of individuals assigned correctly. Moreover, all trophi analyzed from individuals representing four populations of

species “A” had a small projection on their left ramus, which was not observed in the other putative cryptic species (Figure 3.2). However, a similar projection on the ramus has been found in a population of *E. dilatata* from Italy (Parise, 1966). In Discriminant Analysis, function 1 (72% of variation) was associated with fulcrum length and function 2 (21% of variation) was associated with manubria length.

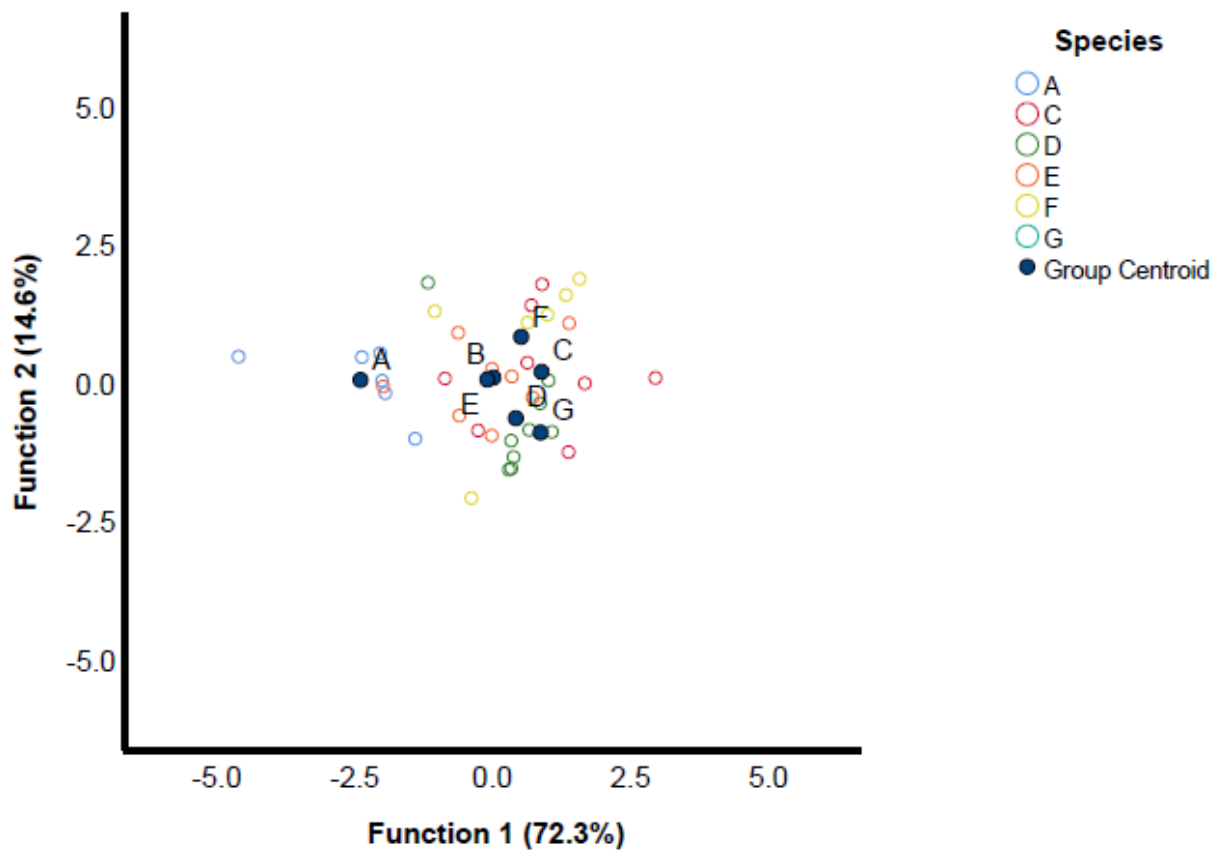


Figure 3.1. Discriminant Analysis based on length of rami, manubria, and fulcrum of trophi from seven *Euchlanis dilatata* cryptic species. The amount variation explained by the first two discriminant functions are shown in parentheses.

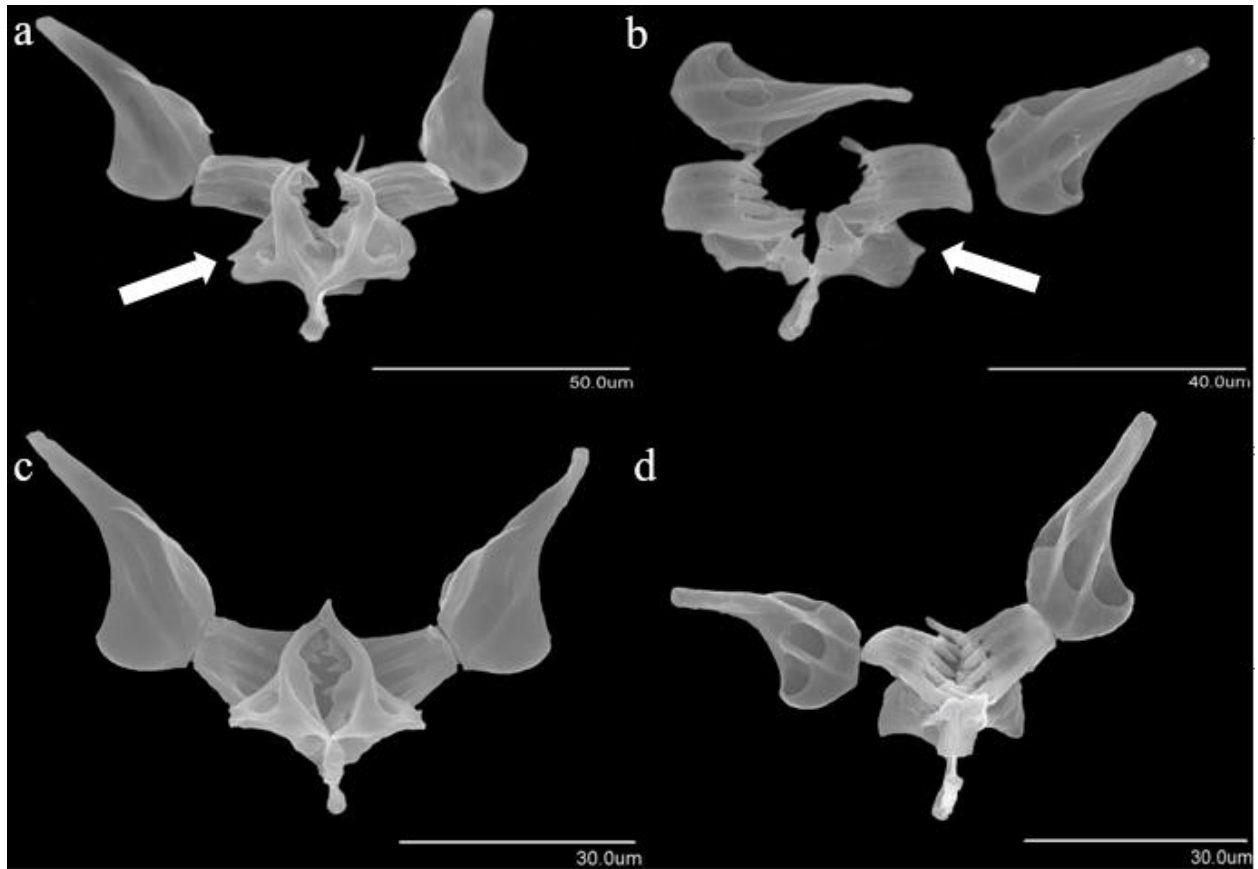


Figure 3.2. Trophi of the *Euchlanis dilatata* a) cryptic species “A” frontal view, b) cryptic species “A” caudal view, c) cryptic species “F” frontal view, d) cryptic species “F” caudal view as representative of the cryptic species without the ramus small projection. Arrow shows the projection on left ramus of cryptic species “A” trophi.

Life table experiments

Age-specific survivorship (l_x), fecundity (m_x), and life expectancy (e_x)

Water temperature, cryptic species, and the interaction between temperature and cryptic species had significant effects on $l_x m_x$ (Linear Mixed-effects Model, $p < 0.001$). Water temperature, conductivity, cryptic species, and the interaction between temperature and cryptic species had significant effects on e_x (Linear Mixed-effects Model, $p < 0.01$). Higher values of $l_x m_x$

were observed at temperature 27 °C (Figure 3.3, Table 3.4). Life expectancy decreased under high temperature and high conductivity (Table 3.4).

Generation time (T), net reproductive rate (R_0), and intrinsic rate of population increase (r) among cryptic species under the four experiment conditions were examined using the exact permutation test in R v 3.4.3 (R core team, 2017). Only significant differences among cryptic species in each treatment are reported below. In all cases the p value was 0.03 unless it is specified.

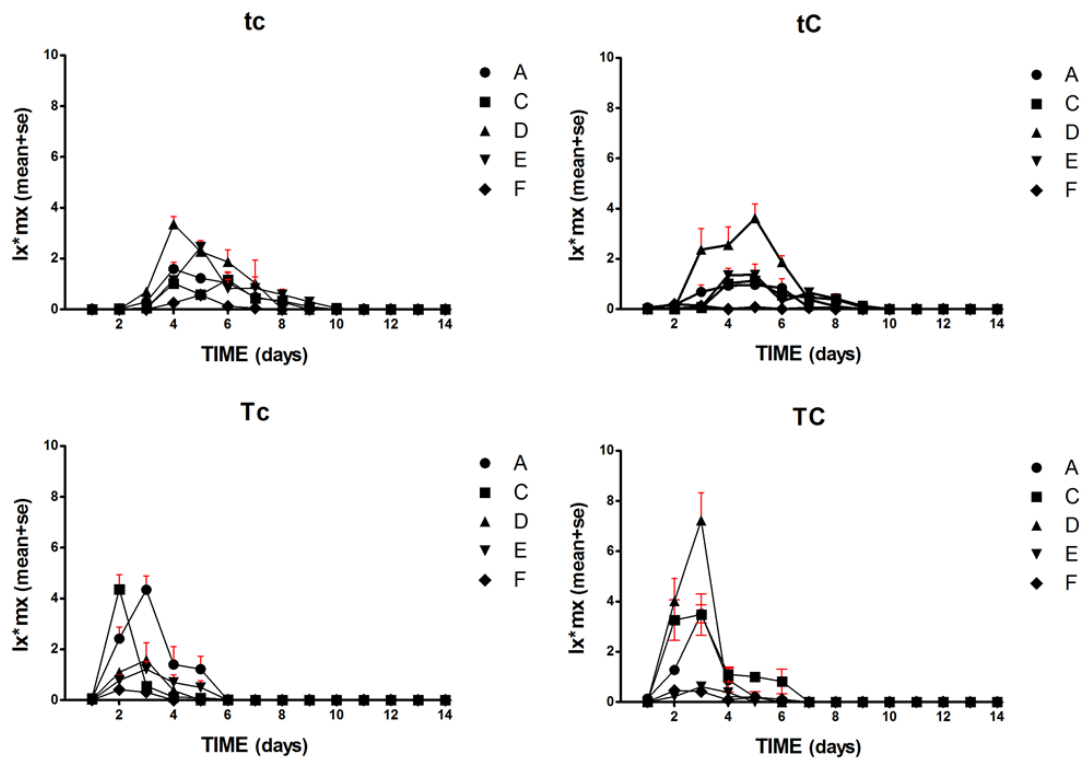


Figure 3.3. Age-specific survivorship and fecundity ($l_x m_x$) of five *Euchlanis dilatata* cryptic species under four conditions: (1) Low temperature, low conductivity (tc: temperature: 20°C, conductivity: 180 μ S/cm), (2) Low temperature, high conductivity (tC: temperature: 20°C, conductivity: 1800 μ S/cm), (3) High temperature, low conductivity (Tc: temperature: 27°C, conductivity: 180 μ S/cm), and (4) High temperature, high conductivity (TC: temperature: 27°C, conductivity: 1800 μ S/cm). Each line on the graph represents a cryptic lineage.

Generation time (T)

For all cryptic species, generation time (T) was the longest under tc conditions. Cryptic species A and E had the shortest generation time under TC treatments while cryptic species C, D and F had the shortest generation time under Tc treatments (Table 3.4).

In tc treatments, generation time ranged from 4.8-5.6 days, but there was no significant difference among cryptic species. Under tC, generation time ranged from 3.3-5.4 days. In these treatments cryptic species E had the longest generation time (5.4 ± 0.06) and was significantly different from cryptic species A (3.9 ± 0.75) and D (4.6 ± 0.17). Under Tc, generation time ranged from 2.2-3.2 days. Cryptic species A (3.1 ± 0.18) and E (3.2 ± 0.17) had longer generation time compared to cryptic species C (2.2 ± 0.09) and F (2.7 ± 0.15). Under TC, generation time ranged from 2.7-3.3 days. In these treatments, generation time of cryptic species E (3.1 ± 0.06) was longer than that of cryptic species D (2.7 ± 0.09) (Table 3.4).

Net reproductive rate (R_0)

Cryptic species C, D, and F showed the highest net reproductive rate (R_0) under TC. Cryptic species A had the highest net reproductive rate under Tc. Finally, cryptic species E had the highest net reproductive rate under tc. For cryptic species A and F, the lowest net reproductive rate was under tC conditions. Cryptic species D and E had their lowest net reproductive rate under Tc. Cryptic species C showed the lowest value of net reproductive rate under tc and tC (Table 3.4).

Under tc, net reproductive rate ranged from 1.0-9.2. Cryptic species F showed the lowest net reproductive rate (1.0 ± 0.17) that was significantly lower than the other four cryptic species. Net reproductive rate of cryptic species D (9.2 ± 1.54) was significantly higher than that of A and C. Cryptic species C (3.7 ± 0.39) had a lower R_0 compared to cryptic species E (6.3 ± 0.68).

Under tC, net reproductive rate ranged from 0.5-10.9. Net reproductive rate of cryptic species D (10.9 ± 0.96) was the highest, and that of cryptic species F (0.5 ± 0.15) was the lowest in these treatments. Under Tc, net reproductive rate ranged from 0.7-9.5. Net reproductive rate of cryptic species A (9.4 ± 1.04) was the highest and net reproductive rate of cryptic species F (0.7 ± 0.25) was the lowest in these treatments. Net reproductive rate of cryptic species C (5.2 ± 0.73) was lower than that of cryptic species A ($p = 0.05$). Cryptic species D (3.1 ± 0.60) had lower net reproductive rate than cryptic species C. Under TC, net reproductive rate ranged from 1.2-11.7. Net reproductive rate of cryptic species E (1.2 ± 0.43) and F (1.3 ± 0.40) were significantly lower compared to the other three cryptic species (Table 3.4).

Intrinsic rate of population increase (r)

Cryptic species A, C, and E had the highest intrinsic rate of population increase (r) under Tc treatments. Cryptic species D and F had the highest intrinsic rate of population increase under TC conditions. Intrinsic rate of population increase was the lowest under tC conditions for cryptic species A and F. Cryptic species C showed the lowest value of r under tc and tC conditions. For cryptic species D, the lowest value of intrinsic rate of population increase was under Tc treatments. Cryptic species E had the lowest intrinsic rate of population increase under TC (Table 3.4).

Under tc, the intrinsic rate of population increase was -0.02 to 0.45. Cryptic species D (0.4 ± 0.02) had the highest, and cryptic species F (-0.02 ± 0.04) showed the lowest values of intrinsic rate of population increase in these treatments. The intrinsic rate of population increase of cryptic species A (0.3 ± 0.01) and E (0.3 ± 0.01) were larger than cryptic species C (0.2 ± 0.01). Under tC, the intrinsic rate of population increase ranged from -0.32 to 0.51. The intrinsic rate of population increase of cryptic species D (0.5 ± 0.03) was larger than the other cryptic

species (between cryptic species A and D, $p= 0.05$). Cryptic species F (-0.3 ± 0.15) had a smaller intrinsic rate of population increase than cryptic species A (0.2 ± 0.11) ($p= 0.05$), C (0.2 ± 0.03), and E (0.3 ± 0.04). Under Tc, the intrinsic rate of population increase was -0.31 to 0.74 . The intrinsic rate of population increase of cryptic species A (0.7 ± 0.05) and C (0.7 ± 0.04) were larger than the other three cryptic species. Cryptic species D (0.4 ± 0.08) showed a larger intrinsic rate of population increase than F (-0.3 ± 0.22). Under TC, the intrinsic rate of population increase ranged from -0.04 to 0.90 . The intrinsic rate of population increase of cryptic species E (-0.04 ± 0.17) and F (0.01 ± 0.09) were lower than that of cryptic species A (0.6 ± 0.02), C (0.7 ± 0.08), and D (0.9 ± 0.05) (between cryptic species A and E, $p= 0.05$). Cryptic species A had a lower intrinsic rate of population increase than cryptic species D ($p= 0.05$) (Table 3.4).

Table 3. 4. Generation time (T), net reproductive rate (R_0), intrinsic rate of population increase (r), age-specific survivorship and fecundity ($l_x m_x$), and life expectancy (e_x) for five cryptic species of *Euchlanis dilatata* (mean \pm SE). **tc:** 20°C, 180 μ S/cm, **tC:** 20°C, 1800 μ S/cm, **Tc:** 27°C, 180 μ S/cm, and **TC:** 27°C, 1800 μ S/cm.

Cryptic species	Parameter mean \pm SE	tc	tC	Tc	TC
A	T	5.1 \pm 0.30	3.9 \pm 0.75	3.1 \pm 0.18	2.9 \pm 0.18
	R_0	5.0 \pm 0.34	3.8 \pm 1.53	9.4 \pm 1.04	6.0 \pm 0.92
	r	0.3 \pm 0.01	0.2 \pm 0.11	0.7 \pm 0.05	0.6 \pm 0.02
	$l_x m_x$	0.6 \pm 0.18	0.5 \pm 0.25	1.9 \pm 0.45	1.2 \pm 0.27
	e_x	2.1 \pm 0.41	1.7 \pm 0.41	1.6 \pm 0.18	1.1 \pm 0.18
C	T	5.6 \pm 0.14	5.4 \pm 0.23	2.2 \pm 0.09	3.3 \pm 0.22
	R_0	3.7 \pm 0.39	3.7 \pm 0.78	5.2 \pm 0.73	9.7 \pm 2.08
	r	0.2 \pm 0.01	0.2 \pm 0.03	0.7 \pm 0.04	0.7 \pm 0.08
	$l_x m_x$	0.4 \pm 0.09	0.4 \pm 0.12	0.9 \pm 0.16	1.6 \pm 0.43
	e_x	2.3 \pm 0.22	2.3 \pm 0.48	1.3 \pm 0.22	1.5 \pm 0.27
D	T	4.8 \pm 0.15	4.6 \pm 0.17	2.7 \pm 0.19	2.7 \pm 0.09
	R_0	9.2 \pm 1.54	10.9 \pm 0.96	3.1 \pm 0.60	11.6 \pm 1.78
	r	0.4 \pm 0.02	0.5 \pm 0.03	0.8 \pm 0.08	0.9 \pm 0.05
	$l_x m_x$	1.3 \pm 0.31	1.4 \pm 0.34	0.8 \pm 0.29	2.3 \pm 0.48
	e_x	2.3 \pm 0.14	2.1 \pm 0.15	1.0 \pm 0.13	1.0 \pm 0.10
E	T	5.6 \pm 0.23	5.4 \pm 0.06	3.2 \pm 0.17	3.1 \pm 0.06
	R_0	6.3 \pm 0.68	4.4 \pm 0.80	3.2 \pm 0.61	1.2 \pm 0.43
	r	0.3 \pm 0.01	0.2 \pm 0.04	0.3 \pm 0.05	-0.04 \pm 0.17
	$l_x m_x$	0.6 \pm 0.16	0.5 \pm 0.13	0.6 \pm 0.22	0.3 \pm 0.12
	e_x	2.4 \pm 0.36	2.3 \pm 0.21	1.5 \pm 0.18	1.0 \pm 0.13
F	T	4.8 \pm 0.29	3.3 \pm 0.88	2.7 \pm 0.15	2.9 \pm 0.34
	R_0	1.0 \pm 0.17	0.5 \pm 0.15	0.7 \pm 0.25	1.3 \pm 0.40
	r	-0.02 \pm 0.04	-0.3 \pm 0.15	-0.3 \pm 0.22	0.01 \pm 0.09
	$l_x m_x$	0.1 \pm 0.07	0.1 \pm 0.06	0.2 \pm 0.08	0.2 \pm 0.09
	e_x	1.4 \pm 0.37	1.4 \pm 0.15	0.8 \pm 0.07	1.1 \pm 0.17

DISCUSSION

Euchlanis dilatata is a species complex, with at least seven cryptic species (see Chapter

1). In this study, I observed reproductive isolation among six, and ecological differentiation

among five of these cryptic species. Moreover, one of the cryptic species (cryptic species A) showed morphological differences in trophi shape and size with the rest of cryptic species.

Reproductive isolation can be mediated through pre-mating and/or post-mating reproductive barriers. Reproductive isolation has been examined among cryptic species of many microinvertebrates. For example, F2 hybrids between two lineages of *Eurytemora affinis* (Poppe, 1880) were not viable in a study by Lee (2000). There was reproductive isolation among populations of *Acanthocyclops vernalis* Fischer A., 1853 (Dodson et al., 2003) from North America. In some studies, reproductive isolation among cryptic species is implied based on molecular data (e.g., allozyme analyses for amphipods in the genus *Hyaella*: Wellborn & Cothran (2004); genetic variation in 16S rRNA gene sequences for three cryptic species of the isopod *Acanthaspidia drygalskii* Vanhöffen, 1914: Raupach & Wägele, 2006).

In rotifers, pre-mating barriers include differentiation in timing and cues of shifting from asexual to sexual reproduction (e.g., *E. hawaiiensis* and *E. chihuahuaensis*: Schröder & Walsh, 2010), and failure in recognizing individuals of other species as potential mates (e.g., *B. plicatilis* species complex: Kotani et al., 1997; Gribble & Mark Welch, 2012). Post-mating barriers are categorized as the lack of resting eggs production after copulation, production of unviable resting eggs, and/or female mortality after copulation (e.g., *E. ukera* and *E. chihuahuaensis*: Schröder & Walsh, 2007) and unviable and/or sterile F1 females (e.g., *B. plicatilis* species complex: Suatoni et al., 2006). In this study, resting eggs were not produced in cross mating trials between cryptic species with one exception. A single resting egg was produced in a mating between a female of cryptic species E and a male of cryptic species F, despite high genetic differentiation between them based on both markers. I did not determine whether this resting egg could hatch into a viable F1 hybrid. Therefore, considering the high genetic variation between species E and F, I

cannot be certain whether gene flow between these two species occurs. On the other hand, cryptic species A and B were reproductively isolated based on my results. The genetic distance between cryptic species A and B in the ITS region was 1.2% and 11.1% in the COI gene. It is possible that when there is no or limited gene flow between cryptic species of *E. dilatata*, the COI gene accumulates genetic variation at a higher rate compared to the ITS region. This could be caused by faster rate of evolution for COI gene compared to the ITS region as addressed by Cruickshank (2002) and Vilas et al., (2005). The lower variability of ITS region compared to COI gene has been suggested as a reason for discordance between these two markers for multiple rotifer species complexes by Obertegger et al. (2018). Although based on Chi-Square tests, the inter-clonal mating success rates within cryptic species were lower than the positive controls (intra-clonal mating experiments) ($p < 0.001$), I observed successful trials for all the within cryptic species cross-mating experiments (1.25-17.9%). These findings suggest that there is gene flow within cryptic species although it was at a smaller rate compared to positive controls. However, I used the production of resting eggs as an indicator of successful mating without specifically determining the role of pre- and post-mating reproductive barriers in reproductive isolation. To fully understand the mechanisms of reproductive isolation among cryptic species of *E. dilatata*, I recommend studying variation in the ploidy number, mixis induction, differentiation in mating behaviors, and the viability of hybrids among cryptic species of *E. dilatata*.

True cryptic species are not easily distinguishable based on morphology (Bickford et al., 2007). However, there are several findings of morphological variation among cryptic species of rotifers (see Fu et al., 1991; Ciroso-Pérez et al., 2001; Campillo et al., 2005; Anitha & George, 2006; Hwang et al., 2013; Michaloudi et al., 2016 for *B. plicatilis*; Schröder & Walsh, 2007 for

the *Epiphanes senta* (Müller, 1773); Fontaneto et al., 2007 for *Rotaria magnacalcarata* (Parsons, 1892)). The term pseudocryptic species refers to cryptic species that show morphological variation after more comprehensive morphological examinations (Knowlton, 1993). Here, I examined trophi morphology of *E. dilatata* populations. Based on trophi size, in general only 64% of individuals were assigned correctly to cryptic species. Individuals of cryptic species A had the highest rate of accurate assignment to their cryptic species (83%). In addition to variation in trophi size for cryptic species A, I observed a projection on the left ramus of trophi that was specific to this cryptic species. A population of *E. dilatata* collected in Italy had a projection similar to what I found for cryptic species A. Molecular analyses are necessary to determine whether that population can be assigned to cryptic species A. Based on my results, at least six cryptic species of *E. dilatata* cannot be distinguished based on trophi morphology. Lack of robust morphological variation in trophi among these cryptic species could be considered a case of morphological stasis despite high genetic variation. Yet, differentiation in body size that was related to the ploidy level has been reported within *E. dilatata* populations (Walsh & Zhang, 1992). Therefore, there could be variation in body size among cryptic species as well which remains to be investigated.

Life history parameters of rotifers can be affected by various factors (Table 3.5). In this study, the temperature had a significant effect on age-specific survivorship (l_x), fecundity (m_x), and life expectancy (e_x). Water conductivity was only correlated with variation in life expectancy. As poikilotherm, rotifers are known to exhibit a positive correlation between development rates and temperature, while life expectancy tends to be negatively correlated with temperature (e.g., Pavón-Meza et al. (2005); Saucedo-Ríos et al. (2017); Ogello et al. (2016)). For instance, Pavón-Meza et al. (2005) recorded lower life expectancy and generation time, and

higher net reproductive rate and population growth at a temperature 25 °C as compared to 15 °C for *B. havanaensis*. *Lecane papuana* (Murray, 1913), *L. bulla* (Gosse, 1851) and *L. cornuta* (Müller, 1786) showed an increase in life expectancy with the decrease of temperature (Saucedo-Ríos et al., 2017). Ogello et al. (2016) observed a longer life expectancy at lower temperature for a Kenyan strain of the rotifer *Brachionus angularis* Gosse, 1851. In my study, cryptic species of *E. dilatata* had higher age-specific survivorship and fecundity, and lower life expectancy at a temperature 27 °C as compared to 20 °C.

Table 3. 5. Example of studies on life table characteristics of rotifers in response to a variety of environmental factors.

Environmental variable	Reference(s)
Water temperature	Stelzer, 2002; Derry et al., 2003; Xiang et al., 2010; Wang et al., 2014; Gabaldón et al., 2015
Salinity	Derry et al., 2003; Malekzadeh-Viayeh et al., 2014; Wang et al., 2014; Gabaldón et al., 2015
Food density and/or food type	Kirk, 1997; Sarma et al., 2001, 2007; Li et al., 2010; Malekzadeh Viayeh et al., 2010; Espinosa-Rodríguez et al., 2012; Farhadian et al., 2013; Pan et al., 2016; Gorokhova, 2017
Competition	Espinosa-Rodríguez et al., 2012
Predation	Santos Medrano et al., 2016
Being hatched from resting versus subitaneous eggs	Gilbert, 2004
Caloric restriction	Gribble & Mark Welch, 2013
Mercury concentration	Ramírez-Pérez et al., 2004; Pan et al., 2016
Methyl parathion concentration	Sarma et al., 2001

I observed variation in life table parameters among five examined cryptic species. For example, cryptic species D had the highest rate of age-specific survivorship and fecundity under all experiment conditions except Tc, and species F had the lowest values under all experiment conditions. For life expectancy, cryptic species A had the highest value under Tc, and cryptic species C had the highest value under TC. Species F had the lowest life expectancy under all experiments except for TC. I observed the highest generation time for all cryptic species under

tc. With an increase of temperature, the generation time for all species decreased. Generation time decreases under high temperatures for poikilotherms (Gillooly, 2000) including rotifers (e.g., Galkovskaja, 1987; Pavón-Meza et al., 2005; Xiang et al., 2010; Wang et al., 2014). The generation time for species A and E was lower under TC. For cryptic species C, D, and F, generation time was the lowest under Tc. As I observed in my study, intrinsic rate of population growth is higher when temperature increases (e.g., Fernández-Araiza et al., 2005; Yin & Zhao, 2008; Wang et al., 2014). I also noted all cryptic species had higher net reproductive rates and intrinsic rates of population increase under temperature 27°C. For example, cryptic species A, had the highest net reproduction rate and intrinsic rate of population increase under Tc. For cryptic species D and F, the highest net reproduction rate and intrinsic rate of population increase were under TC. Cryptic species C had its highest net reproduction rate under Tc and the highest intrinsic rate of population increase under TC. The exception was cryptic species E with a higher net reproductive rate under tc. Yet, it showed the highest intrinsic rate of population increase under Tc. For most species, an increase in temperature caused a decrease in generation time and an increase in reproduction rate and population growth. In this study, under high temperatures, cryptic species showed variation in generation time, reproduction rate and population growth in response to water conductivity. Because I used NaCl to increase the conductivity of MBL to 1,800 $\mu\text{S}/\text{cm}^2$, conductivity in my experiments represents salinity. The variation in life history parameters in response to environmental conditions may stem from genetic variation as noted for net reproductive rate of *B. calyciflorus* cryptic species by Wang et al. (2014). Differential response to water salinity among cryptic species of rotifers has been addressed. *Brachionus plicatilis* had higher reproduction rate compared to *B. manjavacas* in lower salinities (Gabaldón et al., 2015). Malekzadeh Viayeh et al. (2010) recorded variation in response to salinity in

intrinsic rate of population growth among six lineages of *B. plicatilis* from Iran. On the other hand, Leasi et al. (2013) did not find variation in the occurrence of cryptic species of *Testudinella clypeata* in relation to salinity.

Life history characteristics of *E. dilatata* has been studied, for instance in response to competition and/or food type (Espinosa-Rodríguez et al., 2012; Farhadian et al., 2013), combined effects of methyl parathion and food density (Sarma et al., 2001), cadmium, lead, mercury and methyl parathion concentration (Arias-Almeida & Rico-Martínez, 2011), and predation (Nandini et al., 2011). Moreover, Walsh & Zhang (1992) found that large morphotype of *E. dilatata* was triploid and had a longer maturity time compared to maturity time of the small diploid morphotype. Here, I provided evidence of variation in survivorship, reproduction rate and population growth in response to water temperature and conductivity among genetically distinct isolates. Kordbacheh et al. (2017) reported co-occurrence of cryptic species C and D in Laguna Prieta, Hueco Tanks State Park and Historic Site, El Paso Co., TX. Cryptic species C was hatched from rehydrated sediments and active population representing cryptic species D was collected in 2013. Those species may be temporally isolated which could have been resulted from the ecological differentiation between them. The sympatry of cryptic species of *B. plicatilis* with ecological variation was shown by Montero-Pau et al. (2011) and Wang et al. (2014). Furthermore, the observed variation in life history parameters highlights potential ecological niche differentiation among *E. dilatata* cryptic species. Niche differentiation can be a major contributor to the genetic divergence among *E. dilatata* cryptic species.

Several cryptic species of invertebrates have been described in previous studies based on diagnostic nucleotides (e.g., Brower, 2010; Johnson et al., 2015; Delić et al., 2017). Although I did not find morphological variation among cryptic species of *E. dilatata* (except for cryptic

species A), I documented reproductive isolation among six, and ecological differentiation among five cryptic species. Here, I described five cryptic species of *E. dilatata* using diagnostic nucleotides in the ITS region sequence following Jörger and Schrödl (2013) guidelines. To illuminate the mechanisms involved in speciation within *E. dilatata* and other rotifer species complexes, future studies can focus on specifying the pre- and post-mating reproductive barriers among cryptic species, for example the role of variation in ploidy level in reproductive isolation among cryptic species. To further study the ecological niche differentiation, other environmental variables such as food density and predation should be included in life table experiments of these cryptic species, and the genetic basis of variation in ecological adaptation among them should be explored. Integrating mating experiments to examine the strength of reproductive isolation, life table experiments to investigate ecological differentiation, and studying morphological and behavioral variation among cryptic species of rotifers and other microorganisms will provide support for species boundaries.

DESCRIPTION OF NEW SPECIES

Euchlanis dilatata (cryptic species “A”)

Neotype locality: Rio Grande, Sierra Co., NM, USA, 33.110039 °N, -107.297839 °W, 1288 m.

Diagnosis: This species is distinguished from other cryptic species of *Euchlanis dilatata* complex in the ITS region based on following character states with respect to other individuals of *E. dilatata* in this study: 156A; 350T. The morphological diagnostic feature is a small projection on the left ramus (Figure 3.2).

Neotype: An amictic female on a permanent microscopic slide, and approximately 30 amictic females preserved in 95% ethanol deposited in the rotifer collection of the Academy of Natural Sciences of Drexel University; Paratypes (one permanent microscopic slide of amictic females, and approximately 30 amictic females preserved in 95% ethanol) deposited in UTEP Biodiversity Collections (UTEP:Zoo:69). ITS region and COI gene sequences are deposited in GenBank (accession numbers, ITS: KU665929-45, COI: KU665853-69).

Etymology: A specimen from the population at Rio Grande, Sierra Co., NM, USA (cryptic species A) was designated as neotype for *Euchlanis dilatata* because this species had the widest geographic distribution compared to other cryptic species in this study. Moreover, the projection on the trophi that was observed in this species has been also recorded for a population collected in Italy (Parise, 1966).

Other examined populations: Alto Reservoir, Lincoln Co., NM, USA (33.395833 °N, -105.671944 °W), Bear Canyon Lake, Grant Co., NM, USA (32.8846 °N, -107.998033 °W), Chicken Creek Reservoir, Juab Co., UT, USA (39.49185 °N, -111.95760 °W), Lake Mendota, Dane Co., WI, USA (43.0789083 °N, -089.4192250 °W), Schmitthenner Lake, Wyoming Co., PA, USA (41.43738 °N, -76.24304 °W), Detroit Lake State Park, Marion Co., OR, USA (44.700211 °N, -122.183492 °W), Santaquin, Juab Co., UT, USA (39.955778 °N, -111.780283 °W), Presa de la Boquilla, Chihuahua, Mexico (27.5361333 °N, -105.4011333), Centinela, Imperial Co., CA, USA (33.987892 °N, -118.406403 °W), Lago Colina, Chihuahua, Mexico (27.5724 °N, -105.4004666 °W), Presa Chihuahua, Chihuahua, Mexico (28.5762166 °N, -106.1711833 °W), Rio Grande, Fabens, El Paso Co., TX, USA (31.430277 °N, -106.14222 °W), Madeleine Lake, Oneida Co., WI, USA (45.889733 °N, -89.643833 °W), Mescalero Lake, Otero Co., NM, USA (33.2984 °N, -105.6886 °W), Oknoname 085006 Reservoir, Love Co., OK, USA

(33.927583 °N, -97.301067 °W), Poza Azul, Coahuila, Mexico (26.986111 °N, -102.066389 °W), Shafter stream, Presidio Co., TX, USA (29.8143166 °N, -104.3071333 °W), Lake Travis, Travis Co., TX, USA (30.402417 °N, -97.947967 °W), Storrie Lake, San Miguel Co., NM, USA (35.6606694 °N, -105.2345833 °W), Panther Hollow Lake, Allegheny Co., PA, USA (40.436856 °N, -79.948825 °W), Silver Creek, Schuylkill Co., PA, USA (40.543206 °N, -75.304106 °W), Walter E. Long Lake, Travis Co., TX, USA (30.284417 °N, -97.608383 °W), Lake Okeechobee, Glades Co., FL, USA (26.830456 °N, -80.941303 °W).

Morphology: The morphology is typical of *E. dilatata* with no distinguishing feature. Body is oval. Lorica is truncated at the anterior and rounded at the posterior part. Cross-section of the lorica is arc of circle. Foot is slender, with two joints, toes are parallel-sided with sharp tip. Trophi has four stout unci teeth, with inner denticulate comb at the tip of rami. Fulcrum is club shaped. There is a projection on the left ramus.

Ecology and distribution: This species was mostly found in streams, permanent lakes and reservoirs from Texas, Wisconsin, Oregon, California, Pennsylvania, New Mexico, Florida and Mexico. The habitats pH ranged 7.7-9.0, temperature ranged 14.7- 27.7 °C and conductivity ranged 230-1638 µS/cm.

Euchlanis dilatata cryptic species “B”

Type locality: Fish Pond, Nockamixon State Park, Bucks Co., PA, USA, 40.472567 °N, -75.224823 °W, 131 m.

Diagnosis: This species is distinguished from other cryptic species of *Euchlanis dilatata* complex in the ITS region based on following character states with respect to other individuals of *E. dilatata* in this study: 309C; a deletion at 350.

Holotype: An amictic female on a permanent microscopic slide and approximately 30 amictic females preserved in 95% ethanol deposited in the rotifer collection of the Academy of Natural Sciences of Drexel University; Paratypes (one permanent microscopic slide of amictic females, and approximately 30 amictic females preserved in 95% ethanol) deposited in UTEP Biodiversity Collections (UTEP:Zoo:91). ITS region and COI gene sequences are deposited in GenBank (accession numbers, ITS: KX714930, COI: KX714920).

Etymology:

Other examined populations: American River, San Joaquin Co., CA, USA (38.57221207 °N, -121.3531190 °W), Echo Lake, El Dorado Co., CA, USA (38.834557 °N, -120.046143 °W), Lodi Lake, San Joaquin Co., CA, USA (38.147222 °N, -121.292723 °W), Timber Lake ditch, Mount Hood National Forest, Clackamas Co., OR, USA (45.083424 °N, -122.050234 °W).

Morphology: The morphology is typical of *E. dilatata* with no distinguishing feature. Body is oval. Lorica is truncated at the anterior and rounded at the posterior part. Cross-section of the lorica is arc of circle. Foot is slender, with two joints, toes are parallel-sided with sharp tip. Trophi has four stout unci teeth, with inner denticulate comb at the tip of rami. Fulcrum is club shaped.

Ecology and distribution: This species was found in ponds, lakes and streams from California, Pennsylvania and Oregon. The habitat pH was 6.7, temperature was 17.1 °C and conductivity was 104 µS/cm.

Euchlanis dilatata cryptic species “C”

Type locality: Rio Grande, El Paso Co., TX, USA, 31.784234 °N, -106.527845 °W, 1136 m.

Diagnosis: This species is distinguished from other cryptic species of *Euchlanis dilatata* complex in the ITS region based on following character states with respect to other individuals of *E. dilatata* in this study: 644C.

Holotype: An amictic female on a permanent microscopic slide, and approximately 30 amictic females preserved in 95% ethanol deposited in the rotifer collection of the Academy of Natural Sciences of Drexel University; Paratypes (one permanent microscopic slide of amictic females, and approximately 30 amictic females preserved in 95% ethanol) deposited in UTEP Biodiversity Collections (UTEP:Zoo:127). ITS region and COI gene sequences are deposited in GenBank (accession numbers, ITS: KU665946, COI: KU665851).

Etymology:

Other examined populations: Behind Mescalero Canyon playa, Hueco Tanks State Park and Historic Site, El Paso Co., TX, USA (31.9190694 °N, -106.0408305 °W), Corral Tank, Hudspeth Co., TX, USA (30.8237166 °N, -105.3155833 °W), Feather Lake Wildlife Sanctuary, El Paso Co., TX, USA (31.6890972 °N, -106.3052666 °W), Glenn Springs, pool 3, Brewster Co., TX, USA (29.1744166 °N, -103.1575 °W), Glenn Springs, pool 6, Brewster Co., TX, USA (29.1744166 °N, -103.1575 °W), Roadside Pond, Jefferson Co., TX, USA (29.834722 °N, -94.482222 °W), Lake Okeechobee, Glades Co., FL, USA (26.830456 °N, -80.941303 °W), Laguna Prieta, Hueco Tanks State Park and Historic Site, El Paso Co., TX, USA (31.9246388 °N, -106.046675 °W), Mesocosm, Hueco Tanks State Park and Historic Site, El Paso Co., TX, USA (31.9188166 °N, -106.040366 °W), Miller Ranch, Jeff Davis Co., TX, USA (30.623845 °N, -104.674005 °W), Sam Rayburn State Park, Sabine Co., TX, USA (31.061244 °N, -94.106127

°W), La Mesa Canyon Tule spring, Lower Canyons, Mexico (29.75111 °N, -102.58305 °W), Shorty Howell pond, Gwinnett Co., GA, USA (33.97455 °N, -84.14936 °W), Triangle Pond, Buenos Aires National Wildlife Refuge, Pima Co., AZ, USA (31.55 °N, -111.533889 °W), Palo Pinto Canyon stream, Presidio Co., TX, USA (30.0308666 °N, -104.4684333 °W).

Morphology: The morphology is typical of *E. dilatata* with no distinguishing feature. Body is oval. Lorica is truncated at the anterior and rounded at the posterior part. Cross-section of the lorica is arc of circle. Foot is slender, with two joints, toes are parallel-sided with sharp tip. Trophi has four stout unci teeth, with inner denticulate comb at the tip of rami. Fulcrum is club shaped.

Ecology and distribution: This species was found in a variety of habitats from temporary ponds and playas to permanent lakes from Texas, Florida, Arizona and Mexico. The habitats pH ranged 6.4-9.4, temperature ranged 7.0-33.6 °C and conductivity ranged 179-1110 µS/cm.

Euchlanis dilatata cryptic species “D”

Type locality: Former cattle tank, White Sands National Monument, Doña Ana Co., NM, USA, 32.67485 °N, -106.44345 °W, 1213 m.

Diagnosis: This species is distinguished from other cryptic species of *Euchlanis dilatata* complex in the ITS region based on following character states with respect to other individuals of *E. dilatata* in this study: 366A; 756T.

Holotype: An amictic female on a permanent microscopic slide and approximately 30 amictic females preserved in 95% ethanol deposited in the rotifer collection of the Academy of Natural Sciences of Drexel University; Paratypes (one permanent microscopic slide of amictic

females and approximately 30 amictic females preserved in 95% ethanol) deposited in UTEP Biodiversity Collections (UTEP:Zoo:24). ITS region and COI gene sequences are deposited in GenBank (accession numbers, ITS: KU665978, COI: KU665883).

Etymology:

Other examined populations: Alazan Bayou Wildlife Management Area, Nacogdoches Co., TX, USA (31.5033389 °N, -094.7546583 °W), Mescalero Canyon playa, Hueco Tanks State Park and Historic Site, El Paso Co., TX, USA (31.9188166 °N, -106.0403666 °W), Red Tank, Hudspeth Co., TX, USA (30.7303083 °N, -104.9891083 °W), Peccary Tank, Hudspeth Co., TX, USA (30.7555556 °N, -105.0041667 °W), Behind Ranch House playa, Hueco Tanks State Park and Historic Site, El Paso Co., TX, USA (31.924072 °N, -106.041589 °W), Laguna Prieta sediments, Hueco Tanks State Park and Historic Site, El Paso Co., TX, USA (31.9246388 °N, -106.046675 °W), Paint Gap Cattle Tank, Brewster Co., TX, USA (29.3878555 °N, -103.302675 °W), Ojo de Santa Maria, Chihuahua, Mexico (31.1552777 °N, -107.3172222 °W).

Morphology: The morphology is typical of *E. dilatata* with no distinguishing feature. Body is oval. Lorica is truncated at the anterior and rounded at the posterior part. Cross-section of the lorica is arc of circle. Foot is slender, with two joints, toes are parallel-sided with sharp tip. Trophi has four stout unci teeth, with inner denticulate comb at the tip of rami. Fulcrum is club shaped.

Ecology and distribution: This species was found in various habitats including artificial temporary tanks, temporary playas in Texas and Mexico. The habitats pH ranged 8.4-9.3, temperature ranged 23.6-34.3 °C and conductivity ranged 137-988 µS/cm.

Euchlanis dilatata cryptic species “F”

Type locality: Krome pond, Miami-Dade Co., FL, USA, 25.883615 °N, -80.484920 °W, 3.3 m.

Diagnosis: This species is distinguished from other cryptic species of *Euchlanis dilatata* complex in the ITS region based on following character states that are specific to cryptic species “F” with respect to other individuals of *E. dilatata* in this study: 29T; 54T; 55T; 92C; 180C; 186G; 189G; 232T; 233C; 259A; 260C; 264T; 277T; 278G; 288A; 307G; 312T; 314A; 344C; 369T; 657G; 693G; 70A; 702A; 708G; 756C.

Holotype: An amictic female on a permanent microscopic slide, and approximately 30 amictic females preserved in 95% ethanol deposited in the rotifer collection of the Academy of Natural Sciences of Drexel University; Paratypes (one permanent microscopic slide of amictic females, and approximately 30 amictic females preserved in 95% ethanol) deposited in UTEP Biodiversity Collections (UTEP:Zoo:129). ITS region and COI gene sequences are deposited in GenBank (accession numbers, ITS: KU665985 and KX714931, COI: KU665896 and KX714921).

Etymology:

Other examined populations: Buttrill Springs, Brewster Co., TX, USA (29.54585 °N, -103.2738 °W), Cattail Falls, pool C', Brewster Co., TX, USA (29.2731833 °N, -103.3361638 °W), Cattail Falls, pool D, Brewster Co., TX, USA (29.2731527 °N, -103.3358277 °W), Cattail Falls, pool E, Brewster Co., TX, USA (29.2731444 °N, -103.3361638 °W), Cattail Falls, pool G, Brewster Co., TX, USA (29.2731666 °N, -103.3361638 °W), Cattail Falls, pool H, Brewster Co., TX, USA (29.2731694 °N, -103.3362388 °W), Duck Pond, Beaver Co., OK, USA (35.551944 °N, -97.574722 °W), Lake June in the Winter, Highlands Co., FL, USA (27.30715 °N, -81.37542 °W), Lake Jackson, Highlands Co., FL, USA (27.48775 °N, -81.47664 °W).

Morphology: The morphology is typical of *E. dilatata* with no distinguishing feature. Body is oval. Lorica is truncated at the anterior and rounded at the posterior part. Cross-section of the lorica is arc of circle. Foot is slender, with two joints, toes are parallel-sided with sharp tip. Trophi has four stout unci teeth, with inner denticulate comb at the tip of rami. Fulcrum is club shaped (Figure 3.2).

Ecology and distribution: This species was found in a variety of habitats that includes ponds, permanent lakes and natural springs in Texas, Florida and Oklahoma. The habitats pH ranged 5.9-7.9, temperature ranged 7.5-22.6 °C and conductivity ranged 405-523 $\mu\text{S}/\text{cm}$.

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Chapter 4: Detecting adaptive genetic variation in cryptic species of *Euchlanis dilatata* using a next generation sequencing approach

ABSTRACT

Despite the importance of ecological adaptation in promoting speciation, little is known about the molecular basis of adaptive traits. This is especially true for cryptic species. Molecular methods used to detect cryptic species are generally based on neutral markers. Thus, they lack the resolution to reveal whether there is variation in the genomic coding regions with adaptive functions among cryptic species. I hypothesized that there is differentiation between two cryptic species of the rotifer *Euchlanis dilatata* (species “C” and species “D”) in genetic regions that play role in adaptation. I used ddRAD-Seq for single nucleotide polymorphisms discovery and to find loci that were candidate for selection in two cryptic species. Those cryptic species were delimited based on ITS region sequences. I obtained 107 loci with SNPs from four populations representing species C and three populations from species D. F_{ST} values ranged from 0-0.95 indicating there was high genetic differentiation between them. There was high genetic variation among populations from different cryptic species. However, F_{ST} value between Cattle Tank, NM (cryptic species D) and Triangle Pond, AZ (cryptic species C) was 0. Lack of genetic variation between these two populations could be caused by high level of admixture, or low resolution of obtained loci in showing genetic divergence among populations. Population structure analysis grouped populations into two clusters (STRUCTURE, $\Delta K[2]$: 2874) that corresponded to the two cryptic species. Discriminant Analysis of Principal Components identified seven groups, each representing one of the studied populations. My results provided evidence that genetic variation within and between cryptic species of *E. dilatata* may be related to their habitat features. To identify the genomic regions that are under selection and are important in ecological adaptation, further studies should include higher number of samples and use methods that target coding regions of genome.

INTRODUCTION

Different genotypes within the distribution range of a species may show niche differentiation (Peterson & Holt, 2003). Niche differentiation and local adaptation can be major drivers of speciation (Wu, 2001; Presgraves et al., 2003) through divergent selection. Divergent selection on populations in ecologically different environments can lead to genetic differentiation and consequent reproductive isolation (Funk, 1998; Schluter, 2001). The role of divergent selection in reproductive isolation has been shown in the mimetic butterflies *Heliconius melpomene* (Linnaeus, 1758) and *H. cydno* (Doubleday, 1847) (Jiggins, 2008), the threespine stickleback *Gasterosteus aculeatus williamsoni* Girard, 1854 (Rundle & Schluter, 2012) and the apple maggot fly *Rhagoletis pomonella* (Walsh, 1867) (Powell et al., 2014).

Niche differentiation reinforcing reproductive isolation has been documented in cryptic species as well. For instance, Funk (1998) studied two cryptic species of the herbivorous beetle *Neochlamisus bebbianae* (Brown, 1943) that showed host associated ecological and physiological isolation. He suggested divergent selection on different host populations resulted in adaptive and reproductive isolation, and eventual ecological speciation. In another study, temporal isolation was suggested as the driving factor of speciation for two sympatric cryptic species the bee mites *Chaetodactylus lithurgi* Klimov & OConnor, 2004 and *C. abditus* (Klimov & OConnor, 2004). In a study by Rissler & Apodaca (2007), four genetically differentiated lineages of the Black Salamander *Aneides flavipunctatus* (Strauch, 1870) were found. Using environmental niche modeling, the authors showed that each lineage had unique environmental requirements. Goetze et al. (2016) showed that there are ecological dispersal barriers among populations of the copepod *Pleuromamma xiphias* (Giesbrecht, 1889). In another study, there was variation in mating behaviors between two lineages of the copepod

Acanthodiptomus denticornis (Wierzejski, 1887) because of their difference in adaptation to the presence of a predator (Sereda et al., 2016). Based on all of these findings, differentiation through ecological adaptation is probably common among cryptic species. Thus examining ecological niche variation will assist in understanding speciation mechanisms for cryptic species.

Despite the importance of ecological adaptation in promoting speciation (Feder et al., 2012), little is known about the molecular basis of adaptive traits. This is especially true in cryptic species. Studying genetic variation that has adaptive significance can lead to the identification of genes responsible for evolutionary differences among species (Wagner, 2007; Olson-Manning et al., 2012), and can help to elucidate the molecular basis of ecological adaptations (Watt et al., 1983; Bailey & Bataillon, 2016). Cryptic species can be distinguished through molecular studies based on the levels of genetic differentiation among them (Bickford et al., 2007; Fontaneto et al., 2015). However, molecular methods used to delimit cryptic species are generally based on neutral markers. Thus, they lack variation in genes that play a role in ecological adaptation. To identify genetic divergence that can be adaptive, signals of selection need to be examined (Williamson et al., 2014).

With the advent of next generation sequencing, population genetic measures can be examined across the entire genome enabling the identification of genomic regions that are differentiated among populations (Willing et al., 2012). All genomic loci are affected similarly by genetic drift. However, loci that are under selection may show different patterns of differentiation. Therefore, one of the methods for identifying candidate genes for selection is using single nucleotide polymorphisms (SNPs) and identifying the F_{ST} values deviating from neutral distribution (López et al., 2015). Restriction Site-Associated DNA sequencing (RAD-Seq) provide a useful tool for identifying large numbers of loci for SNPs discovery (Etter et al.,

2011; Andrews et al., 2016) without prior genomic information (Andrews et al., 2016). This sequencing method has been used to identify markers that can be used to investigate population structure, and to identify adaptive genetic differentiation in non-model organisms such as the fish *Gasterosteus aculeatus* (Hohenlohe et al., 2010), the European green crab *Carcinus maenas* (Linnaeus, 1758) (Jeffery et al., 2017) and the copepod *Centropages typicus* Krøyer, 1849 (Blanco-Bercial & Bucklin, 2016).

Rotifers, are a good model to study adaptive genetic variation, especially among cryptic species. There are many examples of cryptic species in this phylum (e.g., Gilbert & Walsh, 2005; Fontaneto et al., 2011; Leasi et al., 2013; Tang et al., 2014; Kimpel et al., 2015; Papakostas et al., 2016; Mill et al., 2017; Kordbacheh et al., 2017). Ecological differentiation has been addressed for some rotifer cryptic species. For example, variation in response to water temperature and salinity in the *Brachionus plicatilis* Müller, 1786 species complex (Gómez et al., 1995; Ortells et al., 2003; Montero-Pau et al., 2011), the correlation between phosphorous concentration and occurrence of cryptic species within *Synchaeta* spp. (Obertegger et al., 2012), the correlation between altitude, silica concentration, temperature, conductivity, lake depth and occurrence of *Polyarthra dolichoptera* Idelson, 1925 cryptic species (Obertegger et al., 2014), and variation in response to Chlorophyll-a in *B. calyciflorus* Pallas, 1766 (Michaloudi et al., 2016). However, those studies o used ecological differentiation to distinguish among cryptic species rather than investigating potential roles of ecological speciation leading to cryptic species.

As discussed in Chapter 1, I found high genetic differentiation in two markers (the cytochrome *c* oxidase subunit I (COI) gene and the internal transcribed spacer region of nuclear ribosomal complex (ITS)) among 62 populations of the rotifer *Euchlanis dilatata* Ehrenberg, 1830 occurring in the United States and Mexico. Those populations were classified into seven

putative cryptic species based on ITS region sequences. Although the COI gene and ITS region had the resolution to distinguish among cryptic species of *E. dilatata*, they lack the resolution to reveal genetic variation in loci that are under selection because they are neutral markers. I hypothesize that there is genetic differentiation among these cryptic species in genomic regions that are under selection. I used double-digest RAD sequencing (ddRAD-Seq) for SNP discovery for a) analyzing population structure within *E. dilatata*, and b) detecting loci that are potentially under selection and could be important for ecological adaptation in *E. dilatata*.

METHODS

DNA extraction

I cultured 110 clonal lineages from seven populations representing two cryptic species from the *Euchlanis dilatata* species complex (57 individuals/four populations from cryptic species C, 53 individuals/three populations from cryptic species D, Table 4.1). Each clonal lineage was initiated from one asexual female. Asexual females that were used to start the clonal lineages were either obtained from field collections of active populations or were hatched from resting eggs collected from sediments that were stored in the laboratory for 1-8 years. Clonal lineages were cultured in modified MBL medium (Stemberger, 1981) and were fed the algae *Chlorella vulgaris* Berijerinck, 1890 (Culture Collection of Algae at the University of Texas at Austin [UTEX] strain 30) and *Chlamydomonas reinhardtii* Dangeard, 1888 (UTEX strain 90). From each clonal lineage, approximately 100 asexual females were isolated without food 12-18 hrs prior to DNA extraction. DNA was extracted using 16 µl Chelex[®]-100 and 1µl proteinase K solution (20 mg/ml) incubating at 65 °C for 40 min followed by 95 °C for 10 min. Because single extractions did not yield sufficient DNA (at least 40 ng), I extracted DNA 2-3 times separately for each clonal lineage and combined the products. DNA samples were stored at -80 °C until

sequenced. DNA was measured using a Qubit dsDNA Assay Kit (Invitrogen™, Carlsbad, CA) at the BBRC Genomic Analysis Core Facility at University of Texas at El Paso.

Table 4. 1. Collection sites of *Euchlanis dilatata* clonal lineages that were selected for ddRAD sequencing, GPS coordinates, and source of clonal lineages are shown. Number of examined clonal lineages for each population is indicated in parentheses.

Cryptic species	Populations	Source of clonal lineages	Collection date(s)	GPS coordinates (decimal degrees N/W)
C	Laguna Prieta, Hueco Tanks State Park and Historic Site, El Paso Co., TX (n=16)	Resting eggs	09.18.2015	31.9246388/ -106.046675
	Mescalero Canyon, Hueco Tanks State Park and Historic Site, El Paso Co., TX (n=16)	Active population	10.11.2015	31.9188166/ -106.0403666
	Miller Ranch, Jeff Davis Co., TX (n=14)	Active population	08.08.2017	30.623845/ - 104.674005
	Triangle Pond, Buenos Aires National Wildlife Refuge, Pima Co., AZ (n=11)	Active population	06.09.2017 & 08.18.2017	31.55/ -111.533889
D	Peccary Tank, Indio Mountains Research Station, Hudspeth Co., TX (n=18)	Resting eggs and active population	10.13.2012 & 05.28.2016	30.7555556/ -105.0041667
	Red Tank, Indio Mountains Research Station, Hudspeth Co., TX (n=18)	Resting eggs	10.11.2015 & 05.28.2016	30.7303083/ -104.9891083
	Cattle Tank, White Sands National Monument, Doña Ana Co., NM (n=17)	Resting eggs	04.16.2008	32.67485/ -106.44345

ddRAD sequencing and preprocessing of reads

A minimum of 40 ng DNA per clonal lineage was sent for ddRAD sequencing at the Environmental Genetics and Genomics (EnGGen) Lab at Northern Arizona University following Peterson et al. (2012) protocol and using the restriction enzymes MspI and EcoRI.

The sequences were demultiplexed using the command-line tool *fastq-multx* and were filtered using the command-line tool *fastq-mcf* (Aronesty, 2013) at EnGGen both available at <https://expressionanalysis.github.io/ea-utils>.

Upon obtaining ddRAD sequences, removal of sequences derived from the algal food or other contaminants (such as bacterial genes) was performed by using a set of known contaminant sequences obtained from NCBI (available at <https://www.ncbi.nlm.nih.gov>) and the program *kgrep* (<https://github.com/abremges/kgrep>) using Bioinformatics servers at University of Texas at El Paso. All reads were then trimmed to 70 bp using *fastx_trimmer* (http://hannonlab.cshl.edu/fastx_toolkit/).

SNP genotyping

Filtered and trimmed reads were analyzed in STACKS v 1.35 (Catchen et al., 2013) for the *de novo* assembly of sequence stacks. All sequences were processed in *ustacks*, which takes short-read sequences, aligns similar sequences into stacks, and merges stacks to form putative loci for SNP detection using a maximum-likelihood framework. The minimum depth of coverage for a stack (-m) was set at five, and the maximum distance allowed between stacks (-M) was set to four nucleotides. Then *cstacks* was used to construct a catalog of consensus loci based on stacks that were generated in *ustacks*. *sstacks* was used to compare genotypes against catalog of consensus loci. Using the *populations* script within STACKS, ddRAD-Seq loci with a single SNP present in at least 40% of the individuals from each population, and found in at least three populations, with minimum of 5X coverage per allele were obtained. Obtained loci were blasted against NCBI's nucleotide database using *blastn* tool, and bacterial and algal sequences (contaminants) that were not filtered using the program *kgrep* were identified. I used the *populations* script's *blacklist* option in STACKS to remove the contaminants (Supplemental

Table S4.1), and to extract the final set of loci. PGDSpider v 2.1.1.3 (Lischer & Excoffier, 2012) was used to convert the file formats for input into downstream analyses.

Population structure analyses

Population structure was analyzed using three methods. First, Discriminant Analysis of Principal Components (DAPC) and Bayesian clustering were implemented using the R package *adegenet* v 2.1.0. DAPC optimizes clustering to minimize within groups and maximize among groups genetic variation (Jombart et al., 2010). Genotypes used to run DAPC were based on SNP data and the *find.clusters* command was used to find the optimum number of clusters. Second, STRUCTURE v 2.3 (Pritchard et al., 2000) was used to assign individuals to genetic populations (K). STRUCTURE was run for 100,000 generations with an additional 10,000 generations burn-in, and 10 times iterations (replicates) using K = 1 to 8 under an admixture model. The likelihood of K values was visualized using the web-based program STRUCTURE HARVESTER (Earl & Vonholdt, 2012; available at <http://taylor0.biology.ucla.edu/structureHarvester>) and the model with highest value of ΔK was selected. Finally, Analysis of Molecular Variance (AMOVA) (Excoffier et al., 1992) was performed in GenoDive v 2.0b23 (Meirmans & Van Tienderen, 2004) using a stepwise model. GenoDive v 2.0b23 was run with 999 random permutations to test the significance of Wright's inbreeding coefficient (F_{ST}). The program GenoDive v 2.0b23 was also run with 999 permutations to measure genetic variation within populations based on observed heterozygosity (H_O), expected heterozygosity (H_e) and the coefficient of intrapopulation inbreeding (G_{IS}), and to examine genetic differentiation among populations based on pairwise F_{ST} (Wright, 1946).

Relationship between genetic and geographic distance

A geographic distance matrix was obtained using the Geographic Distance Matrix Generator v 1.2.3 (Ersts, 2006). Mantel tests were run in the R package *ecodist* v 1.2.9 (Goslee & Urban, 2007) with 50,000 permutations to investigate a) the relationship between genetic variation among populations (F_{ST}) and geographic distances (log transformed) (km) among them, and b) the relationship between log transformed F_{ST} values and log transformed genetic distances among populations.

RESULTS

Sequence analysis and SNP genotyping

I obtained 55,102,555 reads for 110 individuals. After removing 429,898 reads as algal (*Chlorella vulgaris* and *Chlamydomonas reinhardtii*) and bacterial contaminants through filtering, 546,726,57 reads were retained. The average number of stacks per individual with 5X coverage was 12,963. After merging the stacks, the final catalog had total of 521,572 loci. 107 loci with one SNP were present in at least 40% of individuals in each population and in at least three populations. Those 107 loci were included in downstream analyses. Only three out of 107 loci were present in at least 80% of individuals of each population. In addition, most of these loci were present in few individuals of populations. Therefore, because of low coverage of the obtained loci, I used them only for population structure analyses. Since loci obtained in my study were not found across high number of individuals and populations, they could not be efficient in investigating signals of selection.

Population structure analyses

Observed heterozygosity (H_o) ranged from 0.08-0.13 within cryptic species C and 0.02-0.14 within cryptic species D (Table 4.2). There was an excess of homozygous individuals in populations from Mescalero Canyon and Triangle Pond from cryptic species C (G_{is} : 0.01 and 0.69, respectively) and in the population from Red Tank (cryptic species D, G_{is} : 0.08) because the observed heterozygosity (H_o) was lower than expected (H_e). For the rest of populations, H_o was slightly higher than H_e . Pairwise F_{ST} value ranged from 0.38-0.68 within cryptic species C and 0.22-0.34 within cryptic species D. Between cryptic species, genetic variation ranged from 0 to 0.95 (Table 4.3, shown in bold). AMOVA showed high genetic differentiation in my study (F_{ST} = 0.11, p =0.001, Supplemental Table S4.2). Most of the observed variation was within populations (89%).

Table 4. 2. Mean observed heterozygosity (H_o), expected heterozygosity (H_e), and intrapopulation inbreeding coefficient (G_{is}) for seven population of *Euchlanis dilatata* representing two cryptic species.

Cryptic species	Population	H_o	H_e	G_{is}
C	Laguna Prieta, TX	0.10	0.10	-0.004
	Mescalero Canyon, TX	0.13	0.14	0.01
	Miller Ranch, TX	0.08	0.13	-0.05
	Triangle Pond, AZ	0.04	0.73	0.69
D	Cattle Tank, NM	0.14	0.12	-0.02
	Red Tank, TX	0.02	0.10	0.08
	Peccary Tank, TX	0.07	0.06	-0.01

Table 4. 3. Pairwise F_{ST} comparison (below diagonal) between populations of *Euchlanis dilatata* and their corresponding p values (above diagonal). Species C: Triangle Pond, AZ, Laguna Prieta, TX, Miller Ranch, TX, and Mescalero Canyon, TX. Species D: Red Tank, TX, Peccary Tank, TX, and Cattle Tank, NM. Values between cryptic species are shown in bold.

	Triangle Pond	Laguna Prieta	Miller Ranch	Mescalero Canyon	Red Tank	Peccary Tank	Cattle Tank
F_{ST}							
Triangle Pond	-	0.001	0.001	0.001	0.005	0.001	0.487

Laguna Prieta	0.68	-	0.001	0.001	0.001	0.001	0.001
Miller Ranch	0.63	0.58	-	0.001	0.433	0.015	0.466
Mescalero Canyon	0.66	0.47	0.38	-	0.001	0.001	0.001
Red Tank	0.36	0.47	0.01	0.49	-	0.021	0.001
Peccary Tank	0.95	0.86	0.90	0.10	0.33	-	0.001
Cattle Tank	0.00	0.82	0.01	0.66	0.34	0.22	-

In the DAPC analysis, the first two discriminant functions (the combination of alleles that were the most efficient in separating the clusters) explained 31% of the total variation among individuals. All three populations from cryptic species D were clustered together and were separated from populations representing cryptic species C (Figure 4.1). Cryptic species C was separated into two groups. One group consisted of populations from Laguna Prieta and Mescalero Canyon, both temporary habitats from the same vicinity in TX, and the other was comprised of populations from permanent habitats at Miller Ranch, TX and Triangle Pond, Buenos Aires National Wildlife Refuge, AZ (permanent habitats). K = 7 was the optimal number of clusters as identified by the BIC value (DAPC, K[7]= 373.5).

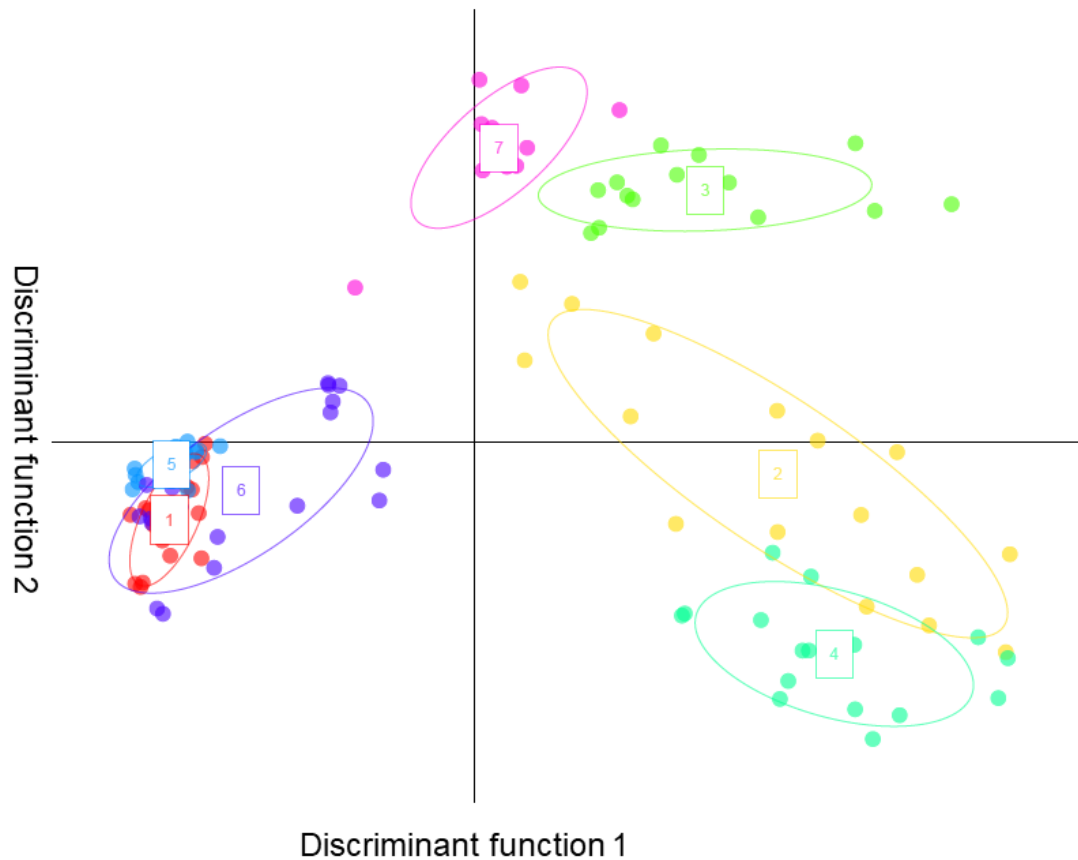


Figure 4.1. Discriminant Analysis of Principal Components (DAPC) of 110 clonal lineages of *Euchlanis dilatata* at 107 variable loci identified seven major groups representing the seven populations studied. Cryptic species C; 2: Mescalero Canyon, TX, 3: Miller Ranch, TX, 4: Laguna Prieta, TX, 7: Triangle Pond, AZ. Cryptic species D; 1: Cattle Tank, NM, 5: Peccary Tank, TX, 6: Red Tank, TX.

Based on STRUCTURE analyses, $K = 2$ was the best-supported model ($\Delta K = 2874$, Supplemental Table S4.3). Each genetic group represented one of the cryptic species (Figure 4.2). All populations had > 0.93 assignment probability for their individuals (showing some genetic admixture) except for Triangle Pond, AZ from species C which had a 0.68 assignment probability. The lower assignment probability for this population indicates higher genetic

admixture in this population compared to others populations. The STRUCTURE plots for K=1 to 8 are provided in Supplementary Figure S4.1

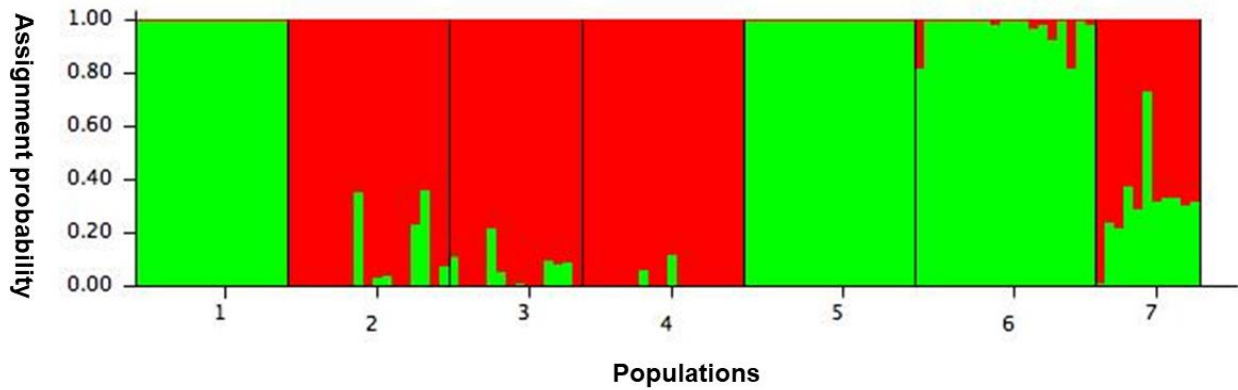


Figure 4.2. Population assignment probabilities of 110 *Euchlanis dilatata* clonal lineages estimated from 107 loci recovered from seven populations representing two cryptic species. K= 2 was the best-supported model ($\Delta K= 2874$, see Supplemental Table 4.3). Cryptic species C; 2: Mescalero Canyon, TX, 3: Miller Ranch, TX, 4: Laguna Prieta, TX, 7: Triangle Pond, AZ. Cryptic species D; 1: Cattle Tank, NM, 5: Peccary Tank, TX, 6: Red Tank, TX.

Relationship between genetic and geographic distance

There was no significant relationship between genetic distance (F_{ST}) at 107 loci and the geographic distance (log transformed) among populations (Mantel test: $r=0.06$, with 95% confidence interval of -0.17-0.27, $p=0.43$). Moreover, the log transformed (F_{ST}) values genetic variation among populations was not significantly correlated to log transformed geographic distance among them (Mantel test: $r= -0.7$, with 95% confidence interval of -0.23 to 0.22, $p=0.53$).

DISCUSSION

In this study I showed that there is genetic differentiation between cryptic species of *Euchlanis dilatata*. The genetic variation between these two cryptic species was previously

shown using sequences of the ITS region and COI gene (Chapter 1). The number and the coverage of obtained loci in my study is low compared to those found in other groups (e.g., 675 loci for the copepod *Centropages typicus* Krøyer 1849 (Blanco-Bercial & Bucklin, 2016) to thousands of loci, for instance in the threespine stickleback *Gasterosteus aculeatus* (Hohenlohe et al., 2010)). The number of loci recovered with RAD sequencing methods depends on the genome size and the number of restriction sites (Andrews et al., 2016). It has also been noted by Pante et al. (2015) that the number of loci decreases when genetically distant groups are compared. In my case, due to high genetic differentiation between cryptic species, some loci were present in one cryptic species and were missing from the other. In order to avoid including too many missing loci, I removed those that were present in less than three populations (the lowest number of populations examined for each cryptic species), which resulted in a decrease in the total number of loci for downstream analyses.

SNPs that are discovered through RAD sequencing generally have lower diversity because there are only four possible allelic states available, and they have low mutation rate (Reitzel et al., 2013). However, SNPs discovery using RAD sequencing provides high number of loci from across the genome. Those SNPs are powerful markers for studying population genetic structure (Andrews et al., 2016). *Euchlanis dilatata* cryptic species were delimited based on ITS region sequences (Chapter 1). Based on this marker, the genetic divergence between cryptic species C and D was 1.8 % and the intra-species genetic variation was less than 0.5%. Moreover, the genetic differentiation associated to habitat features within cryptic species C was not found based on ITS region. Despite the low number of loci obtained through RAD sequencing, I uncovered genetic differentiation among populations and within species. Genetic variation within cryptic species C was higher than that found in cryptic species D as seen in pairwise F_{ST}

values, Discriminant Analysis of Principal Components (DAPC), and STRUCTURE analyses. This may have resulted from variation in habitat features within populations of cryptic species C. Two of populations representing this species were collected from temporary ponds (Laguna Prieta and Mescalero Canyon, Hueco Tanks State Park and Historic Site, El Paso Co., TX), and the other two were collected from permanent ponds (Miller Ranch, Jeff Davis Co., TX and Triangle Pond, Pima Co., AZ). In DAPC, the populations from permanent habitats were grouped together, and they were distinct from the populations that were collected from temporary habitats. One possible explanation for the observed genetic similarity between populations from temporary habitats in species C is their geographic proximity (0.9 km apart). Nevertheless, populations from permanent habitats were the most distant populations in this study (662 km apart), and they were genetically the most similar based on DAPC. It should be noted that Laguna Prieta and Mescalero Canyon were as part of the ancient Lake Cabeza de Vaca during Pleistocene which could also explain their genetic relatedness. Three populations representing species D were collected from temporary, man-made tanks and they were clustered together in DAPC. In the STRUCTURE analyses, populations were classified into two genetic groups, each representing one cryptic species. These findings support the genetic differentiation between two cryptic species of *E. dilatata* that was found based on ITS region and COI gene sequences as described in Chapter 1.

Here, STRUCTURE analyses showed that there was probably genetic admixture between cryptic species D and the population from Triangle Pond, AZ (cryptic species C). Rotifers can disperse through their dormant stages (i.e., diapausing eggs, xerosomes; Dumont, 1983; Walsh et al., 2017) and thus maintain gene flow among populations. Dormant forms can be carried by the wind, animals, or water flows (Wallace et al., 2006). While wind is considered as an important

contributor to dispersal of microinvertebrates (Cáceres & Soluk, 2002; Nkem et al., 2006; Rivas et al., 2018), some studies have shown the significance of bird-mediated dispersal as well (e.g., Green & Figuerola, 2005; Frisch et al., 2007). More extensive sampling and analyses are required to study temporal and spatial patterns of gene flow and its underlying mechanisms within and among cryptic species of *E. dilatata*. Based on my results, habitat features could be more important in explaining the genetic variation among populations and between species of *Euchlanis dilatata* than geographic isolation. The weak effect of geographical isolation on genetic variation among populations of rotifers is not unprecedented (e.g., Fontaneto et al., 2008; Xiang et al., 2011; Kimpel et al., 2015; Kordbacheh et al., 2017). The weak signals of geographical isolation may stem from high genetic variation among populations that are geographically close to each other. Moreover, as it was observed in this study, populations that were geographically distant can be genetically similar. On the other hand, ecological adaptation and niche differentiation can promote speciation (Van Valen, 1976). Ecological differentiation has been found in many rotifer cryptic species. For example, there was variation in response to salinity and temperature among *Brachionus plicatilis*, *B. manjavacas* Fontaneto, Giordani, Melone & Serra, 2007 and *B. ibericus* Ciro-Pérez, Gómez & Serra, 2001 (Gomez et al., 1995). Ortells et al. (2003) showed that there was a positive correlation between co-existence of five cryptic species of the *B. plicatilis* complex with pH and dissolved oxygen levels in coastal Mediterranean ponds. Growth rate in response to salinity has been found to vary between coexisting *B. plicatilis* and *B. manjavacas* (Montero-Pau et al., 2011), and density variation of two cryptic species of *B. calyciflorus* was related to Chlorophyll-a concentration (Wen et al., 2016). Example of additional studies that have examined the relationship between ecological variation and speciation in rotifer species complexes can be found in a detailed review by

Gabaldón et al. (2017). Ecological divergence has been reported for some other invertebrates such as two cryptic species of *Acartia tonsa* Dana, 1849 (Chen & Hare, 2008b), the damselfly *Coenagrion scitulum* (Rambur, 1842) (Swaegers et al., 2015), and the copepod *Leptodiaptomus sicilis* (Forbes 1886) (Barrera-Moreno et al., 2015). Moreover, the importance of ecological niche differentiation in restricting gene flow, promoting spatial and/or temporal divergence and speciation has been hypothesized by King (1972) for *E. dilatata* and Gómez et al. (1997) for *B. plicatilis*. Based on my results, I hypothesize that ecological adaptation has been a major force shaping genetic structure of *E. dilatata* cryptic species.

I analyzed a small portion of the genome (~ 10,000 nucleotides covering about 0.007% of the genome, assuming a genome size of 143 Mbp, unpublished data by P. Brown). A few hundred loci can be useful for studying population structures but identifying signals of selection requires a larger dataset (Andrews et al., 2016). Because of the high levels of genetic variation among *E. dilatata* cryptic species and small sample size, I obtained relatively few loci that were shared between cryptic species C and D. Therefore, my sample size was not large enough to capture strong signals of selection, and particularly diversifying selection on adaptive genomic regions.

Despite the low number of loci, my study is significant because to my knowledge this is the first attempt to ddRAD sequencing to investigate population genetic structure of rotifers. However, the patterns of genetic variation observed here may not represent the genetic structure of *E. dilatata* cryptic species because 1) my sample size was small both in terms of number of populations and number of individuals (especially for the population from Triangle Pond), and 2) most of loci had low coverage and were found only in a small portion of my samples. Therefore, these results should be considered with caution. For further studies, I suggest to include more

populations from each cryptic species, and to use sequencing methods that focus on coding regions of the genome such as exome capture and transcriptome sequencing for ecologically differentiated cryptic species. These methods are more likely to target loci that are responsible for functional adaptive variation (Lowry et al., 2017).

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Chapter 5: General Discussion

One of the taxonomic challenges is how to classify organisms and delineate species (Padial et al., 2010). Aristotle was the first, in western societies, to classify all living things in his book *Historia Animalium* based on the presence or absence of certain features, such as blood. Other Greek philosophers, including Theophrastus, Plinius and Dioscrides, contributed to the classification and naming of several plant species based on growth form, morphology and medical properties. With the advent of microscopes at the end of 16th century, it was possible to study morphological characters more closely, and taxonomic work developed enough to replace ancient Greek studies. During this period, Caesalpino, who is also known as the first taxonomist, wrote *De Plantis* regarding 1,500 plant species based on their growth, seed and fruit form. Although in the 17th century English naturalist, John Ray, managed to establish species as the fundamental unit of taxonomy, the 18th century is considered the starting point of modern taxonomy, since Carl Linnaeus introduced a binary system for naming species in his books, *Plantarum* and *Systema Naturae*. He also provided a classification framework for living organisms from kingdom to species level (Manktelow, 2010) and delimited species based on vegetative characteristics. In the 19th century, George Bentham considered species as a group of individuals that are similar because they have a common ancestor. He also stated that the common ancestor cannot be found through direct proof; species can be delimited based on inductive evidence. Moreover, Bentham believed that hierarchical classification is arbitrary and cannot be reliable to delimit groups in nature (Stevens, 2002).

Portions of contemporary taxonomy are still based on Linnaeus' framework. Nevertheless, Linnaeus' approach was challenged by some peers including de Buffon, Adanson, de Jussieu, and de Lamarck (Maguire, 2011). For example, de Lamarck believed that

classification above species level is arbitrary. The term “phylogeny” was first introduced by Haeckel who described it as categorizing organisms based on the presence/absence of similar morphological characteristics (Dayrat, 2003). In the 20th century, phenetics, which is a classification system based on characteristics similarities and differences regardless of their evolution, was favored by most taxonomists (Maguire, 2011). In phenetics, all characters are weighted equally (Sokal, 1963) and are used to show the quantitative measure of differentiation among various taxa including species (Sneath & Sokal, 1963). Mayr (1965) criticized this classification method because it does not incorporate evolutionary history of organisms and variation in evolutionary rate of characters. Therefore, equal weighting of characters would be misleading. Hennig (1965) introduced a new classification method called cladistics (or phylogenetic systematics), which was an objective method for the classification of organisms. Cladistics only takes synapomorphies into consideration for classifying organisms and showing their phylogenetic relationship in the form of a phylogenetic tree. In cladistics morphology, anatomy, chromosomes, biochemistry and proteins can be used as characters, but for a long time morphological features, behavior and geographical location were the only available data (Cook et al., 2010).

Species are independently evolving lineages (De Queiroz, 2007) and may be distinguished using various criteria such as reproductive isolation among them (Mayr, 1942), adaptive variation (Simpson, 1961), differences in evolutionary tendencies and roles (Simpson, 1961) and differentiation in their genetic traits (Avice & Ball, 1990). Patterns of variations among species are diverse and they cannot be explained by one species concept (Donoghue, 1985). There are more than 20 species concepts (Mayden, 1997). Some of these concepts are briefly discussed below. Recognition Species Concept (RSC) is similar to the Biological Species

Concept (BSC, see introduction) and states species are populations of biparental individuals sharing the same breeding system (Paterson, 1985). Similar to BSC, RSC does not include asexual taxa. Moreover, it does not include a lineage component (Mayden, 1997). On the other hand, Evolutionary Species Concept (ESC) considers species as a lineage including ancestral to descendant sequence of populations that are evolving independently from other lineages and have common evolutionary fate (Simpson, 1961). According to Mayden (1997), ESC is the only concept that encompasses the biological diversity because unlike BSC and RSC it can be used to delimit asexual species, and species that are formed through hybridization. But Templeton (1989) argued that deciding the amount of diversity allowed in the evolutionary fate to be still considered common among individuals is subjective. Phylogenetic Species Concepts (PSC) consider species as the smallest distinguishable and monophyletic biological groups (Cracraft, 1983; Nixon & Wheeler, 1990). Donoghue (1985) discussed that PSC should be used as an alternative to Biological Species Concepts, because inbreeding groups are not always monophyletic; they cannot be considered species. However, Wheeler & Meier (2000) discussed that PSC is not reliable for species delimitation within asexual organisms because they can be diagnosable based on plesiomorphic characters and may make nonmonophyletic groups. Templeton (1989) suggested Cohesion Species Concept (CSC) based on strength of biological, evolutionary and recognition species concepts. Cohesion Species Concept groups evolutionary lineages as species if they are inbreeding and show genetic and ecological interchangeability because of cohesion mechanisms. This concept can be used for asexual organisms as well as sexual groups. But it does not specify how much gene flow can occur before genetic interchangeability is interrupted (Hausdorf, 2011). One of the most recent species concepts is the Differential Fitness Species Concept. According to this concept (Hausdorf, 2011), species are

group of individuals distinguished by characteristics that reduce fitness of other groups and are not exchangeable among them. Differences in characteristics among species can be because of variation in adaption due to selection or nonadaptive forces such as genetic drift. Although there are a variety of criteria for species delimitation, many species are identified primarily based on morphological features (Mallet, 1995). Morphological taxonomy has some limitations. It demands high level of expertise and experience (Hebert et al., 2003) and enormous number of species remain undescribed because of the lack of specialists in the field (Padial et al., 2010). Classification that is based solely on morphology will be misleading if the studied characters show phenotypic plasticity. It also overlooks cryptic species (Hebert et al., 2003). By development of DNA sequencing techniques and computer programs to analyze molecular data in 70s, new types of characters were provided which resulted in the improvement of classification (Maguire, 2011). Hebert et al. (2003) suggested DNA barcoding as a tool to improve taxonomical efforts and to overcome limitations of morphology-based taxonomy in capturing species diversity. Molecular studies have provided opportunity to uncover patterns of hidden diversity. However, it is challenging to specify the adequate level of variation to delimit a taxonomical unit (Pires & Marinoni, 2010). In groups with limited morphological characters, multiple approaches should be integrated for species delimitation (Dayrat, 2005). Microorganisms including rotifers do not have too many recognizable morphological characters; many morphologically similar taxa are not readily distinguishable (Artois et al., 2011; Guil, 2011). Furthermore, there have not been enough taxonomical efforts to study them (Fontaneto et al., 2009; Kaya et al., 2009). Morphologically similar species are delimited using DNA taxonomy (Bickford et al., 2007), and boundaries of new species can be tested by an integrative approach (Fišer et al., 2018) and reevaluated with the new methods (Thomson et al., 2018).

Rotifers were first described by Leuwenhoek in the 18th century (Dobell 1958). Subsequently to Leuwenhoek's description, Müller described over 50 species. Cuvier was the first to notice that rotifers are not ciliates and he classified them as the order of Infusoria. At the beginning of 19th century, Bory de St. Vincent, the first rotifer systematist, described and revised many rotifer genera. In 1929, Remane wrote a comprehensive chapter on rotifer biology and systematics that included morphology and taxonomical descriptions (Wallace et al., 2006). Taxonomic problems in rotifers stem from their high phenotypic plasticity, parthenogenesis reproduction and scarcity of taxonomical efforts (Segers & De Smet, 2008). For example, *Keratella cochlearis* (Gosse, 1851), *K. valga* (Ehrenberg, 1834) and *K. quadrata* (Müller, 1786) show variability in caudal spine length, shape, and most of *Keratella* species in development of lorica pustulation. Pattern of sculpture of the dorsal lorica are important in the identification of *Keratella* species. However, some species such as *K. valga* and *K. quadrata* show similar patterns and they cannot be distinguished based on this feature. Thus, using morphology alone may result in misleading classification of *Keratella* species. (Ahlstrom, 1943). Furthermore, in a barcoding study, García-Morales & Elías-Gutiérrez (2013) found two clusters within *K. cochlearis*, differentiated by 7.5% of genetic divergence, indicating possibility of cryptic speciation in this species. In a more recent study, Cieplinski et al. (2017) reported eight putative cryptic species within *K. cochlearis* based on differentiation in the COI gene. Those cryptic species were not distinguishable based on morphology of the spinelets. However, Segers and Babu (1999) noted that the identification of *Polyarthra vulgaris* Carlin, 1943 and *P. dolichoptera* may not be well founded because these species show variability in morphological characters that are used traditionally to distinguish them. Indeed Obberteger et al. (2014) indicated the presence of 12 putative cryptic species within *P. dolichoptera*. Integrative taxonomy has been used within

various rotifer species complexes to delimit cryptic species. Some examples include variation in morphology, reproductive isolation and genetic divergence in the COI gene among *Epiphanes ukera*, *E. hawaiiensis* and *E. chihuahuaensis* (Schröder & Walsh, 2007) and genetic differentiation in the ITS region, ecological and morphological variation among four cryptic species of *Brachionus calyciflorus* (Papakostas et al., 2016). Integration of multiple approaches for species delimitation within rotifer species complexes has shown to be effective in investigating species diversity and provide support for delimited cryptic species.

Here, I investigated genetic differentiation and cryptic diversity within five cosmopolitan rotifer morphospecies, *Euchlanis dilatata*, *Limnias melicerta*, *L. ceratophylli*, *Collotheca campanulata*, and *C. ornata* using a mitochondrial marker (COI gene), and a nuclear marker (ITS region). I showed that all focal morphospecies represent species complexes, each including multiple cryptic species. For *E. dilatata* I conducted cross mating and life table experiments to evaluate the species delimitation based on molecular analyses. While cryptic species of *E. dilatata* were not morphologically distinguishable, they were reproductively isolated and ecologically differentiated. Therefore, they can be delimited using Biological and Ecological Species Concepts.

The results of species delimitation based on ITS region were different from those based on the COI gene. The ITS region showed lower genetic differentiation compared to the COI gene and it obtained more conservative species delimitation results. The COI gene has a faster evolution rate compared to the ITS region (Cruickshank, 2002; Vilas et al., 2005), which explains the higher genetic differentiation I detected here. Overall ITS region is less variable in rotifers (Table 5.1 and Obertegger et al., 2018). I did not concatenate the COI gene and the ITS region sequences for phylogenetic analyses and species delimitation for two reasons. 1) There is

a difference in coalescent time between the COI gene and ITS region (Birky et al., 1989). 2) There was discordance between their phylogenetic trees in my study and for some other rotifer species complexes (see Chapters 1 and 2; Obertegger et al. (2018)).

Because ITS region yielded more conservative results, and it has been suggested as a more reliable marker for species delimitation for two rotifer species complexes, *Brachionus plicatilis* and *B. calyciflorus* (Mills et al., 2016; Papakostas et al., 2016, respectively), I based species delimitation on this marker for *E. dilatata*. However, for *L. melicerta* and *L. ceratophylli*, I used the delimitation results based on COI gene because first, ITS region showed an overall low genetic differentiation among cryptic species. Second, these morphospecies were not distinguishable in phylogenetic analysis based on ITS region. *L. melicerta* and *L. ceratophylli* probably have not diverged long enough to be distinguishable in ITS region, and for recently diverged lineages, mitochondrial markers can be more informative because of their faster rate of evolution (Moore, 1995). For species delimitation, it is recommended to use multiple molecular markers and then to assess their effectiveness for the studied taxa (Shaw, 2002; Xiao et al., 2010; Dupuis et al., 2012; Finnegan et al., 2013; Jörger & Schrödl, 2013; Fontaneto et al., 2015). Here, I provided evidence that for some rotifer species complexes nuclear markers obtain more reliable results (e.g., *Euchlanis dilatata*) while for other species complexes (e.g., *Limnias melicerta* and *L. ceratophylli*) mitochondrial markers show enough variation to delimit species boundaries and it has been shown that these two markers should not be concatenated for downstream analyses (e.g., see Obertegger et al., 2018).

The concept of total evidence states that all available evidence should be considered for testing the probability of a hypothesis (McLaughlin, 1970). For example, in taxonomy all the available character statements should be used to make a decision about classification hypothesis.

The higher level of congruence among character statements adds more credibility to the taxonomic hypothesis (Rieppel, 2004). Thus, the best estimate of phylogeny is obtained when combined datasets are used, and character congruence that aims at finding a fully resolved hypothesis is investigated (Kluge, 1998). The concept of total evidence has been used to investigate phylogenetic relationships and monophyly of taxa. For instance, Kluge (1998) used morphological and biochemical data as available evidence to infer the phylogenetic relationship within the *Epicrates* boa. He showed that there was congruency between those datasets and together they resulted in a robust phylogeny for *Epicrates*. Sørensen & Giribet (2006) used the combination of morphological characters and four molecular markers to explore the phylogenetic relationship between rotifers and Acanthocephala. In a more recent study, using four molecular markers and morphological data, Bianchi et al. (2016) showed that the genus *Euschistus* is not monophyletic and its taxonomic status must be revisited. In another study, Martin et al. (2017) used combination of molecular and morphological data matrices to reconstruct the phylogenetic relationships of the fireflies from family Lampyridae. Using the total evidence approach, they provided support for monophyly of six subfamilies. Only subfamilies that were supported based on both molecular and morphological data were considered monophyletic in this study. I only included two molecular markers in my study, yet I could not find one marker to be appropriate for species delimitation within all focal species complexes. In all the above examples, multiple molecular markers were used along with morphological characteristics for the total evidence approach, and molecular data or their phylogenetic trees were combined as suggested by Levasseur & Lapointe (2001). I could not use the concept of total evidence in the phylogenetic analyses because of discordance between phylogenetic trees based on COI gene and ITS region. Moreover, I did not find any cryptic species that was recovered in the phylogenetic analyses

based on both markers. However, the monophyly of *Limnias melicerta* and *L. ceratophylli* was confirmed by the COI gene and 18S rRNA. It should be noted that cryptic species of *Euchlanis dilatata* were delimited based on all available evidence including molecular analyses, morphology, reproductive isolation and life history characteristics. Integrating these approaches may be considered as a total evidence approach. But it was not feasible to use available evidence in my study as character matrices and combine them to investigate monophyly of each cryptic species. Using multiple markers including COI, 18S rRNA and 28s rRNA genes and morphological character states for other rotifer species complexes will assist in testing whether total evidence approach could be applicable in the phylogenetic analyses and species delimitation of rotifers.

The rate of diversification and genetic differentiation in aquatic habitats may vary among taxa with different life histories (Eastman & Storfer, 2011; Fontaneto et al., 2012; Fluker et al., 2014) and habitat differences (Takeda et al., 2013). Rotifer can be grouped based on their habitat preference; pelagic versus littoral. Pelagic rotifers constantly swim while littoral species can creep and swim, and sessile groups are attached to the substratum in the littoral zones. In littoral zones there is higher habitat diversity provided by vegetation, debris, mosses and filamentous algae compared to the pelagic zone (Wallace et al., 2006). Habitat preference has been reported for some rotifers inhabiting littoral zones such as *Collotheca gracilipes* (Wallace & Edmondson, 1987) and *Euchlanis dilatata* (Walsh, 1989). Therefore, as a result of high habitat differentiation in littoral zones, substantial genetic diversity is expected within and among populations especially for sessile groups because their females are mobile only during their larval stage. Moreover, sessile colonial rotifers exploit different strategies for colony formation. In allorecrutive method, free swimming larva settle on the tube of individuals from other colonies.

In the autorecruitive method, larvae stay within their parental colonies. In the germinative colony formation, juveniles stay together and start a new colony (Wallace et al., 2006). The variation in colony formation can affect the genetic diversity within populations. For example, less genetic variation is expected among allorecruitive versus autorecruitive colonies because of the higher connectivity among allorecruitive ones. *E. dilatata* is a littoral rotifer while the other four morphospecies are sessile. As shown in Table 5.1, the genetic variation in the ITS region for the littoral species (*Euchlanis dilatata* and *Lecane bulla*) was higher than that of pelagic and sessile species complexes. Sessile species, similar to the littoral ones, can show high differentiation in their habitat preference. Therefore, I expected to see similar level of genetic differentiation in the ITS region for sessile morphospecies as well. However, the genetic variation in ITS region in sessile morphospecies was similar to that of pelagic groups. It should be noted that there are few examples of using ITS region to study rotifer cryptic species that have reported the level of differentiation among cryptic lineages (see Table 5.1). Therefore, I think that there may not be sufficient information available to make conclusions about the relationship between life history of rotifers and the genetic differentiation in the ITS region. On the other hand, the difference in diversification in the COI gene between two subclasses of rotifers, Bdelloidea and Monogononta has been reported. It is hypothesized that this variation is related to the difference in reproductive mode between bdelloids and monogononts (cyclical and facultative parthenogenic respectively) (Fontaneto et al., 2012). In this study, for the COI gene, the genetic variation among cryptic species was within the same range for pelagic, littoral and sessile species complexes (Table 5.1). All those species complexes are cyclical parthenogenic which may have caused this similarity in the range of genetic variation within them. However, comparing diversification rate among rotifers with different life history features may not be possible by simply looking at the genetic

variation in the COI gene. To investigate the patterns of diversification for different groups of rotifers, more sophisticated statistical analyses are essential (see Fontaneto et al., 2012).

Table 5.1. Range of genetic divergence (percentage) in ITS region and COI gene sequences of selected pelagic, littoral, and sessile rotifers. "-" indicates that data were not available.

Species complex	Life history	ITS region (% variation)	COI gene (% variation)	Reference
<i>Brachionus plicatilis</i>	Pelagic	≤1.9 within clades ≥ 2.5 between clades	≤13.3 within clades ≥11.9 between clades	Gómez et al., 2002b
<i>Synchaeta</i> spp.	Pelagic and littoral	-	0.2–2.7 within clades 5.9–25.3 between clades	Obertegger et al., 2012
<i>Polyarthra dolichoptera</i>	Pelagic	-	≤4.4 within species ≥5-24 between species	Obertegger et al., 2014
<i>Testudinella clypeata</i>	Littoral	-	0.16-4.5 within clades 16.7-27.7 between clades	Leasi et al., 2013
<i>Lecane bulla</i>	Littoral	0.0-12.5	0.9-16	Walsh et al., 2009
<i>Euchlanis dilatata</i>	Littoral	0.0-5.2% within species 1.0-13.4% among species	0.0-18.7% within species 0.2-21.9% among species	Current study
<i>Limnias melicerta</i>	Sessile	0-1.5% within cryptic 0-2% among species	0-11.4% within species 8-20.5% among species	Current study
<i>L. ceratophylli</i>	Sessile	0.04 to 1.5% within species 0-5.3% among species	0.5-0.6% within species 15.1-21% among species	Current study
<i>Collotheca campanulata</i>	Sessile	-	0.0-11.7% within cryptic 10.8-25.2% among species	Current study
<i>C. ornata</i>	Sessile	-	0.3-20.0% within cryptic 14.6-29.0% among species	Current study

Cryptic species are, by definition, not morphologically distinguishable (Bickford et al., 2007). However, there are many examples of morphological variation among rotifer cryptic species that were found after a more comprehensive analysis (e.g., Fu et al., 1991; Anitha & George, 2006; Schröder & Walsh, 2007; Hwang et al., 2013; Michaloudi et al., 2016). I showed that cryptic species of *E. dilatata*, *L. melicerta* and *L. ceratophylli* could not be distinguished based on trophi morphology. The only exception was cryptic species A that had a projection on the left ramus of trophi. This lack of morphological variation for most cryptic species in my study could be due to morphological stasis. Morphological stasis happens when there is discordance between speciation rate and morphological variation because of stabilizing selection on morphology (Bickford et al., 2007). On the other hand, variation in mating pheromones can result in speciation without selection for morphology (Bickford et al., 2007) as was addressed for *B. plicatilis* and *B. rotundiformis* (Rico-Martinez & Snell, 1997). Moreover, variation in ecological adaptation can decrease gene flow through temporal and spatial isolation and leads to speciation (Wiens & Harrison, 2004) which may not include morphological divergence. In my study, the only exception was cryptic species A of *E. dilatata* with a projection on left ramus of trophi. This projection was specific to this cryptic species and I only observed it using a scanning electron microscope (SEM). This result is another evidence that subtle morphological variation among cryptic species may be identified using more sophisticated analyses. Many cryptic species including rotifers are left unnamed when the morphological variation among them is either not investigated or found. Jörger & Schrödl (2013) suggested a guideline to describe cryptic species based on diagnostic nucleotides where there is no knowledge of morphological variation among them. Several cryptic species have been described based on diagnostic nucleotides (e.g., Brower, 2010; Johnson et al., 2015; Delić et al., 2017). Despite the lack of morphological variation in my

study, and in order to avoid leaving part of rotifer diversity unnamed and unaddressed, I followed Jörger & Schrödl (2013) guidelines to describe cryptic species. I described four cryptic species of *E. dilatata* based on diagnostic nucleotides in the ITS region because mating and life table experiments supported the species delimitation results based on this marker. Moreover, my goal was to set a baseline for other rotiferologists for describing cryptic species rather than leaving them as unnamed lineages.

To further examine species boundaries that were delimited by molecular methods, I focused on cryptic species of *E. dilatata* to accomplish three goals. 1) Determine whether genetic differentiation among cryptic species is accompanied by restricted gene flow and beyond that, reproductive isolation. 2) Examine whether those cryptic species are differentiated in their ecological adaptation. 3) Uncover the genetic basis of ecological adaptation in *E. dilatata* cryptic species.

Different pre-mating and/or post-mating reproductive barriers can contribute to reproductive isolation. In rotifers, differentiation in timing and cues of shifting to sexual reproduction (e.g., *E. hawaiiensis* and *E. chihuahuaensis*: Schröder & Walsh, 2010), and failure in recognizing individuals of other species as a potential mate (e.g., *B. plicatilis* species complex: Kotani et al., 1997; Gribble & Mark Welch, 2012) are among pre-mating barriers. Deficiency to produce resting eggs after copulation, production of unviable resting eggs, and female mortality after copulation (e.g., *E. ukera* and *E. chihuahuaensis*: Schröder & Walsh, 2007) and unviable and/or sterile F1 females (e.g., *B. plicatilis* species complex: Suatoni et al., 2006) can act as post-mating barriers. I examined the reproductive isolation between six cryptic species of *E. dilatata*. Under laboratory conditions, I provided evidence that these cryptic species were reproductively isolated because the interspecies mating success rate was close to zero. There was one successful

mating trial (out of 89 trials) between cryptic species E and F where one diapausing embryo was produced. Speciation could happen before complete reproductive isolation (Claridge, 1990). Because I did not try to hatch this embryo, there is no information regarding whether the hybrid was viable or fertile and whether cryptic species E and F are reproductively isolated. Moreover, I did not specifically investigate whether the observed reproductive barriers concern pre- or post-mating barriers. Therefore, based on my results, it is not possible to know what mechanisms are involved in inhibiting diapausing embryo production between *E. dilatata* cryptic species. Those mechanisms may involve variation in mating behaviors, timing and cues for sexual reproduction induction (Schröder & Walsh, 2007; Schröder & Walsh, 2010) and failure in mate recognition (Kotani et al., 1997; Gribble & Mark Welch, 2012).

While life history characteristics of *E. dilatata* have been studied (Sarma et al., 2001; Arias-Almeida & Rico-Martínez, 2011; Nandini et al., 2011; Espinosa-Rodríguez et al., 2012; Farhadian et al., 2013), the variation among *E. dilatata* cryptic lineages are not explored. To examine ecological differentiation among cryptic species, I carried out life table experiments for five cryptic species of *E. dilatata* using four experiments conditions with various combinations of temperature and conductivity. I found that survivorship, fecundity and population growth increased, and life expectancy and generation time decreased with the increase in temperature. Other rotifer species have exhibited a positive correlation between development rates and temperature, while their life expectancy has been negatively correlated with temperature (e.g., *Brachionus havanaensis* Rousselet, 1911: Pavón-Meza et al. (2005); *Lecane papuana* (Murray, 1913), *Lecane bulla* (Gosse, 1851) and *Lecane cornuta* (Müller, 1786): Saucedo-Ríos et al. (2017); and a Kenyan strain of *B. angularis* Gosse, 1851: Ogello et al. (2016)). In my study, most cryptic species showed similar patterns in response to temperature, and the variation in life

table parameters among them was in response to water conductivity (salinity). For example, the generation time for species A and E was lower under high temperature and high salinity while for cryptic species C, D, and F, generation time was the lowest under high temperature and low salinity. There are multiple examples of rotifer cryptic species that have shown differential response to salinity and temperature. For instance, differential response to salinity and temperature among *B. plicatilis*, *B. manjavacas* and *B. ibericus* has been suggested to result in temporal isolation (Gómez et al., 1995). Ortells et al. (2003) showed occurrence of five cryptic species of the *B. plicatilis* species complex in coastal Mediterranean ponds were negatively correlated with salinity. Malekzadeh Viayeh et al. (2010) addressed variation in population growth in response to salinity among six cryptic lineages of *B. plicatilis* from Iran. *B. plicatilis* was shown to have a higher reproduction rate compared to *B. manjavacas* at lower salinities in a study by Gabaldón et al. (2015) suggesting differentiation in adaptation between them. Thus, there appears to be at least some ecological variation among cryptic species. The observed variation among rotifer cryptic species in response to temperature and salinity may stem from the genetic variation among them.

We know that rotifer cryptic species are genetically differentiated based on neutral markers, and many including *E. dilatata* cryptic species show ecological differentiation (see references mentioned above as examples). Yet, the genetic basis of ecological differentiation among rotifer cryptic species has not been investigated. Studying the genetic basis of ecological adaptation can detect genes responsible for evolutionary differences among species (Wagner, 2007; Olson-Manning et al., 2012). For this reason, I used next generation sequencing to detect genomic regions that are under selection and potentially of adaptive significance in *E. dilatata*. My aim was to investigate population genetic structure, and to find genomic regions that may be

involved in ecological adaptation of two *E. dilatata* cryptic species. I used ddRAD sequencing to identify SNPs for two cryptic species of *E. dilatata*, cryptic species C with four populations and cryptic species D with three populations. Those cryptic species were delimited based on ITS region sequences (see Figure 1.2). There was higher genetic variation within cryptic species C compared to cryptic species D. This variation may be attributed to the differences in habitat features within this species. All three populations of cryptic species D were collected from temporary, artificial tanks while two populations of cryptic species C were collected from permanent habitats and the other two from temporary habitats. Within cryptic species C, based on loci and regardless of geographic distance, the populations from temporary habitats were grouped together and the populations from permanent habitats were grouped together. However, my results may not represent the true patterns of genetic variation among *E. dilatata* populations because of small sample size and low coverage for loci. Moreover, this small sample size could not show to what extent genetic variation among populations is related to the habitat features.

For all the species complexes I examined, the relationship between genetic and geographic distance was weak or lacking based on the COI gene and ITS region. Some populations showed genetic differentiation despite their geographic proximity. For example, in *Limnias melicerta* two populations that were collected from Florida, one from Krome pond and one from Fish Camp Lake were about 8 km apart. But they were classified under different cryptic species, cryptic species M and H respectively. On the other hand, there was variation in life table parameters among *E. dilatata* cryptic species suggesting they are ecologically differentiated. Because ecological differentiation has been discovered among many rotifer cryptic species (e.g., Kirk, 1997; Sarma et al., 2001; Stelzer, 2002; Derry et al., 2003; Ramírez-Pérez et al., 2004; Gilbert, 2004; Xiang et al., 2010; Espinosa-Rodríguez et al., 2012; Farhadian

et al., 2013; Wang et al., 2014; Gabaldón et al., 2015; Pan et al., 2016; Gorokhova, 2017) and while isolation by distance has not had a major impact on genetic variation (e.g., Xiang et al., 2011; Kimpel et al., 2015), I strongly believe that ecological speciation, should be thought of as an important speciation mode in rotifers. The Monopolization Hypothesis (MPH) elucidates why gene flow could be restricted among rotifer populations although they have high dispersal abilities. The MPH hypothesis has three components: persistent founder effect that refers to dilution of migrants' alleles in the local gene pool, local adaptation of the founder population that reduces the survival of the new arrivals, and the resting egg bank of the local population that provides adaptive genotypes from different time periods (De Meester et al., 2002). Low ability of migrants to colonize new habitats because of lack of adaptation and/or rapid monopolization of resources by first colonizing migrants can limit gene flow. Restricted gene flow among populations because of ecological adaptation will generate genetic divergence and potentially new species. This mode of speciation could result from selection through pressures of a physiological nature, without morphological divergence, hence creating cryptic species. The underlying mechanisms of ecological speciation must be studied further in rotifers and other microinvertebrates.

In this study, I used DNA taxonomy to find cryptic species within five rotifer morphospecies. I showed that molecular approaches reveal hidden diversity in taxa with a limited number of morphological traits. Moreover, at least within one of morphospecies in my study, the DNA-based species boundaries were supported by evidence of reproductive isolation and ecological differentiation among cryptic species although they were not supported by all the molecular evidence. Therefore, DNA taxonomy can be an effective tool to study species diversity within groups with high morphological uniformity. However, the species boundaries

defined by DNA taxonomy should be evaluated using other methods as it has been done for many microorganism (e.g., Schröder & Walsh, 2007; Leasi et al., 2013; André et al., 2014; Darienko et al., 2015; Papakostas et al., 2016).

FUTURE DIRECTIONS

To further investigate genetic differentiation, ecological adaptation of genotypes and obtain a more accurate estimate of species diversity within these five species complexes, I recommend including additional populations from ecologically distinct habitats. Additional samples will provide a more comprehensive understanding of differentiation in ecological niche and geographical distribution of cryptic species. During almost four years of maintaining rotifer cultures, I did not observe any population of *L. melicerta*, *L. ceratophylli* and *C. campanulata* undergo mixis. For *C. ornata*, only two populations representing the same cryptic species were exhibited mixis, which is not enough for cross mating experiments. However, finding the cues to induce mixis and to test reproductive isolation within these species complexes will provide more information about pre-mating reproductive barriers among rotifer species. To better understand the mechanisms involved in reproductive isolation among cryptic species, other pre- and post-mating reproductive barriers such as variation in mating behaviors, timing of sexual reproduction, ploidy level, viability of resting eggs and F1 females can be investigated. Moreover, genes involved in sexual reproduction such as *mmr-b* that codes the mate recognition glycoprotein can be sequences. The genetic variation in those genes among cryptic lineages could be related to the strength of reproductive isolation as it was shown for *Brachionus plicatilis* (Gribble & Mark Welch, 2012). Studying reproductive isolation among cryptic species will provide a framework for applying Biological Species Concept to delimit species boundaries. More comprehensive morphological analyses may lead to finding differentiation among cryptic

species. For example, variation in resting egg morphology and for *Limnias melicerta* and *L. ceratophylli* variation in characters such as antennae length, width of dorsal gap of corona and number of dorsal nodules on the neck region can be investigated. Variation in egg and female size and age at metamorphosis has been documented among three lineages of *Collotheca ornata* (unpublished results by A. Shapiro). Therefore, another approach for examining species boundaries within sessile groups is to investigate the variation in males and females size, larvae and eggs morphology and behaviors such as substratum preference, age at metamorphosis and maturity. To study ecological differentiation among cryptic species and its genetic basis, I focused on *E. dilatata*. Life table experiments should be carried out for cryptic species within *L. melicerta*, *L. ceratophylli*, *C. campanulata* and *C. ornata* to gauge the level of ecological variation among them and to apply Ecological Species Concept for species delimitation. Additional environmental variables such as predator densities can be included in life experiments of *E. dilatata* cryptic species. Finally, I suggest using next generation sequencing methods that target coding genomic regions as well as RAD sequencing to investigate the genetic bases of local adaptation in rotifers and ecological differentiation among rotifer cryptic species. The more information we gather on the genes with adaptive significance, the better we can study the importance of ecological speciation in rotifers and other microinvertebrates.

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Appendix

Supplemental Table S1.1. Site of origin of *Euchlanis dilatata* populations and GenBank accession numbers for their corresponding ITS region and COI gene sequences. BIBE=Big Bend National Park, HTSPHS=Hueco Tanks State Park and Historic Site, IMRS=Indio Mountains Research Station. Haplotype group(s) for the ITS region and COI gene for populations are shown. Populations that are not sequenced for one of the markers are specified by “-“ for the haplotype group and GenBank accession number. Samples collected from Cattail Springs and Glenn Springs in BIBE are considered as one population each in all analyses.

Origin of populations	Collection date	Abbreviation in text and figures	GPS coordinates (decimal degrees N/W)	Haplotype group (ITS/COI)	GenBank accession numbers (ITS/COI)
Chicken Creek Reservoir, Juab Co., UT	05.20.2016	Ed.CHIC.UT	39.49185/ -111.95760	6/38	KX714926/ KX714916
Santaquin, Juab Co., UT	05.20.2016	Ed.SEQ.UT	39.955778/ -111.780283	6/39	KX714929/ KX714919
Duck pond, Beaver Co., OK	11.24.2013	Ed.DUC.OK	35.551944/ -97.574722	7/48	KU665956/ KU665890
Oknoname Reservoir 085006, Love Co., OK	11.24.2013	Ed.OKR.OK	33.927583/ -97.301067	4/47	KU665957/ KU665891
Crescent Lake, Burneyville Co., OK	07.23.2014	Ed.CRS.OK	33.928389/ -97.312607	-/5	-/KU665892
Alazan Bayou Wildlife Management Area, Nacogdoches Co., TX	07.30.2013	Ed.AWR.TX	31.5033389/ -094.7546583	5/-	KU665899/-
Sam Rayburn State Park, Sabine Co., TX	07.30.2013	Ed.SAM.TX	31.061244/ -94.106127	3/3	KU665900/ KU665828
Roadside Pond, I-10+65, Jefferson Co., TX	07.30.2013	Ed.I10.TX	29.834722/ -94.482222	3/11	KU665901/ KU665829
Lake Travis (Laguna Vista), Travis Co., TX	01.07.2014	Ed.TRV.TX	30.402417/ -97.947967	4/31	KU665902/ KU665830
Walter E. Long Lake, Travis Co., TX	01.03.2014	Ed.WAL.TX	30.284417/ -97.608383	4/30	KU665903/ KU665831
Buttrill Springs, BIBE, Brewster Co., TX	07.16.2011	Ed.BUBB.TX	29.54585/ -103.2738	7/44	KU665904-5/ KU665832-3/
Cattail Falls pool C', BIBE, Brewster Co., TX	08.08.2006	Ed.CATCpBB.TX	29.2731833/ -103.3361638	7/42	KU665906/ KU665834/
Cattail Falls pool D, BIBE, Brewster Co., TX	01.11.2005	Ed.CATDBB.TX	29.2731527/ -103.3358277	7/43	KU665907/ KU665835
Cattail Falls pool E, BIBE, Brewster Co., TX	01.20.2008	Ed.CATEBB.TX	29.2731444/ -103.3361638	7/42	KU665908/ KU665836
Cattail Falls pool G, BIBE, Brewster Co., TX	01.20.2008 & 06.23.2013	Ed.CATGBB.TX	29.2731666/ -103.3361638	7/42	KU665909- 10/ KU665837-8
Cattail Falls pool H, BIBE, Brewster Co., TX	01.20.2008	Ed.CATHBB.TX	29.2731694/ -103.3362388	7/-	KU665911/-
Glenn Springs pool 3, BIBE, Brewster Co., TX	05.17.2006	Ed.GL03BB.TX	29.1744166/ -103.1575	3/9	KU665912/ KU665839

Glenn Springs pool 6, BIBE, Brewster Co., TX	05.17.2006	Ed.GL06BB.TX	29.1744166/ -103.1575	3/9	KU665913/ KU665840
Paint Gap Cattle Tank, BIBE, Brewster Co., TX	05.14.2006	Ed.PGTBB.TX	29.3878555/ -103.302675	5/24	KU665914/ KU665841
Corral Tank, IMRS, Hudspeth Co., TX	10.06.2013& 06.23.2013	Ed.COT.TX	30.8237166/ -105.3155833	3/8	KU665915-6/ KU665842-3
Peccary Tank, IMRS, Hudspeth Co., TX	06.03.2013	Ed.PEC.TX	30.7555556/ -105.0041667	3/8	KY564363/ KY564362
Red Tank, IMRS, Hudspeth Co., TX	06.04.2014	Ed.RET.TX	30.7303083/ -104.9891083	5/23	KU665917/ KU665844
Miller Ranch, Jeff Davis Co., TX	06.04.2006	Ed.MIL.TX	30.623845/ - 104.674005	3/3	KU665918/ KU665845
Behind Ranch House Pond, HTSPHS, El Paso Co., TX	11.24.2014	Ed.BRH.TX	31.924072/ -106.041589	9/-	KU665919/-
Mescalero Canyon playa sediments, HTSPHS, El Paso Co., TX	-	Ed.MCHT.TX	31.9188166/ -106.0403666	3/5	KU665920/ KU665846
Behind Mescalero Canyon playa, HTSPHS, El Paso Co., TX	11.24.2014	Ed.BMCHT.TX	31.9190694/ -106.0408305	3/3	KU665921/ KU665847
Mesocosm, HTSPHS, El Paso Co., TX	06.19.2007	Ed.MSHT.TX	31.9188166/ -106.040366	3/3	KU665922/ KU665848
Laguna Prieta sediments, HTSPHS, El Paso Co., TX	-	Ed.LPSHT.TX	31.9246388/ -106.046675	5/-	-/ KU665924
Laguna Prieta, HTSPHS, El Paso Co., TX	09.02.2013	Ed.LPHT.TX	31.9246388/ -106.046675	3/3	KU665923/ KU665849
Palo Pinto Canyon Stream, Presidio Co., TX	09.18.2005	Ed.PPC.TX	30.0308666/ -104.4684333	10/10	KU665925/ KU665850/
Shafter Stream, Presidio Co., TX	08.28.2005	Ed.SH.TX	29.8143166/ -104.3071333	4/-	KU665926- 8/-
Feather Lake Wildlife Sanctuary, El Paso Co., TX	10.10.2007	Ed.FL.TX	31.6890972/ -106.3052666	3/4	KU665959/K U665870

Rio Grande, American Dam, El Paso Co., TX	06.19.2013	Ed.AMD.TX	31.784234/-106.527845	3/3	KU665946/ KU665851
Rio Grande, Fabens, El Paso Co., TX	04.25.2005	Ed.F.RG	31.430277/-106.14222	4 & 8/41	KU665947-52/ KU665852
Rio Grande, Williamsburg, Sierra Co., NM	03.01.2005 & 07.24.2013	Ed.W.RG	33.110039/-107.297839	4/3, 5, 6, 7, 26 & 27	KU665929-45/ KU665853-69
former Cattle Tank sediments, White Sands National Monument, Doña Ana Co., NM	09.20.2006	Ed.CTS.NM	32.67485/-106.44345	5/22	KU665978/ KU665883
former Cattle Tank, White Sands National Monument, Doña Ana Co., NM	-	Ed.CT.NM	32.67485/-106.44345	5/-	KU665976-7/-
Dripping Springs Natural Area, Doña Ana Co., NM	08.12.2006	Ed.DRS.NM	32.3231888/-106.5725138	7/41	KU665979/ KU665884
Mescalero Lake, Otero Co., NM	07.05.2013	Ed.MES.NM	33.2984/-105.6886	4/26	KU665980/ KU665885
Bear Canyon Lake, Grant Co., NM	04.23.2014	Ed.BEC.NM	32.8846/-107.998033	6/34	KU665981/ KU665886
Alto Reservoir, Lincoln Co., NM	06.29.2014	Ed.ALT.NM	33.395833/-105.671944	6/35	KU665953/ KU665887
Storrie Lake, San Miguel Co., NM	06.10.2016	Ed.STR.NM	35.6606694/-105.2345833	4/19	KX714923/ KX714913
Triangle Pond, Buenos Aires National Wildlife Refuge, Pima Co., AZ	08.2007	Ed.TRP.AZ	31.55/-111.533889	3/5	KU665955/ KU665889
Centinela, Imperial Co., CA	02. 29.2016	Ed.Cent.CA	33.987892/-118.406403	4/32	KX714924/ KX714914
Echo Lake, El Dorado Co., CA	02. 29.2016	Ed.ECH.CA	38.834557/-120.046143	4/15	KX714925/ KX714915
Lodi Lake, San Joaquin Co., CA	06.23.2013 & 08.16.2014	Ed.LOD.CA	38.147222/-121.292723	2 & 4/18 & 15	KU665969-70/ KU665876-7
American River, San Joaquin Co., CA	08.16.2014	Ed.AMR.CA	38.57221207/-121.3531190	4/14	KU665971/ KU665878
Detroit Lake State Park, Marion Co., OR	05.24.2014	Ed.DTL.OR	44.700211/-122.183492	12/37	KU665974/ KU665881

Timber Lake Ditch, Mount Hood National Forest, Clackamas Co., OR	05.25.2014	Ed.TIM.OR	45.083424/ -122.050234	4/16	KU665975/ KU665882/
Madeleine Lake, Oneida Co., WI	06.23.2013	Ed.MAD.WI	45.889733/ -89.643833	4/17	KU665972/ KU665879
Lake Mendota, Dane Co., WI	07.22.2014	Ed.MEN.WI	43.0789083/ -089.4192250	6/36	KU665973/ KU665880
Schmitthenner Lake, Wyoming Co., PA	05.20.2016	Ed.SCH.PA	41.43738/ -76.24304	6/40	KX714927/ KX714917
Silver Creek, Schuylkill Co., PA	05.20.2016	Ed.SIL.PA	40.543206/ -75.304106	4/38	KX714928/ KX714918
Panther Hollow Lake, Allegheny Co., PA	08.06.2012	Ed.PHL.PA	40.436856/ -79.948825	11/28	KU665954/ KU665888
Nockamixon Fishing Pond, Bucks Co., PA	05.20.2016	Ed.Nock.PA	40.472567/ -75.224823	2/19	KX714930/ KX714920
Shorty Howell pond, Gwinnett Co., GA	08.19.2014	Ed.SHL.GA	33.97455/ -84.14936	3/12	KU665958/ KU665893
Street Pond, Gwinnett Co., GA	04.18.2016	Ed.STP.GA	33.9360833/ -084.1366000	3/20	KX714932/ KX714922
Lake June in the Winter, Highlands Co., FL	01.09.2015	Ed.JUN.FL	27.30715/ -81.37542	7/45	KU665984/ KU665895
Lake Jackson, Highlands Co., FL	01.09.2015	Ed.JAC.FL	27.48775/ -81.47664	7/46	KU665986/ KU665897
Lake Okeechobee, Glades Co., FL	01.09.2015	Ed.LKO.FL	26.830456/ -80.941303	3 & 17/21	KU665982-3/ KU665894
Krome Ave., Miami-Dade Co., FL	01.08.2015 11.24.2015	Ed.KRM.FL	25.883615/ -80.484920	18 & 19/52 & 53	KU665985/ KU665896/ & KX714931/ KX714921
Cinnamon Bay Beach Pond, St. John, U.S. Virgin Islands	05.24.2012	Ed.CBB.VI	18.356281/ -64.752136	13/33	KU665968/ KU665875
Lago Colina, Chihuahua, Mexico	06.20.2007	Ed.COL.M	27.5724/ -105.4004666	4/-	KU665960/-

La Mesa Canyon Tule, Lower Canyons, Mexico	07.31.2008	Ed.T2T2.M	29.75111/ -102.58305	3/-	KU665961/-
Ojo de Santa Maria, Chihuahua, Mexico	07.31.2009	Ed.OSM.M	31.1552777/ -107.3172222	14/25	KU665962/ KU665871
Poza Azul, Coahuila, Mexico	2006	Ed.POZ.M	26.986111/ -102.066389	4/-	KU665963/-
Presa Chihuahua, Chihuahua, Mexico	04.16.2006	Ed.PCH.M	28.5762166/ -106.1711833	4/-	KU665964/-
Presa de la Boquilla, Chihuahua, Mexico	10.11.2007	Ed.BOQ.M	27.5361333/ -105.4011333	15/29	KU665965/ KU665872
Mexico	-	Ed.MC.M	-	16 & 3/49 & 13	KU665966-7/ KU665873-4
Steep Hill Creek, Natchitoches, LA	03.13.2014	E.deflexa.LA	31.466865/ -93.100005	outgroup	KU665987/ KU665898
Moon Lake, Marquette Co., WI	09.28.2014	L.melicerta.WI	43.806367/ -89.366509	outgroup	KU665988/-

Supplemental Table S2.1. Collection sites of *Limnias melicerta* populations and outgroup taxa. GenBank accession numbers for their corresponding partial COI gene, ITS region, and partial 18S rRNA sequences are provided. Haplotype group(s) for each population are also noted. Missing sequences are specified by “-“ for the haplotype group and GenBank accession numbers.

Collection Site	Collection date	Abbreviation in text and figures or outgroup taxon	GPS coordinates (decimal degrees N/W)	Haplotype groups (COI/ITS) or outgroup gene	GenBank accession numbers (COI/ITS/18S)
Canal Road, Fort Bend Co., TX	07.30.2013	L.mel.CRLRd.TX	29.582778/ -95.539444	26/1	MF787082/ MF787121/ MF795114
Lake Bastrop, Bastrop Co., TX	08.20.2014	L.mel.BasLK.TX	30.133333/ -97.283333	24/9	MF787080/ MF787191/-
Cibolo Lake, Guadalupe Co., TX	08.06.2013	L.mel.CIB.TX	28.953056/ -97.873333	16/2	MF787067/ MF787133/-
Inks Lake State Park, Bastrop Co., TX	08.20.2014	L.mel.INK.TX	30.730596/ -98.383275	17/9	MF787070/ MF787190/-
Mescalero Canyon, El Paso Co., TX	11.24.2014	L.mel.EHT.TX	31.9188166/ -06.0403666	8/3	MF787054-8/ MF787137, MF787153, MF787155, MF787157/ MF795101
Rio Grande, American Dam, El Paso Co., TX	12.10.2013	L.mel.AMD.TX	31.784234/ -106.527845	17/8	MF787068-9/ MF787189/ MF795106
Rattlesnake Springs, Carlsbad Caverns National Park, Eddy Co., NM	07.08.2014 & 10.17.2014	L.mel.RAT.NM	32.1097/ -104.471625	20 & 21/1	MF787074-5/ MF787122-3 & MF787174/ MF795102
Balboa Park Natural Area, Los Angeles Co., CA	02.29.2016	L.mel.Balboa.CA	34.1764278/ -118.4729139	17/7	MF787071/ MF787188/-

Glassman pond, Weber Co., UT	05.20.2016	L.mel.Glass.UT	41.179735/ -111.951601	15/3	MF787066/ MF787183/ MF795110
Timber Lake Ditch, Mount Hood National Forest, Clackamas Co., OR	05.25.2014	L.mel.TIM.OR	45.083424/ -122.050234	12/5	MF787087/ MF787178/ MF795103
Devil's Lake Roadside Ditch, Lincoln Co., OR	05.24.2014	L.mel.DEV.OR	44.967222/ -124.016667	-/3	-/MF787134/ MF795098
Devil's Lake, Devil's Lake State Park, Lincoln Co., OR	05.24.2014	L.mel.DEVD.OR	44.970664/ -124.012335	9/3	MF787059/ MF787135/ MF7950100
Minto Park pond, Marion Co., OR	05.25.2014	L.mel.MIN.OR	44.919914/ - 123.060946	-/3	-/ MF787136/-
Flint pond, Hillsborough Co., NH	11.15.2015	L.mel.FLNT.NH	42.74926/ -71.54951	5/3	MF787040 & MF787045- 50/ MF787150-2, MF787154, MF787156, MF787158- 61/ MF795112
Boxford pond, Essex Co., MA	07.16.2017	L.mel.BOX.MA	42.673355/ -71.022617	-/3	-/ MF787184/-
Moon (Birch) Lake, Marquette Co., WI	09.28.2014 & 10.05.2014	L.mel.MN.WI	43.806367/ -89.366509	2/3	MF787018-39 & MF787041- 3/ MF787138- 49, MF787162-3 & MF787169- 73/ MF795099
White River Wildlife Refuge, Marquette Co., WI	07.06.2015	L.mel.WRW.WI	43.925724/ -89.099011	13/5	MF787064/ MF787180-1

Minister Lake, Racine Co., WI	08.09.2015	L.mel.MinLK.WI	44.54277/ -89.26954	14/3	MF787065/ MF787182/-
Carolina pond, James Island, Charleston Co., SC	10.22.2015	L.mel.CP.SC	32.7084/ -79.9518	18 & 19/6	MF787072-3/ MF787185-7/-
Crescent Lake, Beaver Co., OK	06.25.2015	L.mel.CRS.OK	33.927829/- 97.312675	22, 23, & 24/1	MF787076 & MF787078- 9/MF787126 & MF787128- 30/ MF795113
Statue pond, Beaver Co., OK	06.25.2015	L.mel.STA.OK	33.930405/ -97.3103	3/1	MF787077/ MF787127 & MF787131-2/ MF795105
Lake Niskey, Gwinnett Co., GA	04.16.2016	L.mel.Niskey.GA	33.7155/ -84.5311667	10/3	MF787060/ MF787164/ MF795104
Canary Lake, Gwinnett Co., GA	04.17.2016	L.mel.CanLK.GA	33.9771667/ -84.1371667	6/3	MF787051/ MF787165/ MF795107
Berkeley View, Gwinnett Co., GA	04.18.2016	L.mel.BeView.GA	33.99025/ -84.1623833	1/3	MF787017/ MF787166/-
Lauren pond, Gwinnett Co., GA	04.18.2016	L.mael.Lauren.GA	33.9371667/ -84.13575	4/3	MF787044/ MF787167/-
Street pond, Gwinnett Co., GA	04.18.2016	L.mel.STP.GA	33.9360833/ -84.1366	7/3	MF787052/ MF787168/-
Fish Camp, Highlands Co., FL	01.09.2015	L.mel.FishCP.FL	25.941935/ -80.441761	11/4	MF787061-3/ MF787175 & MF787176-7/ MF795109
Krome pond, Miami-Dade Co., FL	01.09.2015	L.mel.KRM.FL	25.883615/ -80.484920	28/10	MF787083/ MF787192/-
Site 4, Miami-	01.09.2015	L.mel.SIT4.FL	25.761889/	29/5	MF787085/

Dade Co., FL			-80.50241		MF787179/-
Lake Jackson, Highlands Co., FL	01.09.2015	L.mel.JAC.FL	27.48775/ -81.47664	25/1	MF787081/ MF787124/ MF795111
Lake Okeechobee, Glades Co., FL	01.09.2015	L.mel.LKO.FL	26.830456/ -80.941303	29/1	MF787084/ MF787125/ MF795108
GenBank	-	L.mel. KT870155	-	-	KT870155/-/-
GenBank	-	L.mel. KT870154	-	-	KT870154/-/-
Glassman pond, Weber Co., UT	05.20.2016	<i>Collotheca campanulata</i>	41.179735/ -111.951601	outgroup for 18S rDNA	-/-/ MF795133
Steep Hill Creek, Natchitoches, LA	03.13.2014	<i>Ptygura pilula</i>	31.466865/- 93.100005	outgroup for COI gene	MG255828/-/-
Buffalo Lake, Marquette Co., WI	12.08.2013	<i>Sinantherina socialis</i>	43.7738/ -89.4092	outgroup for COI gene	MG255829/-/-
Boxford pond, Essex Co., MA	07.16.2017	<i>Floscularia conifera</i>	42.673355/ -71.022617	outgroup for ITS region gene	-/MG263749/-

Supplemental Table S2.2. Collection sites of *Limnias ceratophylli* populations. GenBank accession numbers for their corresponding partial COI gene, ITS region, and partial 18S rRNA sequences are provided. Haplotype group(s) for each population are also noted. Missing sequences are specified by “-“ for the haplotype group and GenBank accession numbers. Outgroups are the same as in Table S2.1.

Collection site	Collection date	Abbreviation in text and figures	GPS coordinates (decimal degrees N/W)	Haplotype group (COI/ITS)	GenBank accession numbers (COI/ITS/18S)
Lake Worth, Tarrant Co., TX	08.19.2013	L.cer.Worth.TX	32.810833/ -97.4325	1&2/1	MF786994-5/ MF787088-91/ MF795127
Lake Waco Wetlands, McLennan Co., TX	12.10.2012	L.cer.Waco.TX	31.5836/ -97.2006	2/3	MF786997/ MF787120/ MF795128
Feather Lake Wildlife Sanctuary, El Paso Co., TX	09.01.2016	L.cer.FL.TX	31.6890972/ -06.305266	6/3	MF787005/ MF787193/ MF795130
Sam Rayburn State Park, Sabine Co., TX	07.30.2013	L.cer.SAM.TX	31.061244/ -94.106127	5/3	MF787003/ MF787093/-
Morphy Lake, Mora Co., NM	06.10.2016	L.cer.Morphy.NM	35.941042/ -05.396167	15/2	MF786993/ MF787092/ MF795115
Echo Lake, El Dorado Co., CA	02.29.2016	L.cer.ECH.CA	34.0705/ -18.260663	11/3	MF787012/ MF787109/ MF795132
Burraston pond, Juab Co., UT	05.20.2016	L.cer.Burraston.UT	39.796162/ -11.865922	-/4	-/MF787118/ MF795121
Blue Lake, Multnomah Co., OR	05.25.2014	L.cer.Blue.OR	45.5565/ -122.4481	4/3	MF787002/ MF787094/ MF795118
Flint pond, Hillsborough Co., NH	04.30.2014	L.cer.FLNT.NH	42.74926/ -71.54951	-/4	-/MF787112/ MF795126
Naticook Lake, Hillsborough Co., NH	07/16/2016	L.cer.NAT.NH	42.8200/ -71.5257	-/3	-/MF787111/ MF795119
The Fishing Pond,	05.20.2016	L.cer.NockFS9PA	40.472567/ -75.224823	11/4	MF787013/ MF787117/

Nockamixon State Park, Bucks Co., PA					MF795120
Lake Nockamixon, Nockamixon State Park, Bucks Co., PA	05.20.2016	L.cer.NockSP.PA	40.462634/ -75.232702	14/11	MF787011/ MF787119/ MF795123
Twin Lakes, Lower Lake, Westmoreland Co., PA	08.06.2012	L.cer.TLL.PA	41.8571827/ -5.3366041	2/-	MF786996/-/-
Gothic Mill pond, Fond Du Lac Co., WI	06.27.2016	L.cer.GMP.WI	43.8427606/ -8.8301113	7/3	MF787006/ MF787110/-
Moon (Birch) Lake, Marquette Co., WI	06.08.2015 & 09.13.2015	L.cer.MN.WI	43.806367/ -89.366509	3 & 8/3	MF786998-7001 & MF787007-8/ MF787096 & MF787098-108/ MF795117
Lake Mendota, Dane Co., WI	07.22.2014	L.cer.MEN.WI	43.0789083/ -9.4192250	9/3	MF787086/ MF787095/ MF795129
Duck pond, Beaver Co., OK	11.24.2013	L.cer.DUC.OK	35.551944/ -97.574722	6/3	MF787004/ MF787097/ MF795125
Piedmont Park Lake, Gwinnett Co., GA	04.16.2016	L.cer.Pied.GA	33.78605/ -4.3722667	11/4	MF787010/ MF787114/-
Hi Loch Lomond, Fulton Co., GA	04.16.2016	L.cer.HiLoch.GA	33.7121167/ -84.545	12/4	MF787014/ MF787116/ MF795116
Norman Lake, Gwinnett Co., GA	04.17.2016	L.cer.NorLK.GA	33.996/ -4.1287167	13/4	MF787016/ MF787115/ MF795122
East Point Reservoir, Fulton Co., GA	04.17.2016	L.cer.EastPoint.GA	33.9360833/ -4.1366000	12/-	MF787015/-/ MF795131

Harold A Campbell pond, Walton Co., FL	11.10.2015	L.cer.HCP.FL	26.338031/ -80.628171	10/4	MF787009/ MF787113/ MF795124
GenBank	-	L.cer. KT870157	-	-	KT870157/-/-

Supplemental Table S2.3. Collection sites of *Collothea campanulata* populations. Haplotype group(s) for each population for the COI gene are also noted.

Collection site	Collection date	Abbreviation in text and figures or outgroup taxon	GPS coordinates (decimal degrees N/W)	Haplotype group (ITS/COI)
Crescent Lake, Beaver Co., OK	06.25.2015	C.cam.CRS.OK	33.927829/-97.312675	9
Corral Tank, IMRS, Hudspeth Co., TX	10.06.2013	C.cam.COT.TX	30.8237166/-105.3155833	13
Devil's Lake Roadside Ditch, Lincoln Co., OR	05.24.2014	C.cam.DEV.OR	44.967222/-124.016667	10
Minto Park pond, Marion Co., OR	05.25.2014	C.cam.MIN.OR	44.919914/-123.060946	10
Moon (Birch) Lake, Marquette Co., WI	2016	C.cam.MN.WI	43.806367/-89.366509	1
White River Wildlife Refuge, Marquette Co., WI	07.06.2015	C.cam.WRW.WI	43.925724/-89.099011	6
Lake Nockamixon, Nockamixon State Park, Bucks Co., PA	05.20.2016	C.cam.NockSP.PA	40.462634/-75.232702	3
Turtle Basking pond, Hennepin Co., MN	07.10.2017	C.cam.TurtleBasking.MN	44.84506/-93.369538	14
Lost Lake, Hennepin Co., MN	07.10.2017	C.cam.LostLake.MN	44.936106/-93.663976	12
Dragonfly pond, Hennepin Co., MN	07.10.2017	C.cam.Dragon.MN	44.879451/-93.683848	11
Flint pond, Hillsborough Co., NH	11.15.2015	C.cam.FLNT.NH	42.74926/-71.54951	2
Lake Jackson, Highlands Co., FL	01.09.2015	C.cam.JAC.FL	27.48775/-81.47664	4
Fish Camp, Highlands Co., FL	01.09.2015	C.cam.FishCP.FL	25.941935/-80.441761	3
Krome pond, Miami-Dade Co., FL	01.09.2015	C.cam.KRM.FL	25.883615/-80.484920	5
Egeland pond 01, Towner Co., ND	05.25.2017	C.cam.EW01.ND	48.320888/-99.259683	7
Egeland pond 06, Towner Co., ND	05.25.2017	C.cam.EW06.ND	48.645165/-99.100287	7
Egeland pond 03, Towner Co., ND	05.25.2017	C.cam.EW03.ND	48.63244/-99.097539	7
Egeland pond 05, Towner Co., ND	05.25.2017	C.cam.EW05.ND	48.644074/-99.094388	7
Glassman pond, Weber Co., UT	05.20.2016	C.cam.Glass.UT	41.179735/-111.951601	8
Naticook pond,	07.16.2016	<i>Collotheca ferox</i>	42.82/	outgroup

Hillsborough Co., NH			-71.5257	
Shorty Howell Lake,	08.19.2014	<i>C. tenuilobata</i>	33.97455/	outgroup
Gwinnett Co., GA			-84.14936	

Supplemental Table S2.4. Collection sites of *Collothea ornata* populations and outgroup taxa. Haplotype group(s) for each population for partial COI gene are also noted.

Collection site	Collection date	Abbreviation in text and figures or outgroup taxon	GPS coordinates (decimal degrees N/W)	COI haplotype groups
Crescent Lake, Beaver Co., OK	06.25.2015	C.orn.CRS.OK	33.927829/ -97.312675	2
Statue pond, Beaver Co., OK	06.25.2015	C.orn.STA.OK	33.930405/ -97.3103	14
Tule Tank, Big Bend National Park, Brewster Co., TX	06.23.2013	C.orn.TuleTank.TX	29.2426/ -103.444	20
Lake Bastrop, Bastrop Co., TX	08.20.2014	C.orn.BasLK.TX	30.133333/ -97.283333	21
Arlington Pond, Tarrant Co., TX	04.29.2017	C.orn.Arlington.TX	32.7505726/- 97.0658379	
Mescalero Canyon sediments, Hueco Tanks State Park and Historic Site, El Paso Co., TX	1998	C.orn.MES.TX	31.9190694/ -106.0408305	11
Red Tank sediments, Indio Mountains Research Station, Hudspeth Co., TX	06.04.2014	C.orn.RET.TX	30.7303083/ -104.9891083	12
Morphy Lake, Mora Co., NM	06.10.2016	C.orn.Morphy.NM	35.941042/ -105.396167	17
Rattlesnake Springs, Carlsbad Caverns National Park, Eddy Co., NM	07.08.2014 & 10.17.2014	C.orn.RAT.NM	32.1097/ -104.471625	4
Triangle pond, Buenos Aires National Wildlife Refuge, Pima CO., AZ	06.09.2017	C.orn.TRP.AZ	31.55/ -111.533889	5
American River, Sacramento Co., CA	08.16.2014	C.orn.AMR.CA	38.57221207/ -121.353119	31
Devil's Lake Roadside	05.24.2014	C.orn.DevilsD.OR	44.967222/	13

Ditch, Lincoln Co., OR			-124.016667	
Blue Lake Regional Park, Multnomah Co., OR	05.25.2014	C.orn.Blue.OR	45.5565/ -122.4481	35
Timber Lake Ditch, Mount Hood National Forest, Clackamas Co., OR	05.25.2014	C.orn.TimberDitch.OR	45.083424/ -122.050234	40
Minto Park pond, Marion Co., OR	05.25.2014	C.orn.MIN.OR	44.919914/ -123.060946	/-
Moon (Birch) Lake, Marquette Co., WI	10.05.2014	C.orn.MN.WI	43.806367/ -89.366509	33
White River Wildlife Refuge, Marquette Co., WI	07.06.2015	C.orn.WRW.WI	43.925724/ -89.099011	34
Twin Lakes Lower Lake, Westmoreland Co., PA	08.06.2012	C.orn.TLL.PA	41.8571827/ -75.3366041	32
Twin Lakes Upper Lake, Westmoreland Co., PA	08.06.2012	C.orn.TLU.PA	41.864246/ -75.338793	32
Lake Nockamixon, Nockamixon State Park, Bucks Co., PA	05.20.2016	C.orn.NockSP.PA	40.462634/ -75.232702	36
Harris pond, Hillsborough Co., NH	07.16.2016	C.orn.Harris.NH	42.018766/ -71.510671	37
Round pond, Hillsborough Co., NH	07.16.2016	C.orn.RoundPond.NH	43.507001/ -71.343171	39
Naticook pond, Hillsborough Co., NH	07.16.2016	C.orn.Naticook.NH	42.82/ -71.5257	38
Flint pond, Hillsborough Co., NH	11.15.2015	C.orn.FLNT.NH	42.74926/ -71.54951	6
Dublin pond, Cheshire Co., NH	07.16.2016	C.orn.Dublin.NH	42.902704/ -72.083412	18
Boxford pond, Essex Co., MA	07.16.2016	C.orn.Boxford.MA	42.673355/ -71.022617	22
Mascuppic Lake, Middlesex Co., MA	07.10.2017	C.orn.MAS.MA	42.672556/ -71.384359	15
Dragonfly pond, Hennepin Co., MN	07.10.2017	C.orn.Dragon.MN	44.879451/ -93.683848	41
Purgatory Creek Wetlands Park, Hennepin Co., MN	07.10.2017	C.orn.Purgatory.MN	44.856886/ -93.44072	2
Red Rock Lake, Hennepin Co., MN	07.10.2017	C.orn.RedRock.MN	44.843811/ -93.470554	12
Empire Pond, Dakota Co., MN	08.21.2017	C.orn.EmpirePond.MN	44.6679/ -93.1267	8
Crosby Lake, Ramsey Co., MN	07.10.2017	C.orn.Crosby.MN	44.882687/ -93.68508	9
Lake Norman, Duluth, GA	04.17.2014	C.orn.Norman.GA	33.9959667/	30

Street pond, Gwinnett Co., GA	04.18.2014	C.orn.STP.GA	-84.1287167 33.9360833/ -84.1366	30
Fish Camp, Highlands Co., FL	01.09.2015	C.orn.FishCP.FL	25.941935/ -80.441761	1
Lake Okeechobee, Glades Co., FL	01.09.2015	C.orn.LKO.FL	26.830456/ -80.941303	3
Tamiami, Miami-Dade Co., FL	01.09.2015	C.orn.Tamiami.FL	25.762214/ -80.507269	16
Site 4, Miami-Dade Co., FL	01.09.2015	C.orn.SIT4.FL	25.761889/ -80.50241	19
Lake June in The Winter, Highlands Co., FL	01.09.2015	C.orn.JUN.FL	27.30715/ -81.37542	25
Lake Jackson, Highlands Co., FL	01.09.2015	C.orn.JAC.FL	27.48775/ -81.47664	26
Lake Annie, Highlands Co., FL	01.09.2015	C.orn.LakeAnnie.FL	27.21027778/ -81.34916667	27
Krome pond, Miami-Dade Co., FL	01.09.2015	C.orn.KRM.FL	25.883615/ -80.484920	28 & 29
Glassman pond, Weber Co., UT	05.20.2016	C.orn.Glass.UT	41.179735/ -111.951601	24
Lake Littra sediments, Chowilla, South Australia	02.2012	C.orn.Littra.Australia	-33.93444/ -80.507269	10
Naticook pond, Hillsborough Co., NH	07.16.2016	<i>Collotheca ferox</i>	42.82/ -71.5257	outgroup
Shorty Howell Lake, Gwinnett Co., GA	08.19.2014	<i>C. teniulobata</i>	33.97455/ -84.14936	outgroup

Supplemental Table S4.1. Contaminant reads and their associated locus number that were removed from ddRAD sequences of *Euchlanis dilatata* using the *blacklist* option in STACKS. Match title shows the GenBank sequence, and their accession number, that had the highest similarity (highest hit score) with the query loci.

Locus	Match Title	Match Accession	% Identity	E-Value
562	<i>Bradyrhizobium japonicum</i> strain J5, complete genome	CP017637.1	94	1.00E-12
2113	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
7320	<i>Caulobacter vibrioides</i> strain CB2 chromosome, complete genome	CP023313.2	100	4.00E-27
9548	Uncultured bacterium clone F5K2Q4C04J3SM2 23S ribosomal RNA gene, partial sequence	GU926857.1	97	8.00E-24
10849	<i>Parastrongyloides trichosuri</i> genome assembly P_trichosuri_KNP, scaffold PTRK_scaffold0000001	LM523158.1	94	5.00E-16
11735	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
12516	<i>Bradyrhizobium</i> sp. CCGE-LA001, complete genome	CP013949.1	99	2.00E-25
12987	<i>Propionibacterium</i> sp. oral taxon 193 strain F0672 plasmid unnamed1, complete sequence	CP017041.1	100	4.00E-27
13252	Uncultured bacterium clone contig79063 genomic sequence	KP447939.1	97	4.00E-22
13652	<i>Bradyrhizobium</i> sp. S23321 DNA, complete genome	AP012279.1	97	8.00E-24
13652	<i>Bradyrhizobium</i> sp. S23321 DNA, complete genome	AP012279.1	97	8.00E-24
13800	<i>Propionibacterium</i> sp. oral taxon 193 strain F0672 plasmid unnamed1, complete sequence	CP017041.1	100	4.00E-27
14098	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	97	8.00E-24
15208	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
15706	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
16317	Uncultured <i>Chlorellales</i> isolate soil 1224 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	MF482435.1	100	4.00E-27
16720	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27

19373	<i>Chlorella vulgaris</i> gene for 28S ribosomal RNA, partial sequence	AB237642.1	100	4.00E-27
19669	<i>Bacterioplanes sanyensis</i> strain NV9, complete genome	CP022530.1	95	1.00E-06
20109	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
20886	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
24063	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
24822	<i>Pongo abelii</i> chromosome 1 clone CH276-56E11, complete sequence	AC275755.1	100	8.00E-04
25013	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
25415	<i>Cutibacterium acnes</i> strain PA_15_1_R1 chromosome, complete genome	CP012355.1	100	1.00E-26
25841	<i>Roseomonas</i> sp. FDAARGOS_362 chromosome, complete genome	CP024588.1	88	6.00E-10
26080	<i>Bradyrhizobium</i> sp. BTAi1 plasmid pBBta01, complete sequence	CP000495.1	94	2.00E-19
26100	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
26339	<i>Bradyrhizobium</i> sp. ORS278, complete sequence	CU234118.1	88	4.00E-07
26851	<i>Caulobacter henricii</i> strain CB4, complete genome	CP013002.1	97	8.00E-24
30845	<i>Bradyrhizobium diazoefficiens</i> strain USDA 122, complete genome	CP013127.1	97	8.00E-24
31008	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
33488	<i>Propionibacterium</i> sp. oral taxon 193 strain F0672, complete genome	CP017040.1	100	4.00E-27
34954	<i>Aureobasidium melanogenum</i> strain SD-47 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	MF467893.1	100	4.00E-27
38199	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27
39609	<i>Human mastadenovirus</i> C isolate human/CHN/BJ04/2012/[P1/H2/F2], complete genome	MF315028.1	100	4.00E-27
42410	<i>Cutibacterium acnes</i> strain A1-14 chromosome	CP013693.1	100	4.00E-27

71053	<i>Bradyrhizobium</i> sp. CCGE-LA001, complete genome	CP013949.1	97	8.00E-24
74837	<i>Escherichia coli</i> strain FDAARGOS_144 plasmid unnamed3	CP014109.1	93	8.00E-19
139072	<i>Cryptosporidium muris</i> RN66 DNA replication licencing factor MCM7, putative, mRNA	XM_002140465.1	91	6.00E-15
143521	<i>Bradyrhizobium diazoefficiens</i> strain USDA 122, complete genome	CP013127.1	97	8.00E-24

Supplemental Table S4.2. Analysis of Molecular Variance (AMOVA) at 107 ddRAD-Seq loci for seven populations of *Euchlanis dilatata* representing cryptic species C and D.

Source of variation	Degrees of freedom	Variance components	Percentage of variation
Among populations	6	10.3	11
Within populations	05	81.2	89
F _{ST} , p value	0.001		

Supplemental Table S4.3. Probability of the number of genetic populations (K) for 110 clonal lineages of *Euchlanis dilatata* calculated by STRUCTURE v 2.3 (Pritchard et al., 2000). K=2 (in bold) had the highest probability. K: genetic populations, Stdev: standard deviation, LnP(K): The log likelihood for each K, Ln'(K): Ln(K)_n- Ln(K)_{n-1}, Ln''(K): Ln'(K)_n- Ln'(K)_{n-1}. Delta K = L''(K)/Stdev.

K	# Replicates	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	Delta K
1	10	-16002	0.23	—	—	—
2	10	-11402	1.14	4600	3301	2874
3	10	-10102	1.36	1299	620	454.71
4	10	-9423	140.76	680	83	0.58
5	10	-8826	2.03	597	161	79.12
6	10	-8391	117.25	435	617	5.25
7	10	-8572	797.24	-181	585	0.73
8	10	-9338	2241.17	-766	—	—

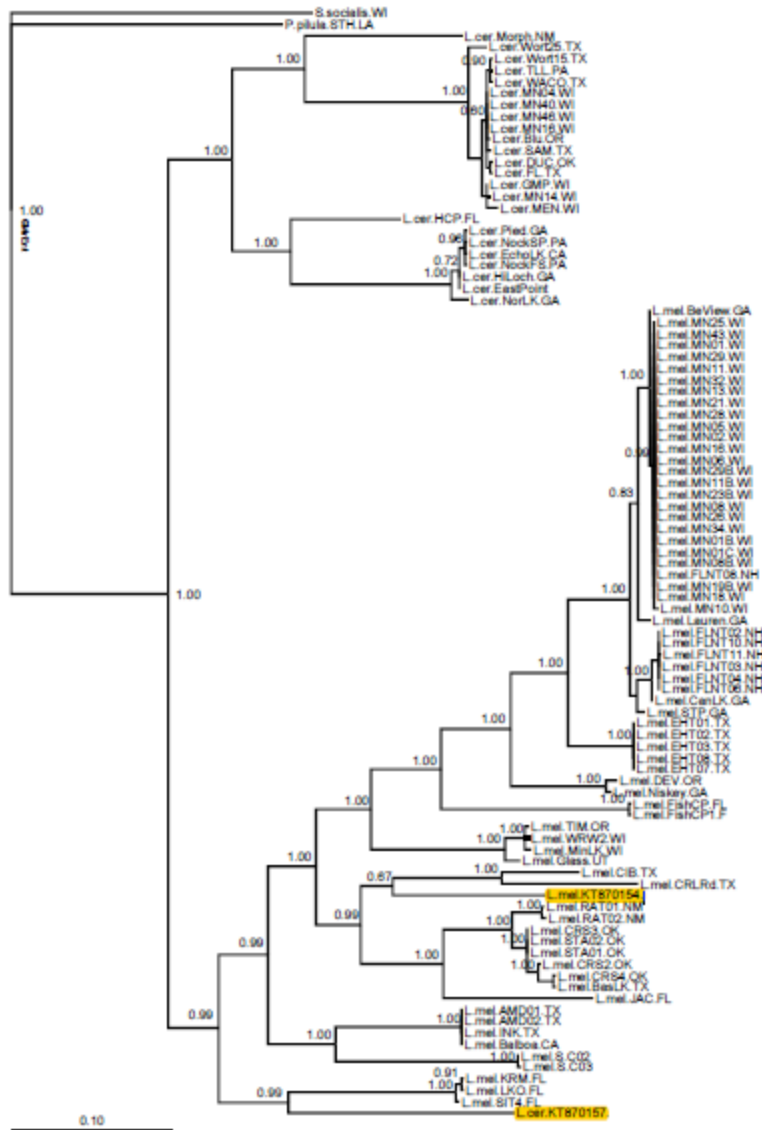


Figure S2.1. The Bayesian inference consensus phylogenetic tree based on partial COI gene sequences of 29 populations of the morphological species *Limnias melicerta*, 20 populations of *L. ceratophylli* and two sequences available at GenBank (L.mel.KT870154 and L.cer.JT870157, highlighted yellow). Abbreviations as in Tables S2.1 and S2.2; independent clonal isolates are indicated by a number (e.g., 01).

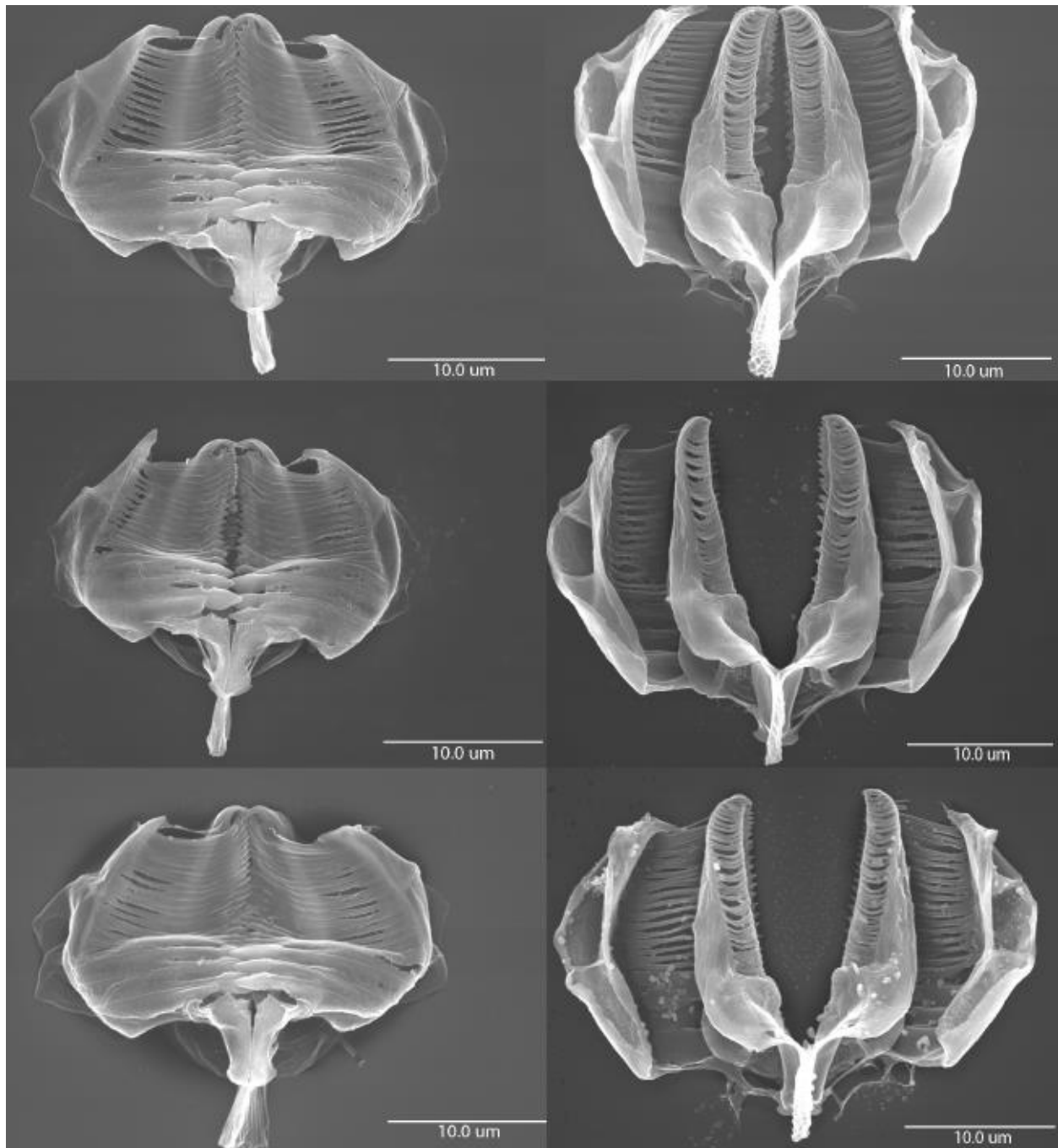


Figure S2.2. Trophi of *Limnias melicerta*. Berkeley View, GA (cryptic species E), caudal view (top left), frontal view (top right), Lake Niskey, GA (cryptic species G), caudal view (middle left), frontal view (middle right), Glassman Pond, UT (cryptic species I), caudal view (bottom left), frontal view (bottom right).

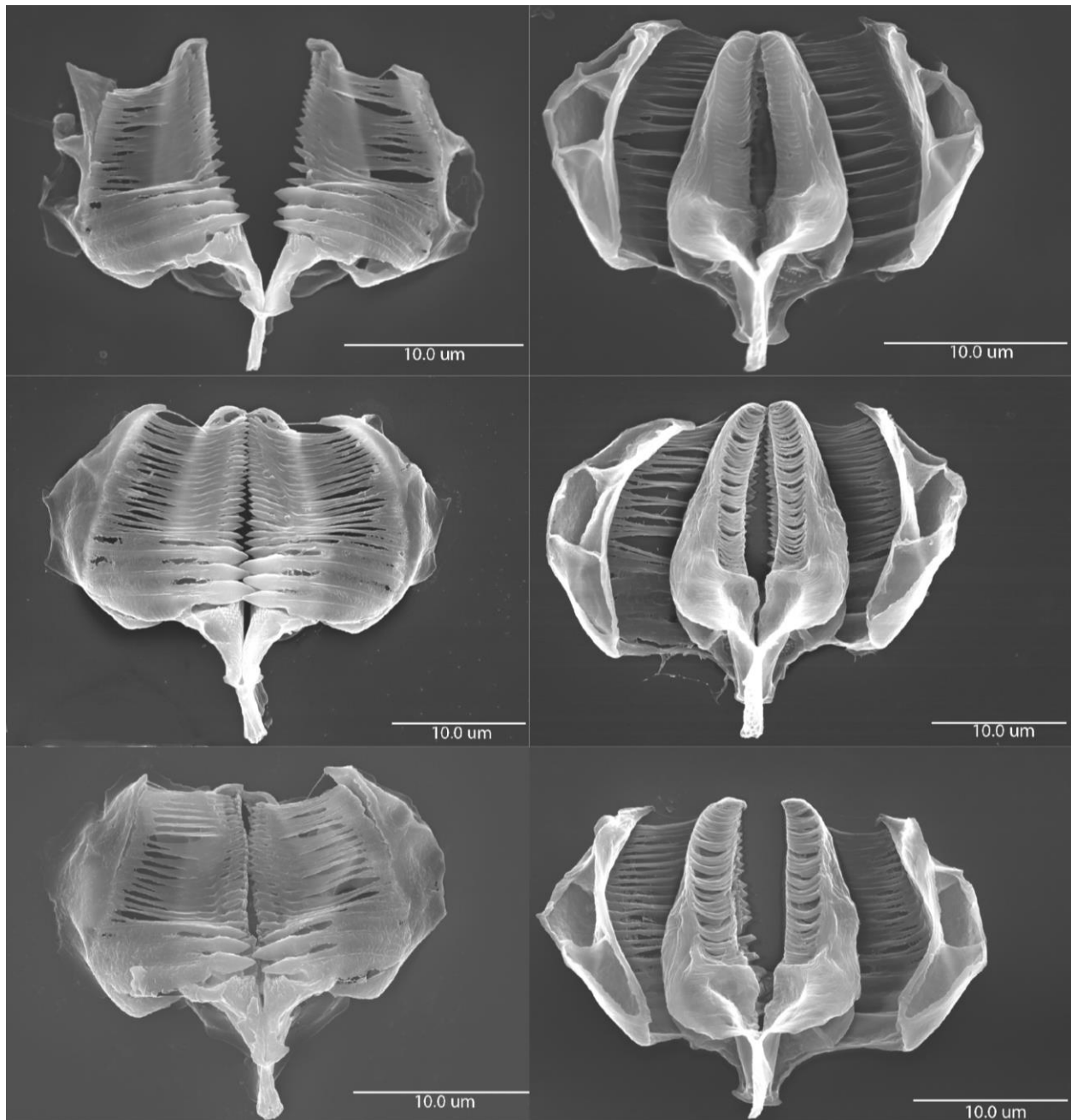


Figure S2.3. Trophi of *Limnias melicerta*. Rattlesnake Spring, NM (cryptic species K), caudal view (top left), frontal view (top right), Rio Grande, TX (cryptic species L), caudal view (middle left), frontal view (middle right), Krome Pond, FL (cryptic species M), caudal view (bottom left), frontal view (bottom right).

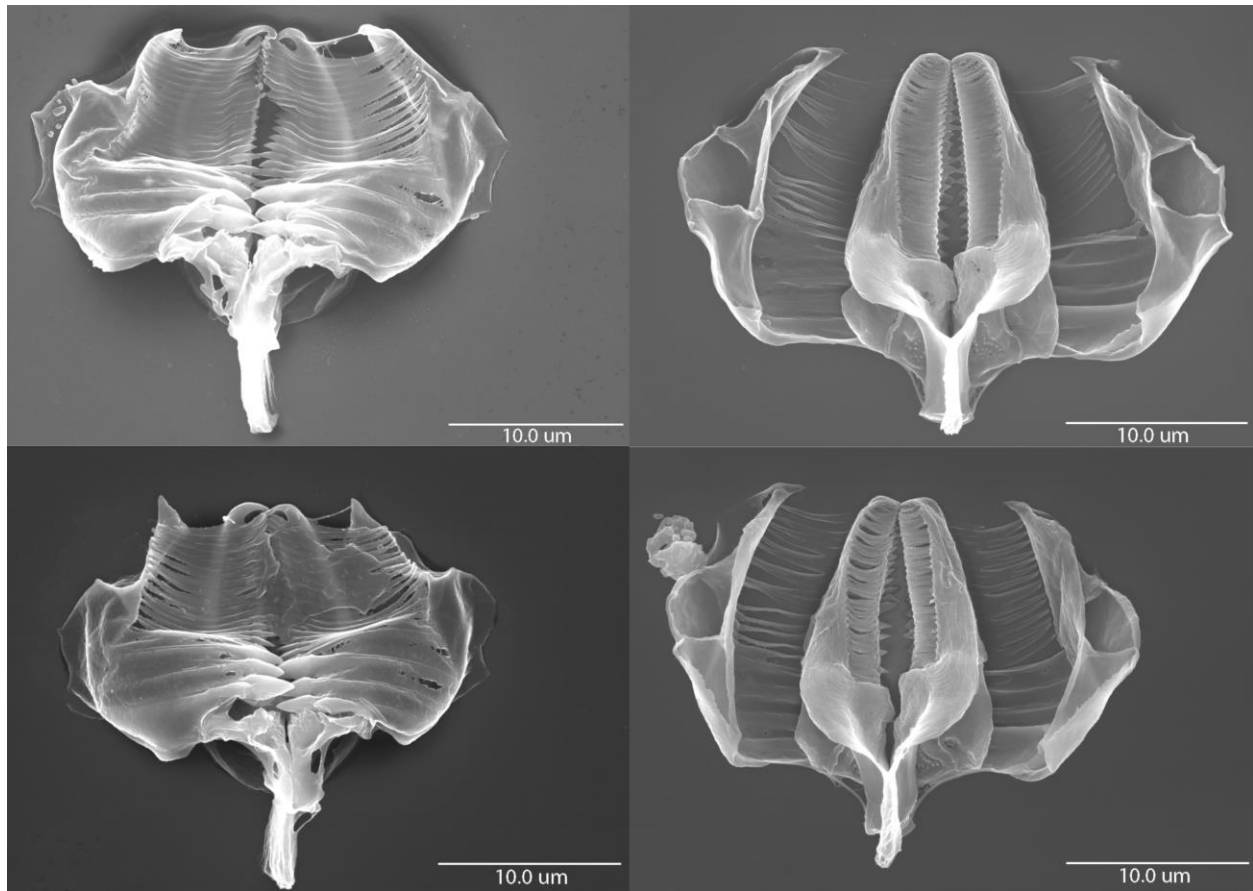


Figure S2.4. Trophi of *Limnias ceratophylli*. Feather Lake Wildlife Sanctuary, TX (cryptic species B), caudal view (top left), frontal view (top right), Norman Lake, GA (cryptic species D), caudal view (bottom left), frontal view (bottom right).

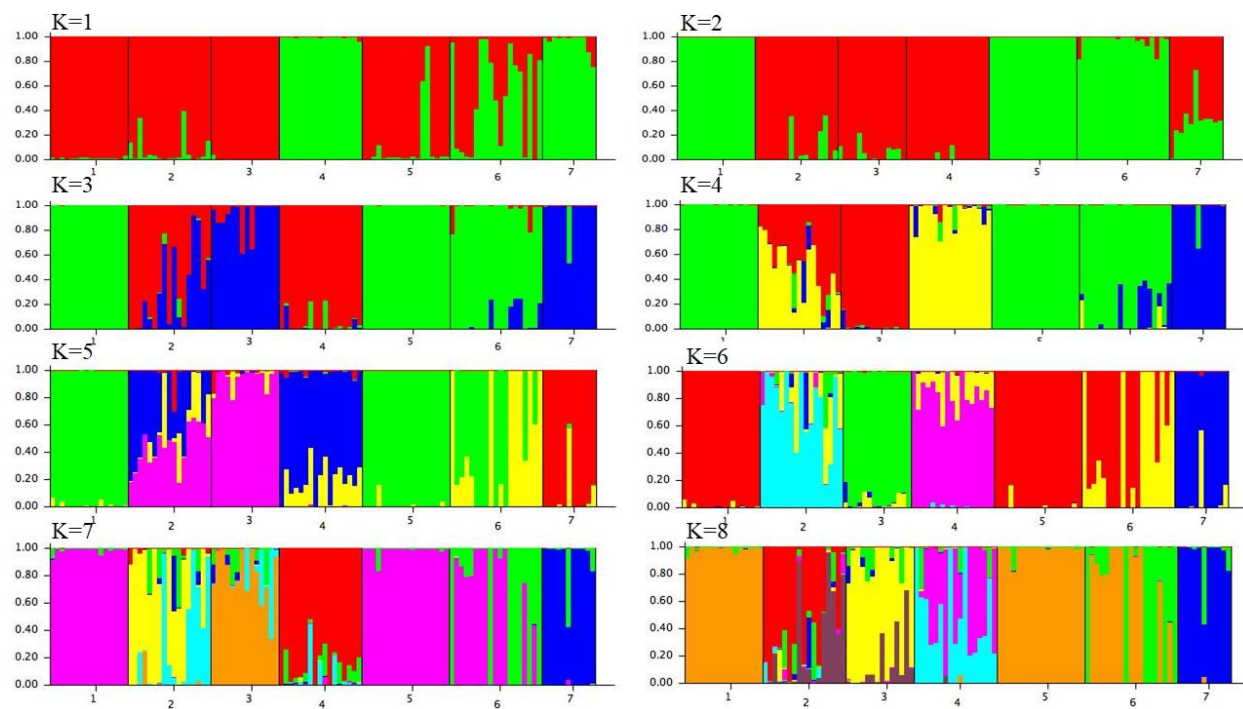


Figure S4.1. Population assignment probabilities (Y-axis) of 110 *Euchlanis dilatata* clonal lineages estimated from 107 ddRAD-Seq loci recovered from seven populations representing two cryptic species for K= 1-7. Cryptic species C; 2: Mescalero Canyon, TX, 3: Miller Ranch, TX, 4: Laguna Prieta, TX, 7: Triangle Pond, AZ. Cryptic species D; 1: Cattle Tank, NM, 5: Peccary Tank, TX, 6: Red Tank, TX. The log likelihood value for each model is given in Supplemental Table S4.2.

Supplemental document S1.3: CLUSTAL format alignment of COI sequences of *Euchlanis dilatata* by MAFFT (v7.380). Abbreviations are the same as in Table S1.1. N= missing data.

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E.ALATA.NH.DQ07 ATATCTTTTTTAAATTCGCTTAGAGCTTGGAACGTGCGCCCCCTAATTGGAGATGAGCAT
E.DEFLEXA.SHC.L ATGTCTTTTTTTATTCGCCTTGAGCTAGGTACAGTAGGCCCCCTTATTGGGACGAGCAT
E.DIL.DQ297773. ATAAGATTTCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.TRP.AZ NNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W10.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W06.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W12.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W02.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W34.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W01.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W26.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W241.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W24.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W27.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
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E.DIL.MIL.TX ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
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E.DIL.AMD.TX ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.FL.TX NNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W33.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W28.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.CRS.OK ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.W11.RG ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
E.DIL.MSHT.TX ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATCGGCCCTTATATTGGGGACGAGCAC
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E.DIL.ROT.TX ATAAGATTTCTAATTCGTCTAGAGCTTGGTGTTATTGGCCCTTATATTGGGGACGAGCAC
E.DIL.COT.TX ATAAGATTTCTAATTCGTCTAGAGCTTGGTGTTATTGGCCCTTATATTGGGGACGAGCAC
E.DIL.GL06BB.TX ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATTGGCCCTTATATTGGGGACGAGCAC
E.DIL.GL03BB.TX ATAAGATTCCTAATTCGTCTAGAGCTTGGTGTTATTGGCCCTTATATTGGGGACGAGCAC
E.DIL.PPC.TX ATAAGATTTCTTATTCGTCTAGAGCTTGGAGTTATTGGGCCTTATATTGGAGACGAACAC
E.DIL.I10.TX ATAAGATTTCTAATTCGTCTAGAGCTTGGTGTAATTGGTCCTTATATTGGGGACGAGCAC
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E.DIL.AMR.CA ATAAGATTTCTTATTCGTCTAGAGCTTGGAGTTATTGGGCCTTATATTGGAGACGAACAC
E.DIL.LOD02.CA NNNNNNNNNNNNATTCGTCTAGAGCTGGGTGTTATTGGTCCTTATATTGGTGATGAACAC
E.DIL.ECH.FL ATGAGATTTTTAATTCGTTTAGAGCTGGGTGTTATTGGTCCTTATATTGGTGATGAACAC
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E.DIL.LOD01.CA ATGAGATTTTTAATTCGTTTAGAGCTAGGTGTTATTGGTCCTTATATTGGTGATGAACAC
E.DIL.STR.NM ATGAGATTTTTAATTCGTTTAGAGCTAGGTGTTATTGGTCCTTATATTGGTGATGAGCAC
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E.DIL.STP.GA ATGAGATTTTTAATTCGTTTAGAGCTAGGTGTTATCGGTCCTTATATTGGTGATGAACAC
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E.DIL.OSM.M ATAAGATTCCTTATTCGTTTAGAGTTAGGGGTTATTGGTCCTTATATTGGGGATGAACAT

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E.DIL.W300.RG	ATAAGGTTTCTTATTCGTTTAGAGCTTGGTGTAATCGGCCCTTATATTGGTGATGAGCAT
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E.DIL.W79.RG	ATAAGGTTTCTTATTCGTTTAGAGCTTGGTGTAATCGGCCCTTATATTGGTGATGAGCAT
E.DIL.PHL.PA	ATAAGGTTTCTTATTCGTTTAGAGCTTGGTGTAATCGGCCCTTATATTGGTGATGAGCAT
E.DIL.BOQ.M	ATAAGGTTTCTTATTCGTTTAGAGCTTGGTGTAATCGGCCCTTATATTGGTGATGAGCAT
E.DIL.DEC.TX	ATAAGGTTTTTAATTCGTTTAGAGCTTGGTGTAATCGGCCCTTATATTGGTGATGAGCAC
E.DIL.TRV.TX	NNNNNNNNNNNNNNNNNNNNNNNGAGCTTGGTGTAATCGGCCCTTATATTGGTGATGAGCAT
E.DIL.CENT.CA	ATAAGGTTTCTTATTCGTTTAGAGCTTGGCGTAATCGGCCCTTATATTGGTGATGAGCAT
E.DIL.CBB.VI	ATGAGATTTTTAATCCGATTAGAGCTTGGTGTAATTGGTCCTTATATTGGTGATGAGCAT
E.DIL.BEC.NM	ATAAGTTTCCTGATCCGTTTAGAACTAGGGGTTATTGGCCCCTATATTGGCGATGAGCAT
E.DIL.ALT.NM	ATAAGCTTCCTCATCCGTTTAGAGCTTGGAGTTATTGGTTCTTATATTGGTGATGAACAT
E.DIL.MEN.WI	ATAAGCTTCCTCATCCGTTTAGAGCTTGGAGTTATTGGTTCTTATATTGGTGATGAACAT
E.DIL.DTL.OR	ATAAGTTTCCTCATTCGTTTAGAACTAGGAGTTATTGGCCCCTATATCGGTGATGAGCAT
E.DIL.SIL.UT	NNNNNNNNNTCATTTCGTTTAGAACTAGGAGTTATTGGTCCTTATATCGGTGATGAGCAT
E.DIL.CHIC.UT	ATAAGTTTCCTCATTCGTTTAGAACTAGGAGTTATTGGTCCTTATATCGGTGATGAGCAT
E.DIL.SEQ.UT	ATAAGTTTCTCATTCGTTTAGAGCTAGGAGTCATCGGTCCCTTATATTGGCGATGAACAC
E.DIL.SCH.PA	ATAAGTTTCTTATTCGTCTAGAATTAGGCGTTATTGGGCCCTTATATTGGAGATGAGCAC
E.DIL.DRS.NM	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.F13.RG	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.CATG01BB.	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.CATG02BB.	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.CATCPBB.T	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.CATEBB.TX	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.CATDBB.TX	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.BUBB3.TX	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.BUBB2.TX	ATAAGTTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.JUN.FL	ATAAGCTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.JAC.FL	ATAAGCTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.OKR.OK	ATAAGCTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.DUC.OK	ATAAGCTTCTTATTCGTCTTGAGTTAGGAGTTATTGGGTCTTATATTGGAGATGAGCAT
E.DIL.MC.M	ATAAGTTTCTTATTCGTTTAGAGTTGGGGTTATTGGTCCTTATATTGGGGACGAGCAT
E.DIL.JX216599.	ATAAGATTCTTAATTCGTTTAGAATTAGGGGTTATTGGGCCTTATATTGGAGATGAACAT
E.DIL.JX216598.	ATAAGATTCTTAATTCGTTTAGAATTAGGGGTTATTGGGCCTTATATTGGAGATGAACAT
E.DIL.KRM01.FL	ATGAGTTTTCTTATTCGTTTAGAGCTTGGTGTTATTGGCCCCTTATATTGGTGATGAGCAT
E.DIL.KRM02.FL	ATGAGTTTTCTTATTCGTTTAGAGCTTGGTATTATTGGCCCCTACATTGGTGATGAGCAT
E.DIL.MC03.M	ATGAGATTTTTGATTTCGTTTAGAATTAGGAGTCATTGGTCCTTATATTGGTGATGAGCAT

E.ALATA.NH.DQ07	CTATACAATGTTGTAGTTACAGCCCATGCATTTATCATAATTTTTTTCATGGTTATGCCA
E.DEFLEXA.SHC.L	CTTTATAATGTTATAGTTACAGCTCATGCTTTTATTATAATTTTTTTCATAGTAATGCCC
E.DIL.DQ297773.	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATACCT
E.DIL.TRP.AZ	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W10.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W06.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W12.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W02.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W34.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W01.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W26.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W241.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W24.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W27.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.W31.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.MIL.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.BMCHT.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.LPHT.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT
E.DIL.SAM.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTATAATTTTCTTCATGGTTATGCCT

E.DIL.AMD.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.FL.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.W33.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTTTTCATGGTTATGCCT
E.DIL.W28.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTTTTCATGGTTATGCCT
E.DIL.CRS.OK	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTTTTCATGGTTATGCCT
E.DIL.W11.RG	TTATACAACGTTATAGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.MSHT.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.W36.RG	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.MCHT.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.ROT.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.COT.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.GL06BB.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.GL03BB.TX	TTATACAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.PPC.TX	CTTTTATAACGTTATGGTAACAGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.I10.TX	CTATATAACGTTATGGTAACGGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.SHL.GA	CTATATAACGTTATGGTAACGGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.MC02.M	CTATACAACGTTATGGTAACGGCTCATGCTTTTGTGTTATAATTTTCTTCATGGTTATGCCT
E.DIL.AMR.CA	CTTTTATAACGTTATGGTAACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.LOD02.CA	CTTTTATAACGTCATGGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATGGTTATGCCT
E.DIL.ECH.FL	CTTTTATAACGTCATGGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATGGTTATGCCT
E.DIL.TIM.OR	CTTTTATAACGTCATGGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATGGTTATGCCT
E.DIL.MAD.WI	CTTTTATAATGTCATGGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATGGTTATGCCT
E.DIL.LOD01.CA	CTTTTATAACGTCATGGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATGGTTATGCCT
E.DIL.STR.NM	CTCTATAATGTCATGGTCACTGCTCATGCTTTTGTGTTATGATTTTCTTCATGGTTATGCCT
E.DIL.NOCK.PA	CTCTATAATGTCATGGTCACTGCTCATGCTTTTGTGTTATGATTTTCTTCATGGTTATGCCT
E.DIL.STP.GA	CTCTATAACGTCATGGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTCATGGTTATGCCT
E.DIL.LKOJC.FL	CTATACAATGTTATAGTTACTGCTCATGCTTTTCGTTATAATTTTTTTTTATGGTTATGCCT
E.DIL.CTS.NM	TTATATAACGTCATGGTTACTGCCCACGCTTTGTTATGATTTTTTTTTATGGTTATGCCT
E.DIL.RET.TX	TTATATAACGTCATGGTTACTGCCCACGCTTTGTTATGATTTTTTTTTATGGTTATACCT
E.DIL.PGTBB.TX	CTATATAATGTTATGGTTACTGCTCATGCTTTTGTGTTATGATTTTTTTTTATGGTTATACCT
E.DIL.OSM.M	CTATATAATGTTATGGTTACTGCTCATGCTTTTGTGTTATGATTTTTTTTTATGGTTATACCT
E.DIL.W300.RG	TTATATAATGTTATAGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATAGTTATGCCA
E.DIL.MES.NM	TTATATAATGTTATAGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATAGTTATGCCA
E.DIL.W79.RG	TTATATAATGTTATAGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATAGTTATGCCA
E.DIL.PHL.PA	TTATATAATGTTATAGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATAGTTATGCCA
E.DIL.BOQ.M	TTATATAATGTTATAGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATAGTTATGCCA
E.DIL.DEC.TX	TTATATAATGTTATGGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATAGTTATGCCA
E.DIL.TRV.TX	TTATATAATGTTATGGTAACGCTCATGCTTTTGTGTTATGATTTTTTTTTATAGTTATGCCA
E.DIL.CENT.CA	TTATACAATGTTATGGTAACGCTCATGCTTTTGTGTTATAATTTTTTTTTATAGTTATACCA
E.DIL.CBB.VI	TTATACAATGTTATGGTTACTGCTCATGCTTTTGTGTTATAATTTTTTTTTATAGTTATGCCC
E.DIL.BEC.NM	TTATATAATGTTATGGTAACAGCTCACGCTTTTATTATAATTTTTTTTCATAGTTATGCCG
E.DIL.ALT.NM	CTATATAATGTTATGGTGACAGCTCACGCTTTTATTATAATCTTTTTTTATAGTTATGCCC
E.DIL.MEN.WI	CTATATAATGTTATGGTGACAGCTCACGCTTTTATTATAATCTTTTTTTATAGTTATGCCA
E.DIL.DTL.OR	TTATATAATGTTATAGTAACAGCTCACGCTTTTATCATAATCTTTTTTTATAGTTATGCCC
E.DIL.SIL.UT	TTATATAATGTTATAGTAACAGCTCACGCTTTTATCATAATCTTTTTTTATAGTTATGCCC
E.DIL.CHIC.UT	TTATATAATGTTATAGTGACAGCTCATGCTTTTATCATAATCTTTTTTTATAGTTATACCT
E.DIL.SEQ.UT	TTGTATAATGTTATAGTTACAGCTCACGCTTTTGTGTTATAATCTTTTTTTATGGTTATGCCA
E.DIL.SCH.PA	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.DRS.NM	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.F13.RG	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.CATG01BB.	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.CATG02BB.	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.CATCPBB.T	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.CATEBB.TX	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.CATDBB.TX	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.BUBB3.TX	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT
E.DIL.BUBB2.TX	CTTTTATAATGTTATAGTCACAGCTCATGCTTTTGTGTTATGATTTTCTTTATAGTTATGCCT

E.DIL.JUN.FL	CTTTATAATGTTATAGTTACAGCTCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT
E.DIL.JAC.FL	CTTTATAATGTTATAGTTACAGCTCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT
E.DIL.OKR.OK	CTTTATAATGTTATAGTTACAGCTCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT
E.DIL.DUC.OK	CTTTATAATGTTATAGTTACAGCTCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT
E.DIL.MC.M	TTATACAATGTTATAGTAACGGCTCATGCTTTTGTTCATGATCTTTTTTATGGTTATGCCT
E.DIL.JX216599.	CTATACAATGTTATGGTCACTGCTCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT
E.DIL.JX216598.	CTATACAATGTTATGGTCACTGCTCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT
E.DIL.KRM01.FL	CTTTATAATGTTATGGTCACTGCCCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT
E.DIL.KRM02.FL	CTTTATAATGTGATGGTCACTGCCCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT
E.DIL.MC03.M	CTTTATAATGTTATAGTAACGCTCATGCTTTTGTTCATGATTTTCTTTATAGTTATGCCT

E.ALATA.NH.DQ07	ATCTCTATGGGTGGCTTTTGGAAATTGATTAATTCCTTTAATACTTGGGGTAGCTGATATG
E.DEFLEXA.SHC.L	ATCTCAATAGGAGGTTTTGGAACTGACTTATTCCTCTTATGCTAGGAGTAGCTGATATA
E.DIL.DQ297773.	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.TRP.AZ	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W10.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W06.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W12.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W02.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W34.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W01.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W26.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W241.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W24.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W27.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W31.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.MIL.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.BMCHT.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.LPHT.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.SAM.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.AMD.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.FL.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W33.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W28.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.CRS.OK	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.W11.RG	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.MSHT.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
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E.DIL.ROT.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.COT.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.GL06BB.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
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E.DIL.I10.TX	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.SHL.GA	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.MC02.M	ATTTCTATGGGTGGCTTTTGGTAACTGGCTTATTCCTTTAATGCTAGGTGTTGCTGATATG
E.DIL.AMR.CA	ATTTCTATAGGTGGTTTTGGTAACTGGCTAATCCCTTTAATGTTGGGTGTTGCCGATATG
E.DIL.LOD02.CA	ATTTCTATGGGTGGCTTTCGGTAACTGACTTATCCCTTTAATGTTAGGTGTTGCTGATATG
E.DIL.ECH.FL	ATTTCTATGGGTGGCTTTCGGTAACTGACTTATCCCTTTAATGTTAGGTGTTGCTGATATG
E.DIL.TIM.OR	ATTTCTATGGGTGGCTTTCGGTAACTGACTTATCCCTTTAATGTTAGGTGTTGCTGATATG
E.DIL.MAD.WI	ATTTCTATGGGTGGCTTTCGGTAACTGACTTATCCCTTTAATGTTAGGTGTTGCTGATATG
E.DIL.LOD01.CA	ATTTCTATGGGTGGCTTTCGGTAACTGACTTATCCCTTTAATGTTAGGTGTTGCTGATATG
E.DIL.STR.NM	ATTTCTATGGGTGGCTTTCGGTAACTGACTTATCCCTTTAATGTTAGGTGTTGCTGATATG
E.DIL.NOCK.PA	ATTTCTATGGGTGGCTTTCGGTAACTGACTTATCCCTTTAATGTTAGGTGTTGCTGATATG
E.DIL.STP.GA	ATTTCTATGGGTGGCTTTCGGTAACTGACTTATCCCTTTAATGTTAGGTGTTGCTGATATG

E.DIL.LKOJC.FL ATTTCTATGGGTGGTTTTGGTAACTGACTAATTCCATTGATGTTAGGTGTTGCCGATATG
 E.DIL.CTS.NM ATTTCTATGGGTGGCTTTGGTAACTGACTTATTCCACTAATGTTGGGTGTTGCTGATATG
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 E.DIL.CBB.VI ATTTCCATAGGGGGTTTTGGTAACTGGCTTATTCCCTTTAATGCTAGGGGTTGCTGATATG
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 E.DIL.SIL.UT ATCTCTATAGGAGGTTTTGGAAATTGATTAATCCCATTAATATTAGGTGTAGTCGATATA
 E.DIL.CHIC.UT ATCTCTATAGGAGGTTTTGGAAATTGATTAATCCCATTAATATTAGGTGTAGTCGATATA
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 E.DIL.CATEBB.TX ATTTCTATAGGGGGTTTTGGTAACTGACTTATTCCCTCTTATGCTAGGTGTTGCTGATATG
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 E.DIL.JX216599. ATTTCTATAGGGGGTTTTGGGAATTGACTTATTCCCTTTAATGCTTGGTGTGCTGATATG
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 E.DIL.MC03.M ATTTCTATAGGAGGTTTTGGTAACTGACTTATTCCATTAATGCTAGGAGTAGCTGATATG

E.ALATA.NH.DQ07 GCTTTCCCTCGTCTTAATAATTTATCTTTCTGACTGCTTCTTCCTTCCTTTGCATTCCCTA
 E.DEFLEXA.SHC.L GCTTTTCCACGCTTAAATAATTTATCCTTTTGACTTCTACTTCCTTCCTTTTAGTTTTTTA
 E.DIL.DQ297773. GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.TRP.AZ GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.W10.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.W06.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.W12.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
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 E.DIL.W34.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.W01.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.W26.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.W241.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.W24.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA
 E.DIL.W27.RG GCCTTTCCCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTA

E.DIL.W31.RG	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.MIL.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.BMCHT.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.LPHT.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.SAM.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.AMD.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.FL.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.W33.RG	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.W28.RG	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.CRS.OK	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.W11.RG	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.MSHT.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.W36.RG	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.MCHT.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.ROT.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.COT.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.GL06BB.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.GL03BB.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.PPC.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGGCTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.I10.TX	GCCTTTCTCGAATGAATAACCTTTCTTTTTGACTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.SHL.GA	GCCTTTCTCGAATGAATAACCTTTCTTTTTGACTTCTTATTCCCTTCATTTACATTTCTA
E.DIL.MC02.M	GCCTTTCTCGAATGAATAATCTTTCTTTTTGACTTCTTATTCCCTTCATTTACATTTTTTA
E.DIL.AMR.CA	GCCTTTCTCGAATGAACAATCTTTCTTTCTGATTACTTATTCCATCTTTTACATTTTTTA
E.DIL.LOD02.CA	GCTTTTCCCCGTATGAACAATCTTTCATTCTGACTTCTTATTCCCTTCTTTTACTTTTTTA
E.DIL.ECH.FL	GCTTTTCCCCGTATGAACAATCTTTCATTCTGACTTCTTATTCCCTTCTTTTACTTTTTTA
E.DIL.TIM.OR	GCTTTTCCCCGTATGAACAATCTTTCATTCTGACTTCTTATTCCCTTCTTTTACTTTTTTA
E.DIL.MAD.WI	GCTTTTCCCTCGTATGAACAATCTTTCATTCTGACTTCTTATTCCCTTCTTTTACTTTTTTA
E.DIL.LOD01.CA	GCTTTTCCCCGTATGAACAATCTTTCTTTCTGACTTCTTATTCCCTTCTTTTACTTTTTTA
E.DIL.STR.NM	GCTTTTCCCCGTATGAACAATCTTTCTTTCTGACTATTAATTCCTTCCCTTACTTTTTTA
E.DIL.NOCK.PA	GCTTTTCCCCGTATGAACAATCTTTCTTTCTGACTATTAATTCCTTCCCTTACTTTTTTA
E.DIL.STP.GA	GCTTTTCCCCGTATGAACAATCTTTCTTTCTGACTATTAATTCCTTCTTTTACTTTTTTA
E.DIL.LKOJC.FL	GCCTTTCTCGAATGAATAATCTTTCTTTTTGACTACTTATTCCCTCTTTTACTTTTTTA
E.DIL.CTS.NM	GCTTTCCCACGTATAAATAATCTTTCTTTCTGGCTTCTTATTCCATCTTTTACTTTTTTA
E.DIL.RET.TX	GCTTTCCCACGTATAAATAATCTTTCTTTCTGGCTTCTTATTCCATCTTTTACTTTTTTA
E.DIL.PGTBB.TX	GCTTTCCCCCGCATAAATAATCTTTCTTTCTGGCTTCTTATTCCATCTTTTACTTTTTTA
E.DIL.OSM.M	GCTTTCCCCCGCATAAATAATCTTTCTTTCTGGCTTCTTATTCCATCTTTTACTTTTTTA
E.DIL.W300.RG	GCTTTCCCCCGAATGAATAATCTTTCTTTTGGACTTCTTATTCCCTTCTTTTACCTTCTTA
E.DIL.MES.NM	GCTTTCCCCCGAATGAATAATCTTTCTTTTGGACTTCTTATTCCCTTCTTTTACCTTCTTA
E.DIL.W79.RG	GCTTTCCCCCGAATGAATAACCTTTCTTTTGGACTTCTTATTCCCTTCTTTTACCTTCTTA
E.DIL.PHL.PA	GCATTCCCCCGAATGAATAACCTTTCTTTTGGACTTCTTATTCCCTTCTTTTACCTTCTTA
E.DIL.BOQ.M	GCTTTCCCCCGAATGAATAACCTTTCTTTTGGACTTCTTATTCCCTTCTTTTACCTTCTTA
E.DIL.DEC.TX	GCTTTCCCCCGAATGAATAACCTTTCTTTTGGACTTCTTATTCCCTTCTTTTACCTTTTTTA
E.DIL.TRV.TX	GCTTTCCCCCGAATGAATAACCTTTCTTTTGGACTTCTTATTCCCTTCTTTTACCTTTTTTA
E.DIL.CENT.CA	GCTTTTCCTCGAATAAATAATCTTTCTTTTGGACTTCTTATTCCCTCTTTCACCTTTTTTA
E.DIL.CBB.VI	GCTTTTCCTCGCATAAATAATCTTTCTTTTGGACTTCTTATCCCTCTTTCACCTTTCTA
E.DIL.BEC.NM	GCCTTTCTCGCATAAATAATCTTTCTTTTGGATTACTAATTCCATCTCTTACATTTTTTA
E.DIL.ALT.NM	GCCTTTCTCGCATAAATAACCTTTCTTTTGGATTACTAATTCCCTCCCTTACTTTTTTA
E.DIL.MEN.WI	GCCTTTCTCGCATAAATAATCTTTCTTTTGGATTACTAATTCCATCCCTTACTTTTTTA
E.DIL.DTL.OR	GCCTTTCTCGCATAAATAATCTTTCTTTTGGATTGCTAATTCCATCCCTTACTTTTTTA
E.DIL.SIL.UT	GCCTTTCTCGCATAAATAATCTTTCTTTTGGATTGCTAATTCCATCCCTTACTTTTTTA
E.DIL.CHIC.UT	GCCTTTCTCGCATAAATAACCTTTCTTTTGGACTACTAATTCCTTCTCTAACTTTTTTA
E.DIL.SEQ.UT	GCATTTCTCGTATAAATAACCTTTCTTTTGGTTACTAATTCCTTCGTTTACTTTTTTA
E.DIL.SCH.PA	GCATTTCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCTTCTTTTACTTTCTT
E.DIL.DRS.NM	GCATTTCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCTTCTTTTACTTTCTT
E.DIL.F13.RG	GCATTTCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCTTCTTTTACTTTCTT
E.DIL.CATG01BB.	GCATTTCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCTTCTTTTACTTTCTT
E.DIL.CATG02BB.	GCATTTCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCTTCTTTTACTTTCTT

E.DIL.CATCPBB.T GCATTTTCCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCCTTCTTTTACTTTTCCTT
 E.DIL.CATEBB.TX GCATTTTCCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCCTTCTTTTACTTTTCCTT
 E.DIL.CATDBB.TX GCATTTTCCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCCTTCTTTTACTTTTCCTT
 E.DIL.BUBB3.TX GCATTTTCCTCGCATAAACAACCTCTCTTTCTGACTTTTAGTTCCCTTCTTTTACTTTTCCTT
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 E.DIL.JUN.FL GCATTTTCCTCGCATAAACAATCTCTCTTTCTGGCTTTTAGTTCCCTTCTTTTACTTTTCCTT
 E.DIL.JAC.FL GCATTTTCCTCGCATAAACAATCTCTCTTTCTGACTTTTAGTTCCCTTCTTTTACTTTTCCTT
 E.DIL.OKR.OK GCATTTTCCTCGCATAAATAACCTCTCTTTTTGACTTTTAGTTCCCTTCTTTTACTTTTCCTT
 E.DIL.DUC.OK GCATTTTCCTCGCATAAATAACCTCTCTTTTTGACTTTTAGTTCCCTTCTTTTACTTTTCCTT
 E.DIL.MC.M GCTTTTCCTCGTATGAATAATCTTTCTTTCTGACTTTTAGTTCCCTTCTTTTACTTTTTTA
 E.DIL.JX216599.GCTTTCCCTCGTATGAATAACCTTTCTTTTTGACTTTTAGTTCCCTTCTTTTACTTTTTTA
 E.DIL.JX216598.GCTTTCCCTCGTATGAATAACCTTTCTTTTTGACTTTTAGTTCCCTTCTTTTACTTTTTTA
 E.DIL.KRM01.FL GCATTTCCCTCGTATAAATAACCTTTCTTTCTGACTTCTTATTCCTTCTTTTTCTTTCCCTT
 E.DIL.KRM02.FL GCGTTCCCTCGTATAAATAACCTTTCTTTCTGATTGCTTATTCCTTCTTTTTCTTTCCCTT
 E.DIL.MC03.M GCATTTTCCTCGTATAAACAATTTGTCTTTTTGACTATTAGTTCCCTTCTTTCTTTTTCTT

E.ALATA.NH.DQ07 CTTCTCTCGTCTATTATTAGAGCAGGTGTAGGCACTGGGTGAACTGTTTACCCTCCCCTT
 E.DEFLEXA.SHC.L CTACTGTCCTCAATTATTAGTGCCGGAGTAGGAACAGGCTGAACTGTTTACCCCCCTTA
 E.DIL.DQ297773.TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACTGTTTACCCCCACTT
 E.DIL.TRP.AZ TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACGGTTTATCCTCCTCTT
 E.DIL.W10.RG TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACTGTTTATCCTCCTCTT
 E.DIL.W06.RG TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACTGTTTATCCTCCTCTT
 E.DIL.W12.RG TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACTGTTTATCCTCCTCTT
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 E.DIL.FL.TX TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACTGTTTATCCTCCTCTT
 E.DIL.W33.RG TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACTGTTTATCCTCCTCTT
 E.DIL.W28.RG TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACTGTTTATCCTCCTCTT
 E.DIL.CRS.OK TTATTATCATCTATCTTAGATGCTGGTGTGGTACTGGTTGAACTGTTTATCCTCCTCTT
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 E.DIL.LOD02.CA TTATTATCTTCTATCCTTGATGCTGGTGTGGTACTGGTTGAACTGTCTATCCTCCTCTT
 E.DIL.ECH.FL TTATTATCTTCTATCCTTGATGCTGGTGTGGTACTGGTTGAACTGTCTATCCTCCTCTT
 E.DIL.TIM.OR TTATTATCTTCTATCCTTGATGCTGGTGTGGTACTGGTTGAACTGTATATCCTCCTCTT

E.DIL.MAD.WI	CTATTGTCTTCTATTCTTGACGCTGGTGTGGTACCGGTTGAACTGTCTATCCTCCTCTT
E.DIL.LOD01.CA	TTACTATCTTCTATTCTTGATGCTGGTGTAGGTACCGGTTGAACTGTCTATCCTCCTCTA
E.DIL.STR.NM	CTACTTTCTTCTATTCTTGATGCTGGTGTAGGTACCGGCTGAACTGTTTATCCTCCTTTG
E.DIL.NOCK.PA	CTACTTTCTTCTATTCTTGATGCTGGTGTAGGTACCGGCTGAACTGTTTATCCTCCTTTG
E.DIL.STP.GA	CTACTGTCTTCTATTCTTGATGCTGGTGTAGGTACCGGCTGAACTGTTTATCCTCCTTTA
E.DIL.LKOJC.FL	TTACTTTCTTCTATTCTAGATGCTGGTGTGGTACTGGTTGAACAGTTTACCCTCCATTA
E.DIL.CTS.NM	TTACTTTCTTCAATTCTTGATGCTGGTGTGGTACGGGTGAACTGTTTACCCTCCCCTA
E.DIL.RET.TX	TTACTTTCTTCAATTCTTGATGCTGGTGTGGTACGGGTGAACTGTTTACCCTCCCCTA
E.DIL.PGTBB.TX	TTACTTTCTTCAATTCTTGATGCTGGTGTGGTACGGGTGAACTGTTTACCCTCCCCTA
E.DIL.OSM.M	TTACTTTCTTCAATTCTTGATGCTGGTGTGGTACGGGTGAACTGTTTACCCTCCCCTA
E.DIL.W300.RG	TTATTATCATCTATTCTAGATGCTGGTGTGGGACAGGATGAACTGTTTATCCTCCCCTC
E.DIL.MES.NM	TTATTATCATCTATTCTAGATGCTGGTGTGGGACAGGATGAACTGTTTATCCTCCCCTC
E.DIL.W79.RG	TTATTATCATCTATTCTAGATGCTGGTGTGGGACAGGATGAACTGTTTATCCTCCCCTC
E.DIL.PHL.PA	TTATTATCATCTATCCTAGATGCTGGTGTGGGACAGGATGAACTGTTTATCCTCCCCTC
E.DIL.BOQ.M	TTATTATCATCTATTCTAGATGCTGGTGTGGGACAGGATGAACTGTTTATCCTCCCCTC
E.DIL.DEC.TX	TTATTATCATCTATTCTAGATGCTGGTGTGGGACAGGATGAACTGTTTACCCCCACTC
E.DIL.TRV.TX	TTATTATCATCTATTCTAGATGCTGGTGTGGGACAGGATGAACTGTTTACCCCCACTC
E.DIL.CENT.CA	TTATTATCATCTATTCTAGATGCTGGTGTGGGACAGGATGAACTGTTTACCCCCCTC
E.DIL.CBB.VI	CTTCTCTTCTATCTTAGATGCTGGTGTGGTACGGGTGAACTGTTTATCCTCCTCTT
E.DIL.BEC.NM	TTACTTTCTTCTATCCTAGACGCAGGTGTAGGTACCGGCTGAACTGTCTACCCCCCTCTC
E.DIL.ALT.NM	TTACTTTCTTCTATTCTAGACGCAGGTGTAGGTACTGGCTGAACTGTTTATCCCCCTCTC
E.DIL.MEN.WI	TTACTTTCTTCTATTCTAGACGCAGGTGTGGGTACTGGCTGAACTGTTTACCCCCCTCTC
E.DIL.DTL.OR	TTACTTTCTTCTATTCTAGACGCAGGTGTAGGTACTGGCTGAACTGTTTATCCTCCCCTC
E.DIL.SIL.UT	TTACTTTCTTCTATTCTAGACGCAGGTGTAGGTACTGGCTGAACTGTTTATCCTCCTCTC
E.DIL.CHIC.UT	TTACTTTCTTCTATTCTAGACGCAGGTGTAGGTACTGGCTGAACTGTTTATCCTCCTCTC
E.DIL.SEQ.UT	TTACTTTCTTCTATTCTAGACGCAGGTGTAGGTACTGGCTGAACTGTTTACCCCCCTCTC
E.DIL.SCH.PA	TTACTTTCTTCTATTCTAGACGCAGGTGTGGTACTGGCTGAACTGTCTACCCTCCACTC
E.DIL.DRS.NM	TTACTTTCTTCTATTTTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.F13.RG	TTACTTTCTTCTATTTTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.CATG01BB.	TTACTTTCTTCTATTCTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.CATG02BB.	TTACTTTCTTCTATTCTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.CATCPBB.T	TTACTTTCTTCTATTCTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.CATEBB.TX	TTACTTTCTTCTATTCTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.CATDBB.TX	TTACTTTCTTCTATTTTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.BUBB3.TX	TTACTTTCTTCTATTTTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.BUBB2.TX	TTACTTTCTTCTATTTTAGACGCTGGAGTAGGCACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.JUN.FL	TTACTTTCTTCTATTTTAGACGCTGGGGTAGGTACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.JAC.FL	TTACTCTCTTCTATTTTAGACGCTGGGGTAGGTACAGGATGAACTGTTTATCCCCCTCTT
E.DIL.OKR.OK	TTACTCTCTTCTATTTTAGACGCTGGGGTAGGTACAGGATGAACTGTTTATCCACCTCTC
E.DIL.DUC.OK	TTACTCTCTTCTATTTTAGACGCTGGGGTAGGTACAGGATGAACTGTTTATCCACCTCTC
E.DIL.MC.M	CTTCTTTCTTCTATCCTGGATGCTGGGGTAGGTACGGGTGAACTGTTTATCCGCTCTT
E.DIL.JX216599.	TTATTGTCTTCTATTTTGATGCTGGGGTAGGTACAGGATGAACTGTATATCCTCCTTTA
E.DIL.JX216598.	TTATTGTCTTCTATTTTGATGCTGGGGTAGGTACAGGATGAACTGTATATCCTCCTTTA
E.DIL.KRM01.FL	CTTCTTTCTTCTATTTTAGACGCAGGTGTTGGTACAGGTGAACTGTTTACCCTCCTCTA
E.DIL.KRM02.FL	CTTCTTTCTTCTATTTTAGACGCAGGTGTTGGTACAGGTGAACTGTTTACCCTCCTCTA
E.DIL.MC03.M	TTACTTTCTTCTATTCTTGATGCCGTGTGGAACTGGCTGAACTGTTTACCCTCCTCTT

E.ALATA.NH.DQ07	TCAGACTCCAAATACCACTCTGGAGTATCAGTTGATCTTGCAATCTTTTCTTTGCATCTA
E.DEFLEXA.SHC.L	TCTGACTCAAATATCATTCTGGTGTTCAGTTGATTTAGCAATTTTTCTCTTTCATCTA
E.DIL.DQ297773.	TCAGACTCTAAGTACCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTTTACATTTA
E.DIL.TRP.AZ	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W10.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W06.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W12.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W02.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W34.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA

E.DIL.W01.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W26.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W241.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W24.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W27.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W31.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.MIL.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.BMCHT.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.LPHT.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.SAM.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.AMD.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.FL.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W33.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W28.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.CRS.OK	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W11.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.MSHT.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.W36.RG	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.MCHT.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.ROT.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.COT.TX	TCAGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.GL06BB.TX	TCAGACTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.GL03BB.TX	TCAGACTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.PPC.TX	TCAGACTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.I10.TX	TCTGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.SHL.GA	TCTGATTCTAAGTATCATTCTGGTATTTCTGTTGACTTAGCTATTTTTAGTCTACATTTA
E.DIL.MC02.M	TCTGATTCTAAGTATCATTCTGGTATTTCTGTTGATTAGCTATTTTTAGTCTACATTTA
E.DIL.AMR.CA	TCTGATTCTAAATATCATTCTGGTATCTCTGTTGATTAGCTATTTTTAGTCTTTCATTTA
E.DIL.LOD02.CA	TCTGATTCTAAGTATCATTCCAGGAATCTCAGTTGATTAGCTATTTTTCAGTCTCCATTTA
E.DIL.ECH.FL	TCTGATTCTAAGTATCATTCCAGGAATCTCAGTTGATTAGCTATTTTTCAGTCTCCATTTA
E.DIL.TIM.OR	TCTGATTCTAAGTATCATTCCAGGAATCTCAGTTGATTAGCTATTTTTCAGTCTCCATTTA
E.DIL.MAD.WI	TCTGATTCTAAGTATCATTCCAGGAATCTCAGTTGATTAGCTATTTTTCAGTCTCCATTTA
E.DIL.LOD01.CA	TCTGATTCTAAATATCATTCCAGGAATTTTCAGTTGATTAGCTATCTTTCAGTCTTTCATTTA
E.DIL.STR.NM	TCTGACTCTAAATACCATTCCAGGAATCTCAGTTGATTAGCTATTTTTCAGTCTTTCATCTA
E.DIL.NOCK.PA	TCTGACTCTAAATACCATTCCAGGAATCTCAGTTGATTAGCTATTTTTCAGTCTTTCATCTA
E.DIL.STP.GA	TCTGACTCTAAATATCATTCCAGGAATTTTCAGTTGATTAGCTATCTTTCAGTCTTTCATCTA
E.DIL.LKOJC.FL	TCTGACTCTAAATATCACTCAGGAGTTTCTGTTGATTGGCTATTTTTCAGTCTTTCATTTA
E.DIL.CTS.NM	TCTGACTCTAAGTATCATTCTGGTATTTCTGTTGATCTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.RET.TX	TCTGACTCTAAGTATCATTCTGGTATTTCTGTTGATCTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.PGTBB.TX	TCTGACTCCAAGTATCATTCTGGTATTTCTGTTGATCTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.OSM.M	TCTGACTCCAAGTATCATTCTGGTATTTCTGTTGATCTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.W300.RG	TCAGATTCTAAATATCACTCTGGCATTTCAGTAGATTTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.MES.NM	TCAGATTCTAAATATCACTCTGGCATTTCAGTAGATTTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.W79.RG	TCAGATTCCAAATATCACTCTGGCATTTCAGTAGATTTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.PHL.PA	TCAGATTCTAAATATCACTCCGGCATTTCAGTTGATCTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.BOQ.M	TCAGATTCTAAATATCACTCTGGCATTTCAGTAGATTTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.DEC.TX	TCAGATTCTAAATATCACTCTGGCATTTCAGTAGATCTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.TRV.TX	TCAGATTCTAAATATCACTCTGGCATTTCAGTAGATCTAGCTATTTTTCAGTCTTTCATTTA
E.DIL.CENT.CA	TCCGATTCTAAATATCACTCTGGCATTTCAGTAGATTTAGCAATTTTTCAGTCTTTCATTTA
E.DIL.CBB.VI	TCTGATTCAAAGTACCACTCAGGAGTTTTCAGTAGATCTAGCTATTTTTCAGGTTACATTTA
E.DIL.BEC.NM	TCCGACTCTAAGTACCACTCAGGGGTTTCTGTAGATTTAGCAATCTTTCAGCCTCCATCTA
E.DIL.ALT.NM	TCTGACTCTAAGTACCACTCAGGAGTTTCTGTAGACTTAGCAATCTTTCAGCCTCCATTTA
E.DIL.MEN.WI	TCTGATTCTAAGTATCACTCAGGAGTTTCTGTAGACTTAGCAATCTTTCAGTCTCCACTTA
E.DIL.DTL.OR	TCTGACTCTAAGTACCACTCAGGAGTTTCTGTAGATTTAGCAATCTTTCAGCCTCCATTTA
E.DIL.SIL.UT	TCTGACTCTAAGTACCACTCAGGAGTTTCTGTAGATTTAGCAATCTTTCAGCCTCCATTTA
E.DIL.CHIC.UT	TCTGACTCTAAGTACCACTCAGGAGTTTCTGTAGATTTAGCAATCTTTCAGCCTCCATTTA
E.DIL.SEQ.UT	TCTGACTCTAAGTACCACTCAGGAGTTTCTGTAGATTTAGCAATCTTTCAGTCTTTCATCTA

E.DIL.SCH.PA	TCTGACTCTAAGTACCACTCAGGAGTTTCTGTAGATTTAGCAATCTTTAGCCTTCATCTA
E.DIL.DRS.NM	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTAGCTATTTTCAGCTTACATTTA
E.DIL.F13.RG	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTAGCTATTTTCAGCTTACATTTA
E.DIL.CATG01BB.	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTGGCTATTTTCAGCTTACATTTA
E.DIL.CATG02BB.	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTGGCTATTTTCAGCTTACATTTA
E.DIL.CATCPBB.T	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTGGCTATTTTCAGCTTACATTTA
E.DIL.CATEBB.TX	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTGGCTATTTTCAGCTTACATTTA
E.DIL.CATDBB.TX	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTGGCTATTTTCAGCTTACATTTA
E.DIL.BUBB3.TX	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTGGCTATTTTCAGCTTACATTTA
E.DIL.BUBB2.TX	TCTGATTCTAAATATCATTCTGGGGTTTTCTGTTGATTTGGCTATTTTCAGCTTACATTTA
E.DIL.JUN.FL	TCTGATTCTAAGTACCACTCTGGTGTCTTCTGTTGATTTAGCTATTTTCAGTTTACATCTA
E.DIL.JAC.FL	TCTGATTCTAAGTATCATTCTGGTGTCTTCTGTTGATTTAGCTATTTTCAGTTTACATCTA
E.DIL.OKR.OK	TCTGACTCTAAGTATCATTCTGGTGTCTTCTGTTGATTTGGCTATTTTCAGTTTACATTTA
E.DIL.DUC.OK	TCTGACTCTAAGTATCATTCTGGTGTCTTCTGTTGATTTGGCTATTTTCAGTTTACATTTA
E.DIL.MC.M	GCAGATTCTAAGTATCATTCTAGGTATTTCTGTTGATTTAGCTATTTTTAGACTTCATTTA
E.DIL.JX216599.	GCTGACTCAAAATATCATTCTAGGTATTTCTGTTGATTTAGCAATTTTTAGTTTACATTTA
E.DIL.JX216598.	GCTGACTCAAAATATCATTCTAGGTATCTCTGTTGATTTAGCAATTTTTAGTTTACATTTA
E.DIL.KRM01.FL	TCTGATTCCAAGTATCACTCTGGAGTATCGGTAGATTTAGCCATTTTTAGCCTACATCTA
E.DIL.KRM02.FL	TCTGATTCCAAGTATCACTCTGGAGTATCGGTAGATTTAGCCATTTTTAGCCTACATCTT
E.DIL.MC03.M	TCAGATTCTAAATATCATTCTAGGTGTGTCTGTAGATTTAGCTATTTTTAGTCTACACTTA

E.ALATA.NH.DQ07	GCTGGTATCTCCTCTATTGCTGGAAGAATTAACCTTTCTAACAACAATCATTGTTGGTCGT
E.DEFLEXA.SHCL	GCCGGAATTTCTTCTATTGCAGGTAGAATTAATTTTCTAACTACTATTATTTGTTCTCGT
E.DIL.DQ297773.	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTCTAACTACTATTATTTGTTCTCGT
E.DIL.TRP.AZ	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W10.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W06.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W12.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W02.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W34.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W01.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W26.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W241.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W24.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W27.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W31.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.MIL.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.BMCHT.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.LPHT.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.SAM.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.AMD.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.FL.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W33.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W28.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.CRS.OK	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W11.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.MSHT.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.W36.RG	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATCTGTTCTCGT
E.DIL.MCHT.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.ROT.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATCTGTTCTCGT
E.DIL.COT.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATCTGTTCTCGT
E.DIL.GL06BB.TX	GCAGGTATTTCTTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATCTGTTCTCGT
E.DIL.GL03BB.TX	GCAGGTATTTCTTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATCTGTTCTCGT
E.DIL.PPC.TX	GCAGGTATTTCTTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATCTGTTCTCGT
E.DIL.I10.TX	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT
E.DIL.SHL.GA	GCAGGTATTTCTCCTCTATTCTTGGTAGAATTAATTTTTTAACTACTATTATTTGTTCTCGT

E.DIL.MC02.M GCAGGTATTTCTCTATTCTTGGTAGAATTAATTTCTTAAGTACTATTATTTGTTCTCGT
 E.DIL.AMR.CA GCAGGTATTTCTTCTATTTTAGGTAGAATCAATTTTCTAAGTACTATTATTTGTTCTCGT
 E.DIL.LOD02.CA GCTGGTATTTCTTCTATCTTAGGTAGAATCAATTTCTTAAGTACTATTATTTGTTCTCGT
 E.DIL.ECH.FL GCTGGTATTTCTTCTATCTTAGGTAGAATCAATTTCTTAAGTACTATTATTTGTTCTCGT
 E.DIL.TIM.OR GCTGGTATTTCTTCTATCTTAGGTAGAATCAATTTTTTAAGTACTATTATTTGTTCTCGT
 E.DIL.MAD.WI GCTGGTATTTCTTCTATCTTAGGTAGAATCAATTTTTTAAGTACTATTATTTGTTCTCGT
 E.DIL.LOD01.CA GCTGGTATTTCTTCTATCTTAGGTAGAATCAATTTTTTAAGTACTATTATTTGTTCTCGT
 E.DIL.STR.NM GCTGGTATTTCTTCTATCTTAGGTAGAATCAATTTTTTAAGTACTATTATTTGTTCTCGT
 E.DIL.NOCK.PA GCTGGTATTTCTTCTATCTTAGGTAGAATCAATTTTTTAAGTACTATTATTTGTTCTCGT
 E.DIL.STP.GA GCTGGTATTTCTTCCATCTTAGGTAGAATCAATTTTTTAAGTACTATTATTTGTTCTCGT
 E.DIL.LKOJC.FL GCAGGTATTTCTTCTATTCTTGGTAGAATCAATTTCTTACTACTATTATTTGTTCTCGA
 E.DIL.CTS.NM GCCGGAATTTCTTCAATTCTTGGTAGAATCAACTTTCTTACTACTATTATTTGTTCTCGC
 E.DIL.RET.TX GCCGGAATTTCTTCAATTCTTGGTAGAATCAACTTTCTTACTACTATTATTTGTTCTCGC
 E.DIL.PGTBB.TX GCCGGAATTTCTTCAATTCTTGGTAGAATCAATTTCTTACTACTATTATTTGTTCTCGC
 E.DIL.OSM.M GCCGGAATTTCTTCAATTCTTGGTAGAATCAATTTCTTACTACTATTATTTGTTCTCGC
 E.DIL.W300.RG GCTGGTATTTCTATCTATCTTAGGTAGTATCAATTTTTTGACTACTATTATCTGTTCTCGT
 E.DIL.MES.NM GCTGGTATTTCTATCTATCTTAGGTAGTATCAATTTTTTGACTACTATTATCTGTTCTCGT
 E.DIL.W79.RG GCTGGTATTTCTATCTATCTTAGGTAGTATCAATTTTTTGACTACTATTATCTGTTCTCGT
 E.DIL.PHL.PA GCTGGTATTTCTATCTATCTTAGGTAGTATCAATTTTTTGACTACTATTATCTGTTCTCGT
 E.DIL.BOQ.M GCTGGTATTTCTATCTATCTTAGGTAGTATCAATTTTTTGACTACTATTATCTGTTCTCGT
 E.DIL.DEC.TX GCTGGTATTTCTATCTATCTTAGGTAGTATCAATTTTTTGACTACTATTATTTGTTCTCGT
 E.DIL.TRV.TX GCTGGTATTTCTATCTATCTTAGGTAGTATCAATTTTTTGACTACTATTATTTGTTCTCGT
 E.DIL.CENT.CA GCTGGTATTTCTATCTATCTTAGGTAGTATCAATTTTTTGACTACTATTATTTGTTCTCGT
 E.DIL.CBB.VI GCTGGTATCTCTTCTATTTTAGGTAGAATTAACTTTTTAAGTACAATTATTTGTTCTCGT
 E.DIL.BEC.NM GCCGGTATCTCTTCTATCCTAGGAAGAATTAATTTCTTGACCACTATTATCTGTTCTCGT
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 E.DIL.DRS.NM GCCGGTGTCTCTTCTATCCTAGGTAGTATTAATTTTTTGACTACTATTATTTGTTCTCGT
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 E.DIL.CATG01BB. GCCGGTGTCTCTTCTATCCTAGGTAGTATTAATTTTTTGACTACTATTATTTGTTCTCGT
 E.DIL.CATG02BB. GCCGGTGTCTCTTCTATCCTAGGTAGTATTAATTTTTTGACTACTATTATTTGTTCTCGT
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 E.DIL.BUBB3.TX GCCGGTGTCTCTTCTATCCTAGGTAGTATTAATTTTTTGACTACTATTATCTGTTCTCGT
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 E.DIL.OKR.OK GCTGGTATCTCTTCTATTTTAGGTAGAATTAATTTTTTGACTACTATTATTTGTTCTCGT
 E.DIL.DUC.OK GCTGGTATCTCTTCTATTTTAGGTAGAATTAATTTTTTGACTACTATTATTTGTTCTCGT
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 E.DIL.JX216598. GCTGGAATTTCTTCTATTTTAGGTAGAATTAATTTCTAAGTACGGTGATTTGTTCTCGA
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 E.DIL.MC03.M GCTGGTATTTCTGTTCTATTTTGGGTAGAATTAATTTTTTAAGTACAATTATTTGTTCTCGA

E.ALATA.NH.DQ07 TCTAATGTCTACCTCTCATTTGCTCGCATGCCCCCTTATGCTTTGAGCTTTTGGTATTACA
 E.DEFLEXA.SHC.L CTTAATTCTTATATTACTTTTGATCGTCTTCCCTTTAATGCTTTGAGCATTTGCAATTACA
 E.DIL.DQ297773. ACAGCTAAGGCCATCTCTCTTGATCGAATGCCTCTTATGCTGTGAGCTTTTGGTGTGACA
 E.DIL.TR.P.AZ ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCGTCACA

E.DIL.W10.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W06.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W12.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W02.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W34.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W01.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W26.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W241.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W24.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W27.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W31.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.MIL.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.BMCHT.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.LPHT.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.SAM.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.AMD.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.FL.TX	ACAGCTAAGGCTATCTCTCTTGATCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W33.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W28.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.CRS.OK	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W11.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.MSHT.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.W36.RG	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.MCHT.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTCACA
E.DIL.ROT.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCTGTTACA
E.DIL.COT.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCTGTTACA
E.DIL.GL06BB.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTTACA
E.DIL.GL03BB.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTTACA
E.DIL.PPC.TX	ACAGCTAAGGCTATCTCTCTTGACCGAATGCCTCTTATGTTGTGGGCTTTGCGCCGTTACA
E.DIL.I10.TX	ACAGCCAAGGCTATCTCTCTTGATCGAATGCCTCTTATGCTATGAGCTTTTGCCGTTACA
E.DIL.SHL.GA	ACAGCCAAGGCTATCTCTCTTGATCGAATGCCTCTTATGTTATGAGCTTTTGCCGTTACA
E.DIL.MC02.M	ACAGCTAAGGCTATCTCTCTTGATCGAATGCCTCTTATGTTGTGAGCTTTTGCCGTTACA
E.DIL.AMR.CA	ACAGCAAAAGCAATTTCTCTTGATCGTATGCCTCTTATGCTATGAGCATTTGCGGTCACT
E.DIL.LOD02.CA	ACGGCTAAAGCTATTTCTCTTGATCGTATGCCTCTTATGCTTTGAGCTTTTGCTGTAAC
E.DIL.ECH.FL	ACGGCTAAAGCTATTTCTCTTGATCGTATGCCTCTTATGCTTTGAGCTTTTGCTGTAAC
E.DIL.TIM.OR	ACAGCCAAGCTATTTCTCTTGATCGTATGCCTCTTATGCTTTGAGCTTTTTCTGTAAC
E.DIL.MAD.WI	ACAGCTAAAGCTATTTCTCTTGACCGTATGCCTCTTATGCTTTGGGCTTTTGCTGTAAC
E.DIL.LOD01.CA	ACAGCTAAAGCTATTTCTCTTGATCGTATGCCTCTTATGCTTTGAGCTTTTGCTGTCACT
E.DIL.STR.NM	ACCGCTAAAGCTATTTCTCTTGATCGTATGCCTCTTATGCTTTGAGCTTTTGCTGTTACT
E.DIL.NOCK.PA	ACCGCTAAAGCTATTTCTCTTGATCGTATGCCTCTTATGCTTTGAGCTTTTGCTGTTACT
E.DIL.STP.GA	ACAGCTAAAGCTATTTCTCTTGATCGTATGCCTCTTATGCTTTGAGCTTTTGCTGTTACT
E.DIL.LKOJC.FL	ACAGCAAAAGCTATCTCACTAGATCGAATGCCTCTTATGTTATGAGCATTTGCTGTCAACA
E.DIL.CTS.NM	ACAGCAAAAGCTATTTCTCTAGATCGTATGCCTTTAATGTTATGGGCGTTTGCTGTTACT
E.DIL.RET.TX	ACAGCAAAAGCTATTTCTCTAGATCGTATGCCTTTAATATTATGGGCGTTTGCTGTTACT
E.DIL.PGTBB.TX	ACAGCAAAAGCTATTTCTCTAGATCGTATGCCTTTAATATTATGGGCGTTTGCTGTGACT
E.DIL.OSM.M	ACAGCAAAAGCTATTTCTCTAGATCGTATGCCTTTAATATTATGGGCGTTTGCTGTGACT
E.DIL.W300.RG	ACAGCAAAAGCTATTTCACTCGATCGTATGCCTCTTATGTTGTGAGCATTTGCTGTTACC
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E.DIL.W79.RG	ACAGCAAAAGCTATTTCACTCGATCGTATGCCTCTTATGTTGTGAGCATTTGCTGTTACC
E.DIL.PHL.PA	ACAGCAAAAGCTATTTCACTCGATCGTATGCCTCTTATGTTGTGAGCATTTGCTGTTACC
E.DIL.BOQ.M	ACAGCAAAAGCTATTTCACTCGATCGTATGCCTCTTATGTTGTGAGCATTTGCTGTTACC
E.DIL.DEC.TX	ACAGCAAAAGCTATTTCACTCGATCGTATGCCTCTTATGTTGTGGGCATTTGCTGTTACT
E.DIL.TRV.TX	ACAGCAAAAGCTATTTCACTCGATCGTATGCCTCTTATGTTGTGGGCATTTGCTGTTACT
E.DIL.CENT.CA	ACAGCAAAAGCTATTTCACTCGATCGTATGCCTCTTATGTTGTGAGCCTTTGCTGTTACA
E.DIL.CBB.VI	ACCGCAAAAGCAATTTCACTAGATCGTATGCCTTTAATGTTATGGGCGTTTGCGGTTACA
E.DIL.BEC.NM	ACGGCAAAAGCAATCTCTTTAGATCGTATACCTCTTATGCTATGAGCCTTTGCCGTTACT
E.DIL.ALT.NM	ACGGCAAAAGCAATCTCTTTAGACCGTATGCCTCTTATGTTATGGGCTTTGCCGTTACT

E.DIL.MEN.WI ACGGCAAAAGCAATCTCTTTAGACCGTATACCTCTTATGTTATGGGCCTTTGCCGTTACT
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 E.DIL.CHIC.UT ACGGCAAAAGCAATCTCTTTAGACCGTATACCTCTTATATTATGGGCCTTTGCCGTTACT
 E.DIL.SEQ.UT ACGGCAAAAGCAATCTCTTTAGACCGTATACCTCTTATATTATGGGCCTTTGCCGTTACT
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 E.DIL.CATG01BB. ACTACTAAAGCCATTTCTCTAGATCGTATGCCTCTATTACTTTGGGCTTTTTTCAGTTACT
 E.DIL.CATG02BB. ACTACTAAAGCCATTTCTCTAGATCGTATGCCTCTATTACTTTGGGCTTTTTTCAGTTACT
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 E.DIL.MC.M ACGGCTAAAGCTATTTCTTTAGATCGTATGCCCTTAATACTTTGGGCTTTTTGCTGTTACA
 E.DIL.JX216599. ACTTCGAAAGCTATTTTCATTAGACCGTATGCCTTTAATATTATGGGCTTTTTTCAGTTACT
 E.DIL.JX216598. ACTTCGAAAGCTATTTTCATTAGATCGTATGCCTTTAATATTATGGGCTTTTTTCAGTTACT
 E.DIL.KRM01.FL ACTACTAAAGCTATTTCCCTTAGACCGCATGCCCCCTTATACTTTGGGCTTTTTTCAGTTACA
 E.DIL.KRM02.FL ACTACTAAAGCTATTTCCCTTAGACCGCATGCCCCCTTATTCTTTGGGCTTTTTTCAGTTACA
 E.DIL.MC03.M ACAACAAAAGCTATCTCTTTAGATCGAATGCCTCTTATTTTGTGAGCTTTTTTCTGTTACT

E.ALATA.NH.DQ07 TCAGTGCTTCTTATTGTTTCCCTCCCAGTTCTAGCTGGAGCTATTACAATGCTTCTAACA
 E.DEFLEXA.SHC.L TCTGTTCTTCTTGTTACAAGTTTACCAGTACTAGCTGGGGCTATTACAATGCTTTTAAACC
 E.DIL.DQ297773. TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.TRP.AZ TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
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 E.DIL.W26.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.W241.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.W24.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.W27.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.W31.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.MIL.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.BMCHT.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.LPHT.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.SAM.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.AMD.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.FL.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.W33.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.W28.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.CRS.OK TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.W11.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.MSHT.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.W36.RG TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.MCHT.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.ROT.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
 E.DIL.COT.TX TCTATTCTTCTTGTAAGTACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT

E.DIL.GL06BB.TX TCTATTCTTCTTGTGACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
E.DIL.GL03BB.TX TCTATTCTTCTTGTGACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
E.DIL.PPC.TX TCTATTCTTCTTGTGACTAGTCTACCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
E.DIL.I10.TX TCTATTCTTCTTGTAACTAGTCTACCCGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
E.DIL.SHL.GA TCTATTCTTCTTGTAACTAGTCTACCCGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
E.DIL.MC02.M TCTATTCTTCTTGTAACTAGTCTACCCGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
E.DIL.AMR.CA TCTATTCTTCTTGTTACTAGCCTTCCAGTTTTAGCTGGGGCTATTACTATGCTTTTAACT
E.DIL.LOD02.CA TCTATTCTACTGGTTACTAGGCTTCCTGTTTTAGCTGGTGCTATCACAATGTTGCTTACT
E.DIL.ECH.FL TCTATTCTACTGGTTACTAGGCTTCCTGTTTTAGCTGGTGCTATCACAATGTTGCTTACT
E.DIL.TIM.OR TCTATTTTACTGGTTACTAGGCTGCCTGTTTTAGCTGGTGCTATTACAATGTTGCTTACT
E.DIL.MAD.WI TCTATTTTACTGGTTACTAGGCTTCCTGTTTTAGCTGGTGCTATTACAATGTTGCTTACT
E.DIL.LOD01.CA TCTATTCTTCTTGTTACTAGCCTTCCTGTTTTAGCCGGGGCCATCACAATGCTGTTAACT
E.DIL.STR.NM TCTATCCTGCTTGTTACTAGACTTCCTGTCCTAGCCGGTGCTATCACAATGTTGCTTACT
E.DIL.NOCK.PA TCTATCCTGCTTGTTACTAGACTTCCTGTCCTAGCCGGTGCTATCACAATGTTGCTTACT
E.DIL.STP.GA TCTATCTTGCTTGTTACTAGACTTCCTGTTTTAGCCGGTGCTATCACAATGCTGCTTACT
E.DIL.LKOJC.FL TCTATTCTTCTTGTTACTAGTCTTCCTGTTTTAGCTGGTGCTATTACTATGCTTCTTACT
E.DIL.CTS.NM TCTATTCTTCTTGTTACTAGATTACCCGTTTTAGCTGGTGCCATCACTATGCTTTTAACT
E.DIL.RET.TX TCTATTCTTCTTGTTACTAGATTACCCGTTTTAGCTGGTGCCATCACTATGCTTTTAACT
E.DIL.PGTBB.TX TCTATTCTTCTTGTTACTAGATTACCCGATTAGCTGGTGCTATTACTATGCTTTTAACT
E.DIL.OSM.M TCTATTCTTCTTGTTACTAGGTTACCCGATTAGCTGGTGCTATTACTATGCTTTTAACT
E.DIL.W300.RG TCTGTCCTTCTTGTTACTAGTCTTCCTGTTTTAGCTGGTGCCATTACTATGCTTTTAACT
E.DIL.MES.NM TCTGTCCTTCTTGTTACTAGTCTTCCTGTTTTAGCTGGTGCCATTACTATGCTTTTAACT
E.DIL.W79.RG TCTGTCCTTCTTGTTACTAGTCTTCCTGTTTTAGCTGGTGCCATTACTATGCTTTTAACT
E.DIL.PHL.PA TCTGTCCTTCTTGTTACTAGTCTTCCTGTTTTAGCTGGTGCTATTACTATGCTTTTAACT
E.DIL.BOQ.M TCTGTCCTTCTTGTTACTAGTCTTCCTGTTTTGGCTGGTGCCATTACTATGCTTTTAACT
E.DIL.DEC.TX TCTGTGCTTCTTGTTACTAGTCTTCCTGTTTTAGCTGGTGCCATTACTATGCTTTTAACT
E.DIL.TRV.TX TCTGTGCTTCTTGTTACTAGTCTTCCTGTTTTAGCTGGTGCCATTACTATGCTTTTAACT
E.DIL.CENT.CA TCTCTTCTTCTTGTTACTAGTCTTCCTGTTTTAGCTGGTGCTATTACTATGCTTTTAACT
E.DIL.CBB.VI TCTATTTTGTAGTTACTAGCTGCCAGTTTTAGCGGGTGCTATTACTATGCTTTTAACT
E.DIL.BEC.NM TCTATTCTTCTTGTAACGAGTCTTCCCGTTTTAGCAGGTGCAATCACTATACTTCTGACA
E.DIL.ALT.NM TCTATTCTTCTTGTAACGAGTCTTCCCGTTTTAGCAGGTGCAATCACTATACTTCTAACA
E.DIL.MEN.WI TCTATTCTTCTTGTAACGAGTCTTCCCGTTTTAGCAGGTGCAATCACTATACTTCTAACA
E.DIL.DTL.OR TCTATTCTTCTTGTAACGAGTCTTCCCGTTTTAGCAGGTGCAATCACTATACTTCTAACA
E.DIL.SIL.UT TCTCTTCTTCTTGTAACGAGTCTTCCCGTTTTAGCAGGTGCAATCACTATACTTCTAACA
E.DIL.CHIC.UT TCTCTTCTTCTTGTAACGAGTCTTCCCGTTTTAGCAGGTGCAATCACTATACTTCTAACC
E.DIL.SEQ.UT TCTATTCTCCTTGTAACGAGTCTTCCCGTTTTAGCAGGTGCAATCACTATACTTCTAACA
E.DIL.SCH.PA GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGCGCTATTACTATGCTGTTGACT
E.DIL.DRS.NM GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGCGCTATTACTATGCTGTTGACT
E.DIL.F13.RG GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGCGCTATTACTATGCTGTTGACT
E.DIL.CATG01BB. GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGTGCTATTACTATGCTGTTGACT
E.DIL.CATG02BB. GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGTGCTATTACTATGCTGTTGACT
E.DIL.CATCPBB.T GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGTGCTATTACTATGCTGTTGACT
E.DIL.CATEBB.TX GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGTGCTATTACTATGCTGTTGACT
E.DIL.CATDBB.TX GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGTGCTATTACTATGCTGTTGACT
E.DIL.BUBB3.TX GCTCTTTTATTAGTTACTAGACTTCCTGTTTTAGCTGGTGCTATTACTATGCTGTTGACT
E.DIL.BUBB2.TX GCTCTTTTATTAGTTACTAGGCTTCCTGTTTTAGCTGGGGCTATTACTATGCTGTTGACT
E.DIL.JUN.FL GCTCTTTTATTAGTTACTAGGCTTCCTGTTTTAGCTGGGGCTATTACTATGCTGTTGACT
E.DIL.JAC.FL GCTCTTTTATTGGTCACTAGGCTTCCTGTTTTAGCTGGGGCTATTACTATGCTGTTGACT
E.DIL.OKR.OK GCTCTTTTATTGGTCACTAGGCTTCCTGTTTTAGCTGGGGCTATTACTATGCTGTTGACT
E.DIL.DUC.OK TCGGTTCTTTTAACTACTAGTCTTCCTGTTCTTGCTGGTGCAATTACCATGCTTTTAACT
E.DIL.MC.M GCTGTGCTTTTAACTACTAGACTGCCTGTTTTAGCTGGTGCTATTACTATGCTATTA
E.DIL.JX216599. GCTGTGCTTTTAACTACTAGACTGCCTGTTTTAGCTGGTGCTATTACTATGCTATTA
E.DIL.JX216598. GCCCTTCTTCTAGTTACTAGATTGCCTGTTCTTGCTGGTGCTATTACTATGCTGTTAACT
E.DIL.KRM01.FL GCCCTTCTTCTAGTTACTAGATTGCCTGTTCTTGCTGGAGCTATTACTATGCTCTTAACT
E.DIL.KRM02.FL GCTCTCTTATTAGTTACTAGTCTTCCAGTGTTAGCTGGTGCTATTACTATGTTACTTACC

[illegible]

E.DIL.TRV.TX	GATCGCAATTTTAATACCTCTTTTTTTGACCCTGCAGGTGGAGGTAACCCAGTTCCTTTAC
E.DIL.CENT.CA	GATCGTAACTTTAATACCTCTTTTTTTGATCCTGCAGGTGGAGGTAATCCAGTTCCTTTAC
E.DIL.CBB.VI	GATCGTAATTTCAATACATCTTTCTTTGACCCTGCAGGTGGCGGTAATCCCGTTCCTTTAC
E.DIL.BEC.NM	GATCGAAACTTTAATACGTCTTTTTTTGATCCTGCTGGTGGGGGCAACCCTGTTCTTTAT
E.DIL.ALT.NM	GATCGAAACTTTAATACGTCTTTTTTTGATCCTGCTGGTGGAGGTAATCCTGTTCTTTAT
E.DIL.MEN.WI	GATCGAAACTTTAATACGTCTTTTTTTGATCCTGCTGGTGGAGGTAATCCTGTTCTTTAT
E.DIL.DTL.OR	GATCGAAACTTTAATACGTCTTTTTTTGATCCTGCTGGTGGAGGTAATCCTGTTCTTTAT
E.DIL.SIL.UT	GATCGAAACTTTAATACGNN
E.DIL.CHIC.UT	GATCGAAACTTTAATACGTCTTTTTTTGATCCTGCTGGTGGAGGTAATCCTGTTCTTTAT
E.DIL.SEQ.UT	GATCGAAACTTTAATACATCTTTTTTTGATCCTGCTGGCGGAGGTAACCCGTTCTTTAT
E.DIL.SCH.PA	GATCGAAACTTTAATACATCTTTCTTTTGACCCCGCTGGTGGAGGTAATCCTGTTCTTTAT
E.DIL.DRS.NM	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGTGGGGGTAACCCGTTCTTTAT
E.DIL.F13.RG	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGTGGGGGTAACCCGTTCTTTAT
E.DIL.CATG01BB.	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGGGGGGTAACCCGTTCTTTAT
E.DIL.CATG02BB.	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGGGGGGTAACCCGTTCTTTAT
E.DIL.CATCPBB.T	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGGGGGGTAACCCGTTCTTTAT
E.DIL.CATEBB.TX	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGGGGGGTAACCCGTTCTTTAT
E.DIL.CATDBB.TX	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGGGGGGTAACCCGTTCTTTAT
E.DIL.BUBB3.TX	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGGGGGGTAACCCGTTCTTTAT
E.DIL.BUBB2.TX	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGGGGGGTAACCCGTTCTTTAT
E.DIL.JUN.FL	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGTGGAGGCAACCCTGTTCTTTAT
E.DIL.JAC.FL	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGTGGAGGCAACCCTGTTCTTTAT
E.DIL.OKR.OK	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGCGGAGGTAACCCGTTCTTTAT
E.DIL.DUC.OK	GATCGTAATTTTAATACTTCTTTTTTTGACCCTGCTGGCGGAGGTAACCCGTTCTTTAT
E.DIL.MC.M	GATCGCAATTTTAATACTTCTTTCTTCGATCCAGCTGGAGGAGGTAACCCAGTTCCTTTAT
E.DIL.JX216599.	GATCGTAATTTTAACACTTCTTTTTTTGATCCTGCTGGTGGTGGTAATCCTGTTTTATAC
E.DIL.JX216598.	GATCGTAATTTTAACACTTCTTTTTTTGATCCTGCTGGTGGNNNNNNNNNNNNNNNNNNNN
E.DIL.KRM01.FL	GATCGTAATTTTAACACTTCTTTTTTTGACCCCGCAGGAGGAGGTAATCCCGTTCCTTTAC
E.DIL.KRM02.FL	GATCGTAATTTTAACACTTCTTTTTTTGTCGACCCCGCAGGAGGAGGTAATCCCGTTCCTTTAC
E.DIL.MC03.M	GATCGTAATTTTAACACTTCTTTTTTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

E.DIL.MSHT.TX	CAGCATTTGTTCTGATTTTTTGGTCACNNNNNNNN
E.DIL.W36.RG	CAGCATTTGTTCTGATTTTTTGGTCACCCTGGAN
E.DIL.MCHT.TX	CAGCATTTGTTCTGATTTTTTGGTCACNNNNNNNN
E.DIL.ROT.TX	CAGCATTTGTTCTGATTTTTTGGTCACCCTGAAN
E.DIL.COT.TX	CAGCATTTGTTCTGATTTTTTGGTCACCCTGGAA
E.DIL.GL06BB.TX	CAGCATTTGTTCTGATTTTTTGGTCACNNNNNNNN
E.DIL.GL03BB.TX	CAGCATTTGTTCTGATTTTTTGGTCACCCTGGAA
E.DIL.PPC.TX	CAGCATTTGTTCTGATTTTTTGGTCACNNNNNNNN
E.DIL.I10.TX	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAN
E.DIL.SHL.GA	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.MC02.M	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.AMR.CA	CAGCATTTATTCTGATTTTTTGGTCACCCTGAAN
E.DIL.LOD02.CA	CAGCATCTGTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.ECH.FL	CAGCATCTGTTTTGATTTTTTGNNNNNNNNNNNN
E.DIL.TIM.OR	CAGCATCTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.MAD.WI	CAGCATTTATTTTGATTTTTTGGTCACCCTGAAN
E.DIL.LOD01.CA	CAGCATTTATTCTGATTTTTTGGCCACCCTGGAA
E.DIL.STR.NM	CAACATTTATTTTGATTTTTTGGTCACCCTGAAG
E.DIL.NOCK.PA	CAACATTTATTTTGATTTTTTGGTCACCNNNNNN
E.DIL.STP.GA	CAGCATTTATTTTGATTTTTTGNNNNNNNNNNNN
E.DIL.LKOJC.FL	CAGCATTTATTTTGATTTTTTGGTCACCNNNNNN
E.DIL.CTS.NM	CAACATTTATTTTGATTTTTTGGTCACCCTGAAN
E.DIL.RET.TX	CAACATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.PGTBB.TX	CAACATTTATTTTGATTTTTTGGTCACNNNNNNNN
E.DIL.OSM.M	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.W300.RG	CAGCATTTATTCTGATTTTTTGGTCACCCTGGAA
E.DIL.MES.NM	CAGCATTTATTCTGATTTTTTGGTCACCCTGAAA
E.DIL.W79.RG	CAGCATTTATTCTGATTTTTTGGTCACCCTGGAA
E.DIL.PHL.PA	CAGCATTTATTCTGATTTTTTGGTCACCCTGGAA
E.DIL.BOQ.M	CAGCATCTTTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.DEC.TX	CAGCATTTATTCTGATTTTTTGGTCACCCTGGAA
E.DIL.TRV.TX	CAGCATTTATTCTGATTTTTTGGTCACCCTGGAA
E.DIL.CENT.CA	CAGCATTTATTCTGATTTTTTGNNNNNNNNNNNN
E.DIL.CBB.VI	CAGCATTTATTTTGATTTTTTGGTCACCCTGAAG
E.DIL.BEC.NM	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.ALT.NM	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.MEN.WI	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.DTL.OR	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.SIL.UT	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
E.DIL.CHIC.UT	CAGCATTTATTTTGATTTTTTGGTCACCCNNNNNN
E.DIL.SEQ.UT	CAGCATTTATTTTGATTTTTTGGTCACNNNNNNNN
E.DIL.SCH.PA	CAGCATTTATTTTGATTTTTTGGTCACNNNNNNNN
E.DIL.DRS.NM	CAGCATTTATTTTGATTTTTTGGTCACCCTGGAA
E.DIL.F13.RG	CAGCATTTATTTTGATTTTTTGGTCACCCGGGAA
E.DIL.CATG01BB.	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.CATG02BB.	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAN
E.DIL.CATCPBB.T	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.CATEBB.TX	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.CATDBB.TX	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAN
E.DIL.BUBB3.TX	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.BUBB2.TX	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.JUN.FL	CAGCATTTGTTTTGATTTTTTGNNNNNNNNNNNN
E.DIL.JAC.FL	CAGCATTTGTTTTGATTTTTTGGTCACCCNNNNNN
E.DIL.OKR.OK	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAN
E.DIL.DUC.OK	CAGCATTTGTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.MC.M	CAGCATCTTTTTTGATTTTTTGGTCACCCTGGAA
E.DIL.JX216599.	CAACATTTATTTNNNNNNNNNNNNNNNNNNNNNN

Supplemental document S1.4: CLUSTAL format alignment of ITS sequences of *Euchlanis dilatata* by MAFFT v 7.380. The diagnostic nucleotides used for species description and their position in this alignment (highlighted in green) are used for species description. Abbreviations are the same as in Table S1.1. N= missing data. -= gaps.

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E.DIL.W79.RG	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.PHL.PA	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.W90.RG	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.LKOSC.FL	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.SIL.UT	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTGCACGCGC-AATACACTCATGTGT
E.DIL.F3.RG	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.F74.RG	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.DEC.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.AMD.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.BMCHT.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.COT.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.FL.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.GL03BB.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.GL06BB.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.I10.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.LK01.FL	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.LPHT.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.MC02.M	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.MIL.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.MSHT.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.ROT.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.SAM.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.SHL.GA	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.T2T2BB.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.TRP.AZ	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.PPC.TX	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.AWR.TX	CATTATCCTTTTGCCTAGTATT--TTAATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.CT3.NM	CATTATCCTTTTGCCTAGTATT--TTAATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.MCHT.TX	CATTATCCTTTTGCCTAGTATT--TTAATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.RET.TX	CATTATCCTTTTGCCTAGTATT--TTAATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.PEC.TX	CATTATCCTTTTGCCTAGTATT--TTAATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.CT1.NM	CATTATCCTTTTGCCTAGTATT--TTAATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.BRH.TX	CATTATCCTTTTGCCTAGTATT--TTAATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.LPSHT.TX	CATTATCCTTTTGCCTAGTATT--TTTATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.OSM.M	CATTATCCTTTTGCCTAGTATT--TTTATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.PGTBB.TX	CATTATCCTTTTGCCTAGTATT--TTTATAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.CTS.NM	CATTATCCTTTTGCCTAGTATT--TTTACGAATACTACACGCGC-AATACACTCATGTGT
E.DIL.AMR.CA	CATTATCCTTTTGCCTAGTATT--TTTACTAATACTACACGCGC-AATACACTCATGTGT
E.DIL.ECH.CA	CATTATCCTTTTGCCTAGTATT--TTTACTAATACTACACGCGC-AATACACTCATGTGT
E.DIL.LOD02.CA	CATTATCCTTTTGCCTAGTATT--TTTACTAATACTACACGCGC-AATACACTCATGTGT
E.DIL.TIM.OR	CATTATCCTTTTGCCTAGTATT--TTTACTAATACTACACGCGC-AATACACTCATGTGT
E.DIL.LOD01.CA	CATTATCCTTTTGCCTAGTATT--TTTACTAATACTACACGCGC-AATACACTCATGTGT
E.DIL.NOCK.PA	CATTATCCTTTTGCCTAGTATT--TTTACTAATACTACACGCGC-AATACACTCATGTGT
E.DIL.CBB.VI	CATTATCCTTTTGCCTAGTGTT--TTTACAAATACTACACGCGC-AATACACTCAAGTGT
E.DIL.BUBB2.TX	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.BUBB3.TX	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.CATCPBB.T	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.CATDBB.TX	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.CATEBB.TX	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.CATG1B.TX	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.CATG2B.TX	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.CATHBB.TX	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.DRS.NM	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.DUC.OK	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.JAC.FL	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.JUN.FL	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT
E.DIL.KRM01.FL	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATGCACTTTTCGTGT

E.DIL.KRM02.FL	CATTATCCTTTTGCCTAGTATT--AACTTTAATACTACACGCGC-AATACACTTTTGTGT
E.DIL.MC.M	CATTATCCTTTTGCCTAGTATC--TTAAAAATACTGCACGCGC-AATACACTAAAGTGT

E.DEFLEXA.SHC.L	ATGCAAAACAAAGCAAATGGATTATAAATGCTTGTTTATAATCGATTTAAATCCATGCTT
L.MELICERTA.BCH	TTGCGTTAATACGCACGACGACTATGCTTATC--ATAATCGTCATCTTATAACCATACTT
E.DIL.ALT.NM	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.BEC.NM	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.CHIC.UT	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.MEN.WI	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.SCH.PA	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.DTL.OR	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.SEQ.UT	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.BOQ.M	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.CENT.CA	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.CIH.M	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.COL.M	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.F13.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.F68.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.F76.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.F85.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.MAD.WI	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.MES.NM	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.OKR.OK	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.POZ.M	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.S31.TX	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.S44.TX	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.S47.TX	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.STR.NM	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.TRV.TX	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W101.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W106.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W116.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W129.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W13.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W146.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W157.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W159.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W163.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W173.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W25.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W300.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W55.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W56.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W57.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W79.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.PHL.PA	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.W90.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.LKOSC.FL	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.SIL.UT	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.F3.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.F74.RG	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.DEC.TX	TTGCGAAAAAATGCACATCGGCTATAAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.AMD.TX	TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.BMCHT.TX	TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.COT.TX	TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
E.DIL.FL.TX	TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT

E.DIL.GL03BB.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.GL06BB.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.I10.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.LK01.FL TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.LPHT.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.MC02.M TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.MIL.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.MSHT.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.ROT.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.SAM.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.SHL.GA TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.T2T2BB.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.TRP.AZ TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.PPC.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGTCG-CTAAAATCCATACTT
 E.DIL.AWR.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.CT3.NM TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.MCHT.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.RET.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.PEC.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.CT1.NM TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.BRH.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.LPSHT.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.OSM.M TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
 E.DIL.PGTBB.TX TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTTAAATCCATACTT
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 E.DIL.AMR.CA TTGCGAAAAAATGCACATCGGCTATAGATGCTTGTTTATAGCCG-CTAAAATCCATACTT
 E.DIL.ECH.CA TTGCGAAAAAATGCACATCGGCTATAGATGCTTGTTTATAGCCG-CTAAAATCCATACTT
 E.DIL.LOD02.CA TTGCGAAAAAATGCACATCGGCTATAGATGCTTGTTTATAGCCG-CTAAAATCCATACTT
 E.DIL.TIM.OR TTGCGAAAAAATGCACATCGGCTATAGATGCTTGTTTATAGCCG-CTAAAATCCATACTT
 E.DIL.LOD01.CA TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTAAAATCCATACTT
 E.DIL.NOCK.PA TTGCGAAAAAATGCACATCGGCTATAGATGCTTGTTTATAGCCG-CTAAAATCCATACTT
 E.DIL.CBB.VI TTGCGAAAAAATGCACATCGGCTATGAATGCTTGTTTATAGCCG-CTAAAATCCATACTT
 E.DIL.BUBB2.TX TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.BUBB3.TX TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.CATCPBB.T TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
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 E.DIL.CATEBB.TX TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.CATG1B.TX TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.CATG2B.TX TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.CATHBB.TX TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.DRS.NM TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.DUC.OK TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.JAC.FL TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.JUN.FL TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.KRM01.FL TTGCGAAAATTTGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.KRM02.FL TTGCGAAAAAATGCACATCGACTATAGATGCTTGTTTATAGTCGTTTTAAATCCATACTT
 E.DIL.MC.M TTGCGATAATTTGCACATCGACTATAAATGCTTGTTTATAGGAGATTCAAATCCATGCTT

E.DEFLEXA.SHC.L TCTT-GAGTATGGTCGGGTACCTATGAATG-TGCTTGCACATCGTAAGCG-----GTAAT
 L.MELICERTA.BCH GCTTCGAGTATGGTCGGGTACCTTTGCGTTTGTTTACCACACAAACATAAGCGTTCA
 E.DIL.ALT.NM GCTT-TAGTATGGTCGGGTACCTATGAA---GTGTATAACTTCATAAGCA-----GTTTT
 E.DIL.BEC.NM GCTT-TAGTATGGTCGGGTACCTATGAA---GTGTATAACTTCATAAGCA-----GTTTT
 E.DIL.CHIC.UT GCTT-TAGTATGGTCGGGTACCTATGAA---GTGTATAACTTCATAAGCA-----GTTTT
 E.DIL.MEN.WI GCTT-TAGTATGGTCGGGTACCTATGAA---GTGTATAACTTCATAAGCA-----GTTTT
 E.DIL.SCH.PA GCTT-TAGTATGGTCGGGTACCTATGAA---GTGTATAACTTCATAAGCA-----GTTTT
 E.DIL.DTL.OR GCTT-TAGTATGGTCGGGTACCTATGAA---GTGTATAACTTCATAAGCA-----GTTTT

[illegible]

E.DIL.TRP.AZ	GCTT-TAGTATGGTCGGGTACCTATGAA---GTGTCTAACTTCATAAGCA-----GTTTT
E.DIL.PPC.TX	GCTT-TAGTATGGTCGGGTACCTATGAA---GTGTCTAACTTCATAAGCA-----GTTTT
E.DIL.AWR.TX	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.CT3.NM	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.MCHT.TX	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.RET.TX	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.PEC.TX	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.CT1.NM	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.BRH.TX	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.LPSHT.TX	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.OSM.M	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.PGTBB.TX	GCTT-TAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.CTS.NM	GCTT-GAGTATGGTCGGGTACCTATGAA---GTTTCTCACTTCATAAGCA-----GTTTT
E.DIL.AMR.CA	GCTT-GAGTATGGTCGGGTACCTATGAA---GTTTCTAACTTCATAAGCA-----GTTTT
E.DIL.ECH.CA	GCTT-GAGTATGGTCGGGTACCTATGAA---GTTTCTAACTTCATAAGCA-----GTTTT
E.DIL.LOD02.CA	GCTT-GAGTATGGTCGGGTACCTATGAA---GTTTCTAACTTCATAAGCA-----GTTTT
E.DIL.TIM.OR	GCTT-GAGTATGGTCGGGTACCTATGAA---GTTTCTAACTTCATAAGCA-----GTTTT
E.DIL.LOD01.CA	GCTT-GAGTATGGTCGGGTACCTATGAA---GTTTCTAACTTCATAAGCA-----GTTTT
E.DIL.NOCK.PA	GCTT-GAGTATGGTCGGGTACCTATGAA---GTTTCTAACTTCATAAGCA-----GTTTT
E.DIL.CBB.VI	GCTT-GAGTGTGGTCGGGTACCTATGAA---GTGTCTCACTTCATAAGCA-----GTTTT
E.DIL.BUBB2.TX	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.BUBB3.TX	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.CATCPBB.T	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.CATDBB.TX	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.CATEBB.TX	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.CATG1B.TX	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.CATG2B.TX	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.CATHBB.TX	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.DRS.NM	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.DUC.OK	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.JAC.FL	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.JUN.FL	GCTT-GAGTATGGTCGGGTACCTATGGG---GTTATTTACTTCATAAGCA-----GTTTC
E.DIL.KRM01.FL	GCTT-GAGTATGGTCGGGTACCTATGAA---GTAATTTACTTCATAAGCA-----GTTTC
E.DIL.KRM02.FL	GCTT-TAGTATGGTCGGGTACCTATGAA---GTATTTTACTTCATAAGCA-----GTTTC
E.DIL.MC.M	GCTT-AAGTATGGTCGGGTACCTATGAA---GTGTTTCACTTCATAAGCA-----GTTTA

E.DEFLEXA.SHC.L	TAGCTGTTACCGTATGGAGTAAAGATTATTCAACTATTTGAATAGCGCCCGTA-----TT
L.MELICERTA.BCH	TTCCTACGATTG---ATCGTGAAGGTGTAAAGATCAGTAAATGACGCCCGCTTGCGATA
E.DIL.ALT.NM	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.BEC.NM	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.CHIC.UT	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.MEN.WI	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.SCH.PA	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.DTL.OR	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.SEQ.UT	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.BOQ.M	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.CENT.CA	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.CIH.M	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.COL.M	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.F13.RG	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.F68.RG	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.F76.RG	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.F85.RG	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.MAD.WI	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.MES.NM	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.OKR.OK	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA

[illegible]

E.DIL.CTS.NM	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.AMR.CA	AGCTAAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.ECH.CA	AGCTAAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.LOD02.CA	AGCTAAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.TIM.OR	AGCTAAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.LOD01.CA	AGCTAAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.NOCK.PA	AGCTAAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.CBB.VI	AGCATAAGACTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGCT-----TA
E.DIL.BUBB2.TX	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.BUBB3.TX	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.CATCPBB.T	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.CATDBB.TX	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.CATDBB.TX	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.CATG1B.TX	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.CATG2B.TX	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.CATHBB.TX	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.DRS.NM	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.DUC.OK	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.JAC.FL	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.JUN.FL	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.KRM01.FL	GGCAAGGAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.KRM02.FL	GGCTTGAAGCTGTGTGGTGTAAAGATTATTCAACTATTTGAATAACGCCCGTC-----TA
E.DIL.MC.M	AGCATTAAACTGTGTGGTGTAAAGATTATTTAACTATTTAAATAACGCCCGCT-----TA

E.DEFLEXA.SHC.L	GCTTATTTTAAAACTA-----TTTAAATCGCATTTACTATGTCTTA-TGTGAACTTATG
L.MELICERTA.BCH	ATTTTAATTGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAATACGCT
E.DIL.ALT.NM	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.BEC.NM	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.CHIC.UT	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.MEN.WI	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.SCH.PA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.DTL.OR	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.SEQ.UT	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.BOQ.M	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.CENT.CA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.CIH.M	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.COL.M	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.F13.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.F68.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.F76.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.F85.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.MAD.WI	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.MES.NM	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.OKR.OK	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.POZ.M	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.S31.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.S44.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.S47.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.STR.NM	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.TRV.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W101.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W106.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W116.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W129.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W13.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W146.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT

E.DIL.W157.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W159.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W163.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W173.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W25.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W300.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W55.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W56.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W57.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W79.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.PHL.PA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.W90.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.LKOSC.FL	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.SIL.UT	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.F3.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.F74.RG	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.DEC.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.AMD.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.BMCHT.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.COT.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.FL.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.GL03BB.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.GL06BB.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.I10.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.LK01.FL	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.LPHT.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.MC02.M	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.MIL.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.MSHT.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.ROT.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.SAM.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.SHL.GA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.T2T2BB.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.TRP.AZ	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.PPC.TX	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.AWR.TX	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.CT3.NM	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.MCHT.TX	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.RET.TX	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.PEC.TX	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.CT1.NM	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.BRH.TX	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.LPSHT.TX	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.OSM.M	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.PGTBB.TX	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.CTS.NM	GCTTATTATAAAAATACACTATATAAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.AMR.CA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.ECH.CA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.LOD02.CA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.TIM.OR	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.LOD01.CA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.NOCK.PA	GCTTATTGTAAAATACACTATATAAAAAATTGCATTAAAGGTTATTTT-TGTGA-TATTTT
E.DIL.CBB.VI	GCTTATTATAAAAATATACTATTTTAAAAATTGCATTTAAGGTTATTTT-TGTGA-TATTTT
E.DIL.BUBB2.TX	GCTTATTTTATTATATACACTTTTAAAAATTGCATTTTGGGTTTTTTTTATGTGA-TATTTG
E.DIL.BUBB3.TX	GCTTATTTTATTATATACACTTTTAAAAATTGCATTTTGGGTTTTTTTTATGTGA-TATTTG
E.DIL.CATCPBB.T	GCTTATTTTATTATATACACTTTTAAAAATTGCATTTTGGGTTTTTTTTATGTGA-TATTTG
E.DIL.CATDBB.TX	GCTTATTTTATTATATACACTTTTAAAAATTGCATTTTGGGTTTTTTTTATGTGA-TATTTG

E.DIL.CATEBB.TX GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.CATG1B.TX GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.CATG2B.TX GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.CATHBB.TX GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.DRS.NM GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.DUC.OK GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.JAC.FL GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.JUN.FL GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.KRM01.FL GCTTATTTTATTATATACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.KRM02.FL GCTTATTTTATTATACACACTTTTAAAATTGCATTTTGGGTTTTTTTATGTGA-TATTTG
 E.DIL.MC.M GCTTAAATTATTATACACTATTTAAAATTGCATTTAAGGTTTTTTTTTGTGA-AATTTG

E.DEFLEXA.SHCL TGTTGCTATGAGAGGGTTTTTGATTCTAT-----AATTAAAAACATAATAG----
 L.MELICERTA.BCH GGTACTAAAGTACTGTTGCACATTGTTATGCGTTAACATGTAAGACGTATTAAGGTATC
 E.DIL.ALT.NM GATCTC--TTAGTTACTTAGT-----GACTTATAGAG----
 E.DIL.BEC.NM GATCTC--TTAGTTACTTAGT-----GACTTATAGAG----
 E.DIL.CHIC.UT GATCTC--TTAGTTACTTAGT-----GACTTATAGAG----
 E.DIL.MEN.WI GATCTC--TTAGTTACTTAGT-----GACTTATAGAG----
 E.DIL.SCH.PA GATCTC--TTAGTTACTTAGT-----GACTTATAGAG----
 E.DIL.DTL.OR GATCTC--TTAGTTACTTAGT-----GACTTATAGAG----
 E.DIL.SEQ.UT GATCTC--TTAGTTACTTAGT-----GACTTATAGAG----
 E.DIL.BOQ.M GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.CENT.CA GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.CIH.M GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.COL.M GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.F13.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.F68.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.F76.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.F85.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.MAD.WI GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.MES.NM GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.OKR.OK GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.POZ.M GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.S31.TX GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.S44.TX GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.S47.TX GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.STR.NM GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.TRV.TX GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W101.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W106.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W116.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W129.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W13.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W146.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W157.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W159.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W163.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W173.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W25.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W300.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W55.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W56.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W57.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W79.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.PHL.PA GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
 E.DIL.W90.RG GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----

E.DIL.LKOSC.FL	GATCTC--TTGGTTACTTAGT-----GACTTTTAGAG----
E.DIL.SIL.UT	GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
E.DIL.F3.RG	GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
E.DIL.F74.RG	GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
E.DIL.DEC.TX	GATTTTC--TTAGTTACTTAGT-----GACTTTTAGAG----
E.DIL.AMD.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.BMCHT.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.COT.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.FL.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.GL03BB.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.GL06BB.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.I10.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.LK01.FL	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.LPHT.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.MC02.M	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.MIL.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.MSHT.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.ROT.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.SAM.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.SHL.GA	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.T2T2BB.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.TRP.AZ	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.PPC.TX	GATCTC--TTAGTTACTTAGT-----GACTATTAGAG----
E.DIL.AWR.TX	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.CT3.NM	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.MCHT.TX	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.RET.TX	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.PEC.TX	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.CT1.NM	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.BRH.TX	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.LPSHT.TX	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.OSM.M	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.PGTBB.TX	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.CTS.NM	GATCTC--TTAGTTACTCAGT-----GACTATTAGAG----
E.DIL.AMR.CA	GATCTC--CTAGTTACTTAGT-----GACTTTAGAG----
E.DIL.ECH.CA	GATCTC--CTAGTTACTTAGT-----GACTTTAGAG----
E.DIL.LOD02.CA	GATCTC--CTAGTTACTTAGT-----GACTTTAGAG----
E.DIL.TIM.OR	GATCTC--CTAGTTACTTAGT-----GACTTTAGAG----
E.DIL.LOD01.CA	GATCTC--CTAGTTACTTAGT-----GACTTTAGAG----
E.DIL.NOCK.PA	GATCTC--CTAGTTACTTAGT-----GACTTTAGAG----
E.DIL.CBB.VI	GATCTC--TTTGTCACTCAGT-----GACTATTAGAG----
E.DIL.BUBB2.TX	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.BUBB3.TX	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.CATCPBB.T	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.CATDBB.TX	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.CATEBB.TX	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.CATG1B.TX	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.CATG2B.TX	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.CATHBB.TX	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.DRS.NM	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.DUC.OK	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.JAC.FL	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.JUN.FL	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.KRM01.FL	GCTCTTGATAATTAACCTTAATACTATTAT-----TAGGCAAACCTATTAAAG----
E.DIL.KRM02.FL	GCTCTCGATTGTTAACTTAATACTATTAT-----TAAGCATGCGATTAAAG----
E.DIL.MC.M	GCTCTCTATAAGTTACTCAATACTATTAT-----TAAGTAACTATTAAAG----

E.DEFLEXA.SHC.L ----TAAACAAAAAAGCACAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 L.MELICERTA.BCH GGCTAAAACTGTAACACAAAATACAACCCTATGCGGTGGATCACTAGGCTCGCGAGTCGA
 E.DIL.ALT.NM ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.BEC.NM ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.CHIC.UT ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.MEN.WI ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.SCH.PA ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.DTL.OR ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.SEQ.UT ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.BOQ.M ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.CENT.CA ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.CIH.M ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.COL.M ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.F13.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.F68.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.F76.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.F85.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.MAD.WI ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.MES.NM ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.OKR.OK ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.POZ.M ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.S31.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.S44.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.S47.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.STR.NM ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.TRV.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W101.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W106.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W116.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W129.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W13.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W146.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W157.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W159.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W163.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W173.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W25.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W300.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W55.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W56.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W57.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W79.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.PHL.PA ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.W90.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.LKOSC.FL ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.SIL.UT ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.F3.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.F74.RG ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.DEC.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.AMD.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.BMCHT.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.COT.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.FL.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.GL03BB.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.GL06BB.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
 E.DIL.I10.TX ----AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA

E.DIL.LK01.FL	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.LPHT.TX	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.MC02.M	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.MIL.TX	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.MSHT.TX	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.ROT.TX	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.SAM.TX	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.SHL.GA	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.T2T2BB.TX	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.TRP.AZ	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.PPC.TX	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.AWR.TX	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CT3.NM	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.MCHT.TX	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.RET.TX	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.PEC.TX	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CT1.NM	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.BRH.TX	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.LPSHT.TX	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.OSM.M	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.PGTBB.TX	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CTS.NM	----	AACAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.AMR.CA	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.ECH.CA	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.LOD02.CA	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.TIM.OR	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.LOD01.CA	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.NOCK.PA	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CBB.VI	----	AGCAATATTAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.BUBB2.TX	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.BUBB3.TX	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CATCPBB.T	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CATDBB.TX	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CATEBB.TX	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CATG1B.TX	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CATG2B.TX	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.CATHBB.TX	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.DRS.NM	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.DUC.OK	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.JAC.FL	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.JUN.FL	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.KRM01.FL	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.KRM02.FL	----	ACCATTTTAAACACGAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA
E.DIL.MC.M	----	ACCAACAAAAACACAAAAACAACCCTATGCGGTGGATCACTTGGCTCGCGAGTCGA

E.DEFLEXA.SHC.L	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
L.MELICERTA.BCH	TGAAGAGCGCAGCAAAG	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.ALT.NM	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.BEC.NM	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CHIC.UT	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.MEN.WI	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.SCH.PA	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.DTL.OR	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.SEQ.UT	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.BOQ.M	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CENT.CA	TGAAGAGCGCAGCAAAC	TGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA

[illegible]

E.DIL.CT3.NM	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.MCHT.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.RET.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.PEC.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CT1.NM	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.BRH.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.LPSHT.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.OSM.M	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.PGTBB.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CTS.NM	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.AMR.CA	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.ECH.CA	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.LOD02.CA	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.TIM.OR	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.LOD01.CA	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.NOCK.PA	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CBB.VI	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.BUBB2.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.BUBB3.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CATCPBB.T	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CATDBB.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CATEBB.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CATG1B.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CATG2B.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.CATHBB.TX	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.DRS.NM	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.DUC.OK	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.JAC.FL	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.JUN.FL	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.KRM01.FL	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.KRM02.FL	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA
E.DIL.MC.M	TGAAGAGCGCAGCAAACCTGCGTGAATTAATGTGATTTGCAGGACACATTGATCATCGATA

E.DEFLEXA.SHC.L	TCTTGAACGCATATTGCGGTTACGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
L.MELICERTA.BCH	TCTTGAACGCATATTGCGGTTACGGTTTCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.ALT.NM	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.BEC.NM	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CHIC.UT	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.MEN.WI	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.SCH.PA	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.DTL.OR	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.SEQ.UT	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.BOQ.M	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CENT.CA	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CIH.M	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.COL.M	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.F13.RG	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.F68.RG	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.F76.RG	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.F85.RG	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.MAD.WI	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.MES.NM	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.OKR.OK	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.POZ.M	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.S31.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.S44.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT

[illegible]

E.DIL.LOD02.CA	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.TIM.OR	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.LOD01.CA	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.NOCK.PA	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CBB.VI	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.BUBB2.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.BUBB3.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CATCPBB.T	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CATDBB.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CATEBB.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CATG1B.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CATG2B.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.CATHBB.TX	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.DRS.NM	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.DUC.OK	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.JAC.FL	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.JUN.FL	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.KRM01.FL	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.KRM02.FL	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT
E.DIL.MC.M	TCTTGAACGCATATTGCGGTTATGGATCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGT

E.DEFLEXA.SHC.L	ATAAATATGCAAATATGTGAAAAATGTCTA-ATCATTTTTGTTTGGTCGTTAAAAATCAA
L.MELICERTA.BCH	TTACATATGTCTATACGTGAAAAGTGTGCT-CGCACTTTTGCTCGGTCGTTTTAAGTGAG
E.DIL.ALT.NM	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.BEC.NM	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.CHIC.UT	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.MEN.WI	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.SCH.PA	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.DTL.OR	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.SEQ.UT	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.BOQ.M	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.CENT.CA	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.CIH.M	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.COL.M	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.F13.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.F68.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.F76.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.F85.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.MAD.WI	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.MES.NM	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.OKR.OK	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.POZ.M	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.S31.TX	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.S44.TX	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.S47.TX	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.STR.NM	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.TRV.TX	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W101.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W106.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W116.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W129.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W13.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W146.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W157.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W159.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----
E.DIL.W163.RG	ATTAATATGTAAATAAGTGAAAAGTGATCATGTGCGCTTTTGCTTGGCTGTTAAA-----

[illegible]

E.DIL.CATHBB.TX ATTAATATGTAAAAATGTGAAAAGCGATCATGTCGCTTTTGCTTGGCTGTTAAAGTTT--
E.DIL.DRS.NM ATTAATATGTAAAAATGTGAAAAGCGATCATGTCGCTTTTGCTTGGCTGTTAAAGTTT--
E.DIL.DUC.OK ATTAATATGTAAAAATGTGAAAAGCGATCATGTCGCTTTTGCTTGGCTGTTAAAGTTT--
E.DIL.JAC.FL ATTAATATGTAAAAATGTGAAAAGCGATCATGTCGCTTTTGCTTGGCTGTTAAAGTTT--
E.DIL.JUN.FL ATTAATATGTAAAAATGTGAAAAGCGATCATGTCGCTTTTGCTTGGCTGTTAAAGTTT--
E.DIL.KRM01.FL ATTAATATGTAAAAATGTGAAAAGCGATCATGTCGCTTTTGCTTGGCTGTTAAAGTTT--
E.DIL.KRM02.FL ATTAATATGTAAATATGTGAAAGGCGATCATGTCGCTTTTGCTTGGCTGTTAAATTTT--
E.DIL.MC.M ATTAATATGTAAATATGTGAAAAGCGATTATTTTCGCTTTTGCTTGGCTGTTAAATAA--

E.DEFLEXA.SHC.L G---TGTTTTTATCAGCTTAAGTAAATTAA--TCTAATC--TCA--TTAGATAAAGTGC
L.MELICERTA.BCH CTCTCACTTTTATCAGCTTCAGATCTATGGATTACTAATTCGTAAAATTAGTAAAAATGC
E.DIL.ALT.NM -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.BEC.NM -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.CHIC.UT -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.MEN.WI -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.SCH.PA -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.DTL.OR -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.SEQ.UT -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.BOQ.M -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.CENT.CA -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.CIH.M -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.COL.M -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.F13.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.F68.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.F76.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.F85.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.MAD.WI -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.MES.NM -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.OKR.OK -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.POZ.M -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.S31.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.S44.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.S47.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.STR.NM -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.TRV.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W101.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W106.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W116.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W129.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W13.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W146.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W157.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W159.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W163.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W173.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W25.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W300.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W55.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W56.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W57.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W79.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.PHL.PA -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.W90.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.LKOSC.FL -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.SIL.UT -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.F3.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC

E.DIL.F74.RG -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.DEC.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.AMD.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.BMCHT.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.COT.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.FL.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.GL03BB.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.GL06BB.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.I10.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.LK01.FL -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.LPHT.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.MC02.M -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.MIL.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.MSHT.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.ROT.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.SAM.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.SHL.GA -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.T2T2BB.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.TRP.AZ -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.PPC.TX -----GTTTTTATCAGCTTAAGAATATATTA--ACTAATC--TCATGTTAGTTAAAATAC
E.DIL.AWR.TX -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.CT3.NM -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.MCHT.TX -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.RET.TX -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.PEC.TX -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.CT1.NM -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.BRH.TX -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.LPSHT.TX -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.OSM.M -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.PGTBB.TX -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.CTS.NM -----GTTTTTATCAGCTTAAGAATATTTAA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.AMR.CA -----GGTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.ECH.CA -----GGTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.LOD02.CA -----GGTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.TIM.OR -----GGTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.LOD01.CA -----GGTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.NOCK.PA -----GGTTTTATCAGCTTAAGAATATATTA--ACTAATC--TTATGTTAGTTAAAATAC
E.DIL.CBB.VI -----GATTTTATCAGCTTAAGAATCTGA--ACTAATC--TTTTGTTAGTTCAAATAC
E.DIL.BUBB2.TX ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.BUBB3.TX ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.CATCPBB.T ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.CATDBB.TX ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.CATEBB.TX ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.CATG1B.TX ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.CATG2B.TX ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.CATHBB.TX ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.DRS.NM ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.DUC.OK ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.JAC.FL ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.JUN.FL ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.KRM01.FL ----TAATTTTATCAGCTTAAGAATTTTAGA--ACTAACC--TTGTGTTAGTT-AAGTAC
E.DIL.KRM02.FL ----TATTTTATCAGCTTAAGAAATTTAG--ACTAACC--TTGCGTTAGTT-AAGTAC
E.DIL.MC.M ----TATTTTATCAGCTTAAGATTATTCAA--GCTAATC--TTATATTAGTTTAAATAC

E.DEFLEXA.SHC.L ACAATGTTATTTTCATTGACGTTGAATATTTCTGATTGCTTTAGGCAAACAAAAATTGCAA
L.MELICERTA.BCH ATATAGTAGCACTCAATTCGATTG-----CTAATGAATGCTAACAACAAAAATTGCTT

E.DIL.MIL.TX	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.MSHT.TX	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.ROT.TX	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.SAM.TX	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.SHL.GA	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.T2T2BB.TX	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.TRP.AZ	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.PPC.TX	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.AWR.TX	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.CT3.NM	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.MCHT.TX	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.RET.TX	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.PEC.TX	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.CT1.NM	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.BRH.TX	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.LPSHT.TX	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.OSM.M	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.PGTBB.TX	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.CTS.NM	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.AMR.CA	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.ECH.CA	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.LOD02.CA	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.TIM.OR	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.LOD01.CA	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.NOCK.PA	ACAATGTTGTTTCATTAGTGTTAA-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.CBB.VI	ACAATGTTGTTTCATTAGTGTTAG-----TCTTTTGCTTTGAGCAAACAAAAATTGCTT
E.DIL.BUBB2.TX	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.BUBB3.TX	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.CATCPBB.T	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.CATDBB.TX	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.CATEBB.TX	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.CATG1B.TX	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.CATG2B.TX	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.CATHBB.TX	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.DRS.NM	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.DUC.OK	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.JAC.FL	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.JUN.FL	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.KRM01.FL	ACAATGTTGTTTCATTTGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.KRM02.FL	ACAATGTTGTTTCATTAGTGTTAA-----TCGGTTGCTATAAGCAAGCAAAAAATTGCTT
E.DIL.MC.M	ACAATGTTGTTTCATTAGTGTTAA-----TCAGTTGCTTTGAGCAAACAAAAATTGCTT

E.DEFLEXA.SHC.L	AGCTTCTAAAGATTTGTTTGTTT---CTGTTATCAGATATTAACCTAAAGAATGAAAATAC
L.MELICERTA.BCH	AGCT--CTTTAATTTGTTTGCTTAGCTTCGTAGTTAGCTTTTCAATTTGTTGTTATACTAG
E.DIL.ALT.NM	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAGGATTAACCTTAAAGTGAATCATC
E.DIL.BEC.NM	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAGGATTAACCTTAAAGTGAATCATC
E.DIL.CHIC.UT	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAGGATTAACCTTAAAGTGAATCATC
E.DIL.MEN.WI	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAGGATTAACCTTAAAGTGAATCATC
E.DIL.SCH.PA	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAGGATTAACCTTAAAGTGAATCATC
E.DIL.DTL.OR	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAGGATTAACCTTAAAGTGAATCATC
E.DIL.SEQ.UT	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAGGATTAACCTTAAAGTGAATCATC
E.DIL.BOQ.M	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAAGATTAACCTTAAAGTGAATCAGC
E.DIL.CENT.CA	AGATAACTCTTATTTGTTGGCTC---ATAGTTTATAAGATTAACCTTAAAGTGAATCAGC
E.DIL.CIH.M	AGATAACTCTTATTTGTTGGCTC---ATAGTTTATAAGATTAACCTTAAAGTGAATCAGC
E.DIL.COL.M	AGATAACTCTTATTTGTTGGCTC---ATAGTTTATAAGATTAACCTTAAAGTGAATCAGC
E.DIL.F13.RG	AGATAACTCTTATTTGTTGGCTC---ATAGTTTATAAGATTAACCTTAAAGTGAATCAGC

[illegible]

E.DIL.PEC.TX	AGATTACTCTTATTTGTTGGCTC---TTAGTTTATTAGATTAAACCTTAAAGTGAATCAAC
E.DIL.CT1.NM	AGATTACTCTTATTTGTTGGCTC---TTAGTTTATTAGATTAAACCTTAAAGTGAATCAAC
E.DIL.BRH.TX	AGATTACTCTTATTTGTTGGCTC---TTAGTTTATTAGATTAAACCTTAAAGTGAATCAAC
E.DIL.LPSHT.TX	AGATTACTCTTATTTGTTGGCTC---TTAGTTTATTAGATTAAACCTTAAAGTGAATCAAC
E.DIL.OSM.M	AGATTACTCTTATTTGTTGGCTC---TTAGTTTATTAGATTAAACCTTAAAGTGAATCAAC
E.DIL.PGTBB.TX	AGATTACTCTTATTTGTTGGCTC---TTAGTTTATTAGATTAAACCTTAAAGTGAATCAAC
E.DIL.CTS.NM	AGATTACTCTTATTTGTTGGCTC---TTAGTTTATTAGATTAAACCTTAAAGTGAATCAAC
E.DIL.AMR.CA	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAAGATTAAACCGTAAAGTGAAATGAA
E.DIL.ECH.CA	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAAGATTAAACCGTAAAGTGAAATGAA
E.DIL.LOD02.CA	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAAGATTAAACCGTAAAGTGAAATGAA
E.DIL.TIM.OR	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAAGATTAAACCGTAAAGTGAAATGAA
E.DIL.LOD01.CA	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAAGATTAAACCTTAAAGTGAAATGAA
E.DIL.NOCK.PA	AGATAACTCTTATTTGTTGGCTC---CTAGTTTATAAGATTAAACCTTAAAGTGAAATGAA
E.DIL.CBB.VI	AGAATACTCTTATTTGTTAGCTA---TTAGTTTATATGATTAAACCTTAAAGTGAATCAAT
E.DIL.BUBB2.TX	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.BUBB3.TX	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.CATCPBB.T	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.CATDBB.TX	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.CATEBB.TX	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.CATG1B.TX	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.CATG2B.TX	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.CATHBB.TX	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.DRS.NM	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.DUC.OK	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.JAC.FL	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.JUN.FL	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.KRM01.FL	TGAATACTTAAATTTGTTAGCTT---GTAGTTTATCTGATTAAACCTTATAATGAAACGAA
E.DIL.KRM02.FL	TGAATACTTTAATTTGCAAGCTT---CTAGTGTATCTGATTAACTATATAATGAAACGAA
E.DIL.MC.M	AGAATTCTCTTATTTGTTTGCTT---GTAGTTAATATGATTTACCTAAAAGTGAAGCAA

E.DEFLEXA.SHC.L	GAAAATG--TGTATTATTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
L.MELICERTA.BCH	TAATATGTTTGTACTTTTTAAAGTGCATAT--AAAAGCTATATCATA-----
E.DIL.ALT.NM	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.BEC.NM	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CHIC.UT	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.MEN.WI	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.SCH.PA	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.DTL.OR	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.SEQ.UT	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.BOQ.M	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CENT.CA	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CIH.M	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.COL.M	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.F13.RG	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.F68.RG	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.F76.RG	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.F85.RG	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.MAD.WI	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.MES.NM	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.OKR.OK	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.POZ.M	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.S31.TX	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.S44.TX	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.S47.TX	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.STR.NM	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.TRV.TX	TAAAAGG--TGTAATTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC

[illegible]

E.DIL.NOCK.PA	TAAAAAG--TGTAATTTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CBB.VI	AAAAAAG--TGTAACTTTATAACTTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.BUBB2.TX	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.BUBB3.TX	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CATCPBB.T	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CATDBB.TX	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CATEBB.TX	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CATG1B.TX	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CATG2B.TX	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.CATHBB.TX	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.DRS.NM	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.DUC.OK	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.JAC.FL	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.JUN.FL	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.KRM01.FL	TAATAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.KRM02.FL	TAAAAAG--TGTAATTTTAAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC
E.DIL.MC.M	TAGAACG--TGTATAACTTAATTTTCATATTTTCGACCTCAGATCAGACGAGATTACCCGC

E.DEFLEXA.SHC.L	TGAATTTAA
L.MELICERTA.BCH	-----TTC
E.DIL.ALT.NM	TGAATTTAA
E.DIL.BEC.NM	TGAATTTAA
E.DIL.CHIC.UT	TGAATTTAA
E.DIL.MEN.WI	TGAATTTAA
E.DIL.SCH.PA	TGAATTTAA
E.DIL.DTL.OR	TGAATTTAA
E.DIL.SEQ.UT	TGAATTTAA
E.DIL.BOQ.M	TGAATTTAA
E.DIL.CENT.CA	TGAATTTAA
E.DIL.CIH.M	TGAATTTAA
E.DIL.COL.M	TGAATTTAA
E.DIL.F13.RG	TGAATTTAA
E.DIL.F68.RG	TGAATTTAA
E.DIL.F76.RG	TGAATTTAA
E.DIL.F85.RG	TGAATTTAA
E.DIL.MAD.WI	TGAATTTAA
E.DIL.MES.NM	TGAATTTAA
E.DIL.OKR.OK	TGAATTTAA
E.DIL.POZ.M	TGAATTTAA
E.DIL.S31.TX	TGAATTTAA
E.DIL.S44.TX	TGAATTTAA
E.DIL.S47.TX	TGAATTTAA
E.DIL.STR.NM	TGAATTTAA
E.DIL.TRV.TX	TGAATTTAA
E.DIL.W101.RG	TGAATTTAA
E.DIL.W106.RG	TGAATTTAA
E.DIL.W116.RG	TGAATTTAA
E.DIL.W129.RG	TGAATTTAA
E.DIL.W13.RG	TGAATTTAA
E.DIL.W146.RG	TGAATTTAA
E.DIL.W157.RG	TGAATTTAA
E.DIL.W159.RG	TGAATTTAA
E.DIL.W163.RG	TGAATTTAA
E.DIL.W173.RG	TGAATTTAA
E.DIL.W25.RG	TGAATTTAA
E.DIL.W300.RG	TGAATTTAA

E.DIL.W55.RG	TGAATTTAA
E.DIL.W56.RG	TGAATTTAA
E.DIL.W57.RG	TGAATTTAA
E.DIL.W79.RG	TGAATTTAA
E.DIL.PHL.PA	TGAATTTAA
E.DIL.W90.RG	TGAATTTAA
E.DIL.LKOSC.FL	TGAATTTAA
E.DIL.SIL.UT	TGAATTTAA
E.DIL.F3.RG	TGAATTTAA
E.DIL.F74.RG	TGAATTTAA
E.DIL.DEC.TX	TGAATTTAA
E.DIL.AMD.TX	TGAATTTAA
E.DIL.BMCHT.TX	TGAATTTAA
E.DIL.COT.TX	TGAATTTAA
E.DIL.FL.TX	TGAATTTAA
E.DIL.GL03BB.TX	TGAATTTAA
E.DIL.GL06BB.TX	TGAATTTAA
E.DIL.I10.TX	TGAATTTAA
E.DIL.LK01.FL	TGAATTTAA
E.DIL.LPHT.TX	TGAATTTAA
E.DIL.MC02.M	TGAATTTAA
E.DIL.MIL.TX	TGAATTTAA
E.DIL.MSHT.TX	TGAATTTAA
E.DIL.ROT.TX	TGAATTTAA
E.DIL.SAM.TX	TGAATTTAA
E.DIL.SHL.GA	TGAATTTAA
E.DIL.T2T2BB.TX	TGAATTTAA
E.DIL.TRP.AZ	TGAATTTAA
E.DIL.PPC.TX	TGAATTTAA
E.DIL.AWR.TX	TGAATTTAA
E.DIL.CT3.NM	TGAATTTAA
E.DIL.MCHT.TX	TGAATTTAA
E.DIL.RET.TX	TGAATTTAA
E.DIL.PEC.TX	TGAATTTAA
E.DIL.CT1.NM	TGAATTTAA
E.DIL.BRH.TX	TGAATTTAA
E.DIL.LPSHT.TX	TGAATTTAA
E.DIL.OSM.M	TGAATTTAA
E.DIL.PGTBB.TX	TGAATTTAA
E.DIL.CTS.NM	TGAATTTAA
E.DIL.AMR.CA	TGAATTTAA
E.DIL.ECH.CA	TGAATTTAA
E.DIL.LOD02.CA	TGAATTTAA
E.DIL.TIM.OR	TGAATTTAA
E.DIL.LOD01.CA	TGAATTTAA
E.DIL.NOCK.PA	TGAATTTAA
E.DIL.CBB.VI	TGAATTTAA
E.DIL.BUBB2.TX	TGAATTTAA
E.DIL.BUBB3.TX	TGAATTTAA
E.DIL.CATCPBB.T	TGAATTTAA
E.DIL.CATDBB.TX	TGAATTTAA
E.DIL.CATEBB.TX	TGAATTTAA
E.DIL.CATG1B.TX	TGAATTTAA
E.DIL.CATG2B.TX	TGAATTTAA
E.DIL.CATHBB.TX	TGAATTTAA
E.DIL.DRS.NM	TGAATTTAA
E.DIL.DUC.OK	TGAATTTAA

E.DIL.JAC.FL	TGAATTTAA
E.DIL.JUN.FL	TGAATTTAA
E.DIL.KRM01.FL	TGAATTTAA
E.DIL.KRM02.FL	TGAATTTAA
E.DIL.MC.M	TGAATTTAA

Supplemental document S2.6: CLUSTAL format alignment of COI sequences of *Limnias melicerta* and *L. ceratophylli* by MAFFT (v7.380). Abbreviations are the same as Tables S2.1 and S2.2. N= missing data.

L.CER.MORPH.NM	ATAAGTGTCAATTATTCGTGTGGAGCTAGGTGTTGTAGGCCCTTTTTAGGGGATGATCAT
L.CER.WORT25.TX	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGTGATGACCAT
L.CER.WORT15.TX	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.TLL.PA	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.WACO.TX	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.MN04.WI	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.MN40.WI	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.MN46.WI	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.MN16.WI	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.BLU.OR	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.SAM.TX	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.DUC.OK	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.FL.TX	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.GMP.WI	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.MN14.WI	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.MEN.WI	ATGAGGGTTCTTATTCGTGTAGAGTTGGGTGTAGTGGGACCTTTCTTAGGCGATGACCAT
L.CER.HCP.FL	ATAAGTGTTTTAATTCGCGTTGAGTTAGGTGTTGTGGGTCTTTTTTGGGAGATGATCAT
L.CER.PIED.GA	ATAAGCGTCTTAATTCGAGTGGAGTTAGGTGTGGTTGGACCTTTTCTTGGTGATGATCAC
L.CER.NOCKSP.PA	ATAAGCGTCTTAATTCGAGTGGAGTTAGGTGTGGTTGGACCTTTTCTTGGTGATGATCAC
L.CER.ECHOLK.CA	ATAAGCGTCTTAATTCGAGTGGAGTTAGGTGTGGTTGGACCTTTTCTTGGTGATGATCAC
L.CER.NOCKFS.PA	ATAAGCGTCTTAATTCGAGTGGAGTTAGGTGTGGTTGGACCTTTTCTTGGTGATGATCAC
L.CER.HILOCH.GA	ATAAGCGTCTTAATTCGAGTGGAGTTAGGTGTGGTTGGACCTTTTCTTGGTGATGATCAC
L.CER.EASTPOI.GA	ATAAGCGTCTTAATTCGAGTGGAGTTAGGTGTGGTTGGACCTTTTCTTGGTGATGATCAC
L.CER.NORLK.GA	ATAAGCGTCTTAATTCGAGTGGAGTTAGGTGTAGTTGGACCTTTTCTTGGTGATGATCAC
L.MEL.BEVIEW.GA	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN25.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN43.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN01.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN29.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN11.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN32.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN13.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN21.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN28.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN05.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN02.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN16.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN06.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
L.MEL.MN29B.WI	ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC

L.MEL.MN11B.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN23B.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN08.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN26.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN34.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN01B.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN01C.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN08B.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.FLNT08.NH ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN19B.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN18.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.MN10.WI ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.LAUREN.GA ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGCCCATTTTTGGGTGACGACCAC
 L.MEL.FLNT02.NH ATAAGAGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTCTTGGGTGACGACCAC
 L.MEL.FLNT10.NH ATAAGAGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTCTTGGGTGACGACCAC
 L.MEL.FLNT11.NH ATAAGAGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTCTTGGGTGACGACCAC
 L.MEL.FLNT03.NH ATAAGAGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTCTTGGGTGACGACCAC
 L.MEL.FLNT04.NH ATAAGAGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTCTTGGGTGACGACCAC
 L.MEL.FLNT06.NH ATAAGAGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTCTTGGGTGACGACCAC
 L.MEL.CANLK.GA ATAAGAGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.STP.GA ATAAGGGTTCTTATCCGGGTGGAGTTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.EHT01.TX ATAAGGGTTCTTATTCGAGTAGAATTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.EHT02.TX ATAAGGGTTCTTATTCGAGTAGAATTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.EHT03.TX ATAAGGGTTCTTATTCGAGTAGAATTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.EHT08.TX ATAAGGGTTCTTATTCGAGTAGAATTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.EHT07.TX ATAAGGGTTCTTATTCGAGTAGAATTGGGGGTTATTGGTCCATTTTTGGGTGACGACCAC
 L.MEL.DEV.OR ATGAGGGTTCTTATTCGGGTAGAGTTAGGGGTTATCGGGCCATTTTTGGGTGATGACCAC
 L.MEL.NISKEY.GA ATGAGGGTTCTTATTCGGGTAGAGTTAGGGGTTATCGGGCCATTTTTGGGTGATGACCAC
 L.MEL.FISHCP2.FL ATAAGGGTCTTGATCCGGGTGAGTTGGGGGTTATTGGCCCATTTCTGGGGGATGACCAT
 L.MEL.FISHCP1.FL ATAAGGGTCTTGATCCGGGTGAGTTGGGGGTTATTGGCCCATTTCTGGGGGATGACCAT
 L.MEL.TIM.OR ATAAGGGTTCTCATCCGTGTGGAGCTTGGTGTTATTGGGCCATTTTTGGGGGATGATCAT
 L.MEL.WRW2.WI ATAAGGGTTCTCATCCGTGTGGAGCTTGGTGTTATTGGGCCATTTTTGGGGGATGATCAT
 L.MEL.MINLK.WI ATAAGGGTTCTCATCCGTGTGGAGCTTGGTGTTATTGGGCCATTTTTGGGGGATGATCAT
 L.MEL.GLASS.UT ATAAGGGTTCTTATCCGGGTGGAGCTTGGTGTTATTGGGCCATTCTTGGGGGATGATCAT
 L.MEL.CIB.TX ATAAGTGTATTATTTCGGGTAGAGTTAGGGGTTGTTGGGCCATTCTTGGTGATGACCAC
 L.MEL.AMD01.TX ATGAGAGTTATTATTTCGTGTGGAGCTGGGTGTGGTTCGGACCTTTTTTAGGGGATGACCAC
 L.MEL.AMD02.TX ATGAGAGTTATTATTTCGTGTGGAGCTGGGTGTGGTTCGGACCTTTTTTAGGGGATGACCAC
 L.MEL.INK.TX ATGAGAGTTATTATTTCGTGTGGAGCTGGGTGTGGTTCGGACCTTTTTTAGGGGATGACCAC
 L.MEL.BALBOA.CA ATGAGAGTTATTATTTCGTGTGGAGCTGGGTGTGGTTCGGACCTTTTTTAGGGGATGACCAC
 L.MEL.CP02.SC ATGAGGGTAATTATTTCGAGTGGAGTTGGGTGTAGTGGGGCCTTTTTGGGTGATGACCAC
 L.MEL.CP03.SC ATGAGGGTAATTATTTCGAGTGGAGTTGGGTGTAGTGGGGCCTTTTTGGGTGATGACCAC
 L.MEL.RAT01.NM ATGAGTGTCAATTATTTCGGGTAGAGCTTGGGGTGGTTGGCCCCCTTTTTAGGAGATGACCAT
 L.MEL.RAT02.NM ATGAGTGTCAATTATTTCGGGTAGAGCTTGGGGTGGTTGGCCCCCTTTTTAGGAGATGACCAT
 L.MEL.NOIC3.OK ATGAGTGTCAATTATTTCGGGTAGAGCTTGGCGTGGTTGGCCCCCTTTTTAGGAGATGATCAT
 L.MEL.STA02.OK ATGAGTGTCAATTATTTCGGGTAGAGCTTGGCGTGGTTGGCCCCCTTTTTAGGAGATGATCAT
 L.MEL.STA01.OK ATGAGTGTCAATTATTTCGGGTAGAGCTTGGCGTGGTTGGCCCCCTTTTTAGGAGATGATCAT
 L.MEL.NOIC2.OK ATGAGTGTCAATTATTTCGAGTAGAGCTTGGGGTGGTTGGCCCCCTTTTTAGGAGATGATCAT
 L.MEL.NOIC4.OK ATGAGTGTCAATTATTTCGAGTAGAGCTTGGGGTGGTTGGCCCCCTTTTTAGGAGATGATCAT
 L.MEL.BASLK.TX ATGAGTGTCAATTATTTCGAGTAGAGCTTGGGGTGGTTGGCCCCCTTTTTAGGAGATGATCAT
 L.MEL.JAC.FL ATGAGTGTATTATTTCGGGTGGAGTTAGGGGTGGTTGGACCTTTTTTGGGCGATGATCAT
 L.MEL.CRLRD.TX ATGAGAGTTATTATTTCGGGTGGAGTTGGGAGTGGTTGGACCATTCTTGGGCGATGATCAT
 L.MEL.KRM.FL ATGAGTGTCAATTATTTCGAGTAGAGTTAGGTGTAGTGGGTCTTTCTTGGGCGATGACCAT
 L.MEL.LKO.FL ATGAGTGTCAATTATTTCGAGTAGAGTTAGGTGTAGTGGGTCTTTCTTGGGCGATGACCAT
 L.MEL.SIT4.FL ATGAGTGTCAATTATTTCGAGTAGAGTTAGGTGTAGTGGGTCTTTCTTGGGCGATGACCAT

L.CER.MORPH.NM ATTTATAACGTAATTGTAACAGCCCACGCGTTTGTATAATCTTCTTCATGGTTATACCT

L.CER.WORT25.TX	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATTATAAATTTTTTTTATAGTTATGCCT
L.CER.WORT15.TX	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.TLL.PA	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.WACO.TX	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.MN04.WI	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.MN40.WI	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.MN46.WI	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.MN16.WI	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.BLU.OR	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.SAM.TX	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.DUC.OK	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.FL.TX	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.GMP.WI	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.MN14.WI	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.MEN.WI	ATTTATAATGTGATTGTAACAGCTCATGCTTTTATCATGATTTTTTTTTTATAGTTATGCCT
L.CER.HCP.FL	ATCTATAATGTTATTGTTACGGCACATGCTTTTATTATAAATTTTTTTTTATGGTTATGCCT
L.CER.PIED.GA	ATTTACAATGTTATTGTTAACGGCTCACGCTTTTATTATGATTTTTTTTTTATGGTTATGCCC
L.CER.NOCKSP.PA	ATTTACAATGTTATTGTTAACGGCTCACGCTTTTATTATGATTTTTTTTTTATGGTTATGCCC
L.CER.ECHOLK.CA	ATTTACAATGTTATTGTTAACGGCTCACGCTTTTATTATGATTTTTTTTTTATGGTTATGCCC
L.CER.NOCKFS.PA	ATTTACAATGTTATTGTTAACGGCTCACGCTTTTATTATGATTTTTTTTTTATGGTTATGCCC
L.CER.HILOCH.GA	ATTTACAATGTTATTGTTAACGGCTCACGCTTTTATTATGATTTTTTTTTTATGGTTATGCCC
L.CER.EASTPOI.GA	ATTTACAATGTTATTGTTAACGGCTCACGCTTTTATTATGATTTTTTTTTTATGGTTATGCCC
L.CER.NORLK.GA	ATTTACAACGTTATTGTTAACGGCTCACGCTTTTATCATGATTTTTTTTTTATGGTTATGCCC
L.MEL.BEVIEW.GA	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN25.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN43.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN01.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN29.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN11.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN32.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN13.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN21.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN28.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN05.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN02.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN16.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN06.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN29B.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN11B.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN23B.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN08.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN26.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN34.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN01B.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN01C.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN08B.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.FLNT08.NH	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN19B.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN18.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.MN10.WI	ATCTATAATGTTATTGTTACTGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.LAUREN.GA	ATCTATAATGTTATTGTCACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.FLNT02.NH	ATCTATAATGTTATTGTCACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.FLNT10.NH	ATCTATAATGTTATTGTCACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.FLNT11.NH	ATCTATAATGTTATTGTCACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.FLNT03.NH	ATCTATAATGTTATTGTCACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.FLNT04.NH	ATCTATAATGTTATTGTCACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.FLNT06.NH	ATCTATAATGTTATTGTCACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT

L.MEL.CANLK.GA	ATCTATAATGTTATTGTACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.STP.GA	ATCTATAATGTTATTGTACGGCACATGCTTTTATCATGATTTTCTTCATGGTGATGCCT
L.MEL.EHT01.TX	ATCTATAATGTTATTGTTACAGCACATGCTTTTATCATGATTTTCTTTATGGTGATGCCT
L.MEL.EHT02.TX	ATCTATAATGTTATTGTTACAGCACATGCTTTTATCATGATTTTCTTTATGGTGATGCCT
L.MEL.EHT03.TX	ATCTATAATGTTATTGTTACAGCACATGCTTTTATCATGATTTTCTTTATGGTGATGCCT
L.MEL.EHT08.TX	ATCTATAATGTTATTGTTACAGCACATGCTTTTATCATGATTTTCTTTATGGTGATGCCT
L.MEL.EHT07.TX	ATCTATAATGTTATTGTTACAGCACATGCTTTTATCATGATTTTCTTTATGGTGATGCCT
L.MEL.DEV.OR	ATCTATAATGTTATTGTTACGGCACATGCTTTTATCATAATTTTCTTTATGGTGATGCCT
L.MEL.NISKEY.GA	ATCTATAATGTTATTGTTACGGCACATGCTTTTATCATAATTTTTTTTATGGTGATGCCT
L.MEL.FISHCP2.FL	ATTTATAATGTTATTGTTACGGCTCACGCTTTTATCATAATCTTTTTCATAGTTATGCC
L.MEL.FISHCP1.FL	ATTTATAATGTTATTGTTACGGCTCACGCTTTTATCATAATCTTTTTCATAGTTATGCC
L.MEL.TIM.OR	ATTTATAATGTTATCGTCACGGCACATGCTTTTATTATGATTTTTTTTATAGTTATGCC
L.MEL.WRW2.WI	ATTTATAATGTTATCGTCACGGCACATGCTTTTATTATGATTTTTTTTATAGTTATGCC
L.MEL.MINLK.WI	ATTTATAATGTTATCGTCACGGCACATGCTTTTATTATGATTTTTTTTATAGTTATGCC
L.MEL.GLASS.UT	ATTTATAATGTTATCGTCACGGCACATGCTTTTATTATGATTTTTTTTATAGTTATGCC
L.MEL.CIB.TX	ATCTATAATGTTATTGTTACTGCTCACGCTTTTATTATGATTTTCTTTATGGTTATGCC
L.MEL.AMD01.TX	ATCTATAATGTCATTGTGACGGCCCATGCTTTTATTATAATTTTCTTTATGGTTATACC
L.MEL.AMD02.TX	ATCTATAATGTCATTGTGACGGCCCATGCTTTTATTATAATTTTCTTTATGGTTATACC
L.MEL.INK.TX	ATCTATAATGTCATTGTGACGGCCCATGCTTTTATTATAATTTTCTTTATGGTTATACC
L.MEL.BALBOA.CA	ATCTATAATGTCATTGTGACGGCCCATGCTTTTATTATAATTTTCTTTATGGTTATACC
L.MEL.CP02.SC	ATCTATAATGTTATTGTTACGGCTCATGCTTTTATTATGATTTTTTTTCATGGTTATGCC
L.MEL.CP03.SC	ATCTATAATGTTATTGTTACGGCTCATGCTTTTATTATGATTTTTTTTCATGGTTATGCC
L.MEL.RAT01.NM	ATTTATAATGTTGTAGTCACGGCGCATGCTTTTATTATAATTTTTTTTATGGTAATGCC
L.MEL.RAT02.NM	ATTTATGATGTTGTAGTCACGGCGCATGCTTTTATTATAATTTTTTTTATGGTAATGCC
L.MEL.NOIC3.OK	ATTTATAATGTTGTAGTTACGGCGCATGCTTTTATTATAATTTTTTTTATGGTAATACC
L.MEL.STA02.OK	ATTTATAATGTTGTAGTTACGGCGCATGCTTTTATTATAATTTTTTTTATGGTAATACC
L.MEL.STA01.OK	ATTTATAATGTTGTAGTTACGGCGCATGCTTTTATTATAATTTTTTTTATGGTAATACC
L.MEL.NOIC2.OK	ATTTATAATGTTGTAGTTACGGCGCATGCTTTTATTATAATTTTTTTTATGGTAATACC
L.MEL.NOIC4.OK	ATTTATAATGTTGTAGTTACGGCGCATGCTTTTATTATAATTTTTTTTATAGTAATGCC
L.MEL.BASLK.TX	ATTTATAATGTTGTAGTTACGGCGCATGCTTTTATTATAATTTTTTTTATAGTAATGCC
L.MEL.JAC.FL	ATTTATAATGTTGTTGTTACAGCTCACGCTTTTATTATGATTTTCTTTATGGTTATGCC
L.MEL.CRLRD.TX	ATCTATAACGTAATTGTAACCGCTCATGCCTTCATTATAATTTTCTTTATGGTAATGCC
L.MEL.KRM.FL	ATCTACAATGTGATTGTGACAGCCCATGCTTTTGTATGATTTTCTTTATAGTTATGCC
L.MEL.LKO.FL	ATCTACAATGTGATTGTGACAGCCCATGCTTTTGTATGATTTTCTTTATAGTTATGCC
L.MEL.SIT4.FL	ATCTACAATGTGATTGTGACAGCCCATGCTTTTGTATGATTTTCTTTATAGTTATGCC

L.CER.MORPH.NM	ATCGCTATTGGAGGTTTTCGGTAACCTGGTTGATTCCGTTAATACTAGGTTGCGTAGATATG
L.CER.WORT25.TX	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.WORT15.TX	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.TLL.PA	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.WACO.TX	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.MN04.WI	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.MN40.WI	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.MN46.WI	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.MN16.WI	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.BLU.OR	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.SAM.TX	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.DUC.OK	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.FL.TX	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.GMP.WI	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.MN14.WI	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATGCTAGGTTGTGTAGACATA
L.CER.MEN.WI	GCTGCGATTGGAGGTTTTGGAAATTGACTCATCCCTTTAATACTAGGTTGTGTAGACATA
L.CER.HCP.FL	GTTGCTATTGGAGGATTCGGTAACCTGACTTATTCCGTTAATGTTAGGGTGTGTTGATATG
L.CER.PIED.GA	GTTGCTATTGGGGGTTTTCGGTAACCTGGCTTATTCCGTTAATGCTAGGGTGTGTAGATATG
L.CER.NOCKSP.PA	GTTGCTATTGGGGGTTTTCGGTAACCTGGCTTATTCCGTTAATGCTAGGGTGTGTAGATATG
L.CER.ECHOLK.CA	GTTGCTATTGGGGGTTTTCGGTAACCTGGCTTATTCCGTTAATGCTAGGGTGTGTAGATATG

L.CER.NOCKFS.PA	GTTGCTATTGGGGGTTTTCGGTAACCTGGCTTATTCCGTTAATGCTAGGGTGTGTAGATATG
L.CER.HILOCH.GA	GTTGCTATTGGGGGTTTTCGGTAACCTGGCTTATTCCGTTAATGCTAGGGTGTGTAGATATG
L.CER.EASTPOI.GA	GTTGCTATTGGGGGTTTTCGGTAACCTGGCTTATTCCGTTAATGCTAGGGTGTGTAGATATG
L.CER.NORLK.GA	GTTGCTATTGGGGGTTTTCGGTAACCTGGCTTATCCCGTTAATGCTAGGGTGTGTAGATATG
L.MEL.BEVIEW.GA	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN25.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN43.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN01.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN29.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN11.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN32.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN13.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN21.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN28.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN05.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN02.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN16.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN06.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN29B.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN11B.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN23B.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN08.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN26.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN34.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN01B.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN01C.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN08B.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.FLNT08.NH	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN19B.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN18.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.MN10.WI	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.LAUREN.GA	ATGGCTATTGGGGGTTTTGGTAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGACATG
L.MEL.FLNT02.NH	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGATATG
L.MEL.FLNT10.NH	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGATATG
L.MEL.FLNT11.NH	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGATATG
L.MEL.FLNT03.NH	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGATATG
L.MEL.FLNT04.NH	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGATATG
L.MEL.FLNT06.NH	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGATATG
L.MEL.CANLK.GA	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGATATG
L.MEL.STP.GA	ATGGCTATTGGGGGTTTTGGCAATTGGCTGATTCCCTATGATGCTGGGTGTGTAGATATG
L.MEL.EHT01.TX	ATAGCTATTGGGGGTTTTCGGCAATTGGTTAATTCCTATGATGCTGGGTGTGTAGATATG
L.MEL.EHT02.TX	ATAGCTATTGGGGGTTTTCGGCAATTGGTTAATTCCTATGATGCTGGGTGTGTAGATATG
L.MEL.EHT03.TX	ATAGCTATTGGGGGTTTTCGGCAATTGGTTAATTCCTATGATGCTGGGTGTGTAGATATG
L.MEL.EHT08.TX	ATAGCTATTGGGGGTTTTCGGCAATTGGTTAATTCCTATGATGCTGGGTGTGTAGATATG
L.MEL.EHT07.TX	ATAGCTATTGGGGGTTTTCGGCAATTGGTTAATTCCTATGATGCTGGGTGTGTAGATATG
L.MEL.DEV.OR	ATGGCCATCGGAGGTTTTGGTAACCTGATTAATTCCTATGATATTAGGGTGTGTTGATATA
L.MEL.NISKEY.GA	ATGGCCATTGGAGGTTTTGGTAACCTGATTAATTCCTATGATATTAGGGTGTGTTGATATA
L.MEL.FISHCP2.FL	ATGGCTATTGGTGGTTTTGGGAATTGGTTGATTCCCTATAATGTTAGGGTGTGTGGACATG
L.MEL.FISHCP1.FL	ATGGCTATTGGTGGTTTTGGGAATTGGTTGATTCCCTATAATGTTAGGGTGTGTGGACATG
L.MEL.TIM.OR	ATAGCTATTGGAGGTTTTGGGAATTGGCTGATCCCTATGATGTTGGGGTGTGTGGATATA
L.MEL.WRW2.WI	ATAGCTATTGGAGGTTTTGGGAATTGGCTGATCCCTATGATGTTGGGGTGTGTGGATATA
L.MEL.MINLK.WI	ATAGCTATTGGAGGTTTTGGGAATTGGCTGATCCCTATGATGTTGGGGTGTGTGGATATA
L.MEL.GLASS.UT	ATAGCTATTGGAGGTTTTGGGAATTGGCTGATCCCTATAATGTTGGGGTGTGTGGATATA
L.MEL.CIB.TX	ATGGCTATTGGGGGCTTTGGAAATTGGTTGATCCCATGATGTTGGGCTGTGTTGACATA
L.MEL.AMD01.TX	ATGGCTATTGGAGGTTTTCGGTAACCTGACTAATCCCTATGATGTTAGGGTGTGTTGACATA
L.MEL.AMD02.TX	ATGGCTATTGGAGGTTTTCGGTAACCTGACTAATCCCTATGATGTTAGGGTGTGTTGACATA
L.MEL.INK.TX	ATGGCTATTGGAGGTTTTCGGTAACCTGACTAATCCCTATGATGTTAGGGTGTGTTGACATA

L.MEL.BALBOA.CA	ATGGCTATTGGAGGTTTTCGGTAAGTACTGACTAATCCCTATGATGTTAGGGTGTGTTGACATA
L.MEL.CP02.SC	ATGGCTATTGGAGGTTTTGGTAATTGACTAATCCCCATGATGCTTGGTTGTGTGGACATG
L.MEL.CP03.SC	ATGGCTATTGGAGGTTTTGGTAATTGACTAATCCCCATGATGCTTGGTTGTGTGGACATG
L.MEL.RAT01.NM	ATGGCTATTGGTGGCTTTTGGTAATTGGTTGATCCCTTTGATGTTGGGGTGTGTTGATATG
L.MEL.RAT02.NM	ATGGCTATTGGTGGCTTTTGGTAATTGGTTGATCCCTTTGATGTTGGGGTGTGTTGATATG
L.MEL.NOIC3.OK	ATGGCTATTGGTGGCTTTTGGTAATTGGTTGATCCCTTTGATGTTGGGGTGTGTTGATATG
L.MEL.STA02.OK	ATGGCTATTGGTGGCTTTTGGTAATTGGTTGATCCCTTTGATGTTGGGGTGTGTTGATATG
L.MEL.STA01.OK	ATGGCTATTGGTGGCTTTTGGTAATTGGTTGATCCCTTTGATGTTGGGGTGTGTTGATATG
L.MEL.NOIC2.OK	ATGGCTATTGGTGGCTTTTGGTAATTGGTTGATCCCTTTGATGTTGGGGTGTGTTGATATG
L.MEL.NOIC4.OK	ATGGCTATTGGTGGCTTTTGGTAATTGGTTGATCCCTTTGATGTTGGGGTGTGTTGATATG
L.MEL.BASLK.TX	ATGGCTATTGGTGGCTTTTGGTAATTGGTTGATCCCTTTGATGTTGGGGTGTGTTGATATG
L.MEL.JAC.FL	ATGGCTATCGGTGGTTTTTGGTAAGTACTGTTAATCCCTTTAATGCTTGGGTGTGTCGATATG
L.MEL.CRLRD.TX	ATGGCTATTGGGGGCTTTTGGAAATTGGTTGATCCCATGATGTTGGGCTGTGTTGACATA
L.MEL.KRM.FL	ATGGCTATTGGGGGATTTTGGAAATTGGCTGATTCCCTATGATATTAGGATGTGTGGATATG
L.MEL.LKO.FL	ATGGCTATTGGGGGATTTTGGAAATTGGCTGATTCCCTATGATATTAGGATGTGTGGATATG
L.MEL.SIT4.FL	ATGGCTATTGGGGGATTTTGGAAATTGGCTGATTCCCTATGATATTAGGATGTGTGGATATA

L.CER.MORPH.NM	GTTTTTCCTCGTATGAACAATTTGTCTGTTCTGGTTACTCATTCCAGCATTAAACACTTTT
L.CER.WORT25.TX	GTATTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.WORT15.TX	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.TLL.PA	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.WACO.TX	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.MN04.WI	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.MN40.WI	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.MN46.WI	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.MN16.WI	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.BLU.OR	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.SAM.TX	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.DUC.OK	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.FL.TX	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.GMP.WI	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.MN14.WI	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTCTGCTA
L.CER.MEN.WI	GTTTTTCCTCGTATAAATAATTTATCGTTTTGACTTTTAATCCCCTCCTTGTCTTTACTA
L.CER.HCP.FL	GTTTTTCCTCGTATAAATAATTTATCTTTTTGACTTTTGATTCCCTTCTCTGTCACTTCTT
L.CER.PIED.GA	GTATTCCTCCCGTATGAATAACTTGTCTTTTTGACTTTTGATTCCCTTCTCTTTCTCTTCTT
L.CER.NOCKSP.PA	GTATTCCTCCCGTATGAATAACTTGTCTTTTTGACTTTTGATTCCCTTCTCTTTCTCTTCTT
L.CER.ECHOLK.CA	GTATTCCTCCCGTATGAATAACTTGTCTTTTTGACTTTTGATTCCCTTCTCTTTCTCTTCTT
L.CER.NOCKFS.PA	GTATTCCTCCCGTATGAATAACTTGTCTTTTTGACTTTTGATTCCCTTCTCTTTCTCTTCTT
L.CER.HILOCH.GA	GTATTCCTCCCGTATGAATAATTTGTCTTTTTGACTTTTGATTCCCTTCTCTTTCTCTTCTT
L.CER.EASTPOI.GA	GTATTCCTCCCGTATGAATAATTTGTCTTTTTGACTTTTGATTCCCTTCTCTTTCTCTTCTT
L.CER.NORLK.GA	GTATTCCTCCCGTATAAATAATTTGTCTTTTTGACTTTTGATTCCCTTCTCTTTCTCTTCTT
L.MEL.BEVIEW.GA	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN25.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN43.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN01.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN29.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN11.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN32.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN13.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN21.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN28.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN05.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN02.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN16.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN06.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
L.MEL.MN29B.WI	GTATTCCTCCCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA

L.MEL.MN11B.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN23B.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN08.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN26.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN34.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN01B.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN01C.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN08B.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.FLNT08.NH GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN19B.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN18.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.MN10.WI GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.LAUREN.GA GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATTCCTTCTTTGACTTTATTA
 L.MEL.FLNT02.NH GTATTTCCCGCGTATAAATAACCTTTCTTTCTGGTTGTTAATCCCTTCTTTGACTTTATTG
 L.MEL.FLNT10.NH GTATTTCCCGCGTATAAATAACCTTTCTTTCTGGTTGTTAATCCCTTCTTTGACTTTATTG
 L.MEL.FLNT11.NH GTATTTCCCGCGTATAAATAACCTTTCTTTCTGGTTGTTAATCCCTTCTTTGACTTTATTG
 L.MEL.FLNT03.NH GTATTTCCCGCGTATAAATAACCTTTCTTTCTGGTTGTTAATCCCTTCTTTGACTTTATTG
 L.MEL.FLNT04.NH GTATTTCCCGCGTATAAATAACCTTTCTTTCTGGTTGTTAATCCCTTCTTTGACTTTATTG
 L.MEL.FLNT06.NH GTATTTCCCGCGTATAAATAACCTTTCTTTCTGGTTGTTAATCCCTTCTTTGACTTTATTG
 L.MEL.CANLK.GA GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATCCCTTCTTTGACTTTATTG
 L.MEL.STP.GA GTATTTCCCGCGTATAAATAACCTTTCTTTTTGGTTGTTAATCCCTTCTTTGACTTTATTA
 L.MEL.EHT01.TX GTATTTCCCTCGTATAAATAATCTCTCTTTTTGGTTATTAATTCCTTCTTTGACTTTATTA
 L.MEL.EHT02.TX GTATTTCCCTCGTATAAATAATCTCTCTTTTTGGTTATTAATTCCTTCTTTGACTTTATTA
 L.MEL.EHT03.TX GTATTTCCCTCGTATAAATAATCTCTCTTTTTGGTTATTAATTCCTTCTTTGACTTTATTA
 L.MEL.EHT08.TX GTATTTCCCTCGTATAAATAATCTCTCTTTTTGGTTATTAATTCCTTCTTTGACTTTATTA
 L.MEL.EHT07.TX GTATTTCCCTCGTATAAATAATCTCTCTTTTTGGTTATTAATTCCTTCTTTGACTTTATTA
 L.MEL.DEV.OR GTATTTCCCTCGTATAAATAACCTCTCTTTTTGATTACTAATTCCTTCTTTGACTTTATTG
 L.MEL.NISKEY.GA GTATTTCCCTCGTATAAATAACCTCTCTTTTTGATTACTAATTCCTTCTTTGACTTTATTG
 L.MEL.FISHCP2.FL GTGTTCCCGCGCATGAATAATTTATCTTTTTGGTTGTTGATCCCTCACTGACTCTACTA
 L.MEL.FISHCP1.FL GTGTTCCCGCGCATGAATAATTTATCTTTTTGGTTGTTGATCCCTCACTGACTCTACTA
 L.MEL.TIM.OR GTATTTCCCTCGCATAAATAATCTATCTTTTTGGTTATTAATTCCTTCTTTAACTTTATTA
 L.MEL.WR2.WI GTATTTCCCTCGTATAAATAATCTATCTTTTTGGTTATTAATTCCTTCTTTAACTTTATTA
 L.MEL.MINLK.WI GTATTTCCCTCGTATAAATAATCTATCTTTTTGGTTATTAATTCCTTCTTTAACTTTATTA
 L.MEL.GLASS.UT GTATTTCCCTCGTATAAACAATCTATCTTTTTGGTTATTAATTCCTTCTTTAACTTTATTG
 L.MEL.CIB.TX GTTTTTCCCTCGAATGAATAACCTGTCTTTTTGGTTATTAATTCATCGTTAACTTTGCTG
 L.MEL.AMD01.TX GTTTTTCCCTCGGATGAATAACCTATCATTTTTGGTTACTTATCCCTCTTTAACTCTTTTA
 L.MEL.AMD02.TX GTTTTTCCCTCGGATGAATAACCTATCATTTTTGGTTACTTATCCCTCTTTAACTCTTTTA
 L.MEL.INK.TX GTTTTTCCCTCGGATGAATAACCTATCATTTTTGGTTACTTATCCCTCTTTAACTCTTTTA
 L.MEL.BALBOA.CA GTTTTTCCCTCGGATGAATAACCTATCATTTTTGGTTACTTATCCCTCTTTAACTCTTTTA
 L.MEL.CP02.SC GTTTTTCCCCCGGATGAATAATCTTTTCATTTTTGGTTGTTGATCCCTCTTTAAACGCTTTTG
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 L.MEL.RAT01.NM GTTTTTCCCTCGTATGAATAATCTTTCTTTTTGACTCCTTATTCCTTCTTTGACTCTTCTT
 L.MEL.RAT02.NM GTTTTTCCCTCGTATGAATAATCTTTCTTTTTGACTCCTTATTCCTTCTTTGACTCTTCTT
 L.MEL.NOIC3.OK GTTTTTCCCTCGTATGAATAATCTTTCTTTTTGGCTCCTTATTCCTTCTTTGAGTCTTCTT
 L.MEL.STA02.OK GTTTTTCCCTCGTATGAATAATCTTTCTTTTTGGCTCCTTATTCCTTCTTTGAGTCTTCTT
 L.MEL.STA01.OK GTTTTTCCCTCGTATGAATAATCTTTCTTTTTGGCTCCTTATTCCTTCTTTGAGTCTTCTT
 L.MEL.NOIC2.OK GTTTTTCCCTCGTATGAATAATCTTTCTTTTTGGCTCCTTATTCCTTCTTTGAGTCTTCTT
 L.MEL.NOIC4.OK GTTTTTCCCTCGTATGAATAATCTTTCTTTTTGGCTCCTTATTCCTTCTTTGAGTCTTCTT
 L.MEL.BASLK.TX GTTTTTCCCTCGTATGAATAATCTTTCTTTTTGGCTCCTTATTCCTTCTTTGAGTCTTCTT
 L.MEL.JAC.FL GTCTTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTATCCCTCTTTGAGTCTTCTG
 L.MEL.CRLRD.TX GTTTTTCCCTCGAATGAATAACCTGTCTTTTTGGTTATTAATTCATCGTTAACTTTGCTG
 L.MEL.KRM.FL GTTTTTCCCTCGTATAAATAATTTATCTTTTTGGCTTTTAATCCCATCTTTGACCCTTCTT
 L.MEL.LKO.FL GTTTTTCCCTCGTATAAATAATTTATCTTTTTGGCTTTTAATCCCATCTTTGACCCTTCTT
 L.MEL.SIT4.FL GTTTTTCCCTCGTATAAATAATTTATCTTTTTGGCTTTTAATCCCATCTTTGACCCTTCTT

L.CER.MORPH.NM CTTCTCTCTTCTTTAGTTGACTCTGGTGCTGGGACAGGTTGAACAGTATATCCCCCCTC

L.CER.WORT25.TX CTACTCTCCTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTACCCTCCTTTA
 L.CER.WORT15.TX CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.TLL.PA CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.WACO.TX CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.MN04.WI CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.MN40.WI CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.MN46.WI CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.MN16.WI CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.BLU.OR CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.SAM.TX CTACTTTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.DUC.OK CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.FL.TX CTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.GMP.WI TTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.MN14.WI TTACTCTCTTCTTTAGTAGACTCAGGGGCAGGTACTGGTTGAACGGTTTATCCTCCCTTG
 L.CER.MEN.WI TTACTCTCTTCTTTAGTAGACTCAGGAGCAGGTACTGGTTGAACGGTTTATCCTCCCTTA
 L.CER.HCP.FL CTTTTATCTTCTTTGGTAGATT CAGGAGCTGGGACTGGTTGAACTGTATACCCTCCGCTA
 L.CER.PIED.GA CTTCTCTCATCTCTTGTGGACTCGGGGGCTGGGACTGGGTGAACTGTTTATCCTCCCCTT
 L.CER.NOCKSP.PA CTTCTCTCATCTCTTGTGGACTCGGGGGCTGGGACTGGGTGAACTGTTTATCCTCCCCTT
 L.CER.ECHOLK.CA CTTCTCTCATCTCTTGTGGACTCGGGGGCTGGGACTGGGTGAACTGTTTATCCTCCCCTT
 L.CER.NOCKFS.PA CTTCTCTCATCTCTTGTGGACTCGGGGGCTGGGACTGGGTGAACTGTTTATCCTCCCCTT
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 L.CER.NORLK.GA CTTCTTTTCATCTCTTGTGGACTCGGGGGCTGGGACTGGGTGAACTGTTTATCCTCCCCTT
 L.MEL.BEVIEW.GA TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCCTTTA
 L.MEL.MN25.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN43.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN01.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN29.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN11.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
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 L.MEL.MN28.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
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 L.MEL.MN16.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN06.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN29B.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN11B.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
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 L.MEL.MN08.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
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 L.MEL.MN34.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN01B.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN01C.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.MN08B.WI TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
 L.MEL.FLNT08.NH TTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCTTTA
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 L.MEL.FLNT02.NH TTACTGTCTTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCCTTTA
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 L.MEL.FLNT04.NH TTACTGTCTTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCCTTTA
 L.MEL.FLNT06.NH TTACTGTCTTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCGCCCTTTA

L.MEL.CANLK.GA TTACTGTCTTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCCCCTTTA
 L.MEL.STP.GA CTACTGTCCTCTATAGTGGATTCTGGTGCTGGTACTGGTTGGACTGTCTACCCCCCTTTA
 L.MEL.EHT01.TX CTACTGTCCTCTATAGTGGATTCTGGTGCTGGAAGTGGTTGGACTGTTTACCCCCCTTTA
 L.MEL.EHT02.TX CTACTGTCCTCTATAGTGGATTCTGGTGCTGGAAGTGGTTGGACTGTTTACCCCCCTTTA
 L.MEL.EHT03.TX CTACTGTCCTCTATAGTGGATTCTGGTGCTGGAAGTGGTTGGACTGTTTACCCCCCTTTA
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 L.MEL.DEV.OR CTACTATCTTCTATGGTAGACTCTGGTGCTGGCACTGGTTGGACTGTTTACCCGCCCTTA
 L.MEL.NISKEY.GA CTACTATCTTCTATGGTAGATTCTGGCGCTGGCACTGGTTGGACTGTTTACCCGCCCTTA
 L.MEL.FISHCP2.FL CTTTTGTCTTTCAGTGGGGGATTCTGGTGCTGGCACTGGTTGAACTGTTTACCCCCCATTA
 L.MEL.FISHCP1.FL CTTTTGTCTTTCAGTGGATTCTGGTGCTGGCACTGGTTGAACTGTTTACCCCCCATTA
 L.MEL.TIM.OR CTTCTTTCTTCTATGGTGGACTCGGGGGCTGGAAGTGGATGGACTGTTTATCCTCCTTTG
 L.MEL.WRW2.WI CTTCTTTCTTCTATGGTGGACTCGGGGGCTGGAAGTGGATGGACTGTTTATCCTCCTTTG
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 L.MEL.JAC.FL CTCCTCTCTTCTATGGTGGACTCTGGTGCGGGTACTGGGTGAAGTGGTTTACCCTCCCCTA
 L.MEL.CRLRD.TX TTGTTATCTTCTTTGGTGGATTCTGGGGCTGGTACTGGGTGGACTGTTTACCCCCCTCTT
 L.MEL.KRM.FL CTTTTGTCTTCATTGGTGGACTCAGGTGCTGGTACTGGTTGAACTGTGTACCCCCCTTTA
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 L.MEL.SIT4.FL CTTTTGTCTTCATTGGTGGACTCAGGTGCTGGTACTGGTTGAACTGTGTACCCCCCTTTA

L.CER.MORPH.NM TCTGATGCTGTTTTTCATTTCAGGGGCTTCTGTAGATTTAGCAATCTTTAGCCTCCACCTT
 L.CER.WORT25.TX TCAGATGCTAAGTTTTCACTCTGGGGCCTCTGTGGACTTAGCCATTTTTAGCCTCCATTTA
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 L.CER.DUC.OK TCAGATGCTAAGTTTTCACTCTGGGGCCTCTGTGGACTTAGCCATTTTTAGCCTCCATTTA
 L.CER.FL.TX TCAGATGCTAAGTTTTCACTCTGGGGCCTCTGTGGACTTAGCCATTTTTAGCCTCCATTTA
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L.CER.NOCKFS.PA	TCAGATGCTAAGTTTCATTCTGGAGCTTCTGTGGATCTTGCTATCTTTAGCTTGCACTTA
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L.CER.NORLK.GA	TCAGATGCTAAGTTTCATTCTGGAGCTTCTGTGGATCTTGCTATCTTTAGCTTGCACTTA
L.MEL.BEVIEW.GA	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN25.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
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L.MEL.MN16.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
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L.MEL.MN29B.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN11B.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN23B.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN08.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
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L.MEL.MN01B.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN01C.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN08B.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.FLNT08.NH	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN19B.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN18.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.MN10.WI	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
L.MEL.LAUREN.GA	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
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L.MEL.STP.GA	GCTGATTCTAAGTTTCACCTCTGGTGCCTCTGTTGATCTTGCTATCTTTAGCCTACATTTG
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L.MEL.EHT03.TX	GCTGACTCTAAGTTCCACTCGGGTGCTTCTGTTGATCTTGCTATCTTTAGCCTGCATTTG
L.MEL.EHT08.TX	GCTGACTCTAAGTTCCACTCGGGTGCTTCTGTTGATCTTGCTATCTTTAGCCTGCATTTG
L.MEL.EHT07.TX	GCTGACTCTAAGTTCCACTCGGGTGCTTCTGTTGATCTTGCTATCTTTAGCCTGCATTTG
L.MEL.DEV.OR	GCTGATTCCAAGTTCCACTCTGGTGCCTCTGTTGATTTAGCTATTTTTCAGTCTACATTTG
L.MEL.NISKEY.GA	GCTGATTCCAAGTTCCACTCTGGTGCCTCTGTTGATTTAGCTATTTTTCAGTCTACATTTG
L.MEL.FISHCP2.FL	GCTGACTCTAAGTTTCATTCTGGTGCCTCTGTTGATCTGGCTATTTTTAGTTTACATTTG
L.MEL.FISHCP1.FL	GCTGACTCTAAGTTTCATTCTGGTGCCTCTGTTGATCTGGCTATTTTTAGTTTACATTTG
L.MEL.TIM.OR	GCTGATTCTAAGTTCCATTCTGGTGCATCTGTAGACCTTGCTATTTTTAGGCTTCATTTG
L.MEL.WRW2.WI	GCTGATTCTAAGTTCCATTCTGGTGCATCTGTAGACCTTGCTATTTTTAGGCTTCATTTG
L.MEL.MINLK.WI	GCTGATTCTAAGTTCCATTCTGGTGCATCTGTAGACCTTGCTATTTTTAGGCTTCATTTG
L.MEL.GLASS.UT	GCTGACTCTAAGTTCCATTCTGGTGCATCTGTAGACCTCGCTATTTTTAGTCTTCATTTG
L.MEL.CIB.TX	GCTGACGCTAAATTCCATTCTGGGGCTTCAGTGGATTTGGCTATCTTTAGTCTTCATCTT
L.MEL.AMD01.TX	TCTGATGCTAAGTTTCATTCTGGGGCTCTGTTGACTTAGCTATTTTTAGCCTTCATTTA
L.MEL.AMD02.TX	TCTGATGCTAAGTTTCATTCTGGGGCTCTGTTGACTTAGCTATTTTTAGCCTTCATTTA
L.MEL.INK.TX	TCTGATGCTAAGTTTCATTCTGGGGCTCTGTTGACTTAGCTATTTTTAGCCTTCATTTA

L.MEL.BALBOA.CA	TCTGATGCTAAGTTTCATTCTGGGGGCTCTGTTGACTTAGCTATTTTTAGCCTTCATTTA
L.MEL.CP02.SC	TCAGATGCTAAGTTTCACTCTGGAGCTTCTGTTGATCTTGCTATCTTTAGCCTTCATTTG
L.MEL.CP03.SC	TCAGATGCTAAGTTTCACTCTGGAGCTTCTGTTGATCTTGCTATCTTTAGCCTTCATTTG
L.MEL.RAT01.NM	GCTGATGCTAAATTCCACTCAGGTGCATCTGTAGATTTAGCTATCTTTAGTCTCCACTTA
L.MEL.RAT02.NM	GCTGATGCTAAATTCCACTCAGGTGCATCTGTAGATTTAGCTATCTTTAGTCTCCACTTA
L.MEL.NOIC3.OK	GCTGATGCTAAATTCCACTCAGGTGCGTCTGTAGATTTAGCTATCTTTAGTCTCCACTTA
L.MEL.STA02.OK	GCTGATGCTAAATTCCACTCAGGTGCGTCTGTAGATTTAGCTATCTTTAGTCTCCACTTA
L.MEL.STA01.OK	GCTGATGCTAAATTCCACTCAGGTGCGTCTGTAGATTTAGCTATCTTTAGTCTCCACTTA
L.MEL.NOIC2.OK	GCTGATGCTAAATTCCACTCAGGTGCGTCTGTAGATTTAGCTATCTTTAGTCTCCACTTA
L.MEL.NOIC4.OK	GCTGATGCTAAATTCCACTCAGGTGCGTCTGTAGATTTAGCTATCTTTAGTCTCCACTTA
L.MEL.BASLK.TX	GCTGATGCTAAATTCCACTCAGGTGCGTCTGTAGATTTAGCTATCTTTAGTCTCCACTTA
L.MEL.JAC.FL	GCTGATGCTAAATTCCACTCAGGGGCATCTGTAGATTTGGCTATTTTTAGGCTCCATTTA
L.MEL.CRLRD.TX	GCTGACGCTAAATTCCATTCTGGGGCTTCAGTGGATTTGGCTATCTTTAGTCTTCATCTT
L.MEL.KRM.FL	GCAGATTCTAAGTTCCATTCTGGGGCTTCAGTCGATTTAGCTATTTTTAGCCTTCACTTG
L.MEL.LKO.FL	GCAGATTCTAAGTTCCATTCTGGGGCTTCAGTCGATTTAGCTATTTTTAGCCTTCACTTG
L.MEL.SIT4.FL	GCAGATTCTAAGTTCCATTCTGGGGCTTCAGTCGATTTAGCTATTTTTAGCCTTCACTTG

L.CER.MORPH.NM	GCTGGTGTTTCTTCTATTTTTAGGGTCAATTAATTTCTTATGTACAGTTGCCATGGCCCGA
L.CER.WORT25.TX	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.WORT15.TX	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.TLL.PA	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.WACO.TX	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.MN04.WI	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.MN40.WI	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.MN46.WI	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.MN16.WI	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.BLU.OR	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.SAM.TX	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.DUC.OK	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTTTAAGCACTATTGCTATGGCTCGC
L.CER.FL.TX	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTTTAAGCACTATTGCTATGGCTCGC
L.CER.GMP.WI	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.MN14.WI	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.MEN.WI	GCAGGTGTTTCTTCAATCCTGGGCTCTATCAACTTTCTAAGCACTATTGCTATGGCTCGC
L.CER.HCP.FL	GCTGGGGTTTCTTCTATTTTTAGGGTCTATTAATTTTTTGAAGCACTATTGCCATAGCTCGT
L.CER.PIED.GA	GCGGGGGTATCCTCCATTCTTGGGTCTATTAACCTTCTTAAGCACTATTGCCATAGCTCGT
L.CER.NOCKSP.PA	GCGGGGGTATCCTCCATTCTTGGGTCTATTAACCTTCTTAAGCACTATTGCCATAGCTCGT
L.CER.ECHOLK.CA	GCGGGGGTATCCTCCATTCTTGGGTCTATTAACCTTCTTAAGCACTATTGCCATAGCTCGT
L.CER.NOCKFS.PA	GCGGGGGTATCCTCCATTCTTGGGTCTATTAACCTTCTTAAGCACTATTGCCATAGCTCGT
L.CER.HILOCH.GA	GCGGGGGTATCCTCCATTCTTGGGTCTATTAACCTTCTTAAGCACTATTGCCATAGCTCGT
L.CER.EASTPOI.GA	GCGGGGGTATCCTCCATTCTTGGGTCTATTAACCTTCTTAAGCACTATTGCCATAGCTCGT
L.CER.NORLK.GA	GCGGGGGTATCCTCCATTCTTGGGTCTATTAACCTTCTTAAGCACTATTGCCATAGCTCGT
L.MEL.BEVIEW.GA	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN25.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN43.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN01.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN29.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN11.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN32.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN13.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN21.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN28.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN05.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN02.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN16.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN06.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT
L.MEL.MN29B.WI	GCAGGAATTTCTTCTATTTTTAGGGTCCATCAATTTCCCTTTGCACAATTGCTATAGCTCGT

L.MEL.MN11B.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN23B.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN08.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN26.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN34.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN01B.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN01C.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN08B.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.FLNT08.NH GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN19B.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN18.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.MN10.WI GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGCACAATTGCTATAGCTCGT
 L.MEL.LAUREN.GA GCAGGAATTTCTTCTATTTTAGGGTCCATCAATTTCTTTGTACAATCGCTATAGCTCGT
 L.MEL.FLNT02.NH GCAGGAATTTCTTCTATTTTAGGATCTATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.FLNT10.NH GCAGGAATTTCTTCTATTTTAGGATCTATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.FLNT11.NH GCAGGAATTTCTTCTATTTTAGGATCTATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.FLNT03.NH GCAGGAATTTCTTCTATTTTAGGATCTATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.FLNT04.NH GCAGGAATTTCTTCTATTTTAGGATCTATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.FLNT06.NH GCAGGAATTTCTTCTATTTTAGGATCTATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.CANLK.GA GCAGGAATTTCTTCTATTTTAGGATCTATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.STP.GA GCAGGAATTTCTTCTATTTTAGGATCCATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.EHT01.TX GCAGGAATTTCTTCTATTTTAGGATCCATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.EHT02.TX GCAGGAATTTCTTCTATTTTAGGATCCATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.EHT03.TX GCAGGAATTTCTTCTATTTTAGGATCCATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.EHT08.TX GCAGGAATTTCTTCTATTTTAGGATCCATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.EHT07.TX GCAGGAATTTCTTCTATTTTAGGATCCATCAATTTCTTTGCACAATCGCTATAGCTCGT
 L.MEL.DEV.OR GCAGGAATTTCTTCTATTTTAGGATCCATCAATTTCTTTGTACAATTGCTATAGCTCGT
 L.MEL.NISKEY.GA GCAGGAATTTCTTCTATTTTAGGATCCATCAATTTCTTTGTACAATTGCTATAGCTCGT
 L.MEL.FISHCP2.FL GCTGGTGTCTCTTCTATCTTGGGTCCATCAATTTCTTTGTACGATCGCTATGGCTCGT
 L.MEL.FISHCP1.FL GCTGGTGTCTCTTCTATCTTGGGTCCATCAATTTCTTTGTACGATCGCTATGGCTCGT
 L.MEL.TIM.OR GCTGGAATTTCTTCTATTTTAGGGTCCATTAATTTTGTGCACTATTGCGATAGCTCGT
 L.MEL.WRW2.WI GCTGGAATTTCTTCTATTTTAGGGTCCATTAATTTTGTGCACTATTGCGATAGCTCGT
 L.MEL.MINLK.WI GCTGGAATTTCTTCTATTTTAGGGTCCATTAATTTTGTGCACTATTGCGATAGCTCGT
 L.MEL.GLASS.UT GCTGGAATTTCTTCTATTTTAGGGTCCATTAATTTTGTGCACTATTGCGATAGCTCGT
 L.MEL.CIB.TX GCTGGTATTTCTTCTATTTTAGGGTCCATTAATTTTGTGCACTATTGCCATGGCTCGT
 L.MEL.AMD01.TX GCTGGAATTTCTTCAATTTTAGGGTCTATTAATTTTCTTTGTACTATTGCTATGGCTCGT
 L.MEL.AMD02.TX GCTGGAATTTCTTCAATTTTAGGGTCTATTAATTTTCTTTGTACTATTGCTATGGCTCGT
 L.MEL.INK.TX GCTGGAATTTCTTCAATTTTAGGGTCTATTAATTTTCTTTGTACTATTGCTATGGCTCGT
 L.MEL.BALBOA.CA GCTGGAATTTCTTCAATTTTAGGGTCTATTAATTTTCTTTGTACTATTGCTATGGCTCGT
 L.MEL.CP02.SC GCTGGAATCTCTTCGATTCTAGGGTCTATTAATTTCTGTGTACGATAGCCATAGCTCGT
 L.MEL.CP03.SC GCTGGAATCTCTTCGATTCTAGGGTCTATTAATTTCTGTGTACGATAGCCATAGCTCGT
 L.MEL.RAT01.NM GCTGGCATCTCTTCTATTTTAGGCTCTATTAATTTTGTGTACTATTGCTACGGCTCGT
 L.MEL.RAT02.NM GCTGGCATCTCTTCTATTTTAGGCTCTATTAATTTTGTGTACTATTGCTACGGCTCGT
 L.MEL.NOIC3.OK GCTGGCATTCTCTTCTATTTTAGGTTCTATTAATTTTGTGTACTATTGCTATGGCTCGT
 L.MEL.STA02.OK GCTGGCATTCTCTTCTATTTTAGGTTCTATTAATTTTGTGTACTATTGCTATGGCTCGT
 L.MEL.STA01.OK GCTGGCATTCTCTTCTATTTTAGGTTCTATTAATTTTGTGTACTATTGCTATGGCTCGT
 L.MEL.NOIC2.OK GCTGGCATTCTCTTCTATTTTAGGTTCTATTAATTTTGTGTACTATTGCTATGGCTCGT
 L.MEL.NOIC4.OK GCTGGCATTCTCTTCTATTTTAGGTTCTATTAATTTTGTGTACTATTGCTATGGCTCGT
 L.MEL.BASLK.TX GCTGGCATTCTCTTCTATTTTAGGTTCTATTAATTTTGTGTACTATTGCTATGGCTCGT
 L.MEL.JAC.FL GCTGGTATTTCTTCTATTTTAGGGTCTATTAATTTCTTTGTGACGATTGCCATGGCTCGT
 L.MEL.CRLRD.TX GCCGGAATTTCTTCCATTTTAGGATCAATCAACTTTCTATGTACAATTGCTATGGCTCGC
 L.MEL.KRM.FL GCCGGGATTTCTTCAATCTTGGGGTCTATTAATTTCTTTGTACTATTGCTATGGCTCGT
 L.MEL.LKO.FL GCCGGGATTTCTTCAATCTTGGGGTCTATTAATTTCTTTGTACTATTGCTATGGCTCGT
 L.MEL.SIT4.FL GCCGGGATTTCTTCAATCTTGGGGTCTATTAATTTCTTTGTACTATTGCTATGGCTCGT

L.CER.MORPH.NM TCTTCATGAAAATTCTCTCTTGAATATCTTCCCCTTTTTCTTTGAGCTGTTTCTATCACA

L.CER.WORT25.TX	TCCTCGTGAAAGTTTTCTCTTGAATATCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.WORT15.TX	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.TLL.PA	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.WACO.TX	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.MN04.WI	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.MN40.WI	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.MN46.WI	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.MN16.WI	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.BLU.OR	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.SAM.TX	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.DUC.OK	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.FL.TX	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.GMP.WI	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.MN14.WI	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.MEN.WI	TCCTCGTGAAAGTTTTCTCTTGAATACCTTCCTCTTTTCCTTTGAGCCGTTGGAATTACT
L.CER.HCP.FL	TCCTCTTGAAAATTTTCGCTTGAGTATCTTCCTCTATTCTTGTTGGGCTGTTGGTATTACT
L.CER.PIED.GA	TCCTCTTGGAAGTTTTCTCTTGAATACCTACCTCTATTTTTATGAGCTGTTGGTATCACT
L.CER.NOCKSP.PA	TCCTCTTGGAAGTTTTCTCTTGAATACCTACCTCTATTTTTATGAGCTGTTGGTATCACT
L.CER.ECHOLK.CA	TCCTCTTGGAAGTTTTCTCTTGAATACCTACCTCTATTTTTATGAGCTGTTGGTATCACT
L.CER.NOCKFS.PA	TCCTCTTGGAAGTTTTCTCTTGAATACCTACCTCTATTTTTATGAGCTGTTGGTATCACT
L.CER.HILOCH.GA	TCCTCTTGGAAGTTTTCTCTTGAATACCTACCTCTATTTTTATGAGCTGTTGGTATCACT
L.CER.EASTPOI.GA	TCCTCTTGGAAGTTTTCTCTTGAATACCTACCTCTATTTTTATGAGCTGTTGGTATCACT
L.CER.NORLK.GA	TCCTCTTGGAAGTTTTCTCTTGAATACCTACCTCTATTTTTATGAGCTGTTGGTATCACT
L.MEL.BEVIEW.GA	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN25.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN43.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN01.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN29.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN11.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN32.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN13.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN21.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN28.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN05.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN02.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN16.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN06.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN29B.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN11B.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN23B.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN08.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN26.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN34.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN01B.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN01C.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN08B.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.FLNT08.NH	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN19B.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN18.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.MN10.WI	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.LAUREN.GA	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.FLNT02.NH	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.FLNT10.NH	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.FLNT11.NH	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.FLNT03.NH	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.FLNT04.NH	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
L.MEL.FLNT06.NH	TCTTCTTGGAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT

L.MEL.CANLK.GA TCTTCTTGAAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
 L.MEL.STP.GA TCTTCTTGAAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGAGCTGTAGGTATTACT
 L.MEL.EHT01.TX TCTTCTTGAAAGTTCTCTTTAGAATATTTACCATTATTTTTGTGGGCTGTAGGTATTACC
 L.MEL.EHT02.TX TCTTCTTGAAAGTTCTCTTTAGAATATTTACCATTATTTTTGTGGGCTGTAGGTATTACC
 L.MEL.EHT03.TX TCTTCTTGAAAGTTCTCTTTAGAATATTTACCATTATTTTTGTGGGCTGTAGGTATTACC
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 L.MEL.EHT07.TX TCTTCTTGAAAGTTCTCTTTAGAATATTTACCATTATTTTTGTGGGCTGTAGGTATTACC
 L.MEL.DEV.OR TCTTCTTGAAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGGGCTGTAGGCATTACT
 L.MEL.NISKEY.GA TCTTCTTGAAAGTTTTCTTTAGAATATTTACCATTATTTTTGTGGGCTGTAGGCATTACT
 L.MEL.FISHCP2.FL TCTTCTTGAAAATTCTCTCTAGAATACTTGCCTCTGTTTTGTGGGCTGTAGGGATTACT
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 L.MEL.TIM.OR TCTTCTTGAAAGTTTTCAATTGGAGTACCTTCCTTTGTTTTCTATGGGCTGTTGGTATTACG
 L.MEL.WRW2.WI TCTTCTTGAAAGTTTTCAATTGGAGTACCTTCCTTTGTTTTCTATGGGCTGTTGGTATTACG
 L.MEL.MINLK.WI TCTTCTTGAAAGTTTTCAATTGGAGTACCTTCCTTTGTTTTCTATGGGCTGTTGGTATTACG
 L.MEL.GLASS.UT TCTTCTTGAAAGTTTTCACTGGAGTACCTTCCTTTGTTTTCTATGGGCTGTTGGTATTACG
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 L.MEL.AMD01.TX TCTTCGTGAAAATTTTTCTCTTGAGTATCTCCCCTTATTTTTGTGGGCTGTCGGAATTACT
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 L.MEL.INK.TX TCTTCGTGAAAATTTTTCTCTTGAGTATCTCCCCTTATTTTTGTGGGCTGTCGGAATTACT
 L.MEL.BALBOA.CA TCTTCGTGAAAATTTTTCTCTTGAGTATCTCCCCTTATTTTTGTGGGCTGTCGGAATTACT
 L.MEL.CP02.SC TCTTCTTGGAAGTTTTCGCTTGAATACCTCCCCTTGTTTCTATGGGCTGTTGGAATTACT
 L.MEL.CP03.SC TCTTCTTGGAAGTTTTCGCTTGAATACCTCCCCTTGTTTCTATGGGCTGTTGGAATTACT
 L.MEL.RAT01.NM TCTTCATGAAAGTTTTCTCTTGAGTATCTTCCTTTATTTTTATGGGCAGTTGGTATCACT
 L.MEL.RAT02.NM TCTTCATGAAAGTTTTCTCTTGAGTATCTTCCTTTATTTTTATGGGCAGTTGGTATCACT
 L.MEL.NOIC3.OK TCTTCATGAAAGTTTTCTCTTGAAATATCTTCCTTTATTTTTATGGGCAGTTGGTATTACT
 L.MEL.STA02.OK TCTTCATGAAAGTTTTCTCTTGAAATATCTTCCTTTATTTTTATGGGCAGTTGGTATTACT
 L.MEL.STA01.OK TCTTCATGAAAGTTTTCTCTTGAAATATCTTCCTTTATTTTTATGGGCAGTTGGTATTACT
 L.MEL.NOIC2.OK TCTTCATGAAAGTTTTCTCTTGAAATATCTTCCTTTATTTTTATGGGCAGTTGGTATTACT
 L.MEL.NOIC4.OK TCTTCATGAAAGTTTTCTCTTGAAATATCTTCCTTTATTTTTATGGGCAGTTGGTATTACT
 L.MEL.BASLK.TX TCTTCATGAAAGTTTTCTCTTGAAATATCTTCCTTTATTTTTATGGGCAGTTGGTATTACT
 L.MEL.JAC.FL TCTTCATGAAAATTTTTCTCTTGAGTACCTTCCTCTGTTCTTGTTGGGCGGTGGGTATTACT
 L.MEL.CRLRD.TX TCCTCTTGGAAGTTTTCTCTAGAGTACCTTCCTCTGTTCTTGTTGGGCGGTGGGTATTACT
 L.MEL.KRM.FL TCTTCTTGGAAGTTTTCTTTGGAATACCTGCCATTGTTTTGTGAGCTGTAGGAATTACA
 L.MEL.LKO.FL TCTTCTTGGAAGTTTTCTTTGGAATACCTGCCATTGTTTTGTGAGCTGTAGGAATTACA
 L.MEL.SIT4.FL TCTTCTTGGAAGTTTTCTTTGGAATACCTGCCATTGTTTTGTGAGCTGTAGGAATTACA

L.CER.MORPH.NM GCTGTATTGTTAGTAACTTCTTTACCAGTGCTGGCTGGTGCTATTACTATGCTTTTAACT
 L.CER.WORT25.TX GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.WORT15.TX GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATTACCATGCTATTA
 L.CER.TLL.PA GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATTACCATGCTATTA
 L.CER.WACO.TX GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.MN04.WI GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.MN40.WI GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.MN46.WI GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.MN16.WI GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.BLU.OR GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.SAM.TX GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.DUC.OK GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.FL.TX GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.GMP.WI GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.MN14.WI GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.MEN.WI GCTATTTTGTGGTTACCTCTCTTCCTGTTTTAGCAGGTGCTATCACCATGCTATTA
 L.CER.HCP.FL GCTGTGTTGTTGGTTACTTCACTCCCTGTACTAGCGGGTGCTATCACTATGCTGTTGACG
 L.CER.PIED.GA GCGGTTCTTCTAGTAACTTCCCTTCCTGTACTGGCTGGTGCTATTACTATACTTTTAACT
 L.CER.NOCKSP.PA GCGGTTCTTCTAGTAACTTCCCTTCCTGTACTGGCTGGTGCTATTACTATACTTTTAACT
 L.CER.ECHOLK.CA GCGGTTCTTCTAGTAACTTCCCTTCCTGTACTGGCTGGTGCTATTACTATACTTTTAACT

L.CER.NOCKFS.PA	GCGGTTCTTCTAGTAACTTCCCTTCCTGTACTGGCTGGTGCTATTACTATACTTTTAACT
L.CER.HILOCH.GA	GCGGTTCTTCTAGTAACTTCCCTTCCTGTACTGGCTGGTGCTATTACTATACTTTTAACT
L.CER.EASTPOI.GA	GCGGTTCTTCTAGTAACTTCCCTTCCTGTACTGGCTGGTGCTATTACTATACTTTTAACT
L.CER.NORLK.GA	GCGGTTCTTCTAGTAACTTCCCTTCCTGTACTGGCTGGTGCTATTACTATACTTTTAACT
L.MEL.BEVIEW.GA	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN25.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN43.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN01.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN29.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN11.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN32.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN13.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN21.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN28.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN05.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN02.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN16.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN06.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN29B.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN11B.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN23B.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN08.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN26.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN34.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN01B.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN01C.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN08B.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.FLNT08.NH	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN19B.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN18.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.MN10.WI	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.LAUREN.GA	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.FLNT02.NH	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.FLNT10.NH	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.FLNT11.NH	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.FLNT03.NH	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.FLNT04.NH	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.FLNT06.NH	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.CANLK.GA	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCTGGTGCTATTACTATGCTACTTACC
L.MEL.STP.GA	GCAGTCCTATTGGTAACCTCTCTTCCTGTGCTAGCCGGTGCTATTACTATGCTACTTACC
L.MEL.EHT01.TX	GCAGTCCTGTTGGTTACCTCTCTTCCTGTATTAGCTGGTGCTATTACTATACTCCTTACC
L.MEL.EHT02.TX	GCAGTCCTGTTGGTTACCTCTCTTCCTGTATTAGCTGGTGCTATTACTATACTCCTTACC
L.MEL.EHT03.TX	GCAGTCCTGTTGGTTACCTCTCTTCCTGTATTAGCTGGTGCTATTACTATACTCCTTACC
L.MEL.EHT08.TX	GCAGTCCTGTTGGTTACCTCTCTTCCTGTATTAGCTGGTGCTATTACTATACTCCTTACC
L.MEL.EHT07.TX	GCAGTCCTGTTGGTTACCTCTCTTCCTGTATTAGCTGGTGCTATTACTATACTCCTTACC
L.MEL.DEV.OR	GCAGTCCTATTGGTAACCTTCCCTCCCTGTGCTGGCTGGTGCTATTACTATACTTCTTACC
L.MEL.NISKEY.GA	GCAGTCCTATTGGTAACCTTCCCTCCCTGTGCTGGCTGGTGCTATTACTATACTTCTTACC
L.MEL.FISHCP2.FL	GCGGTTTTACTGGTTACGTCACTTCCTGTCTTGGCGGGTGCAATTACTATGCTGCTCACT
L.MEL.FISHCP1.FL	GCGGTTTTACTGGTTACGTCACTTCCTGTCTTGGCGGGTGCAATTACTATGCTGCTCACT
L.MEL.TIM.OR	GCAGTTCTGTTGGTTACTTCCCTTCCAGTCTTAGCTGGGGCAATCACTATATTATTGACT
L.MEL.WRW2.WI	GCAGTTCTGTTGGTTACTTCCCTTCCAGTCTTAGCTGGGGCAATCACTATATTATTGACT
L.MEL.MINLK.WI	GCAGTTCTGTTGGTTACTTCCCTTCCAGTCTTAGCTGGGGCAATCACTATATTATTGACT
L.MEL.GLASS.UT	GCAGTTCTGTTGGTTACTTCCCTTCCAGTCTTAGCTGGGGCAATCACTATACTATTGACT
L.MEL.CIB.TX	GCAGTCCTGTTGGTTACATCTCTCCCTGTTTTAGCTGGGGCTATTACTATGTTGTTGACA
L.MEL.AMD01.TX	GCTGTTTTGTTAGTTACTTCTTTGCCTGTTTTGGCGGGGGCTATTACTATGTTATTAACC
L.MEL.AMD02.TX	GCTGTTTTGTTAGTTACTTCTTTGCCTGTTTTGGCGGGGGCTATTACTATGTTATTAACC
L.MEL.INK.TX	GCTGTTTTGTTAGTTACTTCTTTGCCTGTTTTGGCGGGGGCTATTACTATGTTATTAACC

L.MEL.BALBOA.CA	GCTGTTTTGTTAGTTACTTCTTTGCCTGTTTTGGCGGGGGCTATTACTATGTTATTAACC
L.MEL.CP02.SC	GCTGTGTTATTAGTAACATCTTTGCCTGTTTTAGCTGGGGCTATTACTATGTTGTTAACA
L.MEL.CP03.SC	GCTGTGTTATTAGTAACATCTTTGCCTGTTTTAGCTGGGGCTATTACTATGTTGTTAACA
L.MEL.RAT01.NM	GCAGTTTTGTTGGTTACTTCCCTGCCTGTTTTGGCTGGGGCTATTACTATGCTGTTAACT
L.MEL.RAT02.NM	GCAGTTTTGTTGGTTACTTCCCTGCCTGTTTTGGCTGGGGCTATTACTATGCTGTTAACT
L.MEL.NOIC3.OK	GCAGTTTTGTTGGTTACTTCTCTGCCTGTTTTGGCTGGGGCTATTACTATGTTGTTAACT
L.MEL.STA02.OK	GCAGTTTTGTTGGTTACTTCTCTGCCTGTTTTGGCTGGGGCTATTACTATGTTGTTAACT
L.MEL.STA01.OK	GCAGTTTTGTTGGTTACTTCTCTGCCTGTTTTGGCTGGGGCTATTACTATGTTGTTAACT
L.MEL.NOIC2.OK	GCAGTTTTGTTGGTTACTTCTCTGCCTGTTTTGGCTGGGGCTATTACTATGTTGTTAACT
L.MEL.NOIC4.OK	GCAGTTTTGTTGGTTACTTCTCTGCCTGTTTTGGCTGGGGCTATTACTATGTTGTTAACT
L.MEL.BASLK.TX	GCAGTTTTGTTGGTTACTTCTCTGCCTGTTTTGGCTGGGGCTATTACTATGTTGTTAACT
L.MEL.JAC.FL	GCAGTCTTGCTGGTTACTTCTTTGCCCGTTTTAGCTGGGGCTATTACTATGTTACTGACT
L.MEL.CRLRD.TX	GCAGTTTTGTTAGTTACCTCTTTACCTGTTCTCGCTGGGGCAATCACTATACTGCTGACT
L.MEL.KRM.FL	GCTGTTTTATTAGTCACTTCTTTACCAGTGTTAGCGGGGGCTATTACTATGCTCCTGACC
L.MEL.LKO.FL	GCTGTTTTATTAGTCACTTCTTTACCAGTGTTAGCGGGGGCTATTACTATGCTCCTGACC
L.MEL.SIT4.FL	GCTGTTTTATTAGTCACTTCTTTACCAGTGTTAGCGGGGGCTATTACTATGCTCCTGACC

L.CER.MORPH.NM	GATCGTAACTTTAATACATCATTTTTTTGACCCTTCTGGTGGTGGAACCCAGTATTATAC
L.CER.WORT25.TX	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAATCCCGTGTTGTAT
L.CER.WORT15.TX	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.TLL.PA	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.WACO.TX	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.MN04.WI	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.MN40.WI	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.MN46.WI	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.MN16.WI	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.BLU.OR	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.SAM.TX	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.DUC.OK	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.FL.TX	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.GMP.WI	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.MN14.WI	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.MEN.WI	GATCGAACTTCAACACCTCTTTTTTTGACCCTTCTGGGGGCGGTAACCCCGTGTTGTAT
L.CER.HCP.FL	GACCGTAATTTTAATACCTCTTTTTTTGACCCGTCGGGGGAGGCAATCCCATTTTGTAC
L.CER.PIED.GA	GATCGTAATTTTAATACTTCTTTCTTTGACCCATCGGGTGGTGGTAATCCCATCTTGTAC
L.CER.NOCKSP.PA	GATCGTAATTTTAATACTTCTTTCTTTGACCCATCGGGTGGTGGTAATCCCATCTTGTAC
L.CER.ECHOLK.CA	GATCGTAATTTTAATACTTCTTTCTTTGACCCATCGGGTGGTGGTAATCCCATCTTGTAC
L.CER.NOCKFS.PA	GATCGTAATTTTAATACTTCTTTCTTTGACCCATCGGGTGGTGGTAATCCCATCTTGTAC
L.CER.HILOCH.GA	GATCGTAATTTTAATACTTCTTTCTTTGACCCATCGGGTGGTGGTAATCCCATCTTGTAC
L.CER.EASTPOI.GA	GATCGTAATTTTAATACTTCTTTCTTTGACCCATCGGGTGGTGGTAATCCCATCTTGTAC
L.CER.NORLK.GA	GATCGTAATTTTAATACTTCTTTCTTTGACCCATCGGGTGGTGGTAATCCCATCTTGTAC
L.MEL.BEVIEW.GA	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN25.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN43.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN01.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN29.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN11.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN32.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN13.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN21.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN28.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN05.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN02.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN16.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN06.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC
L.MEL.MN29B.WI	GACCGGAACCTTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCATCCTTTTAC

L.MEL.MN11B.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN23B.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN08.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN26.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN34.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN01B.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN01C.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN08B.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.FLNT08.NH GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN19B.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN18.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.MN10.WI GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.LAUREN.GA GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.FLNT02.NH GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCCATCCTTTTAC
 L.MEL.FLNT10.NH GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCCATCCTTTTAC
 L.MEL.FLNT11.NH GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCCATCCTTTTAC
 L.MEL.FLNT03.NH GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCCATCCTTTTAC
 L.MEL.FLNT04.NH GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCCATCCTTTTAC
 L.MEL.FLNT06.NH GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCCATCCTTTTAC
 L.MEL.CANLK.GA GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCCATCCTTTTAC
 L.MEL.STP.GA GACCGGAAC TTCAACACTTCTTTCTTCGATCCATCTGGTGGTGGTAACCCTATCCTTTTAC
 L.MEL.EHT01.TX GATCGGAAC TTCAATACTTCTTTCTTTGACCCATCTGGAGGTGGTAACCCTATTCTTTTAC
 L.MEL.EHT02.TX GATCGGAAC TTCAATACTTCTTTCTTTGACCCATCTGGAGGTGGTAACCCTATTCTTTTAC
 L.MEL.EHT03.TX GATCGGAAC TTCAATACTTCTTTCTTTGACCCATCTGGAGGTGGTAACCCTATTCTTTTAC
 L.MEL.EHT08.TX GATCGGAAC TTCAATACTTCTTTCTTTGACCCATCTGGAGGTGGTAACCCTATTCTTTTAC
 L.MEL.EHT07.TX GATCGGAAC TTCAATACTTCTTTCTTTGACCCATCTGGAGGTGGTAACCCTATTCTTTTAC
 L.MEL.DEV.OR GATCGCAAC TTTAATACTTCTTTCTTTGACCCGTCTGGCGGGGGTAATCCTATCCTTTTAT
 L.MEL.NISKEY.GA GATCGCAAC TTTAATACTTCTTTCTTTGACCCGTCTGGCGGGGGTAATCCTATCCTTTTAT
 L.MEL.FISHCP2.FL GATCGTAAC TTTAATACTTCTTTCTTTGACCCGTCTGGTGGGGGAACCCATTCTTTTATAC
 L.MEL.FISHCP1.FL GATCGTAAC TTTAATACTTCTTTCTTTGACCCGTCTGGTGGGGGAACCCATTCTTTTATAC
 L.MEL.TIM.OR GATCGCAAT TTTAATACTTCTTTCTTTGATCCTTCTGGTGGGGGAACCCATTCTCTAC
 L.MEL.WRW2.WI GATCGCAAT TTTAATACTTCTTTCTTTGATCCTTCTGGTGGGGGAACCCATTCTCTAC
 L.MEL.MINLK.WI GATCGCAAT TTTAATACTTCTTTCTTTGATCCTTCTGGTGGGGGAACCCATTCTCTAT
 L.MEL.GLASS.UT GATCGCAAT TTTAATACTTCTTTCTTTGATCCTTCTGGTGGGGGAACCCATTCTCTAC
 L.MEL.CIB.TX GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTGGTGGGGGAACCCATTCTCTAC
 L.MEL.AMD01.TX GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTGGGAGGGGGGAACCCATTCTTTTAC
 L.MEL.AMD02.TX GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTGGGAGGGGGGAACCCATTCTTTTAC
 L.MEL.INK.TX GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTGGGAGGGGGGAACCCATTCTTTTAC
 L.MEL.BALBOA.CA GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTGGGAGGGGGGAACCCATTCTTTTAC
 L.MEL.CP02.SC GATCGTAAC TTTAATACTTCTTTCTTTGACCCCTCGGGGGGTGGGAACCCGTTCTTTTAC
 L.MEL.CP03.SC GATCGTAAC TTTAATACTTCTTTCTTTGACCCCTCGGGGGGTGGGAACCCGTTCTTTTAC
 L.MEL.RAT01.NM GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.RAT02.NM GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.NOIC3.OK GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.STA02.OK GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.STA01.OK GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.NOIC2.OK GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.NOIC4.OK GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.BASLK.TX GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.JAC.FL GATCGTAAC TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.CRLRD.TX GATCGTAAT TTTAATACTTCTTTCTTTGATCCTTCTCAGGCGGGGGGAAATCCCATTCTATAC
 L.MEL.KRM.FL GACCGTAAC TTTAATACTTCTTTCTTTGATCCTTCTCAGGTGGTGGGAATCCTATTTTGTAC
 L.MEL.LKO.FL GACCGTAAC TTTAATACTTCTTTCTTTGATCCTTCTCAGGTGGTGGGAATCCTATTTTGTAC
 L.MEL.SIT4.FL GACCGTAAC TTTAATACTTCTTTCTTTGATCCTTCTCAGGTGGTGGGAATCCTATTTTGTAC

L.CER.MORPH.NM CAACATCTTTTTTGATTTTTTGG

L.CER.WORT25.TX	CAGCATCTTTTTTGATTTTTTGG
L.CER.WORT15.TX	CAGCATCTTTTTTGATTTTTTGG
L.CER.TLL.PA	CAGCATCTTTTTTGATTTTTTGG
L.CER.WACO.TX	CAGCATCTTTTTTGATTTTTTGG
L.CER.MN04.WI	CAGCATCTTTTTTGATTTTTTGG
L.CER.MN40.WI	CAGCATCTTTTTTGATTTTTTGG
L.CER.MN46.WI	CAGCATCTTTTTTGATTTTTTGG
L.CER.MN16.WI	CAGCATCTTTTTTGATTTTTTGG
L.CER.BLU.OR	CAGCATCTTTTTTGATTTTTTGG
L.CER.SAM.TX	CAGCATCTTTTTTGATTTTTTGG
L.CER.DUC.OK	CAGCATCTTTTTTGATTTTTTGG
L.CER.FL.TX	CAGCATCTTTTTTGATTTTTTGG
L.CER.GMP.WI	CAGCATCTTTTTTGATTTTTTGG
L.CER.MN14.WI	CAGCATCTTTTTTGATTTTTTGG
L.CER.MEN.WI	CAGCATCTTTTTTGATTTTTTGG
L.CER.HCP.FL	CAACATTTGTTTTGATTTTTTGG
L.CER.PIED.GA	CAACATCTTTTTTGATTTTTTGG
L.CER.NOCKSP.PA	CAACATCTTTTTTGATTTTTTGG
L.CER.ECHOLK.CA	CAACATCTTTTTTGATTTTTTGG
L.CER.NOCKFS.PA	CAACATCTTTTTTGATTTTTTGG
L.CER.HILOCH.GA	CAACATCTTTTTTGATTTTTTGG
L.CER.EASTPOI.GA	CAACATCTTTTTTGATTTTTTGG
L.CER.NORLK.GA	CAACATCTCTTTTGATTTTTTGG
L.MEL.BEVIEW.GA	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN25.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN43.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN01.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN29.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN11.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN32.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN13.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN21.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN28.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN05.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN02.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN16.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN06.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN29B.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN11B.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN23B.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN08.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN26.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN34.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN01B.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN01C.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN08B.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.FLNT08.NH	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN19B.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN18.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.MN10.WI	CAGCATTTGTTTTGATTTTTTGG
L.MEL.LAUREN.GA	CAGCATTTGTTTTGATTTTTTGG
L.MEL.FLNT02.NH	CAGCATTTGTTTTGATTTTTTGG
L.MEL.FLNT10.NH	CAGCATTTGTTTTGATTTTTTGG
L.MEL.FLNT11.NH	CAGCATTTGTTTTGATTTTTTGG
L.MEL.FLNT03.NH	CAGCATTTGTTTTGATTTTTTGG
L.MEL.FLNT04.NH	CAGCATTTGTTTTGATTTTTTGG
L.MEL.FLNT06.NH	CAGCATTTGTTTTGATTTTTTGG

L.MEL.CANLK.GA	CAGCATTTGTTTTGATTTTTTGG
L.MEL.STP.GA	CAGCATTTGTTTTGATTTTTTGG
L.MEL.EHT01.TX	CAGCATTTGTTTTGATTTTTTGG
L.MEL.EHT02.TX	CAGCATTTGTTTTGATTTTTTGG
L.MEL.EHT03.TX	CAGCATTTGTTTTGATTTTTTGG
L.MEL.EHT08.TX	CAGCATTTGTTTTGATTTTTTGG
L.MEL.EHT07.TX	CAGCATTTGTTTTGATTTTTTGG
L.MEL.DEV.OR	CAACATTTGTTTTGATTTTTTGG
L.MEL.NISKEY.GA	CAACATTTGTTTTGATTTTTTGG
L.MEL.FISHCP2.FL	CAGCATTTGTTTTGATTTTTTGG
L.MEL.FISHCP1.FL	CAGCATTTGTTTTGATTTTTTGG
L.MEL.TIM.OR	CAACATCTATTTTGATTTTTTGG
L.MEL.WRW2.WI	CAACATCTATTTTGATTTTTTGG
L.MEL.MINLK.WI	CAACATCTATTTTGATTTTTTGG
L.MEL.GLASS.UT	CAACATCTATTTTGATTTTTTGG
L.MEL.CIB.TX	CAGCATCTTTTTTGATTTTTTGG
L.MEL.AMD01.TX	CAGCATTTATTCTGATTTTTTGG
L.MEL.AMD02.TX	CAGCATTTATTCTGATTTTTTGG
L.MEL.INK.TX	CAGCATTTATTCTGATTTTTTGG
L.MEL.BALBOA.CA	CAGCATTTATTCTGATTTTTTGG
L.MEL.CP02.SC	CAGCATCTATTTTGATTTTTTGG
L.MEL.CP03.SC	CAGCATCTTTTTTGATTTTTTGG
L.MEL.RAT01.NM	CAGCATCTTTTTTGATTTTTTGG
L.MEL.RAT02.NM	CAGCATCTTTTTTGATTTTTTGG
L.MEL.NOIC3.OK	CAGCATCTTTTTTGATTTTTTGG
L.MEL.STA02.OK	CAGCATCTTTTTTGATTTTTTGG
L.MEL.STA01.OK	CAGCATCTTTTTTGATTTTTTGG
L.MEL.NOIC2.OK	CAGCATCTTTTTTGATTTTTTGG
L.MEL.NOIC4.OK	CAGCATCTTTTTTGATTTTTTGG
L.MEL.BASLK.TX	CAGCATCTTTTTTGATTTTTTGG
L.MEL.JAC.FL	CAGCATCTTTTTTGATTTTTTGG
L.MEL.CRLRD.TX	CAACATCTTTTCTGATTTTTTGG
L.MEL.KRM.FL	CAACATTTATTTTGATTTTTTGG
L.MEL.LKO.FL	CAACATTTATTTTGATTTTTTGG
L.MEL.SIT4.FL	CAGCATTTATTTTGATTTTTTGG

Supplemental document S2.7: CLUSTAL format alignment of 18S rRNA sequences of *Limnias melicerta* and *L. ceratophylli* by MAFFT (v7.380). Abbreviations are the same as Tables S2.1 and S2.2. N= missing data.

C.CAM.GLASSMAN.UT	AGCAGGCGCGCAAATTACCCACTCCTAGATCGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.DEV.OR	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.MN02.WI	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.DEVD.OR	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.EHT.TX	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.RAT.NM	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.KM873599.	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.TIM.OR	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.NISKEY.GA	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.STA.OK	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.AMD.TX	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.CANLK.GA	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.LKO.FL	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.FISHCAMP.FL	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.GLASSMAN.UT	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.JAC02.FL	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.FLNT.NH	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.NIOC.OK	NNNAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.MEL.CNLRD.TX	NNNNNGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.HILOCH.GA	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.MN.WI	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.BLUE.OR	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.KM873598.	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.NAT01.NH	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.NOCKFS.PA	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CERBURRISTON.UT	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.NORMLK.GA	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.NOCKSP.PA	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.HCP.FL	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.DUC.OK	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.FLNT.NH	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.WORTH.TX	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.WACO01.TX	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.MORPHY.NM	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.MEN01.WI	AGCAGGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.FL.TX	NNNNNNNGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC
L.CER.EASTPOIN.GA	NNNAGTGACGAAAAATAACAATAC
L.CER.ECH.CA	NNNNNGCGCGCAAATTACCCACTCCTAGAACGGGGAGGTAGTGACGAAAAATAACAATAC

C.CAM.GLASSMAN.UT	CGGACTCTAAGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.DEV.OR	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.MN02.WI	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.DEVD.OR	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.EHT.TX	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.RAT.NM	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.KM873599.	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.TIM.OR	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.NISKEY.GA	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.STA.OK	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.AMD.TX	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.CANLK.GA	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.LKO.FL	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.FISHCAMP.FL	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.GLASSMAN.UT	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.JAC02.FL	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.FLNT.NH	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.MEL.NIOC.OK	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT

L.MEL.CNLRD.TX	CGGACTCATTGAGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.HILOCH.GA	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.MN.WI	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.BLUE.OR	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.KM873598.	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.NAT01.NH	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.NOCKFS.PA	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CERBURRISTON.UT	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.NORMLK.GA	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.NOCKSP.PA	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.HCP.FL	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.DUC.OK	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.FLNT.NH	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.WORTH.TX	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.WACO01.TX	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.MORPHY.NM	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.MEN01.WI	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.FL.TX	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.EASTPOIN.GA	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT
L.CER.ECH.CA	CGGACTCAAATGGGCTCGGTAATTGAAATGAGTACAGTTTAAAACCTTTAACGAGGATCT

C.CAM.GLASSMAN.UT	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.DEV.OR	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.MN02.WI	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.DEVD.OR	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.EHT.TX	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.RAT.NM	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.KM873599.	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.TIM.OR	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.NISKEY.GA	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.STA.OK	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.AMD.TX	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.CANLK.GA	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.LKO.FL	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.FISHCAMP.FL	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.GLASSMAN.UT	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.JAC02.FL	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.FLNT.NH	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.NIOC.OK	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.MEL.CNLRD.TX	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.HILOCH.GA	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.MN.WI	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.BLUE.OR	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.KM873598.	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.NAT01.NH	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.NOCKFS.PA	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CERBURRISTON.UT	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.NORMLK.GA	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.NOCKSP.PA	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.HCP.FL	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.DUC.OK	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.FLNT.NH	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.WORTH.TX	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.WACO01.TX	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.MORPHY.NM	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.MEN01.WI	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.FL.TX	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.EASTPOIN.GA	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA
L.CER.ECH.CA	ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTA

C.CAM.GLASSMAN.UT	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGTTAGCGGTACGCTTC
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L.MEL.DEV.OR	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.MN02.WI	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.DEVD.OR	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.EHT.TX	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.RAT.NM	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.KM873599.	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.TIM.OR	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.NISKEY.GA	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.STA.OK	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.AMD.TX	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.CANLK.GA	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.LKO.FL	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.FISHCAMP.FL	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.GLASSMAN.UT	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.JAC02.FL	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.FLNT.NH	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.NIOC.OK	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.MEL.CNLRD.TX	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.HILOCH.GA	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.MN.WI	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.BLUE.OR	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.KM873598.	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.NAT01.NH	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.NOCKFS.PA	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CERBURRISTON.UT	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.NORMLK.GA	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.NOCKSP.PA	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.HCP.FL	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.DUC.OK	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.FLNT.NH	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.WORTH.TX	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.WAC001.TX	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.MORPHY.NM	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.MEN01.WI	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.FL.TX	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.EASTPOIN.GA	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA
L.CER.ECH.CA	AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTCGGGTGCCAGCTTGTGGTACGCTTA

C.CAM.GLASSMAN.UT	ACTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.DEV.OR	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.MN02.WI	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.DEVD.OR	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.EHT.TX	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.RAT.NM	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.KM873599.	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.TIM.OR	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.NISKEY.GA	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.STA.OK	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.AMD.TX	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.CANLK.GA	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.LKO.FL	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.FISHCAMP.FL	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.GLASSMAN.UT	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.JAC02.FL	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.FLNT.NH	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.NIOC.OK	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.MEL.CNLRD.TX	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.HILOCH.GA	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.MN.WI	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.BLUE.OR	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.KM873598.	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.NAT01.NH	ATTGCGTTACTGCTTGCTCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG

L.CER.NOCKFS.PA	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CERBURRISTON.UT	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.NORMLK.GA	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.NOCKSP.PA	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.HCP.FL	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.DUC.OK	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.FLNT.NH	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.WORTH.TX	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.WACO01.TX	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.MORPHY.NM	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.MEN01.WI	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.FL.TX	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.EASTPOIN.GA	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG
L.CER.ECH.CA	ATTGCGTTACTGCTTGCTGGCCCTAATCAACCGGTTGGCCGTTTATGCCCTTTATTGGG

C.CAM.GLASSMAN.UT	TGTTTACGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCCTTAC
L.MEL.DEV.OR	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.MN02.WI	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.DEVD.OR	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.EHT.TX	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.RAT.NM	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.KM873599.	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.TIM.OR	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.NISKEY.GA	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.STA.OK	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.AMD.TX	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.CANLK.GA	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.LKO.FL	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.FISHCAMP.FL	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.GLASSMAN.UT	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.JAC02.FL	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.FLNT.NH	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.NIOC.OK	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.MEL.CNLRD.TX	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.HILOCH.GA	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.MN.WI	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.BLUE.OR	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.KM873598.	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.NAT01.NH	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.NOCKFS.PA	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CERBURRISTON.UT	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.NORMLK.GA	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.NOCKSP.PA	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.HCP.FL	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.DUC.OK	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.FLNT.NH	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.WORTH.TX	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.WACO01.TX	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.MORPHY.NM	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.MEN01.WI	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.FL.TX	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.EASTPOIN.GA	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT
L.CER.ECH.CA	TGTTTTCGGTAGCCGGTACGTTTACTTTGAGAAAATTAGAGTGCTTAAAGCAGGCAATCT

C.CAM.GLASSMAN.UT	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTTG
L.MEL.DEV.OR	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTTG
L.MEL.MN02.WI	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTTG
L.MEL.DEVD.OR	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTTG
L.MEL.EHT.TX	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTTG
L.MEL.RAT.NM	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTTG
L.MEL.KM873599.	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTTG

L.MEL.TIM.OR	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.NISKEY.GA	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.STA.OK	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.AMD.TX	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.CANLK.GA	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.LKO.FL	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.FISHCAMP.FL	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.GLASSMAN.UT	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.JAC02.FL	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.FLNT.NH	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.NIOC.OK	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.MEL.CNLRD.TX	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.HILOCH.GA	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.MN.WI	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.BLUE.OR	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.KM873598.	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.NAT01.NH	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.NOCKFS.PA	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CERBURRISTON.UT	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.NORMLK.GA	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.NOCKSP.PA	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.HCP.FL	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.DUC.OK	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.FLNT.NH	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.WORTH.TX	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.WACO01.TX	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.MORPHY.NM	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.MEN01.WI	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.FL.TX	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.EASTPOIN.GA	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG
L.CER.ECH.CA	GCCTGAATAATGTTGCATGGAATAATAGAATAGGACCTCGGTTCTATTTTGTGGTTTTG

C.CAM.GLASSMAN.UT	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.DEV.OR	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.MN02.WI	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.DEVD.OR	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.EHT.TX	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.RAT.NM	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.KM873599.	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.TIM.OR	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.NISKEY.GA	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.STA.OK	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.AMD.TX	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.CANLK.GA	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.LKO.FL	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.FISHCAMP.FL	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.GLASSMAN.UT	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.JAC02.FL	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.FLNT.NH	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.NIOC.OK	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.MEL.CNLRD.TX	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.HILOCH.GA	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.MN.WI	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.BLUE.OR	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.KM873598.	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.NAT01.NH	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.NOCKFS.PA	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CERBURRISTON.UT	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.NORMLK.GA	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.NOCKSP.PA	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.HCP.FL	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.DUC.OK	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA

L.CER.FLNT.NH	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.WORTH.TX	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.WACO01.TX	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.MORPHY.NM	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.MEN01.WI	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.FL.TX	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.EASTPOIN.GA	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA
L.CER.ECH.CA	TAGAGCATTGAGGTAATGATTAATAGGGACAGACGGGGGCATTTCGTATTGCGGTGTTAGA

C.CAM.GLASSMAN.UT	GGTGAAATTCTTGGATCGCCGCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.DEV.OR	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.MN02.WI	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.DEVD.OR	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.EHT.TX	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.RAT.NM	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.KM873599.	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.TIM.OR	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.NISKEY.GA	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.STA.OK	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.AMD.TX	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.CANLK.GA	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.LKO.FL	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.FISHCAMP.FL	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.GLASSMAN.UT	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.JAC02.FL	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.FLNT.NH	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.NIOC.OK	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.MEL.CNLRD.TX	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.HILOCH.GA	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.MN.WI	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.BLUE.OR	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.KM873598.	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.NAT01.NH	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.NOCKFS.PA	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CERBURRISTON.UT	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.NORMLK.GA	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.NOCKSP.PA	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.HCP.FL	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.DUC.OK	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.FLNT.NH	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.WORTH.TX	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.WACO01.TX	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.MORPHY.NM	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.MEN01.WI	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.FL.TX	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.EASTPOIN.GA	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT
L.CER.ECH.CA	GGTGAAATTCTTGGATCACC GCAAGACGAACAACCTGCGAAAGCATTTGCCAAGAATGTTT

C.CAM.GLASSMAN.UT	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.DEV.OR	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.MN02.WI	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.DEVD.OR	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.EHT.TX	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.RAT.NM	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.KM873599.	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.TIM.OR	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.NISKEY.GA	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.STA.OK	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.AMD.TX	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.CANLK.GA	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.LKO.FL	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA

L.MEL.FISHCAMP.FL	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.GLASSMAN.UT	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.JAC02.FL	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.FLNT.NH	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.NIOC.OK	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.MEL.CNLRD.TX	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.HILOCH.GA	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.MN.WI	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.BLUE.OR	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.KM873598.	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.NAT01.NH	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.NOCKFS.PA	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CERBURRISTON.UT	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.NORMLK.GA	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.NOCKSP.PA	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.HCP.FL	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.DUC.OK	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.FLNT.NH	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.WORTH.TX	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.WACO01.TX	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.MORPHY.NM	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.MEN01.WI	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.FL.TX	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.EASTPOIN.GA	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA
L.CER.ECH.CA	TCATTAATCAAGAACGAAAGTTGGAGGTTCTGAAGACGATTAGATACCGTCCTAGTTCCAA

C.CAM.GLASSMAN.UT	CCCTAAACTATGCCAACTAAGGATCCGTCGCACTTAAATTAATGAGTCGACGGGCACTTT
L.MEL.DEV.OR	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.MN02.WI	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.DEVD.OR	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.EHT.TX	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.RAT.NM	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.KM873599.	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.TIM.OR	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.NISKEY.GA	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.STA.OK	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.AMD.TX	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.CANLK.GA	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.LKO.FL	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.FISHCAMP.FL	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.GLASSMAN.UT	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.JAC02.FL	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.FLNT.NH	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.NIOC.OK	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.MEL.CNLRD.TX	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.HILOCH.GA	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.MN.WI	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.BLUE.OR	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.KM873598.	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.NAT01.NH	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.NOCKFS.PA	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CERBURRISTON.UT	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.NORMLK.GA	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.NOCKSP.PA	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.HCP.FL	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.DUC.OK	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.FLNT.NH	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.WORTH.TX	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.WACO01.TX	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.MORPHY.NM	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.MEN01.WI	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT
L.CER.FL.TX	CCCTAAACTATGCCAACTAACGATGCGTCGCACTTAAATTAATGAGTCGGCGTGGAGTTT

L.CER.EASTPOIN.GA CCCTAAACTATGCCAACTAACGATGCGTCGCACTTACTTAAATGAGTCGGCGTGGAGTTT
L.CER.ECH.CA CCCTAAACTATGCCAACTAACGATGCGTCGCACTTACTTAAATGAGTCGGCGTGGAGTTT

C.CAM.GLASSMAN.UT CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.DEV.OR CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.MN02.WI CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.DEVD.OR CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.EHT.TX CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.RAT.NM CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.KM873599. CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.TIM.OR CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.NISKEY.GA CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.STA.OK CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.AMD.TX CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.CANLK.GA CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.LKO.FL CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.FISHCAMP.FL CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.GLASSMAN.UT CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.JAC02.FL CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.FLNT.NH CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.NIOC.OK CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.MEL.CNLRD.TX CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.HILOCH.GA CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.MN.WI CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.BLUE.OR CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.KM873599. CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.NAT01.NH CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.NOCKFS.PA CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CERBURRISTON.UT CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.NORMLK.GA CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.NOCKSP.PA CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.HCP.FL CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.DUC.OK CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.FLNT.NH CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.WORTH.TX CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.WACO01.TX CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.MORPHY.NM CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.MEN01.WI CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.FL.TX CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.EASTPOIN.GA CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG
L.CER.ECH.CA CCGGGAACCAAAGTGTTTGGGTTCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAG

C.CAM.GLASSMAN.UT GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.DEV.OR GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.MN02.WI GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.DEVD.OR GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.EHT.TX GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.RAT.NM GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.KM873599. GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.TIM.OR GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.NISKEY.GA GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.STA.OK GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.AMD.TX GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.CANLK.GA GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.LKO.FL GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.FISHCAMP.FL GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.GLASSMAN.UT GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.JAC02.FL GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.FLNT.NH GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.NIOC.OK GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.MEL.CNLRD.TX GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG

L.CER.HILOCH.GA	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.MN.WI	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.BLUE.OR	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.KM873598.	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.NAT01.NH	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.NOCKFS.PA	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CERBURRISTON.UT	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.NORMLK.GA	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.NOCKSP.PA	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.HCP.FL	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.DUC.OK	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.FLNT.NH	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.WORTH.TX	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.WACO01.TX	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.MORPHY.NM	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.MEN01.WI	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.FL.TX	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.EASTPOIN.GA	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG
L.CER.ECH.CA	GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG

C.CAM.GLASSMAN.UT	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.DEV.OR	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.MN02.WI	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.DEVD.OR	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.EHT.TX	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.RAT.NM	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.KM873599.	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.TIM.OR	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.NISKEY.GA	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.STA.OK	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.AMD.TX	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.CANLK.GA	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.LKO.FL	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.FISHCAMP.FL	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.GLASSMAN.UT	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.JAC02.FL	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.FLNT.NH	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.NIOC.OK	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.MEL.CNLRD.TX	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.HILOCH.GA	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.MN.WI	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.BLUE.OR	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.KM873598.	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.NAT01.NH	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.NOCKFS.PA	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CERBURRISTON.UT	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.NORMLK.GA	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.NOCKSP.PA	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.HCP.FL	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.DUC.OK	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.FLNT.NH	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.WORTH.TX	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.WACO01.TX	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.MORPHY.NM	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.MEN01.WI	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.FL.TX	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.EASTPOIN.GA	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG
L.CER.ECH.CA	AAAACCTACCCGCCCCGGACACTGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTCG

C.CAM.GLASSMAN.UT	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.DEV.OR	GTGGGTGGTGGTGCATGGCCGTTCT

L.MEL.MN02.WI	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.DEVD.OR	GTGGGTGGTGGTGCATGGCCGTTNN
L.MEL.EHT.TX	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.RAT.NM	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.KM873599.	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.TIM.OR	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.NISKEY.GA	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.STA.OK	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.AMD.TX	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.CANLK.GA	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.LKO.FL	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.FISHCAMP.FL	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.GLASSMAN.UT	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.JAC02.FL	GTGGGTGGTGNNNNNNNNNNNNNNNN
L.MEL.FLNT.NH	GTGGGTGGTGGTGCATGNCCGTTCT
L.MEL.NIOC.OK	GTGGGTGGTGGTGCATGGCCGTTCT
L.MEL.CNLRD.TX	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.HILOCH.GA	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.MN.WI	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.BLUE.OR	GTGGGTGGTGGTGCATGGCNNNNNN
L.CER.KM873598.	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.NAT01.NH	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.NOCKFS.PA	GTGGGTGGTGGTGCATGGCCGTTCT
L.CERBURRISTON.UT	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.NORMLK.GA	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.NOCKSP.PA	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.HCP.FL	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.DUC.OK	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.FLNT.NH	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.WORTH.TX	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.WACO01.TX	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.MORPHY.NM	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.MEN01.WI	GTGGGTGGTGGTGCATGGNCGTTCT
L.CER.FL.TX	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.EASTPOIN.GA	GTGGGTGGTGGTGCATGGCCGTTCT
L.CER.ECH.CA	GTGGGTGGTGGTGCATGGCCGTTCT

Supplemental document S2.8: CLUSTAL format alignment of ITS sequences of *Limnias melicerta* and *L. ceratophylli* by MAFFT (v7.380). Abbreviations are the same as Tables S2.1 and S2.2. - = gaps.

F.CONIFERA.MA	ATCGCATTCACATATCGTATATAGTGCTGCGTTTGCATCGCACAA----CAATTGTAGATA
P.BRACHIATA.WI	ATCACATGCGTTATCGTATGTGTTTTCAAATACACA-CAAGTGATTTGTAACATACACTA
L.CER.SAM.TX	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA
L.MEL.CIB.TX	ACTACAAGCGCTAACACTACAAGTGTTGCGTTTATA-CGCACGA----CGACTATGCTTA
L.MEL.DEV.OR	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA
L.MEL.DEVD.OR	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA
L.MEL.MINTO.OR	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA
L.MEL.EHT02.TX	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA
L.MEL.MN01.WI	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA
L.MEL.MN10.WI	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA
L.MEL.MN02.WI	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA
L.MEL.MN26.WI	ACTACAAGCGCTAACACTACAAGTGTTGCGTTAATA-CGCACGA----CGACTATGCTTA

[illegible]

F.CONIFERA.MA	CATCTCGTAGATTCAATTGCTTGTTC----	AAAACCCATACGTGCGT-GCGTGTGGTCA
P.BRACHIATA.WI	-----TAGCTGCAATCACTTGCTGACTGAATCCACACGTGCGT-TCGTGTGGTGG	
L.CER.SAM.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.CIB.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.DEV.OR	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.DEVD.OR	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MINTO.OR	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.EHT02.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN01.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN10.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN02.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN26.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN20.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN27.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN23.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN13.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MELMN16.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN34.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN24.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN29.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLNT01.NH	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLNT07.NH	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLNT04.NH	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.ETH06.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLN06.NH	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.ETH04.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLNT03.NH	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.ETH05.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLNT08.NH	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLNT02.NH	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLNT10.NH	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FLNT10B.N	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN01B.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN08C.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.NISKEY.GA	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.CANLK.GA	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.BEVIEW.GA	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.LAUREN.GA	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.STP.GA	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN32.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN43.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN31.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN08B.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MN06B.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.ETH04B.NM	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FISHCP.FL	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FISHLK.FL	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.FISHCP01.	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.TIM.OR	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.SIT4.FL	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.WRW2.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.WRW1.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.MINLK.WI	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.GLASS.UT	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.BOXFORD.M	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.CP02.SC	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.CP01.SC	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.CP03.SC	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.BALBOA.CA	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.AMD.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG
L.MEL.INK.TX	-----TCATAATCGTCATCT----	TATAACCATACTTGCTTCGAGTATGGTCG

L.MEL.BASLK.TX -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.KRM.FL -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.CRLRD.TX -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.RAT02.NM -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.RAT02B.NM -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.JAC.FL -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.LKO.FL -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.NIOC03.OK -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.STA05.OK -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.NIOC04.OK -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.NIOC01.OK -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.NIOC02.OK -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.STA02.OK -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG
 L.MEL.STA01.OK -----TCATAATCGTCATCT----TATAACCATACTTGCTTCGAGTATGGTCG

F.CONIFERA.MA GGTACCTACGAGTTTACGTAT-----ACGTAAACATAAACGTTCAAT--GAGTG
 P.BRACHIATA.WI GGTACCTATGCGTTTATGTATATTACTTGATATGCATAACATAAGCGTTCAAT--GCGTA
 L.CER.SAM.TX GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.CIB.TX GGTACCTTTGCGTTTGTGTTTC-----ATCACACAAACATAAGCGTTCAATCCTATGA
 L.MEL.DEV.OR GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.DEVD.OR GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MINTO.OR GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.EHT02.TX GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN01.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
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 L.MEL.MN26.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN20.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN27.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN23.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN13.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MELMN16.TX GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN34.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN24.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN29.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.FLNT01.NH GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.FLNT07.NH GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.FLNT04.NH GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.ETH06.TX GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
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 L.MEL.FLNT10.NH GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.FLNT10B.N GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN01B.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN08C.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.NISKEY.GA GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.CANLK.GA GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.BEVIEW.GA GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.LAUREN.GA GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.STP.GA GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN32.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN43.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN31.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN08B.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.MN06B.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.ETH04B.NM GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.FISHCP.FL GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA
 L.MEL.FISHLK.FL GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCCTACGA

L.MEL.FISHCP01. GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCATTCTCTACGA
 L.MEL.TIM.OR GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCATTCTCTACGA
 L.MEL.SIT4.FL GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCATTCTCTACGA
 L.MEL.WRW2.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCATTCTCTACGA
 L.MEL.WRW1.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCATTCTCTACGA
 L.MEL.MINLK.WI GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCATTCTCTACGA
 L.MEL.GLASS.UT GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCATTCTCTACGA
 L.MEL.BOXFORD.M GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCATTCTCTACGA
 L.MEL.CP02.SC GGTACCTTTGCGTTTGTGTTTC-----ACCACGCAAACATAAGCGTTCAATCTCTACGA
 L.MEL.CP01.SC GGTACCTTTGCGTTTGTGTTTC-----ACCACGCAAACATAAGCGTTCAATCTCTACGA
 L.MEL.CP03.SC GGTACCTTTGCGTTTGTGTTTC-----ACCACGCAAACATAAGCGTTCAATCTCTACGA
 L.MEL.BALBOA.CA GGTACCTTTGCGTTTGTGTTTC-----ACCACGCAAACATAAGCGTTCAATCTCTACGA
 L.MEL.AMD.TX GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.INK.TX GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.BASLK.TX GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.KRM.FL GGTACCTTTGCGTTTGTGTTTC-----ACCACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.CRLRD.TX GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.RAT02.NM GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.RAT02B.NM GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.JAC.FL GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.LKO.FL GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.NIOC03.OK GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.STA05.OK GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.NIOC04.OK GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.NIOC01.OK GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.NIOC02.OK GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.STA02.OK GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA
 L.MEL.STA01.OK GGTACCTTTGCGTTTGTGTTTC-----ACTACACAAACATAAGCGTTCAATCTCTACGA

F.CONIFERA.MA TTGATCGTGAAGGTGTAAAGATCATATTTATTTATGACGCCGTGATCCGCTTAAACACT
 P.BRACHIATA.WI TTGATCGTGAAGGTGTAAAGATCATTTGTAATGATGACGCCCTTTTGC-----TTAAA
 L.CER.SAM.TX TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGCTAATTTTAAAT
 L.MEL.CIB.TX TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.DEV.OR TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.DEVD.OR TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.MINTO.OR TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.EHT02.TX TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN01.WI TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN10.WI TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN02.WI TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN26.WI TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
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 L.MEL.MN27.WI TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
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 L.MEL.MN13.WI TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
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 L.MEL.FLNT02.NH TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
 L.MEL.FLNT10.NH TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT
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 L.MEL.MN01B.WI TTGATCGTGAAGGTGTAAAGATCAGT----AAAATGACGCCCGCTTGCGATAATTTTAAAT

L.MEL.MN08C.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.NISKEY.GA TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.CANLK.GA TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.BEVIEU.GA TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.LAUREN.GA TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.STP.GA TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN32.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN43.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN31.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN08B.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.MN06B.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.ETH04B.NM TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.FISHCP.FL TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.FISHLK.FL TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.FISHCP01. TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.TIM.OR TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.SIT4.FL TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.WRW2.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.WRW1.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.MINLK.WI TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.GLASS.UT TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.BOXFORD.M TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.CP02.SC TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.CP01.SC TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.CP03.SC TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.BALBOA.CA TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.AMD.TX TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.INK.TX TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.BASLK.TX TTGATCGTGAAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.KRM.FL TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.CRLRD.TX TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.RAT02.NM TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.RAT02B.NM TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.JAC.FL TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.LKO.FL TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.NIOC03.OK TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.STA05.OK TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.NIOC04.OK TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.NIOC01.OK TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.NIOC02.OK TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.STA02.OK TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT
 L.MEL.STA01.OK TTGATCGTGGAGGTGTAAAGATCAGT-----AAAATGACGCCCCGCTTGCGATAATTTTAAAT

F.CONIFERA.MA TGCATTTTATTTTATTTTCATCGCTAATGCTATTTCGCGTTGTGAATGT-----
 P.BRACHIATA.WI ATCCTTTTATTATTTTCA-----TGTTTTCCATTGCTACAGCT-ACTTTGTTGTGA
 L.CER.SAM.TX TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGATTGTGTGAAT-ACGCTGGTACTA
 L.MEL.CIB.TX TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGCTACTA
 L.MEL.DEV.OR TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.DEVD.OR TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MINTO.OR TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.EHT02.TX TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN01.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN10.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN02.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN26.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN20.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN27.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN23.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN13.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MELMN16.TX TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN34.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN24.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA

L.MEL.MN29.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.FLNT01.NH TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.FLNT07.NH TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.FLNT04.NH TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.ETH06.TX TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.FLN06.NH TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
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 L.MEL.FLNT10B.N TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN01B.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN08C.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.NISKEY.GA TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.CANLK.GA TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.BEVIEW.GA TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.LAUREN.GA TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.STP.GA TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN32.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN43.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN31.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN08B.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MN06B.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.ETH04B.NM TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.FISHCP.FL TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.FISHLK.FL TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.FISHCP01. TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.TIM.OR TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.SIT4.FL TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.WRW2.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.WRW1.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.MINLK.WI TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.GLASS.UT TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.BOXFORD.M TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.CP02.SC TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ATGCTGGTACTA
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 L.MEL.CP03.SC TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ATGCTGGTACTA
 L.MEL.BALBOA.CA TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ATTCTGGTACTA
 L.MEL.AMD.TX TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.INK.TX TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAATAACGCTGGTACTA
 L.MEL.BASLK.TX TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAATAACGCTGGTACTA
 L.MEL.KRM.FL TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
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 L.MEL.RAT02.NM TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.RAT02B.NM TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
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 L.MEL.LKO.FL TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.NIOC03.OK TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.STA05.OK TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.NIOC04.OK TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
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 L.MEL.STA02.OK TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA
 L.MEL.STA01.OK TGATTCTTACTATTTTAAATTGTTATTTATGTTGTGCTTGTGTGAAT-ACGCTGGTACTA

F.CONIFERA.MA -----GTACGTTGGTTTATTTTAAATTCACCTGAATTAACACTACTACTAACGTC
 P.BRACHIATA.WI ATGTG----TAAACGTTTTCTAATTTCTAATTAGATGACGT-----T
 L.CER.SAM.TX AAGTACTGTTGCACATTGTTATGCGTTTAGCATGTAAGACGTATTAAGGTATCGGCTAAA
 L.MEL.CIB.TX AAGTACTGTTGCACATTGTTATGCAATTAACATGTAAGACGTATTAAGGTATCGGCTAAA
 L.MEL.DEV.OR AAGTACTGTTGCACATTGTTATGCGTTTAAACATGTAAGACGTATTAAGGTATCGGCTAAA

[illegible]

L.MEL.NIOC03.OK AAGTACTGTTGCACATTGTTATGCGTTTAAACATGTAAGACGTATTAAAGTATCGGCTTAA
L.MEL.STA05.OK AAGTACTGTTGCACATTGTTATGCGTTTAAACATGTAAGACGTATTAAAGTATCGGCTTAA
L.MEL.NIOC04.OK AAGTACTGTTGCACATTGTTATGCGTTTAAACATGTAAGACGTATTAAAGTATCGGCTTAA
L.MEL.NIOC01.OK AAGTACTGTTGCACATTGTTATGCGTTTAAACATGTAAGACGTATTAAAGTATCGGCTTAA
L.MEL.NIOC02.OK AAGTACTGTTGCACATTGTTATGCGTTTAAACATGTAAGACGTATTAAAGTATCGGCTTAA
L.MEL.STA02.OK AAGTACTGTTGCACATTGTTATGCGTTTAAACATGTAAGACGTATTAAAGTATCGGCTTAA
L.MEL.STA01.OK AAGTACTGTTGCACATTGTTATGCGTTTAAACATGTAAGACGTATTAAAGTATCGGCTTAA

F.CONIFERA.MA AAACAAACACAAAACACAACCCCTATGCGGTGGATCACTTGGCTCGCGAGTCGATGAAGAG
P.BRACHIATA.WI AGCTCAACACAAAACACAACCCCTATGCGGTGGATCACTTGGCTCGCGAGTCGATGAAGAG
L.CER.SAM.TX ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.CIB.TX ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.DEV.OR ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.DEVD.OR ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MINTO.OR ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.EHT02.TX ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN01.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
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L.MEL.MN02.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN26.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN20.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN27.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN23.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN13.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MELMN16.TX ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN34.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN24.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN29.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.FLNT01.NH ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
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L.MEL.FLNT04.NH ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.ETH06.TX ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.FLN06.NH ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
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L.MEL.FLNT03.NH ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.ETH05.TX ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
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L.MEL.FLNT10B.N ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN01B.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN08C.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.NISKEY.GA ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.CANLK.GA ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.BEVIEW.GA ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.LAUREN.GA ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.STP.GA ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN32.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN43.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
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L.MEL.MN08B.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MN06B.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.ETH04B.NM ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.FISHCP.FL ACTGTAACACAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.FISHLK.FL ACTGTAACACAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.FISHCP01. ACTGTAACACAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.TIM.OR ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.SIT4.FL ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.WRW2.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.WRW1.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.MINLK.WI ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
L.MEL.GLASS.UT ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG

L.MEL.BOXFORD.M ACTGTAACACAAAATACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.CP02.SC ACTGTAACACAAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.CP01.SC ACTGTAACACAAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.CP03.SC ACTGTAACACAAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.BALBOA.CA ACTGTAACACAAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.AMD.TX ACTGTAACACAAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
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 L.MEL.BASLK.TX ACTGTAACACAAAATTACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
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 L.MEL.JAC.FL ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.LKO.FL ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.NIOC03.OK ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.STA05.OK ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.NIOC04.OK ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.NIOC01.OK ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.NIOC02.OK ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.STA02.OK ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG
 L.MEL.STA01.OK ACTGTAACACAAAACACAACCCCTATGCGGTGGATCACTAGGCTCGCGAGTCGATGAAGAG

F.CONIFERA.MA CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 P.BRACHIATA.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.CER.SAM.TX CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.CIB.TX CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.DEV.OR CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.DEVD.OR CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.MINTO.OR CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.EHT02.TX CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.MN01.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
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 L.MEL.MN26.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.MN20.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.MN27.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
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 L.MELMN16.TX CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.MN34.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.MN24.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.MN29.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.FLNT01.NH CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
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 L.MEL.FLNT10B.N CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
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 L.MEL.MN08C.WI CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
 L.MEL.NISKEY.GA CGCAGCAAAGTGCGTGAATTAATGTGATTGTCAGGACACATTGATCATCGATATCTTGAA
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 P.BRACHIATA.WI CGCATATTGCGGTTACGGTTCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGTTTAAATA
 L.CER.SAM.TX CGCATATTGCGGTTACGGTTCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGTTTACATA
 L.MEL.CIB.TX CGCATATTGCGGTTACGGTTCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGTTTACATA
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 L.MEL.DEVD.OR CGCATATTGCGGTTACGGTTCGCTTCCGTGACCACGCCTGTCTGAGGGTCGGTTTACATA
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 L.CER.SAM.TX TGTCTATACGTGAAAAGTG TGCT--CGCAC TTTTGCTCGGTCGTTTTAAGTGAGCT----
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 L.MEL.DEV.OR TGTCTATACGTGAAAAGTG TGCT--CGCAC TTTTGCTCGGTCGTTTTAAGTGAGCT----
 L.MEL.DEVD.OR TGTCTATACGTGAAAAGTG TGCT--CGCAC TTTTGCTCGGTCGTTTTAAGTGAGCT----
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F.CONIFERA.MA	ATTGCTTTTATCGACTTTAGATACAT-ATTTACTAATCTCTATAGTTAGTAAAAAATGCA
P.BRACHIATA.WI	ATTGCTTTTATCGACTTTAGATACATGAATACTAGTCTCTATAGATTAGT-AAAAATGCA
L.CER.SAM.TX	CTCACTTTTATCGACTTTAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.CIB.TX	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.DEV.OR	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.DEVD.OR	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MINTO.OR	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.EHT02.TX	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN01.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN10.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN02.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN26.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN20.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN27.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN23.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN13.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MELMN16.TX	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN34.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN24.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN29.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLNT01.NH	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLNT07.NH	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLNT04.NH	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.ETH06.TX	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLN06.NH	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.ETH04.TX	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLNT03.NH	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.ETH05.TX	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLNT08.NH	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLNT02.NH	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLNT10.NH	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FLNT10B.N	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN01B.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN08C.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.NISKEY.GA	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.CANLK.GA	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.BEVIEW.GA	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.LAUREN.GA	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.STP.GA	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN32.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN43.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN31.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN08B.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MN06B.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.ETH04B.NM	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FISHCP.FL	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FISHLK.FL	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.FISHCP01.	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.TIM.OR	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.SIT4.FL	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.WRW2.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.WRW1.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.MINLK.WI	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.GLASS.UT	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.BOXFORD.M	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.CP02.SC	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.CP01.SC	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.CP03.SC	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.BALBOA.CA	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.AMD.TX	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA
L.MEL.INK.TX	CTCACTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAAATTAGT-AAAAATGCA

L.MEL.BASLK.TX CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.KRM.FL CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.CRLRD.TX CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.RAT02.NM CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.RAT02B.NM CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.JAC.FL CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.LKO.FL CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.NIOC03.OK CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.STA05.OK CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.NIOC04.OK CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
 L.MEL.NIOC01.OK CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA
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 L.MEL.STA01.OK CTCACCTTTTATCGACTTCAGATCTATGGATTACTAATTCGTAAAATTAGT-AAAAATGCA

F.CONIFERA.MA TA-----AAATAGCATTCTAGCTGTTGCTTTTCGCGCTATTAAATGCTGATCACAAAACAA
 P.BRACHIATA.WI TAAGAACTAGCAGTA-TTACTTTGTT-----GCTTCTCGTATGCTATTCACAAAACAA
 L.CER.SAM.TX TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA----CAAGCAA
 L.MEL.CIB.TX TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAGCAA
 L.MEL.DEV.OR TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.DEVD.OR TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MINTO.OR TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.EHT02.TX TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN01.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN10.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN02.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN26.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN20.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN27.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
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 L.MELMN16.TX TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN34.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
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 L.MEL.FLNT07.NH TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.FLNT04.NH TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.ETH06.TX TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
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 L.MEL.FLNT10.NH TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.FLNT10B.N TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN01B.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN08C.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.NISKEY.GA TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.CANLK.GA TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.BEVIEW.GA TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.LAUREN.GA TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.STP.GA TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN32.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN43.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN31.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN08B.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.MN06B.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.ETH04B.NM TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.FISHCP.FL TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA
 L.MEL.FISHLK.FL TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA----CAAACAA

L.MEL.FISHCP01. TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA-----CAAACAA
 L.MEL.TIM.OR TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA-----CAAACAA
 L.MEL.SIT4.FL TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA-----CAAACAA
 L.MEL.WRW2.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA-----CAAACAA
 L.MEL.WRW1.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA-----CAAACAA
 L.MEL.MINLK.WI TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA-----CAAACAA
 L.MEL.GLASS.UT TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA-----CAAACAA
 L.MEL.BOXFORD.M TA-----TAGTAGCACTCAATTCGAT-----TGCTAATGAATGCTAA-----CAAACAA
 L.MEL.CP02.SC TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA-----CAAGCAA
 L.MEL.CP01.SC TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA-----CAAGCAA
 L.MEL.CP03.SC TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA-----CAAGCAA
 L.MEL.BALBOA.CA TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA-----CAAGCAA
 L.MEL.AMD.TX TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA-----CAAGCAA
 L.MEL.INK.TX TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA-----CAAGCAA
 L.MEL.BASLK.TX TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA-----CAAGCAA
 L.MEL.KRM.FL TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTAA-----CAAGCAA
 L.MEL.CRLRD.TX TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.RAT02.NM TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.RAT02B.NM TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.JAC.FL TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.LKO.FL TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.NIOC03.OK TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.STA05.OK TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.NIOC04.OK TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.NIOC01.OK TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.NIOC02.OK TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.STA02.OK TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA
 L.MEL.STA01.OK TA-----TAGTAGCACTCAATTTGAT-----TGCTAATGAATGCTTA-----CAAACAA

F.CONIFERA.MA AAATTGCTTAGCGTATCTTATTTGTTTTGATGATCTAGTGTTTGATACACAGT---TTG
 P.BRACHIATA.WI AAATTGCTTAGCTAACTTCGTTTGTTGAT-AGTGATATAAGTAATGCATGCTT---GTT
 L.CER.SAM.TX AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAACTTTCATTTTGTGTTG
 L.MEL.CIB.TX AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.DEV.OR AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.DEVD.OR AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MINTO.OR AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.EHT02.TX AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN01.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN10.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN02.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
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 L.MEL.MN20.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN27.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
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 L.MEL.MN13.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MELMN16.TX AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN34.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
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 L.MEL.FLNT04.NH AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
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 L.MEL.FLNT02.NH AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.FLNT10.NH AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.FLNT10B.N AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN01B.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG

L.MEL.MN08C.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.NISKEY.GA AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.CANLK.GA AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.BEVIEU.GA AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
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 L.MEL.STP.GA AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN32.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN43.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN31.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN08B.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MN06B.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.ETH04B.NM AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.FISHCP.FL AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.FISHLK.FL AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.FISHCP01.L AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.TIM.OR AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.SIT4.FL AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.WRW2.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.WRW1.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.MINLK.WI AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.GLASS.UT AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.BOXFORD.M AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.CP02.SC AAATTGCTTAGCT-ATTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.CP01.SC AAATTGCTTAGCT-ATTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.CP03.SC AAATTGCTTAGCT-ATTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.BALBOA.CA AAATTGCTTAGCT-ATTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.AMD.TX AAATTGCTTAGCT-ATTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.INK.TX AAATTGCTTAGCT-ATTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.BASLK.TX AAATTGCTTAGCT-ATTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.KRM.FL AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.CRLRD.TX AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.RAT02.NM AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.RAT02B.NM AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.JAC.FL AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.LKO.FL AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.NIOC03.OK AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.STA05.OK AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.NIOC04.OK AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.NIOC01.OK AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.NIOC02.OK AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.STA02.OK AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG
 L.MEL.STA01.OK AAATTGCTTAGCT-CTTTAATTTGTTTGC-TTAGCTTCGTAGTTAGCTTTCATT---TTG

F.CONIFERA.MA TGAATGCTGTAAAAAACTATGCTTACAACACAAAAATTTTAT-TTTATTCGACCTC
 P.BRACHIATA.WI TAA-----CTATGCTAAGCTAAAGAATTAATTTTTTTTTTGTCTTTTCGACCTC
 L.CER.SAM.TX TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTTAAAGTGC
 L.MEL.CIB.TX TTG-----CTATACTAG-----TAATATGCTTGTACTTTTTTAAAGTGC
 L.MEL.DEV.OR TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.DEVD.OR TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MINTO.OR TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.EHT02.TX TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN01.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN10.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN02.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN26.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN20.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN27.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN23.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN13.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN16.TX TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN34.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC
 L.MEL.MN24.WI TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTTAAAGTGC

L.MEL.MN29.WI	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLNT01.NH	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLNT07.NH	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLNT04.NH	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.ETH06.TX	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLN06.NH	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.ETH04.TX	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLNT03.NH	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.ETH05.TX	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLNT08.NH	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLNT02.NH	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLNT10.NH	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FLNT10B.N	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.MN01B.WI	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.MN08C.WI	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.NISKEY.GA	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.CANLK.GA	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.BEVIEW.GA	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.LAUREN.GA	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.STP.GA	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.MN32.WI	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.MN43.WI	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.MN31.WI	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.MN08B.WI	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.MN06B.WI	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.ETH04B.NM	TTG-----TTATACTAG-----TAATATGTTTGTACTTTTTAAAGTGC
L.MEL.FISHCP.FL	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.FISHLK.FL	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.FISHCP01.	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.TIM.OR	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.SIT4.FL	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.WRW2.WI	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.WRW1.WI	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.MINLK.WI	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.GLASS.UT	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.BOXFORD.M	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.CP02.SC	TTG-----TTATACTAT-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.CP01.SC	TTG-----TTATACTAT-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.CP03.SC	TTG-----TTATACTAT-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.BALBOA.CA	TTG-----TTATACTAT-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.AMD.TX	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.INK.TX	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.BASLK.TX	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.KRM.FL	TTG-----TTATACTAG-----TAATATGCTTGTACTTTTTAAAGTGC
L.MEL.CRLRD.TX	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.RAT02.NM	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.RAT02B.NM	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.JAC.FL	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.LKO.FL	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.NIOC03.OK	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.STA05.OK	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.NIOC04.OK	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.NIOC01.OK	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.NIOC02.OK	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.STA02.OK	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC
L.MEL.STA01.OK	TTG-----TTTATACTAG-----TATTATGCTTGTACTTTTTAAAGTGC

Supplemental document S2.9: CLUSTAL format alignment of COI sequences of *Collothea campanulata* by MAFFT v 7.380. Abbreviations are the same as Tables S2.3.

C.TENUIOBATA.GA	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C.CAM.MN.WI	ATAAGAGTTATTATTCGTTTAGAGCTAGGAGTTGTTGGTTCCTTTATCTCTGATGATCAT
C.CAM.FLNT.NH	ATGAGAGTTTTGATTCGTGTGCAATTAGGTGTTGTTGGTTCCTTTATTTCTGATGAGCAC
C.CAM.NOCKSP.PA	ATGAGAGTTTTGATTCGTGTGCAATTAGGTGTTGTTGGTTCCTTTATTTCTGATGAGCAC
C.CAM.FISHCAMP.FL	ATGAGAGTTTTGATTCGTGTGCAATTAGGTGTTGTTGGTTCCTTTATTTCTGATGAGCAC
C.CAM.JACKSON.FL	ATGAGAGTTTTGATTCGTGTGCAATTAGGTGTTGTTGGTTCCTTTATTTCTGATGAGCAC
C.CAM.KRM01.FL	ATGAGAGTTTTGATTCGTGTGCAATTAGGTGTTGTTGGTTCCTTTATTTCTGATGAGCAC
C.CAM.KRM02.FL	ATGAGAGTTTTGATTCGTGTGCAATTAGGTGTTGTTGGTTCCTTTATTTCTGATGAGCAC
C.CAM.WRW.WI	ATAAGAGTTTTGATTCGTGTAGAATTGGGTGTAGTAGGTTCAATTTATCTCTGATGAGCAT
C.CAM.EW01.ND	ATAAGAGTTTTGATTCGTGTAGAATTGGGTGTAGTAGGTTCAATTTATCTCTGATGAGCAT
C.CAM.EW03.ND	ATAAGAGTTTTGATTCGTGTAGAATTGGGTGTAGTAGGTTCAATTTATCTCTGATGAGCAT
C.CAM.EW05.ND	ATAAGAGTTTTGATTCGTGTAGAATTGGGTGTAGTAGGTTCAATTTATCTCTGATGAGCAT
C.CAM.EW06.ND	ATAAGAGTTTTGATTCGTGTAGAATTGGGTGTAGTAGGTTCAATTTATCTCTGATGAGCAT
C.CAM.GLASSMAN.UT	ATAAGAGTTTTGATTCGTGTAGAATTGGGTGTAGTAGGTTCAATTTATCTCTGATGAGCAT
C.CAM.CRS.OK	ATAAGAGTTTTGATTCGTGTAGAATTAGGTGTAGTAGGCTCAATTTATTTCTGATGAGCAC
C.CAM.DEVILSD.OR	ATAAGGGTGTTAATTCGTGTAGAGTTAGGGGTGTTGGCTCAATTTATTTCTGATGAACAT
C.CAM.MINT01.OR	ATAAGGGTGTTAATTCGTGTAGAGTTAGGGGTGTTGGCTCAATTTATTTCTGATGAACAT
C.CAM.MINT02.OR	ATAAGGGTGTTAATTCGTGTAGAGTTAGGGGTGTTGGCTCAATTTATTTCTGATGAACAT
C.CAM.DEVILSD02.OR	ATAAGGGTGTTAATTCGTGTAGAGTTAGGGGTGTTGGCTCAATTTATTTCTGATGAACAT
C.CAM.DRAGON.OR	ATAAGGGTGTTAATTCGTGTAGAGTTAGGGGTGTTGGCTCAATTTATTTCTGATGAACAT
C.CAM.LOASTLAKE.MN	ATAAGGGTCTTAATTCGTGTAGAGTTAGGGGTGTTGGCTCAATTTATTTCTGATGAACAT
C.CAM.COT.TX	ATGAGTGTTTTGATTCGAGTAGAGTTAGGTGTTACGGGCTCTTTTATTGGTGATGATCAT
C.CAM.TURTLEBASKING01.MN	ATAAGGGTGTTGATTCGTGTTGAGCTGGGTGTTACTGGTTCCTTTTATTGGTGATGATCAT
C.CAM.TURTLEBASKING02.MN	ATAAGGGTGTTGATTCGTGTTGAGCTGGGTGTTACTGGTTCCTTTTATTGGTGATGATCAT
C.CAM.GENBANK	ATAAGAGTTATTATTCGTATTGAATTAGGTATTGTGGGAGGTTTTATTTCTGATTCTCAC
C.FEROX.NH	ATAAGTGTTATTATTCGTATTGAATTGGGAGTTTTAGGCACCTTTATTTTCAGACGAACAT
C.TENUIOBATA.GA	GTTTATAACGTAGTAGTCACTGCTCACGCCCTTTATTATAATTTTTTTCATGGCTATGCCC
C.CAM.MN.WI	ATTTATAATGTTCTTGTTACGGCTCATGCTTTCGTTATAATCTTTTTTATAGTTATGCCT
C.CAM.FLNT.NH	ATTTATAATGTTCTGGTCACAGCACATGCGTTTATTATAATTTTCTTTATAGTAATGCCT
C.CAM.NOCKSP.PA	ATTTATAATGTTCTGGTCACAGCACATGCGTTTATTATAATTTTCTTTATAGTAATGCCT
C.CAM.FISHCAMP.FL	ATTTATAATGTTCTGGTCACAGCACATGCGTTTATTATAATTTTCTTTATAGTAATGCCT
C.CAM.JACKSON.FL	ATTTATAATGTTCTAGTCACAGCACATGCATTTATTATAATTTTCTTCATAGTAATGCCT
C.CAM.KRM01.FL	ATTTATAATGTTCTAGTCACAGCACATGCATTTATTATAATTTTCTTTATAGTAATGCCT
C.CAM.KRM02.FL	ATTTATAATGTTCTAGTCACAGCACATGCATTTATTATAATTTTCTTTATAGTAATGCCT
C.CAM.WRW.WI	ATTTATAATGTTTTGGTCACTGCTCATGCATTTATTATGATTTTCTTTATAGTTATGCCC
C.CAM.EW01.ND	ATTTATAATGTTTTGGTCACTGCTCATGCATTTATTATGATTTTCTTTATAGTTATGCCC
C.CAM.EW03.ND	ATTTATAATGTTTTGGTCACTGCTCATGCATTTATTATGATTTTCTTTATAGTTATGCCC
C.CAM.EW05.ND	ATTTATAATGTTTTGGTCACTGCTCATGCATTTATTATGATTTTCTTTATAGTTATGCCC
C.CAM.EW06.ND	ATTTATAATGTTTTGGTCACTGCTCATGCATTTATTATGATTTTCTTTATAGTTATGCCC
C.CAM.GLASSMAN.UT	ATTTATAATGTTTTGGTCACTGCTCATGCATTTATTATGATTTTCTTTATAGTTATGCCC
C.CAM.CRS.OK	ATTTATAATGTTTTGGTCACTGCTCATGCGTTTATCATAATTTTCTTTATGGTTATGCCT
C.CAM.DEVILSD.OR	ATTTATAATGTTTTAGTAACAGCTCATGCGTTTATTATAATTTTTTTTATGGTAATACCA
C.CAM.MINT01.OR	ATTTATAATGTTTTAGTAACAGCTCATGCGTTTATTATAATTTTTTTTATGGTAATACCA
C.CAM.MINT02.OR	ATTTATAATGTTTTAGTAACAGCTCATGCGTTTATTATAATTTTTTTTATGGTAATACCA
C.CAM.DEVILSD02.OR	ATTTATAATGTTTTAGTAACAGCTCATGCGTTTATTATAATTTTTTTTATGGTAATACCA
C.CAM.DRAGON.OR	ATTTATAATGTTTTAGTAACAGCTCATGCGTTTATTATAATTTTTTTTATGGTAATACCA
C.CAM.LOASTLAKE.MN	ATTTATAATGTTTTAGTAACAGCTCATGCGTTTATTATAATTTTTTTTATGGTAATACCA
C.CAM.COT.TX	CTTTACAATGTTTTGGTCACAGCTCATGCTTTTGTTATAATTTTTTTTATAGTTATACCA
C.CAM.TURTLEBASKING01.MN	CTATACAACGTTTTGGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTCATACCC
C.CAM.TURTLEBASKING02.MN	CTATACAACGTTTTGGTTACTGCTCATGCTTTTGTTATAATTTTTTTTATAGTCATACCC
C.CAM.GENBANK	ATTTACAATGTTATTGTAACAGCTCACGCTTTTGTTGATGATTTTTTTTATGGTGATACCT
C.FEROX.NH	ATTTATAATGTTATTGTTACAGCTCATGCTTTTGTTATAATTTTCTTTATAGTAATACCT
C.TENUIOBATA.GA	ATGGCTGTAGGTGGTTTTGGAACTGACTGATTCCTTTAATATTGGGCTCTCTGATATG

C.CAM.MN.WI	ATGGCTATTGGAGGCTTTGGAACTGATTAATCCCTATAAATTAGGTTGTGTTGATATA
C.CAM.FLNT.NH	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGCTAGGGTGTGTTGATATG
C.CAM.NOCKSP.PA	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGCTAGGGTGTGTTGATATA
C.CAM.FISHCAMP.FL	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGCTAGGGTGTGTTGATATA
C.CAM.JACKSON.FL	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTCATGTTAGGGTGTGTTGATATA
C.CAM.KRM01.FL	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTCATGTTAGGGTGTGTTGATATA
C.CAM.KRM02.FL	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTCATGTTAGGGTGTGTTGATATA
C.CAM.WRW.WI	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.EW01.ND	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.EW03.ND	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.EW05.ND	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.EW06.ND	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.GLASSMAN.UT	GTTGCTATTGGTGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.CRS.OK	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.DEVILSD.OR	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.MINT01.OR	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.MINT02.OR	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.DEVILSD02.OR	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.DRAGON.OR	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.LOASTLAKE.MN	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.COT.TX	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.TURTLEBASKING01.MN	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.TURTLEBASKING02.MN	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.GENBANK	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG
C.CAM.FEROX.NH	GTTGCTATTGGGTTTTGGTAACTGACTTATCCCTCTTATGTTAGGGTGTGTTGATATG

C.TENUIOBATA.GA	GTATTTCCACGAATAAATAATTTATCTTTTTGGCTTCTTGTCCCCTCTTTTACACTCCTG
C.CAM.MN.WI	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGATTATTGATTCCTTCTTTTAGATTATTA
C.CAM.FLNT.NH	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.NOCKSP.PA	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.FISHCAMP.FL	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.JACKSON.FL	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTACCTTCTTTTCTTTATTA
C.CAM.KRM01.FL	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTACCTTCTTTTCTTTATTA
C.CAM.KRM02.FL	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTACCTTCTTTTCTTTATTA
C.CAM.WRW.WI	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.EW01.ND	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.EW03.ND	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.EW05.ND	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.EW06.ND	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.GLASSMAN.UT	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.CRS.OK	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.DEVILSD.OR	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.MINT01.OR	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.MINT02.OR	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.DEVILSD02.OR	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.DRAGON.OR	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.LOASTLAKE.MN	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.COT.TX	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.TURTLEBASKING01.MN	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.TURTLEBASKING02.MN	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.GENBANK	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA
C.CAM.FEROX.NH	GTATTTCCCTCGTATAAATAATCTTTCTTTTTGGTTGCTTGTTCCTTCTTTTCTTTATTA

C.TENUIOBATA.GA	CTTTTATCCTCAGTAGTTGATTCTGAGGAGCAGGTACAGGCTGAACTGTGTATCCTCCCCCTC
C.CAM.MN.WI	TTATTGTCTTCTTATTGATTCTGGGGCTGGAAGTGGTGGACAGTGTACCCCCCTTTA
C.CAM.FLNT.NH	TTACTTTCTAGTTTAGTTGATTCTGGGGCTGGTACGGGTGGACTGTTTACCTCCTTTA
C.CAM.NOCKSP.PA	TTACTTTCTAGTTTAGTTGATTCTGGGGCTGGTACGGGTGGACTGTTTACCTCCTTTA
C.CAM.FISHCAMP.FL	TTACTTTCTAGTTTAGTTGATTCTGGGGCTGGTACGGGTGGACTGTTTACCTCCTTTA
C.CAM.JACKSON.FL	TTACTTTCTAGTTTAGTTGATTCTGGGGCTGGTACGGGTGGACTGTTTACCTCCTTTA
C.CAM.KRM01.FL	TTACTTTCTAGTTTAGTTGATTCTGGGGCTGGTACGGGTGGACTGTTTACCTCCTTTA
C.CAM.KRM02.FL	TTACTTTCTAGTTTAGTTGATTCTGGGGCTGGTACGGGTGGACTGTTTACCTCCTTTA

C.CAM.WRW.WI	TTACTTTCTAGTTTAGTTGATTCTGGGGCAGGTACTGGCTGAACTGTTTATCCCCCTTTA
C.CAM.EW01.ND	TTACTTTCTAGTTTAGTTGATTCTGGGGCAGGTACTGGCTGAACTGTTTATCCCCCTTTA
C.CAM.EW03.ND	TTACTTTCTAGTTTAGTTGATTCTGGGGCAGGTACTGGCTGAACTGTTTATCCCCCTTTA
C.CAM.EW05.ND	TTACTTTCTAGTTTAGTTGATTCTGGGGCAGGTACTGGCTGAACTGTTTATCCCCCTTTA
C.CAM.EW06.ND	TTACTTTCTAGTTTAGTTGATTCTGGGGCAGGTACTGGCTGAACTGTTTATCCCCCTTTA
C.CAM.GLASSMAN.UT	TTACTTTCTAGTTTAGTTGATTCTGGGGCAGGTACTGGCTGAACTGTTTATCCCCCTTTA
C.CAM.CRS.OK	CTTCTTTCTAGTTTAGTTGATTCTGGTGCTGGTACAGGTTGAACTGTGTATCCCCCTCTG
C.CAM.DEVILSD.OR	TTACTATCTAGTTTAGTTGACTCTGGGGCAGGCACTGGTTGAACTGTTTATCCTCCTTTG
C.CAM.MINT01.OR	TTACTATCTAGTTTAGTTGACTCTGGGGCAGGCACTGGTTGAACTGTTTATCCTCCTTTG
C.CAM.MINT02.OR	TTACTATCTAGTTTAGTTGACTCTGGGGCAGGCACTGGTTGAACTGTTTATCCTCCTTTG
C.CAM.DEVILSD02.OR	TTACTATCTAGTTTAGTTGACTCTGGGGCAGGCACTGGTTGAACTGTTTATCCTCCTTTG
C.CAM.DRAGON.OR	TTACTATCTAGTTTAGTTGACTCTGGGGCAGGCACTGGTTGAACTGTTTATCCTCCTTTG
C.CAM.LOASTLAKE.MN	TTACTATCTAGTTTAGTTGACTCTGGGGCAGGCACTGGTTGAACTGTTTACCCTCCTTTG
C.CAM.COT.TX	CTTCTCTCTGCTTTAGTTGACACTGGTGCTGGGACAGGTTGAACGGTTTATCCTCCTCTG
C.CAM.TURTLEBASKING01.MN	CTCTTATCTGCTTTGGTTGACACAGGTGCAGGAACAGGTTGAACTGTGTATCCTCCTCTT
C.CAM.TURTLEBASKING02.MN	CTCTTATCTGCTTTGGTTGACACAGGTGCAGGAACAGGTTGAACTGTGTATCCTCCTCTT
C.CAM.GENBANK	TTAGTATCTTCATTAGTTGATTCTGGGGCAGGTACGGGGTGGACTGTTTACCCCCCTCTA
C.FEROX.NH	TTATTATCTTCCCTTGTGGATTACAGGGCGGGTACTGGTTGAACAGTTTATCCCCCTCTG

C.TENUIOBATA.GA	TCTGACTTTAAATTTTCATTCTGGAGTTTCCGTCGACATGGCTATTTTTAGATTACATTTA
C.CAM.MN.WI	TCAGATGTCTCTTATCATTAGGTGTTTTCTGTTGATATGGCTATTTTTAGCCTTCATTTG
C.CAM.FLNT.NH	TCTGATTTTAAATATCATTCTGGTGTTTTCCGTTGACATGGCTATTTTTAGTCTTCATCTT
C.CAM.NOCKSP.PA	TCTGATTTTAAATATCATTCTGGTGTTTTCCGTTGACATGGCTATTTTTAGTCTTCATCTT
C.CAM.FISHCAMP.FL	TCTGATTTTAAATATCATTCTGGTGTTTTCCGTTGACATGGCTATTTTTAGTCTTCATCTT
C.CAM.JACKSON.FL	TCTGATTTTAAATATCATTCTGGTGTTTTCCGTCGATATGGCTATTTTTAGCCTTCATCTG
C.CAM.KRM01.FL	TCTGATTTTAAATATCATTCTGGTGTTTTCCGTCGATATGGCTATTTTTAGCCTTCATCTG
C.CAM.KRM02.FL	TCTGATTTTAAATATCATTCTGGTGTTTTCCGTCGATATGGCTATTTTTAGCCTTCATCTG
C.CAM.WRW.WI	TCTGATTTTAAATATCATTCTGGCGTGTCTGTTGATATAGCAATTTTTAGTCTTCATCTA
C.CAM.EW01.ND	TCTGATTTTAAAGTATCAGTCTGGTGCTGCTGTTGATATAGCAATTTTTAGTCTTCATTTA
C.CAM.EW03.ND	TCTGATTTTAAAGTATCAGTCTGGTGCTGCTGTTGATATAGCAATTTTTAGTCTTCATTTA
C.CAM.EW05.ND	TCTGATTTTAAAGTATCAGTCTGGTGCTGCTGTTGATATAGCAATTTTTAGTCTTCATTTA
C.CAM.EW06.ND	TCTGATTTTAAAGTATCAGTCTGGTGCTGCTGTTGATATAGCAATTTTTAGTCTTCATTTA
C.CAM.GLASSMAN.UT	TCTGATTTTAAAGTATCAGTCTGGTGCTGCTGTTGATATAGCAATTTTTAGTCTTCATTTA
C.CAM.CRS.OK	TCTGATTTCAAATATCATTCTGGGGTGTCTGTTGATATGGCAATTTTTAGTCTTCATCTA
C.CAM.DEVILSD.OR	TCCGACTTTAAATATCATTCTGGGGTCTCAGTTGATATGGCTATTTTTAGTCTTCATCTC
C.CAM.MINT01.OR	TCCGACTTTAAATATCATTCTGGGGTCTCAGTTGATATGGCTATTTTTAGTCTTCATCTC
C.CAM.MINT02.OR	TCCGACTTTAAATATCATTCTGGGGTCTCAGTTGATATGGCTATTTTTAGTCTTCATCTC
C.CAM.DEVILSD02.OR	TCCGACTTTAAATATCATTCTGGGGTCTCAGTTGATATGGCTATTTTTAGTCTTCATCTC
C.CAM.DRAGON.OR	TCCGACTTTAAATATCATTCTGGGGTCTCAGTTGATATGGCTATTTTTAGCCTTCATCTC
C.CAM.LOASTLAKE.MN	TCCGACTTTAAATATCATTCTGGGGTCTCAGTTGATATGGCTATTTTTAGTCTTCATCTC
C.CAM.COT.TX	TCTGATGTGAAGTTTCATTCTGGCATTTCGTGCGATTTGGCTATTTTCAGTTTACACATT
C.CAM.TURTLEBASKING01.MN	TCAGATATTAATTTTCATTCTGGGGTTCCTGGGATTTAGCTATTTTTAGTTTGCATGTT
C.CAM.TURTLEBASKING02.MN	TCAGATATTAATTTTCATTCTGGGGTTCCTGGGATTTAGCTATTTTTAGTTTGCATGTT
C.CAM.GENBANK	TCAGACTACAAGTTTTCATTACAGGGGTTTCAGTAGATATGGCAATTTTTAGTCTTCATTTG
C.FEROX.NH	TCTGATTATAAATTTTCATTCTGGTGATCTGTTGACATAGCAATTTTTAGTCTTCATTTA

C.TENUIOBATA.GA	GCCGGAGTAAGCTCTATTCTAGGCTCAATTAATTTTTTAACCACTATTTTAGTTGCCCGC
C.CAM.MN.WI	GCTGGAGTGAGGTCAATTCTAGGTTCAATTAATTTTTATCAACAATTATTTGTGCTCGT
C.CAM.FLNT.NH	GCGGGGGTTAGCTCTATTCTGGTTCTATTAATTTTTATCGACTGTAATTTGTAGTCGT
C.CAM.NOCKSP.PA	GCGGGGGTTAGCTCTATTCTGGTTCTATTAATTTTTATCGACTGTAATTTGTAGTCGT
C.CAM.FISHCAMP.FL	GCGGGGGTTAGCTCTATTCTGGTTCTATTAATTTTTATCGACTGTAATTTGTAGTCGT
C.CAM.JACKSON.FL	GCGGGGGTTAGTTCTATTCTGGCTCTATTAATTTTTATCGACAGTAATTTGTAGTCGT
C.CAM.KRM01.FL	GCGGGGGTTAGTTCTATTCTGGCTCTATTAATTTTTATCGACAGTAATTTGTAGTCGT
C.CAM.KRM02.FL	GCGGGGGTTAGTTCTATTCTGGCTCTATTAATTTTTATCGACAGTAATTTGTAGTCGT
C.CAM.WRW.WI	GCTGGAGTCAGTTCAATTTTAGGTTCTATTAATTTCTTGCTACTGTAATTTGTAGTCGT
C.CAM.EW01.ND	GCTGGAGTCAGTTCAATTTTAGGTTCTATTAATTTCTTGCTACTGTAATTTGTAGTCGT
C.CAM.EW03.ND	GCTGGAGTCAGTTCAATTTTAGGTTCTATTAATTTCTTGCTACTGTAATTTGTAGTCGT
C.CAM.EW05.ND	GCTGGAGTCAGTTCAATTTTAGGTTCTATTAATTTCTTGCTACTGTAATTTGTAGTCGT
C.CAM.EW06.ND	GCTGGAGTCAGTTCAATTTTAGGTTCTATTAATTTCTTGCTACTGTAATTTGTAGTCGT
C.CAM.GLASSMAN.UT	GCTGGAGTCAGTTCAATTTTAGGTTCTATTAATTTCTTGCTACTGTAATTTGTAGTCGT
C.CAM.CRS.OK	GCTGGTGAGGTCTATTTTAGGTTCTATTAATTTTTATCTACTGTAATTTGTAGTCGT

C.CAM.DEVILSD.OR	GCAGGGGTTAGCTCTATTTTAGGGTCTATTAATTTCCCTATCTACTGTAATTTGTAGTCGT
C.CAM.MINT01.OR	GCAGGGGTTAGCTCTATTTTAGGGTCTATTAATTTCCCTATCTACTGTAATTTGTAGTCGT
C.CAM.MINT02.OR	GCAGGGGTTAGCTCTATTTTAGGGTCTATTAATTTCCCTATCTACTGTAATTTGTAGTCGT
C.CAM.DEVILSD02.OR	GCAGGGGTTAGCTCTATTTTAGGGTCTATTAATTTCCCTATCTACTGTAATTTGTAGTCGT
C.CAM.DRAGON.OR	GCAGGGGTTAGCTCTATTTTAGGGTCTATTAATTTCCCTATCTACTGTAATTTGTAGCCGT
C.CAM.LOASTLAKE.MN	GCAGGGGTTAGCTCTATTTTAGGGTCTATTAATTTCCCTATCTACTGTAATTTGTAGTCGT
C.CAM.COT.TX	GCTGGTGCAAGTTCAATTATAGGCTCAATTAATTTCTTATCAACTATTATTTGTGCTCGT
C.CAM.TURTLEBASKING01.MN	GCTGGTGCTAGTTCAATTATAGGTTCTATTAACCTTTATATCTACTATTATTTGTGCTCGC
C.CAM.TURTLEBASKING02.MN	GCTGGTGCTAGTTCAATTATAGGTTCTATTAACCTTTATATCTACTATTATTTGTGCTCGC
C.CAM.GENBANK	GCAGGTGTTAGTTCTATTTTAGGTTCAATTAACCTTTTTGTCCACTATTATTTGTGCTCGT
C.FEROX.NH	GCTGGTATTAGTTCAATCTTGGGCTCTATTAATTTCTTGACAACCTATTATCACTGCTCGG

C.TENUIOBATA.GA	TCTGATTATTCTTACACACTTAGTCTCCTCCCTTATTTTTATGATCTATTATTATTACT
C.CAM.MN.WI	AGCACTTTTAAAGTTTACATTAGACTATTTACCTTTATTTCTGTGGGCTGTTTCTATTACA
C.CAM.FLNT.NH	AGCTCTTTTAAAATTCAAGGTCGATTATCTTCCTTTATTTCTTTGAGCTGTTTCTATTACA
C.CAM.NOCKSP.PA	AGCTCTTTTAAAATTCAAGGTCGATTATCTTCCTTTATTTCTTTGAGCTGTTTCTATTACA
C.CAM.FISHCAMP.FL	AGTTCCTTTGAAATTCAAGGTCGATTATCTTCCTTTATTTCTTTGAGCTGTTTCTATTACA
C.CAM.JACKSON.FL	AGTTCCTTTGAAATTCAAGGTCGATTATCTTCCTTTATTTCTTTGAGCTGTTTCTATTACG
C.CAM.KRM01.FL	AGTTCCTTTGAAATTCAAGGTCGATTATCTTCCTTTATTTCTTTGAGCTGTTTCTATTACG
C.CAM.KRM02.FL	AGTTCCTTTGAAATTCAAGGTCGATTATCTTCCTTTATTTCTTTGAGCTGTTTCTATTACG
C.CAM.WRW.WI	AGCAGTTTAAAGTTTAAAGTTGATTATCTTCCTTTATTTCTTTGGGCAGTGTCTATTACA
C.CAM.EW01.ND	AGCAGTCTAAAGTTTAAAGTTGATTACCTTCCTTTATTTCTTTGGGCAGTGTCTATCACA
C.CAM.EW03.ND	AGCAGTCTAAAGTTTAAAGTTGATTACCTTCCTTTATTTCTTTGGGCAGTGTCTATCACA
C.CAM.EW05.ND	AGCAGTCTAAAGTTTAAAGTTGATTACCTTCCTTTATTTCTTTGGGCAGTGTCTATCACA
C.CAM.EW06.ND	AGCAGTCTAAAGTTTAAAGTTGATTACCTTCCTTTATTTCTTTGGGCAGTGTCTATCACA
C.CAM.GLASSMAN.UT	AGTAGTTTAAAGTTTAAAGTTGATTATCTTCCTTTATTTCTTTGAGCAGTTTCTATTACG
C.CAM.CRS.OK	AGTAGTTTAAAGTTTAAAGTTGATTATCTTCCTTTATTTCTTTGAGCAGTTTCTATTACG
C.CAM.DEVILSD.OR	AGTAGTTTAAAGTTTAAAGTTGATTACTTGCCTTTATTCCTTTGGGCTGTTTCTATTACG
C.CAM.MINT01.OR	AGTAGTTTAAAGTTTAAAGTTGATTACTTGCCTTTATTCCTTTGGGCTGTTTCTATTACG
C.CAM.MINT02.OR	AGTAGTTTAAAGTTTAAAGTTGATTACTTGCCTTTATTCCTTTGGGCTGTTTCTATTACG
C.CAM.DEVILSD02.OR	AGTAGTTTAAAGTTTAAAGTTGATTACTTGCCTTTATTCCTTTGGGCTGTTTCTATTACG
C.CAM.DRAGON.OR	AGTAGTTTAAAGTTTAAAGTTGATTACTTGCCTTTATTCCTTTGGGCTGTTTCTATTACG
C.CAM.LOASTLAKE.MN	AGTAGTTTAAAGTTTAAAGTTGATTACTTGCCTTTATTCCTTTGGGCTGTTTCTATTACG
C.CAM.COT.TX	TCTTCTGATAAGTTTTCTATTGATATATTGCCTTTGTTTTGTGGGCTGTTGCTATTACA
C.CAM.TURTLEBASKING01.MN	TCTTCTGGTAAAGTTTTCCATCGATATGCTTCCTTTATTTCTTTGGGCTGTTTCTATTACT
C.CAM.TURTLEBASKING02.MN	TCTTCTGGTAAAGTTTTCCATCGATATGCTTCCTTTATTTCTTTGGGCTGTTTCTATTACT
C.CAM.GENBANK	TCGAGCTCTAAGTTTATGATTAGATCATATTCCTCTTTTCCCTTTGGGCTGTGCTATTACA
C.FEROX.NH	GCTAATTCCAAGTTTTCTGTTGATTATTTACCTTTATTCCTTTGGGCTATTGTTGTAACA

C.TENUIOBATA.GA	GCTATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACCATGCTTTTAAACA
C.CAM.MN.WI	GCTATTTTATTGATTTTAAAGTTTACCTGTATTAGCTGGTGCTATCACCATGCTTCTTACA
C.CAM.FLNT.NH	GCTATCTTACTTATTCTAAGACTACCAGTTTATAGCTGGTGGTATTACCATGCTATTGACT
C.CAM.NOCKSP.PA	GCTATCTTACTTATTCTAAGACTACCAGTTTATAGCTGGTGGTATTACTATGCTATTGACT
C.CAM.FISHCAMP.FL	GCTATCTTACTTATTCTAAGACTACCAGTTTATAGCTGGTGGTATTACTATGCTATTGACT
C.CAM.JACKSON.FL	GCTATTCTACTTATTTTAAAGATTGCCTGTTTTAGCTGGCGGTATTACCATGCTATTGACT
C.CAM.KRM01.FL	GCTATTCTACTTATTTTAAAGATTGCCCGTTTTAGCTGGCGGTATTACCATGCTATTGACT
C.CAM.KRM02.FL	GCTATTCTACTTATTTTAAAGATTGCCCGTTTTAGCTGGCGGTATTACCATGCTATTGACT
C.CAM.WRW.WI	GCTATTTTACTTATTTTAAAGTTTACCAGTATTGGCTGGTGGTATTACTATGTTGTTAACA
C.CAM.EW01.ND	GCTATTTTACTTATTTTAAAGTTTACCAGTATTAGCTGGTGGTATTACTATGTTGTTAACA
C.CAM.EW03.ND	GCTATTTTACTTATTTTAAAGTTTACCAGTATTAGCTGGTGGTATTACTATGTTGTTAACA
C.CAM.EW05.ND	GCTATTTTACTTATTTTAAAGTTTACCAGTATTAGCTGGTGGTATTACTATGTTGTTAACA
C.CAM.EW06.ND	GCTATTTTACTTATTTTAAAGTTTACCAGTATTAGCTGGTGGTATTACTATGTTGTTAACA
C.CAM.GLASSMAN.UT	GCTATTTTACTTATTTTAAAGTTTACCAGTATTAGCTGGTGGTATTACTATGTTGTTAACA
C.CAM.CRS.OK	GCTATTTTACTTATTTTAAAGTTTACCTGTCTTGGCTGGGGGTATTACAATATTATTAACA
C.CAM.DEVILSD.OR	GCTATTCTCCTTATTTTGAAGTTTCCCTGTGTTAGCTGGTGAATCACTATGTTATTAAC
C.CAM.MINT01.OR	GCTATTCTCCTTATTTTGAAGTTTCCCTGTGTTAGCTGGTGAATCACTATGTTATTAAC
C.CAM.MINT02.OR	GCTATTCTCCTTATTTTGAAGTTTCCCTGTGTTAGCTGGTGAATCACTATGTTATTAAC
C.CAM.DEVILSD02.OR	GCTATTCTCCTTATTTTGAAGTTTCCCTGTGTTAGCTGGTGAATCACTATGTTATTAAC
C.CAM.DRAGON.OR	GCTATTCTCCTTATTTTGAAGTTTCCCTGTGTTAGCTGGTGAATCACTATGTTATTAACA
C.CAM.LOASTLAKE.MN	GCTATTCTCCTTATTTTGAAGTTTCCCTGTGTTAGCTGGTGAATCACTATGTTATTAACA
C.CAM.COT.TX	GCAATTTTACTAGTTTTTAAAGCTTACCTGTCTTAGCAGGTGCTATTACTATCTTTAACT

C.CAM.TURTLEBASKING01.MN	GCTATTTTGTAAATTTTGTAGTTTGCCCGTTCTAGCTGGCGCTATTACAATACTTCTTACT
C.CAM.TURTLEBASKING02.MN	GCTATTTTGTAAATTTTGTAGTTTGCCCGTTCTAGCTGGCGCTATTACAATACTTCTTACT
C.CAM.GENBANK	GCTATTCTATTGATCCTTAGTTTGCCGTGTATTAGCTGGTGCTATTACTATGCTTTTAAACA
C.FEROX.NH	GCTATTCTGTAAATCCTTACTCTTCTCTGTTCTAGCAGGGGCGATTACAATGCTACTAACT

C.TENUIOBATA.GA	GATCGAAATTTTAACACAAGCTTTTTTGTATCCAAGAGGCGGAGGAAATCCGGTTCTATAC
C.CAM.MN.WI	GATCGTAACTTTAATACTAGTTTTTTTTGATCCAAGGGGAGGGGGGAATCCTGTATTGTAC
C.CAM.FLNT.NH	GATCGTAATTTTAATACGAGTTTTTTTTGATCCTAGAGGAGGAGGTAATCCTATTTTGTAC
C.CAM.NOCKSP.PA	GATCGTAATTTTAATACGAGTTTTTTTTGATCCTAGAGGAGGAGGTAATCCTATTTTGTAC
C.CAM.FISHCAMP.FL	GATCGTAATTTTAATACGAGTTTTTTTTGATCCTAGAGGAGGAGGTAATCCTATTTTGTAC
C.CAM.JACKSON.FL	GATCGTAATTTTAATACAAGTTTTTTTTGATCCTAGGGGGGAGGAAACCTATTTTATAT
C.CAM.KRM01.FL	GATCGTAATTTTAATACAAGTTTTTTTTGATCCTAGGGGCGGAGGAAACCTATTTTATAT
C.CAM.KRM02.FL	GATCGTAATTTTAATACAAGTTTTTTTTGATCCTAGGGGCGGAGGAAACCTATTTTATAT
C.CAM.WRW.WI	GATCGTAATTTTAATACAAGTTTTTTTTGATCCTAGAGGAGGTGGTAATCCTATTTTATAC
C.CAM.EW01.ND	GATCGTAACTTTAATACAAGTTTTTTGACCCTAGAGGAGGGGGTAACCTATTTTATAC
C.CAM.EW03.ND	GATCGTAACTTTAATACAAGTTTTTTGACCCTAGAGGAGGGGGTAACCTATTTTATAC
C.CAM.EW05.ND	GATCGTAACTTTAATACAAGTTTTTTGACCCTAGAGGAGGGGGTAACCTATTTTATAC
C.CAM.EW06.ND	GATCGTAACTTTAATACAAGTTTTTTGACCCTAGAGGAGGGGGTAACCTATTTTATAC
C.CAM.GLASSMAN.UT	GATCGTAACTTTAATACAAGTTTTTTGACCCTAGAGGAGGGGGTAACCTATTTTATAC
C.CAM.CRS.OK	GATCGAACTTTTAATACAAGTTTTTTGATCCTAGAGGAGGGGGTAATCCTATTTTATAT
C.CAM.DEVILSD.OR	GATCGTAATTTTAATACTAGCTTTTTTGACCCAAGGGGAGGAGGTAATCCTATTTTATAC
C.CAM.MINT01.OR	GATCGTAATTTTAATACTAGCTTTTTTGACCCAAGGGGAGGAGGTAATCCTATTTTATAC
C.CAM.MINT02.OR	GATCGTAATTTTAATACTAGCTTTTTTGACCCAAGGGGAGGAGGTAATCCTATTTTATAC
C.CAM.DEVILSD02.OR	GATCGTAATTTTAATACTAGCTTTTTTGACCCAAGGGGAGGAGGTAATCCTATTTTATAC
C.CAM.DRAGON.OR	GATCGTAATTTTAATACTAGCTTTTTTGACCCAAGGGGGGAGGTAATCCTATTTTATAC
C.CAM.LOASTLAKE.MN	GATCGTAATTTTAATACTAGCTTTTTTGACCCAAGGGGGGAGGTAATCCTATTTTATAC
C.CAM.COT.TX	GATCGTAACTTTAACACCAGTTTTTTGATCCTAGGGGAGGAGGTAACCCAGTTTTATAC
C.CAM.TURTLEBASKING01.MN	GACCGGAATTTTAATACCAGTTTTTTGATCCTAGAGGGGCGGGAACCCAGTTCTTTAT
C.CAM.TURTLEBASKING02.MN	GACCGGAATTTTAATACCAGTTTTTTGATCCTAGAGGGGCGGGAACCCAGTTCTTTAT
C.CAM.GENBANK	GATCGAACTTTTAATACTAGCTTTTTTGACCCTAGTGGTGGTGGAAATCCAGTTTTATAT
C.FEROX.NH	GATCGTAACTTTAATACTAGTTTCTTCGACCCAAGAGGAGGGGGTAATCCTGTCTTTAC

C.TENUIOBATA.GA	CAGCATTTATTTTGATTTTTTG
C.CAM.MN.WI	CAGCATCTATTTTGATTTTTTG
C.CAM.FLNT.NH	CAACATTTATTTTGATTTTTTG
C.CAM.NOCKSP.PA	CAACATTTATTTTGATTTTTTG
C.CAM.FISHCAMP.FL	CAACATTTATTTTGATTTTTTG
C.CAM.JACKSON.FL	CAACATTTATTTTGATTTTTTG
C.CAM.KRM01.FL	CAACATTTATTTTGATTTTTTG
C.CAM.KRM02.FL	CAACATTTATTTTGATTTTTTG
C.CAM.WRW.WI	CAGCATTTATTTTGATTTTTTG
C.CAM.EW01.ND	CAGCATTTATTTTGATTTTTTG
C.CAM.EW03.ND	CAGCATTTATTTTGATTTTTTG
C.CAM.EW05.ND	CAGCATTTATTTTGATTTTTTG
C.CAM.EW06.ND	CAGCATTTATTTTGATTTTTTG
C.CAM.GLASSMAN.UT	CAGCATTTATTTTGATTTTTTG
C.CAM.CRS.OK	CAACATTTATTTTGATTTTTTG
C.CAM.DEVILSD.OR	CAGCATTTGTTTTGATTTTTTG
C.CAM.MINT01.OR	CAGCATTTGTTTTGATTTTTTG
C.CAM.MINT02.OR	CAGCATTTGTTTTGATTTTTTG
C.CAM.DEVILSD02.OR	CAGCATTTGTTTTGATTTTTTG
C.CAM.DRAGON.OR	CAGCATTTGTTTTGATTTTTTG
C.CAM.LOASTLAKE.MN	CAGCATTTGTTTTGATTTTTTG
C.CAM.COT.TX	CAGCATTTATTTTGATTTTTTG
C.CAM.TURTLEBASKING01.MN	CAGCATTTATTCTGATTTTTTG
C.CAM.TURTLEBASKING02.MN	CAGCATTTATTCTGATTTTTTG
C.CAM.GENBANK	CAACATCNNNNNNNNNNNNNNNN
C.FEROX.NH	CAACATCTGTTCTGATTTTTTG

Supplemental document S2.10: CLUSTAL format alignment of COI sequences of *Collothea ornata* by MAFFT v 7.380. Abbreviations are the same as Tables S2.4.

C. FEROX.NH	ATAAGAGTTATTATTCGTTTAGAGCTAGGAGTTGTTGGTTCTTTTATCTCTGATGATCAT
C. ORN. TENUILOBATA. GA	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C. ORN. PURGATORY. MN	ATAAGATTTATTATTCGTGTCGAGCTAGGTACTTATGGTTCATTCTTGTCTGACGAACAC
C. ORN. LKO. FL	ATAAGTGTAATTATTCGTATTGAGTTGGGTGTTGTAGGAAGTTTTATTTTCAGACGATCAT
C. ORN. RAT. MN	ATAAGTGTTATCATTCGTATTGAATTGGGTGTAGTAGGGAGCTTTATTTCTGATGATCAT
C. ORN. TRP. AZ	ATAAGTGTTATCATTCGTATTGAATTGGGTGTAGTAGGAAGCTTCATTTCTGATGACCAT
C. ORN. FLNT01. NH	ATAAGTGTCATCATTCGTATTGAATTGGGTGTAGTAGGAAGCTTTATTTCTGATGATCAT
C. ORN. FLNT02. NH	ATAAGTGTCATCATTCGTATTGAATTGGGTGTAGTAGGAAGCTTTATTTCTGATGATCAT
C. ORN. CRS02. OK	ATAAGTGTTATCATTCGTATTGAACTGGGTGTAGTAGGAAGCTTTATTTCTGATGATCAT
C. ORN. CRS01. OK	ATAAGTGTTATCATTCGTATTGAACTGGGTGTAGTAGGAAGCTTTATTTCTGATGATCAT
C. ORN. EMPIREPOND. MN	ATAAGTGTTATCATTCGTATTGAATTGGGTGTAGTAGGAAGCTTTATTTCTGATGATCAT
C. ORN. CROSBY. MN	ATAAGTGTTATCATTCGTATTGAATTGGGTGTAGTAGGAAGCTTTATTTCTGATGATCAT
C. ORN. LITTRA. AUSTRALIA	ATAAGAGTGATTATTCGTATTGAGTTGGGTGTCGTAGGAAGTTTTATTTCTGATGACCAT
C. ORN. MES01. TX	ATAAGGGTTGTTATTCGTATTGAGTTAGGTGTTGTTGGAAGTTTCATTTCTGATGACCAT
C. ORN. MES02. TX	ATAAGGGTTGTTATTCGTATTGAGTTAGGTGTTGTTGGAAGTTTCATTTCTGATGACCAT
C. ORN. RET02. TX	ATAAGGGTTGTTATTCGTATTGAGTTAGGTGTTGTTGGAAGTTTCATTTCTGATGACCAT
C. ORN. RET01. TX	ATAAGGGTTGTTATTCGTATTGAGTTAGGTGTTGTTGGAAGTTTCATTTCTGATGACCAT
C. ORN. DEVILSD. OR	ATAAGCGTTATTATTCGTGTTGAGCTAGGTGTTGTTGGTACATTTATTTCTGATGATCAC
C. ORN. STA. OK	ATAAGCGTTATTATTCGTGTTGAGCTAGGTGTTGTTGGTACATTTATTTCTGATGATCAC
C. ORN. MAS. MA	ATAAGCGTTATTATTCGTGTTGAGCTTGGTGTTGTTGGTACATTTATTTCTGATGATCAC
C. ORN. NORMAN. GA	ATAAGCGTTATTATTCGTGTTGAGCTTGGTGTTGTTGGTACATTTATTTCTGATGATCAC
C. ORN. TAMIAMI. FL	ATAAGAGTTATTATTCGTGTAGAATTAGGTGTTGTTGGTACTTTTATTTCTGATGATCAT
C. ORN. MORPHY. NM	ATGAGGGTGATTATTCGTGTGGAGCTGGGTGTGGTTGGTAGATTTCATTTCTGACGATCAT
C. ORN. DUBLIN. NH	ATAAGCGTTATTATTCGGGTAGAGTTAGGTGTTGGTTGGTACTTTTATTTCTGATGATCAT
C. ORN. SITE4. FL	ATAAGGGTTATCATCCGTATTGAGCTAGGCGTAGTAGGTAGTTTTATCTCTGACGATCAC
C. ORN. TULETANK. TX	ATAAGTGTAATTATTCGTGTAGAATTGGGGTAATCGGAAGTTTTATTTCTGATGACCAT
C. ORN. BAS. TX	ATAAGTGTTATAATTCCGAATTGAGTTGGGGGTATTAGGTAGGTTTATTTCTGACGATCAC
C. ORN. BOXFORD01. MA	ATAAGTGTTATTATTCGAATCGAATTGGGTGTGGTAGGGAGCTTTATTGGTGACGACCAT
C. ORN. BOXFORD02. MA	ATAAGAGTAATTATTCGTATTGAGTTAGGGTAATTGGCAGCTTTATTTCTGATGACCAT
C. ORN. FISHCAMP. FL	ATGAGAGTTATTATTCGAGTAGAATTAGGGGTCTTGGCCCATTTTTAGGAGACGACCAT
C. ORN. GLASSMAN. UT	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C. ORN. JUN. FL	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C. ORN. JACKSON. FL	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C. ORN. LAKEANNIE. FL	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C. ORN. KRM01. FL	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C. ORN. KRM02. FL	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATATGATGAGCAT
C. ORN. STP. GA	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C. ORN. NORMAN. GA	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAT
C. ORN. AMR01. CA	ATGAGTTTTATTATTCGTGTCGAGTTAGGAACCTATGGCTCATTTTTATCTGATGAACAT
C. ORN. AMR02. CA	ATGAGTTTTATTATTCGTGTCGAGTTAGGAACCTATGGCTCATTTTTATCTGATGAACAT
C. ORN. TLL. PA	ATGAGTTTTATTATTCGTGTCGAGTTAGGAACCTATGGCTCATTTTTATCTGATGAACAT
C. ORN. TLU. PA	ATGAGTTTTATTATTCGTGTCGAGTTAGGAACCTATGGCTCATTTTTATCTGATGAACAT
C. ORN. MN. WI	ATGAGTTTTATTATTCGTGTCGAGTTAGGAACCTATGGCTCATTTTTATCTGATGAACAT
C. ORN. WRW5. WI	ATGAGTTTTATTATTCGTGTCGAGTTANNNNCTTATGGCTCATTTTTATCTGATGAACAT
C. ORN. BLUE. OR	ATAAGTTTTATTATTCGTGTTGAGTTAGGAACCTATGGCTCATTTCTATCTGATGAACAT
C. ORN. NOCKFS. PA	ATAAGTTTTATTATTCGTGTTGAGTTAGGAACCTATGGCTCATTTTTATCTGATGAACAT
C. ORN. HARRIS. MA	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAC
C. ORN. NATICOOK. NH	ATAAGGTTTATTATTCGTGTTGAGTTAGGAACCTACGGCTCATTTTTATCTGATGAGCAC
C. ORN. PURGATORY. MN	ATAAGATTTATTATTCGTGTCGAGCTAGGTACTTATGGTTCATTCTTGTCTGACGAACAC
C. ORN. CROSBY. MN	ATAAGATTTATTATTCGTGTCGAGCTAGGTACTTATGGTTCATTCTTGTCTGACGAACAC
C. ORN. ROUNDPOND. NH	ATAAGTTTCATTATTCGTGTTGAATTAGGAACCTATGGTTCATTTTTATCTGATGAGCAT
C. ORN. TIMBERDITCH. OR	ATAAGATTTATCATTCGAGTTGAACCTCGGTACTTATGGTACTTTCTATCTGATGACCAT
C. ORN. DRAGON. MN	ATAAGTTTTATTATTCGTGTTGAGCTAGGCATTTATGGTGC GTTCTCTCAGATGATCAT

C.FEROX.NH
 C.ORN.TENUILOBATA.GA
 C.ORN.PURGATORY.MN
 C.ORN.LKO.FL
 C.ORN.RAT.MN
 C.ORN.TRP.AZ
 C.ORN.FLNT01.NH
 C.ORN.FLNT02.NH
 C.ORN.CRS02.OK
 C.ORN.CRS01.OK
 C.ORN.EMPIREPOND.MN
 C.ORN.CROSBY.MN
 C.ORN.LITTRA.AUSTRALIA
 C.ORN.MES01.TX
 C.ORN.MES02.TX
 C.ORN.RET02.TX
 C.ORN.RET01.TX
 C.ORN.DEVILSD.OR
 C.ORN.STA.OK
 C.ORN.MAS.MA
 C.ORN.NORMAN.GA
 C.ORN.TAMIAMI.FL
 C.ORN.MORPHY.NM
 C.ORN.DUBLIN.NH
 C.ORN.SITE4.FL
 C.ORN.TULETANK.TX
 C.ORN.BAS.TX
 C.ORN.BOXFORD01.MA
 C.ORN.BOXFORD02.MA
 C.ORN.FISHCAMP.FL
 C.ORN.GLASSMAN.UT
 C.ORN.JUN.FL
 C.ORN.JACKSON.FL
 C.ORN.LAKEANNIE.FL
 C.ORN.KRM01.FL
 C.ORN.KRM02.FL
 C.ORN.STP.GA
 C.ORN.NORMAN.GA
 C.ORN.AMR01.CA
 C.ORN.AMR02.CA
 C.ORN.TLL.PA
 C.ORN.TLU.PA
 C.ORN.MN.WI
 C.ORN.WRW5.WI
 C.ORN.BLUE.OR
 C.ORN.NOCKFS.PA
 C.ORN.HARRIS.MA
 C.ORN.NATICOOK.NH
 C.ORN.PURGATORY.MN
 C.ORN.CROSBY.MN
 C.ORN.ROUNDPOND.NH
 C.ORN.TIMBERDITCH.OR
 C.ORN.DRAGON.MN

ATTTATAATGTTCTTGTTACGGCTCATGCTTTCGTTATAATCTTTTTTATAGTTATGCCT
 GTTTATAACGTAGTAGTCACTGCTCAGCCTTTATTATAATTTTTTTCATGGCTATGCCC
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 GTTTATAATGTTGTTGTACAGCTCATGCTTTTATTATGATTTTCTTTATGGCAATACCC

C.FEROX.NH
 C.ORN.TENUILOBATA.GA
 C.ORN.PURGATORY.MN
 C.ORN.LKO.FL
 C.ORN.RAT.MN
 C.ORN.TRP.AZ
 C.ORN.FLNT01.NH
 C.ORN.FLNT02.NH

ATGGCTATTGGAGGCTTTGGAACTGATTAATCCCTATAATATTAGGTTGTGTTGATATA
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 ATAGCAATTGGAGGATTTGGAACTGGCTAATTCCTATAATGTTAGGGTGTGTCGATATA

C.ORN.CRS02.OK	ATAGCAATTGGAGGGTTTGGAACTGGTTAATTCCTATAATGTTAGGGTGTGTTGATATG
C.ORN.CRS01.OK	ATAGCAATTGGAGGGTTTGGAACTGGTTAATTCCTATAATGTTAGGGTGTGTTGATATG
C.ORN.EMPIREPOND.MN	ATAGCAATTGGAGGATTTGGAACTGGCTAATTCCTATAATGTTAGGGTGTGTTGATATA
C.ORN.CROSBY.MN	ATAGCAATTGGAGGATTTGGAACTGACTAATTCCTATGATGTTAGGGTGTGTTGATATA
C.ORN.LITTRA.AUSTRALIA	ATGGCTATTGGAGGGTTTCGGTAATTGGTTGATTCCCTCTTATGCTGGGTTGTGTAGATATG
C.ORN.MES01.TX	ATGGCTATTGGCGGGTTTGGTAATTGATTAATCCCCTTAATGTTGGGTTGTGTTGATATG
C.ORN.MES02.TX	ATGGCTATTGGCGGGTTTGGTAATTGATTAATCCCCTTAATGTTGGGTTGTGTTGATATG
C.ORN.RET02.TX	ATGGCTATTGGCGGGTTTGGTAATTGATTAATCCCCTTAATGTTGGGTTGTGTTGATATG
C.ORN.RET01.TX	ATGGCTATTGGCGGGTTTGGTAATTGATTAATCCCCTTAATGTTGGGTTGTGTTGATATG
C.ORN.DEVILSD.OR	ATGGCAATTGGTGGTTTTGGCAATTGGTTGATTCCATTGATGTTAGGTTGTGTTGATATA
C.ORN.STA.OK	ATGGCAATTGGTGGTTTTGGCAATTGGTTGATTCCATTGATGTTAGGTTGTGTTGATATA
C.ORN.MAS.MA	ATGGCAATTGGTGGTTTTGGCAATTGGTTGATTCCATTGATGTTAGGTTGTGTTGATATA
C.ORN.NORMAN.GA	ATGGCAATTGGTGGTTTTGGCAATTGGTTGATTCCATTGATGTTAGGTTGTGTTGATATA
C.ORN.TAMIAMI.FL	ATGGCTATTGGTGGTTTTGGTAATTGACTAATTCATTAATGTTAGGGTGTGTAGATATA
C.ORN.MORPHY.NM	ATGGCTATTGGTGGGTTTTGGTAAGTGGTTAATTCCTCTTATATTAGGTTGTGTAGACATA
C.ORN.DUBLIN.NH	ATGGCTATTGGTGGTTTTGGTAAGTGGTTAATTCCTCTTATATTAGGGTGTGTGATATA
C.ORN.SITE4.FL	ATGGCTATCGGTGGTTTTGGCAATTGACTTATTCCTATAATGTTAGGCTGCGTAGATATA
C.ORN.TULETANK.TX	ATAGCAATTGGCGGGTTTCGGTAACGATTAAATTCCTTTAATATTAGGGTGTGTTGATATA
C.ORN.BAS.TX	ATGGCTGTGGGTGGGTTTCGGTAAGTGGCTGATTCCAATAATGCTGGGGTGTGTAGATATG
C.ORN.BOXFORD01.MA	ATAGCAATTGGTGGTTTTCGGAATTGACTTATCCCCTAATGCTAGGTTGTGTTGATATA
C.ORN.BOXFORD02.MA	ATAGCAATTGGTGGTTTTCGGAATTGACTTATCCCCTAATGCTAGGTTGTGTTGATATA
C.ORN.FISHCAMP.FL	ATGGCAATTGGTGGGTTTTGGTAATTGATTAATTCCTTTAATGTTAGGGTGTGTAGATATA
C.ORN.GLASSMAN.UT	ATGGCTATTGGTGGTTTTGGGAATTGATTGATTCCATTAATACTTGGGTGTGTAGATATG
C.ORN.JUN.FL	ATGGCTGTAGGTGGTTTTGGAACTGACTGATTCCCTTTAATATTGGGCTCTCCTGATATG
C.ORN.JACKSON.FL	ATGGCTGTAGGTGGTTTTGGAACTGACTGATTCCCTTTAATATTGGGCTCTCCTGATATG
C.ORN.LAKEANNIE.FL	ATGGCTGTAGGTGGTTTTGGAACTGACTGATTCCCTTTAATATTGGGCTCTCCTGATATG
C.ORN.KRM01.FL	ATGGCTGTAGGTGGTTTTGGAACTGACTGATTCCCTTTAATATTGGGCTCTCCTGATATG
C.ORN.KRM02.FL	ATGGCTGTAGGTGGTTTTGGAACTGACTGATTCCCTTTAATATTGGGCTCTCCTGATATG
C.ORN.STP.GA	ATGGCTGTAGGCGGTTTTGGGAAGTGGCTGATTCCCTTTAATATTGGGTTCTCCTGATATG
C.ORN.NORMAN.GA	ATGGCTGTAGGCGGTTTTGGGAAGTGGCTGATTCCCTTTAATATTGGGTTCTCCTGATATG
C.ORN.AMR01.CA	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTTTAATATTGGGTTCCCTGATATG
C.ORN.AMR02.CA	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTTTAATATTGGGTTCCCTGATATG
C.ORN.TLL.PA	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTTTAATATTGGGTTCCCTGATATG
C.ORN.TLU.PA	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTTTAATATTGGGTTCCCTGATATG
C.ORN.MN.WI	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTTTAATATTGGGTTCCCTGATATG
C.ORN.WRW5.WI	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTTTAATATTGGGTTCCCTGATATG
C.ORN.BLUE.OR	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTTTAATATTAGGTTCTCCTGATATG
C.ORN.NOCKFS.PA	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTTTAATATTGGGTTCCCTGATATG
C.ORN.HARRIS.MA	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTCTGATATTGGGTTCTCCTGATATA
C.ORN.NATICOOK.NH	ATAGCTGTAGGGGGTTTTGGAACTGGCTGATTCCCTCTGATATTGGGTTCTCCTGATATA
C.ORN.PURGATORY.MN	ATGGCTGTAGGAGGGTTTGGCAATTGATTGATTCCCTTTAATACTGGGCTCTCCTGATATG
C.ORN.CROSBY.MN	ATGGCTGTAGGAGGGTTTGGCAATTGATTAAATTCCTTTAATACTGGGCTCTCCTGATATG
C.ORN.ROUNDPOND.NH	ATAGCGGTAGGAGGTTTTGGTAAGTGGCTTATTCCTCTTATACTAGGTTCTCCCGACATA
C.ORN.TIMBERDITCH.OR	ATGGCTGTTGGAGGTTTTGGTAATTGATTAATTCCTCTCATGCTAGGTTCTCCTGATATA
C.ORN.DRAGON.MN	ATGGCTGTAGGAGGGTTTGGCAACTGGTTAATTCCTTTAATGCTCGGTTCCCCAGACATA

C.FEROX.NH	GTATTTCCCTCGTATAAATAATCTTTCTTTTGGATTATTGATTCCCTTCCTTTAGATTATTA
C.ORN.TENUILOBATA.GA	GTATTTCCACGAATAAATAATTTATCTTTTGGCTTCTTGTCCCTCTTTTACACTCCTG
C.ORN.PURGATORY.MN	GTTTTCCCTCGAATAAATAATCTGTCTTTTGGCTTCTTATTCCTTCTTTTACGCTTTTA
C.ORN.LKO.FL	GCATTTCCCCGTATAAACAATTTGTCTTTTCTGTTACTTATTCCTCCTTTTCTTTTATTG
C.ORN.RAT.MN	GCATTTCCCCGTATAAATAATCTCTCTTTTGGTTATTAATCCCTTCATTTAGTTTGTTA
C.ORN.TRP.AZ	GCATTTCCCCGTATAAATAATCTCTCTTTTGGTTACTAATCCCTTCATTTAGTTTGTTA
C.ORN.FLNT01.NH	GCATTTCCCTCGTATAAATAATCTCTCTTTTGGTTACTAATCCCTTCATTTAGTTTGTTA
C.ORN.FLNT02.NH	GCATTTCCCTCGTATAAATAATCTCTCTTTTGGTTACTAATCCCTTCATTTAGTTTGTTA
C.ORN.CRS02.OK	GCATTTCCCTCGTATAAATAATCTCTCTTTTGGTTATTAATTCCTTCATTTAGTTTGTTA
C.ORN.CRS01.OK	GCATTTCCCTCGTATAAATAATCTCTCTTTTGGTTATTAATTCCTTCATTTAGTTTGTTA
C.ORN.EMPIREPOND.MN	GCATTTCCCTCGTATAAATAATCTCTCTTTTGGTTACTAATCCCTTCATTTAGTTTGTTA
C.ORN.CROSBY.MN	GCATTTCCCTCGTATAAATAATCTCTCTTTTGGTTACTAATCCCTTCATTTAGTTTGTTA
C.ORN.LITTRA.AUSTRALIA	GCATTTCCCCGTATAAATAATTTGTCATTCTGGTTACTAATCCCTTCATTTCTCCTGCTG
C.ORN.MES01.TX	GCTTTTCCCCGTATGAATAACCTATCCTTTTGGCTTCTTATTCCTTCTTTTTCATTATTA
C.ORN.MES02.TX	GCTTTTCCCCGTATGAATAACCTATCCTTTTGGCTTCTTATTCCTTCTTTTTCATTATTA
C.ORN.RET02.TX	GCTTTTCCCCGTATGAATAATCTATCCTTTTGGCTTCTTATTCCTTCTTTTTCATTATTA

C.ORN.RET01.TX
C.ORN.DEVILSD.OR
C.ORN.STA.OK
C.ORN.MAS.MA
C.ORN.NORMAN.GA
C.ORN.TAMiami.FL
C.ORN.MORPHY.NM
C.ORN.DUBLIN.NH
C.ORN.SITE4.FL
C.ORN.TULETANK.TX
C.ORN.BAS.TX
C.ORN.BOXFORD01.MA
C.ORN.BOXFORD02.MA
C.ORN.FISHCAMP.FL
C.ORN.GLASSMAN.UT
C.ORN.JUN.FL
C.ORN.JACKSON.FL
C.ORN.LAKEANNIE.FL
C.ORN.KRM01.FL
C.ORN.KRM02.FL
C.ORN.STP.GA
C.ORN.NORMAN.GA
C.ORN.AMR01.CA
C.ORN.AMR02.CA
C.ORN.TLL.PA
C.ORN.TLU.PA
C.ORN.MN.WI
C.ORN.WRW5.WI
C.ORN.BLUE.OR
C.ORN.NOCKFS.PA
C.ORN.HARRIS.MA
C.ORN.NATICOOK.NH
C.ORN.PURGATORY.MN
C.ORN.CROSBY.MN
C.ORN.ROUNDPOND.NH
C.ORN.TIMBERDITCH.OR
C.ORN.DRAGON.MN

GCTTTTCCCGTATGAATAATCTATCCTTTTGGCTTCTTATTCCTTCTTTTTCATTATTA
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C.ORN.SITE4.FL
C.ORN.TULETANK.TX
C.ORN.BAS.TX
C.ORN.BOXFORD01.MA
C.ORN.BOXFORD02.MA
C.ORN.FISHCAMP.FL
C.ORN.GLASSMAN.UT
C.ORN.JUN.FL
C.ORN.JACKSON.FL
C.ORN.LAKEANNIE.FL
C.ORN.KRM01.FL
C.ORN.KRM02.FL
C.ORN.STP.GA
C.ORN.NORMAN.GA
C.ORN.AMR01.CA
C.ORN.AMR02.CA
C.ORN.TLL.PA
C.ORN.TLU.PA
C.ORN.MN.WI
C.ORN.WRW5.WI
C.ORN.BLUE.OR
C.ORN.NOCKFS.PA
C.ORN.HARRIS.MA
C.ORN.NATICOOK.NH
C.ORN.PURGATORY.MN
C.ORN.CROSBY.MN
C.ORN.ROUNDPOND.NH
C.ORN.TIMBERDITCH.OR
C.ORN.DRAGON.MN

C.FEROX.NH
C.ORN.TENUILOBATA.GA
C.ORN.PURGATORY.MN
C.ORN.LKO.FL
C.ORN.RAT.MN
C.ORN.TRP.AZ
C.ORN.FLNT01.NH
C.ORN.FLNT02.NH
C.ORN.CRS02.OK
C.ORN.CRS01.OK
C.ORN.EMPIREPOND.MN
C.ORN.CROSBY.MN
C.ORN.LITTRA.AUSTRALIA
C.ORN.MES01.TX
C.ORN.MES02.TX
C.ORN.RET02.TX
C.ORN.RET01.TX
C.ORN.DEVILSD.OR
C.ORN.STA.OK
C.ORN.MAS.MA
C.ORN.NORMAN.GA
C.ORN.TAMIAMI.FL
C.ORN.MORPHY.NM
C.ORN.DUBLIN.NH
C.ORN.SITE4.FL
C.ORN.TULETANK.TX
C.ORN.BAS.TX
C.ORN.BOXFORD01.MA
C.ORN.BOXFORD02.MA
C.ORN.FISHCAMP.FL
C.ORN.GLASSMAN.UT
C.ORN.JUN.FL

[illegible]

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GCCGGAGTAAGTTCTATTTTAGGCTCAATCAATTTTTTAACCACATATTTAGTTGCCCGC
GCCGGAGTAAGTTCTATTTTAGGCTCAATCAATTTTTTAACCACATATTTAGTTGCCCGC

C.ORN.TLL.PA
C.ORN.TLU.PA
C.ORN.MN.WI
C.ORN.WRW5.WI
C.ORN.BLUE.OR
C.ORN.NOCKFS.PA
C.ORN.HARRIS.MA
C.ORN.NATICOOK.NH
C.ORN.PURGATORY.MN
C.ORN.CROSBY.MN
C.ORN.ROUNDPOND.NH
C.ORN.TIMBERDITCH.OR
C.ORN.DRAGON.MN

C.FEROX.NH
C.ORN.TENUILOBATA.GA
C.ORN.PURGATORY.MN
C.ORN.LKO.FL
C.ORN.RAT.MN
C.ORN.TRP.AZ
C.ORN.FLNT01.NH
C.ORN.FLNT02.NH
C.ORN.CRS02.OK
C.ORN.CRS01.OKT
C.ORN.EMPIREPOND.MN
C.ORN.CROSBY.MN
C.ORN.LITTRA.AUSTRALIA
C.ORN.MES01.TX
C.ORN.MES02.TX
C.ORN.RET02.TX
C.ORN.RET01.TX
C.ORN.DEVILSD.OR
C.ORN.STA.OK
C.ORN.MAS.MA
C.ORN.NORMAN.GA
C.ORN.TAMIAMI.FL
C.ORN.MORPHY.NM
C.ORN.DUBLIN.NH
C.ORN.SITE4.FL
C.ORN.TULETANK.TX
C.ORN.BAS.TX
C.ORN.BOXFORD01.MA
C.ORN.BOXFORD02.MA
C.ORN.FISHCAMP.FL
C.ORN.GLASSMAN.UT
C.ORN.JUN.FL
C.ORN.JACKSON.FL
C.ORN.LAKEANNIE.FL
C.ORN.KRM01.FL
C.ORN.KRM02.FL
C.ORN.STP.GA
C.ORN.NORMAN.GA
C.ORN.AMR01.CA
C.ORN.AMR02.CA
C.ORN.TLL.PA
C.ORN.TLU.PA
C.ORN.MN.WI
C.ORN.WRW5.WI
C.ORN.BLUE.OR
C.ORN.NOCKFS.PA
C.ORN.HARRIS.MA
C.ORN.NATICOOK.NH
C.ORN.PURGATORY.MN

C. ORN. CROSBY. MN	TCTGACTATTCTTTTTCTCTTAGTCTTCTTCCTTTGTTTTTATGATCTATTGTATTACT
C. ORN. ROUNDPOND. NH	TCTGATTATTCTTTTACTCTAAGTCTTCTACCTTTATTTTTATGGTCTATTATAATTACA
C. ORN. TIMBERDITCH. OR	TCTGACTATTCTTTTACAGCCTTAGCTTACTACCTCTATTTTTATGATCTATTATAATTACA
C. ORN. DRAGON. MN	TCTGATTACTCATTTAGTCTTAGAATACTTCCTTTGTTTTTATGATCTATTATAATTACA

C. FEROX. NH	GCTATTTTATTGATTTTAAAGTTTACCTGTATTAGCTGGTGCTATCACCATGCTTCTTACA
C. ORN. TENUILOBATA. GA	GCTATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACCATGCTTTTAACA
C. ORN. PURGATORY. MN	GCTATTCTTTTGATTCTTTTCACTTCCTGTTTTAGCAGGTGCTATTACCATGCTTCTGACA
C. ORN. LKO. FL	GCGGTACTTCTAATTTTAAAGCTTGCCAGTTCTTGCCGGAGCAATCACCATACTATTAACA
C. ORN. RAT. MN	GCTGTGTTACTAATTTTAAAGCTTCTCTGTTTTAGCAGGCGCTATCACAATACTGCTGACT
C. ORN. TRP. AZ	GCTGTATTATTAATTTTAAAGCCTTCTCTGTTTTAGCAGGCGCCATCACTATGCTGTGACT
C. ORN. FLNT01. NH	GCTGTATTACTAATTTTAAAGCCTTCTCTGTCCTAGCAGGCGCTATTACTATGCTCCTAACT
C. ORN. FLNT02. NH	GCTGTATTACTAATTTTAAAGCCTTCTCTGTCCTAGCAGGCGCTATTACTATGCTCCTAACT
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C. ORN. EMPIREPOND. MN	GCTGTACTACTAATTTTAAAGCCTTCTCTGTTTTAGCGGGTGCTATTACTATGCTCCTAACT
C. ORN. CROSBY. MN	GCGGAATAACTAATTTTAAAGCCTTCTCTGTTTTAGCAGGCGCCATTACTATGCTCCTAACT
C. ORN. LITTRA. AUSTRALIA	GCTGTTTTACTAATTTTAAAGTTTCCCGTTTTAGCGGGGGCAATCACCATGTTACTTACT
C. ORN. MES01. TX	GCAGTTCTTTTAGTTTTAAAGCTACCTGTATTAGCGGGGGCTATCACCATGCTTTTAACC
C. ORN. MES02. TX	GCAGTTCTTTTAGTTTTAAAGCTACCTGTATTAGCGGGGGCTATCACCATGCTTTTAACC
C. ORN. RET02. TX	GCAGTTCTTTTAGTTTTAAAGCTACCTGTATTAGCGGGGGCTATCACCATGCTTTTAACC
C. ORN. RET01. TX	GCAGTTCTTTTAGTTTTAAAGCTACCTGTATTAGCGGGGGCTATCACCATGCTTTTAACC
C. ORN. DEVILSD. OR	GCTATTTTGTTAAATTCTAAGGTTGCCAGTCTTAGCAGGGGCAATTACTATGCTTTTAACC
C. ORN. STA. OK	GCTATTTTGTTAAATTCTAAGGTTGCCAGTCTTAGCAGGGGCAATTACTATGCTTTTAACC
C. ORN. MAS. MA	GCTATTTTATTGATTCTAAGGTTGCCAGTCTTAGCAGGGGCAATTACTATGCTTTTAACC
C. ORN. NORMAN. GA	GCTATTTTATTGATTCTAAGGTTGCCAGTCTTAGCAGGGGCAATTACTATGCTTTTAACC
C. ORN. TAMIAMI. FL	GCCATTTTATTGATTTTAAAGTTTGCCAGTATTAGCAGGGGCTATTACTATGCTTTTAACC
C. ORN. MORPHY. NM	GCTATTTTATTAATTCTAAGCTTGCCAGTTTTGCGAGGAGCAATCACCATGCTTTTAACC
C. ORN. DUBLIN. NH	GCTATTTTATTAATTTTAAAGGCTACCAGTATTAGCGGGTGCTATTACAATATTACTTACT
C. ORN. SITE4. FL	GCTGTTTTACTTATTCTAAGCCTACCAGTGCTTGCTGGTGCTATCACTATGCTCCTAACC
C. ORN. TULETANK. TX	GCAATTTTACTAATTTCTTTTACCTGTATTAGCTGGAGCAATTACTATGCTATTAAACC
C. ORN. BAS. TX	GCTGTTCTATTAAATTTTAAAGTTTACCAGTATTAGCTGGAGCTATCAATGCTTCACT
C. ORN. BOXFORD01. MA	GCTGTGTTGTTAGTTTTATCACTACCTGTTTTAGCCGGAGCTATCACAATATTGTTAACC
C. ORN. BOXFORD02. MA	GCTGTGTTGTTAGTTTTATCACTACCTGTTTTAGCCGGAGCTATCACAATATTGTTAACC
C. ORN. FISHCAMP. FL	GCCATTTTATTGATTTTGAGTTTACCAGTTCTAGCAGGTGCAATCACTATACTTTTAACC
C. ORN. GLASSMAN. UT	GCATTGTTGTTGGTGCTGAGTCTTCCGGTACTTGCTGGGGGTATTACCATGTTATTAACA
C. ORN. JUN. FL	GCTATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGGGCTATTACCATGCTTTTAACA
C. ORN. JACKSON. FL	GCTATTCTTTTGATTCTTTTCCCTCCCTGTTTTAGCAGGAGCTATTACCATGCTTTTAACA
C. ORN. LAKEANNIE. FL	GCTATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACCATGCTTTTAACA
C. ORN. KRM01. FL	GCTATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACCATGCTTTTAACA
C. ORN. KRM02. FL	GCTATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACCATGCTTTTAACA
C. ORN. STP. GA	GCTATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACG
C. ORN. NORMAN. GA	GCTATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACG
C. ORN. AMR01. CA	GCGATTCTTTTGATTCTTTCTCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. AMR02. CA	GCGATTCTTTTGATTCTTTCTCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. TLL. PA	GCGATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. TLU. PA	GCGATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. MN. WI	GCGATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. WRW5. WI	GCGATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. BLUE. OR	GCGATTCTTTTGATTCTTTCCCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. NOCKFS. PA	GCGATTCTTTTGATTCTTTCTCTCCCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. HARRIS. MA	GCGATTCTTTTGATTCTTTCCCTTCTCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. NATICOOK. NH	GCGATTCTTTTGATTCTTTCCCTTCTCTGTTTTAGCAGGAGCTATTACTATGCTTTTAACA
C. ORN. PURGATORY. MN	GCTATTCTTTTGATTCTTTTCACTTCTCTGTTTTAGCAGGTGCTATTACCATGCTTCTGACA
C. ORN. CROSBY. MN	GCTATTCTTTTGATTCTTTTCACTTCTCTGTTTTAGCAGGTGCTATTACCATGCTTCTGACA
C. ORN. ROUNDPOND. NH	GCAATTCTCCTTATCCTTTCTCTCCCTGTACTTGCAAGTGAATTACAATACTCTTAACC
C. ORN. TIMBERDITCH. OR	GCGGTTCTTCTTATTTTATCTTTACCAGTTCTTGCAAGGAGCTATTACTATACTTTTAACA
C. ORN. DRAGON. MN	GCAGTCTTGCTCATCTTGCTTTTACCTGTTCTTGCTGGTGCTATTACTATGCTCCTTACG

C. FEROX. NH	GATCGTAACTTTAATACTAGTTTTTTTATGATCCAAGGGGAGGGGGAATCCTGTATTGTAC
C. ORN. TENUILOBATA. GA	GATCGAAATTTTAAACACAAGCTTTTTTATGATCCAAGAGGCGGAGGAAATCCGGTCTATAC
C. ORN. PURGATORY. MN	GATCGTAACTTTAACAATACTAGTTTTTTTATGATCCAAGAGGCGGAGGAAATCCGGTCTTAC

C.ORN.LKO.FL	GATCGTAACTTTAATACAAGATTTTTGATCCAAGGGGTGGTGGTAATCCTGTCTTGTAT
C.ORN.RAT.MN	GACCGTAACTTCAATACTAGTTTTTTTGACCCAAGTGGTGGTGGTAATCCTGTGTTGTAT
C.ORN.TRP.AZ	GACCGTAACTTCAATACTAGTTTTTTTGACCCAAGTGGTGGTGGTAACCTGTGTTATAT
C.ORN.FLNT01.NH	GACCGTAACTTCAATACTAGTTTTTTTGATCCCAAGTGGTGGTGGTAATCCTGTATTATAC
C.ORN.FLNT02.NH	GACCGTAACTTCAATACTAGTTTTTTTGATCCCAAGTGGTGGTGGTAATCCTGTATTATAT
C.ORN.CRS02.OK	GACCGTAACTTCAATACTAGTTTTTTTGACCCAAGTGGTGGTGGTGGTAATCCTGTATTATAT
C.ORN.CRS01.OK	GACCGTAACTTCAATACTAGTTTTTTTGACCCAAGTGGTGGTGGTGGTAATCCTGTATTATAT
C.ORN.EMPIREPOND.MN	GACCGTAACTTCAATACTAGTTTTTTTGACCCAAGTGGTGGTGGTGGTAATCCTGTATTATAT
C.ORN.CROSBY.MN	GACCGTAACTTCAATACTAGTTTTTTTGACCCAAGTGGTGGTGGTGGTAATCCTGTATTATAT
C.ORN.LITTRA.AUSTRALIA	GATCGTAACTTTAACAAGTTTTTTGACCCAAGTGGTGGTGGTGGTAATCCTGTATTATAT
C.ORN.MES01.TX	GACCGTAACTTTAATACAAGTTTTTTTGATCCCAAGTGGTGGGGAACCCGGTTTTGTAT
C.ORN.MES02.TX	GACCGTAACTTTAATACAAGTTTTTTTGATCCCAAGTGGTGGGGAACCCGGTTTTGTAT
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C.ORN.RET01.TX	GACCGTAACTTCAATAACAAGTTTTTTTGATCCCAAGTGGTGGGGAACCCGGTTTTGTAT
C.ORN.DEVILSD.OR	GATCGAAACTTTAATACCAGATTCTTTGATCCTAGTGGTGGTGGTAATCCTGTGCTATAC
C.ORN.STA.OK	GATCGCAACTTTAATACCAGATTCTTTGATCCTAGTGGTGGTGGTAATCCTGTGCTATAC
C.ORN.MAS.MA	GATCGAAACTTTAATACCAGATTCTTTGATCCTAGTGGTGGTGGTAATCCTGTGCTATAC
C.ORN.NORMAN.GA	GATCGAAACTTTAATACCAGATTCTTTGATCCTAGTGGTGGTGGTAATCCTGTGCTATAC
C.ORN.TAMIAMI.FL	GATCGAAATTTTAAATACAAGATTCTTTGATCCTAGGGGAGGTGGTAATCCTGTTCTTTAC
C.ORN.MORPHY.NM	GATCGTAATTTTCAATACTAGTTTTTTTGATCCAAGGGGTGGTGGTAATCCTGTTCTTTAC
C.ORN.DUBLIN.NH	GATCGTAATTTTAACTAGTTTTTTTGACCCGAGAGGAGGTGGTAATCCGGTACTCTAC
C.ORN.SITE4.FL	GATCGAAACTTTAATACTAGCTTCTTTGACCCAGTGGTGGTGGTAATCCTGTACTTTAC
C.ORN.TULETANK.TX	GACCGTAACTTTAATACGAGTTTTTTGACCCAGAGGAGGTGGGAATCCTGTCTATAT
C.ORN.BAS.TX	GATCGTAATTTCAATAACCAGATTCTTCGACCCTAGTGGTGGTGGTAATCCTGTCTATAT
C.ORN.BOXFORD01.MA	GATCGCAATTTTAAATACTAGTTTTTTTGACCCAGAGGGGTGGTAATCCTGTCTATAC
C.ORN.BOXFORD02.MA	GATCGCAATTTTAAATACTAGTTTTTTTGACCCAGAGGGGTGGTAATCCTGTCTATAC
C.ORN.FISHCAMP.FL	GATCGTAATTTTAAATACTAGATTCTTCGACCCTAGAGGGGGGGAACCCGGTCTTATAC
C.ORN.GLASSMAN.UT	GATCGAAATTTTAAATACTANATTTTTTGACCCAAGGGGAGGGGGAATCCTATTTTATAT
C.ORN.JUN.FL	GATCGAAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGAGGAAATCCGGTCTATAC
C.ORN.JACKSON.FL	GATCGAAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGAGGAAATCCGGTCTATAC
C.ORN.LAKEANNIE.FL	GATCGAAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGAAATCCGGTCTATAC
C.ORN.KRM01.FL	GATCGAAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGAGGAAATCCGGTCTATAC
C.ORN.KRM02.FL	GATCGAAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGAGGAAATCCGGTCTATAC
C.ORN.STP.GA	GATCGAAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGAGGAAATCCGGTCTGTAC
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C.ORN.AMR01.CA	GATCGTAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
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C.ORN.TLL.PA	GATCGTAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
C.ORN.TLU.PA	GATCGTAATTTTAAACACNAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
C.ORN.MN.WI	GATCGTAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
C.ORN.WRW5.WI	GATCGTAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
C.ORN.BLUE.OR	GATCGTAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
C.ORN.NOCKFS.PA	GATCGTAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
C.ORN.HARRIS.MA	GATCGTAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
C.ORN.NATICOOK.NH	GATCGTAATTTTAAACACAAGCTTTTTTGATCCAAGAGGCGGGGGAAATCCGGTCTATAC
C.ORN.PURGATORY.MN	GATCGTAACTTTAACAAGTTTTTTTGACCCAGTGGGGGAGGAAATCCGGTCTTTTAC
C.ORN.CROSBY.MN	GATCGTAACTTTAACAAGTTTTTTTGACCCAGTGGGGGAGGAAATCCGGTCTTTTAC
C.ORN.ROUNDPOND.NH	GATCGTAATTTTAAACACCAGTTTTTTTGACCCAGTGGAGGAGGAAACCTGTCTTTAT
C.ORN.TIMBERDITCH.OR	GACCGTAACTTTAATACAAGCTTTTTTGACCCAAGGGGAGGAGGCAATCCAATTCTTTAT
C.ORN.DRAGON.MN	GACCGTAATTTTAAATACTAGCTTCTTTGATCCAAGGGGAGGAGGGAATCCAATTCTCTAC

C.FEROX.NH	CAGCATCTATTTTGATTTTTTG
C.ORN.TENUILOBATA.GA	CAGCATTTATTTTGATTTTTTG
C.ORN.PURGATORY.MN	CAGCATTTATTTTGATTTTTTG
C.ORN.LKO.FL	CAGCATTTGTTTTGATTTTTTG
C.ORN.RAT.MN	CAGCATTTATTTTGATTTTTTG
C.ORN.TRP.AZ	CAGCATTTATTTTGATTTTTTG
C.ORN.FLNT01.NH	CAGCATTTATTTTGATTTTTTG
C.ORN.FLNT02.NH	CAGCATTTATTTTGATTTTTTG
C.ORN.CRS02.OK	CAGCATTTATTTTGATTTTTTG
C.ORN.CRS01.OK	CAGCATTTATTTTGATTTTTTG
C.ORN.EMPIREPOND.MN	CAGCATTTATTTTGATTTTTTG

C.ORN.CROSBY.MN	CAGCATTTATTTTGATTTTTTG
C.ORN.LITTRA.AUSTRALIA	CAACACTTGTTTTGATTTTTTG
C.ORN.MES01.TX	CAACATTTATTTTGATTTTTTG
C.ORN.MES02.TX	CAACATTTATTTTGATTTTTTG
C.ORN.RET02.TX	CAACATTTATTTTGATTTTTTG
C.ORN.RET01.TX	CAACATTTATTTTGATTTTTTG
C.ORN.DEVILSD.OR	CAACATCTATTTTGATTTTTTG
C.ORN.STA.OK	CAACATCTATTTTGATTTTTTG
C.ORN.MAS.MA	CAACATCTATTTTGATTTTTTG
C.ORN.NORMAN.GA	CAACATCTATTTTGATTTTTTG
C.ORN.TAMIAMI.FL	CAGCACTTATTTTGATTTTTTG
C.ORN.MORPHY.NM	CAGCATTTATTTTGATTTTTTG
C.ORN.DUBLIN.NH	CAACATTTATTTTGATTTTTTG
C.ORN.SITE4.FL	CAGCATCTATTTTGATTTTTTG
C.ORN.TULETANK.TX	CAACATTTATTTCTGATTTTTTG
C.ORN.BAS.TX	CAACATTTATTTTGATTTTTTG
C.ORN.BOXFORD01.MA	CAGCACTTATTTTGATTTTTTG
C.ORN.BOXFORD02.MA	CAGCACTTATTTTGATTTTTTG
C.ORN.FISHCAMP.FL	CAGCATCTTTTTTGATTTTTTG
C.ORN.GLASSMAN.UT	CAACATCTTTTTTGATTTTTTG
C.ORN.JUN.FL	CAGCATTTATTTTGATTTTTTG
C.ORN.JACKSON.FL	CAGCATTTATTTTGATTTTTTG
C.ORN.LAKEANNIE.FL	CAGCATTTATTTTGATTTTTTG
C.ORN.KRM01.FL	CAGCATTTATTTTGATTTTTTG
C.ORN.KRM02.FL	CAGCATTTATTTTGATTTTTTG
C.ORN.STP.GA	CAGCATTTATTTTGATTTTTTG
C.ORN.NORMAN.GA	CAGCATTTATTTTGATTTTTTG
C.ORN.AMR01.CA	CAGCATTTATTTTGATTTTTTG
C.ORN.AMR02.CA	CAGCATTTATTTTGATTTTTTG
C.ORN.TLL.PA	CAGCATTTATTTTGATTTTTTG
C.ORN.TLU.PA	CAGCATTTATTTTGATTTTTTG
C.ORN.MN.WI	CAGCATTTATTTTGATTTTTTG
C.ORN.WRW5.WI	CAGCATTTATTTTGATTTTTTG
C.ORN.BLUE.OR	CAGCATTTATTTTGATTTTTTG
C.ORN.NOCKFS.PA	CAGCATTTATTTTGATTTTTTG
C.ORN.HARRIS.MA	CAGCATTTATTTTGATTTTTTG
C.ORN.NATICOOK.NH	CAGCATTTATTTTGATTTTTTG
C.ORN.PURGATORY.MN	CAGCATTTATTTTGATTTTTTG
C.ORN.CROSBY.MN	CAGCATTTATTTTGATTTTTTG
C.ORN.ROUNDPOND.NH	CAACACTTATTTCTGATTTTTTG
C.ORN.TIMBERDITCH.OR	CAACACCTCTTTTGATTTTTTG
C.ORN.DRAGON.MN	CAACACCTCTTTTGATTTTTTG

Population structure and cryptic species in the cosmopolitan rotifer *Euchlanis dilatata*

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Determining genetic structure is fundamental to our understanding of how populations adapt and evolve. Increasingly cryptic species complexes are being discovered in zooplankton, including rotifers. We used three molecular markers to investigate partitioning of genetic diversity within five populations of the cosmopolitan rotifer *Euchlanis dilatata*. We also investigated genetic differentiation among 62 populations across a broad area of North America. DNA fingerprinting showed low levels of divergence (~1%) among four local populations within a river system but high levels of population sub-structuring and polymorphic loci (up to 66%). One population was assayed for ITS and *COI* markers and also showed low divergence (0 and <1%, respectively). Overall, ITS sequences were less variable (0–13.4%) than *COI* sequences (0.0–21.9%). When sequences were used for phylogenetic analysis, we found substantial differentiation among populations and seven putative cryptic species based on Bayesian Species Delimitation (ITS: 0–5.2% genetic divergence within, and 1.0–13.4% between putative species). Cryptic lineages varied from occurring in a single locality, broadly, or even overlapping suggesting that they may differ in their capabilities to disperse, colonize and persist in new habitats. Accordingly, *E. dilatata* can be considered a species complex, and additional species are likely to be uncovered.

ADDITIONAL KEYWORDS: AFLP – DNA Taxonomy – isolation by distance – species delimitation.

INTRODUCTION

Studying population genetic structure informs our understanding of how populations evolve under evolutionary forces such as gene flow. There is a growing number of examples of small organisms that disperse passively over long distances implying that, for these taxa, gene flow can occur even among geographically distant populations. However, many of these taxa show high levels of genetic differentiation and form cryptic species complexes, even across small spatial scales within the range of their dispersal (e.g. Zeller, Reusch & Lampert, 2006; Fontaneto, Boschetti & Ricci, 2008b; Xiang *et al.*, 2011). Rotifers, a common constituent of freshwater ecosystems, possess the ability for passive, long-distance dispersal through their diapausing stages (e.g. resting eggs, xerosomes (Dumont, 1980; Walsh, May & Wallace, 2017)). These propagules

transported with dust during wind events, can be dispersed by animals, or through water flow (Fontaneto, 2011). Based on the high likelihood of passive dispersal, most rotifer species are assumed to have cosmopolitan distributions. Nevertheless, application of molecular, behavioral and morphological methods has revealed high numbers of cryptic species complexes within the phylum (e.g. *Brachionus plicatilis* Müller, 1786 [Gómez & Snell, 1996; Mills *et al.*, 2017], *B. calyciflorus* Pallas, 1766 [Xiang *et al.*, 2011; Papakostas *et al.*, 2016], *Lecane bulla* (Gosse, 1851) [Walsh *et al.*, 2009], *Epiphanes senta* (Müller, 1773) [Schröder & Walsh, 2007, 2010], *Testudinella clypeata* (Müller, 1786) [Leasi *et al.*, 2013], *Polyarthra dolichoptera* Idelson, 1925 [Obertegger, Flaim & Fontaneto, 2014], *Synchaeta pectinata* Ehrenberg, 1832 [Kimpel *et al.*, 2015] and a number of bdelloid species [Fontaneto *et al.* 2007; Fontaneto *et al.* 2011; Xiang *et al.* 2016]).

Vita

Azar Kordbacheh was awarded Bachelor of Science degree in Zoology from University of Tehran, Iran in 2007. In 2010, she received her Master of Science degree in Animal Biosystematics from University of Tehran, Iran. She was admitted to the Ecology and Evolutionary Biology doctoral program at University of Texas at El Paso in 2012. She was awarded teaching assistant positions in Topics in Study of Life and Organismal Biology laboratories. Azar also obtained DNA sequences for gnesiotrochan rotifers as a research assistant in Dr. Walsh's laboratory under her grant from National Science Foundation (DEB 0516032, 1257068). During her doctoral studies, Azar was the recipient of multiple research grants and scholarships including a Sigma XI Grants-in-Aid of Research (2012; G2012162274), three University of Texas at El Paso Dodson Research Grants (2014-2016), a University of Texas at El Paso College of Science Research Award supported by a grant from NIH (2016; 2G12MD007592), a Research Assistant Fellowship from University of Texas at El Paso Office of the Provost and Graduate School (2017), a University of Texas at El Paso Frank B. Cotton Trust Scholarship (2014), a Krutilek Memorial Graduate Fellowship (2016), and University of Texas Student Government Association Travel Grants (2013, 2014 and 2016). She presented her doctoral research in six international conferences including International Rotifer Symposium (2012 and 2015), Association for the Sciences of Limnology and Oceanography (2013 and 2014), Evolution Meeting (2016 and 2017). Based on her research, she has published two manuscripts and she has another three manuscripts in preparation.

Azar has volunteered as a graduate student representative in a search committee for a tenure track position at the Department of Biological Sciences at University of Texas at El Paso (2016) and as a judge in COURI Symposium at University of Texas at El Paso (2014, 2015 and 2016). Azar is interested in population genetics and conservation in aquatic habitats, and she is planning to pursue her career as a professor researching those topics.

This dissertation was typed by Azar Kordbacheh.