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Genetic Population Structure of the Federally Endangered Etowah Darter, *Etheostoma etowahae*

Shane Ritchea

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**Genetic Population Structure of the Federally
Endangered Etowah Darter, *Etheostoma etowahae***

**A Thesis Presented to the Graduate School of Environmental Science and
Management**

Duquesne University

In partial fulfillment of the requirements for the
Degree of MASTER OF SCIENCE IN ENVIRONMENTAL SCIENCE AND
MANAGEMENT

By

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ABSTRACT

The Etowah darter is a recently described member of the *Etheostoma* (*Nothonotus*) *jordani* species group believed to be geographically restricted to the Upper Etowah River in Georgia. The most geographically proximal records of the relatively abundant Greenbreast darter, *E. jordani*, were reported from Stamp Creek; however, in recent surveys *Nothonotus* individuals have been documented from intermediate localities and appear to be morphological mixtures of *E. jordani* and *E. etowahae*. These localities may indicate syntopy and/or hybridization, or alternatively, morphological characters promoted in the formal species descriptions may be incapable of definitively identifying all *Nothonotus* specimens from the Etowah River. In this study 2020bp of mtDNA from 123 *Nothonotus* specimens have been sequenced to provide a means for genetic identification, examine population structure, and redefine geographic distributions. Phylogeographic analysis documents that *E. etowahae* haplotypes occur in several small fragmented streams ~110 km downstream from where it was first described in 1993.

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INTRODUCTION

History of Darter Taxonomy

There are currently four genera of North American darters: *Ammocrypta* (6 species), *Crystallaria* (with one species, *C. asprella*), *Etheostoma* (136 species), and *Percina* (41 species), giving a total of close to 200 described species (Nelson *et al.*, 2004). There has been much study of North American darters, with many new species described in the last few decades (Nelson *et al.*, 2004); (Burr *et al.*, 1993; Page *et al.*, 2003). However, the systematics of darters has long been troubled (Bailey *et al.*, 1988), in part because morphological characters often are convergent and overlap broadly, leading to difficulties in examining higher order relationships in the group (Bailey *et al.*, 1955; Page, 1981), (Turner, 1987).

Initially, in the “Golden Age” of darter taxonomy (1841-1897), there were many more subgenera than now. Nearly 100 new species were described and a large number of darter genera were designated without careful consideration of the underlying relationships of these fishes (Collette, 1967). In 1930, a study by Jordan, Everman, and Clark listed 31 genera and 104 species. Twenty five years later, a landmark study conducted by Bailey and Gosline (1955) reduced the number of darter genera to three, subsuming many subgenera, all based on vertebral number. The three genera recognized were *Percina* (8 subgenera), *Ammocrypta* (2) and *Etheostoma* (12). A survey based on breeding tubercles by Collette in 1965 adopted essentially the same arrangement as Bailey and Gosline (1955) (Bailey *et al.*, 1988).

An example of the numerous historic changes in darter taxonomy is illustrated by the crystal darter. In 1882, Jordan and Gilbert reassigned the crystal darter, *Crystallaria asprella*, to the genus *Ammocrypta* (Jordan *et al.*, 1882), then three years later, returned it to the genus *Crystallaria* (Jordan, 1885). Later, Bailey (Bailey *et al.*, 1954; Bailey *et al.*, 1955) demoted *Crystallaria* to a monotypic subgenus in the genus *Ammocrypta*. Today *Crystallaria* is recognized as a distinct genus due to a cladistic study by Simons (1991), but it is uncertain how long we can expect this arrangement to last. As more research continues, additional data (both morphological and molecular) may arise to support its return to *Ammocrypta*, an example of the problematic and contentious systematics of darters.

Genus *Etheostoma* Rafinesque, 1819

Etymology—*Etheostoma*, derivation uncertain, the word *Etheostoma*, according to Rafinesque, means “various mouth.”

Etheostoma is the largest and most speciose genus of fishes in North America, with 136 described species (Nelson, 2006), and the description of additional species is anticipated. Bailey and Gosline listed 12 subgenera in 1955, and during the following 25 years the genus remained in a state of flux as species were resurrected and/or removed following studies conducted by major contributors to the field such as Collette (1962), Collette (1965), Cole (1967), Howell (1968), Page and Witt (1973b), Williams and Robison (1980), and Page (1981b). The last of these increased the current number of recognized subgenera of *Etheostoma* from 12 to 17.

Males of most species of *Etheostoma* display brilliant colors, especially during the breeding season (Kuehne *et al.*, 1983). Many can produce Schreckstoff substances (an alarm pheromone released by specialized skin cells when damaged) that serve to warn nearby fish in case of an attack (Boschung, *et al.*, 2004). Food of all species for which information is available consists primarily of the immature stages of aquatic insects (Kuehne *et al.*, 1983). Darters in the genus *Etheostoma* have radiated into a wide variety of habitats ranging from stagnant waters and organic substrates of swamps to shoreline areas of lakes, from pools and sandy areas to boulder riffles, large creeks and rivers, and tiny springs (Kuehne *et al.*, 1983). They often are abundant in streams smaller than those invaded by the other darter genera (Kuehne *et al.*, 1983).

Etheostoma darters utilize four distinct egg-deposition strategies: egg-burying, egg-attaching, egg-clustering, and egg-clumping; whereas the other three darter genera use only one method, egg burying (the hypothesized ancestral behavior) (Page *et al.*, 1982, Page *et al.*, 1984, Page, 1985, Bart *et al.*, 1992). Egg-attaching behavior is a derived behavior known among percids only in *Etheostoma* (Page, 1985).

Subgenus *Nothonotus* Putnam, 1863

Etymology—*Nothonotus*, from the Latin word *nothus*, “bastard” and possible *notutus*, “spotted.”

Subgenus *Nothonotus* was described as a subgenus of *Etheostoma* by Bailey (1959), and supported by Zorach (1972), Page (1981), and Wood (1996). Etnier and Williams (1989) and Wood (1996) presented evidence of monophyly and hypothesized relationships of the species (Mettee, *et al.*, 1996). It is presumed to be a monophyletic

assemblage of fishes united by a suite of morphological characters (Page, 1981, 1983; Etnier *et al.*, 1989) including the following synapomorphies: a rather deep body as compared to other darters; slab-sided body shape; darkened anterior membranes in the spinous portion of the dorsal fin; thin, dark, horizontal lines on the lateral sides, and an absence of nuptial tubercles (Bailey *et al.*, 1988). Most species are of moderate size, but *E. tippecanoe* (Jordan *et al.*, 1890) is one of the smallest of darters (at only 43mm adult length) and the only *Nothonotus* which consistently has an incomplete lateral line (Bailey *et al.*, 1988). The lack of tubercles in all species of the subgenera *Nothonotus* has been used to support the monophyly of and further indicates the compact nature of this subgenera (Collette, 1965).

A recent study by Near and Keck (2005), based upon cytochrome *b*, has suggested the elevation of *Nothonotus* to generic status (along with *Allohistium*), due to a basal arrangement of this group compared to other members of the genus *Etheostoma* and the genera *Percina*, *Crystallaria*, and *Ammocrypta*. However, for this study I have chosen to follow the traditional view of *Nothonotus* as a subgenus within *Etheostoma* until additional supporting evidence shows otherwise.

The species in *Nothonotus* frequently are difficult to distinguish because the most important character, color, fades quickly in preservative. Meristic characters are not always satisfactory because of broad overlap in counts (Zorach, 1972). Thus, at times geographic range or a combination of characters must be utilized (Zorach, 1972). The females may be difficult to distinguish.

Nothonotus darters inhabit riffle habitats of large creeks and rivers primarily over mixed gravel and boulder patches with moderate to strong flow. These patches are often

widely dispersed and densities of *Nothonotus* darters may vary greatly from year to year in the same sites (Trautman, 1981). Dispersal-vicariance analyses suggest that the ancestral area for *Nothonotus* is the Eastern and Interior Highlands (Near *et al.*, 2005).

***Etheostoma (Nothonotus) jordani* Species Complex**

Rivers of the Mobile Basin contain one of the most distinctive ichthyofaunas in North America, characterized by at least 41 endemic species (Swift *et al.*, 1986; Burr *et al.*, 1992; Wood and Mayden, 1993; Burkhead *et al.*, 1997). There are two hypotheses for this faunal diversification: a long history of drainage exchange and isolation of gene pools, combined with a limited impact of processes associated with Pleistocene glaciation (Swift *et al.*, 1986; Wiley *et al.*, 1985; Mayden, 1988); and the Central Highlands Vicariance Hypothesis, which proposes vicariance as opposed to dispersal from centers of origin as the mechanism responsible for the geographic pattern of speciation (Near *et al.*, 2005).

Over the past decade or two, thorough studies of the morphological, behavioral, ecological, and genetic variation in species have resulted in the “splitting” of several fairly well-known polytypic *Nothonotus* species into numerous “new” species (Butler *et al.*, 2003). Until recently, the Greenbreast darter, *Etheostoma jordani* Gilbert (1891), endemic to the Mobile Basin primarily above the Fall Line (type locality, Choccolocco Creek, tributary of Coosa River, Calhoun County, Alabama) (Figure 1), had been considered a single species (Zorach, 1969). However, Zorach (1969) had noted some variation within Greenbreast darters. Some specimens from the Black Warrior River system lacked opercular scales entirely or may have had embedded scales on the opercle, whereas all other populations had scaled opercles. Zorach (1969) also noted that a single

sample from the Etowah River (although inadequate) had low scale counts and high fin-ray counts explaining this finding as possible infraspecific population.

Evaluation of variation in morphology and color in the Greenbreast darter from throughout its range has revealed that in reality four distinct species are represented (Wood and Mayden, 1993). The four species described out of the *E. jordani* species complex by Wood and Mayden (1993), (Figure 2) are as follows.

Etheostoma jordani Gilbert, Greenbreast Darter

E. jordani is distinguished from other members of the species group by presence of red spots on breeding males without dark halos on side of body, olivaceous lips, blue-turquoise anal fin, and exposed scales on opercles (Wood and Mayden, 1993). It is distributed throughout the Coosa River System, including the Conasauga and Coosawattee rivers, the Cahaba River System, and the Tallapoosa River system below the Fall Line (Wood and Mayden, 1993) (Figure 1).

Etymology—the species epithet *jordani* is used in honor of David Starr Jordan. The common name Greenbreast darter refers to the blue-green coloration on the breast and underside of head.

Etheostoma douglasi Wood & Mayden, New Species, Tuskaloosa Darter

E. douglasi is distinguished from the other members by the combination of no red spots along flanks of breeding males, no scales on opercles, and no trace of red pigmentation on the lips or in the anal fin (Wood and Mayden, 1993).

Etymology—named for Dr. Neil H. Douglas, Director and Curator, Northeast Louisiana University Museum of Zoology, in recognition of his contributions to our

understanding of the freshwater fish fauna of Louisiana and his dedication to teaching.

The common name, Tuskaloosa darter, is in reference to the Mississippian chieftan met by Hernando de Soto and to the Choctaw Indian name for Black Warrior, the river system to which this species is endemic.

Etheostoma etowahae Wood & Mayden, New Species, Etowah Darter

E. etowahae is distinguished from other members of the group by absence of red spots on flanks of breeding males, lack of red pigment on lips, lack of a red band in anal fin, and presence of scales on opercle. Additionally, *E. etowahae* differs from the remaining three members of the *E. jordani* species group in having a mean of 12.7 transverse scale rows; 45.5 lateral line scales; and a mean of 17.1 caudal peduncle scale rows (Wood and Mayden, 1993). It is restricted to the upper Etowah River System of Georgia above Lake Allatoona (Figure 1).

Etymology—the species epithet *etowahae* is an adjective referring to the Etowah River to which the new species is endemic. The common name, Etowah darter, also refers to the Etowah River.

Etheostoma chuckwachatte Wood & Mayden, New Species, Lipstick Darter

E. chuckwachatte is distinguished from other members of the group by presence of red lips, bright red spots along flanks of breeding males, a broad red band in the anal fin of adult males, and scales on opercles (Wood and Mayden, 1993). It is known from throughout the Tallapoosa River System above the Fall Line in Alabama and Georgia (Wood and Mayden, 1993).

Etymology—*Etheostoma chuckwachatte* is named from the anglicized version of the Creek Indian words for mouth, chuckwe; and red, chattee; and refers to the bright red

lips of this species. The common name, lipstick darter, is also in reference to the bright red lips on breeding males.

Distinguishing Characters Promoted to Identify the Four Individuals Described out of the *E. jordani* Species Complex by Wood and Mayden (1993)

The four species are distinguished from one another on the basis of squamation, meristic characters, general head and body shape, and pigmentation patterns (Table 1). *E. douglasi* is distinguished from the other members of the species group, and all other members of *Nothonotus* except *E. auticeps*, by its lack of exposed scales on the opercle. While meristic characters among the remaining three species are similar, *E. etowahae* generally has fewer lateral line scales, fewer scale rows above and below the lateral line at the caudal peduncle, and fewer transverse scale rows than the remaining three species in the group. Generally *E. etowahae* has a shorter head, snout, and pectoral fins, and a longer anal fin base than the other three species in the group. This pattern of interspecific variation is further summarized by principal component analysis of meristic variables for both males and females in which *E. etowahae* is almost completely separated from the remaining three species along principal component one (meristic variables for males and females). *E. chuckwachatte* generally has a longer head, and shorter pectoral, pelvic, and caudal fins relative to populations of *E. jordani* in closest geographic proximity.

Wood and Mayden (1993) describe several pigmentation characters indicative of the breeding males which also serve to distinguish the four species in the group (Table 1). Males of *E. jordani* and *E. chuckwachatte* are distinguished from those of *E. etowahae* and *E. douglasi* by the presence of red spots on the body. Males of *E. chuckwachatte* are

distinguished from all other members of *Nothonotus*, except *E. rufilineatum*, by the presence of red lips; they are further distinguished from all other members of the *E. jordani* group by this character and the presence of a broad red band through a typically blue-turquoise anal fin.

Conservation Status

Often, newly discovered fish taxa are on the brink of extinction (e.g., Williams and Clemmer 1991; Boschung *et al.* 1992; Warren *et al.* 1994), and the lack of critical information on their habitats and life histories precludes informed recovery efforts (Warren *et al.* 2000). The conservation status of the newly described members of the *E. jordani* complex as recommended by Wood and Mayden (1993) is that of threatened to *E. douglasi*, and *E. chuckwachatte*. *E. etowahae* merits endangered status and it was listed as a federally endangered species on December 20th, 1994, approximately a year after its initial species description, and has been accused (along with *E. scotti*, the Cherokee darter) of “breaking the back” or “the final straw” in alleged problems with the Endangered Species Act (Mann *et al.*, 1995).

The Etowah darter is endemic to the Etowah Basin in north Georgia (Burkhead 1992), which lies on the north edge of the Atlanta metropolitan area. The Etowah darter’s habitat has been degraded by increased urbanization in the Atlanta metropolitan area and has experienced habitat loss due to impoundments, siltation, and pollution from municipal and industrial waste discharges, runoff from monoculture agriculture and poultry farms, poultry processing plants, and silvicultural activities (USFWS, 1993, 1994).

Study Rationale and Research Objectives

The diagnostic morphological characters promoted in the formal description of *E. etowahae* do not appear to adequately define the identity of all male *Nothonotus* specimens taken from several localities in the Etowah and Upper Coosa River Systems. One of the most conspicuous field characters promoted for *E. etowahae* is the absence of red spots on the body of the breeding male (Wood and Mayden, 1993). Specimens taken from the Upper Etowah System (Long Swamp Creek, Cherokee Co., GA on 6 May, 2001 by Dr. Byron J. Freeman) contained both red spotted and immaculate (unspotted) males in the same seine hauls. Similar observations were made in the Upper Coosa System (Terrapin Creek, Cherokee Co., AL on 19 October, 2001 by the Freeman Lab), but the non-spotted males were assumed to be *E. jordani* out of peak coloration rather than representing a potential mixture of two syntopic species (this site is reported to only contain the red spotted *E. jordani* males). Since *E. etowahae* and *E. jordani* are not reported to be in syntopy, we are at a loss to definitively identify specimens taken from some localities based on the presence or absence of the red spotted male character.

Furthermore, the “diagnostic” meristic characters (lateral, transverse, and caudal peduncle scale rows) of Wood and Mayden (1993) need to be carefully counted in the lab under a microscope to obtain an accurate count; and although the two species are reported to differ significantly in modal counts, the ranges largely overlap (Figure 3). A preliminary study by the Freeman lab (2003) shows that seven out of 25 specimens from a single Long Swamp Creek, Cherokee Co., GA collection had at least one meristic count that fell outside the reported range of *E. etowahae*, confounding them with *E. jordani*. One of the specimens from this collection (with red spots before preservation) had all three

meristic counts falling outside of the range of *E. etowahae* and would be considered an uncontested *E. jordani* using all of Wood and Mayden's diagnostic meristic characters. The most upstream record of the Greenbreast darter, *E. jordani*, in the Etowah system is reported to be Stamp Creek, Bartow Co., GA (Wood and Mayden, 1993). However, in recent surveys *Nothonotus* individuals have been found in Smithwick and Long Swamp Creeks, and these specimens appear to be a morphological mixture of *E. jordani* and *E. etowahae* (Figure 3). These localities may represent the first report of syntopy and/or hybridization between these two species. Alternatively, the morphological characters reported in the species descriptions (Wood and Mayden, 1993) may not be completely useful in definitively identifying all individuals to species level in the upper Etowah and Coosa systems. In theory, identification problems can result whenever "diagnostic modes" are promoted as the primary difference among closely related species, for modes are a characteristic of a population and do not help to assign identification of an individual to a species.

The ability to definitively identify a Federally Endangered Species and delineate its current geographic distribution is paramount for recovery efforts. From a management perspective the habitat critical for the protection of populations and those populations requiring prioritization for protection must be understood. This study is designed to reveal significant genetic differences between *E. etowahae* and *E. jordani* using mitochondrial DNA (mtDNA) sequence data in order to delineate the true range of each of these species in the Etowah River System using phylogeography. There are well-recognized advantages of using mtDNA sequences for phylogenetic studies, i.e., relative ease of collecting sequence data due to the compact and conservative gene organization without introns in

mitochondrial genes, and clear orthology of homologous gene sequences due to the rare, if any, DNA recombination and gene duplication and, for purposes of microevolutionary analysis, a rapid pace of evolution such that new character states commonly arise within the lifespan of a species (Avisé *et al.*, 1987; Wolstenholme 1992; Boore 1999; Saccone *et al.*, 2002).

In addition, a genetic characterization of population structure for the Etowah darter will allow estimates of fragmentation and degree of isolation of populations and prioritize management decisions should significant genetic partitioning justify evolutionary significant unit (ESU) status to specific populations, as in the case with the sympatric Cherokee darter (Storey 2003; Storey *et al.*, in prep).

The hypothesis that will be investigated is that the geographic distribution of *E. jordani* and *E. etowahae* in the Etowah basin is as described by Wood and Mayden (1993). If this distribution is refuted then two alternative hypotheses will be considered. One, the newly discovered localities may indicate syntopy and/or hybridization between these two species, or alternatively, morphological characters promoted in the formal species descriptions may be problematic and incapable of definitively identifying all *Nothonotus* specimens from the Etowah River. Either call raises questions as to the classification status of these newly documented populations and the true geographic ranges of these sister species.

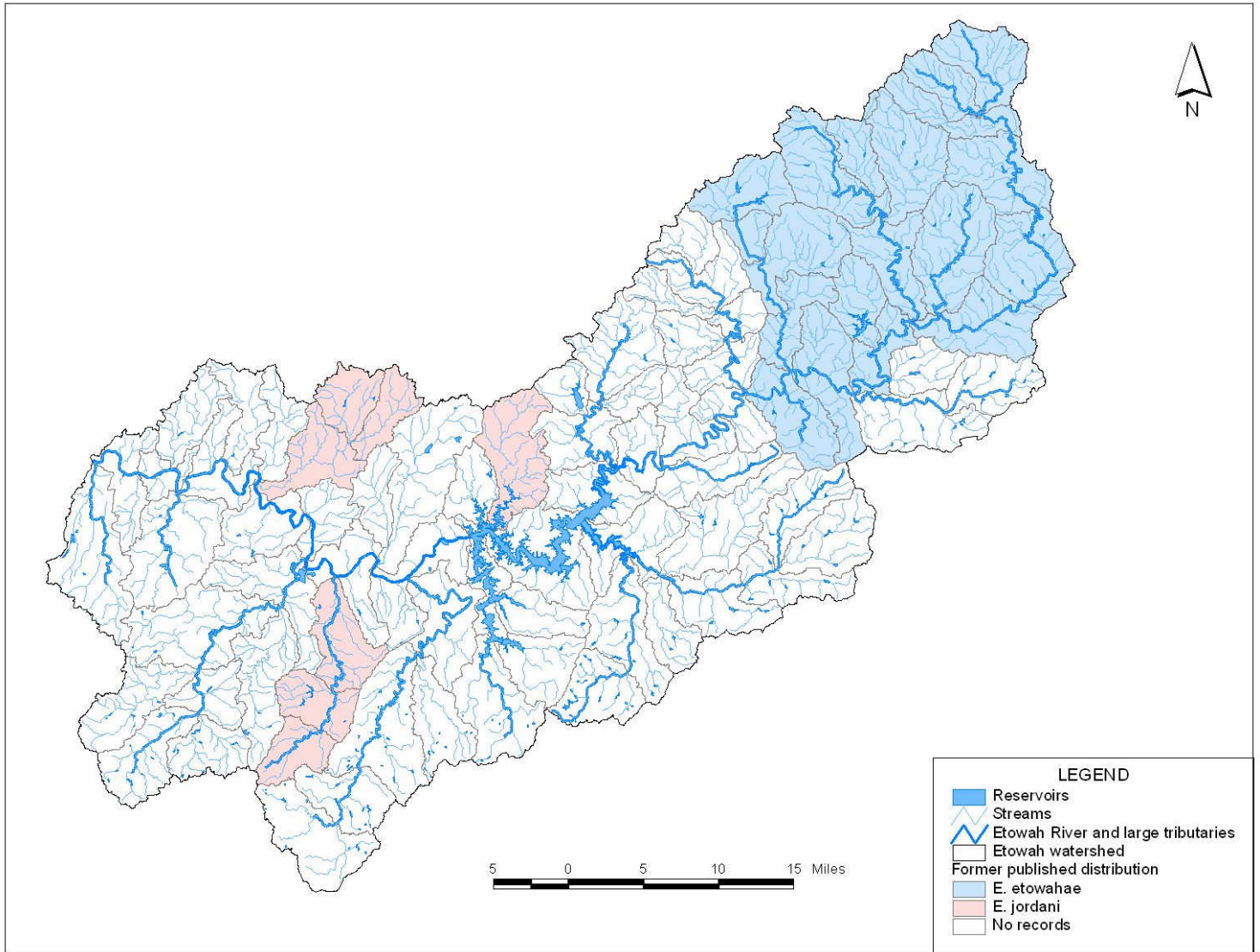


Figure 1. Published distribution from Wood and Mayden (1993) of *E. etowahae* and *E. jordani* in the Etowah River watershed. The distribution of *E. etowahae* is shaded in blue and that of *E. jordani* is shaded in pink. The distribution of *E. jordani* also occurs in several adjacent drainages outside the range of this map in the Conasauga, Coosawatee, Oostanaula, Coosa, and lower Tallapoosa River systems.



E. jordani
Greenbreast darter



E. chuckwachatte
Lipstick darter



E. douglasi
Tuskaloosa darter



E. etowahae
Etowah darter

Figure 2. The four species described out of the *Etheostoma jordani* species complex group, by Wood and Maiden (1993). Illustrations by Karl J. Scheidegger in *Fishes of Alabama and the Mobile Basin* (Metee *et. al.*, 1996).

Table 1. The diagnostic ranges of meristic (lateral line [LL], transverse [TV], and caudal peduncle [CP] scale rows) and morphological characters used to distinguish members of the *E. jordani* species complex by Wood and Mayden (1993).

Characteristic	<i>E. jordani</i>	<i>E. douglasi</i>	<i>E. etowahae</i>	<i>E. chuckwachatte</i>
Lateral line scale rows	44-52	44-55	42-51	44-52
Transverse scale rows	14-16	13-17	11-15	13-16
Caudal peduncle scale rows	17-22	18-24	15-19	17-22
Red spots on side of body	present	absent	absent	present
Red stripe in anal fin	absent	absent	absent	present
Red pigment on lips	absent	absent	absent	present
Scales on opercle	present	absent	present	present

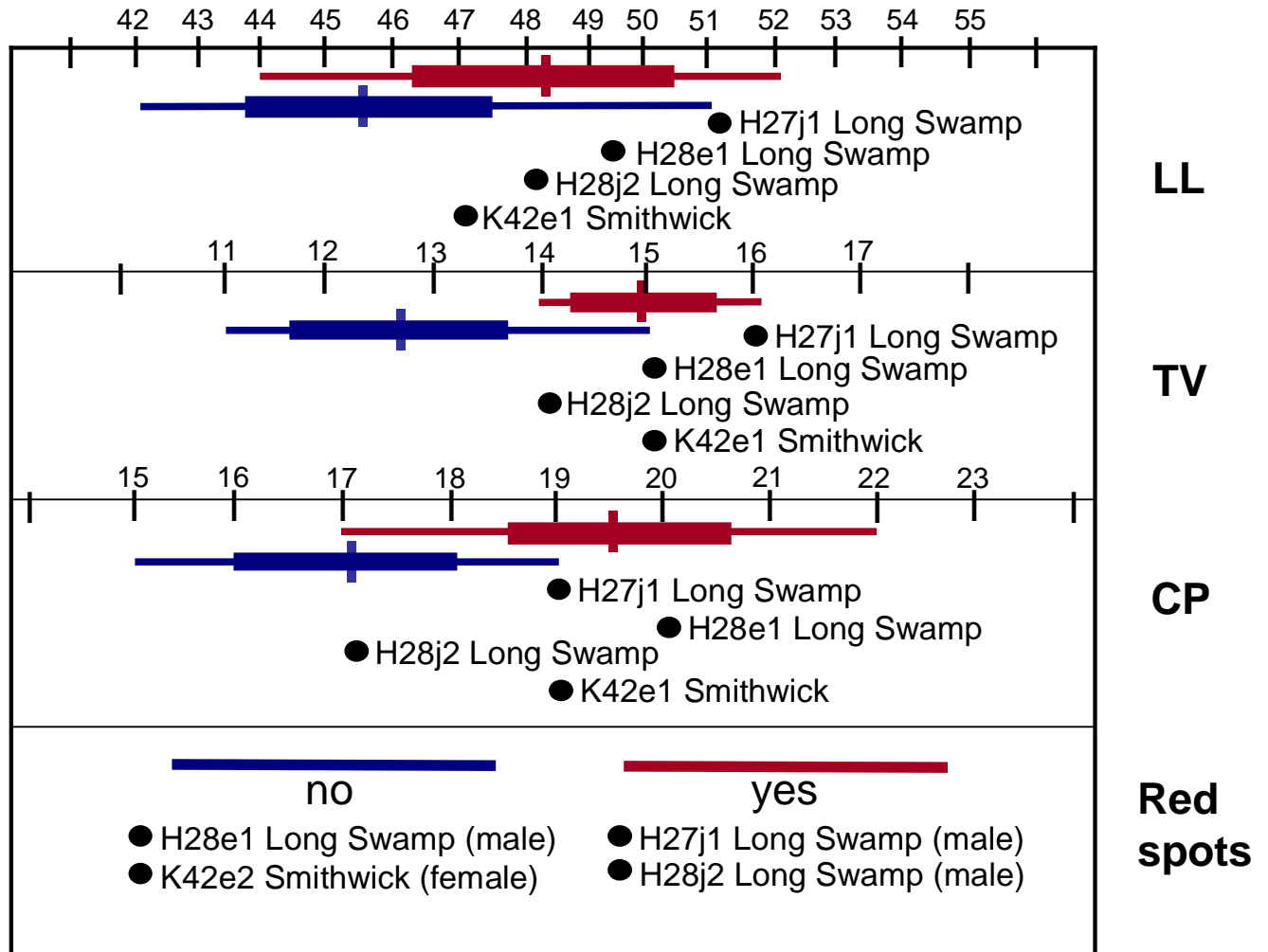


Figure 3. Rainey Plot depicting the overlap of morphometric characters for *E. etowahae* (in blue) and *E. jordani* (in red). Thin horizontal bars represent ranges, the thicker horizontal bars represent standard deviation from the mean, and the vertical bars represent the means. Some representatives from the “atypical” *Nothonotus* from Long Swamp and Smithwick Creeks are included for comparison and to illustrate problematic identification.

MATERIALS AND METHODS

Sample Collections

All samples for this study were collected by seine and/or electrofisher. Samples of Tuskaloosa (*E. douglasi*) darters were collected from two localities in Alabama by Dr. Brady A. Porter (Appendix A). In collaboration with Dr. Byron J. Freeman at the University of Georgia, samples of Lipstick (*E. chuckwachatte*), Greenbreast (*E. jordani*), and Etowah (*E. etowahae*) darters were obtained from 28 localities during fish surveys conducted from 2001 to 2005 in the State of Georgia by the Institute of Ecology, University of Georgia (Appendix A). Under permission from a Federal Endangered Species Collection Permit and a Georgia Scientific Collecting Permit, a small fin clip (approximately 1-2mm square) was taken from the caudal fin of individuals identified as *E. etowahae*, and the fish were released. Whole fish and/or fin clip samples were collected from individuals identified by geographic range as *E. douglasi*, *E. chuckwachatte*, or *E. jordani*. All samples were preserved in absolute ethanol on site, and are vouchered with the Georgia Museum of Natural History DNA Archive.

Genetic Analyses

For samples in which the whole fish was preserved, an approximately 0.5cm square of muscle tissue was dissected from the right caudal peduncle area of whole fish, leaving the left side of the fish in tact for morphological analysis. Skin was removed and the muscle tissue was blotted dry of ethanol, minced into small pieces, and placed into a 1.5ml microcentrifuge tube. Fin clips taken from specimens that were caught and released in the field were blotted dry of ethanol, left whole (not minced) and placed into 1.5ml

microcentrifuge tubes. 500µl lysis buffer (0.1M Tris, 4M urea, 0.2M NaCl, 0.01M CDTA, 0.5% lauroyl sarcosine) with proteinase K solution (0.1mg/ml concentration) was added, and the samples were incubated overnight at 55°C. DNA was extracted from the muscle/fin digestion using a standard phenol:chloroform protocol (Maniatis *et al.*, 1982). The extracted DNA was resuspended in 50µl (fin tissue) or 100µl (muscle tissue) HPLC grade water and stored at 4°C.

Gene Selection

Three genes were amplified and sequenced for this study. The mtDNA control region was first selected in order to assist with comparisons of levels of divergence with the Cherokee darter conducted in the same system (Storey 2003). Initial phylogenetic trees were constructed from the control region data and 11 specimens from divergent areas of the trees were chosen to sequence for the cytochrome *b* (*cyt b*) gene. In order to find a highly variable gene, mtDNA sequences were downloaded from GenBank for full genome sequences from related fish species (Table 2) and percents of variable sites and pairwise distance averages per species group were computed using MEGA v 3.1.2 (Kumar *et al.*, 2004) (Table 3) in order to find the three most variable mtDNA genes in fishes. The three most variable genes were determined to be ND2, ND4, and *cyt b*. Next, sequences (ND2, ND4, and *cyt b*) were downloaded from GenBank from nine darter species (Table 4) in order to analyze the variability of three genes between darter species. Percents of average variable sites and pairwise distance averages per species group were computed using MEGA v 3.1.2 (Kumar *et al.*, 2004) (Table 5). The NADH Dehydrogenase Subunit 2 (ND2) gene proved to be the most variable gene amongst darters and was selected as the third gene to sequence in this study.

Extracted DNA was amplified using previously published PCR primers (Kocher *et al.*, 1995; Porter, 1999; Porter *et al.*, 2002; Storey 2003; Storey *et al.*, in prep.), (Table 6), (Figures 4 and 5). The mtDNA sequences include 973 base pairs encompassing the alignable portion of the mtDNA control region (837 bp), the tRNA-Phe gene (68 bp), and part of the 12S rRNA gene (68 bp); a portion of the *cyt b* gene (1114 bp); and the complete ND2 gene (1047 bp). Each 50µl reaction contained ~25-1000ng of genomic DNA as template, along with 2.5mM MgCl₂, 2 mM of each dNTP, 0.5 units *Taq* DNA polymerase (Fisher Brand), 5pM each of a pair of oligonucleotide primers (Table 6), (Figures 4 and 5), and 1X Fisher buffer B (Porter, *et al.*, 2002). PCR was conducted in a DNA Dyad Thermalcycler (MJ Technologies) with the following profiles: 2 minute hot start at 93°C, followed by 32 cycles of 45 seconds at 93°C, 1 minute at 58°C (control region and ND2 only; *cyt b* had an annealing temperature of 45°C), and 2 minutes at 72°C, with a final extension step of 10 minutes at 72°C. For templates that wouldn't amplify under these conditions, an extended program was used which increased the number of cycles to 45.

Electrophoresis was conducted with 5µl aliquots of PCR product using a 3% SB agarose gel containing ethidium bromide and SB buffer (Brody *et al.*, 2004) at 300 V for 10 minutes. Successful PCR products were cleaned by column centrifugation using Princeton separation columns with Sephadex® G-50 (Sigma). The clean PCR products were quantified by spectrophotometer and saved for cycle sequencing. Sequencing reactions were conducted using ¼ reactions with BigDye® v 3.1 cycle sequencing kit (ABI). Reactions consisted of 2µl BigDye® master mix, 1µM sequencing primer (Table 6), (Figures 4 and 5), 1x sequencing buffer, and ~40-80ng of clean PCR product + HPLC

water to make a total volume of 20µls. Samples were cycled 55-75 times in a DNA Dyad Thermalcycler (MJ Technologies) according to manufacturer's suggestion.

Following the cycle sequencing reaction, products were again cleaned by Sephadex® G-50 column centrifugation and placed into a DNA SpeedVac on medium heat for about 30 minutes or until dry. The dry samples were reconstituted with 10µl of DI formamide and transferred to 96 well plates, denatured for 2 minutes at 95°C, and snap cooled on ice. Sequences were analyzed on an ABI PRISM® 3100-Avant Genetic Analyzer following the manufacturer's settings.

All sequences were edited and aligned to the outgroup, *E. tippecanoe*, using the Eyeball Sequence Editor (ESEE3S ver. 3.0s; Cabot *et al.*, 1989) and contigs were created by locating areas of complimentary overlap in forward and reverse primer regions. The contigs were aligned in CLUSTALX (Thompson *et al.*, 1997) using the parameters gap opening penalty = 5 and gap extension = 0.1. The alignments were exported to MEGA v 3.1.2 (Kumar *et al.*, 2004) and corrected by eye (Appendix B). The alignments for the protein coding genes (*cyt b* and ND2) were checked for the presence of stop codons. Novel haplotypes were revealed by sequence divergence as small as one base pair substitution for the entire region. The ND2 alignment was appended with the control region alignment to comprise a fourth dataset ("combined data").

The aligned sequence data was analyzed using Neighbor-Joining (MEGA v3.2.1) (control region, *cyt b*, ND2, combined data), Maximum Parsimony (MEGA v3.2.1) (*cyt b*), and Bayesian Likelihood (MrBayes v3.1.2, Huelsenbeck *et al.*, 2001) (control region, ND2, combined data), for phylogenetic reconstruction. Neighbor-joining (NJ) trees were constructed in MEGA with 1,000 bootstrap replicates, and bootstrap supports greater than

50% were placed on each node. An analysis of nucleotide saturation was conducted by plotting pairwise frequencies of transitions and transversions against uncorrected pairwise nucleotide sequence divergence from data generated in MEGA for DOS 1.02 (Kumar, *et al.*, 1993) and plotted in Microsoft Excel. The model of DNA that best fit the data for Bayesian analysis was determined using MrModelTest v2 (Nylander, 2004). The selected likelihood models were: Hasegawa-Kishino-Yano model with among-site substitution-rate heterogeneity described by a gamma distribution and a fraction of sites constrained to be invariable (HKY+I+G) for the control region; and general time reversible model with among-site substitution-rate heterogeneity described by a gamma distribution and a fraction of sites constrained to be invariable (GTR+I+G) for the ND2 gene and combined data. The Bayesian likelihood analysis is based on Markov chain Monte-Carlo (MCMC) method using the program MrBayes v3.1.2 (Huelsenbeck *et al.*, 2001). Four MCMC simulations were run in parallel for 1,500,000 generations, sampling every 100th tree. The generations before the MCMC converged on optimal maximum likelihood scores were discarded (burn-in period) and the consensus tree was computed. Posterior probability scores above 50% were placed on each node. A maximum parsimony analysis was conducted on the *cyt b* alignment (MEGA v3.2.1) using a heuristic branch and bound search with 1,000 bootstrap replicates and bootstrap support over 50% was placed on each node. Due to the large size of the other datasets, parsimony analysis was unable to be completed with bootstrap or jackknife support because of computational constraints in MEGA or PAUP v. 4 (Swofford, 2000), instead the combined dataset was run through PAUP without bootstrapping in order to analyze branching and topology for congruence with the other tree building methods.

Table 2. Taxa and GenBank Accession Numbers for full mitochondrial genome sequences from related fish species used to find a highly variable gene.

Species	GenBank Accession number
<i>Onchorhynchus clarki henshawi</i> (Lahontan cutthroat trout)	AY886762
<i>Onchorhynchus mykiss</i> (rainbow trout)	L29771
<i>Onchorhynchus tshawytscha</i> (Chinook salmon)	AF392054
<i>Pagrus auriga</i> (redbanded seabream)	AB124801
<i>Pagrus major</i> (red seabream)	AP002949
<i>Thunnus alalunga</i> (albacore tuna)	AB101291
<i>Thunnus thynnus thynnus</i> (Atlantic northern bluefin tuna)	AY302574

Table 3. Percent variable sites and average pairwise distance by gene across species pairs.

Gene	Variable sites:			Average pairwise distance:		
	<i>Oncorhynchus</i>	<i>Pagrus</i>	<i>Thunnus</i>	<i>Oncorhynchus</i>	<i>Pagrus</i>	<i>Thunnus</i>
ND1	12%	13%	5%	8.8%	14.0%	5.2%
ND2	13%	17%	4%	9.6%	19.5%	4.2%
COX1	9%	11%	2%	6.3%	12.2%	1.6%
COX2	8%	8%	1%	5.7%	9.1%	1.3%
ATP8	4%	11%	0%	2.6%	12.7%	0%
ATP6	12%	12%	4%	9.1%	13.6%	4.6%
COX3	8%	10%	3%	6.0%	11.2%	2.9%
ND3	9%	16%	4%	6.9%	18.3%	4.1%
ND4L	8%	15%	6%	6.0%	17.1%	6.0%
ND4	12%	15%	5%	9.0%	16.9%	5.5%
ND5	11%	12%	4%	7.9%	13.9%	3.8%
ND6	13%	14%	5%	9.2%	16.2%	4.8%
Cyt b	10%	15%	3%	7.1%	16.9%	3.0%

Table 4. Taxa and GenBank Accession Numbers for 9 *Etheostoma* species for 3 genes: ND2, ND4, and Cyt *b*.

Species	GenBank Accession number:		
	ND2	ND4	Cyt <i>b</i>
<i>Etheostoma</i>			
<i>radiosum</i> (orangebelly darter)	AY341348	AY341348	AY341348
<i>virgatum</i> (striped darter)	AF412553	AY251552	AF412536
<i>striatulum</i> (striated darter)	AF412547	AY251547	AF123042
<i>smithi</i> (slabrok darter)	AF412456	AY251545	AY374275
<i>obeyense</i> (barcheck darter)	AF412544	AY251543	AF123035
<i>barbouri</i> (teardrop darter)	AF412543	AY251541	AF123028
<i>kennicotti</i> (stripetail darter)	AF412541	AY251542	AF045341
<i>percnum</i> (duskytail darter)	AF412539	AY251544	AF123038
<i>squamiceps</i> (spottail darter)	AF412537	AY251546	AF123041

Table 5. Percent variable sites and average pairwise distance for three genes for the nine species of *Etheostoma* surveyed.

Gene	Variable sites:	Average pairwise distance:
ND2	0.42%	20.0%
ND4	0.38%	19.1%
Cyt <i>b</i>	0.35%	17.4%

Table 6. Primers used in PCR and Sequencing of the following mitochondrial genes: control region (also includes tRNA-Phe gene and partial 12S rRNA gene), cytochrome *b*, and ND2.

Control Region primers:		
LPRO	5'AACTCTCACCCCTAGCTCCCAAAG3'	Forward PCR primer
12Sa-rev	5'TAGTGGGGTATCTAATCCCAG3'	Reverse PCR primer
BAPD.1N	5'ATCTCGCATACCTCAAATCTT3'	Forward sequencing primer
TDKDN	5'CCTGAAGTAGGAACCAGATG3'	Reverse sequencing primer
12S.1-rev	5'GGGTGTGGCTTAGCAAGGCGT3'	Reverse sequencing primer
Cytochrome <i>b</i> primers:		
THR	5'TCCGACATTCGGTTTACAAG3'	Forward PCR & sequencing primer
GLU	5'GACTTGAAGAACCACCGTTG3'	Forward PCR & sequencing primer
ND2 primers:		
ASN	5'CGCGTTTAGCTGTAACTAA3'	Reverse PCR primer
GLN	5'CTACCTGAAGAGATCAAAC3'	Forward PCR & sequencing primer
MET	5'CATACCCCAAACATGTTGGT3'	Forward sequencing primer
TRP	5'GAGATTTTCACTCCCGCTTA3'	Reverse sequencing primer
SBRF	5'GGCTTATCCTCTCGACCTG3'	Forward sequencing primer
RGLN	5'TCATGCGTTGGTGGTGCTGG3'	Reverse sequencing primer

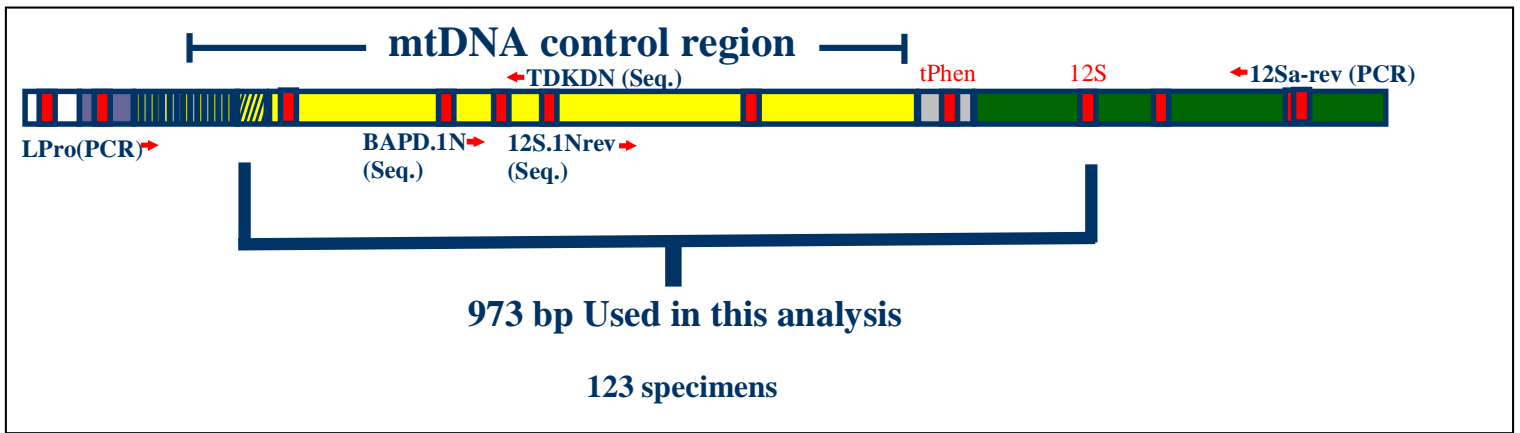


Figure 4. Cartoon depicting the 973 base pairs encompassing the alignable portion of the mtDNA control region (837 bp), the tRNA-Phe gene (68 bp), and part of the 12S rRNA gene (68 bp) that was amplified in PCR reactions. The primers used for sequencing and PCR reactions and their locations within the mitochondrial genome are labeled with red arrows.

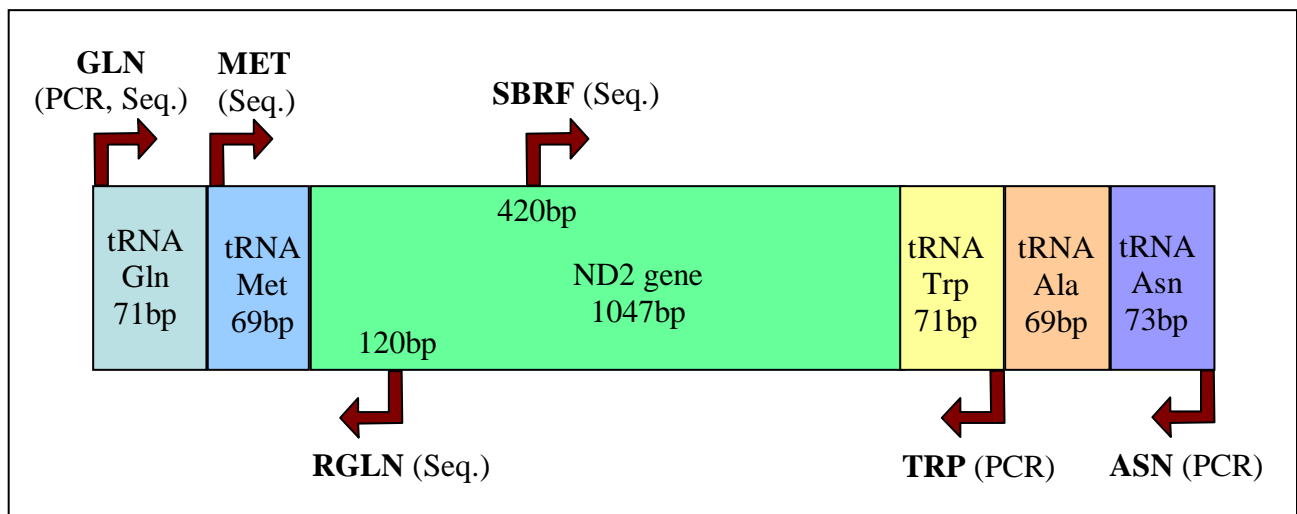


Figure 5. Cartoon depicting the 1047 base pairs of mtDNA for the ND2 gene that was amplified in PCR reactions. The primers used for sequencing and PCR reactions and their locations within the mitochondrial genome are labeled with red arrows. Sequencing was optimized by using the three primers GLN, SBRF, and RGLN.

RESULTS

Control Region Results:

Analysis of Alignment

973 base pairs of mtDNA were amplified and sequenced encompassing the alignable portion of the mtDNA control region (837 bp), the tRNA-Phe gene (68 bp), and part of the 12S rRNA gene (68 bp). In the process of sequence alignment the hypervariable and degraded repeat portion of the control region was excluded from the analysis as warranted through the potential for homoplasy (Porter *et al.*, 2002; Faber *et al.*, 1997). This region may be of interest in future studies on infraspecific variation in darters.

Sequencing revealed 56 distinct mtDNA haplotypes within the 123 assayed specimens. Within the 56 haplotypes, 79 of 973 sites were variable and 47 of these sites were potentially informative for parsimony analysis. Nucleotide composition averages consisted of: A=30.5%, T=30.7%, C=22%, and G=16.8%. The content of A+T (61.2%) was higher than that of C+G (38.3%), showing a bias in base content of A+T. Saturation plots show linear relationships between uncorrected sequence divergence and both proportion transitions and transversions (Figures 6 and 7).

Phylogenetic Analyses

Neighbor-Joining Tree

The control region Neighbor-Joining tree (Figure 12) revealed four unified groups with high bootstrap support representing a monophyletic clade of *E. chuckwachatte* as the most ancestral lineage of the *E. jordani* species complex; a clade of *E. douglasi* as being the sister to both *E. jordani* and *E. etowahae*; an assemblage of *E. jordani*; and an

assemblage of *E. etowahae*. The node between *E. jordani* and *E. etowahae* was supported by 51% bootstrap confidence. Within the *E. jordani* assemblage there is a clade of Hatchett Creek fishes with 84% bootstrap support. Other than this Hatchett Creek clade, there is little phylogeographic signal within either *E. jordani* or *E. etowahae* populations.

Bayesian Likelihood Tree

The results from the control region Bayesian tree (Figure 13) reflected those found in the Neighbor-Joining analysis. The analysis was congruent in all major branching and topology, and clading of all taxa are largely consistent. The node separating *E. jordani* and *E. etowahae* had a strong posterior probability value of 82%.

Cytochrome *b* Gene Results:

Analysis of Alignment

1114 base pairs of the cyt *b* gene were amplified and sequenced for 11 individuals selected from divergent areas found from the control region phylogenetic trees. Within the alignment, 864 of 1114 sites were variable and 180 of these were potentially informative for parsimony analysis. Nucleotide composition averages consisted of: A=22.1%, T=29.9%, C=31.2%, and G=16.8%. The content of A+T (52%) was relatively equal to that of C+G (48%), showing only a slight bias in nucleotide base composition. Saturation plots show linear relationships between uncorrected sequence divergence and both proportion transitions and transversions (Figures 8 and 9). No stop codons were present in any of the sequences examined and no insertions or deletions were observed. For these reasons, it is believed that no pseudogenes were sequenced, and all sequences analyzed

represent *cyt b*. All sequences began with the start codon AAA, which codes for the amino acid phenylalanine.

Phylogenetic Analyses

The *cyt b* Neighbor-Joining and Maximum Parsimony trees (Figures 14 and 15) were largely congruent with the results found in the control region phylogenetic analyses except with the relationship of *E. douglasi*. The Maximum Parsimony tree placed *E. douglasi* as more closely related to *E. jordani* than to *E. etowahae* with 80% bootstrap confidence. The clade of *E. etowahae* was represented by a 100% bootstrap confidence value.

ND2 Gene Results:

Analysis of Alignment

1047 base pairs encompassing the entire ND2 gene were amplified and sequenced. The primers: ASN, GLN, MET, and TRP, (Table 6), (Figure 5) were tested to find which would work best for sequencing. GLN worked well to capture the beginning of the gene but the reverse primer ASN did not work effectively. A new forward primer was designed, SBRF (Table 6), (Figure 5), which worked well to overlap the end of GLN, starting at ~420 bp, and completed the sequence of the gene. These two primers worked well for the majority of the specimens, but failed to provide high quality sequence of the first ~120 bp of the ND2 gene in 16 of the individuals. Therefore another primer was designed, RGLN (Table 6), (Figure 5), to catch at about 210 bp of the ND2 gene and run reverse in order to complete sequencing of the beginning of the gene.

Sequencing revealed 105 distinct haplotypes. Within the 105 haplotypes, 319 of 1047 sites were variable and 209 of these were potentially informative for parsimony analysis. Nucleotide composition averages consisted of: A=24.3%, T=25.1%, C=34.5%, and G=16.1%. The content of A+T (49.4%) was relatively equal to that of C+G (50.5%), showing no bias in nucleotide base composition. Saturation plots show linear relationships between uncorrected sequence divergence and both proportion of transitions and transversions (Figures 10 and 11). No stop codons were present in any of the sequences examined and no insertions or deletions were observed. For these reasons, it is believed that no pseudogenes were sequenced, and all sequences analyzed represent ND2. All sequences began with the codon ATG, which codes for the amino acid methionine.

Phylogenetic Analyses

Neighbor-Joining Tree

Results of the ND2 Neighbor-Joining Tree (Figure 16) produced similar topologies and placement of groups as in the control region and *cyt b* trees with a few notable differences. The placement of *E. douglasi* was more closely related to *E. jordani* than *E. etowahae* (as in *cyt b* Maximum Parsimony tree) and four haplotypes had disparate clading. High bootstrap values were present at the nodes of the four major groups. A clade of Little Armuchee Creek fishes in the *E. jordani* assemblage was revealed with 74% bootstrap support and the Hatchett Creek clade node was supported by a 99% bootstrap value. Little phylogeographic structure was present except for the Hatchett Creek and Little Armuchee Creek clades.

Bayesian Likelihood Tree

Results of the ND2 Bayesian Maximum Likelihood tree (Figure 17) reflected those found from the ND2 Neighbor-Joining tree. 100% posterior probability values were present at nodes between the four major groups.

Combined Data Results:

Analysis of Alignment

Aligned sequence data from the mtDNA control region (containing the tRNA-Phe gene, partial 12S rRNA gene) and ND2 gene were combined into a single data set comprising 2020 base pairs for phylogenetic analysis, since mtDNA is inherited as a single locus. The dataset contained 393 variable sites, 255 of which were informative for parsimony.

Phylogenetic Analyses

Results of the combined data Neighbor-Joining (Figure 18) and Bayesian Likelihood (Figure 19) trees were consistent with results obtained from the ND2 phylogenetic analyses. Also, the tree produced by PAUP for testing the topology and branching order with Maximum Parsimony was largely congruent.

Phylogeographic Analysis

Genetic analysis (Figure 20) and the corresponding phylogeographic analysis (Figure 21) document that *E. etowahae* haplotypes occur in two additional isolated populations located approximately 110 river kilometers downstream in the Etowah River system from the most downstream range reported in the species description by Wood and Mayden (1993). *E. jordani* and *E. etowahae* haplotypes appear to be in syntopy in two

areas (Raccoon Creek, six haplotypes; and the Lower Etowah River, five haplotypes) as revealed by genetic analysis.

DISCUSSION

All of the phylogenetic reconstruction methods (Neighbor-Joining, Bayesian Likelihood, and Maximum Parsimony) consistently revealed four distinct groups in phylogenetic trees representing *E. jordani* and the three species described out of the *E. jordani* species complex group by Wood and Mayden (1993). This pattern supports the recognition of *E. jordani*, *E. etowahae*, *E. douglasi*, and *E. chuckwachatte* as separate distinct species and each species exhibited its own unique set of mtDNA haplotypes.

The phylogenetic analyses were investigated using three different mitochondrial DNA genes (control region, cytochrome *b*, and ND2). An unresolved relationship of *E. douglasi* was represented by it being placed more closely related to *E. jordani* in the more variable ND2 gene phylogenies than in either the Control Region or *cyt b* analyses. The ND2 gene analyses also contained two haplotypes which claded differently than in the control region phylogenies: BAP1178j2 and BAP1178j3 (both from Raccoon Creek). The control region phylogenies placed them as clading with *E. etowahae*, but the ND2 analyses assigned them to the *E. jordani* clade. One explanation for this would be that the ND2 gene is more variable and contains more phylogenetic characters to help resolve the true relationship of these closely related sister species. This rationale would seem logical given the findings of the search for a highly variable gene from the data obtained from GenBank. And also, a study done with mammals has shown that the ND2 gene is evolving more rapidly than other mitochondrial proteins (Anderson *et al.*, 1982). Phylogenetic analyses with the ND2 gene also provided notably higher confidence, in the terms of bootstrap and

posterior probability values, of phylogenetic nodes and provided better population-level resolution for all four species.

Genetic analysis revealed *E. etowahae* haplotypes occurring in two additional isolated populations located approximately 110 river kilometers downstream in the Etowah River system from the most downstream range reported in the species description by Wood and Mayden (1993), which may have implications on management efforts in the Etowah River Basin and also on the status of this species under the Endangered Species Act. It points to a need to place Stamp Creek, Raccon Creek, and a portion of the Lower Etowah River under the Etowah Habitat Conservation Program and protect these additional areas under the ESA. Two areas were revealed as possible sites of syntopy between the Etowah and Greenbreast darters. This syntopy in Raccoon Creek and the Lower Etowah River may be the first report of this kind for *E. etowahae* and *E. jordani* sharing the same range. Or alternatively, this may be the first report of hybridization between the two species. The discovery of syntopy between *E. etowahae* and *E. jordani* doesn't immediately suggest hybridization. Due to the maternally inherited nature of mtDNA the true paternal parentage of the analyzed individuals cannot be determined with the methods utilized in this study. Other types of analyses can confirm/reject this hypothesis. Nuclear DNA markers, such as microsattelite analyses (which have proven effective in other closely related darter species) are needed to more fully address this problem.

The current morphological and meristic diagnostic characters have been shown to be inadequate or there is hybridization from Long Swamp/Smithwick Creeks down into Stamp Creek, Raccoon Creek, and the Lower Etowah River. Mistakes in specimen identifications made in the field based on the promoted diagnostic characters and/or

historic range have been made in Long Swamp Creek, based upon the mitochondrial DNA genetic analyses in this study. Little phylogeographic (no phylogenetic signal) structure is found within either *E. jordani* or *E. etowahae* throughout their respective ranges except for the Hatchett Creek clade (and possibly the Little Armuchee Creek clade) within the *E. jordani* assemblage. The Hatchett Creek population should be considered for possible evolutionarily significant unit (ESU) recognition and, if granted this status, might be managed separately in the most appropriate manner.

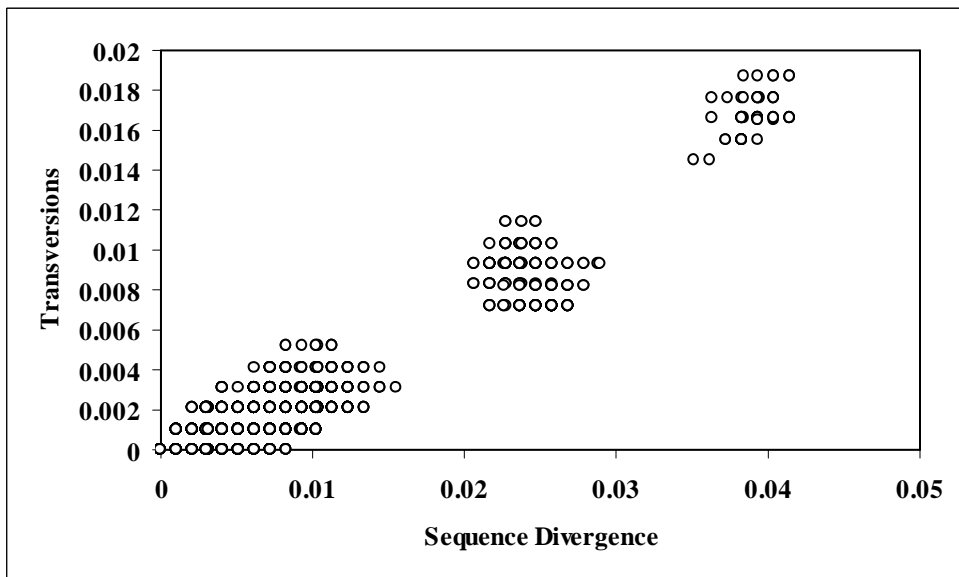
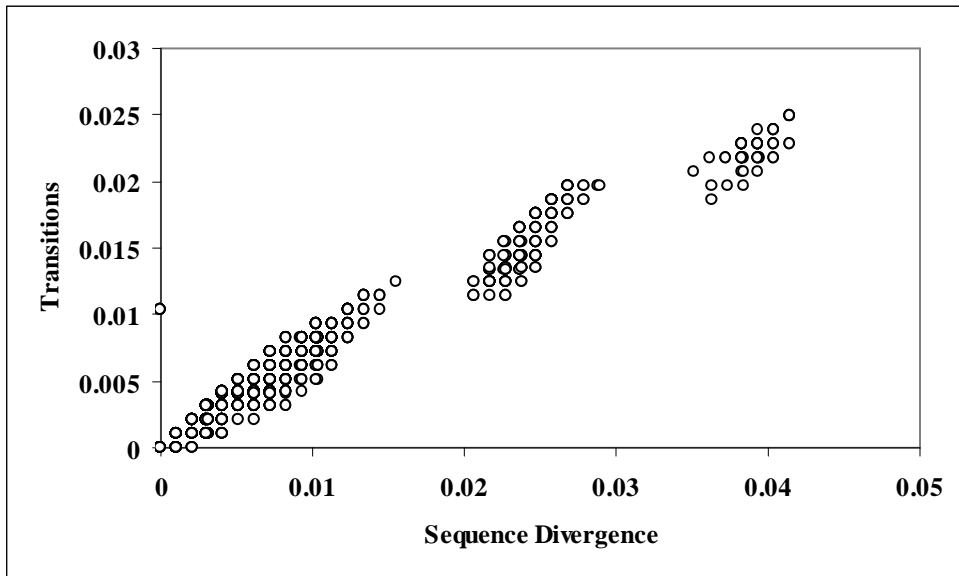
Comparative Biogeography

Geographic ranges of *Nothonotus* and *Ulocentra* overall seem to have a high level of concordance with phylogeography within the Mobile System. *E. etowahae* has a similar geographic range with the threatened Cherokee darter, *E. scotti*, and both are endemic to the Etowah River basin. Furthermore, the sister species to *E. etowahae*, *E. jordani*, has a strikingly similar geographic distribution to *E. coosae* in the Conasauga, Coosawattee, Oostanaula, Coosa, and Lower Etowah. A study by Storey (2003) reports three evolutionary significant units (ESU) of *E. scotti* occupying the Upper, Middle, and Lower sections of the Etowah River. *E. etowahae*, however, shows surprisingly little phylogenetic structure throughout the Etowah System; phylogenetic analysis documents haplotypes occupying the type locality of *E. etowahae* in the upper portion of the Etowah River grouping with samples taken from areas from the lower portion (e.g., Stamp Creek and the Lower Etowah River). The border between these two sister species pairs (*E. etowahae*/*E. jordani* and *E. scotti*/*E. coosae*) occurs near the physiogeographic province division of the Blue Ridge and Piedmont physiogeographic zones. Racoon Creek (which

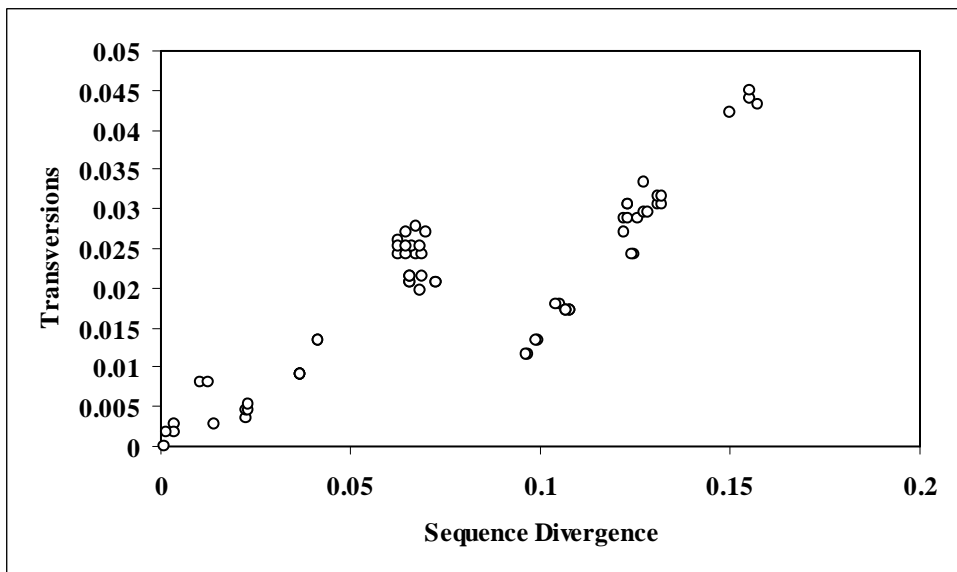
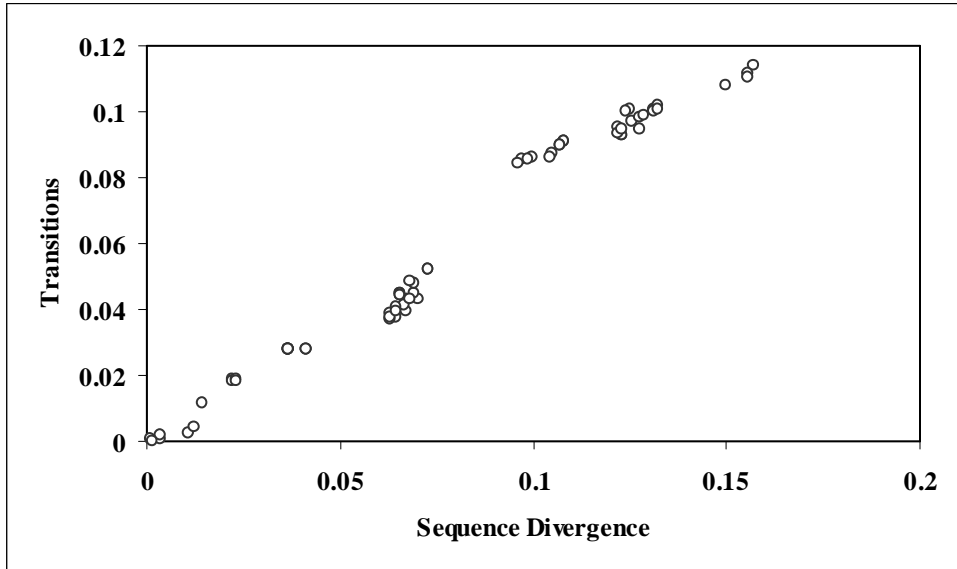
has its headwaters in the Piedmont) has both *E. etowahae* and *E. jordani* haplotypes, along with *E. scotti* and *E. coosae* haplotypes. Therefore, this is a syntopic region for both species pairs. The Lower ESU of *E. scotti* and *E. coosae* appears to be hybridizing in Pettit Creek, and although no *Nothonotus* have been found in Pettit Creek, both *E. jordani* and *E. etowahae* haplotypes have been found in the mainstem of the Lower Etowah River (approximately 25 river km downstream from the mouth of Pettit Creek). Both Pettit Creek and the Lower Etowah River are in the Blue Ridge geographic system wherein both cases we have found a narrow region of syntopy right at the physiogeographic region boundary.

Future Directions

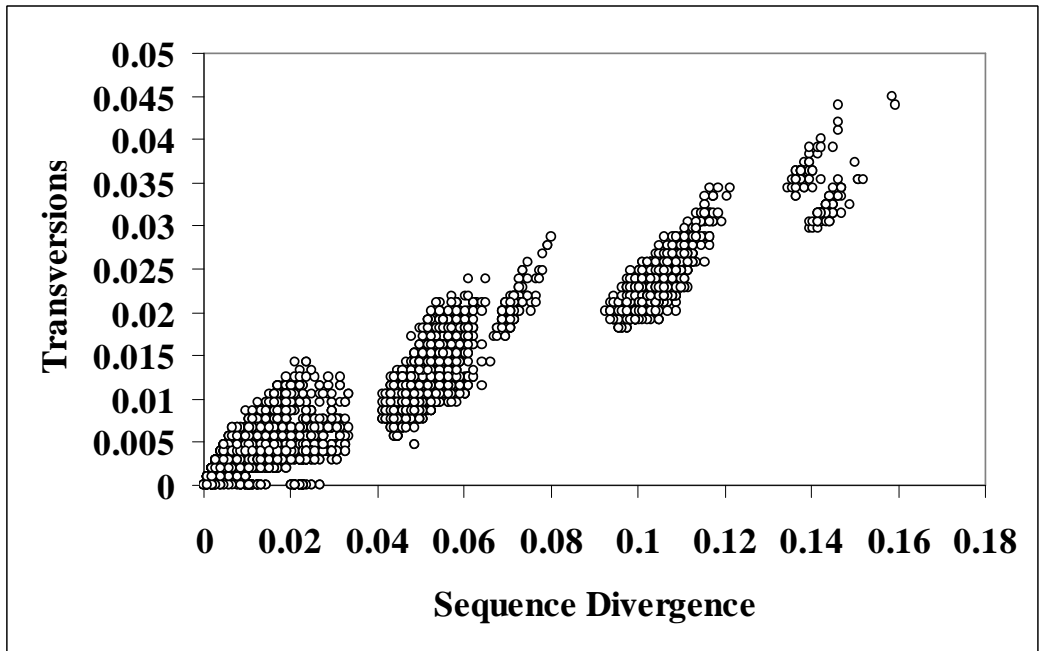
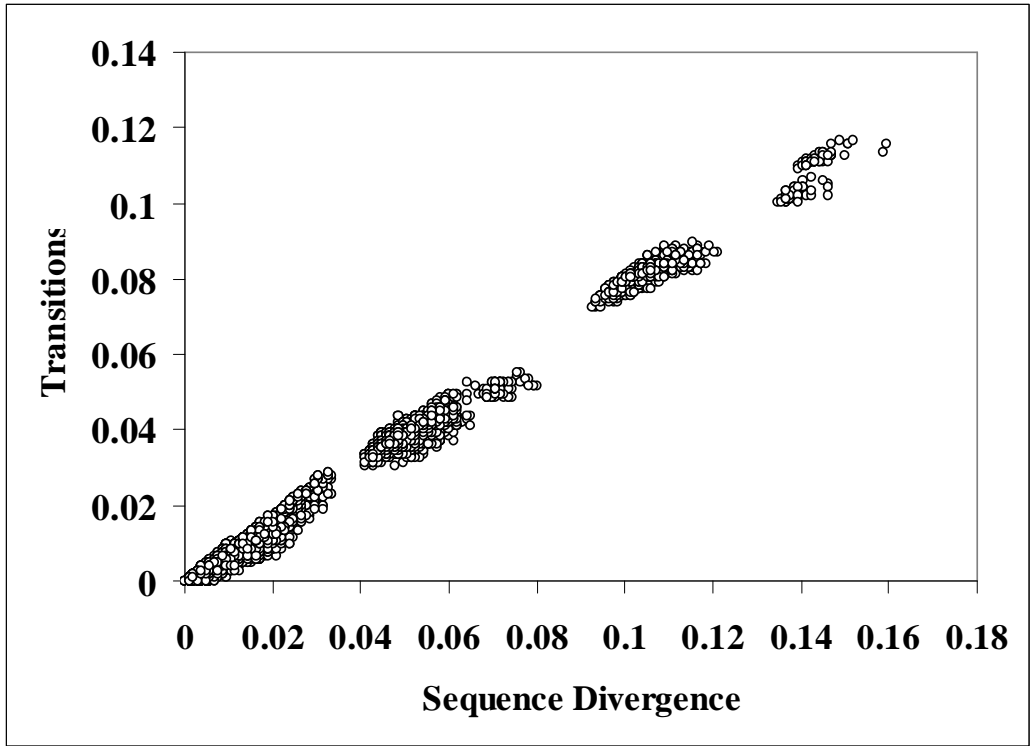
The next step in clarifying the relationships of Etowah and Greenbreast darters will be to conduct nuclear DNA analyses in order to confirm or reject the hypothesis of hybridization and to further ascertain the true geographic range of each of these sister species. The results of these analyses will also dictate the methods of management and status under the Endangered Species Act. A thorough meristic and morphologic investigation (including scale counts and osteology) will also be necessary in order to achieve the goal of finding enough morphological markers to be able to provide a sound redescription of these fishes.



Figures 6 and 7. Control region frequencies of pairwise observed transitions (top) and transversions (bottom) plotted against nucleotide sequence divergence.



Figures 8 and 9. Cytochrome *b* frequencies of pairwise observed transitions (top) and transversions (bottom) plotted against nucleotide sequence divergence.



Figures 10 and 11. ND2 Frequencies of pairwise observed transitions (top) and transversions (bottom) plotted against nucleotide sequence divergence.

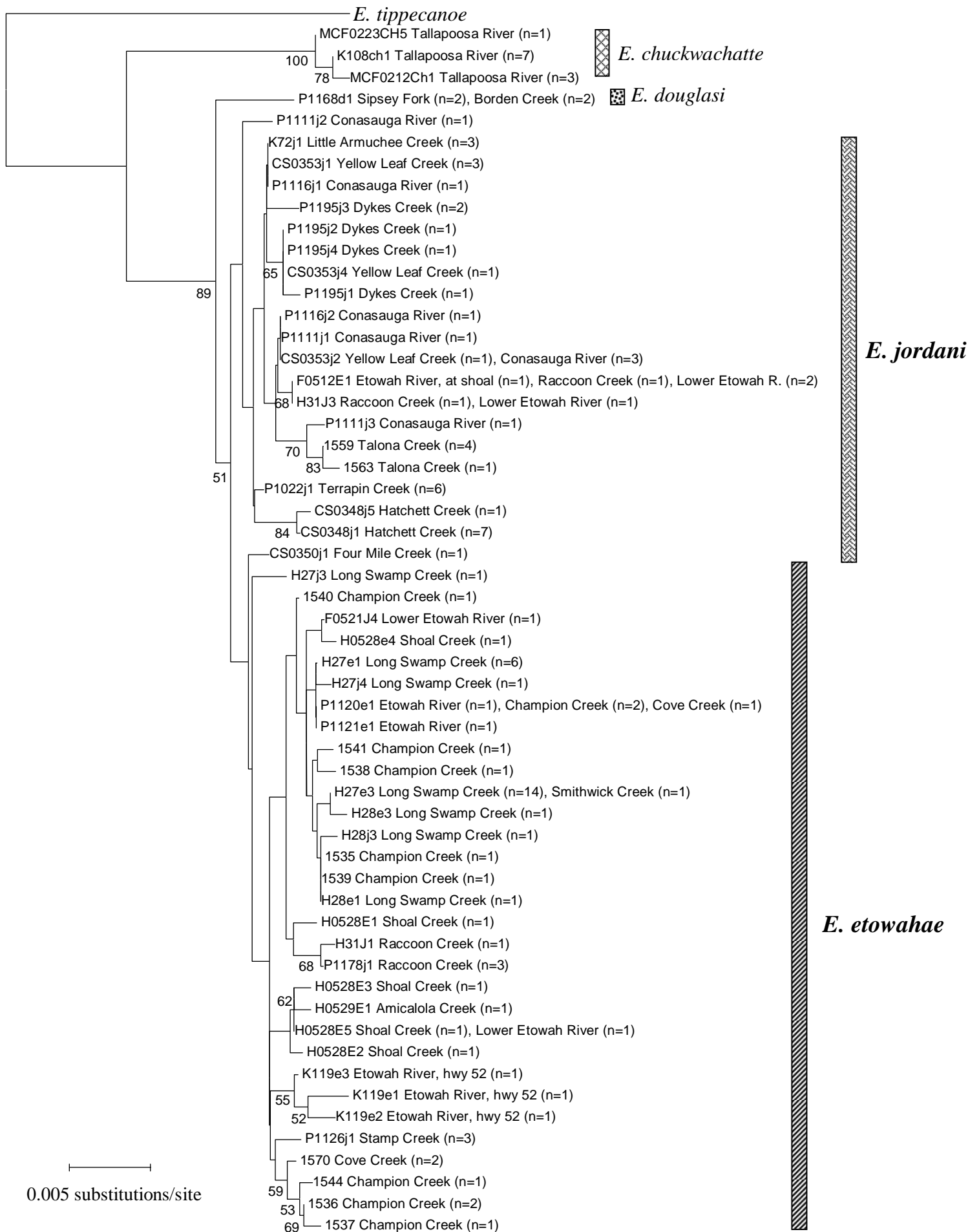


Figure 12. Control Region Neighbor-Joining Tree, conducted in MEGA v 3.1 (Kumar *et al.*, 2004), rooted with *E. tippecanoe*. Numbers below nodes represent bootstrap values greater than 50%.

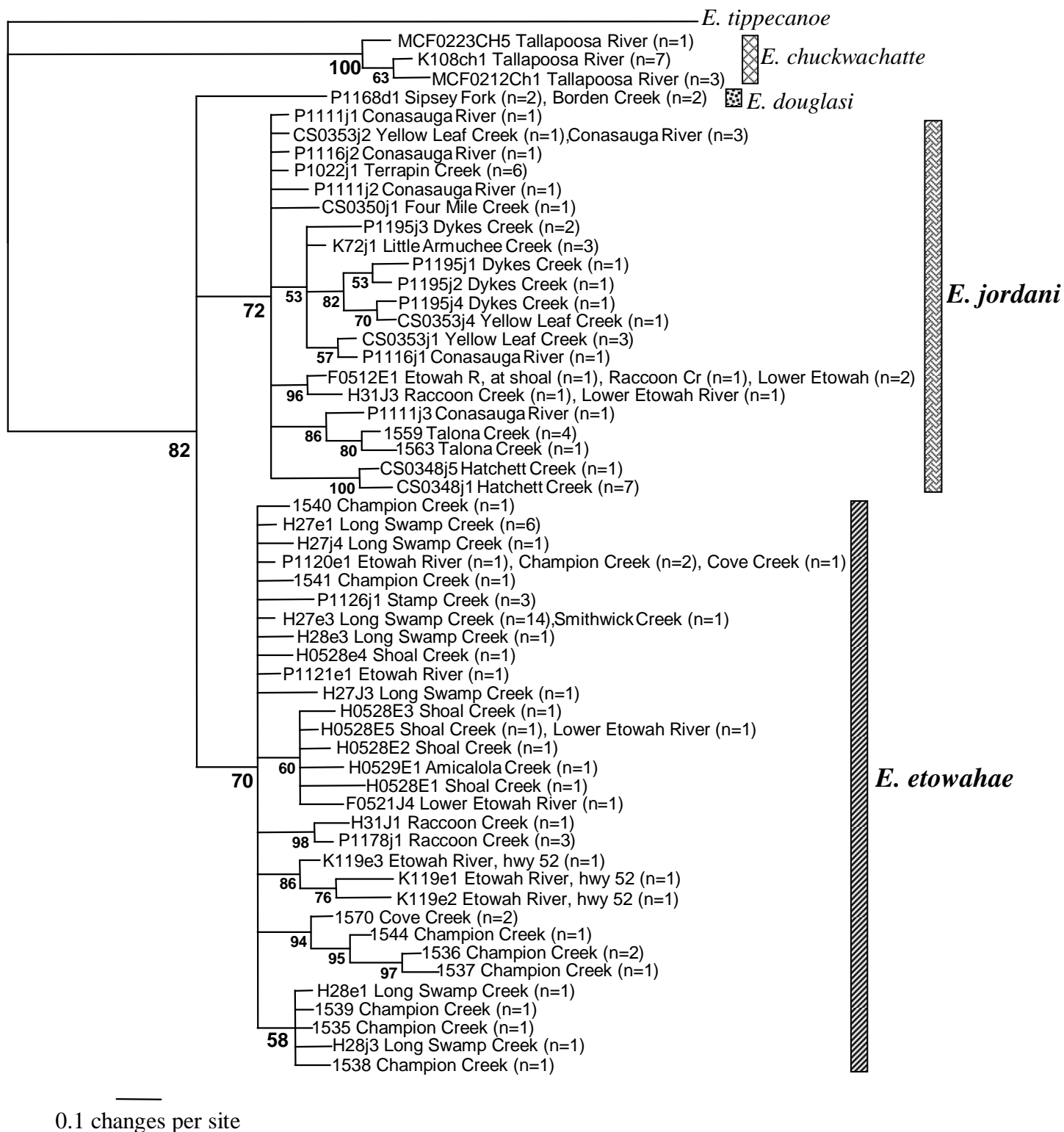


Figure 13. Control Region Bayesian Likelihood Tree, Constructed with MrBayes v3.1 (Huelsenbeck and Ronquist, 2001). Consensus tree with posterior probability support greater than 50% below corresponding nodes. Rooted with *E. tippecanoe*

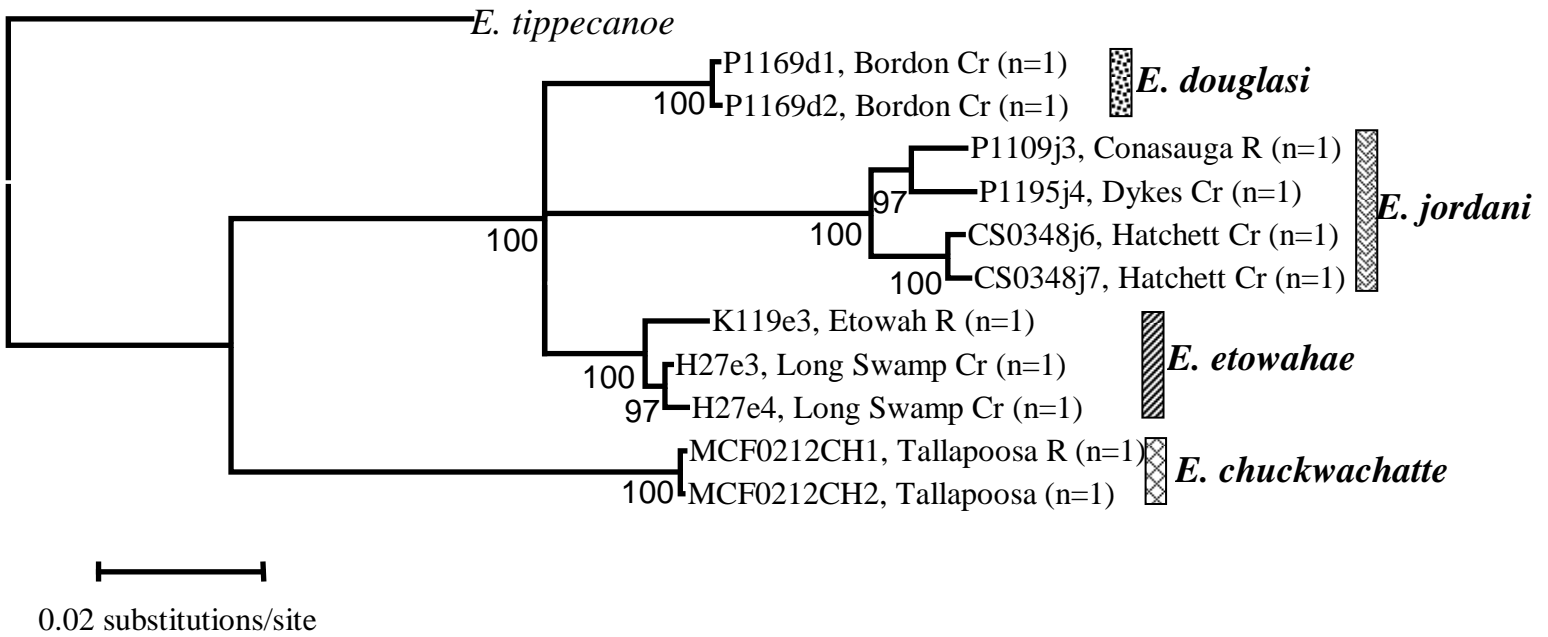


Figure 14. Cyt *b* Neighbor-Joining Tree, conducted in MEGA v 3.1 (Kumar *et al.*, 2004), rooted with *E. tippecanoe*. Numbers below nodes represent bootstrap values greater than 50%.

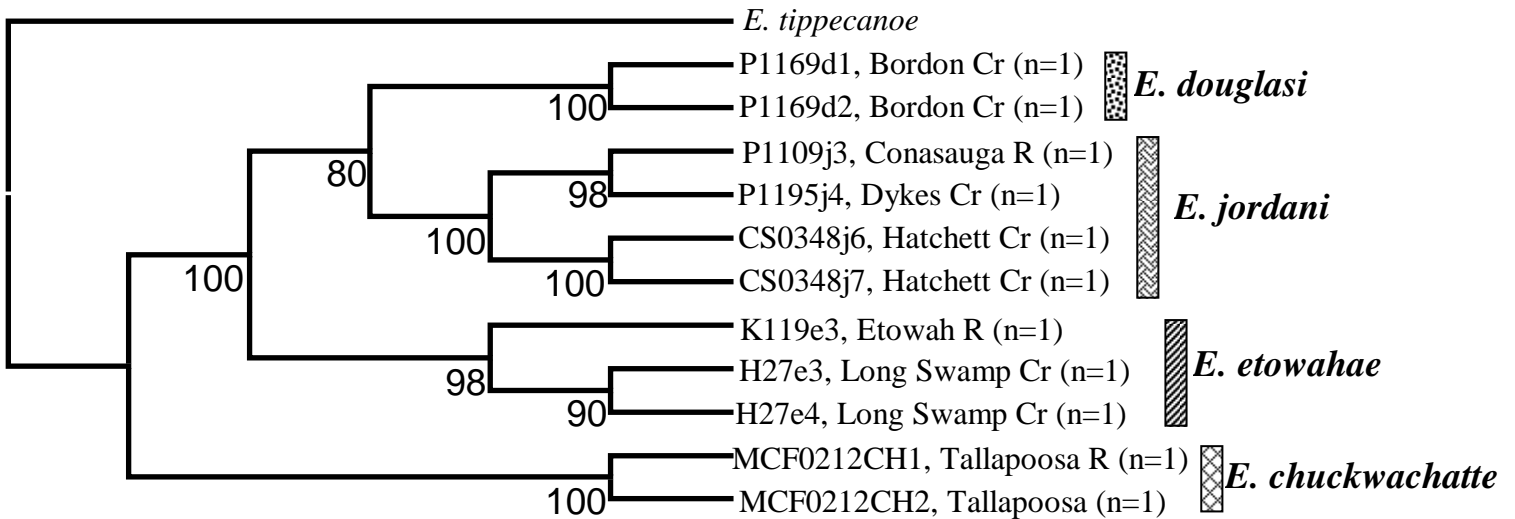


Figure 15. Cyt *b* Maximum Parsimony Tree, conducted in MEGA v 3.1 (Kumar *et al.*, 2004), branch and bound heuristic search with 1,000 bootstrap replicates, rooted with *E. tippecanoe*. Numbers below nodes represent bootstrap values greater than 50%.

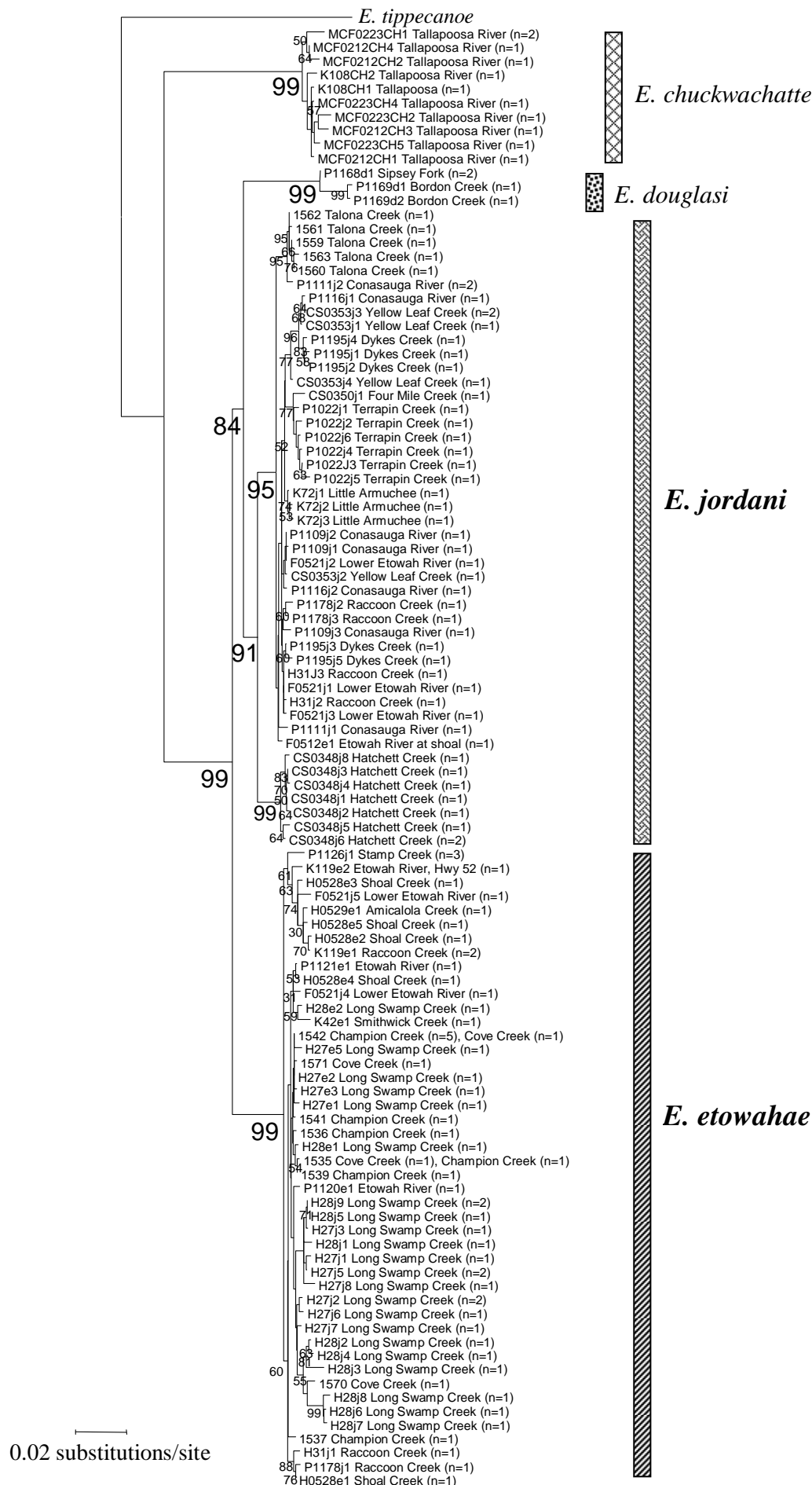


Figure 16. ND2 Neighbor-Joining Tree, conducted in MEGA v 3.1 (Kumar *et al.*, 2004), rooted with *E. tippecanoe*. Numbers below nodes represent bootstrap values greater than 50%.

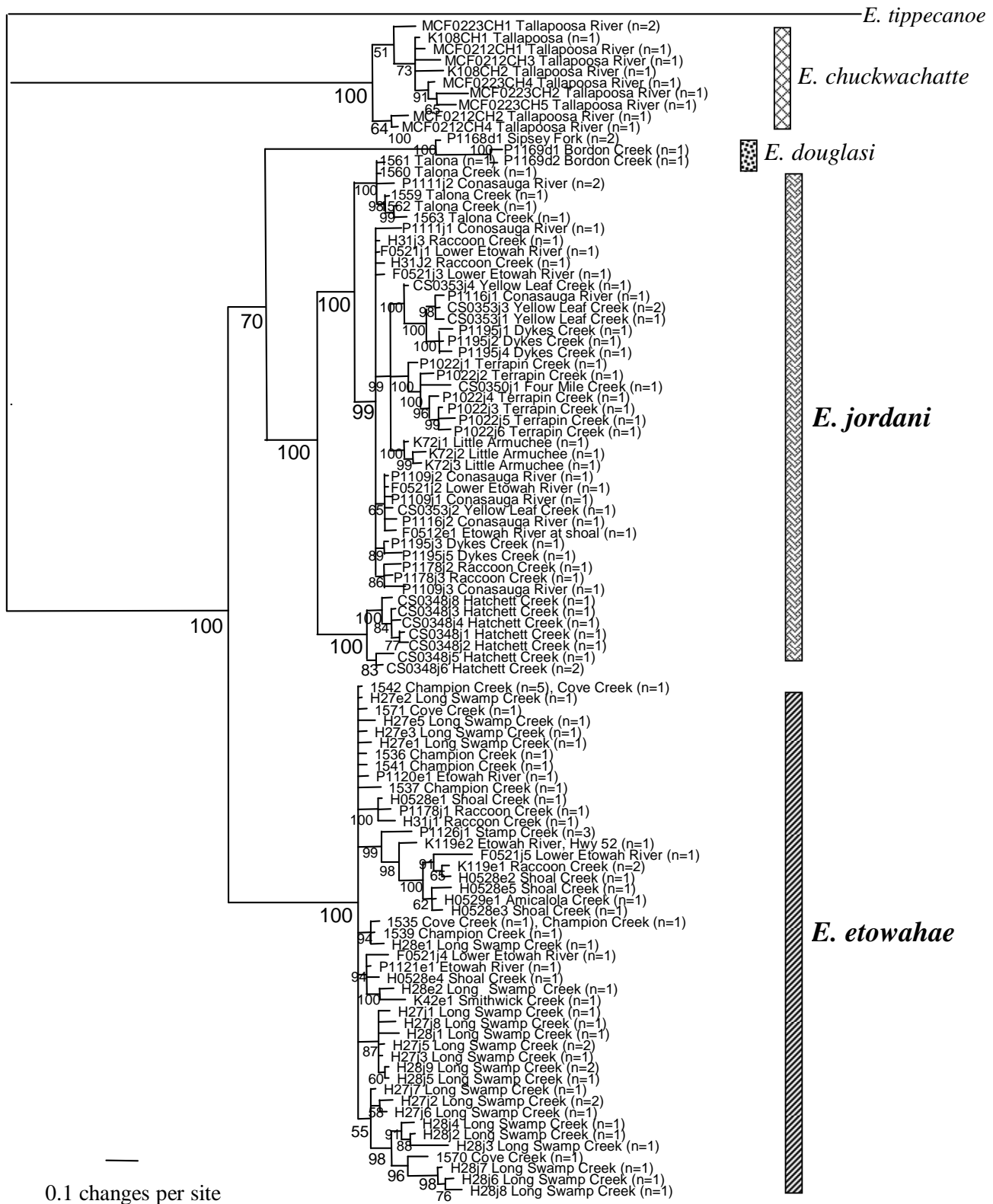


Figure 17. ND2 Bayesian Likelihood Tree Constructed with MrBayes v3.1 (Huelsenbeck and Ronquist, 2001). Consensus tree with posterior probability support greater than 50% below corresponding nodes. Rooted with *E. tippecanoe*

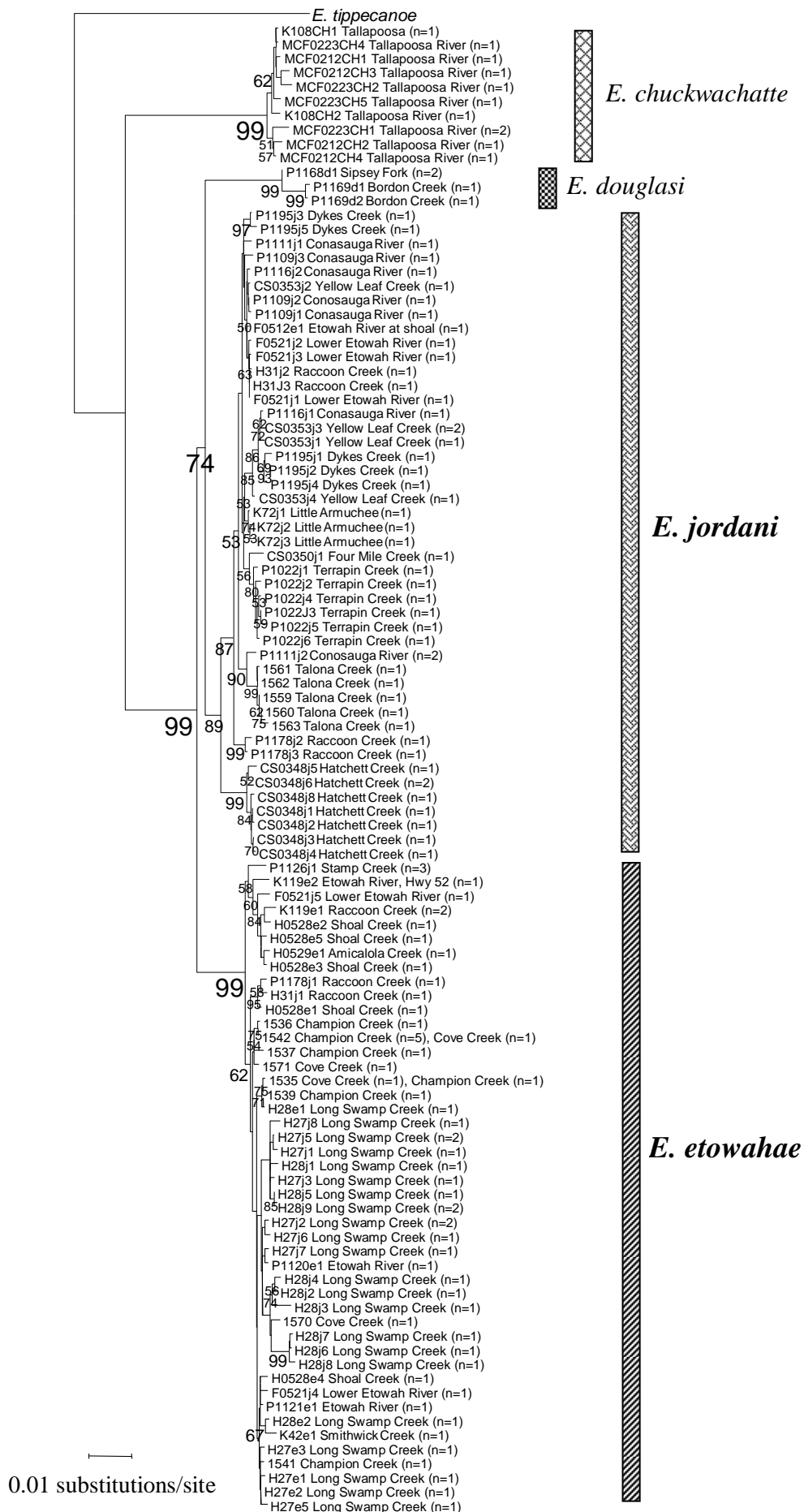


Figure 18. Combined Data Neighbor-Joining Tree conducted in MEGA v 3.1 (Kumar *et al.*, 2004), rooted with *E. tippecanoe*. Numbers below nodes represent bootstrap values greater than 50%.

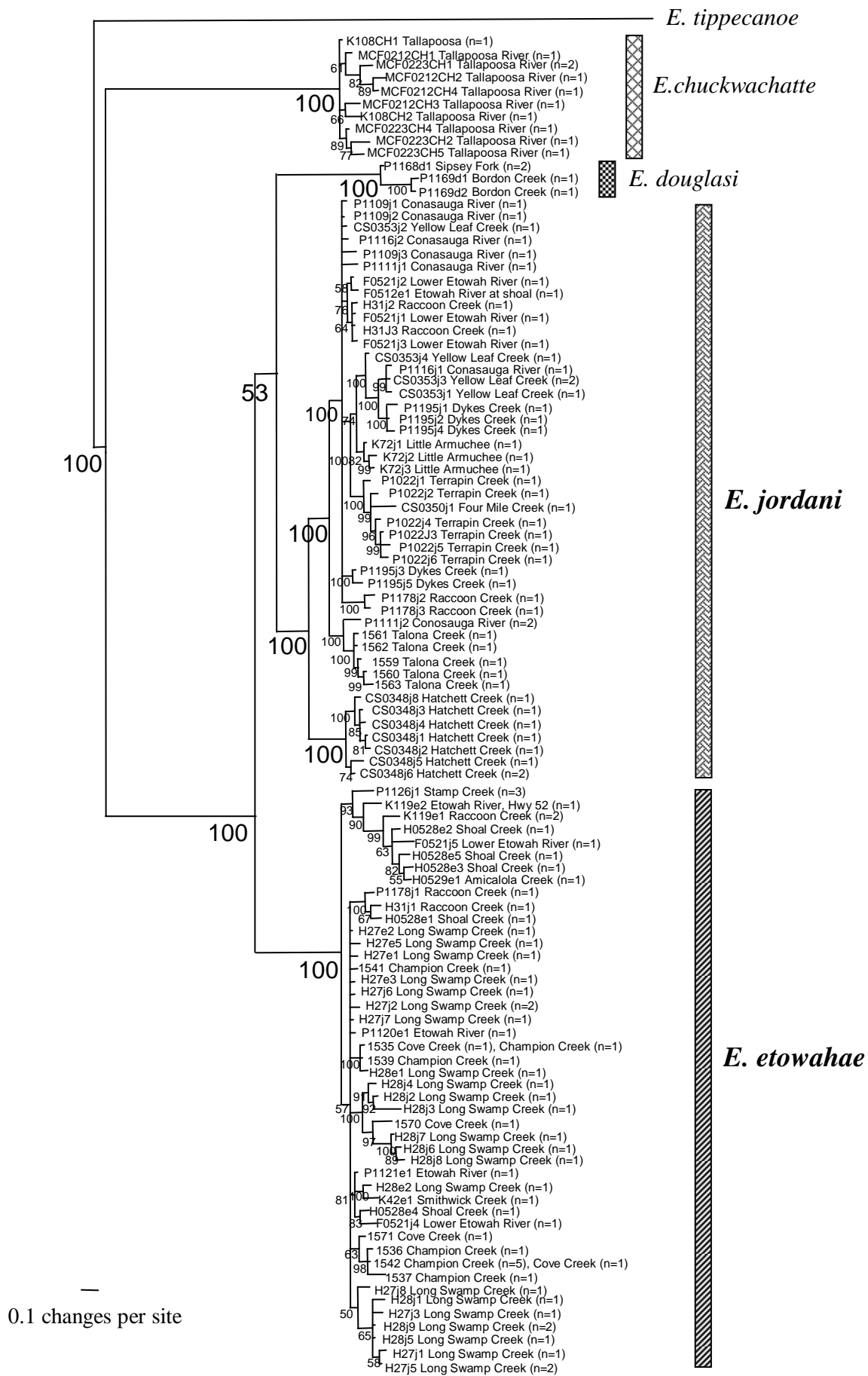


Figure 19. Combined Data Bayesian Likelihood Tree Constructed with MrBayes v3.1 (Huelsenbeck and Ronquist, 2001). Consensus tree with posterior probability support greater than 50% below corresponding nodes. Rooted with *E. tippecanoe*

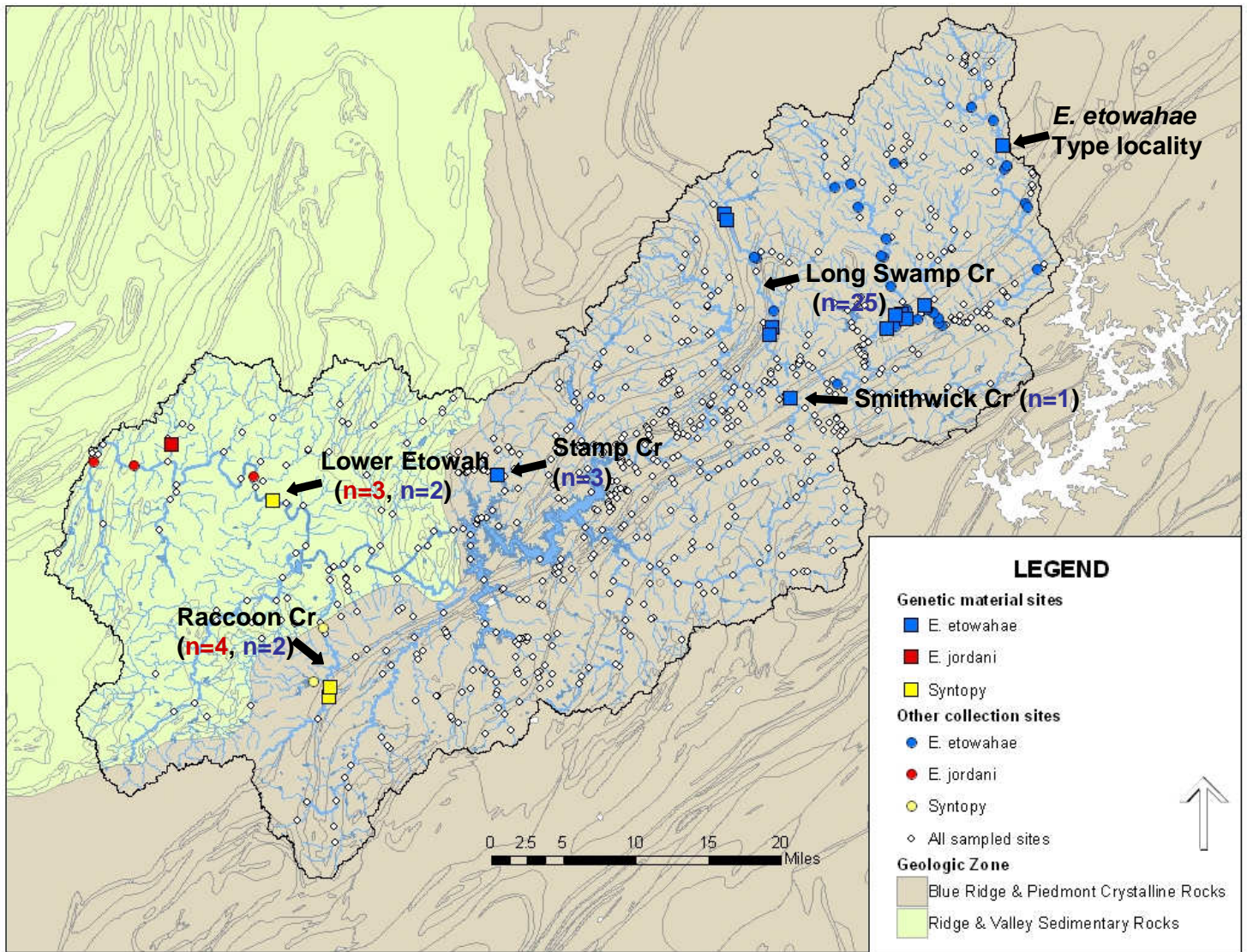


Figure 20. Distribution of *E. etowahae* (blue) and *E. jordani* (red) in the Etowah River System as determined by genetic analysis. Areas of syntopy are in yellow. Colored squares represent genetically analyzed specimens whereas colored circles represent historic collections archived in the Georgia Museum of Natural History. Open (white) circles indicate areas sampled where no *Nothonotus* individuals have been found.

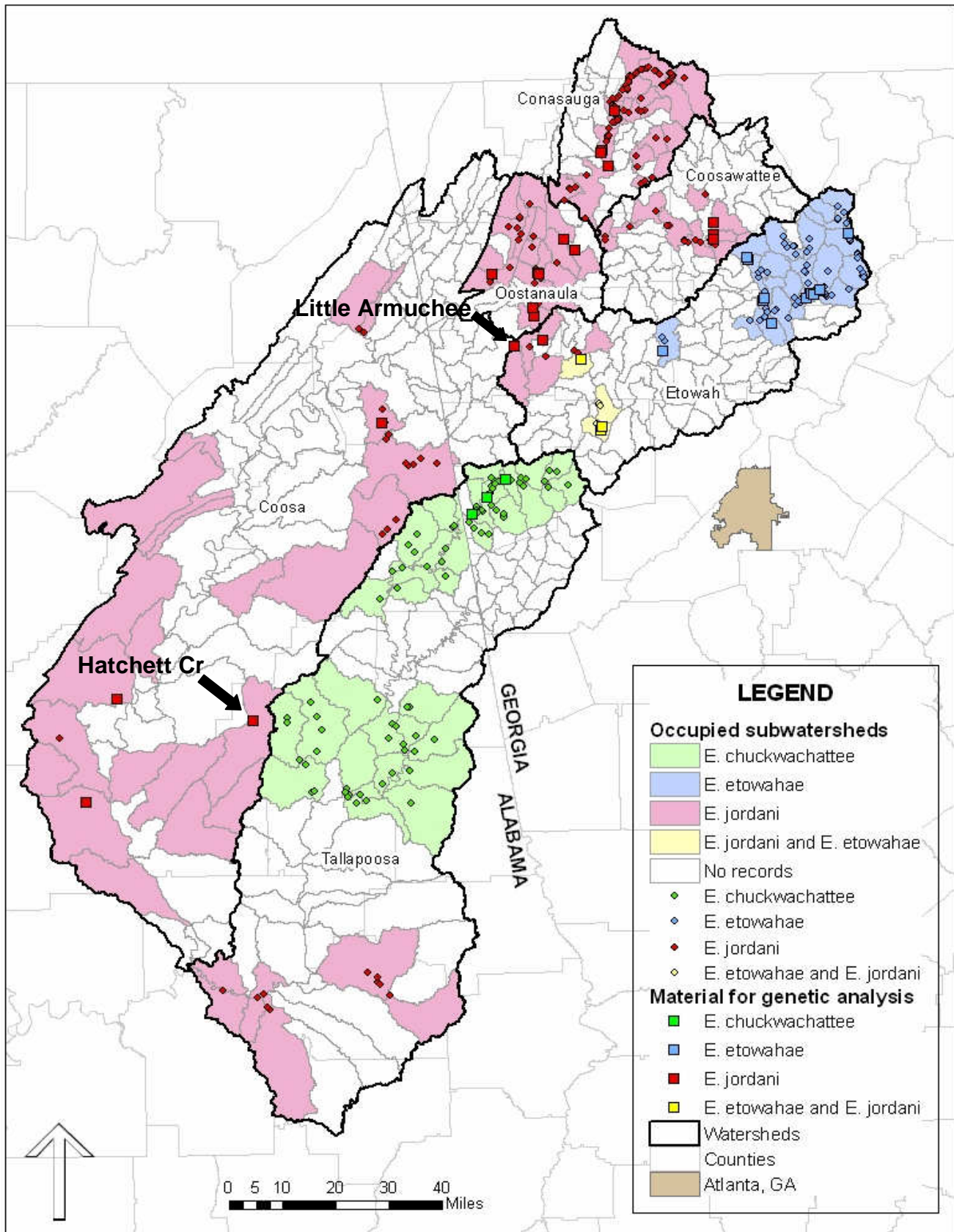


Figure 21. Phylogeography of *E. chuckwachattee*, *E. etowahae*, and *E. jordani* in Georgia and Alabama. *E. douglasi* is not represented because its range is beyond the range of this map. The two phylogeographic significant sites (Hatchett and Little Armuchee Creeks) are labeled.

Works Cited

- Anderson, S., de Bruijn, M. H. L., Coulson, A. R., Eperon, I. C., Sanger, F., and Young, I. G. (1982). Complete sequence of bovine mitochondrial DNA: Conserved features of the mammalian mitochondrial genome. *J. Mol. Biol.* **156**:683-717.
- Avise, J. C. (2000). *Phylogeography*, Harvard Univ. Press, London.
- Avise, J. C., Arnold, J., Ball, R. M., Bermingham, E., Lamb, T., Neigel, J. E., Reeb, C. A., Saunders, N. C. (1987). Intraspecific Phylogeography: The mitochondrial DNA bridge between population genetics and systematics. *Ann. Rev. Ecol. Syst.* **18**:489-522.
- Bailey, R.M. (1959). *Etheostoma acuticeps*, a new darter from the Tennessee River system, with remarks on the subgenus *Nothonotus*. *Occasional Papers of the Museum of Zoology*, Univ. of Michigan, no. 603. 10 pp.
- Bailey, R. M., Winn, H. E., and Smith, C. L. (1954). Fishes from the Escambia River, Alabama and Florida, with ecologic and taxonomic notes. *Proc. Acad. Nat. Sci. Phila.* **106**:109-164.
- Bailey, R. M., and Gosline, W. A. (1955). Variation and systematic significance of vertebral counts in the American fishes of the family Percidae. *Misc. Pub. Mus. Zool. Univ. Michigan* **93**:1-44.
- Bailey, R. M., and Etnier, D. A. (1988). Comments on the subgenera of darters (Percidae) with descriptions of two new species of *Etheostoma* (*Ulocentra*) from southeastern United States. *Misc. Pub. Mus. Zool. Univ. Michigan* **175**:1-48.
- Bart, H. L., Jr., and Page, L. M. (1992). The influence of size and phylogeny on life history variation in North American percids, p. 573-599. In: Systematics, historical ecology, and North American freshwater fishes. R. L. Mayden (ed.). Stanford Univ. Press, Stanford, CA.
- Boore, J. L. (1999). Animal mitochondrial genomes. *Nucleic Acids Res.* **27**:1767-1780.
- Boschung, H. T., Mayden, R. L., and Tomelleri, J. R. (1992). *Etheostoma chermoki*, a new species of darter (Teleostei: Percidae) from the Black Warrior River drainage of Alabama. *Bull. Alabama Mus. Nat. Hist.* **13**:11-20.
- Boschung, H. T., and Mayden, R.L. (2004). Fishes of Alabama, Smithsonian Institution. Washington D.C.
- Brody, J. R., and Kern, S. E. (2004). Sodium Boric Acid: A tris-free, cooler conductive medium for DNA electrophoresis. *Biotechniques* **36**:214-216.

- Burkhead, N. M. (1992). Results of a conservation status survey for two freshwater fishes, the Cherokee and Etowah darters (Pices, Percidae), endemic to the Etowah River System of North Georgia. Report to the Jacksonville, Florida Office of the U.S. Fish and Wildlife Service, Jacksonville, Florida.
- Burkhead, N. M., S. J. Walsh, B. J. Freeman, and J. D. Williams. (1997). Status and Restoration of the Etowah River, an imperiled Southern Appalachian ecosystem. In: Aquatic fauna in peril: the Southeastern perspective. G. W. Benz and D. E. Collins, eds. Special Publication I, Southeast Aquatic Research Institute, Decatur, GA.
- Burr, B. M., and Mayden, R. L. (1992). Phylogenetics and North American freshwater fishes, p. 18-75. In: Systematics, historical ecology, and North American freshwater fishes. R. L. Mayden (ed.). Stanford Univ. Press, Stanford, CA.
- Butler, R. S., and Mayden, R. L. (2003). Cryptic Biodiversity. *Endangered Species Bulletin*, March/April, Volume XXVII, 2:24-26.
- Cabot, E. L., and Beckenbach, A. T. (1989). Simultaneous editing of multiple nucleic acid and protein sequences with ESEE. *Comput. Appl. Biosci.* 5:233-234.
- Claridge, M.F., Dawah, H.A. & Wilson, M.R. (1997). Species in insect herbivores and parasitoids – sibling species, host races and biotypes. In Species. *The Units of Biodiversity*, eds Claridge, M.F., Dawah, H.A. & Wilson, M.R. pp.247-272. The Systematics Association Special Volume Series 54. Chapman & Hall, London.
- Cole, C. F. (1967). A study of the eastern Johnny darter, *Etheostoma olmstedi* Storer (Teleostei, Percidae). *Chesapeake Sci.* 8:28-51.
- Collette, B. B. (1962). The swamp darters of the subgenus *Hololepis* (Pices, Percidae). *Tulane Stud. Zool.* 9:115-211.
- Collette, B. B. (1965). Systematic significance of breeding tubercles in fishes of the family Percidae. *Proc. U.S. Nat. Mus.* 17:567-614.
- Collette, B. B. (1967). The taxonomic history of the darters (Percidae: Etheostomatini). *Copeia* 1967:814-819.
- Etnier, D. A., and Bailey, R. M. (1989). *Etheostoma (Ulocentra) flavum*, a new darter from the Tennessee and Cumberland drainages. *Occas. Pap. Michigan Mus. Zool.* 717:1-24.
- Etnier, D. A., and Williams, J. D. (1989). *Etheostoma (Nothonotus) wapiti* (Osteichthyes: Percidae), a new darter from the southern bend of the Tennessee River system in Alabama and Tennessee. *Proc. Of the Biol. Society of Washington* 102:987-1000.

- Faber, J.E. and C.A. Stepien. (1997). The utility of mitochondrial DNA control region sequences for analyzing phylogenetic relationships among populations, species and genera of the Percidae. pp. 125-139, In: T.D. Kocher and C.A. Stepien (eds), *Molecular Systematics of Fishes*. Academic Press, San Diego, CA.
- Frankham, R., Ballou, J. D., Briscoe, D. A. (2002). Introduction to Conservation Genetics. Cambridge University Press.
- Gilbert, C. H. (1891). Report of explorations made in Alabama during 1889, with notes on the fishes of the Tennessee, Alabama, and Escambia rivers. *Bull. U.S. Fish Comm.*, **9**:143-159.
- Howell, W. M. (1968). Taxonomy and distribution of the percid fish, *Etheostoma stigmaeum* (Jordan), with the validation and redescription of *Etheostoma davisoni* Hay. Unpubl. PhD. Diss. Univ. Alabama. 113 pp.
- Jordan, D. S. (1885). A catalog of the fishes known to inhabit the waters of North America, north of the Tropic of Cancer, with notes on the species discovered in 1883. *Ann. Rep. Comm. Fish and Fish*. pt. 13, pp. 789-973.
- Jordan, D. S., and Evermann, B. W. (1890). Description of a new species of fish from Tippecanoe River, Indiana. *Proc. U.S. Nat. Mus.* **13**:3-4.
- Jordan, D. S., Evermann, B. W., Clark, H. W. (1930). Checklist of the fish and fishlike vertebrates of North and Middle America north of the boundary of Venezuela and Columbia. *Rep. U.S. Comm. Fish.*, App. 10, Washington, D.C.
- Jordan, D.S. and Gilbert, C. H. (1882). Synopsis of the Fishes of North America. 8vo, pp. 1018, Washington.
- Kocher, T. D., Conroy, J. A., McKaye, K. R., Stauffer, J. R., and Lockwood, S. F. (1995). Evolution of NADH Dehydrogenase Subunit 2 in East African Cichlid Fish. *Molecular Phylogenetics and Evolution* **4**:420-432.
- Kuehne, R. A., and Barbour, R. W. (1983). The American darters. Univ. Press of Kentucky, Lexington.
- Kumar, S., Tamura, K., and Nei, M. (1993). *MEGA1.02*: Molecular Evolutionary Genetics Analysis. The Pennsylvania State University.
- Kumar, S., Tamura, K., and Nei, M. (2004). *MEGA3*: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. *Briefings in Bioinformatics* **5**:150-163.
- Mann, C. C., and Plummer, M. (2005). Is the Endangered Species Act in danger? *Science* **267**:1256-1258.

- Maniatis, T., Fritsch, E. F., and Sambrook, J. (1982). Molecular Cloning. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
- Mayden, R. L. (1988). Vicariance biogeography, parsimony, and evolution in North American freshwater fishes. *Syst. Zool.* **37**:329-355.
- Mettee, M. F., O'Neil, P.E., and Pierson, J. M. (1996). Fishes of Alabama and the Mobile Basin. Oxmoor House. Birmingham, AL.
- Moritz, C. (1995). Uses of molecular phylogenies for conservation. *Phil. Trans. Roy. Soc. Lond.* **349**:113-118.
- Near, T. J., and Keck, B. P. (2005). Dispersal, vicariance, and timing of diversification in *Nothonotus* darters. *Molecular Ecology* **14**:3485-3496.
- Nelson, J. S., Crossman, E. J., Espinoza-Perez, Findley, L. T., Gilbert, C. R., Lea, R. N., and Williams, J. D. (2004). Common and Scientific Names of Fishes from the United States, Canada, and Mexico. *Am. Fish. Soc.*, Sp. Pub. 29, Bethesda, MD.
- Nelson, J.S. (2006). Fishes of the World (fourth edition). Wiley & Sons, New York.
- Nylander, J. A. A. (2004). MrModelTest v2, Program distributed by author. Evolutionary Biology Centre, Uppsala University.
- Page, L. M. (1981b). The genera and subgenera of darters (Percidae, Etheostomatini). *Occas. Papers. Mus. Nat. Hist. Univ. Kansas* **90**:1-69.
- Page, L. M. (1983). Handbook of darters. T. F. H. Publications, Inc., Neptune City, N.J., 271 pp.
- Page, L. M., and Whitt, G. S. (1973b). Lactate dehydrogenase isozymes, malate dehydrogenase isozymes and tetrazolium oxidase mobilities of darters (Etheostomatini). *Comp. Biochem. Physio.* **44B**:611-623.
- Page, L. M., and Retzer, M. E. (1982). Spawning behavior in seven species of darters (Pices: Percidae). *Brimeleyana* **8**:135-143.
- Page, L. M., and Swofford, D. L. (1984). Morphological correlates of ecological specialization in darters. *Environ. Biol. Fish.* **11**:139-159.
- Page, L. M., Hardman, M., and Near, T. J. (2003). Phylogenetic relationships of barcheek darters (Percidae: *Etheostoma*, Subgenus: *Catonotus*) with descriptions of two new species. *Copeia* **3**:512-530.
- Page, R. D. M. (1996). TREEVIEW: An application to display phylogenetic trees on

- personal computers. *Computer Applications in the Biosciences* **12**:357-358.
- Porter, B. A. (1999). Phylogeny, Evolution, and Biogeography of the Darter Subgenus *Ulocentra* (Genus *Etheostoma*, Family Percidae). Ph.D. thesis, The Ohio State University, Columbus.
- Porter, B. A., Cavender, T. M., and Fuerst, P.A. (2002). Molecular phylogeny of the Snubnose Darters, subgenus *Ulocentra* (Genus *Etheostoma*, Family *Percidae*). *Molecular Phylogenetics and Evolution* **22**:364-374.
- Ronquist, F. and Huelsenbeck, J. P. (2001). MRBAYES: Bayesian inference of phylogeny. *Bioinformatics* **17**:754-755.
- Ronquist, F. and Huelsenbeck, J. P. (2003). MRBAYES 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**:1572-1574.
- Saccone, C., Gissi, C., Reyes, A., Larizza, A., Sbisà, E., Pesole, G. (2002). Mitochondrial DNA in metazoan: degree of freedom in a frozen event. *Gene*, **286**:3-12.
- Simons, A. M. (1991). Phylogenetic relationships of the crystal darter, *Crystallaria asprella* (Teleostei: Percidae). *Copeia* **4**:927-936.
- Storey, C. M. (2003). Genetic population structure and life history aspects of the federally threatened Cherokee darter, *Etheostoma scotti*. Masters Thesis, University of Georgia, Athens, GA. 96 pp.
- Swift, C. C., Gilbert, C. R., Bortone, S. A., Burgess, G. H., and Yerger, R. W. (1986). Zoogeography of the freshwater fishes of the south-eastern United States: Savannah river to lake Pontchartrain. *Zoogeography of North American Freshwater Fishes* (eds C. H. Hocutt and E. O. Wiley). Wiley-Interscience, New York, pp. 213-265.
- Swofford, D. L. 2000. PAUP*. Phylogenetic Analysis Using Parsimony (*and Other Methods). Version 4. Sinauer Associates, Sunderland, Massachusetts.
- Thompson, J. D., Gibson, T. J., Plewniak, F., Jeanmougin, F. and Higgins, D. G. (1997) The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research*, **25**:4876-4882.
- Trautman, M. B. (1981). The Fishes of Ohio. Ohio State Univ. Press, Columbus, 782pp.
- Turner, T. F. (1987). Mitochondrial control region sequences and phylogenetic systematics of Darters (Teleostei: Percidae). *Copeia* **2**:319-338.
- U.S. Fish and Wildlife Service (USFWS). (1993). Proposed threatened status for

- the Cherokee darter and proposed endangered status for the Etowah darter. Federal Register 58(199):53696-53702.
- U.S. Fish and Wildlife Service (USFWS). (1994). Determination of threatened status for the Cherokee darter and endangered status for the Etowah darter. Federal Register 59(243):65505-12.
- Wiley, E. O., and Mayden, R. L. (1985). Species and speciation in phylogenetic systematics, with examples from the North American fish fauna. *Ann. Mo. Bot. Gard.* **72**:596-635.
- Williams, J. D., and Robison, H. W. (1980). *Ozarka*, a new subgenus of *Etheostoma* (Pices: Percidae). *Brimleyana* **4**:149-156.
- Williams, J. D., and Clemmer, G. H. (1991). *Scaphirhynchus suttkusi*, a new sturgeon from the Mobile Basin of Alabama and Mississippi. *Bull. Alabama Mus. Nat. Hist.* **10**:17-31.
- Wolstenholme, D. R. (1992). Animal mitochondrial DNA: structure and evolution. *Int. Rev. Cytol.* **141**:173-216.
- Wood, R. M. (1996). Phylogenetic systematics of the darter subgenus *Nothonotus* (Teleostei: Percidae). *Copeia* **2**:300-318.
- Wood, R. M., and Mayden, R.L. (1993). Systematics of the *Etheostoma jordani* Species Group (Teleostei: Percidae), with descriptions of three new species. *Bull. Alabama Mus. Nat. Hist.* **16**:31-46.
- Zorach, T. (1972). Systematics of the percid fishes, *Etheostoma camurum* and *E. chlorobranchium* new species, with a discussion of the subgenus *Nothonotus*. *Copeia* **3**:427-447.

APPENDIX A

Table 1. Field site numbers and specimen labels (species were identified, at time of collection, based on external morphology and historic ranges).

	GENUS	SPECIES	FIELD SITE#	Specimen ID
1	<i>Etheostoma</i>	<i>chuckwachatte</i>	JRK108	K108c1
2	<i>Etheostoma</i>	<i>chuckwachatte</i>	JRK108	K108c2
3	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0212	MCF0212c1
4	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0212	MCF0212c2
5	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0212	MCF0212c3
6	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0212	MCF0212c4
7	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0223	MCF0223c1
8	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0223	MCF0223c2
9	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0223	MCF0223c3
10	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0223	MCF0223c4
11	<i>Etheostoma</i>	<i>chuckwachatte</i>	MCF0223	MCF0223c5
12	<i>Etheostoma</i>	<i>douglasi</i>	BAP1168	P1168d1
13	<i>Etheostoma</i>	<i>douglasi</i>	BAP1168	P1168d2
14	<i>Etheostoma</i>	<i>douglasi</i>	BAP1169	P1169d1
15	<i>Etheostoma</i>	<i>douglasi</i>	BAP1169	P1169d2
16	<i>Etheostoma</i>	<i>etowahae</i>	MMH0528	H0528e1
17	<i>Etheostoma</i>	<i>etowahae</i>	MMH0528	H0528e2
18	<i>Etheostoma</i>	<i>etowahae</i>	MMH0528	H0528e3
19	<i>Etheostoma</i>	<i>etowahae</i>	MMH0528	H0528e4
20	<i>Etheostoma</i>	<i>etowahae</i>	MMH0528	H0528e5
21	<i>Etheostoma</i>	<i>etowahae</i>	MMH0529	H0529e1
22	<i>Etheostoma</i>	<i>etowahae</i>	BJF0512	F0512e1
23	<i>Etheostoma</i>	<i>etowahae</i>	MMH0127	H27e1
24	<i>Etheostoma</i>	<i>etowahae</i>	MMH0127	H27e2
25	<i>Etheostoma</i>	<i>etowahae</i>	MMH0127	H27e3
26	<i>Etheostoma</i>	<i>etowahae</i>	MMH0127	H27e4
27	<i>Etheostoma</i>	<i>etowahae</i>	MMH0127	H27e5
28	<i>Etheostoma</i>	<i>etowahae</i>	MMH0128	H28e1
29	<i>Etheostoma</i>	<i>etowahae</i>	MMH0128	H28e2
30	<i>Etheostoma</i>	<i>etowahae</i>	MMH0128	H28e3
31	<i>Etheostoma</i>	<i>etowahae</i>	JRK0142	K42e1
32	<i>Etheostoma</i>	<i>etowahae</i>	JRK01119	K119e1
33	<i>Etheostoma</i>	<i>etowahae</i>	JRK01119	K119e2
34	<i>Etheostoma</i>	<i>etowahae</i>	JRK01119	K119e3
35	<i>Etheostoma</i>	<i>etowahae</i>	JER0445	1570
36	<i>Etheostoma</i>	<i>etowahae</i>	JER0445	1571
37	<i>Etheostoma</i>	<i>etowahae</i>	JER0445	1572
38	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1535

39	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1536
40	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1537
41	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1538
42	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1539
43	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1540
44	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1541
45	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1542
46	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1543
47	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1544
48	<i>Etheostoma</i>	<i>etowahae</i>	JER0444	1545
49	<i>Etheostoma</i>	<i>etowahae</i>	BAP1120	P1120e1
50	<i>Etheostoma</i>	<i>etowahae</i>	BAP1121	P1121e1
51	<i>Etheostoma</i>	<i>jordani</i>	BAP1178	BAP1178j1
52	<i>Etheostoma</i>	<i>jordani</i>	BAP1178	BAP1178j2
53	<i>Etheostoma</i>	<i>jordani</i>	BAP1178	BAP1178j3
54	<i>Etheostoma</i>	<i>jordani</i>	MMH0231	H31j1
55	<i>Etheostoma</i>	<i>jordani</i>	MMH0231	H31j2
56	<i>Etheostoma</i>	<i>jordani</i>	MMH0231	H31j3
57	<i>Etheostoma</i>	<i>jordani</i>	BJF0521	F0521j1
58	<i>Etheostoma</i>	<i>jordani</i>	BJF0521	F0521j2
59	<i>Etheostoma</i>	<i>jordani</i>	BJF0521	F0521j3
60	<i>Etheostoma</i>	<i>jordani</i>	BJF0521	F0521j4
61	<i>Etheostoma</i>	<i>jordani</i>	BJF0521	F0521j5
62	<i>Etheostoma</i>	<i>jordani</i>	BAP1022	P1022j1
63	<i>Etheostoma</i>	<i>jordani</i>	BAP1022	P1022j2
64	<i>Etheostoma</i>	<i>jordani</i>	BAP1022	P1022j3
65	<i>Etheostoma</i>	<i>jordani</i>	BAP1022	P1022j4
66	<i>Etheostoma</i>	<i>jordani</i>	BAP1022	P1022j5
67	<i>Etheostoma</i>	<i>jordani</i>	BAP1022	P1022j6
68	<i>Etheostoma</i>	<i>jordani</i>	JRK0172	K72j1
69	<i>Etheostoma</i>	<i>jordani</i>	JRK0172	K72j2
70	<i>Etheostoma</i>	<i>jordani</i>	JRK0172	K72j3
71	<i>Etheostoma</i>	<i>jordani</i>	BAP1111	P1111j1
72	<i>Etheostoma</i>	<i>jordani</i>	BAP1111	P1111j2
73	<i>Etheostoma</i>	<i>jordani</i>	BAP1111	P1111j3
74	<i>Etheostoma</i>	<i>jordani</i>	MMH0127	H27j1
75	<i>Etheostoma</i>	<i>jordani</i>	MMH0127	H27j2
76	<i>Etheostoma</i>	<i>jordani</i>	MMH0127	H27j3
77	<i>Etheostoma</i>	<i>jordani</i>	MMH0127	H27j4
78	<i>Etheostoma</i>	<i>jordani</i>	MMH0127	H27j5
79	<i>Etheostoma</i>	<i>jordani</i>	MMH0127	H27j6
80	<i>Etheostoma</i>	<i>jordani</i>	MMH0127	H27j7
81	<i>Etheostoma</i>	<i>jordani</i>	MMH0127	H27j8
82	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j1
83	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j2

84	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j3
85	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j4
86	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j5
87	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j6
88	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j7
89	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j8
90	<i>Etheostoma</i>	<i>jordani</i>	MMH0128	H28j9
91	<i>Etheostoma</i>	<i>jordani</i>	BAP1126	P1126j1
92	<i>Etheostoma</i>	<i>jordani</i>	BAP1126	P1126j2
93	<i>Etheostoma</i>	<i>jordani</i>	BAP1126	P1126j3
94	<i>Etheostoma</i>	<i>jordani</i>	CS0348	CS0348j1
95	<i>Etheostoma</i>	<i>jordani</i>	CS0348	CS0348j2
96	<i>Etheostoma</i>	<i>jordani</i>	CS0348	CS0348j3
97	<i>Etheostoma</i>	<i>jordani</i>	CS0348	CS0348j4
98	<i>Etheostoma</i>	<i>jordani</i>	CS0348	CS0348j5
99	<i>Etheostoma</i>	<i>jordani</i>	CS0348	CS0348j6
100	<i>Etheostoma</i>	<i>jordani</i>	CS0348	CS0348j7
101	<i>Etheostoma</i>	<i>jordani</i>	CS0348	CS0348j8
102	<i>Etheostoma</i>	<i>jordani</i>	CS0350	CS0350j1
103	<i>Etheostoma</i>	<i>jordani</i>	CS0353	CS0353j1
104	<i>Etheostoma</i>	<i>jordani</i>	CS0353	CS0353j2
105	<i>Etheostoma</i>	<i>jordani</i>	CS0353	CS0353j3
106	<i>Etheostoma</i>	<i>jordani</i>	CS0353	CS0353j4
107	<i>Etheostoma</i>	<i>jordani</i>	CS0353	CS0353j5
108	<i>Etheostoma</i>	<i>jordani</i>	BAP1116	P1116j1
109	<i>Etheostoma</i>	<i>jordani</i>	BAP1116	P1116j2
110	<i>Etheostoma</i>	<i>jordani</i>	BAP1109	P1109j1
111	<i>Etheostoma</i>	<i>jordani</i>	BAP1109	P1109j2
112	<i>Etheostoma</i>	<i>jordani</i>	BAP1109	P1109j3
113	<i>Etheostoma</i>	<i>jordani</i>	BAP1195	P1195j1
114	<i>Etheostoma</i>	<i>jordani</i>	BAP1195	P1195j2
115	<i>Etheostoma</i>	<i>jordani</i>	BAP1195	P1195j3
116	<i>Etheostoma</i>	<i>jordani</i>	BAP1195	P1195j4
117	<i>Etheostoma</i>	<i>jordani</i>	BAP1195	P1195j5
118	<i>Etheostoma</i>	<i>jordani</i>	PAM0419	1559
119	<i>Etheostoma</i>	<i>jordani</i>	PAM0419	1560
120	<i>Etheostoma</i>	<i>jordani</i>	PAM0419	1561
121	<i>Etheostoma</i>	<i>jordani</i>	PAM0419	1562
122	<i>Etheostoma</i>	<i>jordani</i>	PAM0419	1563

Table 2. Collection Locations for each Field Number

Field #	Stream Name	Locality
JRK01108	Tallapoosa River	Tallapoosa River at State Hwy 27, 4.5 air miles NNW of Buchanan, GA city center, Haralson County.
MCF0212	Tallapoosa River	Tallapoosa River at County Route 146 (Broad Street), 2.4 miles NW of Tallapoosa, GA city center, Haralson County.
MCF0223	Tallapoosa River	MCF02-23 -Tallapoosa River at County Route 189 (Poplar Springs Road), 4.7 air miles NNE of Tallapoosa, GA city center, Haralson County.
BAP1168	Sipsey Fork of Black Warrior R.	Sipsey Fork of the Black Warrior River at canoe ramp just downstream of SR33 bridge, 5.4 air mi. NE Double Springs, Winston Co., AL
BAP1169	Bordon Creek	Bordon Creek on Forest Service Rd to Bordon Creek trail head off CR 6, ~ 2miles N Lawrence/Winston Co. line, ~4.7 air mi. NW Grayson, Lawrence Co., AL
MMH0528	Shoal Creek	Shoal Creek upstream from mouth approximately 0.4 river miles, at powerline cut in Dawson Forest, Dawson County GA.
MMH0529	Amicalola Creek	Amicalola Creek upstream from mouth approximately 0.2 river miles in Dawson Forest, Dawson County, GA
BJF0512	Etowah River	Etowah River at shoal with a small island 0.67 river miles upstream of the mouth of Amicalola Creek in the Dawson Forest (Yellow Creek Site 1).
JRK0142	Smithwick Creek	Smithwick Creek 1.5 river miles downstream of County Route 204 (Julius Bridge Road), 4.6 air miles SE of Ball Ground, GA city center, Cherokee Co.
JRK01119	Etowah River	Etowah River at State Route 52, 4.5 air miles W Dahunega, GA city center.
JER0445	Cove Creek	Cove Creek ~ 125 meters upstream of CR 294 (Cove Rd.), ~ 1.5 airmiles east of Jasper
JER0444	Champion Creek	Champion Creek ~125 meters upstream of Old Cove Rd.
BAP1120	Etowah River	Etowah River at the first shoal downstream from the confluence of Amicalola Creek, 5.9 air miles SW of Dawsonville, GA city center.
BAP1121	Etowah River	Etowah River just downstream of Kelly Bridge road, 0.2 miles from boatramp (380486° E, 0756694° N)
BAP1178	Raccoon Creek	Raccoon Creek at Raccoon Creek road, 0.72 air miles upstream of Braswell Mountain road, 4.2 air miles E of Braswell, GA
MMH0231	Raccoon Creek	Raccoon Creek at Raccoon Creek road, 0.72 air miles upstream of Braswell Mountain road, 4.2 air miles E of Braswell, GA
BJF0521	Etowah River	Etowah River, 1.25 air miles SE of US Highway 411 crossing at downstream end of island, 2.7 air miles SSW of Kingston, GA city center.
BAP1022	Terrapin Creek	Terrapin Creek at canoe takeout along State Route 9, 5.1 air miles NW of Spring Garden, AL city center.
JRK0172	Little Armuchee	Little Armuchee Creek at at Hwy 27 10.16 air kilometers SSW of the intersection of SR 100 and SR 1, City of Summerville at highway 27, Summerville, Chatooga Co., GA
BAP1111	Conasauga River	Conasauga River, 0.7 river miles downstream of U.S. Highway 76 / State Route 52, 5.2 air miles ENE of Dalton, GA city center.

MMH0127	Long Swamp Creek	Long Swamp Creek at large shoal ca 100m downstream of trib. draining Blue Circle Gravel quarry, 2.1 air miles NE of Ball Ground, GA city center.
MMH0128	Long Swamp Creek	Long Swamp Creek 0.8 road miles downstream of tributary draining Blue Circle Gravel quarry, 2.5m upstream of County road 275 (Conn's Creek road)
BAP1126	Stamp Creek	Stamp Creek at State Route 20 (Brandon Farm Road) crossing 0.6 air miles east of Corbin, 7.6 air miles ENE of Cartersville, GA city center.
CS0348	Hatchett Creek	Hatchett Creek at Highway 148, Clay Co., AL
CS0350	Four Mile Creek	Four Mile Creek at CR 61, Shelby Co., AL
CS0353	Yellow Leaf Creek	Yellow Leaf Creek at County road 61 near confluence with Blue Gut Creek 7.07airmiles NE of Lomax, Alabama
BAP1116	Conasauga River	Conasauga River, 0.5 river miles upstream of Whitfield County Route 100 (Tibbs Bridge Road), 6.8 air miles ESE of Dalton, GA city center.
BAP1109	Conasauga River	Conasauga River at shoal immediately upstream of U.S. Highway 76 / State Route 52, 4.84 air miles W of Chatsworth (center), GA.
BAP1195	Dykes Creek	Dykes Creek at Rt 293 Kingston Hwy, Floyd Co., GA
PAM0419	Talona Creek	Talona Creek upstream of Whitestone Road crossing and fork in system. Left fork (Talona Creek) samples. 8/14/04

APPENDIX B

Table 1. Control Region alignment created in Clustal X and corrected by eye in MEGA v 3.1.2. *E. tippecanoe* is used as a reference sequence. Dashes represent insertion/deletion events and dots represent common bases.

	123	456	789	111	111	111	122	222	222	223	333	333	333	444	444	444
	123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678
tippecanoe	-AA	ATA	CAC	GTA	TGT	ATT	TAC	ACC	ATA	CAT	TTA	TAT	TAA	CCA	TAT	AAG
P1168d1	-..
K108c1	-..
MCF0212c1	-..
H0127e1	-..
H0127e3	-..
H0128e1	-..
H0128e3	-..
K119e1	-..
K119e2	-..
K119e3	-..
P1195j1	A..
P1195j2	A..
P1195j3	A..
P1195j4	A..
MCF0223c5	-..
1540	A..
H0528e1	A..
H0528e2	A..
H0528e3	A..
H0528e4	A..
H0528e5	A..
F0512e1	-..
F0521j4	A..
H02H31j1	A..
H02H31j3	-..
H0529e1	A..
CS0348j5	-..
CS0353j1	-..
P1120e1	A..
P1121e1	A..
1535	A..
1536	A..
1537	A..
1538	A..
1539	A..
1541	A..
1544	A..
1559	-..
1563	-..
1570	A..
P1022j1	-..
P1126j1	-..
P1111j1	-..
P1111j2	-..
P1111j3	-..

K0172j1	-
H0127j3	-
H0127j4	-
H0128j3	-
P1178j1	-
CS0350j1	-
CS0348j1	-
CS0353j2	-
CS0353j4	-
P1116j1	-
P1116j2	-
	455	555	555	556	666	666	666	777	777	777	788	888	888	889	999	999	
	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456	
tippecanoe	GGG	CAT	TCA	AGT	ACA	TAT	ATG	TTT	AAT	CAA	CAT	ATC	TAG	GAT	TAC	CCC	
P1168d1	T.A.
K108c1	T.	T.	.	.	.A.
MCF0212c1	T.	T.	.	.	.A.
H0127e1	T.A.
H0127e3	T.A.
H0128e1	T.A.
H0128e3	T.A.
K119e1	T.A.
K119e2	T.A.
K119e3	T.A.
P1195j1	T.A.
P1195j2	T.A.
P1195j3	T.A.
P1195j4	T.A.
MCF0223c5	T.	T.	.	.	.A.
1540	T.A.
H0528e1	T.A.
H0528e2	T.A.
H0528e3	T.A.
H0528e4	T.A.
H0528e5	T.A.
F0512e1	T.A.
F0521j4	T.A.
H02H31j1	T.A.
H02H31j3	T.A.
H0529e1	T.A.
CS0348j5	T.A.
CS0353j1	T.A.
P1120e1	T.A.
P1121e1	T.A.
1535	T.A.
1536	T.A.
1537	T.A.
1538	T.A.
1539	T.A.
1541	T.A.
1544	T.A.
1559	T.A.
1563	T.A.
1570	T.A.
P1022j1	T.A.
P1126j1	T.A.

P1111j1	T..A.
P1111j2	T..A.
P1111j3	T..
K0172j1	T..A.
H0127j3	T..A.
H0127j4	T..A.
H0128j3	T..A.
P1178j1	T..A.
CS0350j1	T..A.
CS0348j1	T..A.
CS0353j2	T..A.
CS0353j4	T..A.
P1116j1	T..A.
P1116j2	T..A.

		111	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111
	999	000	000	000	011	111	111	112	222	222	222	333	333	333	344	444	
	789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234	
tippecanoe	ATT	CAT	ATA	TCA	CCA	TAT	AAC	TAA	GGG	TTA	CAT	AAA	GCA	TCT	ATA	GGT	
P1168d1	A..A	C..
K108c1TA	C..A.
MCF0212c1TA	C..A.
H0127e1	A..C	C..A.
H0127e3	A..C	C..A.
H0128e1	A..C	C..A.
H0128e3	A..C	C..A.
K119e1	A..C	C..A.
K119e2	A..C	C..A.
K119e3	A..C	C..A.
P1195j1	A..C	C..A.
P1195j2	A..C	C..A.
P1195j3	A..C	C..A.
P1195j4	A..C	C..A.
MCF0223c5TA	C..A.
1540	A..C	C..A.
H0528e1	A..C	C..A.
H0528e2	A..C	C..A.
H0528e3	A..C	C..A.
H0528e4	A..C	C..A.
H0528e5	A..C	C..A.
F0512e1	A..C	C..A.
F0521j4	A..C	C..A.
H02H31j1	A..C	C..A.
H02H31j3	A..C	C..A.
H0529e1	A..C	C..A.
CS0348j5	A..C	C..A.
CS0353j1	A..C	C..A.
P1120e1	A..C	C..A.
P1121e1	A..C	C..A.
1535	A..C	C..A.
1536	A..C	C..A.
1537	A..C	C..A.
1538	A..C	C..A.
1539	A..C	C..A.
1541	A..C	C..A.
1544	A..C	C..A.
1559	A..C	C..A.

1539C.	...T	-..	A..T
1541C.	...T	-..	A..T
1544C.	...T	-..	A..T
1559C.	...-	...	A..C
1563C.	...-	...	A..C
1570C.	...T	-..	A..T
P1022j1C.	...-	...	A..T
P1126j1C.	...T	-..	A..T	..C
P1111j1C.	...-	...	A..C
P1111j2C.	...-	...	A..T	...A.
P1111j3C.	...-	...	A..C
K0172j1C.	...-	...	A..C
H0127j3C.	...T	-..	A..T
H0127j4C.	...T	-..	A..T
H0128j3C.	...T	-..	A..T
P1178j1C.	...T	-..	A..T
CS0350j1C.	...-	...	A..T
CS0348j1C.	...T	-..	A..T
CS0353j2C.	...-	...	A..C
CS0353j4C.	...-	...	A..C
P1116j1C.	...-	...	A..C
P1116j2C.	...-	...	A..C
		111	111	122	222	222	222	222	222	222	222	222	222	222	222	222
		999	999	900	000	000	001	111	111	111	222	222	222	233	333	333
		345	678	901	234	567	890	123	456	789	012	345	678	901	234	567
tippecanoe	ACA	CAA	ATA	CTC	ATA	AGT	TAA	GTT	ATA	CGT	TTA	CCT	GAC	ATC	TCG	TCA
P1168d1
K108c1
MCF0212c1
H0127e1
H0127e3
H0128e1
H0128e3
K119e1
K119e2
K119e3
P1195j1
P1195j2
P1195j3
P1195j4
MCF0223c5
1540
H0528e1
H0528e2
H0528e3
H0528e4
H0528e5
F0512e1
F0521j4
H02H31j1
H02H31j3
H0529e1
CS0348j5
CS0353j1
P1120e1
P1121e1

1535
1536
1537
1538
1539
1541
1544
1559
1563
1570
P1022j1
P1126j1
P1111j1
P1111j2
P1111j3
K0172j1
H0127j3
H0127j4
H0128j3
P1178j1
CS0350j1
CS0348j1
CS0353j2
CS0353j4
P1116j1
P1116j2
	222	222	222	222	222	222	222	222	222	222	222	222	222	222	222	222
	444	444	444	555	555	555	566	666	666	667	777	777	777	888	888	888
	123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678
tippecanoe	TAT	CTC	AGA	A-T	CTT	AAT	GTA	GTA	AGA	GCC	TAC	CAT	CAG	TTG	ATT	TCT
P1168d1	..CA.	.-.	T..	C..
K108c1	..CA.	.-.
MCF0212c1	..CA.	.-.
H0127e1A.	.-.	T..
H0127e3A.	.-.	T..
H0128e1	..CA.	.-.	T..
H0128e3A.	.-.	T..
K119e1	..CA.	.-.	T..
K119e2	..CA.	.-.	T..
K119e3	..CA.	.-.	T..
P1195j1	..CA.	.C.	-..
P1195j2	..CA.	.C.	-..
P1195j3	..CA.	.C.	-..
P1195j4	..CA.	.-.	T..
MCF0223c5	..CA.	.-.
1540	..CA.	.T.	..-
H0528e1	..CA.	.T.	..-
H0528e2A.	.T.	..-
H0528e3	..CA.	.T.	..-
H0528e4A.	.T.	T.-
H0528e5	..CA.	.T.	..-
F0512e1	..CA.	.C.	-..
F0521j4A.	.T.	..-
H02H31j1	..CA.	.-.	T..
H02H31j3	..CA.	.-.	T..
H0529e1	..CA.	.-.	T..G

CS0348j5	..CA.	.C.	-..
CS0353j1	..CA.	-.T.
P1120e1A.	-.T.
P1121e1A.	-.T.
1535	..CA.	-.T.
1536	..CA.	.C.	-..
1537	..CA.	.C.	-..
1538	..CA.	-.T.
1539	..CA.	-.T.
1541A.	-.T.
1544A.	-.T.
1559	..CA.	.C.	-..
1563	..CA.	.C.	-..
1570A.	-.T.
P1022j1	..CA.	.C.	-..
P1126j1	..CA.	-.T.
P1111j1	..CA.	.C.	-..
P1111j2	..CA.	.C.	-..
P1111j3	..CA.	.C.	-..
K0172j1	..CA.	.C.	-..
H0127j3A.	-.T.
H0127j4A.	-.T.
H0128j3	..CA.	-.T.
P1178j1	..CA.	-.T.
CS0350j1	..CA.	.C.	-..
CS0348j1	..CA.	.C.	-..
CS0353j2	..CA.	.C.	-..
CS0353j4	..CA.	-.T.
P1116j1	..CA.	-.T.
P1116j2	..CA.	.C.	-..
		222	222	222	223	333	333	333	333	333	333	333	333	333	333	333	333
		899	999	999	990	000	000	000	111	111	111	122	222	222	223	333	333
		901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	TAA	TGC	-CA	ACG	GTT	ATT	GAA	GGT	GAG	GGA	CAA	CTA	TTG	TGG	GGG	TTT	
P1168d1	T-
K108c1A	T..	-..
MCF0212c1A	T..	-..
H0127e1-	T..
H0127e3	-..
H0128e1-	T..
H0128e3	-..
K119e1-	T..
K119e2-	T..
K119e3-	T..
P1195j1	-..
P1195j2	-..
P1195j3	-..
P1195j4	-..
MCF0223c5A	T..	-..
1540-	T..
H0528e1-	T..
H0528e2-	T..
H0528e3-	T..
H0528e4	-..
H0528e5-	T..
F0512e1	-..

F0521j4-	T..
H02H31j1-	T..
H02H31j3	-..
H0529e1-	T..
CS0348j5	-..
CS0353j1	-..
P1120e1-	T..
P1121e1	-..
1535-	T..
1536-	T..A.
1537-	T..A.
1538-	T..C.
1539-	T..
1541-	T..C.
1544-	T..A.
1559	-..
1563	-..C.
1570-	T..
P1022j1	-..
P1126j1	-..
P1111j1	-..
P1111j2	-..
P1111j3	-..
K0172j1	-..
H0127j3	-..
H0127j4-	T..
H0128j3-	T..
P1178j1-	T..
CS0350j1	-..
CS0348j1	-..
CS0353j2	-..
CS0353j4	-..
P1116j1	-..
P1116j2	-..
		333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333
		333	444	444	444	455	555	555	556	666	666	666	777	777	777	788	888
		789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234
tippecanoe	CAC	ACA	GTG	AAT	TAT	TCC	TGG	CAT	TTG	GTT	CCT	ACT	TCA	GGG	CCA	TTT	
P1168d1
K108c1
MCF0212c1
H0127e1
H0127e3
H0128e1
H0128e3
K119e1
K119e2
K119e3
P1195j1C.
P1195j2C.
P1195j3
P1195j4C.
MCF0223c5
1540
H0528e1
H0528e2

H0528e3
H0528e4
H0528e5
F0512e1
F0521j4
H02H31j1
H02H31j3
H0529e1
CS0348j5
CS0353j1
P1120e1
P1121e1
1535
1536
1537
1538
1539
1541
1544
1559
1563
1570
P1022j1
P1126j1
P1111j1
P1111j2
P1111j3	C..
K0172j1
H0127j3
H0127j4	C..
H0128j3
P1178j1
CS0350j1
CS0348j1
CS0353j2
CS0353j4	C..
P1116j1
P1116j2
	333	333	333	333	333	444	444	444	444	444	444	444	444	444	444	444	444
	888	889	999	999	999	000	000	000	011	111	111	112	222	222	222	333	
	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012	
tippecanoe	ATT	GAT	ATT	ATT	CCT	CAC	ACT	TTC	ATC	GAC	GCT	GAC	ATA	AGT	-AA	TGG	
P1168d1	T..	...
K108c1C.	T..	...
MCF0212c1C.	T..	...
H0127e1C.	T..	...
H0127e3	G..C.	T..	...
H0128e1	G..C.	T..	...
H0128e3	G..C.	T..	...
K119e1C.	T..	...
K119e2C.	T..	...
K119e3C.	T..	...
P1195j1	T..	...
P1195j2	T..	...
P1195j3	C.C	T..	...
P1195j4	T..	...

MCF0223c5C.	T..	...
1540C.	T..	...
H0528e1	T..	...
H0528e2C.	T..	...
H0528e3C.	T..	...
H0528e4	G..C.	T..	...
H0528e5C.	T..	...
F0512e1	T..	...
F0521j4C.	T..	...
H02H31j1C.	T..	...
H02H31j3	T..	...
H0529e1C.	T..	...
CS0348j5	T..	...
CS0353j1	T..	...
P1120e1C.	T..	...
P1121e1C.	T..	...
1535	G..C.	T..	...
1536C.	T..	...
1537C.	T..	...
1538	G..C.	T..	...
1539	G..C.	T..	...
1541C.	T..	...
1544C.	T..	...
1559	T..	...
1563	T..	...
1570C.	T..	...
P1022j1	T..	...
P1126j1C.	T..	...
P1111j1	T..	...
P1111j2	T..	...
P1111j3	T..	...
K0172j1	T..	...
H0127j3	G..	T..	...
H0127j4C.	T..	...
H0128j3	G..C.	T..	...
P1178j1C.	T..	...
CS0350j1C.	T..	...
CS0348j1	T..	...
CS0353j2	T..	...
CS0353j4	T..	...
P1116j1	T..	...
P1116j2	T..	...
		444	444	444	444	444	444	444	444	444	444	444	444	444	444	444	444	444
		333	333	344	444	444	445	555	555	555	666	666	666	677	777	777	778	778
		345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890	890
tippecanoe	TGG	AGT	ACA	TAC	TCC	TCG	TTA	CCC	ACC	AAG	CCG	GGC	GTT	CTT	TCC	ATC		
P1168d1
K108c1	A..
MCF0212c1	A..
H0127e1	A..
H0127e3	A..
H0128e1	A..
H0128e3	A..
K119e1	A..
K119e2	A..
K119e3	A..

P1195j1	A..
P1195j2	A..
P1195j3	A..
P1195j4	A..
MCF0223c5	A..
1540	A..
H0528e1
H0528e2	A..
H0528e3	G..	A..
H0528e4	A..
H0528e5	A..
F0512e1	A..
F0521j4	A..
H02H31j1
H02H31j3	A..
H0529e1	A..
CS0348j5
CS0353j1	A..
P1120e1	A..
P1121e1	A..
1535	A..
1536	A..
1537	A..
1538	A..
1539	A..
1541	A..
1544	A..
1559
1563
1570	A..
P1022j1	A..
P1126j1	A..
P1111j1	A..
P1111j2	A..
P1111j3	A..
K0172j1	A..
H0127j3	A..
H0127j4	A..
H0128j3	A..
P1178j1
CS0350j1	A..
CS0348j1
CS0353j2	A..
CS0353j4	A..
P1116j1	A..
P1116j2	A..
tippecanoe	GGG	CAA	CTG	GTT	TTT	TTT	TTC	TAT	TTC	CTT	TCA	CTT	GGC	ATT	TCA	GAG	
P1168d1	C.CT	.T.	TC.	C..	
K108c1	C.CT	.T.	TC.	C..	
MCF0212c1	C.CT	.T.	TC.	C..	
H0127e1	C.CT	.T.	TC.	C..	
H0127e3	C.CT	.T.	TC.	C..	
H0128e1	C.CT	.T.	TC.	C..	

H0128e3	C.CT	.T.	TC.	C..
K119e1	C.CT	.T.	TC.	C..
K119e2	C.CT	.T.	TC.	C..
K119e3	C.CT	.T.	TC.	C..
P1195j1	C.CT	.T.	TC.	C..
P1195j2	C.CT	.T.	TC.	C..
P1195j3	C.CT	.T.	TC.	C..
P1195j4	C.CT	.T.	TC.	C..
MCF0223c5	C.CT	.T.	TC.	C..
1540	C.CT	.T.	TC.	C..
H0528e1	C.CT	.T.	TCG	C..
H0528e2	C.CT	.T.	TCG	C..
H0528e3	C.CT	.T.	TCG	C..
H0528e4	C.CT	.T.	TCG	C..
H0528e5	C.CT	.T.	TCG	C..
F0512e1	C.CT	.T.	TCG	C..
F0521j4	C.CT	.T.	TCG	C..
H02H31j1	C.CT	.T.	TCG	C..
H02H31j3	C.CT	.T.	TCG	C..
H0529e1	C.CT	.T.	TCG	C..
CS0348j5	C.CT	.T.	TC.	C..
CS0353j1	C.CT	.T.	TC.	C..
P1120e1	C.CT	.T.	TC.	C..
P1121e1	C.CT	.T.	TC.	C..
1535	C.CT	.T.	TC.	C..
1536	C.CT	.T.	TC.	C..
1537	C.CT	.T.	TC.	C..
1538	C.CT	.T.	TC.	C..
1539	C.CT	.T.	TC.	C..
1541	C.CT	.T.	TC.	C..
1544	C.CT	.T.	TC.	C..
1559	C.CT	.T.	TC.	C..
1563	C.CT	.T.	TC.	C..
1570	C.CT	.T.	TC.	C..
P1022j1	C.CT	.T.	TC.	C..
P1126j1	C.CT	.T.	TC.	C..
P1111j1	C.CT	.T.	TC.	C..
P1111j2	C.CT	.T.	TC.	C..
P1111j3	C.CT	.T.	TC.	C..
K0172j1	C.CT	.T.	TC.	C..
H0127j3	C.CT	.T.	TC.	C..
H0127j4	C.CT	.T.	TC.	C..
H0128j3	C.CT	.T.	TC.	C..
P1178j1	C.CT	.T.	TC.	C..
CS0350j1	C.CT	.T.	TC.	C..
CS0348j1	C.CT	.T.	TC.	C..
CS0353j2	C.CT	.T.	TC.	C..
CS0353j4	C.CT	.T.	TC.	C..
P1116j1	C.CT	.T.	TC.	C..
P1116j2	C.CT	.T.	TC.	C..
	555	555	555	555	555	555	555	555	555	555	555	555	555	555	555	555
	233	333	333	334	444	444	444	555	555	555	566	666	666	667	777	777
	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	TGC	ACA	CGG	GAT	TAA	CAG	ACA	AGG	CAG	AAC	ATT	TAC	TTT	GCG	CGG	GTA
P1168d1GC	...
K108c1G	.G.

MCF0212c1G	.G.
H0127e1GA	...
H0127e3GA	...
H0128e1GA	...
H0128e3GC.A	...
K119e1G
K119e2GA	...
K119e3G
P1195j1G
P1195j2G
P1195j3G
P1195j4G
MCF0223c5G	.G.
1540GA	...
H0528e1G
H0528e2G
H0528e3G
H0528e4GA	...
H0528e5G
F0512e1G
F0521j4GA	...
H02H31j1GA	...
H02H31j3G
H0529e1G
CS0348j5G
CS0353j1G
P1120e1GA	...
P1121e1GA	...
1535GA	...
1536GA	...
1537GA	...
1538GA	...
1539GA	...
1541GA	...
1544GA	...
1559G
1563G
1570GA	...
P1022j1G
P1126j1GA	...
P1111j1G
P1111j2G
P1111j3G
K0172j1G
H0127j3G
H0127j4GA	...
H0128j3GA	...
P1178j1GA	...
CS0350j1G
CS0348j1G
CS0353j2G
CS0353j4G
P1116j1G
P1116j2G
	555	555	555	555	555	555	555	555	556	666	666	666	666	666	666	666
	777	888	888	888	899	999	999	990	000	000	000	111	111	111	122	222

	789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234
tippecanoe	TAT	AGT	ATG	AAT	GGT	GGA	AAG	AT?	TTA	TAC	AAA	GAA	CCA	CAT	ATT	AGG
P1168d1	A..T	...	ATTA.
K108c1	A..GT	...	ATT
MCF0212c1	A..GT	...	ATT
H0127e1	A..T	...	AT.A.
H0127e3	A..T	...	AT.A.
H0128e1	A..T	...	AT.A.
H0128e3	A..T	...	AT.A.
K119e1	A..T	...	AT.A.
K119e2	A..T	...	AT.	TA.
K119e3	A..T	...	AT.A.
P1195j1	A..T	...	AT.A.
P1195j2	A..T	...	AT.A.
P1195j3	A..T	...	AT.A.
P1195j4	A..T	...	AT.A.
MCF0223c5	A..GT	...	ATT
1540	A..T	...	AT.A.
H0528e1	A..T	...	AT.A.
H0528e2	A..T	...	AT.A.
H0528e3	A..T	...	AT.A.
H0528e4	A..T	...	AT.A.
H0528e5	A..T	...	AT.A.
F0512e1	AG.T	...	AT.A.
F0521j4	A..T	...	AT.A.
H02H31j1	A..T	...	AT.A.
H02H31j3	AG.T	...	AT.A.
H0529e1	A..T	...	AT.A.
CS0348j5	AG.T	...	AT.A.
CS0353j1	A..T	...	AT.A.
P1120e1	A..T	...	AT.A.
P1121e1	A..T	...	AT.A.
1535	A..T	...	AT.A.
1536	A..T	...	AT.A.
1537	A..T	...	AT.A.
1538	A..T	...	AT.A.
1539	A..T	...	AT.A.
1541	A..T	...	AT.A.
1544	A..T	...	AT.A.
1559	AG.T	...	AT.A.
1563	AG.T	...	AT.A.
1570	A..T	...	AT.A.
P1022j1	AG.T	...	AT.A.
P1126j1	A..T	...	AT.A.
P1111j1	AG.T	...	AT.A.
P1111j2	AG.T	...	AT.A.
P1111j3	AG.T	...	AT.A.
K0172j1	A..T	...	AT.A.
H0127j3	A..T	...	AT.A.
H0127j4	A..T	...	AT.A.
H0128j3	A..T	...	AT.A.
P1178j1	A..T	...	AT.A.
CS0350j1	AG.T	...	AT.A.
CS0348j1	A..T	...	AT.A.
CS0353j2	AG.T	...	AT.A.
CS0353j4	A..T	...	AT.A.
P1116j1	A..T	...	AT.A.

P1116j2	AG.
	666	666	666	666	666	666	666	666	666	666	666	666	666	666	666	666	666
	222	223	333	333	333	444	444	444	455	555	555	556	666	666	666	777	
	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012	
tippecanoe	ATA	TCA	TGT	GCA	TAA	GTA	GTG	GTA	ATT	CCT	CCT	AAC	TTC	CCT	AAG	AGA	
P1168d1	AC.	...	T..	T.	...	
K108c1C.	...	T.C	
MCF0212c1C.	...	T.C	
H0127e1	A..	...	T..	T.	...	
H0127e3	A..	...	T..	T.	...	
H0128e1	A..	...	T..	T.	...	
H0128e3	A..	...	T..	T.	...	
K119e1	A..	...	T..	T.	...	
K119e2	A..	...	T..	T.	...	
K119e3	A..	...	T..	T.	...	
P1195j1	AC.	...	T..	T.	...	
P1195j2	AC.	...	T..	T.	...	
P1195j3	AC.	...	T..	T.	...	
P1195j4	AC.	...	T..	T.	...	
MCF0223c5C.	...	T.C	
1540	A..	...	T..	T.	...	
H0528e1	A..	...	T..	T.	...	
H0528e2	A..	...	T..	T.	...	
H0528e3	A..	...	T..	T.	...	
H0528e4	A..	...	T..	T.	...	
H0528e5	A..	...	T..	T.	...	
F0512e1	AC.	...	T..	T.	...	
F0521j4	A..	...	T..	T.	...	
H02H31j1	A..	...	T..	T.	...	
H02H31j3	AC.	...	T..	T.	...	
H0529e1	A..	...	T..	T.	...	
CS0348j5	AC.	...	T..	T.	...	
CS0353j1	AC.	...	T..	T.	...	
P1120e1	A..	...	T..	T.	...	
P1121e1	A..	...	T..	T.	...	
1535	A..	...	T..	T.	...	
1536	A..	...	T..	T.	...	
1537	A..	...	T..	T.	...	
1538	A..	...	T..	T.	...	
1539	A..	...	T..	T.	...	
1541	A..	...	T..	T.	...	
1544	A..	...	T..	T.	...	
1559	AC.	...	T..	T.	...	
1563	AC.	...	T..	T.	...	
1570	A..	...	T..	T.	...	
P1022j1	AC.	...	T..	T.	...	
P1126j1	A..	...	T..	T.	...	
P1111j1	AC.	...	T..	T.	...	
P1111j2	AC.	...	T..	T.	...	
P1111j3	AC.	...	T..	T.	...	
K0172j1	AC.	...	T..	T.	...	
H0127j3	AC.	...	T..	T.	...	
H0127j4	A..	...	T..	T.	...	
H0128j3	A..	...	T..	T.	...	
P1178j1	A..	...	T..	T.	...	
CS0350j1	AC.	...	T..	T.	...	

CS0348j1	AC.	...	T..T.	...
CS0353j2	AC.	...	T..T.	...
CS0353j4	AC.	...	T..T.	...
P1116j1	AC.	...	T..T.	...
P1116j2	AC.	...	T..T.	...
	666	666	666	666	666	666	666	666	666	777	777	777	777	777	777	777
	777	777	788	888	888	889	999	999	999	000	000	000	011	111	111	112
	345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890
tippecanoe	CCC	CCC	TCT	GGG	AT?	TCT	TAC	GGT	TTC	TTT	GCG	TAA	ACC	CCC	CCT	ACC
P1168d1T
K108c1T
MCF0212c1T
H0127e1T
H0127e3T
H0128e1T
H0128e3T
K119e1T
K119e2T
K119e3T
P1195j1T
P1195j2T
P1195j3T
P1195j4T
MCF0223c5T
1540T
H0528e1T
H0528e2T
H0528e3T
H0528e4T
H0528e5T
F0512e1T
F0521j4T
H02H31j1T
H02H31j3T
H0529e1T
CS0348j5T
CS0353j1T
P1120e1T
P1121e1T
1535T
1536T
1537T
1538T
1539T
1541T
1544T
1559T
1563T
1570T
P1022j1T
P1126j1T
P1111j1T
P1111j2T
P1111j3T
K0172j1T
H0127j3T

H0127j4	T
H0128j3	T
P1178j1	T
CS0350j1	T
CS0348j1	T
CS0353j2	T
CS0353j4	T
P1116j1	T
P1116j2	T

	777	777	777	777	777	777	777	777	777	777	777	777	777	777	777	777	777
	222	222	222	333	333	333	344	444	444	445	555	555	555	666	666	666	
	123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678	
tippecanoe	CCC	CCT	AAA	CTC	CTG	AGA	TAG	CTA	TCA	ATC	CTG	CAA	ACC	CCC	CGG	AAA	
P1168d1A	G..	T..
K108c1A	G..
MCF0212c1A	G..
H0127e1A	G..	T..
H0127e3A	G..	T..
H0128e1A	G..	T..
H0128e3A	G..	T..
K119e1A	G..	T..
K119e2A	G..	T..
K119e3A	G..	T..
P1195j1A	G..	T..
P1195j2A	G..	T..
P1195j3A	G..	T..
P1195j4A	G..	T..
MCF0223c5A	G..
1540A	G..	T..
H0528e1A	G..	T..
H0528e2A	G..	T..
H0528e3A	G..	T..
H0528e4A	G..	T..
H0528e5A	G..	T..
F0512e1A	G..	T..
F0521j4A	G..	T..
H02H31j1A	G..	T..
H02H31j3A	G..	T..
H0529e1A	G..	T..
CS0348j5A	G..	T..
CS0353j1A	G..	T..
P1120e1A	G..	T..
P1121e1A	G..	T..
1535A	G..	T..
1536A	G..	T..
1537A	G..	T..
1538A	G..	T..
1539A	G..	T..
1541A	G..	T..
1544A	G..	T..
1559A	G..
1563A	G..
1570A	G..	T..
P1022j1A	G..	T..
P1126j1A	G..	T..
P1111j1A	G..	T..

P1111j2A	G..	T..
P1111j3A	G..
K0172j1A	G..	T..
H0127j3A	G..	T..
H0127j4A	G..	T..
H0128j3A	G..	T..
P1178j1A	G..	T..
CS0350j1A	G..	T..
CS0348j1A	G..	T..
CS0353j2A	G..	T..
CS0353j4A	G..	T..
P1116j1A	G..	T..
P1116j2A	G..	T..

	777	777	777	777	777	777	777	777	777	777	788	888	888	888	888	888
	677	777	777	778	888	888	888	999	999	999	900	000	000	001	111	111
	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	CAG	GAA	AAC	CTC	TAG	AAG	?AT	TTT	TTG	GGG	ATC	CAA	TTT	GTA	TCT	ATT
P1168d1	C..
K108c1	C..
MCF0212c1	C..
H0127e1	C..
H0127e3	C..
H0128e1	C..
H0128e3	C..
K119e1A	...	C..
K119e2	C..
K119e3	C..
P1195j1	C..
P1195j2	C..
P1195j3	C..
P1195j4	C..
MCF0223c5	C..
1540	C..
H0528e1	C..
H0528e2	C..
H0528e3	C..
H0528e4	C..
H0528e5	C..
F0512e1	C..
F0521j4	C..
H02H31j1	C..
H02H31j3	C..
H0529e1	C..
CS0348j5	C..
CS0353j1	C..
P1120e1	C..
P1121e1	C..
1535	C..
1536	C..
1537	C..
1538	C..
1539	C..
1541	C..
1544	C..
1559	C..
1563	C..

1570	C..
P1022j1	C..
P1126j1	C..
P1111j1	C..
P1111j2	C..
P1111j3	C..
K0172j1	C..
H0127j3	C..
H0127j4	C..
H0128j3	C..
P1178j1	C..
CS0350j1	C..
CS0348j1	C..
CS0353j2	C..
CS0353j4	C..
P1116j1	C..
P1116j2	C..
	888	888	888	888	888	888	888	888	888	888	888	888	888	888	888	888
	111	222	222	222	233	333	333	334	444	444	444	555	555	555	566	666
	789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234
tippecanoe	TAC	ATT	ATT	AAA	ATA	ATG	TGT	TTG	CTA	GCG	TAG	CTT	AAT	TAA	AGC	ATA
P1168d1
K108c1
MCF0212c1	T..
H0127e1
H0127e3
H0128e1
H0128e3
K119e1
K119e2
K119e3
P1195j1
P1195j2
P1195j3
P1195j4
MCF0223c5
1540
H0528e1
H0528e2
H0528e3
H0528e4
H0528e5
F0512e1
F0521j4
H02H31j1G
H02H31j3
H0529e1
CS0348j5
CS0353j1
P1120e1
P1121e1
1535
1536
1537
1538
1539

1541
1544
1559
1563
1570
P1022j1
P1126j1
P1111j1
P1111j2
P1111j3
K0172j1
H0127j3
H0127j4
H0128j3
P1178j1G
CS0350j1
CS0348j1
CS0353j2
CS0353j4
P1116j1
P1116j2
	888	888	888	888	888	888	888	888	888	888	888	889	999	999	999	999	
	666	667	777	777	777	888	888	888	899	999	999	990	000	000	000	111	
	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012	
tippecanoe	ACA	CTG	AAG	ATG	TTA	AGA	TGA	GCC	CTA	GAA	AGC	TCC	GCA	GGC	ACA	AAG	
P1168d1	A..TG	A..	
K108c1	A..	
MCF0212c1	A..	
H0127e1	A..TG	A..	
H0127e3	A..TG	A..	
H0128e1	A..TG	A..	
H0128e3	A..TG	A..	
K119e1	A.	...	A..	...	A..	..TG	A..	
K119e2	A..	...	A..	..TG	A..	
K119e3	A..TG	A..	
P1195j1	A..TG	A..	
P1195j2	A..TG	A..	
P1195j3	A..TG	A..	
P1195j4	A..TG	A..	
MCF0223c5	A..	A..	
1540	A..TG	A..	
H0528e1	A..TG	A..	
H0528e2	A..TG	A..	
H0528e3	A..TG	A..	
H0528e4	A..TG	A..	
H0528e5	A..TG	A..	
F0512e1	A..TG	A..	
F0521j4	A..TG	A..	
H02H31j1	A..TG	A..	
H02H31j3	A..TG	A..	
H0529e1	A..TG	A..	
CS0348j5	G..	..G	A..TG	A..	
CS0353j1	A..TG	A..	
P1120e1	A..TG	A..	
P1121e1	A..TG	A..	
1535	A..TG	A..	

1536	A..	TG	A..
1537	A..	TG	A..
1538	A..	TG	A..
1539	A..	TG	A..
1541	A..	TG	A..
1544	A..	TG	A..
1559	A..	TG	A..
1563	A..	TG	A..
1570	A..	TG	A..
P1022j1	A..	TG	A..
P1126j1	A..	TG	A..
P1111j1	A..	TG	A..
P1111j2	A..	TG	A..
P1111j3	A..	TG	A..
K0172j1	A..	TG	A..
H0127j3	A..	TG	A..
H0127j4	A..	TG	A..
H0128j3	A.	...	A..	TG	A..
P1178j1	A..	TG	A..
CS0350j1	A..	TG	A..
CS0348j1	G.	..G	A..	TG	A..
CS0353j2	A..	TG	A..
CS0353j4	A..	TG	A..
P1116j1	A..	TG	A..
P1116j2	A..	TG	A..
	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999
	111	111	122	222	222	223	333	333	333	444	444	444	455	555	555	556	
	345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890	
tippecanoe	GCT	TGG	TCC	TGA	CTT	TAC	TAT	CAA	CTC	TAG	CTG	AAC	TTA	CAC	ATG	CAA	
P1168d1
K108c1T	.GA	..A
MCF0212c1T	.GA	..A
H0127e1G
H0127e3G
H0128e1G
H0128e3G
K119e1T
K119e2T
K119e3T
P1195j1AC
P1195j2A
P1195j3A
P1195j4A
MCF0223c5T	.GA	..A
1540G
H0528e1G
H0528e2
H0528e3
H0528e4G
H0528e5
F0512e1A
F0521j4G
H02H31j1G
H02H31j3A
H0529e1
CS0348j5A

CS0353j1A
P1120e1G
P1121e1G
1535G
1536A
1537A
1538G
1539G
1541G
1544A
1559A
1563A
1570A
P1022j1A
P1126j1
P1111j1A
P1111j2
P1111j3A
K0172j1A
H0127j3G
H0127j4G
H0128j3G
P1178j1G
CS0350j1G
CS0348j1A
CS0353j2A
CS0353j4A
P1116j1A
P1116j2A

999 999 999 999 999 9
666 666 666 777 777 7
123 456 789 012 345 6

tippecanoe	GTA	TCC	GCA	TCC	CCG	T
P1168d1
K108c1
MCF0212c1
H0127e1
H0127e3
H0128e1
H0128e3
K119e1
K119e2
K119e3
P1195j1
P1195j2
P1195j3
P1195j4
MCF0223c5
1540
H0528e1
H0528e2
H0528e3
H0528e4
H0528e5
F0512e1
F0521j4

H02H31j1
H02H31j3
H0529e1
CS0348j5
CS0353j1
P1120e1
P1121e1
1535
1536
1537
1538
1539
1541
1544
1559
1563
1570
P1022j1
P1126j1
P1111j1
P1111j2
P1111j3
K0172j1
H0127j3
H0127j4
H0128j3
P1178j1
CS0350j1
CS0348j1
CS0353j2
CS0353j4
P1116j1
P1116j2

Table 2. Cytochrome *b* alignment created in Clustal X and corrected by eye in MEGA v 3.1.2. *E. tippecanoe* is used as a reference sequence. Dots represent common bases.

				111	111	111	122	222	222	223	333	333	333	444	444	444
	123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678
tippecanoe	AAA	ACC	CAC	CCC	CTA	CTT	AAA	ATT	GCA	AAC	GAC	GCA	CTT	GTT	GAT	CTC
P1109j3TCT
P1195j4TCT
CS0348j6TCT
CS0348j7TCT
K119e3CT
H0127e3CT
H0127e4CT
MCF0212c1CT
MCF0212c2CT
P1169d1CT
P1169d2CT
	455	555	555	556	666	666	666	777	777	777	788	888	888	889	999	999
	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	CCC	GCC	CCC	TCC	AAT	ATC	TCA	GTA	TGA	TGA	AAC	TTC	GGC	TCC	CTA	TTG
P1109j3ATG	C.A
P1195j4ATG	C.A
CS0348j6TATG	C.A
CS0348j7ATG	C.A
K119e3ATG	C.A
H0127e3ATG	C.A
H0127e4ATG	C.A
MCF0212c1T	..T	..AT	..TG	C..
MCF0212c2T	..T	..AT	..TG	C..
P1169d1ATG	C.A
P1169d2ATG	C.A
		111	111	111	111	111	111	111	111	111	111	111	111	111	111	111
	999	000	000	000	011	111	111	112	222	222	222	333	333	333	344	444
	789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234
tippecanoe	GGC	CTT	TGT	TTG	ATT	ACC	CAG	ATT	CTC	ACG	GGA	CTA	TTT	CTG	GCA	ATG
P1109j3	..TC	..A	..CAC	..A	..T	..A
P1195j4	..TC	..A	..CAC	..A	..T	..A
CS0348j6	..TC	..A	..CAC	..A	..T	..A
CS0348j7	..TC	..A	..CAC	..A	..T	..A
K119e3	..TC	..AAC	..A	..T	..A
H0127e3	..TC	..AAC	..A	..T	..A
H0127e4	..TC	..A	G..AC	..A	..T	..A
MCF0212c1	..TC	..AT	..AC	..A	..C	...
MCF0212c2	..TC	..AT	..AC	..A	..C	...
P1169d1	..TCAC	..A	..T	...
P1169d2	..TCAC	..A	..T	...
	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111
	444	445	555	555	555	666	666	666	677	777	777	778	888	888	888	999
	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012
tippecanoe	CAC	TAC	ACC	GCC	GAC	ATC	GCG	ACA	GCC	TTT	TCA	TCG	GTC	GCC	CAT	ATC
P1109j3T	..GGA	..AC	...
P1195j4T	..GA	..GA	..AC	...
CS0348j6T	..GGA	..AC	...

CS0348j7T	..GGA	..AC	...
K119e3T	..GA	..GA	..AC	...
H0127e3T	..GA	..GA	..AC	...
H0127e4T	..GA	..GA	..AC	...
MCF0212c1	..T	..TGA	..GCA	..T	..C	...
MCF0212c2	..T	..TGA	..GCA	..T	..C	...
P1169d1T	..G	..TA	..GAC	...
P1169d2T	..G	..TA	..GAC	...
	111	111	122	222	222	222	222	222	222	222	222	222	222	222	222	222
	999	999	900	000	000	001	111	111	111	222	222	222	233	333	333	334
	345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890
tippecanoe	TGT	CGA	GAT	GTG	AAC	TAC	GGC	TGA	CTT	ATT	CGT	AAC	ATA	CAC	GCC	AAC
P1109j3C	..AT	..TCT
P1195j4C	..AT	..TCT
CS0348j6	..CC	..AT	..TCT
CS0348j7	..CC	..AT	..TCT
K119e3	..CC	..ATCT	..C
H0127e3	..CC	..ATCT
H0127e4	..CC	..ATCT
MCF0212c1C	..A	..T	..TCT	..G
MCF0212c2C	..A	..T	..TCT	..G
P1169d1	..CC	..AT	..TCT
P1169d2	..CC	..AT	..TCT
	222	222	222	222	222	222	222	222	222	222	222	222	222	222	222	222
	444	444	444	555	555	555	566	666	666	667	777	777	777	888	888	888
	123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678
tippecanoe	GGC	GCA	TCT	TTC	TTC	TTC	ATC	TGC	ATC	TAC	CTT	CAC	ATT	GGA	CGA	GGT
P1109j3CT	..T	A.GCC	...
P1195j4CT	..T	A.GCC	...
CS0348j6CT	..T	A.ACC	...
CS0348j7CT	..T	A.ACC	...
K119e3CT	..T	A.GCC	...
H0127e3AT	..T	A.GCC	...
H0127e4AT	..T	A.GCC	...
MCF0212c1C	..TT	..T	..G	..TC	...
MCF0212c2C	..TT	..T	..G	..TC	...
P1169d1CT	..T	A.GC	..GC	...
P1169d2CT	..T	A.GC	..GC	...
	222	222	222	223	333	333	333	333	333	333	333	333	333	333	333	333
	899	999	999	990	000	000	000	111	111	111	122	222	222	223	333	333
	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	CTC	TAC	TAC	GGC	TCC	TAC	CTC	TAT	AAA	GAA	ACG	TGA	AAT	ATT	GGA	GTA
P1109j3	..ATG	..G
P1195j4	..ATG	..G
CS0348j6	..ATG	..G
CS0348j7	..ATG	..G
K119e3	..AG	..G
H0127e3	..AG	..G
H0127e4	..ACG	..G
MCF0212c1	..GTA	..GC
MCF0212c2	..GTA	..GC
P1169d1	..ACG	..G
P1169d2	..ACG	..G

	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333
	333	444	444	444	455	555	555	556	666	666	666	777	777	777	788	888
	789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234
tippecanoe	GTC	CTC	CTC	CTA	CTA	GTA	ATG	ATA	ACA	GCC	TTT	GTC	GGG	TAC	GTT	CTC
P1109j3	..T	T..G	..CT	..AC	...
P1195j4	..T	T..G	..CT	..AC	...
CS0348j6	..T	T..G	..CT	..AC	...
CS0348j7	..T	T..G	..CT	..AC	...
K119e3	..T	T..G	..CT	..AC	...
H0127e3	..T	T..A	..G	..CT	..AC	...
H0127e4	..T	T..A	..G	..CT	..AC	...
MCF0212c1	A.TG	T..ACT
MCF0212c2	A.TG	T..ACT
P1169d1	..T	T..CT
P1169d2	..T	T..CT
	333	333	333	333	333	444	444	444	444	444	444	444	444	444	444	444
	888	889	999	999	999	000	000	000	011	111	111	112	222	222	222	333
	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012
tippecanoe	CCC	TGA	GGA	CAA	ATA	TCA	TTT	TGA	GGC	GCT	ACC	GTT	ATT	ACT	AAC	CTT
P1109j3G	..GCT	...
P1195j4G	..GCT	...
CS0348j6G	..GCT	...
CS0348j7G	..GCT	...
K119e3GCT	...
H0127e3GCT	...
H0127e4GCT	...
MCF0212c1	..T	..GGCCG
MCF0212c2	..T	..GGCCG
P1169d1G	..GT	...
P1169d2G	..GT	...
	444	444	444	444	444	444	444	444	444	444	444	444	444	444	444	444
	333	333	344	444	444	445	555	555	555	666	666	666	677	777	777	778
	345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890
tippecanoe	CTG	TCT	GCG	GTG	CCT	TAT	GTT	GGC	AAC	ACC	CTC	GTT	CAG	TGA	ATC	TGA
P1109j3	T.AA	..AG	..A	..TAA	..G
P1195j4	T.AA	..AG	..G	..TAA	..G
CS0348j6	T.AA	..AG	..G	..TAA	..G
CS0348j7	T.AA	..AG	..G	..TAA	..G
K119e3	..ATG	..T	..TAA	..G	..T	...
H0127e3	T.ATG	..T	..TAA	..G	..T	...
H0127e4	T.ATG	..T	..TAA	..G	..T	...
MCF0212c1	T.AA	..AG	..T	..TAAT	...
MCF0212c2	T.AA	..AG	..T	..TAAT	...
P1169d1	T.AA	..AG	..GAA	..G	..T	...
P1169d2	T.AA	..AG	..GAA	..G	..T	...
	444	444	444	444	444	444	455	555	555	555	555	555	555	555	555	555
	888	888	888	999	999	999	900	000	000	001	111	111	111	222	222	222
	123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678
tippecanoe	GGG	GGC	TTT	TCC	GTA	GAT	AAT	GCC	ACC	CTC	ACC	CGG	TTC	TTC	GCC	TTC
P1109j3	..CCC	..CT	..A	..T
P1195j4	..CCC	..CT	..A	..T
CS0348j6	..CCC	..CT	..A	..T
CS0348j7	..CCC	..CT	..A	..T
K119e3	..CCC	..CT	..A	A..T

H0127e3CC	..CT	..A	..T
H0127e4	..CCC	..CT	..A	..T
MCF0212c1CC	..CT	..A	..T	..TT
MCF0212c2CC	..CT	..A	..T	..TT
P1169d1	..CCC	..CT	..A	..T
P1169d2	..CCC	..CT	..A	..T
	555	555	555	555	555	555	555	555	555	555	555	555	555	555	555	555
	233	333	333	334	444	444	444	555	555	555	566	666	666	666	777	777
	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	CAC	TTC	CTC	TTC	CCC	TTT	GTT	ATC	GCA	GGA	GCC	ACA	CTT	GTG	CAC	CTT
P1109j3	..T	...	TCT	..C	..T	..G	T.A	T.G	CGG	..CG	C.A	CAC	T.G	T.C	AT.	T.C
P1195j4	..T	...	TCT	..C	..T	..G	TAA	T.G	CGG	..CG	C.A	CAC	T.G	T.C	AT.	T.C
CS0348j6	..T	...	TCT	..C	..T	..G	T.A	T.G	CGG	..CG	C.A	CAC	T.G	T.C	AT.	T.C
CS0348j7	..T	...	TCT	..C	..T	..G	T.A	T.G	CGG	..CG	C.A	CAC	T.G	T.C	AT.	T.C
K119e3	..TGT	..G	..CA	..T	...
H0127e3	..TT	..G	..CA	..T	...
H0127e4	..TT	..G	..CA	..T	...
MCF0212c1T	..ATA	..TTT	...
MCF0212c2T	..AA	..TTT	...
P1169d1	..TT	..G	..CT	..T	...
P1169d2	..TG	..T	..G	..CT	..T	...
	555	555	555	555	555	555	555	556	666	666	666	666	666	666	666	666
	777	888	888	888	899	999	999	990	000	000	000	111	111	111	122	222
	789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234
tippecanoe	CTT	TTC	CTC	CAT	CAA	ACG	GGT	TCA	AAC	AAC	CCC	CTT	GGC	TTA	AAC	TCA
P1109j3	TCC	..T	..TA	..CT	..TC	..G
P1195j4	TCC	..T	..TA	..CT	..TC
CS0348j6	TCC	..T	..TCT	..TC
CS0348j7	TCC	..T	..TCT	..TC
K119e3	..C	..TCT	..TC
H0127e3	..C	..TCT	..TC
H0127e4	..C	..TCT	..TC
MCF0212c1A	..CT
MCF0212c2A	..CT
P1169d1	..C	..T	..TCT	..TCG
P1169d2	..C	..T	..TCT	..TCG
	666	666	666	666	666	666	666	666	666	666	666	666	666	666	666	666
	222	223	333	333	333	444	444	444	455	555	555	556	666	666	666	777
	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012
tippecanoe	GAT	GCG	GAC	AAA	ATC	TCC	TTT	CAC	CCC	TAC	TTC	TCC	TAC	AAA	GAC	CTA
P1109j3A	..TT	T.G
P1195j4A	..TT	T.G
CS0348j6A	..TT	T.G
CS0348j7A	..TT	T.G
K119e3	..C	..A	..TCT	T.G
H0127e3	..C	..A	..TCT	T.G
H0127e4	..C	..A	..TCT	T.G
MCF0212c1	..C	..A	..TTG
MCF0212c2	..C	..A	..TTG
P1169d1	..C	..A	..TT	T.G
P1169d2	..C	..A	..TT	T.G
	666	666	666	666	666	666	666	666	666	666	777	777	777	777	777	777
	777	777	788	888	888	889	999	999	999	000	000	000	011	111	111	112

	345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890
tippecanoe	CTT	GGT	TTT	GCA	GTA	CTA	CTT	ATT	GCT	CTA	ACA	GCT	CTT	GCT	CTC	TTT
P1109j3CC	..C	..CC
P1195j4CC	..C	..CC
CS0348j6GCG	A.C	..C	..C
CS0348j7	..GG	..A	..C	A.C	..C	..C
K119e3	..GCC	..C	..C
H0127e3CC	..C	..C
H0127e4GCC	..C	..C
MCF0212c1CT	..CC	..C
MCF0212c2CT	..CC	..C
P1169d1CAC	..C	..C
P1169d2CC	..C	..C
	777	777	777	777	777	777	777	777	777	777	777	777	777	777	777	777
tippecanoe	TCC	CCC	AAT	CTC	TTG	GGA	GAC	CCA	GAC	AAC	TTC	ACC	CCA	GCA	AAT	CCC
P1109j3T	C..CTTC	...
P1195j4T	C..CTT	..G	..C	...
CS0348j6T	C.CCTT	..C	..C	...
CS0348j7T	C.CCTT	..C	..C	...
K119e3T	..C	...	C.CT	..CTT	..G
H0127e3T	..C	...	C.CT	..CTT	..G
H0127e4T	..C	...	C.CT	..CTT	..G
MCF0212c1TAC	..TTC
MCF0212c2TAC	..TTC
P1169d1	C.CCT	..G
P1169d2	C.CCT	..G
	777	777	777	777	777	777	777	777	777	777	788	888	888	888	888	888
tippecanoe	TTA	GTT	ACT	CCC	CCA	CAC	ATT	AAG	CCT	GAG	TGA	TAC	TTC	TTG	TTT	GCC
P1109j3G	..TG
P1195j4G	..TG
CS0348j6	..GG	..T
CS0348j7	..GG	..T
K119e3G	..TA
H0127e3G	..TA
H0127e4G	..TA
MCF0212c1	C.GTA	..G
MCF0212c2	C.GTA	..G
P1169d1CG	..T
P1169d2CG	..T
	888	888	888	888	888	888	888	888	888	888	888	888	888	888	888	888
tippecanoe	TAC	GCC	ATT	CTT	CGT	TCC	ATC	CCC	AAC	AAA	CTG	GGA	GGG	GTT	CTA	GCC
P1109j3C	..G	..CT	..T	..TG
P1195j4C	..A	..CT	..T	..TG	T..	...
CS0348j6C	..G	..CT	..T	..TA	T.G	...
CS0348j7C	..G	..CT	..T	..TA	T.G	...
K119e3G	..CT	..TC	T.G	...
H0127e3G	..CT	..TC	T.G	...
H0127e4G	..CT	..TC	T.G	...

MCF0212c1A	..CT	..T	..TAC	T..	...
MCF0212c2A	..CT	..T	..TAC	T..	...
P1169d1G	..GT	..T	..TA	T.G	...
P1169d2G	..GT	..T	..TA	T.G	...
	888	888	888	888	888	888	888	888	888	888	888	889	999	999	999	999
	666	667	777	777	777	888	888	888	899	999	999	990	000	000	000	111
	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012
tippecanoe	TTA	TTG	GCA	TCC	ATC	CTG	GTC	CTA	ATA	ATT	GTT	CCA	ATC	CTC	CAC	ACA
P1109j3GT	..C	..AC	..G	..T
P1195j4GT	..C	..AGC	..G	..TG
CS0348j6GT	..C	..AGC	..G
CS0348j7GT	..C	..AGC	..G
K119e3GT	..C	..AGC	..GC
H0127e3GT	..C	..AGC	..G
H0127e4GT	..C	..AGC	..G
MCF0212c1C	..G	G.C	..CT
MCF0212c2C	..G	G.C	..CT
P1169d1	..GGT	..T	..AGC	..G
P1169d2	..GGT	..T	..AGC	..G
	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999
	111	111	122	222	222	223	333	333	333	444	444	444	455	555	555	556
	345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890
tippecanoe	TCA	AAA	CAA	CGA	GGC	GTC	ACA	TTC	CGG	CCC	CTC	TCC	CAA	TTC	CTC	TTC
P1109j3C	..TTTG
P1195j4C	..TTG
CS0348j6C	..TTG	C..
CS0348j7C	..TTG	C..
K119e3	..GC	..TT
H0127e3	..GC	..TT
H0127e4	..GC	..TT
MCF0212c1TT
MCF0212c2TT
P1169d1C	..TTG
P1169d2C	..TTG
	999	999	999	999	999	999	999	999	999	999	999	999	999	000	000	000
	666	666	666	777	777	777	788	888	888	889	999	999	999	000	000	000
	123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678
tippecanoe	TGA	ACC	TTA	ATC	GCG	GAC	GTC	GCC	ATT	CTA	ACC	TGA	ATT	GGA	GGT	ATG
P1109j3	..G	G..	..GCCT	..C	..A	...
P1195j4	...	G..	..GCCT	..C	..A	...
CS0348j6	..G	G..	..GCCT	..C
CS0348j7	..G	G..	..GCCT	..C
K119e3	...	G..CCT	..C
H0127e3	...	G..CCT	..C
H0127e4	...	G..CCT	..C
MCF0212c1	C..CA
MCF0212c2	C..CA
P1169d1	...	G..CCT	..C
P1169d2	...	G..CCT	..C
	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111
	000	000	000	000	000	000	000	000	000	000	000	000	000	000	000	000
	011	111	111	112	222	222	222	333	333	333	344	444	444	445	555	555

	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	CCA	GTA	GAA	CAC	CCC	TTT	ATT	ATT	ATT	GGT	CAA	GTC	GCA	TCC	TTC	GTC
P1109j3	..CCC	...	A..T	...	C.G
P1195j4	..CGCC	...	A..T	...	C.G
CS0348j6	..CGCC	...	A..T	...	C.G
CS0348j7	..CGCC	...	A..T	...	C.G
K119e3	..CGC	...	A..T	...	C.G
H0127e3	..CGC	...	A..T	...	C.G
H0127e4	..CGC	...	A..T	...	C.G
MCF0212c1	..CT	A..TT	...	C.T
MCF0212c2	..CT	A..TT	...	C.T
P1169d1	..CGCT	...	C.G
P1169d2	..CGCT	...	C.G

	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111
	000	000	000	000	000	000	000	000	000	000	000	000	000	000	011	111
	555	666	666	666	677	777	777	778	888	888	888	999	999	999	900	000
	789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234
tippecanoe	TAT	TTC	TTC	CTT	TTC	CTC	GTC	CTT	ACC	CCA	ATC	GCG	GGA	TGA	GTC	GAA
P1109j3	..CCG	C..	..A	C..	...
P1195j4	..CA	..CTCCG	C..	..A	C..	...
CS0348j6	..CCC	C..	..A	C..	...
CS0348j7	..CCC	C..	..A	C..	...
K119e3	..CCG	C..	..C	C..	..A	C..	..G
H0127e3	..CCG	..C	..C	C..	..A	C..	...
H0127e4	..CCG	..C	..C	C..	..A	C..	...
MCF0212c1	..CCG	..C	..C	C..	..A	C..	...
MCF0212c2	..CCG	..C	..C	C..	..A	C..	...
P1169d1	..CC	...	A..	A..	..C	G..	..G	C..	..A	C..	...
P1169d2	..CC	...	A..	A..	..C	G..	..G	C..	..A	C..	...

	111	111	111	1
	111	111	111	1
	000	001	111	1
	567	890	123	4
tippecanoe	AAC	AAG	GCC	C
P1109j3
P1195j4
CS0348j6
CS0348j7
K119e3
H0127e3
H0127e4
MCF0212c1	..T
MCF0212c2	..T
P1169d1
P1169d2

Table 3. ND2 alignment created in Clustal X and edited by eye in MEGA v 3.1.2. *E. tippecanoe* is used as a reference sequence and dots represent common bases.

	123	456	789	111	111	111	122	222	222	223	333	333	333	444	444	444
	012	345	678	901	234	567	890	123	456	789	012	345	678			
tippecanoe	ATG	AAC	CCG	TAT	ATT	TTA	GCC	GCC	CTA	CTC	TTT	GGT	CTA	GGC	CTA	GGC
H27j1CCC
H27j2CCC
H27j5CCC
H27j6CCC
H27j7CCC
H27j8CCC
H28e1CCC
H28e2CCC
P1126j1CC	T..C
P1111j1CCC
P1111j2CCC
H28j1CCC
H28j2CCC
H28j3CCC
H28j4CCC
H28j6CCC
H28j7CCC
H28j8CCC
1570CCC
K119e2CCC
K108c1CCC
K108c2CCC
MCF0212c1CC	...	A..C
MCF0212c3CC	...	A..C
P1168d1CCC
P1169d1CCC
P1169d2CCC
CS0348j1CCC
CS0348j2CCC
CS0348j3CCC
CS0348j4CCC
CS0348j8CCC
P1116j1CCC
P1116j2CCC
P1120e1CCC
P1121e1CCC
1535CCC
1536CCC
1539CCC
1541CCC
1542CCC
1559CCC
1560CCC
1561CCC
1562CCC
1563CCC
1571CCC
K72j1CCC
K72j2CCC

K72j3CCC
P1022j1CCC
P1022j2CCC
P1022j3CCC
P1022j4CCC
P1022j5CCC
P1022j6CCC
H28j9CCC
P1109j3CCC
P1195j3CCC
P1195j5CCC
H27e1CCC
H27e2CCC
H27e3CCC
H27e5CCC
MCF0223c1CCC
CS0353j1CCC
CS0353j2CCC
CS0353j3CCC
CS0353j4CCC
CS0348j5CCC
CS0348j6CCC
P1109j1CCC
P1109j2CCC
K119e1CCC
MCF0212c2CCC	...	T..
MCF0212c4CCC
MCF0223c4CCC	...	T..
MCF0223c5CC	A..C	...	T..
CS0350j1CCC	...	T..
P1195j1CCC
P1195j2CCC
P1195j4CCC
H0528j5CCC
K42e1	GCCC
H0528e1CCC
H0528e2CCC
H0528e4CCC
1537CCC
H27j3CCC
P1178j1CCC
P1178j2CCC
P1178j3CCC
H0231j1CCC
H0231j2CCC
H0231j3CCC
H0528e5CCC
F0512e1CCC
F0521j4CCC
H0528e3CCC
H29e1CCC
F0521j5CCC
MCF0223c2CC	A..C	...	T..
F0521j1CCC
F0521j2CCC
F0521j3CCC

	455	555	555	556	666	666	666	777	777	777	788	888	888	889	999	999
	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	ACG	ACA	ATT	ACC	TTC	GCC	AGC	TCA	CAC	TGG	CTC	CTC	GCC	TGA	ATG	GGA
H27j1	..CGT
H27j2	..CGT
H27j5	..CGT
H27j6	..CGT
H27j7	..CGT
H27j8	..CGT
H28e1	..CGT
H28e2	..CGT
P1126j1	..C	...	G..GT
P1111j1	..CGT
P1111j2	..CGT
H28j1	..CGT
H28j2	..CGT
H28j3	..CGT
H28j4	..CGT
H28j6	..CGT
H28j7	..CGT
H28j8	..CGT
1570	..CGT
K119e2	..C	...	G..GT
K108c1	..CGTA	...
K108c2	..CGTA	...
MCF0212c1	..CGTA	...
MCF0212c3	..CGTA	...
P1168d1	..CGTC
P1169d1	..CGTC
P1169d2	..CGTC
CS0348j1	..CGT
CS0348j2	..CGT
CS0348j3	..CGT
CS0348j4	..CGT
CS0348j8	..CGT
P1116j1	..CGT
P1116j2	..CGT
P1120e1	..CGT
P1121e1	..CGT
1535	..CGT
1536	..CGT
1539	..CGT
1541	..CGT
1542	..CGT
1559	..CGT
1560	..CGT
1561	..CGT
1562	..CGT
1563	..CGT
1571	..CGT
K72j1	..CGT
K72j2	..CGT
K72j3	..CGT
P1022j1	..CGT
P1022j2	..CGT
P1022j3	..CGT
P1022j4	..CGTG

P1022j5	..CGT
P1022j6	..CGT
H28j9	..CGT
P1109j3	..CGT
P1195j3	..CGT
P1195j5	..CGT
H27e1	..CGT
H27e2	..CGT
H27e3	..CGT
H27e5	..CGT
MCF0223c1	..CGTA	...
CS0353j1	..CGT
CS0353j2	..CGT
CS0353j3	..CGT
CS0353j4	..CGT
CS0348j5	..CGT
CS0348j6	..CGT
P1109j1	..CGT
P1109j2	..CGT
K119e1	..C	...	G..GT
MCF0212c2	..CGTA	...
MCF0212c4	..CGTA	...
MCF0223c4	..CGTA	...
MCF0223c5	..CGTA	...
CS0350j1	..CGT
P1195j1	..CGT
P1195j2	..CGT
P1195j4	..CGT
H0528j5	..CGT
K42e1	..CGT
H0528e1	..CGT
H0528e2	..C	...	G..GT
H0528e4	..CGT
1537	..CGT
H27j3	..CGT
P1178j1	..CGT
P1178j2	..CGT
P1178j3	..CGT
H0231j1	..CGT
H0231j2	..CGT
H0231j3	..CGT
H0528e5	..C	...	G..GT
F0512e1	..CGT
F0521j4	..CGT
H0528e3	..C	...	G..GT
H29e1	..C	...	G..GT
F0521j5	..C	...	G..GT
MCF0223c2	..CAGTA	...
F0521j1	..CGT
F0521j2	..CGT
F0521j3	..CGT
tippecanoe	TTA	GAA	ATG	AAT	ACT	CTG	GCC	ATC	ATC	CCC	CTG	ATA	GCA	CAG	CAC	CAT
H27j1	C.TAATT	..G
		111	111	111	111	111	111	111	111	111	111	111	111	111	111	111
	999	000	000	000	011	111	111	112	222	222	222	333	333	333	344	444
	789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234

H27j2	C.TAATT	..G
H27j5	C.TAATT	..G
H27j6	C.TAATT	..G
H27j7	C.TAATT	..G
H27j8	C.TAATT	..G
H28e1	C.TAATT	..G
H28e2	C.TAATT	..G
P1126j1	C.TAATT	..G
P1111j1	C.TAATT	..GC
P1111j2	C.TA	..CATT	..GT	..C
H28j1	C.TAATT	..G
H28j2	C.TAATT	..G
H28j3	C.TAATT	..G
H28j4	C.TAATT	..G
H28j6	C.TAATT	..G
H28j7	C.TAATT	..G
H28j8	C.TAATT	..G
1570	C.TAATT	..G
K119e2	C.TAATT	..G
K108c1	C.TAATGAC	...
K108c2	C.TAATGAC	...
MCF0212c1	C.TAATGAC	...
MCF0212c3	C.TAAT	..TGAC	...
P1168d1	C.TA	..CATGAC	...
P1169d1	C.TA	..CATGAC	...
P1169d2	C.TA	..CATGAC	...
CS0348j1	C.TAATGAC	...
CS0348j2	C.TACTGAC	...
CS0348j3	C.TAATGAC	...
CS0348j4	C.TAATGAC	...
CS0348j8	C.TAATGAC	...
P1116j1	C.TAATGAC	...
P1116j2	C.TAATGAC	...
P1120e1	C.TAATGAC	...
P1121e1	C.TAATGAC	...
1535	C.TAATGAC	...
1536	C.TAATGAC	...
1539	C.TAATGAC	...
1541	C.TAATGAC	...
1542	C.TAATGAC	...
1559	C.TA	..CATGTC	...
1560	C.TA	..CATGTC	...
1561	C.TA	..CATGTC	...
1562	C.TA	..CATGTC	...
1563	C.TA	..CATGTC	...
1571	C.TAATGAC	...
K72j1	C.TAATGAC	...
K72j2	C.TAATGAC	...
K72j3	C.TAATGAC	...
P1022j1	C.TAATGAC	...
P1022j2	C.TAATGAC	...
P1022j3	C.TAATGAC	...
P1022j4	C.TAATGAC	...
P1022j5	C.TAATGAC	...
P1022j6	C.TAATGAC	...
H28j9	C.TAATGAC	...
P1109j3	C.TAATGAC	...

P1195j3	C.TAAT	..GC
P1195j5	C.TAAT	..GC
H27e1	C.TAATT	..G
H27e2	C.TAATT	..G
H27e3	C.TAATT	..G
H27e5	C.TAATT	..G
MCF0223c1	C.TATGAC	
CS0353j1	C.TAAT	..GC	
CS0353j2	C.TAAT	..GC	
CS0353j3	C.TAAT	..GC	
CS0353j4	C.TAAT	..GC	
CS0348j5	C.TAAT	..GA	..C	
CS0348j6	C.TAAT	..GA	..C	
P1109j1	C.TAAT	..GC	
P1109j2	C.TAAT	..GC	
K119e1	C.TAATT	..G	
MCF0212c2	C.TATGAC	
MCF0212c4	C.TATGAC	
MCF0223c4	C.TATGAC	
MCF0223c5	C.TATGAC	
CS0350j1	C.TAAT	..GC	
P1195j1	C.TAAT	..GC	
P1195j2	C.TAAT	..GC	
P1195j4	C.TAAT	..GC	
H0528j5	C.TAATT	..G	
K42e1	C.TAATT	..G	
H0528e1	C.TAATT	..G	
H0528e2	C.TAATT	..G	
H0528e4	C.TAATT	..G	
1537	C.TAAT	..G	
H27j3	C.TAATT	..G	
P1178j1	C.TAATT	..G	
P1178j2	C.TAAT	..GC	
P1178j3	C.TAAT	..GC	
H0231j1	C.TAATT	..G	
H0231j2	C.TAAT	..GC	
H0231j3	C.TAAT	..GC	
H0528e5	C.TAATT	..G	
F0512e1	C.TAAT	..GC	
F0521j4	C.TAATT	..G	
H0528e3	C.TAATT	..G	
H29e1	C.TAATT	..G	
F0521j5	C.TAATT	..G	
MCF0223c2	C.TAT	..TGAC	
F0521j1	C.TAAT	..GC	
F0521j2	C.TAAT	..GC	
F0521j3	C.TAAT	..GC	

111	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111	111
444	445	555	555	555	666	666	666	677	777	777	778	888	888	888	999	
567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012	

tippecanoe	CAT	CCC	CGG	GCA	GTA	GAA	GCA	ACC	ACC	AAG	TAT	TTT	CTT	ACC	CAA	GCA
H27j1	..CA	..GG	..CC
H27j2	..CA	..GG	..CC
H27j5	..CA	..GG	..CC
H27j6	..CA	..GG	..CC
H27j7	..CA	..GG	..CC

H27j8	..CA	..GG	..CC
H28e1	..CA	..GG	..CC
H28e2	..CA	..GG	..CC
P1126j1	..CA	..GG	..CC
P1111j1	..CA	..GG	..CCG	...
P1111j2	..CA	..GG	..CCG	...
H28j1	..CA	..GG	..CC
H28j2	..CA	..GG	..CC
H28j3	..CA	..GG	..CC
H28j4	..CA	..GG	..CC
H28j6	..CA	..GG	..CC
H28j7	..CA	..GG	..CC
H28j8	..CA	..GG	..CC
1570	..CA	..GG	..CC
K119e2	..CA	..GG	..CC
K108c1	..CA	..GG	..CTG	...
K108c2	..CA	..GG	..CTG	...
MCF0212c1	..CA	..GG	..CTG	...
MCF0212c3	..CA	..GG	..CTG	...
P1168d1	..CA	..G	..G	..G	..CCG	...
P1169d1	..CA	..G	..G	..G	..CCG	...
P1169d2	..CA	..G	..G	..G	..CCG	...
CS0348j1	..CA	..GG	..CCG	...
CS0348j2	..CA	..GG	..CCG	...
CS0348j3	..CA	..GG	..CCG	...
CS0348j4	..CA	..GG	..CCG	...
CS0348j8	..CA	..GG	..CCG	...
P1116j1	..CA	..GG	..CCG	...
P1116j2	..CA	..GG	..CCG	...
P1120e1	..CA	..GG	..CC
P1121e1	..CA	..GG	..CC
1535	..CA	..GG	..CC
1536	..CA	..GG	..CC
1539	..CA	..GG	..CC
1541	..CA	..GG	..CC
1542	..CA	..GG	..CC
1559	..CA	..GG	..CCG	...
1560	..CA	..GG	..CCG	...
1561	..CA	..GG	..CCG	...
1562	..CA	..GG	..CCG	...
1563	..CA	..GG	..CCG	...
1571	..CA	..GG	..CC
K72j1	..CA	..GG	..CCG	...
K72j2	..CA	..GG	..CCG	...
K72j3	..CA	..GG	..CCG	...
P1022j1	..CA	..GG	..CCG	...
P1022j2	..CA	..GG	..CCG	...
P1022j3	..CA	..GG	..CCG	...
P1022j4	..CA	..GG	..CCG	...
P1022j5	..CA	..GG	..CCG	...
P1022j6	..CA	..GG	..CCG	...
H28j9	..CA	..GG	..CC
P1109j3	..CA	..GG	..CCG	...
P1195j3	..CA	..GG	..CCG	...
P1195j5	..CA	..GG	..CCG	...
H27e1	..CA	..GG	..CC
H27e2	..CA	..GG	..CC

H27e3	..CGG	..CC
H27e5	..CA	..GG	..CC
MCF0223c1	..CA	..GG	..CTG	...
CS0353j1	..CA	..GG	..CCG	...
CS0353j2	..CA	..GG	..CCG	...
CS0353j3	..CA	..GG	..CCG	...
CS0353j4	..CA	..GG	..CCG	...
CS0348j5	..CA	..GG	..CCG	...
CS0348j6	..CA	..GG	..CCG	...
P1109j1	..CA	..GG	..CCG	...
P1109j2	..CA	..GG	..CCG	...
K119e1	..CA	..GG	..CCG	...
MCF0212c2	..CA	..GG	..CTG	...
MCF0212c4	..CA	..GG	..CTG	...
MCF0223c4	..CA	..GG	..CTG	...
MCF0223c5	..CA	..GG	..CTG	...
CS0350j1	..CA	..GG	..CCG	...
P1195j1	..CA	..GG	..CCG	...
P1195j2	..CA	..GG	..CCG	...
P1195j4	..CA	..GG	..CCG	...
H0528j5	..CA	..GG	..CCG	...
K42e1	..CA	..GG	..CCG	...
H0528e1	..CA	..GG	..CCG	...
H0528e2	..CA	..GG	..CCG	...
H0528e4	..CA	..GG	..CCG	...
1537	..CA	..GG	..CCG	...
H27j3	..CA	..GG	..CCG	...
P1178j1	..CA	..GG	..CCG	...
P1178j2	..CA	..GG	..CCG	...
P1178j3	..CA	..GG	..CCG	...
H0231j1	..CA	..GG	..CCG	...
H0231j2	..CA	..GG	..CCG	...
H0231j3	..CA	..GG	..CCG	...
H0528e5	..CA	..GG	..CCG	...
F0512e1	..CA	..GG	..CCG	...
F0521j4	..CA	..GG	..CCG	...
H0528e3	..CA	..GG	..CCG	...
H29e1	..CA	..GG	..CCG	...
F0521j5	..CA	..GG	..CCG	...
MCF0223c2	..CA	..GG	..CTG	...
F0521j1	..CA	..GG	..CCG	...
F0521j2	..CA	..GG	..CCG	...
F0521j3	..CA	..GG	..CCG	...

111	111	122	222	222	222	222	222	222	222	222	222	222	222	222	222	222
999	999	900	000	000	001	111	111	111	222	222	222	233	333	333	334	
345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890	

tippecanoe	ACC	GCA	GCA	GCC	ATA	CTT	CTT	TTT	GCC	AGT	ACC	ACT	AAC	GCA	TGG	CTG
H27j1GC	..CCCA	T..
H27j2GC	..CCCA	T..
H27j5GC	..CCCA	T..
H27j6GC	..CCCA	T..
H27j7GC	..CCCA	T..
H27j8GC	..CCCA	T..
H28e1GC	..CCCA	T..
H28e2GC	..CCCA	T..
P1126j1GC	..CCCA	T..

P1111j1GCCCA	T..
P1111j2GCCCA	T..
H28j1GC	..CCCA	T..
H28j2GC	..CCCA	T..
H28j3GC	..CCCA	T..
H28j4GC	..CCCA	T..
H28j6GC	..CCCA	T..
H28j7GC	..CCCA	T..
H28j8GC	..CCCA	T..
1570GC	..CCCA	T..T
K119e2GC	..CCCA	T..
K108c1G	..GG	..CCCA	...
K108c2G	..GG	..CCCA	...
MCF0212c1G	..GG	..CCCA	...
MCF0212c3G	..GG	..CCCA	...
P1168d1CG	..CCA	T..
P1169d1CG	..CCA	T..
P1169d2CG	..CCA	T..
CS0348j1GCC	..CCA	T..
CS0348j2GCC	..CCA	T..
CS0348j3GCC	..CCA	T..
CS0348j4GCC	..CCA	T..
CS0348j8GCC	..CCA	T..
P1116j1GCC	..CCA	T..
P1116j2GCC	..CCA	T..
P1120e1GC	..CCCA	T..
P1121e1GC	..CCCA	T..
1535GC	..CCCA	T..
1536GC	..CCCA	T..
1539GC	..CCCA	T..
1541GC	..CCCA	T..
1542GC	..CCCA	T..
1559GCC	..CCA	T..
1560GCC	..CCA	T..
1561GCC	..CCA	T..
1562GCC	..CCA	T..
1563GCC	..CCA	T..
1571GC	..CCCA	T..
K72j1GCC	..CCA	T..
K72j2GCC	..CCA	T..
K72j3GCC	..CCA	T..
P1022j1	G..	..GCC	..CCA	T..
P1022j2	G..	..GCC	..CCA	T..
P1022j3	G..	..GCC	..CCA	T..
P1022j4	G..	..GCC	..CCA	T..
P1022j5	G..	..GCC	..CCA	T..
P1022j6	G..	..GCC	..CCA	T..
H28j9GC	..CCCA	T..
P1109j3GCC	..CCA	T..
P1195j3GCC	..CCA	T..
P1195j5GCC	..CCA	T..
H27e1GC	..CCCA	T..
H27e2GC	..CCCA	T..
H27e3GC	..CCCA	T..
H27e5GC	..CCCA	T..
MCF0223c1G	..GG	..CCCA	...
CS0353j1GCC	..CCA	T..

CS0353j2GCCCA	T..
CS0353j3GCCCA	T..
CS0353j4GCCCA	T..
CS0348j5GCCCA	T..
CS0348j6GCCCA	T..
P1109j1GCCCA	T..
P1109j2GCCCA	T..
K119e1GC	..CCCA	T..
MCF0212c2G	..GG	..CCCA	...
MCF0212c4G	..GG	..CCCA	...
MCF0223c4G	..GG	..CCCA	...
MCF0223c5G	..GG	..CCCA	...
CS0350j1	G..	..GCCCA	T..
P1195j1GCCCA	T..
P1195j2GCCCA	T..
P1195j4GCCCA	T..
H0528j5GC	..CCCA	T..
K42e1GC	..CCCA	T..
H0528e1GC	..CCCA	T..
H0528e2GC	..CCCA	T..
H0528e4GC	..CCCA	T..
1537GC	..CCCA	T..
H27j3GC	..CCCA	T..
P1178j1GC	..CCCA	T..
P1178j2GCCCA	T..
P1178j3GCCCA	T..
H0231j1GC	..CCCA	T..
H0231j2GCCCA	T..
H0231j3GCCCA	T..
H0528e5GC	..CCCA	T..
F0512e1GCCCA	T..
F0521j4GC	..CCCA	T..
H0528e3GC	..CCCA	T..
H29e1GC	..CCCA	T..
F0521j5GC	..CCCA	T..
MCF0223c2G	..GG	..CCCA	...
F0521j1GCCCA	T..
F0521j2GCCCA	T..
F0521j3	.A.	..GCCCA	T..

222	222	222	222	222	222	222	222	222	222	222	222	222	222	222	222	222
444	444	444	555	555	555	566	666	666	666	667	777	777	777	888	888	888
123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678	

tippecanoe	ACA	GGA	CAG	TGA	GAC	ATC	CAA	CAG	ATG	ACC	CAC	CCC	CTC	CCC	ATC	ACC
H27j1GGA	G..	..T	G..T
H27j2GGA	G..	..TT
H27j5GGA	G..	..T	G..T
H27j6GGA	G..	..TT
H27j7GGA	G..	..TT
H27j8GGA	G..	..T	G..T
H28e1GGA	G..	..TT
H28e2GGA	G..	..TT
P1126j1GGA	G..	..TT
P1111j1GGA	..A	G..A
P1111j2GGA	..AA
H28j1GGA	G..	..T	G..T
H28j2GGA	G..	..TT

H28j3GGA	G..	..TT
H28j4GGA	G..	..TT
H28j6GGA	G..	..T	G.T
H28j7GGA	G..	..T	G.T
H28j8GGA	GG.	..T	G.T
1570GGA	G..	..TT
K119e2GGA	G..	..TT
K108c1T	..TA	..A	..A	..T	..T
K108c2T	..TA	..A	..A	..T	..T
MCF0212c1T	..TA	..A	..A	..T	..T
MCF0212c3T	..TA	..A	..A	..T	..T
P1168d1GGA	..AT
P1169d1GGA	..AT
P1169d2GGA	..AT
CS0348j1GG	..TA	..ATTT
CS0348j2GG	..TA	..ATTT
CS0348j3GG	..TA	..ATTT
CS0348j4GG	..TA	..ATTT
CS0348j8GG	..TA	..ATTT
P1116j1GGA	..A	G..A
P1116j2GGA	..A	G..A
P1120e1GGA	G..	..TT
P1121e1GGA	G..	..TT
1535GGA	G..	..TT
1536GGA	G..	..TT
1539GGA	G..	..TT
1541GGA	G..	..TT
1542GGA	G..	..TT
1559GGA	..AA
1560GGA	..AA
1561GGA	..AA
1562GGA	..AA
1563GGA	..AA
1571GGA	G..	..TT
K72j1GGA	..A	G..A
K72j2GGA	..A	G..A
K72j3GGA	..A	G..A
P1022j1GGA	..A	G..A
P1022j2GGA	..A	G..A
P1022j3GGA	..A	G..A
P1022j4GGA	..A	G..A
P1022j5GGA	..A	G..A
P1022j6GGA	..A	G..A
H28j9GGA	G..	..T	G.T
P1109j3GGA	..A	G..A
P1195j3GGA	..A	G..A
P1195j5GGA	..A	G..A
H27e1GGA	G..	..TT
H27e2GGA	G..	..TT
H27e3GGA	G..	..TT
H27e5GGA	G..	..TT
MCF0223c1T	..TA	..A	..A	..T	..T
CS0353j1GGA	..A	G..A
CS0353j2GGA	..A	G..A
CS0353j3GGA	..A	G..A
CS0353j4GGA	..A	G..A
CS0348j5GG	..TA	..ATTT

CS0348j6GG	..TA	..ATTT
P1109j1GGA	..A	G..A
P1109j2GGA	..A	G..A
K119e1GGA	..A	G..T
MCF0212c2T	..TA	..A	..A	..T	..T
MCF0212c4T	..TA	..A	..A	..T	..T
MCF0223c4T	..TA	..A	..A	..T	..T
MCF0223c5T	..TA	..A	..A	..T	..T
CS0350j1GGA	..A	G..A
P1195j1GGA	..A	G..A
P1195j2GGA	..A	G..A
P1195j4GGA	..A	G..A
H0528j5GGA	..A	G..	..T	G..T
K42e1GGA	..A	G..	..TT
H0528e1GGA	..A	G..	..TT
H0528e2GGA	..A	G..T
H0528e4GGA	..A	G..	..TT
1537GGA	..A	G..	..TT
H27j3GG	...	H27j3A	..A	G..	..T	G..T
P1178j1GGA	..A	G..	..TT
P1178j2GGA	..A	G..A
P1178j3GGA	..A	G..A
H0231j1GGA	..A	G..	..TT
H0231j2GGG.	..A	..A	..A	G..A
H0231j3GGA	..A	G..A
H0528e5GGA	..A	T..T
F0512e1GGA	..A	G..A
F0521j4GGA	..A	G..	..TT
H0528e3GGA	..A	T..T
H29e1GGA	..A	T..T
F0521j5GGA	..A	G..T
MCF0223c2T	..TA	..A	..A	..T	..T
F0521j1GGA	..A	G..A
F0521j2GGA	..A	G..A
F0521j3GGA	..A	G..A

222	222	222	223	333	333	333	333	333	333	333	333	333	333	333	333	333
899	999	999	990	000	000	000	111	111	111	122	222	222	223	333	333	333
901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789

tippecanoe	CTT	ATT	ACG	CTT	GCC	TTA	GCC	CTA	AAA	ATT	GGT	CTT	GCG	CCT	GTT	CAC
H27j1	..CC	..CACAT
H27j2	..CC	..CACAT
H27j5	..CC	..CACAT
H27j6	..CC	..CACAT
H27j7	..CC	..CACAT
H27j8	..CC	..CACAT
H28e1	..CC	..CACAT
H28e2	..CC	..CACAT
P1126j1	..CC	..CACAT
P1111j1C	..CACAT
P1111j2C	..CACAT
H28j1	..CC	..CACAT
H28j2	..CC	..CACAT
H28j3	..CC	..CACAT
H28j4	..CC	..CACAT
H28j6	..CC	..CACAT
H28j7	..CC	..CACAT

H28j8	..CC	..CACAT
1570	..CC	..CACAT
K119e2	..CC	..CACAT
K108c1	..AC	..CACAT
K108c2	..AC	..CAAAT
MCF0212c1	..AC	..CACAT
MCF0212c3	..AC	..CACAT
P1168d1C	..CG	..A	T..CAT
P1169d1C	..CG	..A	T..CAT
P1169d2C	..CG	..A	T..CAT
CS0348j1	..CC	..CACAT
CS0348j2	..CC	..CACAT
CS0348j3	..CC	..CACAT
CS0348j4	..CC	..CACAT
CS0348j8	..CC	..CACAT
P1116j1C	..CACAT
P1116j2C	..CACAT
P1120e1	..CC	..CACAT
P1121e1	..CC	..CACAT
1535	..CC	..CACAT
1536	..CC	..CACAT
1539	..CC	..CACAT
1541	..CC	..CACAT
1542	..CC	..CACAT
1559C	..CACAT
1560C	..CACAT
1561C	..CACAT
1562C	..CACAT
1563C	..CACAT
1571	..CC	..C	..GACAT
K72j1C	..CACAT
K72j2C	..CACAT
K72j3C	..CACAT
P1022j1C	..CACAT
P1022j2C	..CACAT
P1022j3C	..CACAT
P1022j4C	..CACAT
P1022j5C	..CACAT
P1022j6C	..CACAT
H28j9	..CC	..CACAT
P1109j3C	..CACAT
P1195j3C	..CACAT
P1195j5C	..CACAT
H27e1	..CC	..CACAT
H27e2	..CC	..CACAT
H27e3	..CC	..CACAT
H27e5	..CC	..CG	..ACAT
MCF0223c1	..AC	..CACAT
CS0353j1C	..CACAT
CS0353j2C	..CACAT
CS0353j3C	..CACAT
CS0353j4C	..CACAT
CS0348j5	..CC	..CACAT
CS0348j6	..CC	..CACAT
P1109j1C	..CACAT
P1109j2C	..CACAT
K119e1	..CC	..CACAT

MCF0212c2	..AC	..CAA
MCF0212c4	..AC	..CACA
MCF0223c4	..AC	..CACA
MCF0223c5	..AC	..CA	A..A
CS0350j1C	..CAAT
P1195j1C	..CACAT
P1195j2C	..CACAT
P1195j4C	..CACAT
H0528j5	..CC	..CACAT
K42e1	..CC	..CACAT
H0528e1	..CC	..CACAT
H0528e2	..CC	..CACAT
H0528e4	..CC	..CACAT
1537	..CC	..CACAT
H27j3	..CC	..CACAT
P1178j1	..CC	..CACAT
P1178j2C	..CACAT
P1178j3C	..CACAT
H0231j1	..CC	..CACAT
H0231j2C	..CACAT
H0231j3C	..CACAT
H0528e5	..CC	..CACAT
F0512e1C	..CACAT
F0521j4	..CC	..CACAT
H0528e3	..CC	..CACAT
H29e1	..CC	..CACAT
F0521j5	..CC	..CACAT
MCF0223c2	..AC	..CACA
F0521j1C	..CACAT
F0521j2C	..CACAT
F0521j3C	..CACAT

333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333	333
333	444	444	444	455	555	555	556	666	666	666	777	777	777	788	888	
789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234	

tippecanoe	TCG	TGA	CTA	CCC	GAG	GTT	CTC	CAG	GGA	CTA	GAT	CTT	ACG	ACC	GGA	CTT
H27j1	..ACACTG	...
H27j2	..ACACTG	...
H27j5	..ACACTG	...
H27j6	..ACACTG	...
H27j7	..ACACTG	...
H27j8	..ACACTG	...
H28e1	..ACACTG	...
H28e2	..AGCACTG	...
P1126j1	..ACACTG	...
P1111j1	..ACACT
P1111j2	..ACACT
H28j1	..ACACTG	...
H28j2	..ACACTG	...
H28j3	..ACACTG	...
H28j4	..ACACTG	...
H28j6	..ACACTG	...
H28j7	..ACACTG	...
H28j8	..ACACTG	...
1570	..ACACTG	...
K119e2	..ACACTG	...
K108c1	..AA	..C	..T	..ACTG	..C

K108c2	..AA	..C	..T	..ACTG	..C
MCF0212c1	..AA	..C	..T	..ACTG	..C
MCF0212c3	..AA	..C	..T	..ACTG	..C
P1168d1	..ACACTG	..C	
P1169d1	..ACACTG	..C	
P1169d2	..ACACTG	..C	
CS0348j1	..ACACTG	...	
CS0348j2	..ACACTG	...	
CS0348j3	..ACACTG	...	
CS0348j4	..ACACTG	...	
CS0348j8	..ACACTG	...	
P1116j1	..ACACTG	...	
P1116j2	..ACACTG	...	
P1120e1	..ACACTG	...	
P1121e1	..ACACTG	...	
1535	..ACACTG	...	
1536	..ACACTG	...	
1539	..ACACTG	...	
1541	..ACACTG	...	
1542	..ACACTG	...	
1559	..ACACTG	...	
1560	..ACACTG	...	
1561	..ACACTG	...	
1562	..ACACTG	...	
1563	..ACACTG	...	
1571	..ACACTG	...	
K72j1	..ACACTG	...	
K72j2	..ACACTG	...	
K72j3	..ACACTG	...	
P1022j1	..ACACTG	...	
P1022j2	..ACACTG	...	
P1022j3	..ACACTG	...	
P1022j4	..ACACTG	...	
P1022j5	..ACACTG	...	
P1022j6	..ACACTG	...	
H28j9	..ACACTG	...	
P1109j3	..ACACTG	...	
P1195j3	..ACACTG	...	
P1195j5	..ACACTG	...	
H27e1	..ACACTG	...	
H27e2	..ACACTG	...	
H27e3	..ACACTG	...	
H27e5	..ACACTG	...	
MCF0223c1	..AA	..C	..T	..ACTG	..C	
CS0353j1	..ACACTG	...	
CS0353j2	..ACACTG	...	
CS0353j3	..ACACTG	...	
CS0353j4	..ACACTG	...	
CS0348j5	..ACACTG	...	
CS0348j6	..ACACTG	...	
P1109j1	..ACACTG	...	
P1109j2	..ACACTG	...	
K119e1	..ACACTG	...	
MCF0212c2	..AA	..C	..T	..ACTG	..C	
MCF0212c4	..AA	..C	..T	..ACTG	..C	
MCF0223c4	..AA	..C	..T	..ACTG	..C	
MCF0223c5	..AA	..C	..T	..ACTG	..C	

CS0350j1	..ACACT
P1195j1	..ACACT
P1195j2	..ACACT
P1195j4	..ACACT
H0528j5	..ACACTG	...
K42e1	..AGCACTG	...
H0528e1	..ACACTG	...
H0528e2	..ACACTG	...
H0528e4	..ACACTG	...
1537	..ACACTG	...
H27j3	..ACACTG	...
P1178j1	..ACACTG	...
P1178j2	..ACACTG	...
P1178j3	..ACACTG	...
H0231j1	..ACACTG	...
H0231j2	..ACACTG	...
H0231j3	..ACACTG	...
H0528e5	..ACACTG	...
F0512e1	..ACACTG	...
F0521j4	..ACACTG	...
H0528e3	..ACACTG	...
H29e1	..ACACTG	...
F0521j5	..ACACTG	...
MCF0223c2	..AA	..C	..T	..ACTG	..C
F0521j1	..ACACTG	...
F0521j2	..ACACTG	...
F0521j3	..ACACTG	...

333	333	333	333	333	444	444	444	444	444	444	444	444	444	444	444	444
888	889	999	999	999	000	000	000	011	111	111	112	222	222	222	333	
567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012	

tippecanoe	ATC	CTC	TCC	ACC	TGA	CAA	AAG	CTT	GCC	CCC	TTT	GCC	CTC	CTA	CTA	CAA
H27j1GCTT
H27j2GCTT
H27j5GCTT
H27j6GCTT
H27j7GCTT
H27j8GCTT
H28e1GCTT
H28e2GCTT
P1126j1GCTT
P1111j1CTTG	...
P1111j2A	..CTTG	...
H28j1GCTT
H28j2GCTT
H28j3GCTT
H28j4GCTT
H28j6GCTT
H28j7GCTT
H28j8GCTT
1570GCTT
K119e2GCTT
K108c1ATT
K108c2ATT
MCF0212c1ATTT
MCF0212c3ATT
P1168d1GA	..CTTTT	...

P1169d1GA	..CTTT	...
P1169d2GA	..CTTT	...
CS0348j1CTTG
CS0348j2CTTG
CS0348j3A	..CTTG
CS0348j4A	..CTTG
CS0348j8A	..CTTG
P1116j1A	..CTTG
P1116j2A	..CTTG
P1120e1GCTT
P1121e1GCTT
1535GCTT
1536GCTT
1539GCTT
1541GCTT
1542GCTT
1559A	..CTTG
1560A	..CTTG
1561A	..CTTG
1562A	..CTTG
1563A	..CTTG
1571GCTT
K72j1A	..CTTG
K72j2A	..CTTG
K72j3A	..CTTG
P1022j1A	..CTTG
P1022j2A	..CTTG
P1022j3A	..CTTG
P1022j4A	..CTTG
P1022j5A	..CTTG
P1022j6A	..CTTG
H28j9GCTT
P1109j3CTTG
P1195j3CTTG
P1195j5CTTG
H27e1GCTT
H27e2GCTT
H27e3GCTT
H27e5GCTT
MCF0223c1A	TTT	...
CS0353j1A	..CTTG
CS0353j2CTTG
CS0353j3A	..CTTG
CS0353j4A	..CTTG
CS0348j5A	..CTTG
CS0348j6CTTG
P1109j1CTTG
P1109j2CTTG
K119e1GCTT
MCF0212c2A	TT	...
MCF0212c4A	TT	...
MCF0223c4A	TT	...
MCF0223c5A	TT	...
CS0350j1	A..	..A	..CTTG
P1195j1A	..CTTG
P1195j2A	..CTTG
P1195j4A	..CTTG

H0528j5GCTT
K42e1GCTT
H0528e1GCTT
H0528e2GCTT
H0528e4GCTT
1537GCTTG
H27j3GCTT
P1178j1GCTT
P1178j2GCTTG
P1178j3GCTTG
H0231j1GCTT
H0231j2GCTTG
H0231j3GCTTG
H0528e5GCTTG
F0512e1GCTTG
F0521j4GCTT
H0528e3GCTT
H29e1GCTT
F0521j5GCTT
MCF0223c2GATT
F0521j1GCTTG
F0521j2GCTTG
F0521j3GCTTG

	444	444	444	444	444	444	444	444	444	444	444	444	444	444	444	444
	333	333	344	444	444	445	555	555	555	666	666	666	677	777	777	778
	345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890
tippecanoe	ATT	CAA	CCT	ACC	AAC	TCA	CCT	ATC	TTA	ATT	GCC	TTT	GGC	GTA	GCA	TCA
H27j1	G.G	G..	..A	C..TA	...	A..	..C
H27j2	G.G	G..	..A	C..TA	...	A..	..C
H27j5	G.G	G..	..A	C..TA	...	A..	..C
H27j6	G.G	G..	..A	C..TA	...	A..	..C
H27j7	G.G	G..	..A	C..TA	...	A..	..C
H27j8	G.G	G..	..A	C..TA	...	A..	..C
H28e1	G.G	G..	..A	C..TA	...	A..	..C
H28e2	G.G	G..	..A	C..TA	...	A..	..C
P1126j1	G.G	G..	..A	C.GTA	...	A..	..C
P1111j1	G.G	G..	..A	C.GTA	...	A..	..C
P1111j2	G.A	G..	..A	C.GTA	...	A..	..C
H28j1	G.G	G..	..A	C..TA	...	A..	..C
H28j2	G.G	G..	..A	C..TA	...	A..	..C
H28j3	G.G	G..	..A	C..TA	...	A..	..C
H28j4	G.G	G..	..A	C..TA	...	A..	..C
H28j6	G.G	G..	..A	C..TA	...	A..	..C
H28j7	G.G	G..	..A	C..TA	...	A..	...
H28j8	G.G	G..	..A	C..TA	...	A..	...
1570	G.G	G..	..A	C..TA	...	A..	...
K119e2	G.G	A..	..A	C.GTA	...	A..	..C
K108c1	G..	G..TG	...	A..	...
K108c2	G..	G..TG	...	A..	...
MCF0212c1	G..	G..TG	...	A..	...
MCF0212c3	G..	G..TG	..C	A..	...
P1168d1	G.G	G..	..A	C.GTA	C.G	A..	..C
P1169d1	G.G	G..	..A	C.GTA	C.G	A..	..C
P1169d2	G.G	G..	..A	C.GTA	C.G	A..	..C
CS0348j1	G.A	G..	..A	C.GTA	...	A..	..C
CS0348j2	G.A	G..	..A	C.GTA	...	A..	..C

CS0348j3	G.A	G..	...	C.GTA	...	A..	..C
CS0348j4	G.A	G..	...	C.GTA	...	A..	..C
CS0348j8	G.A	G..	...	C.GTA	...	A..	..C
P1116j1	G.G	G..	...	C.GTG	...	A..	..C
P1116j2	G.G	G..	...	C.GTAC
P1120e1	G.G	G..	..A	C..TA	...	A..	..C
P1121e1	G.G	G..	..A	C..TA	...	A..	..C
1535	G.G	G..	..A	C..TA	...	A..	..C
1536	G.G	G..	..A	C..TA	...	A..	..C
1539	G.G	G..	..A	C..TA	...	A..	..C
1541	G.G	G..	..A	C..TA	...	A..	..C
1542	G.G	G..	..A	C..TA	...	A..	..C
1559	G.A	G..	...	C.GTA	...	A..	..C
1560	G.A	G..	...	C.GTA	...	A..	..C
1561	G.A	G..	...	C.GTA	...	A..	..C
1562	G.A	G..	...	C.GTA	...	A..	..C
1563	G.A	G..	...	C.GTA	...	A..	..C
1571	G.G	G..	..A	C..TA	...	A..	..C
K72j1	G.G	G..	...	C.GTA	...	A..	..C
K72j2	G.G	G..	...	C.GTA	...	A..	..C
K72j3	G.G	G..	...	C.GTA	...	A..	..C
P1022j1	G.G	G..	...	C.GTA	...	A..	..C
P1022j2	G.G	G..	...	C.GTA	...	A..	..C
P1022j3	G.G	G..	...	C.GTA	...	A..	..C
P1022j4	G.G	G..	...	C.GTA	...	A..	..C
P1022j5	G.G	G..	...	C.GTA	...	A..	..C
P1022j6	G.G	G..	...	C.GTA	...	A..	..C
H28j9	G.G	G..	..A	C..TA	...	A..	..C
P1109j3	G.G	G..	...	C.GTA	...	T..	..C
P1195j3	G.G	G..	...	C.GTA	...	A..	..C
P1195j5	G.G	G..	...	C.GTA	...	A..	..C
H27e1	G.G	G..	..A	C..TA	...	A..	..C
H27e2	G.G	G..	..A	C..TA	...	A..	..C
H27e3	G.G	G..	..A	C..TA	...	A..	..C
H27e5	G.G	G..	..A	C..TA	...	A..	..C
MCF0223c1	G..	G..TG	...	A..	...
CS0353j1	G.G	G..	...	C.GTG	...	A..	..C
CS0353j2	G.G	G..	...	C.GTAC
CS0353j3	G.G	G..	...	C.GTG	...	A..	..C
CS0353j4	G.G	G..	...	C.GTG	...	A..	..C
CS0348j5	G.A	G..	...	C.GTA	...	A..	..C
CS0348j6	G.A	G..	...	C.GTA	...	A..	..C
P1109j1	G.G	G..	...	C.GTAC
P1109j2	G.G	G..	...	C.GTAC
K119e1	G.G	G..	..A	C.G	G..	..TA	...	A..	..C
MCF0212c2	G..	G..TG	...	A..	...
MCF0212c4	G..	G..TG	...	A..	...
MCF0223c4	G..	G..TG	...	A..	...
MCF0223c5	G..	G..TG	...	A..	...
CS0350j1	G.G	G..	...	C.GTA	...	A..	..C
P1195j1	G.G	G..	...	C.GTG	...	A..	..C
P1195j2	G.G	G..	...	C.GTG	...	A..	..C
P1195j4	G.G	G..	...	C.GTG	...	A..	..C
H0528j5	G.G	G..	..A	C..TA	...	A..	..C
K42e1	G.G	G..	..A	C.G	G..	..TA	...	A..	..C
H0528e1	G.G	G..	..A	C..TA	...	AT.	..C
H0528e2	G.G	G..	..A	C.G	G..	..TA	...	A..	..C

H0528e4	G.G	G..	..A	C..TA	...	A..	..C
1537	G.G	G..	..A	C.T	T..	..TA	...	A..	..C
H27j3	G.G	G..	..A	C..TA	...	A..	..C
P1178j1	G.G	G..	..A	C..TA	...	AT.	..C
P1178j2	G.G	G..	...	C.GTA	...	A..	..C
P1178j3	G.G	G..	...	C.GTA	...	A..	..C
H0231j1	G.G	G..	..T	C..TA	...	AT.	..C
H0231j2	G.G	G..	...	C.GTA	...	A..	..C
H0231j3	G.G	G..	...	C.GTA	...	A..	..C
H0528e5	G.G	G..	..A	C.G	G..	..TA	...	A..	..C
F0512e1	G.G	G..	...	C.GTAC
F0521j4	G.G	.T.	...	G..	..A	C.TTA	...	A..	..C
H0528e3	G.G	G..	..A	C.GTA	...	A..	..C
H29e1	G.G	G..	..A	C.G	G..	..TA	...	A..	..C
F0521j5	G.G	G..	..A	C.G	G..	..TA	...	A..	..C
MCF0223c2	.G.	G..	G..TG	...	A..	...
F0521j1	G.G	G..	...	C.GTA	...	A..	..C
F0521j2	G.G	G..	...	C.GTAC
F0521j3	G.G	G..	...	C.GTA	...	A..	..C

444	444	444	444	444	444	444	455	555	555	555	555	555	555	555	555	555
888	888	888	999	999	999	999	900	000	000	001	111	111	111	222	222	222
123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678	

tippecanoe	ACT	CTT	GTA	AGA	GGC	TGG	GGC	GGG	TTA	AAT	CAA	ACC	CAA	CTT	CGT	AAG
H27j1	G.GAG
H27j2	G.GAG
H27j5	G.GAG
H27j6	G.GAG
H27j7	G.GAG
H27j8	G.GAG
H28e1	G.GAG
H28e2	G.GAG
P1126j1G	G.GAG	.A.
P1111j1T	G.GA
P1111j2T	G.GA
H28j1	G.GAG
H28j2	G.GAG
H28j3	G.GAG	.A.
H28j4	G.GAG
H28j6	G.GAG
H28j7	G.GAG
H28j8	G.GAG
1570	G.GAG
K119e2	G.GAG
K108c1	G.G	..T	..AAA
K108c2	G.G	..T	..AAA
MCF0212c1	G.G	..T	..AAA
MCF0212c3	G.G	..T	..AAA
P1168d1C	G.GGA
P1169d1C	G.GG	.A.A
P1169d2C	G.GGA
CS0348j1T	G.G
CS0348j2T	G.G
CS0348j3T	G.G
CS0348j4T	G.GG
CS0348j8T	G.G
P1116j1T	G.GA

P1116j2	T	G.G	A
P1120e1		G.G	A	G	...	C.
P1121e1		G.G	A	G
1535		G.G	A	G
1536		G.G	A	G
1539		G.G	A	G
1541		G.G	A	G
1542		G.G	A	G
1559	T	G.G	A
1560	T	G.G	A
1561	T	G.G	A
1562	T	G.G	A
1563	T	G.G	G	C.A
1571		G.G	A	G
K72j1	T	G.G	A
K72j2	T	G.G	CA
K72j3	T	G.G	CA
P1022j1	T	G.G	A
P1022j2	T	G.G	A
P1022j3	T	G.G	A
P1022j4	T	G.G	A
P1022j5	T	G.G	A
P1022j6	T	G.G	A
H28j9		G.G	A	G
P1109j3	T	G.G	A	G
P1195j3	T	G.G	A
P1195j5	T	G.G	A
H27e1		G.G	A	G
H27e2		G.G	A	G
H27e3		G.G	A	G
H27e5		G.G	A	G
MCF0223c1		G.G	...	T	...	A	...	A	A
CS0353j1		G.G	A
CS0353j2	T	G.G	A
CS0353j3	T	G.G	A
CS0353j4	T	G.G	A
CS0348j5	C	G.G
CS0348j6	T	G.G
P1109j1	T	G.G	A
P1109j2	T	G.G	A
K119e1		G.G	A	G
MCF0212c2		G.G	...	T	...	A	...	A	A
MCF0212c4		G.G	...	T	...	A	...	A	A
MCF0223c4		G.G	...	T	...	A	...	A	A
MCF0223c5		G.G	...	T	...	A	...	A	A
CS0350j1	T	G.G	A	G
P1195j1	T	G.G	A
P1195j2	T	G.G	A
P1195j4	T	G.G	A
H0528j5		G.G	A	G
K42e1		G.G	A	G
H0528e1		G.G	A	G
H0528e2		G.G	A	G	A.
H0528e4		G.G	A
1537		G.G	A	G
H27j3		G.G	A	G
P1178j1		G.G	A	G

P1178j2T	G.GA
P1178j3T	G.GA
H0231j1	G.GAG
H0231j2T	G.GA
H0231j3T	G.GA
H0528e5	G.GAG
F0512e1T	G.GA
F0521j4T	G.GAG
H0528e3	G.GAG
H29e1	G.GAG
F0521j5	G.GA
MCF0223c2	G.G	..T	..AAA
F0521j1T	G.GA
F0521j2T	G.GA
F0521j3T	G.GA

	555	555	555	555	555	555	555	555	555	555	555	555	555	555	555	555
	233	333	333	334	444	444	444	555	555	555	566	666	666	667	777	777
	901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456
tippecanoe	ATC	CTT	GCA	TAC	TCG	TCC	ATC	GCC	CAC	CTT	GGC	TGG	ATG	ATT	CTT	GTC
H27j1C	..CATA	G..	..G	..T
H27j2C	..CATAG	..T
H27j5C	..CATA	G..	..G	..T
H27j6C	..CATA	G..	..G	..T
H27j7C	..CATAG	..T
H27j8C	..CATA	G..	..G	..T
H28e1C	..CATA	..AG	..T
H28e2C	..CATAG	..T
P1126j1C	..CATAG	..T
P1111j1C	..CA	GAC	..T
P1111j2C	..CAC	..T
H28j1C	..CATA	G..	..G	..T
H28j2C	..CATAG	..GT
H28j3C	..CATA	..AG	..GT
H28j4C	..CATAG	..T
H28j6C	..CAGA	GG.	..G	..T
H28j7C	..CATA	GG.	..G	..T
H28j8C	..CAG	...	A..A	GG.	..G	..T
1570C	..CATAG	..T
K119e2C	..CATAG	..T
K108c1C	..CAT
K108c2C	..CAT
MCF0212c1C	..CAT
MCF0212c3C	..CAAT
P1168d1C	..CAC	..T
P1169d1C	..CAC	..T
P1169d2C	..CAC	..T
CS0348j1C	..CC	..T
CS0348j2C	..CC	..T
CS0348j3C	..CC	..T
CS0348j4C	..CC	..T
CS0348j8C	..CC	..T
P1116j1C	..CAG.AC	..T
P1116j2C	..CAC	..T
P1120e1C	..CATAG	..T	..T
P1121e1C	..CATAG	..T	..T
1535C	..CATA	..AG	..T	..T

1536C	..CATAG	..T	
1539C	..CATA	..AG	..T
1541C	..CCTAG	..T	
1542C	..CATAG	..T	
1559C	..CAC	..T	
1560C	..CAC	..T	
1561C	..CAC	..T	
1562C	..CAC	..T	
1563C	..CAC	..T	
1571C	..CATA	..AG	..T
K72j1C	..CAC	..T	
K72j2C	..CAC	..T	
K72j3C	..CAC	..T	
P1022j1C	..CAC	..T	
P1022j2C	..CAC	..T	
P1022j3C	..CAC	..T	
P1022j4C	..CAC	..T	
P1022j5C	..CGAC	..T	
P1022j6C	..CAC	..T	
H28j9C	..CATA	..G	..G	..T	
P1109j3C	..CAC	..T	
P1195j3C	..CAC	..T	
P1195j5C	..CAC	..T	
H27e1C	..CATAG	..T	
H27e2C	..CATAG	..T	
H27e3C	..CATAG	..T	
H27e5C	..CAT	..GGAG	..T	
MCF0223c1C	..CAC	..T	
CS0353j1C	..CAAC	..T	
CS0353j2C	..CAC	..T	
CS0353j3C	..CAAC	..T	
CS0353j4C	..CAC	..T	
CS0348j5C	..CAC	..T	
CS0348j6C	..CAC	..T	
P1109j1C	..CAC	..T	
P1109j2C	..CAC	..T	
K119e1C	..CATAG	..T	
MCF0212c2C	..GCAC	..T	
MCF0212c4C	..CAC	..T	
MCF0223c4C	..CAC	..T	
MCF0223c5C	..CAC	..T	
CS0350j1C	..CTAC	..T	
P1195j1C	..CAAC	..T	
P1195j2C	..CAAC	..T	
P1195j4C	..CAAC	..T	
H0528j5C	..CATA	..G	..G	..T	
K42e1C	..CATA	..A	..G	..T	
H0528e1C	..CATAG	..T	
H0528e2C	..CATAG	..T	
H0528e4C	..CATAG	..T	
1537C	..CATAG	..T	
H27j3C	..CATA	..G	..G	..T	
P1178j1C	..CATAG	..T	
P1178j2C	..CAC	..T	
P1178j3C	..CAC	..T	
H0231j1C	..CATAG	..T	
H0231j2C	..CAC	..T	

H0231j3C	..CAC	..T
H0528e5C	..CATAG	..T	
F0512e1C	..CAC	..T	
F0521j4C	..CTAG	..T	
H0528e3C	..CATAG	..T	
H29e1C	..CATAG	..T	
F0521j5C	..CTA	..AG	..T	
MCF0223c2C	..CA	..A	TGT	
F0521j1C	..CAC	..T	
F0521j2C	..CAC	..T	
F0521j3C	..CAC	..T	

555	555	555	555	555	555	555	555	556	666	666	666	666	666	666	666	666
777	888	888	888	899	999	999	999	990	000	000	000	111	111	111	122	222
789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234	

tippecanoe	TTA	CAA	TTT	TCG	CCC	TCC	CTC	ACA	TTT	CTT	ACC	CTC	CTC	ACA	TAT	TTT
H27j1A	G..G	C.C	..CA
H27j2A	G..G	C.C	..CA
H27j5AG	C.C	..CA
H27j6A	G..G	C.C	..CA
H27j7AG	C.C	..CA
H27j8A	G..G	C.C	..CA
H28e1AG	C.C	..CA
H28e2AG	C.C	..CA
P1126j1TAG	C.C	..CA
P1111j1AG	C.C	..CA
P1111j2AG	C.C	..CA
H28j1AG	C.C	..CA
H28j2A	G..G	C.C	..CA
H28j3A	G..G	C.C	..CA
H28j4A	G..G	C.C	..CA
H28j6A	G..G	C.C	..CA
H28j7A	G..G	C.C	..CA
H28j8A	G..G	C.C	..CA
1570AG	C.C	..CA
K119e2AG	C.C	..CA
K108c1AT	..G	C..	..CT	..G
K108c2AT	..G	C..	..C	..T	..T	..G
MCF0212c1AT	..G	C..	..CT	..G
MCF0212c3AT	..G	C..	..C	..T	..T	..G
P1168d1AG	C.C	..CA
P1169d1AG	C.C	..CA
P1169d2AG	C.C	..CA
CS0348j1	C..AG	C.C	..CA
CS0348j2	C..AG	C.C	..CA
CS0348j3	C..AG	C.C	..CA
CS0348j4	C..AG	C.C	..CA
CS0348j8	C..AG	C.C	..CA
P1116j1AG	C.C	..CA
P1116j2AG	C.C	..CA
P1120e1AG	C.C	..CA
P1121e1AG	C.C	..CA
1535AG	C.C	..CA
1536AG	C.C	..CA
1539AG	C.C	..CA
1541AG	C.C	..CA
1542AG	C.C	..CA

1559AG	C.CA
1560AG	C.CA
1561AG	C.C	..CA
1562AG	C.C	..CA
1563AG	C.CA
1571AG	C.C	..CA
K72j1AG	C.C	..CA
K72j2AG	C.C	..CA
K72j3AG	C.C	..CA
P1022j1AG	C.C	..CA
P1022j2AG	C.C	..CA
P1022j3AG	C.C	..C	..AA
P1022j4AG	C.C	..CA
P1022j5AG	C.C	..C	..AA	..A
P1022j6AG	C.C	..C	..AA
H28j9AG	C.C	..CA
P1109j3AG	C.C	..CA
P1195j3AG	C.C	..CA
P1195j5AG	C.C	..CA
H27e1AG	C.C	..CA
H27e2AG	C.C	..CA
H27e3AG	C.C	..CA
H27e5AG	C.C	..CA
MCF0223c1ATG	C..	..CT	..G
CS0353j1AG	C.C	..CA
CS0353j2AG	C.C	..CA
CS0353j3AG	C.C	..CA
CS0353j4AG	C.C	..CA
CS0348j5	C..AG	C.C	..CA
CS0348j6	C..AG	C.C	..CA
P1109j1AG	C.C	..CA
P1109j2AG	C.C	..CA
K119e1AG	C.C	..CA
MCF0212c2ATG	C..	..CT	..G
MCF0212c4ATG	C..	..CT	..G
MCF0223c4ATG	C..	..CT	..G
MCF0223c5ATG	C..	..CT	..G
CS0350j1AG	C.C	..CA
P1195j1AG	C.C	..CA
P1195j2AG	C.C	..CA
P1195j4AAG	C.C	..CA
H0528j5AG	C.C	..CA
K42e1AG	C.C	..CA
H0528e1AG	C.C	..CA
H0528e2AG	C.C	..CA
H0528e4ATG	C.C	..CA
1537AG	C.C	..CA
H27j3AG	C.C	..CA
P1178j1AG	C.C	..CA
P1178j2AG	C.C	..CA
P1178j3AG	C.C	..CA
H0231j1AG	C.C	..CA
H0231j2AG	C.C	..CA
H0231j3AG	C.C	..CA
H0528e5AG	C.C	..CA
F0512e1AG	C.C	..CA
F0521j4AG	C.C	..CA

H0528e3AG	C.C	..CA
H29e1AG	C.C	..CA
F0521j5AG	C.C	..CA
MCF0223c2AT	..G	C..	..C	..T	..T	..G
F0521j1AG	C.C	..CA
F0521j2AG	C.C	..CA
F0521j3AG	C.C	..CA
	666	666	666	666	666	666	666	666	666	666	666	666	666	666	666	666
	222	223	333	333	333	444	444	444	455	555	555	556	666	666	666	777
	567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012
tippecanoe	GTG	ATA	ACG	ATC	TCA	ACA	TTT	CTT	CTA	TTT	AAG	CTC	AGC	AAA	TCT	ACC
H27j1	..A	..G	..A	..AC	...	G..AAC	..T
H27j2	..A	..G	..A	..AC	...	G..AAC	..T
H27j5	..A	..G	..A	..AC	...	G..AAC	..T
H27j6	..A	..G	..A	..AC	...	G..AAC	..T
H27j7	..A	..G	..A	..AC	...	G..AAC	..T
H27j8	..A	..G	..A	..AC	...	G..AAC	..T
H28e1	..A	..G	..A	..AC	...	G..AAC	..T
H28e2	C.A	..G	..A	..AC	...	G..AAC	..T
P1126j1	..A	..G	..A	..AC	...	G..AAC	..T
P1111j1	..A	..G	..A	..AG	..C	..C	G..	..C	..AAC	..T
P1111j2	..A	..G	..A	..AG	..C	..C	G..AAC	..T
H28j1	..A	..G	..A	..AC	...	G..AAC	..T
H28j2	..A	..G	..A	..AC	...	G..AAC	..T
H28j3	..A	..G	..A	..AG	..C	...	G..AAC	..T
H28j4	..A	..G	..A	..AC	...	G..AAC	..T
H28j6	..A	..G	..A	..AC	...	G..AAC	..T
H28j7	..A	..G	..A	..AC	...	G..AAC	..T
H28j8	..A	..G	..A	..AC	...	G..AAC	..T
1570	..A	..G	..A	..AC	...	G..AAC	..T
K119e2	..A	..G	..A	..AC	..C	...	G..AAC	..T
K108c1	..AA	..A	..G	..T	..C	...	G..AAC	..T
K108c2	..AA	..A	..G	..T	..C	...	G..AAC	..T
MCF0212c1	..AA	..A	..G	..T	..C	...	G..AAC	..T
MCF0212c3	..AA	..A	..G	..T	..C	...	G..AAC	..T
P1168d1	..A	..GAC	...	G..AAC	..T
P1169d1	..A	..GAC	...	G..AAC	..T
P1169d2	..A	..GAC	...	G..	...	G.AAC	..T
CS0348j1	..A	..G	..A	..AG	..C	..C	G..AAC	..T
CS0348j2	..A	..G	..A	..AG	..C	..C	G..AAC	..T
CS0348j3	..A	..G	..A	..AG	..C	..C	G..AAC	..T
CS0348j4	..A	..G	..A	..AG	..C	..C	G..AAC	..T
CS0348j8	..A	..G	..A	..AG	..C	..C	G..AAC	..T
P1116j1	..A	..G	..A	..AG	..C	..C	G..	..C	..AAC	..T
P1116j2	..A	..G	..A	..AG	..C	..C	G..	..C	..AAC	..T
P1120e1	..A	..G	..A	..AC	...	G..AAC	..T
P1121e1	C.A	..G	..A	..AC	...	G..AAC	..T
1535	..A	..G	..A	..AC	...	G..AAC	..T
1536	..A	..G	..A	..AC	...	G..AAC	..T
1539	..A	..G	..A	..AC	...	G..AAC	..T
1541	..A	..G	..A	..AC	...	G..AAC	..T
1542	..A	..G	..A	..AC	...	G..AAC	..T
1559	..A	..G	..A	..AG	..C	..C	G..AAC	..T
1560	..A	..G	..A	..AG	..C	..C	G..AAC	..T
1561	..A	..G	..A	..AG	..C	..C	G..AAC	..T
1562	..A	..G	..A	..AG	..C	..C	G..AAC	..T

1563	..A ..G ..A ..AG ..C ..C G..AA.C ..T
1571	..A ..G ..A ..AC ... G..AA.C ..T
K72j1	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
K72j2	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
K72j3	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1022j1	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1022j2	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1022j3	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1022j4	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1022j5	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1022j6	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
H28j9	..A ..G ..A ..AC ... G..AA.C ..T
P1109j3	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1195j3	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1195j5	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
H27e1	..A ..G ..A ..AAC ... G..AA.C ..T
H27e2	..A ..G ..A ..AC ... G..AA.C ..T
H27e3	..A ..G ..A ..AC ... G..AA.C ..T
H27e5	..A ..G ..A ..AC ... G..AA.C ..T
MCF0223c1	..AA ..A ..G .T. ..C ... G..AA.C ..T
CS0353j1	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
CS0353j2	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
CS0353j3	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
CS0353j4	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
CS0348j5	..A ..G ..A ..AG ..C ..C G..AA.C ..T
CS0348j6	..A ..G ..A ..AG ..C ..C G..AA.C ..T
P1109j1	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1109j2	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
K119e1	..A ..G ..A ..AC ... G..AA.C ..T
MCF0212c2	..AA ..A ..G .T. ..C ... G..AA.C ..T
MCF0212c4	..AA ..A ..G .T. ..C ... G..AA.C ..T
MCF0223c4	..AA ..A ..G .T. ..C ... G..AA.C ..T
MCF0223c5	..AA ..A ..G .T. ..C ... G..AA.C ..T
CS0350j1	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1195j1	..A ..G ..A ..AG ..C ..C G.. ..C ..A ..G .A.C ..T
P1195j2	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1195j4	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
H0528j5	..A ..G ..A ..AC ... G..AA.C ..T
K42e1	C.A ..G ..A ..AC ... G..AA.C ..T
H0528e1	..A ..G ..A ..AC ... G..AA.C ..T
H0528e2	..A ..G ..A ..AC ... G..AA.C ..T
H0528e4	C.A ..G ..A ..AC ... G..AA.C ..T
1537	..A ..G ..A ..AC ... G..AA.C ..T
H27j3	..A ..G ..A ..AC ... G..AA.C ..T
P1178j1	..A ..G ..AC ... G..AA.C ..T
P1178j2	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
P1178j3	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
H0231j1	..A ..G ..A ..AC ... G..AA.C ..T
H0231j2	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
H0231j3	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
H0528e5	..A ..G ..A ..AC ... G..AA.C ..T
F0512e1	..A ..G ..A ..AG ..C ..C G.. ..C ..AA.C ..T
F0521j4	C.A ..G ..A ..AC ... G..AA.C ..T
H0528e3	..A ..G ..A ..AC ... G..AA.C ..T
H29e1	..A ..G ..A ..AC ... G..AA.C ..T
F0521j5	..A ..G ..A ..AC ... G..AA.C ..T
MCF0223c2	..AA ..A ..G .T. ..C ... G..AA.C ..T

F0521j1	..A	..G	..A	..AG	..C	..C	G..	..C	..AA.C	..T
F0521j2	..A	..G	..A	..AG	..C	..C	G..	..C	..AA.C	..T
F0521j3	..A	..G	..A	..AG	..C	..C	G..	..C	..AA.C	..T
	666	666	666	666	666	666	666	666	666	777	777	777	777	777	777	777
	777	777	788	888	888	889	999	999	999	000	000	000	011	111	111	112
	345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890
tippecanoe	ACT	ATT	AAT	ATG	CTA	GCC	ACC	TCG	TGA	GCC	AAA	GCA	CCC	GCT	TTA	ACG
H27j1	..C	G.CA	..C	..G	..T
H27j2	..C	G.CA	..C	..G	..T
H27j5	..C	G.CA	..C	..G	..T
H27j6	..C	G.CA	..C	..G	..T
H27j7	..C	G.CA	..C	..G	..T
H27j8	..C	G.CA	..C	..G	..T
H28e1	..C	G.CA	..C	..G	..T
H28e2	..C	G.CA	..C	..G	..T
P1126j1	..C	G.CA	..C	..A	..T
P1111j1	..C	G.CA	..CTG	...
P1111j2	..C	G.CA	..CTG	...
H28j1	..C	G.CA	..C	..G	..T
H28j2	..C	G.CA	..C	..G	..T
H28j3	..C	G.CC	A.C	..G	..T
H28j4	..C	G.CA	..C	..G	..T
H28j6	..C	G.CA	..C	..G	..T
H28j7	..C	G.CA	..C	..G	..T
H28j8	..C	G.CA	..C	..G	..T
1570	..C	G.CA	..C	..G	..T
K119e2	..C	G.CA	..C	..A	..T
K108c1	..C	G.CA	..CA	..GG	..A
K108c2	C.C	G.CA	..CA	..GG	..A
MCF0212c1	..C	G.CA	..CA	..GG	..A
MCF0212c3	..C	G.CA	..CA	..GG	..A
P1168d1	..C	G.CA	..CTGGG	..C
P1169d1	..C	G.CA	..CTGGG	..C
P1169d2	..C	G.CA	..CTGGG	..C
CS0348j1	..C	G.CA	..CTG	...
CS0348j2	..C	G.CA	..CTG	...
CS0348j3	..C	G.CA	..CTG	...
CS0348j4	..C	G.CA	..CTG	...
CS0348j8	..C	G.CA	..CTG	...
P1116j1	..C	G.CA	..CTG	...
P1116j2	..C	G.CA	..CTG	...
P1120e1	..C	G.CA	..C	..G	..T
P1121e1	..C	G.CA	..C	..G	..T
1535	..C	G.CA	..C	..G	..T
1536	..C	G.CA	..C	..G	..T
1539	..C	G.CA	..C	..G	..T
1541	..C	G.CA	..C	..G	..T
1542	..C	G.CA	..C	..G	..T
1559	..C	G.CA	..CTG	...
1560	..C	G.CA	..CTG	...
1561	..C	G.CA	..CTG	...
1562	..C	G.CA	..CTG	...
1563	..C	G.CA	..CTG	...
1571	..C	G.CA	..C	..G	..T
K72j1	..C	G.CA	..CTG	...
K72j2	..C	G.CA	..CTG	...

K72j3	..C	G.CA	..CTG	...
P1022j1	..C	G.CA	..CTG	...
P1022j2	..C	G.CA	..CTG	...
P1022j3	..C	G.CA	..CTG	...
P1022j4	..C	G.CA	..CTG	...
P1022j5	..C	G.CA	..CTG	...
P1022j6	..C	G.CA	..CTG	...
H28j9	..C	G.CA	..C	..G	..TG	...
P1109j3	..C	G.CA	..CTG	...
P1195j3	..C	G.CA	..CTG	...
P1195j5	..C	G.CA	..CTG	...
H27e1	..C	G.CA	..C	..G	..TG	...
H27e2	..C	G.CA	..C	..G	..TG	...
H27e3	..C	G.CA	..C	..G	..TG	...
H27e5	..C	G.CA	..C	..G	..TG	...
MCF0223c1	..C	G.CA	..CA	..GG	..A
CS0353j1	..C	G.CA	..CTG	...
CS0353j2	..C	G.CA	..CTG	...
CS0353j3	..C	G.CA	..CTG	...
CS0353j4	..C	G.CA	..CTG	...
CS0348j5	..C	G.CA	..C	...	G..TG	...
CS0348j6	..C	G.CA	..CTG	...
P1109j1	..C	G.CA	..CTG	..A
P1109j2	..C	G.CA	..CTG	...
K119e1	..C	G.CA	..C	..A	..TG	...
MCF0212c2	..C	G.CA	..CA	..GG	..A
MCF0212c4	..C	G.CA	..CA	..GG	..A
MCF0223c4	..C	G.CA	..CA	..GG	..A
MCF0223c5	..C	G.CA	..CA	..GG	..A
CS0350j1	..C	G.CA	..CTG	...
P1195j1	..C	G.CA	..CTG	...
P1195j2	..C	G.CA	..CTG	...
P1195j4	..C	G.CA	..CTG	...
H0528j5	..C	G.CA	..C	..G	..TG	...
K42e1	..C	G.CA	..C	..G	..TG	...
H0528e1	..C	G.CA	..C	..G	..TG	...
H0528e2	..C	G.CA	..C	..A	..TG	...
H0528e4	..C	G.CA	..C	..G	..TG	...
1537	..C	G.CA	..C	..G	..TG	...
H27j3	..C	G.CA	..C	..G	..TG	...
P1178j1	..C	G.CA	..C	..G	..TG	...
P1178j2	..C	G.CA	..CTG	...
P1178j3	..C	G.CA	..CTG	...
H0231j1	..C	G.CA	..C	..G	..TG	...
H0231j2	..C	G.CA	..CTG	...
H0231j3	..C	G.CA	..CTG	...
H0528e5	..C	G.CA	..C	..A	..TG	...
F0512e1	..C	G.CA	..CTG	...
F0521j4	..C	G.CA	..C	..G	..TG	...
H0528e3	..C	G.CA	..C	..A	..TG	...
H29e1	..C	G.CA	..C	..A	..TG	...
F0521j5	..C	G.CA	..C	..A	..TG	...
MCF0223c2	..C	G.CA	..CA	..GG	..A
F0521j1	..C	G.CA	..CTG	...
F0521j2	..C	G.CA	..CTG	...
F0521j3	..C	G.CA	..CTG	...

	777	777	777	777	777	777	777	777	777	777	777	777	777	777	777	777
	222	222	222	333	333	333	344	444	444	445	555	555	555	666	666	666
	123	456	789	012	345	678	901	234	567	890	123	456	789	012	345	678
tippecanoe	GCC	CTC	ACC	CCC	CTT	GTT	CTT	CTG	TCC	CTA	GGA	GGC	CTT	CCC	CCA	CTA
H27j1T	G..	..A	...	A..GA
H27j2T	G..	..A	...	A..GA
H27j5T	G..	..A	...	A..GA
H27j6T	G..	..A	...	A..GA
H27j7T	G..	..A	...	A..GA
H27j8T	G..	..A	...	A..GA
H28e1T	G..	..A	...	A..GA
H28e2T	G..	..A	...	A..GA
P1126j1T	GT.	..A	...	A..GA
P1111j1T	G..	..G	...	A..G	..GA
P1111j2T	G..	..G	...	A..G	..GA
H28j1T	G..	..A	...	A..GA
H28j2T	G..	..A	...	A..GA
H28j3T	G..	..A	...	A..GA
H28j4	C..	..T	G..	..A	...	A..GA
H28j6T	G..	..A	...	A..GA
H28j7T	G..	..A	...	A..GA
H28j8T	G..	..A	...	A..GA
1570T	G..	..A	...	A..GA	A..	...
K119e2T	G..	..A	...	A..GA
K108c1T	G..	..A	...	A..AC	..A
K108c2T	G..	..A	...	A..AC	..A
MCF0212c1T	G..	..A	...	A..AC	..A
MCF0212c3T	G..	..A	...	A..AC	..A
P1168d1T	G..	..G	...	A..	T.G	..GG
P1169d1T	G..	..G	...	A..	T.G	..TG	..AG	A..	...
P1169d2T	G..	..G	...	A..	T.G	..TG	..AG	A..	...
CS0348j1T	G..	..A	...	A..G	..GA
CS0348j2T	G..	..A	...	A..G	..GA
CS0348j3T	G..	..A	...	A..G	..GA
CS0348j4T	G..	..A	...	A..G	..GA
CS0348j8T	G..	..A	...	A..G	..GA
P1116j1T	G..	..G	...	A..G	..GA
P1116j2T	G..	..G	...	A..G	..GA
P1120e1T	G..	..A	...	A..GA
P1121e1T	G..	..A	...	A..GA
1535T	G..	..A	...	A..GA
1536T	G..	..A	...	A..GA
1539T	G..	..A	...	A..GA
1541T	G..	..A	...	A..GA
1542T	G..	..A	...	A..GA
1559T	G..	..G	...	A..G	..GA
1560T	G..	..G	...	A..G	..GA
1561T	G..	..G	...	A..G	..GA	..C	...
1562T	G..	..G	...	A..G	..GA
1563T	G..	..G	...	A..G	..GA
1571T	G..	..A	...	A..GA
K72j1T	G..	..G	...	A..G	..GA
K72j2T	G..	..G	...	A..G	..GA
K72j3T	G..	..G	...	A..G	..GA
P1022j1T	G..	..G	...	A..G	..GA
P1022j2T	G..	..G	...	A..G	..GAT
P1022j3T	G..	..G	...	A..G	..GAT

P1022j4	...	T	G..	..G	...	A..G	..GAT
P1022j5	...	T	G..	..G	...	A..G	..GAT
P1022j6	...	T	G..	..G	...	A..G	..GAT
H28j9	...	T	G..	..A	...	A..GA
P1109j3	...	T	G..	..G	...	A..G	..GA
P1195j3	...	T	G..	..G	...	A..G	..GA
P1195j5	...	T	G..	..G	...	A..G	..GA
H27e1	...	T	G..	..A	...	A..GA
H27e2	...	T	G..	..A	...	A..GA
H27e3	...	T	G..	..A	...	A..GA
H27e5	...	T	G..	..A	...	A..GA
MCF0223c1	...	T	G..	..A	...	A..AC	..A
CS0353j1	...	T	G..	..G	...	A..G	..GA
CS0353j2	...	T	G..	..G	...	A..G	..GA
CS0353j3	...	T	G..	..G	...	A..G	..GA
CS0353j4	...	T	G..	..G	...	A..G	..GA
CS0348j5	...	T	G..	..A	...	A..G	..GA
CS0348j6	...	T	G..	..A	...	A..G	..GA
P1109j1	...	T	G..	..G	...	A..G	..GA
P1109j2	...	T	G..	..G	...	A..G	..GA
K119e1	...	T	G..	..A	...	A..GG
MCF0212c2	...	T	G..	..A	...	A..AC	..A
MCF0212c4	...	T	G..	..A	...	A..AC	..A
MCF0223c4	...	T	G..	..A	...	A..AC	..A
MCF0223c5	...	T	G..	..A	...	A..AC	..A
CS0350j1	...	T	G..	..G	...	A..G	..GAT
P1195j1	...	T	G..	..G	...	A..G	..GA
P1195j2	...	T	G..	..G	...	A..G	..GA
P1195j4	...	T	G..	..G	...	A..G	..GA
H0528j5	...	T	G..	..A	...	A..GA
K42e1	...	T	G..	..A	...	A..GA
H0528e1	...	T	G..	..A	...	A..GA
H0528e2	...	T	G..	..A	...	A..GG
H0528e4	...	T	G..	..A	...	A..GA
1537	...	T	G..	..A	...	A..GA
H27j3	...	T	G..	..A	...	A..GA
P1178j1	...	T	G..	..A	...	A..GA
P1178j2	...	T	G..	..G	...	A..G	..GA
P1178j3	...	T	G..	..G	...	A..G	..GA
H0231j1	...	T	G..	..A	...	A..GA
H0231j2	...	T	G..	..G	...	A..G	..GA
H0231j3	...	T	G..	..G	...	A..G	..GA
H0528e5	...	T	G..	..A	...	A..GG
F0512e1	...	T	G..	..G	...	A..G	..GA
F0521j4	...	T	G..	..A	...	A..GA
H0528e3	...	T	G..	..A	...	A..GG
H29e1	...	T	G..	..A	...	A..GG
F0521j5	...	T	G..	..A	...	A..GG
MCF0223c2	...	T	G..	..A	...	A..AC	..A
F0521j1	...	T	G..	..G	...	A..G	..GA
F0521j2	...	T	G..	..G	...	A..G	..GA
F0521j3	...	T	G..	..G	...	A..G	..GA
777	777	777	777	777	777	777	777	777	777	777	788	888	888	888	888	888
677	777	777	778	888	888	888	999	999	999	999	900	000	000	001	111	111
901	234	567	890	123	456	789	012	345	678	901	234	567	890	123	456	
tippecanoe	ACT	GGT	TTT	ATG	CCA	AAA	TGG	CTT	ATT	CTT	CAA	GAA	TTA	ACT	AAG	CAG

H27j1	..GCCC
H27j2	..GCCC
H27j5	..GCCC
H27j6	..GCCC
H27j7	..GCCC
H27j8	..GCCC
H28e1	..GCCC
H28e2	..GCCC
P1126j1	..GCCC
P1111j1	..GCG	..G	..CG	..CA
P1111j2	..G	..C	..CG	..G	..CG	..CA
H28j1	..GCG	..G	..CC
H28j2	..GCG	..G	..CC
H28j3	..GCG	..G	..CC
H28j4	..GCG	..G	..CC
H28j6	..GCG	..G	..CC
H28j7	..GCG	..G	..CC
H28j8	..GCG	..G	..CC
1570	..GCG	..G	..CC
K119e2	..GCA	..CC
K108c1	..G	..C	..CG	..A	..C	..CC	..A	..A
K108c2	..G	..C	..CG	..A	..C	..CC	..A	..A
MCF0212c1	..G	..C	..CG	..A	..C	..CC	..A	..A
MCF0212c3	..G	..C	..CG	..A	..C	..CC	..A	..A
P1168d1	..GCG	..G	..CC	..C
P1169d1	..GCG	..G	..CG	..C
P1169d2	..GCG	..G	..CG	..C
CS0348j1	..GCG	..G	..CG	..C
CS0348j2	..GCG	..G	..CG	..C
CS0348j3	..GCG	..G	..CG	..C
CS0348j4	..GCG	..G	..CG	..C
CS0348j8	..GCG	..G	..CG	..C
P1116j1	..ACG	..G	..CG	..CA
P1116j2	..GCG	..G	..CG	..CA
P1120e1	..GCCC
P1121e1	..GCCC
1535	..GCCC
1536	..GCCC
1539	..GCCC
1541	..GCCC
1542	..GCCC
1559	..G	..C	..CG	..G	..CG	..CA
1560	..G	..C	..CG	..G	..CG	..CA
1561	..G	..C	..CG	..G	..CG	..CA
1562	..G	..C	..CG	..G	..CG	..CA
1563	..G	..C	..CG	..G	..CG	..CA
1571	..GCCC
K72j1	..ACG	..G	..CG	..CA
K72j2	..ACG	..G	..CG	..CA
K72j3	..ACG	..G	..CG	..CA
P1022j1	..ACG	..G	..CG	..CA
P1022j2	..ACG	..G	..CG	..CA
P1022j3	..ACG	..G	..CG	..CA
P1022j4	..ACG	..G	..CG	..CA
P1022j5	..ACG	..G	..CG	..CA
P1022j6	..ACG	..G	..CG	..CA
H28j9	..GCCC

P1109j3	..GCGCG	..CA
P1195j3	..GCG	..GCG	..CA
P1195j5	..GCG	..GCG	..CA
H27e1	..GCCC
H27e2	..GCCC
H27e3	..GCCC
H27e5	..GCCC
MCF0223c1	..G	..C	..CG	..A	..C	..CC	..A	..GA	
CS0353j1	..AG	..GCG	..CA
CS0353j2	..GCG	..GCG	..CA
CS0353j3	..AG	..GCG	..CA
CS0353j4	..ACG	..GCG	..CA
CS0348j5	..GCGCG	..C
CS0348j6	..GCGCG	..C
P1109j1	..GCG	..GCG	..CA
P1109j2	..GCG	..GCG	..CA
K119e1	..GCA	..CC
MCF0212c2	..G	..C	..CG	..A	..C	..CC	..A	..GA	
MCF0212c4	..G	..C	..CG	..A	..C	..CC	..A	..GA	
MCF0223c4	..G	..C	..CG	..A	..C	..CC	..A	..A	
MCF0223c5	..G	..C	..CG	..A	..C	..CC	..A	..A	
CS0350j1	..ACG	..GCG	..CA
P1195j1	..AG	..GCG	..CA
P1195j2	..AG	..GCG	..CA
P1195j4	..AG	..GCG	..CA
H0528j5	..GCCC
K42e1	..GCCC
H0528e1	..GCCCA	
H0528e2	..GCA	..CC
H0528e4	..GCCC
1537	..GCCC
H27j3	..GCCC
P1178j1	..GCCCA	
P1178j2	..GCG	..GCG	..C	..A	..A
P1178j3	..GCG	..GCG	..CA
H0231j1	..GCCCA	
H0231j2	..GCG	..GCG	..CA
H0231j3	..GCG	..GCG	..CA
H0528e5	..GCA	..CC
F0512e1	..GCG	..GCG	..CA
F0521j4	..GCCC
H0528e3	..GCA	..CC
H29e1	..GCA	..CC
F0521j5	..GCA	..CC
MCF0223c2	..G	..C	..CG	..A	..C	..CC	..A	..A	
F0521j1	..GCG	..GCG	..CA
F0521j2	..GCG	..GCG	..CA
F0521j3	..GCG	..GCG	..CA

888	888	888	888	888	888	888	888	888	888	888	888	888	888	888	888	888
111	222	222	222	233	333	333	334	444	444	444	555	555	555	566	666	
789	012	345	678	901	234	567	890	123	456	789	012	345	678	901	234	

tippecanoe	GAT	CTT	GCT	CCT	ACA	GCA	ACT	CTA	GCC	GCG	ATA	TCA	GCC	CTC	CTA	AGC
H27j1	G.AC	..G	G..	..GT	...
H27j2AC	..GGT	...
H27j5	G.AC	..G	G..	..GT	...
H27j6A	...	H27	..C	..GGT	...

H27j7AC	..GGT	...
H27j8	G.AC	..G	G..	..GT	...
H28e1AC	..GGT	...
H28e2AC	..GGT	...
P1126j1AC	..GGT	...
P1111j1AG	..C	..GAGT	...
P1111j2AG	..C	..GAGT	...
H28j1	G.AC	..G	G..	..GT	...
H28j2AC	..GGT	...
H28j3AC	..GGT	...
H28j4AC	..GGT	...
H28j6	G.AG	..C	..GGT	...
H28j7	G.AG	..C	..GGT	...
H28j8	G.AG	..C	..GGT	...
1570AG	..C	..GGT	...
K119e2AC	..GGC	...
K108c1	..CAC	..CAT	...
K108c2	..CAC	..CAT	...
MCF0212c1	..CAC	..CAT	...
MCF0212c3	..CAC	..CAT	...
P1168d1AG	..CAGT	...
P1169d1	G.AG	..CAGT	...
P1169d2	G.AG	..CAGT	...
CS0348j1AG	..C	..GAGT	...
CS0348j2AG	..C	..GAGT	...
CS0348j3AG	..C	..GAGT	...
CS0348j4AG	..C	..GAGT	...
CS0348j8AG	..C	..GAGT	...
P1116j1AG	..C	..GAGT	...
P1116j2AG	..C	..GAGT	...
P1120e1AC	..GGT	...
P1121e1AC	..GGT	...
1535AC	..GGT	...
1536AC	..GGT	...
1539AC	..GGT	...
1541AC	..GGT	...
1542AC	..GGT	...
1559AG	..C	..GAGT	...
1560AG	..C	..GAGT	...
1561AG	..C	..GAGT	...
1562AG	..C	..GAGT	...
1563AG	..C	..GAGT	...
1571AC	..GGT	...
K72j1AG	..C	..GAGT	...
K72j2AG	..C	..GAGT	...
K72j3AG	..C	..GAGT	...
P1022j1AG	..C	..GAGT	...
P1022j2AG	..C	..GAGT	...
P1022j3AG	..C	..GAGT	...
P1022j4AG	..C	..GAGT	...
P1022j5AG	..C	..GAGT	...
P1022j6AG	..C	..GAGT	...
H28j9	G.AC	..G	G..	..GT	...
P1109j3AG	..C	..GAGT	...
P1195j3AG	..C	..GAGT	...
P1195j5AG	..C	..GAGT	...
H27e1AC	..GGT	...

H27e2AC	..GGT	...
H27e3AC	..GGT	...
H27e5AC	..GGT	...
MCF0223c1AC	..CAT	..A
CS0353j1AG	..C	..GAGT	...
CS0353j2AG	..C	..GAGT	...
CS0353j3AG	..C	..GAGT	...
CS0353j4AG	..C	..GAGT	...
CS0348j5AG	..C	..GAGT	...
CS0348j6AG	..C	..GAGT	...
P1109j1AG	..C	..GAGT	...
P1109j2AG	..C	..GAGT	...
K119e1AC	..GGC	...
MCF0212c2AC	..CAT	...
MCF0212c4AC	..CAT	...
MCF0223c4	..CAC	..CAT	...
MCF0223c5	..CAC	..CAT	...
CS0350j1AG	..C	..GAGT	...
P1195j1	G..AG	..C	..GAGT	...
P1195j2	G..AG	..C	..GAGT	...
P1195j4	G..AG	..C	..GAGT	...
H0528j5	G..AC	..G	...	G..	..GT	...
K42e1AC	..GGT	...
H0528e1AC	..GGT	...
H0528e2AC	..GGC	...
H0528e4AC	..GGT	...
1537AC	..GGT	...
H27j3	G..AC	..G	...	G..	..GT	...
P1178j1AC	..GGT	...
P1178j2AG	..C	..GAG	T..T	...
P1178j3AG	..C	..GAGT	...
H0231j1AC	..GGT	...
H0231j2AG	..C	..GAGT	...
H0231j3AG	..C	..GAGT	...
H0528e5AC	..GGC	...
F0512e1AG	..C	..GAGT	...
F0521j4AC	..GGT	...
H0528e3AC	..GGC	...
H29e1AC	..GGC	...
F0521j5AC	..GGT	...
MCF0223c2	..CAC	..CAT	...
F0521j1AG	..C	..GAGT	...
F0521j2AG	..C	..GAGT	...
F0521j3AG	..C	..GAGT	...

888	888	888	888	888	888	888	888	888	888	888	888	889	999	999	999	999
666	667	777	777	777	888	888	888	888	899	999	999	990	000	000	000	111
567	890	123	456	789	012	345	678	901	234	567	890	123	456	789	012	

tippecanoe	CTT	TAC	TTT	TAT	TTA	CGA	CTC	TCC	TAT	GCA	ATA	GCC	CTC	ACC	ATG	TCC
H27j1CTGT	..T	..A	...
H27j2CTGT	..T	..A	...
H27j5CTG	..A	..T	..T	..A	...
H27j6CTG	..A	..T	..T	..A	...
H27j7CTG	..A	..T	..T	..A	...
H27j8CTG	..G	..T	..T	..A	...
H28e1CTG	..A	..T	..T	..A	...
H28e2CTG	..A	..T	..T	..A	...

P1126j1CTG	..AT	..A	...
P1111j1CTG	..AA	...
P1111j2CTG	..AA	...
H28j1CTG	..G	..T	..T	..A	...
H28j2CTG	..A	..T	..T	..A	...
H28j3CTG	..A	..T	..T	..A	...
H28j4CTG	..A	..T	..T	..A	...
H28j6CTG	..G	..T	..T	..A	...
H28j7CTG	..G	..T	..T	..A	...
H28j8CTG	..G	..T	..T	..A	...
1570CTG	..G	..T	..T	..A	...
K119e2CTG	..AT	..A	...
K108c1CTG	A..	..A	..A
K108c2CTG	A..	..A	..A
MCF0212c1CTG	A..	..A	..A
MCF0212c3CTG	A..	..A	..A
P1168d1CTG	..A
P1169d1CTG	..A
P1169d2CTG	..A
CS0348j1CTG	..AA	...
CS0348j2CTG	..AA	...
CS0348j3CTG	..AA	...
CS0348j4CTG	..AA	...
CS0348j8CTG	..AA	...
P1116j1CTG	A..AA	G..
P1116j2CTG	..AA	...
P1120e1CTG	..A	..T	..T	..A	...
P1121e1CTG	..A	..T	..T	..A	...
1535CTG	..A	..T	..T	..A	...
1536CTG	..A	..T	..T	..A	...
1539CTG	..A	..T	..T	..A	...
1541CTG	..A	..T	..T	..A	...
1542CTG	..A	..T	..T	..A	...
1559CTG	..AA	...
1560CTG	..AA	...
1561CTG	..AA	...
1562CTG	..AA	...
1563CTG	..AA	...
1571CTG	..A	..T	..T	..A	...
K72j1CTG	..AA	...
K72j2CTG	..AA	...
K72j3CTG	..AA	...
P1022j1CTG	..AA	...
P1022j2CTG	..AA	...
P1022j3CTG	..AA	...
P1022j4CTG	..AA	...
P1022j5CTG	..AA	...
P1022j6CTG	..AA	...
H28j9CTG	..A	..T	..T	..A	...
P1109j3CTG	..AA	...
P1195j3CTG	..AA	...
P1195j5CTG	..AA	...
H27e1CTG	..A	..T	..T	..A	...
H27e2CTG	..A	..T	..T	..A	...
H27e3CTG	..A	..T	..T	..A	...
H27e5CTG	..A	..T	..T	..A	...
MCF0223c1CTG	..G	AA..	..A	..G

CS0353j1CTG	A.AA	G..
CS0353j2CTG	..AA	...
CS0353j3CTG	A.AA	G..
CS0353j4CTG	..AA	...
CS0348j5CTG	..AA	...
CS0348j6CTG	..AA	...
P1109j1CTG	..AA	...
P1109j2CTG	..AA	...
K119e1CTG	..AT	..A	...
MCF0212c2CTG	..G	AA.	..A	..G.
MCF0212c4CTG	..G	AA.	..A
MCF0223c4CTG	A..	..A
MCF0223c5CTG	A..	..A
CS0350j1CTG	..AA	...
P1195j1CA.TG	A.AA	...
P1195j2CA.TG	A.AA	...
P1195j4CA.TG	A.AA	...
H0528j5CTG	..A	..T	..T	..A	...
K42e1CTG	..A	..T	..T	..A	...
H0528e1CTG	..AT	..T	...
H0528e2CTG	..AT	..A	...
H0528e4CTG	..A	..T	..T	..A	...
1537CTG	..A	..T	..T	..A	...
H27j3CTG	..A	..T	..T	..A	...
P1178j1CTG	..AT	..T	...
P1178j2CTG	..AA	...
P1178j3CTG	..AA	...
H0231j1CTG	..AT	..T	...
H0231j2CTG	..AA	...
H0231j3CTG	..AA	...
H0528e5CTG	..AT	..A	...
F0512e1CTG	..AA	...
F0521j4CTG	..A	..T	..T	..A	...
H0528e3CTG	..AT	..A	...
H29e1CTG	..AT	..A	...
F0521j5CAGTG	..AT	..A	...
MCF0223c2CTG	A..	..A
F0521j1CTG	..AA	...
F0521j2CTG	..AA	...
F0521j3CTG	..AA	...

999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999
111	111	122	222	222	223	333	333	333	444	444	444	455	555	555	556		
345	678	901	234	567	890	123	456	789	012	345	678	901	234	567	890		

tippecanoe	CCT	AAC	AAC	CTA	ACA	GGT	ACT	ACC	CCC	TGA	CGC	CTG	CAA	CAA	TCG	CAG
H27j1	..CTG	..G	G.C	..GA	..A	..G	..T	..A	...
H27j2	..CTG	..G	G.C	..GA	..A	..G	..T	..A	...
H27j5	..CTG	..G	G.C	..GA	..A	..G	..T	..A	...
H27j6	..CTG	..G	G.C	..GA	..A	..G	..T	..A	...
H27j7	..CTG	..G	G.C	..GA	..A	..G	..T	..A	...
H27j8	..CTG	..G	G.C	..GA	..A	..G	..T	..A	...
H28e1	..CTG	..G	G.C	..GA	..A	..G	..T	..A	...
H28e2TG	..G	G.C	..GA	..A	..G	..T	..A	...
P1126j1	..CTG	..G	G.C	..GA	..A	..G	..T	..A	...
P1111j1	..CT	...	G.G	..G	GTCA	..AT	..A	...
P1111j2	..CT	...	G.G	..G	GTCA	..AT	..A	...
H28j1	..C	...	G.TG	..G	G.C	..GA	..A	..G	..T	..A	...

CS0348j5T ... G.G ..G .TCA ..AT ..A ...
 CS0348j6T ... G.G ..G .TCA ..AT ..A ...
 P1109j1 ..CT ... G.G ..G GTCA ..AT ..A ...
 P1109j2 ..CT ... G.G ..G GTCA ..AT ..A ...
 K119e1 ..CTG ..G .AC ..GA ..A ..G ..T ..A ...
 MCF0212c2 ..CT.. G.. ..G .TA ..AG ..A ..AC ..A ...
 MCF0212c4 ..CT.. G.. ..G .TA ..AG ..A ..AC ..A ...
 MCF0223c4 ..CT.. G.. ..G .TA ..AG ..A ..AC ..A ...
 MCF0223c5 ..CT.. G.. ..G .TA ..AG ..A ..AC ..A ...
 CS0350j1 ..CT ... G.G ..G GTCA ..AT ..A ...
 P1195j1 ..CGT ... G.G ..G GTCA ..AT ..A ...
 P1195j2 ..CGT ... G.G ..G GTCA ..AT ..A ...
 P1195j4 ..CGT ... G.G ..G GTCA ..AT ..A ...
 H0528j5 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 K42e1TG ..G G.C ..GA ..A ..G ..T ..A ...
 H0528e1 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 H0528e2 ..CTG ..G ..C ..GA ..A ..G ..T ..A ...
 H0528e4 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 1537 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 H27j3 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 P1178j1 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 P1178j2 ..CT ... G.G ..G GTCA ..AT ..A ...
 P1178j3 ..CT ... G.G ..G GTCA ..AT ..A ...
 H0231j1 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 H0231j2 ..CT ... G.G ..G GTCA ..AT ..A ...
 H0231j3 ..CT ... G.G ..G GTCA ..AT ..A ...
 H0528e5 ..CTG ..G .AC ..GA ..A ..G ..T ..A ...
 F0512e1 ..CT ... G.G ..G GTCA ..AT ..A ...
 F0521j4 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 H0528e3 ..CTG ..G G.C ..GA ..A ..G ..T ..A ...
 H29e1 ..CTG ..G ..C ..GA ..A ..G ..T ..A ...
 F0521j5 ..CTG ..G ..C ..GA ..A ..G ..T ..A ...
 MCF0223c2 ..CT.. G.. ..G .TA ..AG ..A ..AC ..A ...
 F0521j1 ..CT ... G.G ..G GTCA ..AT ..A ...
 F0521j2 ..CT ... G.G ..G GTCA ..AT ..A ...
 F0521j3 ..CT ... G.G ..G GTCA ..AT ..A ...

111 111 111

999 999 999 999 999 999 999 999 999 999 999 999 999 999 000 000 000
 666 666 666 777 777 777 788 888 888 889 999 999 999 999 000 000 000
 123 456 789 012 345 678 901 234 567 890 123 456 789 012 345 678

tippecanoe TTT ACA TTA CCC CTA GCC CTT ACA ACC ACT ACC ACC CTT CTG CTG CTT
 H27j1 CCCGGGGA ...
 H27j2 CCGGGGGA ...
 H27j5 CCCGGGGA ...
 H27j6 CCGG .A. ..GGGA ...
 H27j7 CCGG .A. ..GGGA ...
 H27j8 CCGG .A. ..GGGA ...
 H28e1 CCC ... C.GGGA ...
 H28e2 CCCGGGGA ...
 P1126j1 CCCGGGGA ...
 P1111j1 CCGG .A. ..C ..GGC ..A ...
 P1111j2 CCGG .A. ..C ..GGCA ...
 H28j1 CCCG .G. ..GGGA ...
 H28j2 CCGG .G. .A. ..G ..GGA ...
 H28j3 CCGG .G. .A. ..GGGA ...
 H28j4 CCGG .G. .A. ..G ..GGA ...

H28j6	CCG	G.G	.A.	..G	..G	G..	G..A	...
H28j7	CCG	G.G	.A.	..G	..G	G..	G..A	...
H28j8	CCG	G.G	.A.	..G	..G	G..A	...
1570	CCG	G.G	.A.	..G	G..A	...
K119e2	CCCGG	G..A	...
K108c1	..CG	.G.	..CCA	...
K108c2	..CG	.G.	..C	G..CA	...
MCF0212c1	..CG	.G.	..CCA	...
MCF0212c3	..CG	.G.	..CCA	...
P1168d1	CCCG	.G.	..C	..G	GG.A	..A	...
P1169d1	CCCG	.G.	..C	..G	GG.A	..A	...
P1169d2	CCCG	.G.	..C	..G	GG.A	..A	...
CS0348j1	CCC	A..	..GC	..G	G..C
CS0348j2	CCC	A..	..GC	..G	G..C
CS0348j3	CCC	A..	..GC	..G	G..C
CS0348j4	CCC	A..	..GC	..G	G..C
CS0348j8	CCC	A..	..GC	..G	.A.	...	GG.C
P1116j1	CCCC	..G	GG.C	..A
P1116j2	CCCG	.G.	..C	..G	G..C	..A
P1120e1	CCCG	.G.	..G	G..A	...
P1121e1	CCCG	.G.	..G	GG.A	...
1535	CCC	...	C..G	.G.	..G	.A.	GG.A	...
1536	CCCG	.G.	..G	.A.	GG.A	...
1539	CCC	...	C..G	.G.	..G	GG.A	...
1541	CCCG	.G.	..G	GG.A	...
1542	CCCG	.G.	..G	GG.A	...
1559	CCCG	.G.	..C	..G	GG.C
1560	CCCG	.G.	..C	..G	.A.	...	GG.C
1561	CCCG	.G.	..C	..G	GG.C
1562	CCCG	.G.	..C	..G	GG.C
1563	CCCG	.G.	..C	..G	.A.	...	GG.C
1571	CCCG	.G.	..G	GG.A	...
K72j1	CCCGC	..G	GG.C	..A
K72j2	CCCG	.G.	..C	..G	GG.C	..A
K72j3	CCCGC	..G	.A.	...	GG.C	..A
P1022j1	CCCG	.A.	..C	..G	GG.C	..A
P1022j2	CCCG	.G.	..C	..G	GG.C	..A	...	G..
P1022j3	CCCG	.G.	..C	..G	.A.	...	GG.C	..A
P1022j4	CCCG	.G.	..C	..G	.A.	...	GG.C	..A
P1022j5	CCCG	.G.	..C	..G	.A.	...	GG.C	..A
P1022j6	CCCGC	..G	.A.	...	GG.C	..A
H28j9	CCCG	.G.	..G	GG.A	...
P1109j3	CCCG	.G.	..C	..G	.A.	...	GG.C	..A
P1195j3	CCCG	.G.	..C	..G	GG.C	..A	...	G..
P1195j5	CCCG	.T.	..C	..G	GG.C	..A	...	G..
H27e1	CCCG	.G.	..G	GG.A	...
H27e2	CCCG	.G.	..G	GG.A	...
H27e3	CCCG	.G.	..G	GG.A	...
H27e5	CCCG	.G.	..G	GG.A	...
MCF0223c1	..CG	.G.	..C	.G.CA	...
CS0353j1	CCCC	..G	GG.C	..A
CS0353j2	CCCGC	..G	GG.C	..A
CS0353j3	CCCC	..G	GG.C	..A
CS0353j4	CCCC	..G	GG.C	..A
CS0348j5	CCCG	.G.	..C	..G	GG.C
CS0348j6	CCCG	.G.	..C	..G	GG.C
P1109j1	CCCG	.G.	..C	..G	GG.C	..A

P1109j2 CCCG .G. ..C ..G GG.C ..A
 K119e1 CCCG .G. ..G GG.A
 MCF0212c2 G.CG .G. ..CCA
 MCF0212c4 G.CG .G. ..CCA
 MCF0223c4 ..CG .G. ..CCA
 MCF0223c5 ..CG .G. ..CCA
 CS0350j1 CCCG .G. ..C ..G GG.C ..A
 P1195j1 CCCC ..G GG.C ..A
 P1195j2 CCCC ..G GG.C ..A
 P1195j4 CCCC ..G GG.C ..A
 H0528j5 CCCG .G. ..G GG.A
 K42e1 CCCG .G. ..G GG.G.A
 H0528e1 CCCG .G. ..G GG.A
 H0528e2 CCCG .G. ..G GG.A
 H0528e4 CCCG .G. ..G GG.A
 1537 CCCG .G. ..G G..A
 H27j3 CCCG .G. ..G G..A
 P1178j1 CCCG .G. ..G GG.G.A
 P1178j2 CCCG .G. ..C ..G .A. ... GG.C ..A
 P1178j3 CCCG .G. ..C .AG .A. ... GG.C ..A
 H0231j1 CCCG .G. ..G G..G.. ..A
 H0231j2 CCCG .G. ..C ..G GG.C ..A
 H0231j3 CCCG .G. ..C ..G GG.C ..A
 H0528e5 CCCG .G. ..G GG.A
 F0512e1 CCCG .G. ..C ..G GG.CA
 F0521j4 CCCG .G. ..G GG.A
 H0528e3 CCCG .G. ..G G..A
 H29e1 CCCG .G. ..G G..A
 F0521j5 CCCG .G. ..G G..A
 MCF0223c2 ..CG .G. ..CCA
 F0521j1 CCCG .G. ..C ..G GG.C ..A
 F0521j2 CCCG .G. ..C ..G GG.C ..A
 F0521j3 CCCG .G. ..C ..G GG.C ..A

111 111 111 111 111 111 111 111 111 111 111 111 111 111
 000 000 000 000 000 000 000 000 000 000 000 000 000 000
 011 111 111 112 222 222 222 333 333 333 344 444 444
 901 234 567 890 123 456 789 012 345 678 901 234 567

tippecanoe CCA CTC ACA CCC GCA GTA GTG GCA CTA CTC ACT CTT TAA
 H27j1T .TGC ..AA .GC
 H27j2T .TGC ..AA .GC
 H27j5T .TGC ..AA .GC
 H27j6T .TGC ..AA .GC
 H27j7T .TG A.. ..C ..AA .GC
 H27j8T .TG A.. ..C ..AA .GC
 H28e1T .TGC ..AA .GC
 H28e2T .TGC ..AA .GC
 P1126j1T .TGC ..AA .GC
 P1111j1T .TGC ..AA .GC
 P1111j2T .TGC ..AA .GC
 H28j1T .TGC ..AA .GC
 H28j2T .TG A.. ..C ..AA .GC
 H28j3T .TG A.. ..C ..AA .GC
 H28j4T .TG A.. ..T .C ..AA .GC
 H28j6T .TG A.. ..C ..AA .GC
 H28j7T .TG A.. ..C ..AA .GC
 H28j8T .TG A.. ..C ..AA .GC

1570	...	T	.TG	A..C.	..AA	.GC
K119e2	...	T	.TG	C.	..AA	.GC
K108c1	..C	..T	TT.	..TCG	..AGC	..C	...
K108c2	..C	..T	TT.	..TCG	..AC	..C	...
MCF0212c1	..C	..T	TT.	..TCG	..AGC	..C	...
MCF0212c3	..C	..T	TT.	..TCG	..AGC	..C	...
P1168d1	...	T	.T.	CG	..AA	.GC
P1169d1	...	T	.T.	CG	..AA	.GC
P1169d2	...	T	.T.	CG	..AA	.GC
CS0348j1	...	T	.TG	C.	..AG	.GC
CS0348j2	...	T	.TG	C.	..AG	.GC
CS0348j3	...	T	.TG	C.	..AG	.GC
CS0348j4	...	T	.TG	C.	..AG	.GC
CS0348j8	...	T	.TG	C.	..AG	.GC
P1116j1	...	T	.TG	C.	..AA	.GC
P1116j2	...	T	.TG	C.	..AA	.GC
P1120e1	...	T	.TG	A..C.	..AA	.GC
P1121e1	...	T	.TG	C.	..AA	.GC
1535	...	T	.TG	C.	..AA	.GC
1536	...	T	.TG	C.	..AA	.GC
1539	...	T	.TG	C.	..AA	.GC
1541	...	T	.TG	C.	..AA	.GC
1542	...	T	.TG	C.	..AA	.GC
1559	...	T	.TG	C.	..AA	.GC
1560	...	T	.TG	C.	..AA	.GC
1561	...	T	.TG	C.	..AA	.GC
1562	...	T	.TG	C.	..AA	.GC
1563	...	T	.TG	C.	..AA	.GC
1571	...	T	.TG	C.	..AA	.GC
K72j1	...	T	.TG	C.	..AA	.GC
K72j2	...	T	.TG	..GC.	..AA	.GC
K72j3	...	T	.TG	C.	..AA	.GC
P1022j1	...	T	.TG	C.	..AA	.GC
P1022j2	...	T	.TG	..GC.	..AA	.GC
P1022j3	...	T	.TG	C.	..AA	.GC
P1022j4	...	T	.TG	C.	..AA	.GC
P1022j5	...	T	.TG	C.	C.AA	.GC
P1022j6	...	T	.TG	C.	..AA	.GC
H28j9	...	T	.TG	C.	..AA	.GC
P1109j3	...	T	.TG	C.	..AA	.GC
P1195j3	...	T	.TG	C.	..AA	.GC
P1195j5	...	T	.TG	C.	C.AA	.GC
H27e1	...	T	.TG	C.	..AA	.GC
H27e2	...	T	.TG	C.	..AA	.GC
H27e3	...	T	.TG	C.	..AA	.GC
H27e5	...	T	.TG	C.	..AA	.GC
MCF0223c1	..C	..T	TT.	..TCG	..AGC	..C	...
CS0353j1	...	T	.TG	C.	..AA	.GC
CS0353j2	...	T	.TG	C.	..AA	.GC
CS0353j3	...	T	.TG	C.	..AA	.GC
CS0353j4	...	T	.TG	C.	..AA	.GC
CS0348j5	...	T	.TG	C.	..AG	.GCG
CS0348j6	...	T	.TG	C.	..AG	.GCG
P1109j1	...	T	.TG	C.	..AA	.GC
P1109j2	...	T	.TG	C.	..AA	.GC
K119e1	...	T	.TG	C.	..AG	.GC
MCF0212c2	..C	..T	TT.	C.	..AGC

MCF0212c4	..C	..T	TT.C.	..AGC
MCF0223c4	..C	..T	TT.	..TCG	..AGC	..C	...
MCF0223c5	..C	..T	TT.	..TCG	..AGC	..C	...
CS0350j1T	.TGC.	..AA	.GC
P1195j1T	.TGC.	..A	...	G..	..A	.GC
P1195j2T	.TGC.	..AA	.GC
P1195j4T	.TGC.	..AA	.GC
H0528j5T	.TGC.	..AA	.GC
K42e1T	.TGC.	..AA	.GC
H0528e1T	.TGC.	..AA	.GC
H0528e2T	.TGC.	..AG	.GC
H0528e4T	.TGC.	..AA	.GC
1537T	.TGC.	..AA	.GC
H27j3T	.TGC.	..AA	.GC
P1178j1T	.TGC.	..AA	.GC
P1178j2T	.TGC.	..AA	.GC
P1178j3T	.TGC.	..AA	.GC
H0231j1T	.TGC.	..AA	.GC
H0231j2T	.TGC.	..AA	.GC
H0231j3T	.TGC.	..AA	.GC
H0528e5T	.TGC.	..AA	.GC
F0512e1T	.TGC.	..AA	.GC
F0521j4T	.TGC.	..AA	.GC
H0528e3T	.TGC.	..AG	.GC
H29e1T	.TGC.	..AG	.GC
F0521j5T	.TGC.	..AT	.GC
MCF0223c2	..C	..T	TT.	..TCG	..AGC	..C	...
F0521j1T	.TGC.	..AA	.GC
F0521j2T	.TGC.	..AA	.GC
F0521j3T	.TGC.	..AA	.GC