Summer 2014

Phylogeny and Biogeography of the Family Haemulidae Based on a Multigene Approach

Millicent D. Sanciangco
Old Dominion University

Recommended Citation

Sanciangco, Millicent D.. "Phylogeny and Biogeography of the Family Haemulidae Based on a Multigene Approach" (2014). Doctor of Philosophy (PhD), dissertation, Biological Sciences, Old Dominion University, DOI: 10.25777/vkv0-g713
https://digitalcommons.odu.edu/biology_etds/82

PHYLOGENY AND BIOGEOGRAPHY OF THE FAMILY HAEMULIDAE BASED ON A MULTIGENE APPROACH

by

Millicent D. Sanciangco
B.S. Zoology, April 2002, University of the Philippines Los Baños, Philippines
M.S. Biology, May 2007, Old Dominion University

A Dissertation Submitted to the Faculty of
Old Dominion University in Partial Fulfillment of the
Requirements for the Degree of

DOCTOR OF PHILOSOPHY

ECOLOGICAL SCIENCES

OLD DOMINION UNIVERSITY
August 2014

Approved by:

Kent E. Carpenter (Director)

David Gauthier (Member)

John Holsinger (Member)

Mark Westneat (Member)

ABSTRACT

PHYLOGENY AND BIOGEOGRAPHY OF THE FAMILY HAEMULIDAE BASED ON A MULTIGENE APPROACH

Millicent D. Sanciangco
Old Dominion University, 2014
Director: Dr. Kent E. Carpenter

Haemulids are one of the most ecologically and commercially important groups of near-shore fishes. They are very diverse, with 145 putative species belonging to 18 genera. The phylogenetic relationships of the genera within the haemulids, however, are uncertain and the limits and relationships with other percomorphs are undefined.

Here, I present the first comprehensive phylogenetic hypothesis for the family based on a combined dataset of five genes (4731 bp; 16 genera, 56 species). Results show strong support for a monophyletic Haemulidae with the inclusion of the former inermiids. However, results of the analyses call into question the monophyly of a number of genera (e.g. *Pomadasys*). Furthermore, results show Haemulidae as sister to Lutjanidae, and *Hapalogenys* as outside the Haemulidae, based on a limited sampling of outgroups, and suggest further studies are needed that will incorporate a wider subset of taxa and more genes.

I provide a phylogenetic hypothesis of the interfamilial relationships within percomorphs based on RAxML (Randomized Axelerated Maximum Likelihood) analysis of 23-gene dataset (1231 taxa) to determine sister groups of haemulids. This study presents the most comprehensive dataset, encompassing the major lineages within Percomorphaceae, and poses novel hypothesis regarding relationships of many groups. Results show haemulids are sister to Lutjanidae plus Caesionidae in a clade together with Callanthiidae, Malacanthidae, Pomacanthidae, Emmelichthyidae, Acanthuriformes, Monodactylidae, Sciaenidae, Chaetodontidae, and Leiognathidae; however, support for this group is weak.

Further, I test the utility of mitogenomes (14 genera, 26 species; ~16,000 bp) and multi-locus data (22 genes; 19 genera, 82 species) to infer interrelationships within the haemulids in order to address what might have been the limits of the second chapter using RAxML analyses. Similarly, the family Haemulidae and subfamilies Plectorhinchinae and Haemulinae were recovered as monophyletic. Although improvement in nodal support is evident using both datasets, resolution at the species level using the mitogenomes is not possible due to limited availability of mitogenomes for the haemulids. Nevertheless, analyses revealed a possible radiation for the haemulids originating from the Old World to the New World. The more inclusive 22-gene dataset provided resolution for the interrelationships within the family, and better explained the non-monophyly of the genus *Pomadasys*.

This dissertation is dedicated to Jonnell, Andre, and Avery.

ACKNOWLEDGMENTS

The completion of my PhD degree has been one of the most significant challenges of my life. It would not have been possible to see the end of my dissertation without the help and support of the many people around me.

I would like to express my sincerest gratitude to my advisor, Dr. Kent Carpenter, for the support and guidance throughout my journey to graduate school (both Masters and PhD), for trusting me and allowing me to manage the ETOL (Euteleost Tree of Life) project and the lab, and for the many discussions and advice in greatly improving this dissertation. Your role has been invaluable. I am thankful to my Advisory committee, Drs. Kent Carpenter, Timothy Motley, John Holsinger, Lisa Horth, and Mark Westneat, and to my Dissertation Committee, Drs. Kent Carpenter, Mark Westneat, David Gauthier, and John Holsinger, for the recommendations and advice in helping improve this dissertation. It is very unfortunate to have lost Dr. Motley on my fifth year in the program. He was a great mentor and a good friend.

I am thankful to Drs. Luiz Rocha and Kent Carpenter for their advice and suggestions that helped improved the *Zootaxa* paper, which is also the second chapter of this dissertation. I am grateful to Drs. Joseph Brown, Chenhong Li, and Derrick Zwickl for their suggestions on analyzing my preliminary datasets. I am also thankful to Dr. Ricardo Betancur-R for the advice and assistance on the ETOL project and for the help in analyzing the percomorph dataset.

I am grateful to the following for providing tissue samples for this study: A. Bentley and E. Wiley (Biodiversity Institute, U. Kansas), A. Carvalho-Filho (FISH-LTD), B. Collette (National Museum of Natural History, Smithsonian Institution), A. Connell (Durban, South Africa), C. Struthers (Museum of New Zealand, Te Papa Tongarewa), Y. Iwatsuki (U. Miyazaki), P.A. Hastings and H.J. Walker (SIO), S. Knudsen (U Auckland), C. Burridge and K. Clements (U Tasmania), T. Darden (Marine Resources Research Institute, South Carolina Department of Natural Resources), M. McGrouther (Australian Museum), R. Robertson (Smithsonian Tropical Research Institute), and B. Stockwell (ODU). W.N. Eschmeyer and J. Fong provided access to their Catalog of Fishes database (through the ETOL).

I am also very thankful to Eric Womack for being my Research Assistant, for performing independent lab work for some of the percomorph sequences as part of the ETOL quality control, for helping me keep the lab organized, for helping me with the tissue and voucher inventories, and keeping the databases up-to-date.

I am extremely grateful to Jeremy Raynal and April Cobos for proofreading and for their suggestions on improving the writing of this dissertation.

I have learnt a great deal of information and computing skills from attending a number of training courses and workshops, including those hosted by NimBIOS, UC Davis/Bodega Bay, Deepfin, and NESCent. I am also grateful for the scholarships/awards I received that made my participation to those courses possible. BGSO (Biology Graduate Student Organization) and UC Davis funded my participation to the Bodega Bay Applied Phylogenetics workshop. The Deep Fin Initiative provided stipend during my Student Exchange Program in Loyola University Chicago. I am thankful to Drs. Guillermo Orti and Terry Grande for granting me the award, and to Dr. Grande for hosting me in her laboratory. I am thankful to Dr. Wm. Leo Smith and the museum staff for accommodating me at The Field Museum during my visit to look at fish specimens. NIMBioS funded my attendance to High Performance Computing for Phylogenetics tutorial, and Dr. Tandy Warnow and the AToL (Assembling the Tree of Life) project sponsored my participation to the AToL workshop at NESCent.

I am also grateful to Lee Weigt (Director, Laboratories of Analytical Biology (LAB), National Museum of Natural History, Smithsonian Institution) and Dr. Guillermo Orti (The George Washington University, formerly in University of Nebraska Lincoln) for allowing me to process some of my samples in their laboratories. I am very thankful to Lee Weigt and his family for allowing me to stay in their house when I worked in the LAB for two weeks and for the ETOL project that subsidized my three-week stay in UNL to work on the ETOL samples.

I would like to acknowledge the financial, academic, and technical support of Old Dominion University and the Department of Biological Sciences. I thank Dr. Ian Bartol and the College of Sciences for awarding me a University Fellowship. Ruben Igloria (formerly at OCCS, ODU) helped me compile programs and setup my account so I could submit jobs through Zorka/HPC cluster. I am thankful to the ILLIAD staff, OCCS staff, Marla Harvey, Mary Hayward, and Norris for doing the work they do. The International Union for Conservation of Nature/Conservation International, Global Marine Species Assessment project, funded by Tom Haas and the New Hampshire Charitable Foundation, provided travel support to Dr. Carpenter for incidental collection of some specimens (e.g. *Parakuhlia*) used in this study. My dissertation was funded through the ETOL project from NSF award DEB-0732894 to Dr. Carpenter, with me, as the Graduate Research Assistant from 2008 to 2013.

Members of the Carpenter Lab and GMSA folks also deserve my sincerest gratitude. To Amanda Ackiss, Adam Hanson, Dr. Heather Harwell, Andrew Hines, Jeremy Raynal, Mia Raynal, Brian Stockwell, Emily Stump, Kimberly Wieber, and Eric Womack, your friendship and support have meant more to me (and to my family) than I could ever express.

I am indebted to Drs. Ariel and Luna Pinto, Dr. Nido and Rachel Calida, and Dr. Joe and Jennifer Martin for always inviting Andre to play with their kids when I was working in the lab and/or analyzing my data, and also for making sure we remember and celebrate occasions with them. They have been our immediate family here in the US. I am also grateful to Tita Merly Palomar and family for also treating us like relatives and inviting us to many occasions. I thank Dr. Araceli Suzara, (Director, Filipino-American Center, ODU) for inviting me to serve as a board member of the Center's steering committee and inviting us to the Center's events at ODU. I am very fortunate to have met Leslie Belton (and family), who took care of Avery starting when he was two months until when he was about 13 months old, so I could work on my research.

I am grateful for my parents, Panfilo (Jun) and Arlene Domingo; my in-laws, Jessie and Juanita Sanciangco; my sister Audrey Domingo, and brothers-in-law, Johnvil and Jaysee Sanciangco, for the unconditional and financial support, for checking in on us, for just being there, especially for Andre, even though they are all continents away.

Finally, to my family, Jonnell, Andre, and Avery, who have been my sources of great joy, strength, and inspiration, I thank God for having you three in my life. Thank you, Avery, for always keeping us entertained. I feel terrible for sending you to the babysitter/daycare at a very young age because I had to work on my dissertation. Andre, I am very thankful you have a big heart, and understood the demands of my getting a degree. I know I have not been a very "fun" mom since I started my PhD and you only probably remembered me as a student, and therefore had to be always "busy," for as long as you could remember. I promise I will make it up to you, to Avery, and to Dad. To my husband, Jonnell, who had put up with me and probably felt like a widower, especially during the first two years when I was too busy getting PCRs to work in the lab and during the past two years when I was finishing up, you had been very patient, understanding, and supportive. I know you were also exhausted taking care of most of everything including looking after the kids more and making sure you spent time with them when I literally could not. I am very fortunate to have a husband like you. I am looking forward to spending more time with you and our kids when all this is over.

TABLE OF CONTENTS

LIST OF TABLES

Table Page

LIST OF FIGURES

CHAPTER I

GENERAL INTRODUCTION

The family Haemulidae (grunts) is one of the largest percoid families and includes 145 putative species belonging to 18 genera. They are circumglobal and occur in tropical and warm temperate oceans of the Atlantic, Indian, and Pacific. All species are neritic, inhabiting the shallow waters of coral reefs, rocky bottoms, seagrass beds, sand flats, and mud-bottoms in coastal and estuarine waters. Most feed on a wide variety of benthic invertebrates including crustaceans, polychaete worms, clams, and echinoids, while some species primarily feed on plankton (Konchina, 1977; Ogden and Ehrlich, 1977; Williams *et al.*, 2004).

The family name was derived from the Greek word *haimaleos*, which means "bloody gums" and refers to the red coloration of their interior mouth (Brown, 1956). The family common name "grunt" was derived from the distinctive stridulatory sound, which is amplified by the swim bladder, produced when rubbing their pharyngeal teeth during feeding, territorial display, or fright response (Konchina, 1977). Grunts are oblong, compressed, and moderate-sized perch-like fishes with generally small to average-sized mouth. The family is characterized by the presence of series of enlarged sensory chin pores, which range from two to six. They have conical teeth in each jaw but no canines and no teeth on the palate. Their scales (usually ctenoid) extend onto the head except on the snout, lips, and chin (Lindeman and Toxey, 2003; McKay, 1984, 2001; McKay and Schneider, 1995). Other diagnostic features include a single dorsal fin with nine to 15 spines and 11 to 26 rays, moderate to long pectoral fins, each with a single spine and five soft rays, and an anal fin with three spines and six to 13 rays (Lindeman and Toxey, 2003; McKay, 1984, 2001; McKay and Schneider, 1995). Diverse color patterns are distinctive of many adult grunts. Most species of *Plectorhinchus* also go through diverse color pattern changes during juvenile stages presenting challenges for accurate identification. Early juveniles of *Haemulon* can look very similar, with almost identical banding patterns to other members of the same genus (Lindeman, 1986).

The journal model for this dissertation is *Zootaxa*.

Haemulids play a significant role in the ecosystem by providing nutrients, as well as stimulating biological activity, in the reef community (Ogden and Ehrlich, 1977). They also serve as indicators of anthropogenic impacts (e.g. overfishing, cyanide and dynamite fishing) to the reefs (Tupper and Juanes, 1999). Haemulids are also an important component in commercial fisheries, with a global capture production averaging 69,279 tons from 2000 to 2012 (FAO, 2014).

Although haemulids are an ecologically and commercially important group of near-shore fishes, information on the inter- and intrarelationships of the family have remained obscure. Several revisions have been made regarding the diverse taxonomic classification of the family and a number of articles on the systematics and distribution of individual species exist (Courtenay, 1961; Konchina, 1976; Lindeman and Toxey, 2003; McKay, 1984, 2001; Nelson, 1994, 2006), but none exist that could potentially clarify relationships among genera. Furthermore, interfamilial relationships within the ill-defined suborder Percoidei, and order Perciformes, to which haemulids belong, remain to be resolved. Here, I use molecular sequence data to answer three main hypotheses concerning the haemulids.

Question 1: What is the phylogenetic history of the Haemulidae? Do morphological characters support a monophyletic classification for the Haemulidae? Are the two subfamilies, Plectorhinchinae and Haemulinae, and putative genera currently defined by morphological characters valid? The aim of chapter two is to provide a phylogenetic hypothesis for most haemulids using combined mitochondrial and nuclear gene sequences (five genes; 4731 bp) and infer relationships within the family. Several interesting phylogenetic relationships supported by morphological characters were recovered but interrelationships within some genera remain unresolved (chapter published in *Zootaxa*, Sanciangco *et al.* 2011).

Question 2: What are the close relatives of the Haemulidae? Nelson (2006) classified the family Haemulidae in the Order Perciformes, and further, in the suborder Percoidei. Perciformes (*sensu* Nelson, 2006) is the largest group of vertebrates with 10,033 species in 160 families and 20 suborders, including Percoidei (Nelson, 2006). The suborder Percoidei (*sensu* Nelson 2006) is the most species-rich of all perciforms, with 3,176 species belonging to 79 families of unknown integrity (Johnson, 1984; Lauder and Liem, 1983; Nelson, 2006; Wiley and Johnson, 2010). Previous studies have established the limits and relations of some families within percoids using morphological characters and molecular sequences, but they have not been successful in defining the monophyly of the suborder nor in determining broad interfamilial relationships within the percoids (Dettai and Lecointre, 2005; Johnson, 1984, 1993; Johnson and Patterson, 1993; Li *et al.*, 2009; Li *et al.*, 2008; Mahon, 2007; Smith and Craig, 2007). More recently, Betancur-R. *et al.* (2013a) and Near *et al.* (2013) have examined the phylogenetic relationships of most of bony fishes using mutli-gene sequences. Although these studies have presented novel hypotheses for many taxa, the placement of Haemulidae and its closest relatives remained obscure. Understanding these relationships is necessary to determine the evolutionary history of haemulids and also to provide resolution to the "tips" of the greater perciform tree. Information on interrelationships of perciforms will also be useful for selecting outgroups and testing the monophyly of many taxa. The aim of chapter three is to provide a reliable taxonomic framework for the Haemulidae in the greater percomorphs.

Question 3: What is the best set of data to infer the phylogeny of the Haemulidae? The clades recovered from the analyses presented in chapter two call into question the monophyly of a number of haemulid genera. Will the addition of more genes or more taxa help us to understand the evolutionary history of the family? Will extensive sampling of one gene (complete mitochondrial genome) with a limited subset of species, or extensive sampling of the species with incomplete genes resolve interrelationships within the haemulids? The aim of chapter four is to test the utility of the complete mitochondrial genome to infer the relationships of haemulids and compare results with a limited number of genes and of a combined dataset of 22 markers.

CHAPTER II

A MOLECULAR PHYLOGENY OF THE GRUNTS (PERCIFORMES: HAEMULIDAE) INFERRED USING MITOCHONDRIAL AND NUCLEAR GENES

Note: The entirety of this chapter has been published in:

Sanciangco, M. D., Rocha, L. A., Carpenter, K. E., 2011. A molecular phylogeny of the Grunts (Perciformes: Haemulidae) inferred using mitochondrial and nuclear genes. Zootaxa 2966, 37–50.

INTRODUCTION

The family Haemulidae, or grunts, include 18 genera and about 145 species (Nelson, 2006) in the ill-defined order Perciformes, suborder Percoidei (*sensu* Nelson 2006). Grunts are circumglobal and often prominent in both hard and soft-bottom nearshore tropical, subtropical, and warm temperate waters (Lindeman and Toxey, 2003; McKay, 1984, 2001; McKay and Schneider, 1995). Most are carnivorous, feeding opportunistically on a wide variety of benthic invertebrates including crustaceans, polychaete worms, clams, and echinoids, while smaller species primarily feed on plankton (Konchina, 1977; Ogden and Ehrlich, 1977; Williams *et al.*, 2004).

Johnson (1981) used a number of characters to define Haemulidae and its subfamilies, Haemulinae and Plectorhinchinae. He proposed the superfamily Haemuloidea to include the mostly bottom feeding Haemulidae and the planktivorous Inermiidae. The latter family, commonly known as bonnetmouths, contains only two species that are reef-associated, typically small, and specialized for planktivory with highly protrusible jaws and fusiform bodies (Lindeman, 2006; McEachran and Fechhelm, 2005; Nelson, 2006). Johnson (1981) found that the families Haemulidae and Inermiidae share a suspensorium similar to that of the lutjanoids in having little direct osseous articulation and a simple symplectic but having a unique projection on the margin of the metapterygoid, which projects posteriorly as a vertically oriented rounded flange that overlaps the medial side of the lower arm of the hyomandibular. This, in addition to other osteological characters such as the number of branchiostegals; number of openings in pars jugularis; presence of chin pores and scales on lacrimal, snout, and preopercular margin; absence of subocular shelf and trisegmental pterygiophores; and specializations in their infraorbitals, suspensorium, and procurrent spur provide morphological evidence for a monophyletic Haemuloidea.

The presence of enlarged sensory chin pores and the attachment of the sixth infraorbital to the skull in haemulids are characters that are uncommon among percoids (Johnson, 1981). These enlarged pores are also present in the Lobotidae, Hapalogenyidae, Sciaenidae, and several other families. However, these families are easily recognized based on the presence of other anatomical and osteological characters diagnostic of the members of those families. Lobotidae and Hapalogenyidae, for example, have more than six chin pores, while Sciaenidae has only one or two anal fin spines compared to three anal spines in haemulids. The number, shape, and position of chin pores also help diagnose subfamilies and genera within Haemulidae. Plectorhinchines have four to six chin pores while haemulines, including the former inermiids, possess either two chin pores, a median chin groove, or both (Johnson, 1981). While both haemulid subfamilies and some genera appear to be well defined, many haemulid genera are not well defined and diagnosed only with superficial characters. For example, the monotypic *Genyatremus* was originally erected to differentiate what is currently recognized as *Anisotremus interruptus* from other higher bodied species of *Anisotremus* (Gill, 1861), and it appears to have been only incorrectly placed in another genus and recognized as *Genyatremus luteus* (Johnson, 1981; Lindeman and Toxey, 2003). *Orthopristis* (Girard, 1858) was erected based on superficial characters that are not currently used to distinguish members of the genus such as the body configuration and fin meristics (Lindeman and Toxey, 2003; McKay and Schneider, 1995). *Boridia, Conodon, Microlepidotus, Xenichthys,* and *Xenistius* were all designated by monotypy (Eschmeyer, 1990) without extensive morphological comparisons.

A number of recent studies that help define the limits of haemulid species and genera (Courtenay, 1961; Iwatsuki *et al.*, 1998; Konchina, 1976; Miles, 1953; Ren and Zhang, 2007; Rocha *et al.*, 2008), or provide basic regional systematic information (Bernardi and Lape, 2005; Konchina, 1977; Lindeman and Toxey, 2003; McKay, 1984, 2001; McKay and Schneider, 1995; Roux, 1981) are available; however, none of these studies have attempted to infer a phylogeny of the family Haemulidae using either molecular or morphological methods. Johnson (1981) studied the morphology of a number of families thought to be closely related to his proposed haemuloids (Haemulidae and Inermiidae) and suggested two additional superfamilies, the

Sparoidea (including Sparidae, Centracanthidae, Nemipteridae, and Lethrinidae) and Lutjanoidea (including Lutjanidae and Caesionidae), but he could not find evidence to suggest that any of these groups were directly related to one another. He was not confident in polarizing morphological characters of Haemuloidea and therefore chose not to propose a phylogeny.

Recent studies conducted on higher-level relationships of percomorphs and acanthomorphs have shown potential outgroups for haemulids on the basis of molecular characters including Dettai and Lecointre (2005; Syngnathidae, Uranoscopidae + Cheimarrichthyidae + Ammodytidae, Moronidae, Drepanidae, and Scaridae + Labridae); Smith and Craig (2007; Lutjanidae, Lethrinidae + Priacanthidae, Moronidae, and Lobotidae); Craig and Hastings (2007; Moronidae and Cirrhitidae); and Mahon (unpublished; Dinopercidae and Drepanidae + Acanthuridae + Ephippidae). In addition, the interrelationships of families within the putative Percoidei, the suborder to which Haemulidae belongs (Nelson, 2006), are not well understood, hence making it more challenging to define the possible sister-groups of haemulids. *Hapalogenys* has been classified in the Haemulidae because of the presence of chin pores (Iwatsuki and Russell, 2006; Iwatsuki *et al.*, 2000; Richardson, 1844); however, the phylogenetic placement of the Hapalogenyidae (Ren and Zhang, 2007; Springer and Raasch, 1995) within the haemulids has also been controversial (Iwatsuki and Nakabo, 2005; Iwatsuki *et al.*, 2000; Johnson, 1984; Lindeman and Toxey, 2003).

The purpose of this study is to infer a genus-level phylogeny of haemulids, including a former inermiid species, *Emmelichthyops*, test the validity of the two subfamilies, and provide a basis to further test hypotheses of morphological character evolution and biogeography of the family Haemulidae. Here I use molecular data to help frame questions of generic placement within Haemulidae. The markers used for this study include the mitochondrial Cytochrome Oxidase I (COI) and Cytochrome *b* (CYT *b*) and three nuclear markers, Recombination Activation Gene-1 (RAG1), SH3 and PX domain-containing 3-like protein (SH3PX3), and pleiomorphic adenoma proteinlike 2 (PLAGL2) genes. A phylogeny of haemulids from most genera was inferred from maximum parsimony (MP), maximum likelihood (ML), and Bayesian analyses of a combined total of 4731 base pairs.

MATERIALS AND METHODS

Taxon sampling

Ten outgroup taxa were included from the families Nemipteridae (*Nemipterus marginatus*), Lethrinidae (*Lethrinus ornatus*), Lutjanidae (*Aphareus furca* and *Lutjanus fulviflamma*), Sparidae (*Sarpa salpa*), and Hapalogenyidae (*Hapalogenys aya*, *H. kishinouyei*, and *H. nigripinnis*). Lobotidae (*Lobotes pacificus* and *L. surinamensis*), another percoid family that possesses chin pores, was also included in the study. Among the ingroup taxa, 56 species belonging to 18 genera are included among the 144 species and 20 haemulid genera (Appendix A). All genera of haemulids are represented except for the two monotypic genera *Parakuhlia* and *Xenocys*. Specimens were collected by trawling, hook and line, or spearfishing. Samples were also obtained from specimens from fish markets. Muscle tissue of the fish were dissected and preserved in 95% ethanol or DMSO solution (Seutin *et al.*, 1990) and stored at -20°C until processed in the laboratory.

DNA isolation, amplification, and sequencing

Genomic DNA was extracted from approximately 20 mg of tissue following the DNeasy® Kit (Qiagen) protocol and Wizard® SV 96 Genomic DNA Purification System (Promega). Primers used to amplify the mitochondrial and nuclear genes are listed in Table 1. A total of 651 base pairs were amplified using the COI primers under the following conditions: initial denaturation at 95°C for one minute (to activate the Takara Ex Taq HotStart™ DNA polymerase, Takara Bio Inc.), followed by 30 cycles of 95°C for 30 seconds, 52°C for 30 seconds, and 72 °C for 45 seconds; followed by a five minute extension at 72°C. CYT *b* yielded a total of 1140 base pairs, with amplification conditions similar to those of COI but with 32 cycles and annealing temperature of 52 °C for 45 seconds. For all the nuclear genes used, nested PCRs were employed to successfully amplify approximately 1431 base pairs of RAG1 gene, 705 base pairs of SH3PX3 gene, and 804 base pairs of PLAGL2 gene from DNA extracts, with the following amplification settings: initial denaturation at 95 °C for one minute; 30 cycles of 95 °C for ten seconds, 56 °C to 63 °C for 45 seconds, and 72 °C for five minutes; with an additional final extension at 72 °C for five minutes. Amplification conditions for the second set of internal primers for three nuclear genes follow the same protocol as that of the first PCR, except with annealing temperature set to 63 °C for all three genes. A 0.2 μl of ExoSAP-IT® (USB Corporation) master mix (1:5 dilution of the enzyme) was added for every 1 μl of PCR product to purify the target gene, carried out at 37 °C for 30 minutes and 80 °C for 20 minutes. Sequencing reactions were conducted in forward and reverse directions using primers for the second set of PCR. Sequences were assembled and edited in Sequencher version 4.10.1 (Gene Codes). The trimming criteria for sequences include trimming no more than 25% until the first 20 bases contain at least three bases with confidences below 20% for the five-prime end and trimming until the last 20 bases contain less than three bases with confidences below 20% for the three-prime end. Sequences were then trimmed according to a reference sequence for each gene obtained from GenBank, including COI: FJ237890 *Pomadasys maculatus* (Zhang and Hanner, 2008), CYT *b*: EF512297 *Pomadasys maculatus* (Zhu *et al.*, 2007), RAG1: EF095661 *Haemulon aurolineatum* (Chen *et al.*, 2007), SH3PX3: EF033010 *Lutjanus mahogani* (Li *et al.*, 2007); and PLAGL2: EF033023 *Lutjanus mahogani* (Li *et al.*, 2007). Multiple alignments of sequences were performed using ClustalX (Thompson *et al.*, 1997) using default settings (Hall, 2004).

TABLE 1. PCR primer sequences and annealing temperatures used to amplify the five markers used. 1st indicates the first round of nested PCR and 2nd for second round of nested PCR using the following primers for each gene.

Gene	Primers	Sequences	Tm (°C)	PCR	Reference
COI	FISHCO1LBC_F	5' TCAACYAATCAYAAAGATATYGGCAC 3'	52	1st	Ward *et al.*, 2005
	FISHCO1HBC_R	5' ACTTCYGGGTGRCCRAARAATCA 3'		1st	Ward *et al.*, 2005
CYT *b*	CYT*b*_UniF	5' CGAACGTTGATATGAAAAACCATCGT 3'	52	1st	Orrell *et al.*, 2002
	CYT*b*_UniR	5' ATCTTCGGTTTACAAGACCGGTG 3'		1st	Orrell *et al.*, 2002
RAG1	2510F	5' TGGCCATCCGGGTMAACAC 3'	63	1st	Li and Orti, 2007
	RAG1R1	5' CTGAGTCCTTGTGAGCTTCCATRAAYTT 3'		1st	López *et al.*, 2004
	RAG1F1	5' CTGAGCTGCAGTCAGTACCATAAGATGT 3'	63	2nd	López *et al.*, 2004
	RAG1R2	5' TGAGCCTCCATGAACTTCTGAAGRTAYTT 3'		2nd	López *et al.*, 2004
SH3PX3	F35	5' AAAGYGARAACAAGGAGGAGAT 3'	56	1st	Pers. Comm. C. Li*
	R1373	5' AGCGACAGYTTGTCCARCAT 3'		1st	Pers. Comm. C. Li*
	F532	5' GACGTTCCCATGATGGCWAAAAT 3'	63	2nd	Li *et al.*, 2007
	R1299	5' CATCTCYCCGATGTTCTCGTA 3'		2nd	Li *et al.*, 2007
PLAGL2	F9	5' CCACACACTCYCCACAGAA 3'	58	1st	Li *et al.*, 2007
	R1430	5' TCGTACTGAGGCTRGAGCTGAA 3'		1st	Pers. Comm. C. Li*
	F51	5' AAAAGATGTTTCACCGMAAAGA 3'	63	2nd	Li *et al.*, 2007
	R920	5' GGTATGAGGTAGATCCSAGCTG 3'		2nd	Li *et al.*, 2007

Phylogenetic analysis

The concatenated data matrix of five genes was partitioned by gene and by codon position, producing 15 data blocks. Each of the data blocks was initially optimized independently under a GTR + Γ model implemented in MrBayes, with two million MCMC generations and seven chains (Huelsenbeck and Ronquist, 2001; Nylander *et al.*, 2004; Ronquist and Huelsenbeck, 2003). Following Li *et al.* (2008), the overall similarity among data blocks was evaluated on the basis of their estimated parameter values, counting five substitution rates, three base composition proportions, the gamma parameter (alpha), and the rate multiplier for each data block. Using a hierarchical cluster analysis in SAS, each data partition was used as an observation, with the ten independent parameters estimated from MrBayes as values for each observation. The resulting clustering dendrogram was then used as a guide tree to identify the two most similar data blocks for grouping two partitions and subsequently adding one data block at a time based on overall similarity from the guide tree until only one large data block remained. The AIC values and Bayes Factor have proven that partitioning following the guide tree always resulted in better partitioning scheme than randomly grouping two other partitions (Li *et al.*, 2008). To evaluate the best partitioning scheme, the harmonic means for each MrBayes run was recorded to calculate and compare the harmonic means and Bayes Factor (BF = $(-\ln L_i) - (-\ln L\text{best})$). The optimal partitioning strategy is chosen based on the best ln score (top two among all partitioning schemes for comparison) and with the fewest number of parameters. If there is not much difference between the top two ln scores, the one with a fewer number of parameters estimated and has a fewer number of partition is preferred. The best strategy should also have a 2lnBayes factor of more than 10 between that scheme and the next (stepwise) partitioning scheme. A 2ln Bayes factor of ≥ 10 is strong evidence against the alternative hypothesis (Brandley *et al.*, 2005; Kass and Raftery, 1995; Li *et al.*, 2008). I used MP, ML, and Bayesian analyses to infer phylogeny. The minimal length trees were obtained using a heuristic search and 1000 replicates of random taxon addition with tree-bisection-reconnection (TBR) branch swapping algorithm, saving all trees per replicate. In addition to Bremer support (decay index, Sorensen and Franzosa 2007), relative internal branch support was estimated with bootstrap analysis with 1000 replicates, with TBR branch swapping and simple taxon addition. Tree statistics included the consistency index and retention index. MrModelTest2 (Nylander, 2004) was used to determine the best-fit model for each of the data partitions following the best partitioning scheme, with models scored in PAUP* version 4.0b10 (Swofford, 2002). ML was performed using the partition version of the program Genetic Algorithm for Rapid Likelihood Inference (GARLI; Zwickl 2006), with internal branch support estimated with 100 bootstrap replicates for each of the independent search runs. The repeatability of results (recovering the same best scores and same topologies, with very similar log-likelihood scores, at least twice) across independent search replicates indicates the number of search replicates to be conducted. A total of eight independent search replicates were conducted for this study. Trees were collected and scored using Mesquite (Maddison and Maddison, 2007). MrBayes was also used to estimate the evolutionary parameters using posterior probabilities (Ronquist and Huelsenbeck, 2003). The Markov chain Monte Carlo parameters (MCMC) for the final partitioned dataset included 10 million generations with seven chains sampling every one thousand. Convergence was assessed using Tracer looking at the ESS value for each log-likelihood trace and plotting the posterior probability density for the mutation rate (Rambaut and Drummond, 2007) and AWTY (Are We There Yet?) comparing split frequencies, looking at each independent trajectory, and checking for presence of or absence of splits throughout the chain for each one to make sure that the chains are sampling particularly well (Nylander *et al.*, 2008). Resulting topologies for all analyses were viewed in Mesquite (Maddison and Maddison, 2007) and bootstrap values from MP and ML mapped on the Bayesian topology.

RESULTS

The characteristics of the five mitochondrial and nuclear genes are shown in Appendix B. The concatenated dataset of five loci generated a total of 4731 characters for the 66 taxa included in this study. The dataset was partitioned by gene and by codon position yielding 15 block partitions (5 genes x 3 codon positions). Appendix C shows the ten parameters estimated in MrBayes. These parameters were then employed into a hierarchical cluster analysis in SAS. The output from cluster analysis showing which data block should be grouped based on overall similarity using the ten parameters estimated in MrBayes is shown in Figure 1. The resulting dendrogram from SAS is read from left to right looking at the terminal branches, concatenating data blocks on the first node and then concatenating data blocks on the subsequent nodes, adding one data block at a time. Table 2 also shows how the 15 data blocks down to one data block (no partition) were clustered. Starting with 15 partitions (where all data blocks are treated as separate), the 14-partitioning scheme has (SH3PX3_3 and PLAGL2_3) concatenated as one data block, plus the rest of data blocks (13 other data blocks, each treated as separate). The 13-

partitioning strategy has (SH3PX3_3 and PLAGL2_3) as one data block and (COI_3, CYT*b*_3) as another data block, plus the rest of data blocks (11). Data blocks were concatenated following the dendrogram until only one data block with no partition is left. Boxed text indicates the best partitioning schemes, with 11- and 15- data partitions, chosen by different model selection criteria in this study. Although the 15 data block partitioning scheme is the best partition based on the likelihood scores, it has 40 more parameters than the 11 data block partitioning scheme. Also, the difference between the 11- and 12- partitioning schemes has a value of 42.82, which is more than 10 and satisfies the conventional criterion for choosing the best strategy. Hence the 11-data block partitioning scheme was chosen as the best partitioning strategy (Brandley *et al.*, 2005; Li *et al.*, 2008) in this study (Table 3).

In the limited outgroup comparisons of this study, *Hapalogenys* is sister to *Lobotes*. In addition, the lutjanids are sister to haemulids. A monophyletic Haemulidae, including the former inermiids, is well supported in all analyses (with a Bremer support of 66, bootstrap value of 100 for MP and ML and a posterior probability of 1.0 in Bayesian analysis) (Fig. 2). The phylogenetic position of *Haemulon vittatum* (formerly in *Inermia*) first reported in Rocha *et al.* (2008) is

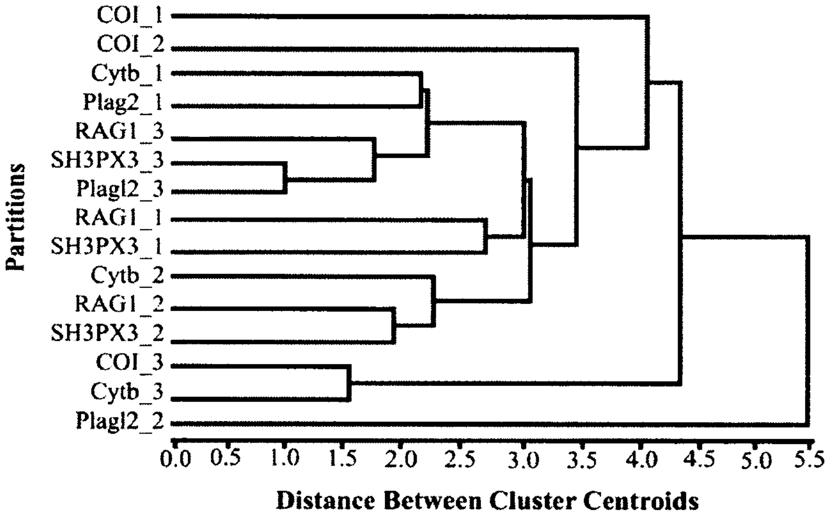


FIGURE 1. Clustering diagram showing overall similarity among 15 data blocks of the full data set (5 genes × 3 codon positions) using SAS. Each block is indicated at the tip of terminal branches by gene name and codon position. Each node shows clustering terminal branches (data set) based on hierarchical clustering algorithm using a Bayesian approach.

TABLE 2. Comparison of log likelihoods and Bayes factors among different partitioning schemes (from one to 15 partitions). Results show the total number of parameters; the harmonic mean of -log likelihood calculated using MrBayes; the Bayes factor calculated by comparing model i to the model with maximum likelihood, BF = (-ln*Li*)- (-ln*L*best); and the clustering of data blocks for each partitioning scheme based on the hierarchical cluster grouping. Boxed text indicates the best partitioning schemes chosen by different model selection criteria. Concatenated data blocks are enclosed in parentheses. S=SH3PX3; P=PLAGL2; R=RAG1; C=COI; Cy=CYT *b*. Numbers (1,2,3) after gene initials refer to codon positions 1, 2, and 3, respectively.

No. of partitions	No. of parameters	Ln	2LnBayes Factor	Data block partition
1	10	-58368.64	233.16	all together
2	20	-58252.06	4483.72	(S3P3R3Cy1P1R1S1R2S2Cy2C2C1C3Cy3) and P2
3	30	-56010.2	144.62	(S3P3R3Cy1P1R1S1R2S2Cy2C2C1)(C3Cy3) and P2
4	40	-55937.89	216.44	(S3P3R3Cy1P1R1S1R2S2Cy2C2)(C3Cy3) and the rest
5	50	-55829.67	466.68	(S3P3R3Cy1P1R1S1R2S2Cy2)(C3Cy3) and the rest
6	60	-55596.33	110.92	(S3P3R3Cy1P1R1S1)(C3Cy3)(R2, S2Cy2) and the rest
7	70	-55540.87	221.58	(S3P3R3Cy1P1)(C3Cy3)(R2S2Cy2)(R1S1) and the rest
8	80	-55430.08	138.16	(S3P3R3Cy1P1)(C3Cy3)(R2S2Cy2) and the rest
9	90	-55361	248.8	(S3P3R3Cy1P1)(C3Cy3)(R2S2) and the rest
10	100	-55236.6	418.44	(S3P3R3)(C3Cy3)(R2S2)(Cy1P1) and the rest
11	110	-55027.38	-145.08	(S3P3R3)(C3Cy3)(R2S2) and the rest
12	120	-55099.92	42.82	(S3P3R3)(C3Cy3) and the rest
13	130	-55078.51	-48.68	(S3P3)(C3Cy3) and the rest
14	140	-55102.85	256.78	(S3P3) and the rest
15	150	-54974.46		all separate

TABLE 3. Models selected by MrModelTest2.0 (Nylander, 2004) under the AIC criterion for the optimal 11-partition scheme for Bayesian analysis, with –lnL values and number of parameters for each data block.

Partition	Data blocks	Model chosen by MrModeltest2.0	-lnL	No. of parameters
1	SH3PX3_3.PLAGL2_3.RAG1_3	GTR+G	11765.64	9
2	COI_3.CYT*b*_3	GTR+I+G	28687.79	10
3	RAG1_2.SH3PX3_2	GTR+I+G	2035.76	10
4	COI_1	GTR+I+G	946.92	10
5	COI_2	F81	350.01	3
6	CYT*b*_1	GTR+I+G	3815.70	10
7	CYT*b*_2	GTR+I+G	1661.82	10
8	RAG1_1	GTR+I+G	2196.07	10
9	SH3PX3_1	JC+G	641.66	1
10	PLAGL2_1	HKY+G	563.80	5
11	PLAGL2_2	F81	460.41	3

confirmed. In addition, *Xenistius californiensis* is also nested within *Haemulon*. *Emmelichthyops* is sister to *Microlepidotus brevipinnis* and these, sister to *Isacia*. These three species are sister to *Orthopristis*.

Two well-supported clades (Bremer support of 56) corresponding to the subfamilies Plectorhinchinae and Haemulinae were recovered in this study (Fig. 2). Within Plectorhinchinae, *Parapristipoma* is sister to a clade containing the members of the genus *Plectorhinchus*, with the inclusion of *Diagramma pictum*. In addition to the *Haemulon* plus *Xenistius* clade noted above, a number of putative haemuline genera appear to be para- and polyphyletic. Species of *Pomadasys* are recovered in three separate clades and the genus is polyphyletic. Within the haemuline assemblage, a clade (*Pomadasys* I) containing *Pomadasys perotaei*, *P. incisus*, and *O. olivaceus* is sister to the rest of the haemulines. Several *Pomadasys*, including *P. striatus*, *P. argyreus*, *P. maculatus*, *P. kaakan*, and *P. stridens* (*Pomadasys* II) plus *Brachydeuterus* were clustered in a separate clade, and is sister to the remaining haemulines. A clade containing additional species of *Pomadasys* (*Pomadasys* III), *Boridia*, *Conodon serrifer*, *Xenichthys*, and *Haemulopsis* and the clade containing species of *Orthopristis*, *Isacia*, *Emmelichthyops*, and *Microlepidotus* is sister to a clade containing *Anisotremus* and *Haemulon*. *Anisotremus* is monophyletic with the inclusion of *Conodon nobilis*. *Conodon*, therefore, is polyphyletic. *Genyatremus* is monophyletic, and the clade containing the three species included in this genus was also recovered by a recent morphological analysis (Tavera *et al.*, 2011), albeit branch ordering within the clade is different.

DISCUSSION

The interrelationships of haemulids

Previous molecular studies on higher-level percomorphs and acanthomorphs have shown possible outgroups for haemulids but did not provide morphological evidence to support their relationship. The outgroup sampling for this study is not exhaustive and obviates definitive statements about sister taxa of the Haemulidae. However, my results do confirm recent conclusions that *Hapalogenys* is not a member of the Haemulidae (Ren and Zhang, 2007; Springer and Raasch, 1995). The presence of short barbels or furlike papillae on the chins of hapalogenyids and antrorse spine before the first dorsal fin spine separate them from the haemulids. There is also some support (a clade supported by a decay index of 4, 100% bootstrap for MP and ML and a posterior probability of 1.0 for Bayesian analysis) that *Lobotes* may be

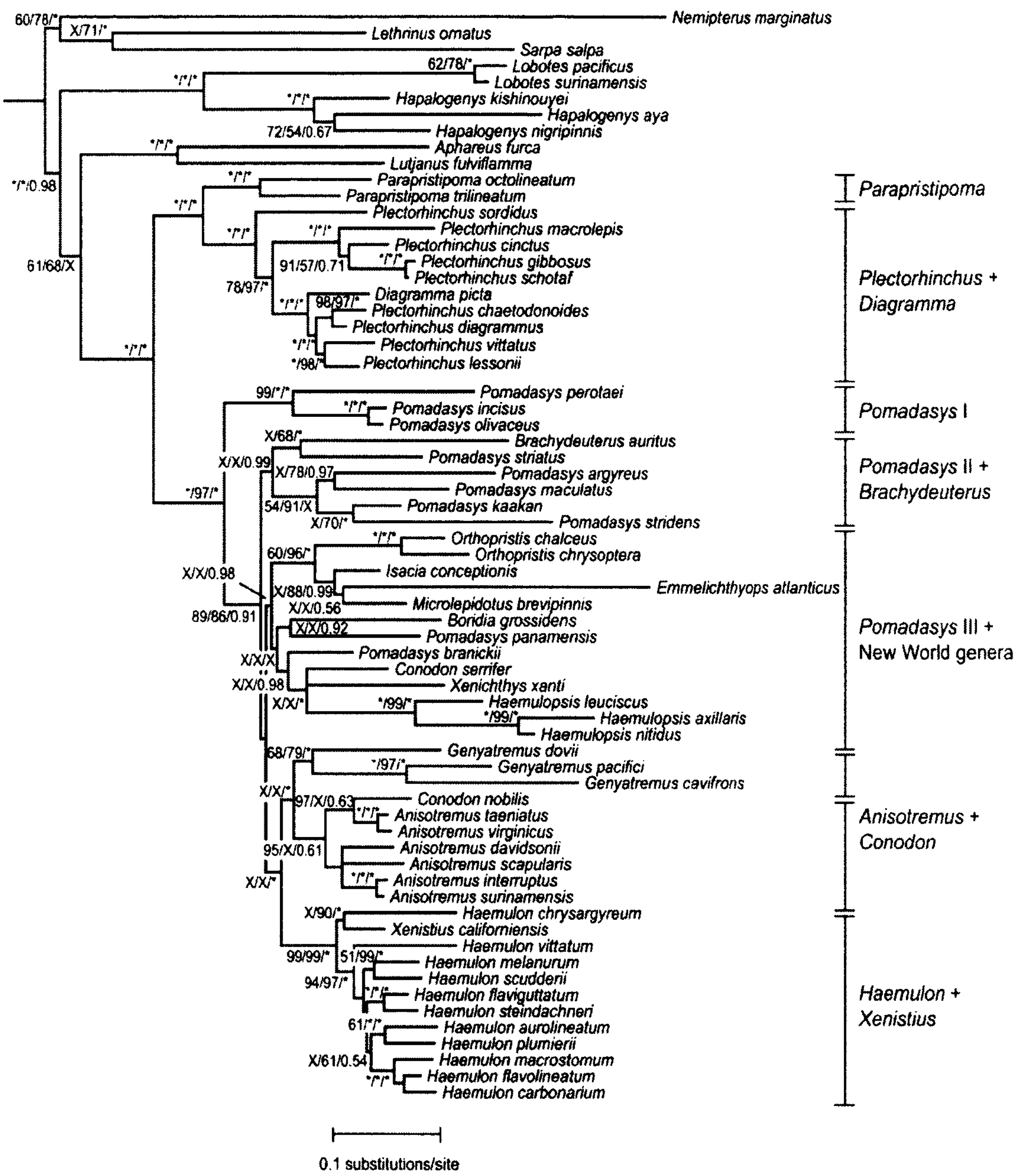


FIGURE 2. The tree represents a 50% majority rule consensus of the Bayesian topology (numbers represent the posterior probability of the clades), with bootstrap values from MP and ML mapped onto the topology. MP, ML, and Bayesian analyses produced similar topologies (MP: TL = 12,869, consistency index CI = 0.2372, retention index RI = 0.4450; ML: Ln Likelihood = -54309.4503) with differences mostly on nodes with low bootstrap support. The numbers on branches are MP and ML bootstrap values and posterior probabilities from Bayesian analysis, respectively. Asterisks indicate a bootstrap value of 100% for MP and ML and 1.0 for Bayesian analysis. Nodes with less than 50% bootstrap value are marked with an X if the clade had less than 50% support in any of the MP, ML, or Bayesian analyses.

sister to *Hapalogenys* (Fig. 2) based on the molecular data and some morphological characters such as the rounded shape of the caudal fin, absence of distinct canines on palatine and vomer, and the presence of more than six sensory pores on the chin. The possession of sensory chin pores, however, does not appear to be a synapomorphy for haemulids plus *Hapalogenys* and *Lobotes*, since my analysis recovers lutjanids as sister to haemulids. More comprehensive taxon sampling of perciform fishes is required to further test this relationship.

The intrarelationships within haemulids

The monophyly of Haemulidae is only well supported if the former inermiids are included. The placement of this species within Haemulidae is not surprising given the many synapomorphies that are shared among them. Johnson (1981) presented a list of shared meristic and osteological characters between "inermiids" and haemulids and also noted the differences between them, most notably the highly protrusible jaws of *Haemulon vittatum* (formerly *Inermia vittata*) and *Emmelichthyops atlanticus*. He noted that the neurocranium bears little resemblance to the typical haemuloid type, which gives way to its modification for the reception of the extremely long ascending processs of the premaxillary, which is a specialization for planktivory. He believed that this degree of morphological and ecological divergence from other haemulids warrants familial recognition. Rocha *et al.* (2008) recovered *Inermia vittata* nested within *Haemulon* and proposed that *Inermia* should be recognized as *Haemulon vittatum* based on both cladistic pattern and genetic sequence divergence. They further hypothesized that the disparity in external morphology between *Haemulon* and *Inermia* can be attributed to the morphological specializations brought about by rapid ecological shifts. The specialization to plankton feeding is also seen in other haemulines, such as in some species of *Anisotremus, Orthopristis, Pomadasys, Haemulon,* and *Xenistius*, although these genera do not possess a highly specialized jaw similar to that of *Haemulon vittatum* and *Emmelichthyops*. Similarly, *Emmelichthyops* appears to have adapted to planktivory. However, unlike *Haemulon vittatum* (which is nested deep within the well-supported genus *Haemulon*), *Emmelichthyops* is on a long branch within a poorly supported clade (low bootstrap, posterior probability, and Bremer support) that includes *Isacia, Microlepidotus,* and *Orthopristis* (Fig. 2). A more precise phylogenetic placement for this species will require exhaustive sampling in the *Orthopristis-Haemulopsis* clade and rigorous morphological comparisons. This study supports the hypothesis by Rocha *et al.* (2008) of the placement of *Haemulon vittatum* and also now provides molecular evidence for the placement of *Emmelichthyops* in Haemulidae. It is important to note that the placement of these two species in the subfamily Haemulinae is also supported by the following morphological characters: two chin pores and low vertebral, pleural, and epipleural rib counts. Therefore, it is recommended that the family Inermiidae should no longer be treated as valid.

The morphological basis for Haemulinae and Plectorhinchinae (Johnson, 1981) is also corroborated by my molecular analyses. The Plectorhinchinae recovered here includes well-supported clades (Bremer support of at least 12 and high bootstrap and posterior probability) for all species of *Parapristipoma* and *Plectorhinchus*. However, the paraphyletic *Plectorhinchus* includes *Diagramma*. These two genera are very similar in appearance externally and differ mostly in dorsal-fin ray counts, scale counts, and shape of the swimbladder (McKay, 2001; Smith, 1962). Final disposition of species within the clade containing all *Plectorhinchus*, including *Diagramma*, should await a more exhaustive sampling of these species and re-examination of morphological characters. It is interesting to note that the colorful Indo-Pacific coral reef *Plectorhinchus* + *Diagramma* form a clade within a clade that includes mostly drab species, including the only member of this group found in the Atlantic.

The clades recovered within the Haemulinae call into question the monophyly of a number of genera (Fig. 2). *Pomadasys* is polyphyletic and found in three separate clades that correspond roughly to different biogeographic regions. Haemulinae clade I is composed of *Pomadasys* found in the eastern Atlantic (although one is also found in the Indian Ocean). Clade II is composed of *Pomadasys* from the Indo-West Pacific and the eastern Atlantic *Brachydeuterus*. Clade III includes only species found in the Americas (New World): two eastern Pacific *Pomadasys* plus eastern Pacific/western Atlantic *Orthopristis*, eastern Pacific *Isacia*, *Haemulopsis*, *Xenichthys*, *Microlepidotus* and *Conodon*, and the western Atlantic *Boridia*. If new morphological information corroborates the polyphyly of *Pomadasys*, this and the other genera in these basal haemuline clades will need to be reclassified. The distinct or nearly distinct geographic distribution of these clades suggests interesting biogeographical relationships that warrant further study.

Two haemulid clades are confined to the New World and are composed primarily of *Haemulon* and *Anisotremus*. As noted above, the *Haemulon* clade is paraphyletic with the inclusion of *Xenistius californiensis*. Jordan and Gilbert (1882) diagnosed *X. californiensis* using several meristic and anatomical characters such as having an oblong body; a moderate, very oblique terminal mouth, with the lower jaw strongly protruding; soft parts of vertical fins densely scaled; the two dorsal fins are almost separate; caudal fin forked; and most notably, having the soft dorsal fin shorter than the spinous dorsal fin and composed of 11 or 12 rays and anal fins also short, with second and third anal spines high. These characters are also diagnostic of the members of the genus *Haemulon* (Courtenay, 1961). The recognition of *Xenistius* under *Haemulon* is supported by my independent and combined analyses of five genes (MP, ML, and Bayesian) and I conclude that *X. californiensis* should be treated as *Haemulon californiensis*.

Similarly, the limits of genera within the *'Anisotremus'* clade also need to be redefined. *Anisotremus* was erected without morphological justification (Gill, 1861) by monotypy (Eschmeyer, 1990) and subsequently recognized to encompass other high-bodied haemulids with black bars (Lindeman and Toxey, 2003; McKay and Schneider, 1995). The molecular analysis appears to support this ill-defined genus with the inclusion of *Conodon nobilis*. Here I follow the taxonomic suggestions of Tavera *et al.* (2011) and classify the former *Anisotremus dovii* and *A. pacifici* in the genus *Genyatremus*. I also use the name *Genyatremus cavifrons* to refer to the species historically identified as *G. luteus*, as suggested by Tavera *et al.* (2011). The molecular and morphological evidence indicates that further comprehensive examination of osteological and other morphological characters of the members of this clade may result in a revision of generic assignments. The monophyly of *Conodon* is also rejected in this study. *Conodon nobilis*, inhabiting the western Atlantic, is clustered within the *Anisotremus* clade as noted above while *C. serrifer* is clustered together in a clade with eastern Pacific species, including *Xenichthys xanti*, *Haemulopsis leuciscus*, *H. axillaris,* and *H. nitidus*. Aiming to avoid future reversals, I defer taxonomic rearrangement of these genera to a future study with better taxon sampling and a more detailed morphological analysis.

The current study presents the first nearly comprehensive phylogenetic hypothesis of haemulid genera. The monophyly of the family and subfamilies and distinct clades within the subfamilies are well supported in all analyses (Bremer support of 56, bootstrap values above 95% and posterior probability of 1.0). This phylogeny calls into question the validity of some haemulid genera and leaves a number of other questions unanswered. The placement of *Xenocys* and *Parakuhlia* within the Haemulidae remains unresolved until specimens become available. However, morphology indicates that their subfamilial designation is Haemulinae. Defining the limits and relationships of the questionable genera will require detailed morphological examination to test and refine the current phylogenetic hypothesis. The molecular data largely corroborate the morphological data that define the family, subfamilies, and some genera. It also appears that the specialization to "extreme" planktivory evolved separately in some haemulines. A closer examination of the feeding apparatus of the "inermiids" may uncover fundamental differences that support alternative sister-species relationships. Detailed morphological examinations are warranted given the results of this study, as are more tests that may help shed light on the biogeographical history of the Haemulidae.

CHAPTER III

A PHYLOGENETIC HYPOTHESIS OF PERCOMORPH FISHES TO DETERMINE THE OUTGROUP OF THE HAEMULIDAE

INTRODUCTION

Percomorph fishes are one of the nine major radiations of jawed vertebrates (Alfaro *et al.*, 2009), including about 55% (>17,000 species) of extant teleost diversity (Betancur-R *et al.*, 2013a; Friedman, 2010; Johnson and Patterson, 1993; Near *et al.*, 2013; Nelson, 1989; Nelson, 2006). Percomorphs have come to be known as the "bush at the top"(Nelson, 1989) of the fish tree of life due to their historical lack of phylogenetic resolution. The Perciformes (perch-like fishes) is the most species-rich order of percomorphs and the largest order of vertebrates. For a long time, the Perciformes has been regarded as a non-monophyletic "wastebasket" (Nelson, 2006; Wiley and Johnson, 2010), with at least 160 families and 20 suborders of dubious phylogenetic integrity placed within the order (Johnson, 1984; Nelson, 2006; Wiley and Johnson, 2010). Several studies using either morphological or molecular data have hypothesized Perciformes as either a para- or polyphyletic group (Chen *et al.*, 2003; Dettai and Lecointre, 2005; Johnson and Patterson, 1993; Lauder and Liem, 1983; Lautredou *et al.*, 2013; Li *et al.*, 2009; Li *et al.*, 2008; Mahon, 2007; Miya *et al.*, 2003; Nelson, 2006; Smith and Craig, 2007; Wiley and Johnson, 2010). Johnson and Patterson (1993) considered that the Perciformes may be monophyletic but only if its taxonomic limits are expanded to include members of the Scorpaeniformes (mail-cheeked fishes), Pleuronectiformes (flatfishes), and Tetraodontiformes (plectognaths). Springer and Johnson (2004) suggested that the plectognaths (including Caproidei) are "pre-perciforms" lineages, whereas Nelson (2006) noted that flatfishes and plectognaths are probably perciform derivatives. Li *et al.* (2008) and Li *et al.* (2009) recovered a polyphyletic Perciformes, in which traditionally-assigned perciform taxa are placed close to the Lophiiformes (anglerfishes), Gasterosteiformes (sticklebacks), Scorpaeniformes, and Mugiliformes (mullets). Wiley and Johnson (2010) also noted the non-monophyly of "Perciformes," but erected monophyletic orders based on morphology for many of the suborders formerly included within the Perciformes *sensu lato*. They also placed the diversity of percomorphs, comprised of Pleuronectiformes, Tetraodontiformes, Lophiiformes, Batrachoidiformes (toadfishes), and Ophidiiformes (cusk-eels), in the division Percomorphacea (formerly Percomorpha). Wiley and Johnson (2010) proposed that Perciformes *sensu stricto* should only include the groups (formerly) placed in the suborder Percoidei (*sensu* Nelson 2006), but provided no evidence for its monophyly.

Percoidei (*sensu* Nelson 2006), the largest perciform suborder, is also notorious for the lack of synapomorphies and resolution among higher-level percomorphs (Johnson, 1984; Nelson, 2006). Regan (1913) defined Percoidei by the absence of special peculiarities that characterize other perciform suborders. Johnson (1984) identified two artificial groupings for percoids: the "basal," or more generalized percoids, and the remaining percoids based on the modifications of the cranial bones in addition to opercular and pectoral series spination. His more generalized percoids include Acropomatidae (lanternbellies), Gerreidae (mojarras), Girellidae, Haemulidae (grunts), Kyphosidae (sea chubs), Sciaenidae (drums and croakers), halfmoons, Sparidae (porgies), and Teraponidae (tigerperches), a group that he also considered to be "more primitive" among a large subgroup of percoid families.

Recently, Smith and Craig (2007), based on 4036 bp of combined mitochondrial and nuclear sequences from a broad array of percomorph taxa, noted that there is no phylogenetic distinction between Perciformes, Percoidei, and Percomorpha because "percoids" are spread throughout the Percomorpha (*sensu* Johnson and Patterson 1993). According to Smith and Craig, members of the Percoidei are placed among lineages of Perciformes, Pleuronectiformes, and Tetraodontiformes, including representatives of Atherinomorpha, Gasterosteiformes, and Scorpaeniformes (Smith and Craig, 2007). Dettai and Lecointre (2005) and Li *et al.* (2009) also obtained percoids in multiple clades together with members of scorpaenids, trachinoids, and ophidiiforms, and emphasized the need for broad-scale taxonomic sampling to resolve percoids, especially for members of dubious morphological affinity. Smith and Craig (2007) proposed a revision for Nelson's (2006) percoid taxonomy by removing Percidae from Percoidei and Trachinidae from Trachinoidei, and by creating a new non-monophyletic 'wastebasket' suborder, the Moronoidei. In the scheme presented by Smith and Craig (2007), Percoidei is the clade stemming from the most recent common ancestor of *Acanthistius*, *Bembrops*, *Bovichthys*, *Etheostoma*, *Harpagifer*, *Niphon*, *Notothenia*, *Perca*, and *Sander*, which is diagnosed by the loss of suborbital stay, the presence of a caudal fin hypurapophysis, and a laterally expanded and posteriorly flattened post-pelvic process (Smith, 2005). Moronoidei is treated as the node-based definition of the clade stemming from the most recent common ancestor of *Morone* and *Polyprion*, and comprise all other taxa excluded from Percoidei *sensu lato*.

More recently, a broad-scale phylogenetic study of bony fishes by the Euteleost Tree of Life (EToL) project examined 21 genetic markers and 1410 taxa in 369 families (Betancur-R *et al.*, 2013a). This study proposed a revised classification of fishes based on molecular data, erecting nine well-supported series under the subdivision Percomorphaceae (Betancur-R *et al.*, 2013a; Betancur-R *et al.*, 2013c). These series include the cusk eels (Ophidiimorpharia, with one order); toadfishes (Batrachoidimorpharia, with one order); kurtids, apogonids, and gobioids (Gobiomorpharia, with two orders); seahorses, pipefishes, gurnards, goatfishes and allies (Syngnathimorpharia, with one order); tunas, mackerels, butterfishes, and allies (Pelagimorpharia, with one order); armored sticklebacks, gouramies, and snakeheads (Anabantomorpharia, with two orders); billfishes, threadfins, jacks, snooks, flatfishes, and allies (Carangimorpharia, with three orders); cichlids, blennies, needlefishes, killifishes, silversides, mullets, and allies (Ovalentaria, with seven orders); and the new "bush at the top," the Percomorpharia, with 11 orders including Perciformes. The new circumscription of Perciformes is putatively monophyletic, comprising 38 families, but 49 families that were not examined were also tentatively included, for a total of 87 families, compared to Nelson's 160 families in this order (Betancur-R *et al.*, 2013a). Previous molecular studies have also included members of these major clades, in combination with other representatives, as well as with different sets of markers (Betancur-R *et al.*, 2013b; Betancur-R and Orti, 2014; Campbell *et al.*, 2013; Chen *et al.*, 2003; Dettai *et al.*, 2004; Dettai and Lecointre, 2005; Kawahara *et al.*, 2008; Li *et al.*, 2009; Li *et al.*, 2011; Miya *et al.*, 2013; Miya *et al.*, 2001; Miya *et al.*, 2005; Miya *et al.*, 2003; Near *et al.*, 2012a; Near *et al.*, 2012b; Thacker, 2009; Wainwright *et al.*, 2012).

Despite significant progress made in accommodating the diversity of percomorph taxa into major clades, phylogenetic resolution within the newly discovered groups is weak and at least five of these are rapid radiations characterized by short basal internodes that require additional study. Betancur-R *et al.* (2013a) also presented a revised time-scale of bony fish evolution based on 60 calibration points, with all major lineages in Percormorphaceae originating between 132 Ma (million years ago) and 82 Ma, before the end of the Cretaceous. More recently, Near *et al.* (2013) published a phylogeny of 579 (mostly acanthomorph) taxa based on a subset of the EToL markers. Their results are largely congruent with those obtained by Betancur-R *et al.* (2013a), although Near *et al.* (2013) chose to delimit 14 percomorph clades instead of nine. It is noteworthy that Near *et al.* (2013) examined 25 families not included in the global EToL phylogeny, many of which had enigmatic phylogenetic status (e.g., Banjosidae, Callanthiidae, Cepolidae, Ostracoberycidae, Pentacerotidae). Problems still exist, however, regarding the classification of several families not included in these studies and those with uncertain placement in the global fish tree.

There are two main goals in this study that will help better define the close relatives of the Haemulidae. First, I investigate the position of eight families that, to the best of my knowledge, have never been included in any large-scale analysis of the percomorphs and provide a more comprehensive framework for defining interfamilial relationships within the percomorphs. These include the marblefishes (Aplodactylidae), bathyclupeids (Bathyclupeidae), picarel porgies (Centracanthidae), kelpfishes (Chironemidae), galjoen fishes (Dichistiidae), barbeled grunters (Hapalogenyidae), trumpeters (Latridae), and slopefishes (Symphysanodontidae). Second, I augment the familial diversity of the EToL dataset by adding families (e.g., lactariids, arripids) that were previously not examined by Betancur-R *et al.* (2013a), but that have been included in other recent molecular studies on percomorphs, albeit with a much smaller taxonomic representation. I expand the taxonomic sampling to incorporate representatives from families from the more recent studies to increase generic and species-level resolution of the global fish tree, but restrict the sampling to only the percomorphs plus selected outgroups. In addition to the EToL markers previously employed, I used two additional fast-evolving mitochondrial genes, COI (cytochrome oxidase I) and CYT *b* (cytochrome *b*), in order to account for the rapid percomorph radiations.

MATERIALS AND METHODS

Phylogenetic Data and Analyses

I restricted the taxonomic sampling to include only percomorph taxa from the global fish dataset (Betancur-R *et al.*, 2013a) and added 51 species for a total of 1231 unique species for this study (Appendix D). For the additional species, I used fresh samples collected from expeditions, bought from fish markets, or gifts from the Ichthyology Collection at University of Kansas and other museums. In addition to determining the placement of new taxa in the expanded percomorph dataset, I investigated the effects of adding new markers in the analysis. I included all the percomorph sequences from the 21-gene dataset and added two additional rapidly evolving mtDNA genes, 815 COI and 388 CYT *b*, for a total of 1203 additional mtDNA sequences (Table 4). These mtDNA sequences were newly generated, collected from previous studies (Sanciangco *et al.*, 2011), or retrieved from NCBI database. DNA isolation, amplification via nested PCR (see Table 4 for list of primers), sequencing, sequence alignment, and phylogenetic analyses were followed from previous studies (Betancur-R *et al.*, 2013a; Sanciangco *et al.*, 2011). I used SequenceMatrix v1.7.8 (Vaidya *et al.*, 2011) and Geneious (Biomatters, 2013) to concatenate individual gene sequences. The final dataset is a concatenation of 1231 taxa from three genes or more plus *Symphysanodon*, which only had two genes sequenced. The dataset has eight partitions, which include three codon positions across all exons for the nuclear genes, three codon positions across all exons for the mitochondrial genes, plus 16S and hoxc6a. I performed rapid bootstrapping algorithm for RAxML (Randomized Axelerated Maximum Likelihood) using 1000 replicates estimated under the GTRCAT model, with the collection of sample trees used to draw the bipartition frequencies on the optimal tree. I performed all RAxML analyses via CIPRES portal v3.1.

RESULTS AND DISCUSSION

The final dataset is a concatenated alignment of 23 genes and is 44.70% complete (presence of sequence for a particular gene) for 1231 perciforms, including an outgroup (*Hoplostethus occidentalis atlanticus*, F. Trachichthyidae, O. Beryciformes). The results of the RAxML analysis (Appendix E) are largely concordant with the results of the two recent fish phylogenies (Betancur-R *et al.*, 2013a; Near *et al.*, 2013). I recovered consistent placement for all major groups, with similar clade components. However, I also found some disparities. Figures 3 to 8 provide higher-resolution versions of Appendix E for the target groups (new additions). I recognize the classification of Betancur-R *et al.* (2013a) for the nine highly supported supraordinal groups for Percomorphaceae. I present the new findings below starting from the most basal taxa to the most apical groups in the percomorph tree.

TABLE 4. List of PCR sequence primers for the percormorph dataset adapted from previous studies.

Gene	Description	Primer name	Primer sequence	Reference
16S	16S rRNA	16sAR	CGCCTGTTTATCAAAAACAT	Betancur-R *et al.* 2013; Cooper *et al.* 2009
		16sBR	CGCGTCTGAACTCAGATCACGT	Betancur-R *et al.* 2013; Cooper *et al.* 2009
COI	Cytochrome oxidase I	CO1LBC_F	TCAACYAATCAYAAAGATATYGGCAC	Ward *et al.* 2005
		CO1HBC_R	ACTTCYGGGTGRCCRAARAATCA	Ward *et al.* 2005
CYT *b*	Cytochrome b	CYT *b*_UniF	CGAACGTTGATATGAAAAACCATCGT	Orrell *et al.* 2002
		CYT *b*_UniR	ATCTTCGGTTTACAAGACCGGTG	Orrell *et al.* 2002
ENC1	Gene for peroxisomal enoyl-CoA hydratase/L-3-hydroxyacyl-CoA dehydrogenase	ENC1_F85	GACATGCTGGAGTTTCAGGA	Li *et al.* 2007
		ENC1_R982	ACTTGTTRGCMACTGGGTCAAA	Li *et al.* 2007
		ENC1_F88	ATGCTGGAGTTTCAGGACAT	Li *et al.* 2007
		ENC1_R975	AGCMACTGGGTCAAACTGCTC	Li *et al.* 2007
FICD	FIC domain	ficd_F166	GTSGTCCARGCGGAYCACCTCTA	Li *et al.* 2011
		ficd_R965	GTGCATTTGGCKATRAATCGRA	Li *et al.* 2011
		ficd_F169	GTCCARGCGGAYCACCTCTACA	Li *et al.* 2011
		ficd_R965	GTGCATTTGGCKATRAATCGRA	Li *et al.* 2011
		ficd_F186	CTACACTAARGCCYTSGCCATCTC	Li *et al.* 2011
		ficd_R941	AAGGGTCGAACRTCSCCCTCRTT	Li *et al.* 2011
GLYT	Glycosyltransferase-like domain containing 2	Glyt_F559	GGACTGTCMAAGATGACCACMT	Li *et al.* 2007
		Glyt_R1562	CCCAAGAGGTTCTTGTTRAAGAT	Li *et al.* 2007
HOX	Homeo box C6a	hoxc6a_F215	ATGGATCAAACGTGTTTCTTCA	Betancur-R *et al.* 2013
		hoxc6a_R1129	GCGATYTCGATGCGTCTGCG	Betancur-R *et al.* 2013
		hoxc6a_F386	GATCTACCCGTGGATGCAGCG	Betancur-R *et al.* 2013
KIAA1239	Leucine-rich repeat and WD repeat-containing protein, KIAA1239-like	KIAA2013_F41	CCAGYCGAACAGTSAACAACACCCT	Li *et al.* 2010
		KIAA2013_R829	CGGGTCCRCAGTACTCRTTGTA	Li *et al.* 2010
		KIAA2013_F49	ACAGTSAACAACACCCTSTACTACAT	Li *et al.* 2010

Table 4. *Continued*

Gene	**Description**	**Primer name**	**Primer sequence**	**Reference**
		KIAA2013_R801	TTTGAAGAGGAASAARTGGAAGAG	Li *et al.* 2010
MYH6	Myosin, heavy polypeptide 6	myh6_F459	CATMTTYTCCATCTCAGATAATGC	Li *et al.* 2007
		myh6_R1325	ATTCTCACCACCATCCAGTTGAA	Li *et al.* 2007
		myh6_F507	GGAGAATCARTCKGTGCTCATCA	Li *et al.* 2007
		myh6_R1322	CTCACCACCATCCAGTTGAACAT	Li *et al.* 2007
PANX2	Pannexin 2			Broughton *et al.* 2013
PLAGL2	Pleiomorphic adenoma genelike 2	PLAGL2_F9	CCACACACTCYCCACAGAA	Li *et al.* 2007
		PLAGL2_R1430	TCGTACTGAGGCTRGAGCTGAA	Pers. Comm. C. Li*
		PLAGL2_F51	AAAAGATGTTTCACCGMAAAGA	Li *et al.* 2007
		PLAGL2_R920	GGTATGAGGTAGATCCSAGCTG	Li *et al.* 2007
PTCHD1 (PTR)	Patched domain containing 4	Ptr_F458	AGAATGGATWACCAACACYTACG	Li *et al.* 2007
		Ptr_R1248	TAAGGCACAGGATTGAGATGCT	Li *et al.* 2007
		Ptr_F463	GGATAACCAACACYTACGTCAA	Li *et al.* 2007
		Ptr_R1242	ACAGGATTGAGATGCTGTCCA	Li *et al.* 2007
RAG1	Recombination activating gene 1	RAG1_2510F	TGGCCATCCGGGTMAACAC	Li and Orti 2007
		RAG1_RAG1R1	CTGAGTCCTTGTGAGCTTCCATRAAYTT	López *et al.* 2004
		RAG1_RAG1F1	CTGAGCTGCAGTCAGTACCATAAGATGT	López *et al.* 2004
		RAG1_RAG1R2	TGAGCCTCCATGAACTTCTGAAGRTAYTT	López *et al.* 2004
RAG2	Recombination activating gene 2	Rag2_Damsel_R2	TCTGCCCTGCARAAGCTCRA	Cooper *et al.* 2009
		Rag2_F1	GAGGGCCATCTCCTTCTCCAA	Cooper *et al.* 2009
		Rag2_F2	GACTGTCCTCCTCAGGTGTTC	Cooper *et al.* 2009
		Rag2_R2	GTCTGTAGAGTCTCACAGGAGAGCA	Cooper *et al.* 2009
		Rag2_R3	GATGGCCTTCCCTCTGTGGGTAC	Cooper *et al.* 2009
RH	Rhodopsin			Betancur-R *et al.* 2013; Cooper *et al.* 2009
RIPK4	Receptor-interacting serinethreonine kinase 4	F57	GCCAAGTTGATGAAGATCCTVCAG	Li *et al.* 2011
		R880	ACAGTYAARATGCTGATAGAAGAGGG	Li *et al.* 2011
		F65	GATGAAGATCCTVCAGCCTCA	Li *et al.* 2011

Table 4. *Continued*

Gene	**Description**	**Primer name**	**Primer sequence**	**Reference**
		R766	CACACCAGCACYTCTCGTCT	Li *et al.* 2011
SH3PX3	Sorting nexin 3; similar to SH3 and PX domain containing 3 gene	SH3PX3_F35	AAAGYGARAACAAGGAGGAGAT	Pers. Comm. C. Li*
		SH3PX3_R1373	AGCGACAGYTTGTCCARCAT	Pers. Comm. C. Li*
		SH3PX3_F532	GACGTTCCCATGATGGCWAAAAT	Li *et al.* 2007
		SH3PX3_R1299	CATCTCYCCGATGTTCTCGTA	Li *et al.* 2007
SIDKEY	si:dkey-174m14.3	F116	CGGATGARGYCTGCAGCAG	Li *et al.* 2010
		R1360	ACAGTCTGACMAARGCCCAGC	Li *et al.* 2010
		F247	GACCTSTACAGCAGYGACAC	Li *et al.* 2010
		R1355	AAGGACAGTCTGACMAAGGC	Li *et al.* 2010
SREB2	G protein-coupled receptor 85	sreb2_F10	ATGGCGAACTAYAGCCATGC	Li *et al.* 2007
		sreb2_R1094	CTGGATTTTCTGCAGTASAGGAG	Li *et al.* 2007
		sreb2_F27	TGCAGGGGACCACAMCAT	Li *et al.* 2007
		*sreb2*_R1082	CAGTASAGGAGCGTGGTGCT	Li *et al.* 2007
SVEP1	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	svep1_F7960	CCTCCNCAYATYGAYTTTGGDGAMTA	Betancur-R *et al.* 2013
		svep1_R8889	TTCAGGWARCCRTGRCTRATRTCCTC	Betancur-R *et al.* 2013
TBR1	T-box, brain, 1b	tbr1_F1	TGTCTACACAGGCTGCGACAT	Li *et al.* 2007
		tbr1_R820	GATGTCCTTRGWGCAGTTTTT	Li *et al.* 2007
		tbr1_F86	GCCATGMCTGGYTCTTTCCT	Li *et al.* 2007
		tbr1_R811	GGAGCAGTTTTTCTCRCATTC	Li *et al.* 2007
VCPIP	Valosin-containing protein p97/p47 complete interacting protein 1	vcpip_F84	CCGGACCCGMARTGYCAGGC	Betancur-R *et al.* 2013
		vcpip_R946	GTGRTTBCKGCYVGAGCTGCTCCABGC	Betancur-R *et al.* 2013
		vcpip_F134	AGCATYGAGTGCACSGASTGCGGMCA	Betancur-R *et al.* 2013
		vcpip_R930	CTGCTCCASGCRATGCAKATGGGYTTG	Betancur-R *et al.* 2013
ZIC1	Zic family member 1	zic1_F9	GGACGCAGGACCGCARTAYC	Li *et al.* 2007
		zic1_R967	CTGTGTGTGTCCTTTTGTGRATYTT	Li *et al.* 2007
		zic1_F16	GGACCGCAGTATCCCACYMT	Li *et al.* 2007
		zic1_R963	GTGTGTCCTTTTGTGAATTTTYAGRT	Li *et al.* 2007

Arripididae: Pelagimorpharia

One of the families not included in the two most recent euteleostean phylogenies (Betancur-R *et al.*, 2013a; Near *et al.*, 2013) is the enigmatic family Arripididae (Australasian salmons or kahawais). The family is comprised of a single genus, *Arripis*, with four putative species, *A. georgianus*, *A. trutta*, *A. truttacea*, and *A. xylabion* (Paulin, 1993). Previous studies regarding the taxonomic classification and relations of the family are very few and have been controversial (Miya *et al.*, 2013; Paulin, 1993; Yagishita *et al.*, 2002; Yagishita *et al.*, 2009). Gill (1893a) was the first to recognize the family as distinct, but also included *Emmelichthys nitidus* (now in Emmelichthyidae) in the group. Subsequent studies have used the nomenclature Arripidae to refer to the group; however, Paulin (1993) indicated that the spelling is incorrect (Steyskal, 1980). Following Steyskal (1980), the basonym *–is* is of feminine gender and has the genitive in *–idis* in its stem, and, therefore, should follow *–id–* since the Greek lexicon of the genus name is *Arripis*. More than 80 years after the family was first recognized, MacDonald (1983), in an unpublished dissertation, provided the preliminary hypothesis regarding the interrelationships within the family based on allozyme markers. Accordingly, he recovered *A. trutta* and *A. truttaceus* as sister-species, and the two, sister to *A. georgianus*. *A. xylabion* was described in 1993, and therefore, was not included at the time (Paulin, 1993). Johnson and Fritzsche (1989) included one of the four species, *A. georgianus*, and some other percoids as outgroups to test the sister-group relationship between the nibblers, *Graus* and *Girella* (Family Kyphosidae, Subfamily Girellinae). Their choice of outgroups is based on Freihofer's (1963) morphological study, suggesting a close relationship between scorpidids (halfmoons), kyphosids (rudderfishes), girellids (nibblers), oplegnathiods (knifejaws), microcanthids, arripids, kuhliids (flagtails), teraponids (tigerperches), pomatomids (bluefishes), nemastistiids (roosterfishes), and several additional families belonging to Stromateoidea. Freihofer (1963) hypothesized that these groups form a natural assemblage by sharing the unique pattern 10 of the ramus lateralis accessorius nerve (RLA), a feature which he described. Freihofer's description of 17 principal patterns of RLA (with marked disparity exemplified by percomorphs) can be defined according to the intra– and extracranial course of the nerve, its relationships with various bones, and its ultimate peripheral distribution to gustatory organs on the head and fins (Freihofer, 1963; Greenwood, 1964). Accordingly, in RLA pattern 10, the orbito-pectoral branch (RLA-OP) reaches the pectoral girdle by passing directly posteriorly from the sphenotic to the posttemporal-supracleithral joint, without crossing medially beneath the pteroic, lateral tabular, and posttemporal, and lying just beneath the skin overlying the levator arcus palatini and dilator and the levator opercula muscles (Johnson and Fritzsche, 1989). In their morphological examination of the above groups, Johnson and Fritzsche (1989) concurred with Freihofer's hypothesis that RLA pattern 10 characterizes a natural assemblage. In an effort to evaluate the RLA pattern 10's usefulness as a phylogenetic marker within the percomorphs, Yagishita *et al.* (2009) analyzed the mitogenome sequences of 13 species, including *A. trutta* plus outgroups, exhibiting RLA pattern 10. They proposed two lineages for species with RLA pattern 10 and at least two independent origins for the character. Interestingly, they recovered a highly supported monophyletic clade comprising of Arripididae, Stromateoidei, and Scombridae.

The close relationship among the arripids, stromateoids, and scombrids has been implied by Yagishita *et al.* (2002) in a previous study, which included *A. georgianus*; however, support for the group was weak (59% bootstrap support, BS). Yagishita *et al.* (2009) further noted that this morphologically diverse group is comprised of pelagic dwellers and are often associated with long distance migrations. Miya *et al.* (2013) used this premise to test evolutionary origins of scombrids and recovered a well-supported monophyletic clade containing all pelagic members, including *A. trutta*, aptly termed Pelagia. In the present study, I was able to include all three species investigated in the initial allozyme study and found the results to be consistent with MacDonald's (1983), placing *A. trutta* and *A. truttacea* as sister-species, and this, sister to *A. georgianus*. My results (Fig. 3) also corroborate the findings of Yagishita *et al.* (2002), Yagishita *et al.* (2009), and Miya *et al.* (2013), placing Arripididae with the pelagic dwellers, scombroids and putative relatives (Pomatomidae and Scombrolabracidae) plus non-scombroid families Bramidae, Chiasmodontids, Icosteidae, Centrolophidae, Nomeidae, Stromateidae, Caristiidae, Ariommatidae, and Tetragonuridae, an assemblage which Miya *et al.* (2013) first reported. However, my results are different from their topology, with Chiasmodontidae as the basal to the rest of Pelagia in my phylogeny. My results also show Scombridae as paraphyletic, but support for this is low. Arripididae is monophyletic, but the hypothesis regarding its sister relationship with other families within the Pelagia remains inconclusive using my dataset that mostly consists of nuclear markers and partial mitochondrial genes, and are not sufficient to resolve the rapid radiation seen in Pelagia (Miya *et al.*, 2013).

Lactariidae: Carangimorpharia

One of the families not included in Betancur-R *et al.*'s (2013a) and Near *et al.*'s (2013) datasets is the monotypic family Lactariidae (false trevally). The available literature on *Lactarius lactarius* mostly reports on the general biology, ecology, and fisheries statistics and do not provide information regarding interfamilial relationships (Apparao, 1966; Hakkimane and Rathod, 2011; James *et al.*, 1974; Kaikini, 1974; Reuben *et al.*, 1993; Zacharia and Jayabalan, 2007). Previous reports have associated the false trevallies with scombrids, pomatomids, and carangids (Bloch and Schneider, 1801; Cuvier, 1830; Cuvier and Valenciennes, 1833). Others have associated them with Sciaenidae(Günther, 1860) and Serranidae (Regan, 1913), based on similarity in general characteristics. In 1923, Jordan erected the familial classification Lactariidae and placed them within the Carangiformes. Jordan's classification, which was also based on external morphology, has been widely accepted ever since (Johnson, 1984; Smith-Vaniz, 1984). In 1994, Leis provided description of eight larval and adult characters namely, the lack of subopercular and interopercular spines on larvae, series of melanophores along the dorsal midline of trunk and tail of larvae; soft-rayed portion of the dorsal and anal fins as long-based; presence of cycloid scales; fusion of hypurals 1 and 2, and 3 and 4; coracoid with a broad anterior lamella, which extends broadly toward the cleithrum; and the length of the hypobranchial process and its attachment to the midline, which suggests that *Lactarius* and *Mene* are sister to the carangoid fishes. Leis noted that these synapomorphies support the conventional placement of *Lactarius* as closely related to carangoids. Moreover, Leis noted that *Lactarius* and *Mene* are successive sister groups to the carangoids based on two equivocal characters, namely the absence of spines on the supracleithrum and on the posttemporal of the larvae for both taxa. He also noted two other characters of uncertain reliability, which are the posterior extension of the swim bladder and the arrangement of neural arches and spines, but these differ in construction from the two taxa and raise the question of homology. Leis further mentioned that relationships of false trevallies remain uncertain pending availability of larvae of *Lactarius* and other carangoids. More recently, Campbell *et al.* (2013), in their assessment of the monophyly of the flatfishes (Pleuronectiformes), provided molecular evidence of the placement of *Lactarius* within the carangimorphs. They recovered *Lactarius* in a clade with *Sphyraena*, *Mene*, *Makaira*, and *Xiphias*, but received no support for the node. Betancur-R and Orti (2014), however, conducted an analysis combining their previous dataset and that of Campbell *et al.*'s and including only the carangimorphs and anabantomorphs, and recovered *Lactarius* as sister to

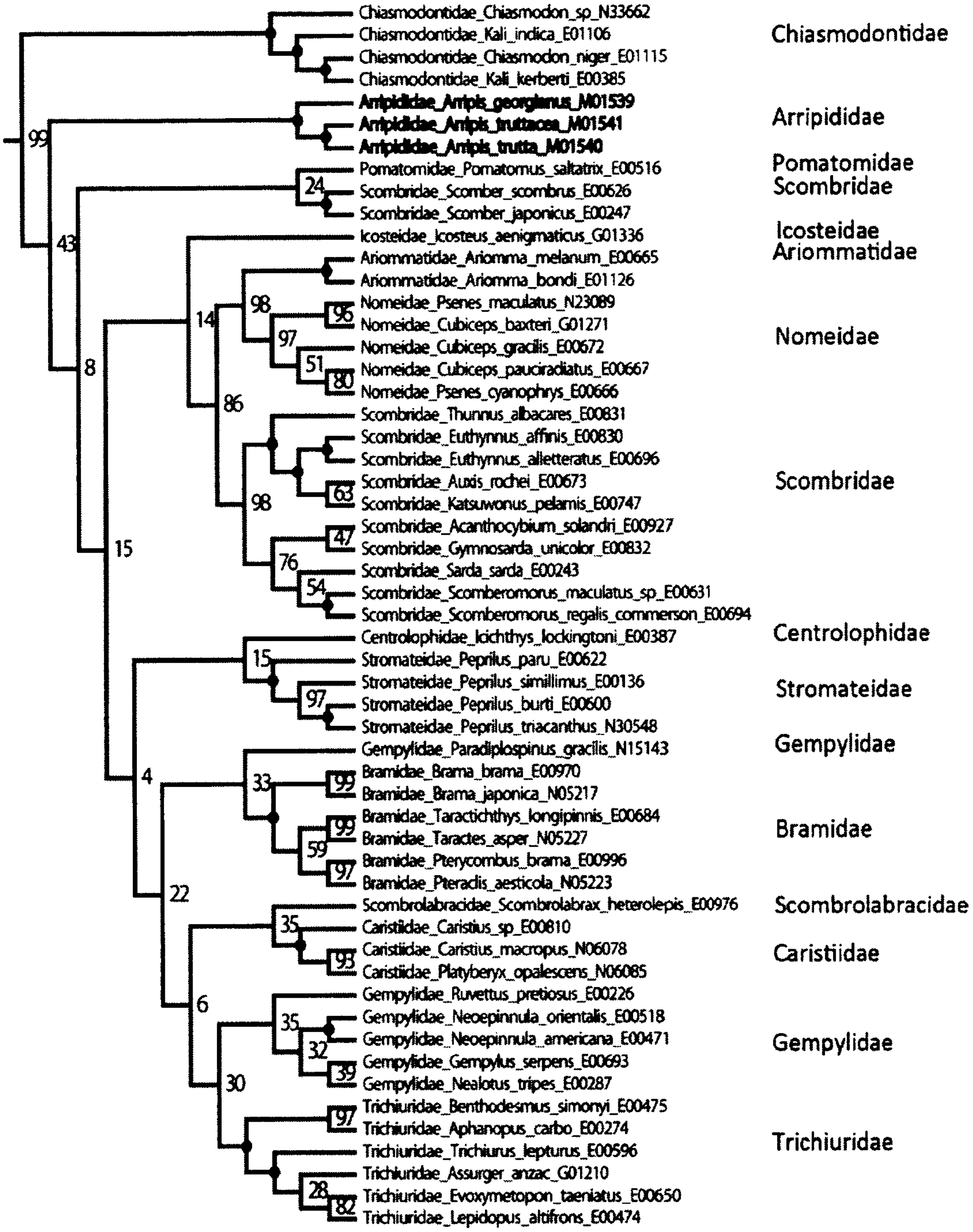


FIGURE 3. Interfamilial relationships of Arripididae (see also Appendix E). Values on the nodes represent bootstrap support from RAxML analysis. Filled black circles on the nodes identify the clades supported with a bootstrap score of 100%.

sphyraenids (60% BS); however, the position of this clade within the carangoids is also not supported.

The results of this study (Fig. 4) corroborate the placement of lactariids within the carangimorphs. These results are concordant with Leis (1994) placing *Lactarius* as sister to Menidae, but support for this is weak. Moreover, *Lactarius* and Menidae are sister to Polynemidae, and this clade is basal to all carangoids. Reexamination of the coracoid and hypobranchial processes, as well as other morphological characters that Leis have investigated, of the carangimorphs will most likely provide more evidence supporting the affinity of these taxa.

In addition, these results corroborate Betancur-R and Orti's (2014) results placing psettodids closer to the flatfishes, than the previous findings in Betancur-R *et al.* (2013a) phylogeny, which is contrary to previous morphological (Chapleau, 1993; Lauder and Liem, 1983; Regan, 1910) and molecular studies that included a limited taxon sampling of pleuronectoids (Berendzen and Dimmick, 2002; Betancur-R *et al.*, 2013b; Near *et al.*, 2013; Pardo *et al.*, 2005), which placed psettodids close to the flatfishes and supported a monophyletic clade for the order. Betancur-R *et al.* (2013a) recovered psettodids in a clade with the nematistiids, rachycentrids, coryphaenids, and echeneids and far from the pleuronectiforms. Their placement of psettodids in the Carangiformes renders the Pleuronectiformes polyphyletic. Campbell *et al.* (2013), in their investigation of the monophyly of the order, recovered psettodids as sister to *Toxotes*, but also found no support for the group. Betancur-R and Orti's(2014) re-analysis of the combined dataset of two previous studies recovered a monophyletic clade for flatfishes (65% BS), with psettodids as the basal group. Their approach analyzed a more restricted dataset of flatfishes and carangimophs and enabled resolution of the flatfishes. Although this approach is highly recommended (Betancur-R and Orti, 2014), especially when monophyly of the target group is ascertained, this study incorporates the entirety of Percomorphaceae and aims to provide hypothesis of previously unclassified groups. The results, however, shows that the addition of new taxa, as well as expanding taxonomic coverage, can completely change the assumed sister-group relationships and affect placement of species within a group, such in the case for *Lactarius*. Inclusion of more specimens and more genes will likely help resolve relationships within the Carangimorphariae as well. Moreover, assessment of morphological characters, such as those examined by Leis (1994), can also be key to understanding the relationships uniting the flatfishes, billfishes, and carangids

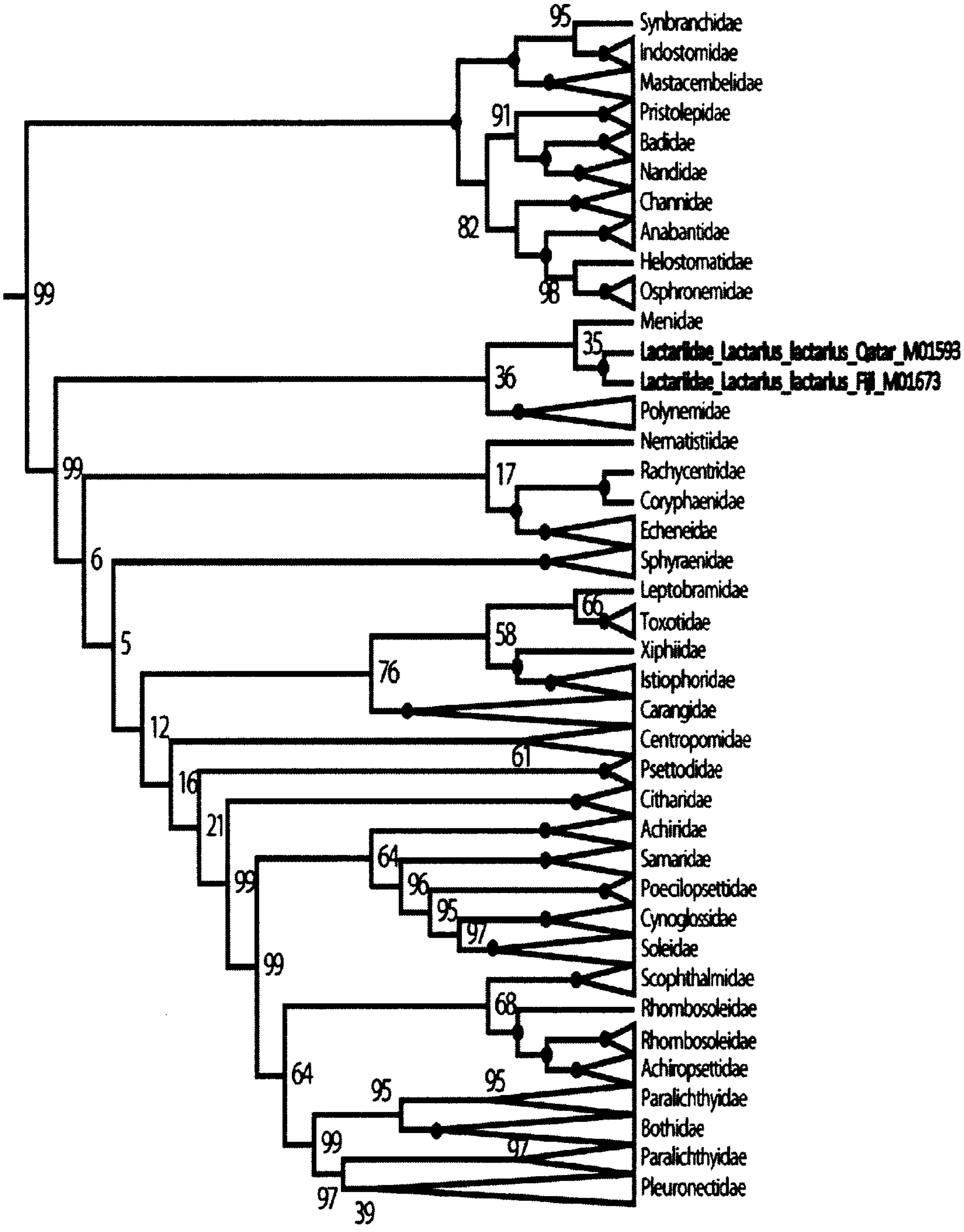


FIGURE 4. Interfamilial relationships of Lactariidae (see also Appendix E). Values on the nodes represent bootstrap support from RAxML analysis. Filled black circles on the nodes identify the clades supported with a bootstrap score of 100%.

(Betancur-R *et al.*, 2013a; Chen *et al.*, 2003; Ishiguro *et al.*, 2003; Johnson, 1984; Li *et al.*, 2009; Little *et al.*, 2010; Smith and Wheeler, 2006). Further examination of morphological characters and gene sequences for members of the Carangimorphariae clade almost certainly will provide more information regarding the close affinity between the carangids and flatfishes.

Callanthiidae, Percomorpharia

The groppos (callanthiids) are one of the families not included in Betancur's *et al.*'s (2013a) fish phylogeny, but are included in the more recent analysis of Near *et al.* (2013). Similar to the bandfishes, Li *et al.* (2009) recovered the groppos in their extended clade, Clade N, and sister to Caproidae (boarfishes). Near *et al.* (2013) recovered the groppos close to sillaginids (sillagos) and emmelichthyids (rovers), but found no support for the group. In the present study (Fig. 5), the genus *Callanthias* is placed close to the tilefishes (Malacanthidae), and nests in a bigger assemblage comprised of haemulids (grunts), lutjanids (snappers) plus caesionids (fusiliers), pomacanthids (angelfishes), chaetodontids (butterflyfishes), emmelichthyids, acanthuriforms, leiognathids, and sciaenids (82% BS).

Hapalogenyidae: Percormorpharia

The family of barbeled grunters, Hapalogenyidae, is one of the enigmatic groups not examined in previous molecular studies that encompass most of percomorphs. The phylogenetic placement of the family within the percomorphs is controversial (Iwatsuki and Nakabo, 2005; Iwatsuki *et al.*, 2000; Johnson, 1984; Lindeman and Toxey, 2003; Ren and Zhang, 2007; Sanciangco *et al.*, 2011; Springer and Raasch, 1995). The members of the family have often been placed in the Haemulidae (Iwatsuki and Russell, 2006; Iwatsuki *et al.*, 2000; McKay, 2001; Nelson, 2006; Richardson, 1844) or classified as *incertae sedis* under the suborder Percoidei (Johnson, 1984). Springer and Raasch (1995) erected the family name, Hapalogenidae (sic Haplogeniidae) for the genus, without strong supporting evidence.McKay (2001) and Iwatsuki and Russell (2006) recognized *Hapalogenys* separate from Haemulidae (grunts), but retained the genus in Haemulidae for convenience, pending further study of more genera.

McKay (2001) also described the genus as similar to the two species of Dinopercidae (cavebasses); however, he observed that species of *Hapalogenys* do not possess the intrinsic muscles on the posterior part of the swimbladder. Leis and Carson-Ewart (2000) observed that *Lobotes*, *Datnioides*, and *Hapalogenys* all shared remarkable similarity in larval morphology, particularly in head spination, pigmentation, early development of the posteriorly-placed pelvic fins, and general body shape, and placed the three genera in an informal group called "*Lobotes*-like." Ren and Zhang (2007), in their study of phylogenetic relationships of 15 haemulids based on the partial mitochondrial 16S gene, recovered *Hapalogenys* outside Haemulidae. Sanciangco *et al.* (2011) corroborated this finding placing *Hapalogenys* outside Haemulidae in their phylogenetic analysis of most genera and species of the family Haemulidae using five genes. Their study provided substantial molecular evidence that *Hapalogenys* is indeed not a haemulid. In addition, their study also confirmed Leis and Carson-Ewart's (2000) hypothesis that *Hapalogenys* is sister to *Lobotes* (*Datnioides* was not sampled in their study). Liang *et al.* (2012) also recovered *Hapalogenys* outside haemulids based on a more limited taxon sampling inferring relationships within the haemulids. However, relationships of *Hapalogenys* within the percomorphs remain inconclusive. Previous studies have included *Hapalogenys* as an outgroup species and none has tested nor included *Hapalogenys* in any molecular analysis within the broader percomorph. The results of my RAxML analysis (Fig. 6) confirms Hapalogenyidae in a clade together with lobotids (Sanciangco *et al.*, 2011) and *Datnioides* (Leis and Carson-Ewart, 2000), and is highly supported (100% BS). Furthermore, I recovered the "lobotes-like" clade in a bigger assemblage comprised of the Spariformes (*sensu* Betancur-R *et al.* 2013c), siganids, scatophagids, priacanthids, cepolids, caproids, lophiiforms, tetraodontiforms, sillaginids, moronids, ephippiforms, and the clade containing the most recent common ancestor of leiognathids, acanthuriforms, callanthiids, haemulids, and lutjanids plus caesionids (82% BS). The inclusion of *Hapalogenys* in this study completely changed the sister grouping for Lobotidae. In Betancur-R *et al.* (2013a), *Lobotes* was recovered as sister to Sillaginidae, but support for this relationship is weak. The results of this study not only corroborate sister-group relationships for *Hapalogenys*, but also present novel hypothesis regarding relationships with other percomorphs.

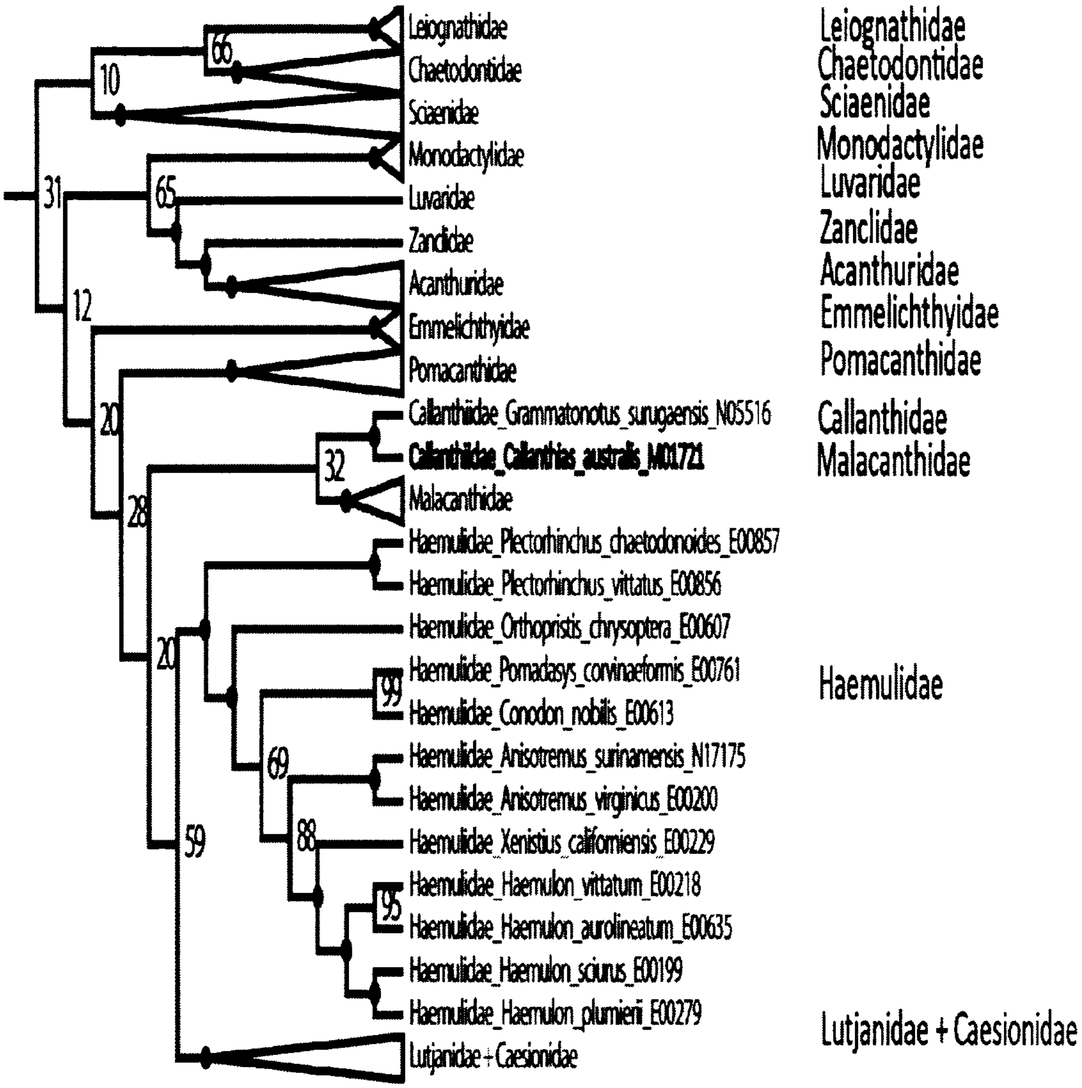


FIGURE 5. Interfamilial relationships of Callanthiidae (see also Appendix E). Values on the nodes represent bootstrap support from RAxML analysis. Filled black circles on the nodes identify the clades supported with a bootstrap score of 100%.

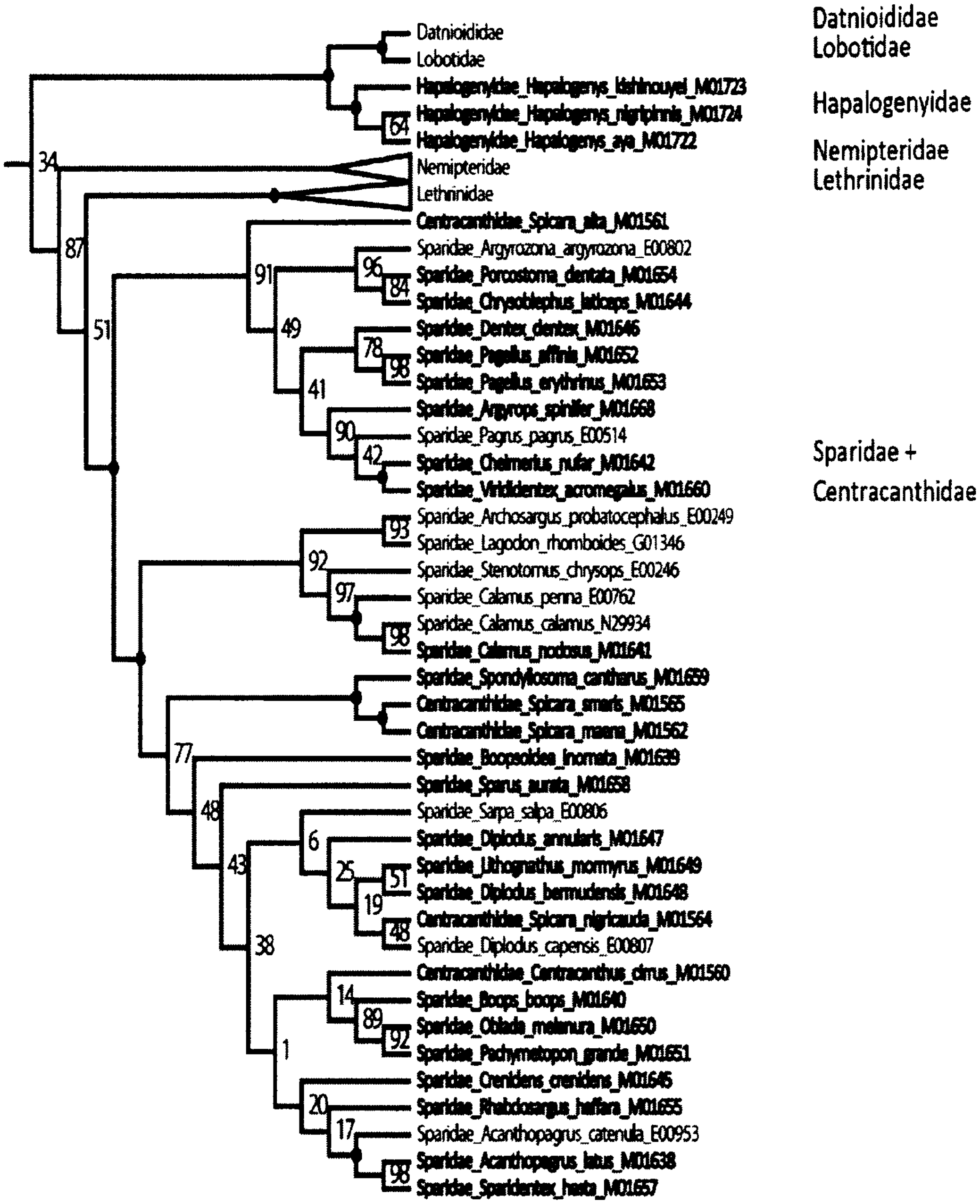


FIGURE 6. Interfamilial relationships of Hapalogenyidae, Sparidae, and Centracanthidae (see also Appendix E). Values on the nodes represent bootstrap support from RAxML analysis. Filled black circles on the nodes identify the clades supported with a bootstrap score of 100%.

Centracanthidae; Spariform fishes

The inclusion of *Centracanthus* in this analysis confirms that the family Centracanthidae (picarel porgies) Gill 1893 should be treated as a junior synonym of Sparidae Rafinesque 1810 (Fig. 6). There are currently two putative genera, namely *Centracanthus* (with one species) and *Spicara* (with nine species), belonging to the family. Previous relations of the centracanthids include *Inermia* and *Emmelichthyops* (Heemstra 1974 as cited in Johnson 1981), which are now in Haemulidae (grunts), and Sparidae (porgies) (Johnson, 1981, 1984; Jordan and Fesler, 1893; Regan, 1913; Smith, 1938). Heemstra (as cited in Johnson 1981), in his delimitation of the family Emmelichthyidae (rovers), placed *Inermia* and *Emmelichthyops*, along with several other genera in a separate family, Centracanthidae, which is diagnosed by the presence of a "joint-like articulation at the distal (ventral) ends of the premaxillary and maxillary bones." Johnson (1981) examined this joint and noted a significant difference in its articulation between that of the former inermiids and centracanthids. Accordingly, in the centracanthids, the distal end of the premaxillary gives rise to two flanges that form a trough that cradles the shaft of the maxillary anterior to a distal, ventral expansion, which is a condition shared by the closely related sparids. As opposed to the inermiids, the premaxillary fits into an acute notch in the ventral margin of the maxillary instead of having grooves where the maxillary is situated.

Heemstra and Randall (1977) also corroborated this finding and noted that centracanthids are sparid derivatives, supported by the presence of sparoid suspensorium, infraorbital configuration, and six branchiostegals. Johnson (1981) further observed that Centracanthidae appears closely related to the Sparidae not only based on similarity of the maxillary-premaxillary articulation, but also on a number of general osteological features. He noted that there are many morphological specializations associated with planktivorous lifestyle, which supports the monophyly of Centracanthidae. Johnson retained the centracanthids in a separate family pending investigation of the interrelationships within the sparoids. Carpenter and Johnson (2002) recovered a monophyletic Sparidae plus Centracanthidae (*Spicara maena*, *S. alta*, and *Centracanthus cirrus*) and found four non-homoplasious synapomorphies: three openings in the lateral wall of pars jugularis, a modified distal end of alveolar ramus of premaxillary to articulate with the distal ventral edge of the maxilla, proximal tips of the first hypural and the parhypural broadly overlap and articulate with the urostyle, and presence of apical pores in the lateral line scales. The monophyletic Sparidae plus Centracanthidae was further supported by subsequent molecular studies that included one or few members of the genus *Spicara* within Sparidae

(Chiba *et al.*, 2009; Day, 2002; Orrell and Carpenter, 2004; Orrell *et al.*, 2002), but did not include *Centracanthus*.

Hanel and Tsigenopoulos (2011) conducted a molecular phylogenetic analysis of the sparids (18 genera; 38 species) that included the two centracanthid genera using 16S rRNA gene. Their topology shows members of centracanthids spread throughout the Sparidae family. They recovered *Spicara melanurus* nested in *Diplodus*. Although this was not included in my molecular analysis, a morphological examination of *S. melanurus* shows that it is probably a *Diplodus* with a highly protrusible jaw and a spot on the caudal peduncle, as in all other *Diplodus*. *S. axillaris* (also not sampled in this study) is placed close to *Sparus* and *Pachymetopon*, *S. maena*, *S. smaris*, and *S. flexuosa* (not sampled) are nested in a clade together with *Spondyliosoma*, *S. alta* is placed close to *Dentex*, and *Centracanthus cirrus* is nested with *Pagellus*. More recently, Santini *et al.* (2014) provided a more comprehensive phylogeny of the sparids + centracanthids (38 genera, 91 species), confirming previous hypothesis that centracanthids are spread throughout the sparids. The results (29 genera, 38 species) are concordant with previous studies, placing centracanthids within the sparids, and with similar clade composition for the major nodes, with some disparities. I recovered *S. maena* and *S. smaris* together with *Spondyliosoma*. *S. alta* (not included in the two most recent studies, but included in Orrell *et al.* 2002) is also nested in a clade with *Dentex* and with *Pagellus*, *Argyrozona*, *Porcostoma*, *Chrysoblephus*, *Argyrops*, *Cheimerius*, and *Viridentex*. I found *S. nigricauda* (not sampled in Hanel and Tsigenopoulos 2011 and Santini *et al.* 2014) together with *Diplodus*, *Lithognathus*, and the rest of sparids. My results are different from Hanel and Tsigenopoulos (2011) in the placement of *C. cirrus*, which is nested together in a clade with *Boops*, *Oblada*, and *Pachymetopon*, but support for this is low. Disparities in the interrelationships within the sparids + centracanthids can be attributed to the limited number of gene sequences for some of the spariform fishes in my dataset, which mostly consisted of COI, CYT *b*, and RAG1, as compared to those taxa with more genes, in which placement were consistent with previous studies. Nevertheless, my results confirmed that centracanthids are indeed sparids. Centracanthidae was erected based on its planktivorous life style and highly protrusible jaw. The present study confirms that this trait is highly plastic and evolved several times within the Sparidae. This is an observation found in other percoid families such as the Lutjanidae-Caesionidae relationship and the Hamulidae-Inermiidae relationships. Sparidae is monophyletic, with the inclusion of *Spicara* (paraphyletic) and *Centracanthus* (100% BS). Two genera, *Diplodus* and *Spicara*, however, are not monophyletic. Further, none of the putative subfamilies are monophyletic (Chiba *et al.*, 2009; Hanel and Sturmbauer, 2000; Orrell and Carpenter, 2004; Orrell *et al.*, 2002; Smith and Heemstra, 1986). My findings do not support the current subfamilial classification based on dentition, spinous and soft fin ray counts, scalation, and body colour for the sparids.

The now expanded Sparidae, Nemipteridae (threadfin breams), and Lethrinidae (emperors), make up the spariform fishes. Akazaki (1962) was the first to recognize the "spariform fish," which included a primitive Nemipteridae, an intermediate Sparidae, and a highly specialized Lethrinidae based on osteological relationships, including dentition. Johnson (1981) expanded Akazaki's spariform and erected the superfamily "Sparoidea" to include the primitive Nemipteridae, intermediate Lethrinidae, and the more derived Sparidae plus Centracanthidae, based on similarity of maxillary-premaxillary distal articulation and other osteological characters. Carpenter and Johnson (2002) also recovered a monophyletic superfamily, substantiated by three non-homoplasious characters: symplectic with dorsal and ventral laminar extensions, broad articulation between hyomandibular and metapterygoid, and anterior extension of suborbital shelf behind second infraorbital, based on cladistic analysis of 54 morphological characters. My results are concordant with that of Johnson (1981) and Carpenter and Johnson (2002) for the relationships within spariform fishes, with strong support (87% BS).

Cepolidae, Percomorpharia

The Cepolidae (bandfishes) is one of the five families not included in the global fish phylogeny (Betancur-R *et al.*, 2013a), but is sampled in the Near *et al.*'s (2013) phylogeny. Previous studies regarding the classification and familial relations of cepolids are scarce. The cepolids were placed in separate families in the past, which are recognized as subfamilies, based on the following synapomorphies: toothless vomer and palatine, dorsal and anal fins not divided, dorsal and anal spines flexible and reduced, and presence of a single postclavicle and six branchiostegals (Nelson, 2006; Smith-Vaniz, 2001; Smith and Heemstra, 1986). At present, there are four putative genera and 19 species belonging to the two subfamilies Cepolinae and Owstoniidae. With regards to familial relations, Li *et al.* (2009) placed the Cepolidae close to Labridae (wrasses) and Scaridae (parrotfishes), and is included in an "extended clade (Clade N)," while Smith and Wheeler (2006) placed them close to Leiognathidae (slipmouths) and Bythitidae (viviparous brotulas). Near *et al.* (2013), however, placed the Cepolidae close to Priacanthidae (bigeyes) and close to Scatophagidae (scats) plus Siganidae (rabbitfishes), Caproidae (boarfishes), lophiiforms, tetraodontiforms, Ephippidae (spadefishes), and Moronidae (temperate basses). With a much broader taxon sampling, the results of this study corroborate this most recent finding, and recovered Cepolidae close to Priacanthidae and Scatophagidae (98% BS) (Fig. 7). This group nests in a bigger assemblage consisting of Lophiiformes (anglerfishes) and Tetraodontiformes (plectognaths), and siganids, with moderate support (86% BS).

Symphysanodontidae, Banjosidae, Pentacerotidae, and Bathyclupeidae: Percomorpharia

The phylogenetic position of slopefishes among the percomorphs has been controversial and its relationships unknown. Most information available regarding the symphysanodontids pertain to species accounts and generalized descriptions for the members of the family (Anderson *et al.*, 2011; Anderson, 2000, 2003; Anderson and Springer, 2005; Nelson, 1994, 2006). The family is comprised of a single genus, *Symphysanodon*, with 12 putative species (Anderson *et al.*, 2011). Members of this family have been mistaken for members of the lanternbellies (Acropomatidae), sea basses (Serranidae), or snappers (Lutjanidae) in the past, but can easily be diagnosed by the absence of distinguishing characters for the other three groups (Anderson and Springer, 2005; Nelson, 1994, 2006). Johnson (1984) provided a hypothesis of evolutionary relationships with the acropomatids (lanternbellies) based on his observation of the larvae of *Symphysanodon sp.*, which he described as possessing hornlike frontal spines similar to those of *Synagrops* (Acropomatidae), and noted that presence of this character is suggestive of their close affinity.

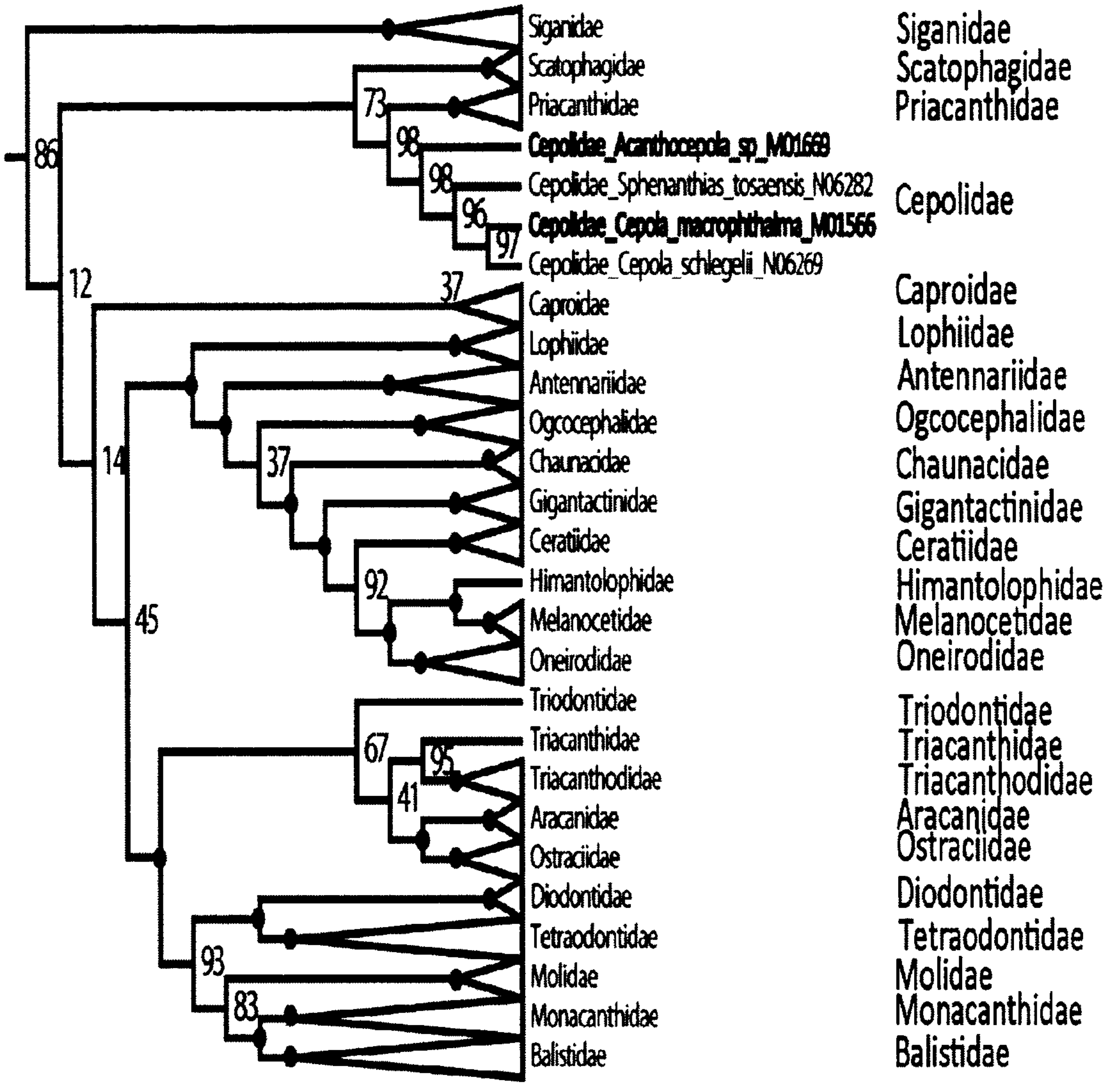


FIGURE 7. Interfamilial relationships of Cepolidae (see also Appendix E). Values on the nodes represent bootstrap support from RAxML analysis. Filled black circles on the nodes identify the clades supported with a bootstrap score of 100%.

My results are concordant with Johnson's observation placing *Symphysanodon* close to acropomatids. Furthermore, I recovered the slopefishes belonging to Pempheriformes *sedis mutabilis sensu* Betancur-R *et al.* (2013c). My results are concordant with Johnson's observation, with the slopefishes closely related to the lanternbellies (Fig. 8). The lanternbellies, however, are not monophyletic, appearing in three different places for each of the three genera represented in this study. Members of the genus *Synagrops* are nested in a group containing the bathyclupeids (also a new addition in this study), wreckfishes (Polyprionidae), banjofishes (Banjosidae), and armorheads (Pentacerotidae). *Malakichthys* is found in a clade together with the Asian seaperches (Lateolabracidae), gapers (Champsodontidae), sandburrowers (Creediidae), duckbills (Percophidae), pearl perches (Glaucosomatidae), and sweepers (Pempheridae). *Acropoma* is nested in a clade comprised of the epigonids, Howellidae, ostracoberycids (Ostracoberycidae), and Symphysanodontidae. This study is the first to include members of the families Symphysanodontidae and Bathyclupeidae in a molecular phylogenetic analysis of the percomorphs, and although support for the relationships within the order is not recovered in this analysis, the hypothesis shows up in a number of different analyses and deserves further testing. The relationships within this entire assemblage has been recovered in part in other fish phylogenies (Betancur-R *et al.*, 2013a; Near *et al.*, 2013), but they also found no support for the group.

Dichistiidae, Percomorpharia

One of the 49 families not included in Betancur-R *et al.*'s (2013a) and Near *et al.*'s (2013) phylogenies is that of the galjoen fishes (Dichistiidae). Similar to many perciform families, the taxonomic history of galjoen fishes has been controversial. The family is comprised of a single genus, *Dichistius*, with two putative species. Members of this family have been placed together with the squamipinnes, porgies, *Girella*, and *Scorpis*, based on superficial external characters (Cuvier, 1830; Fowler, 1934; Günther, 1860; Jordan, 1923). Smith(1935) was the first

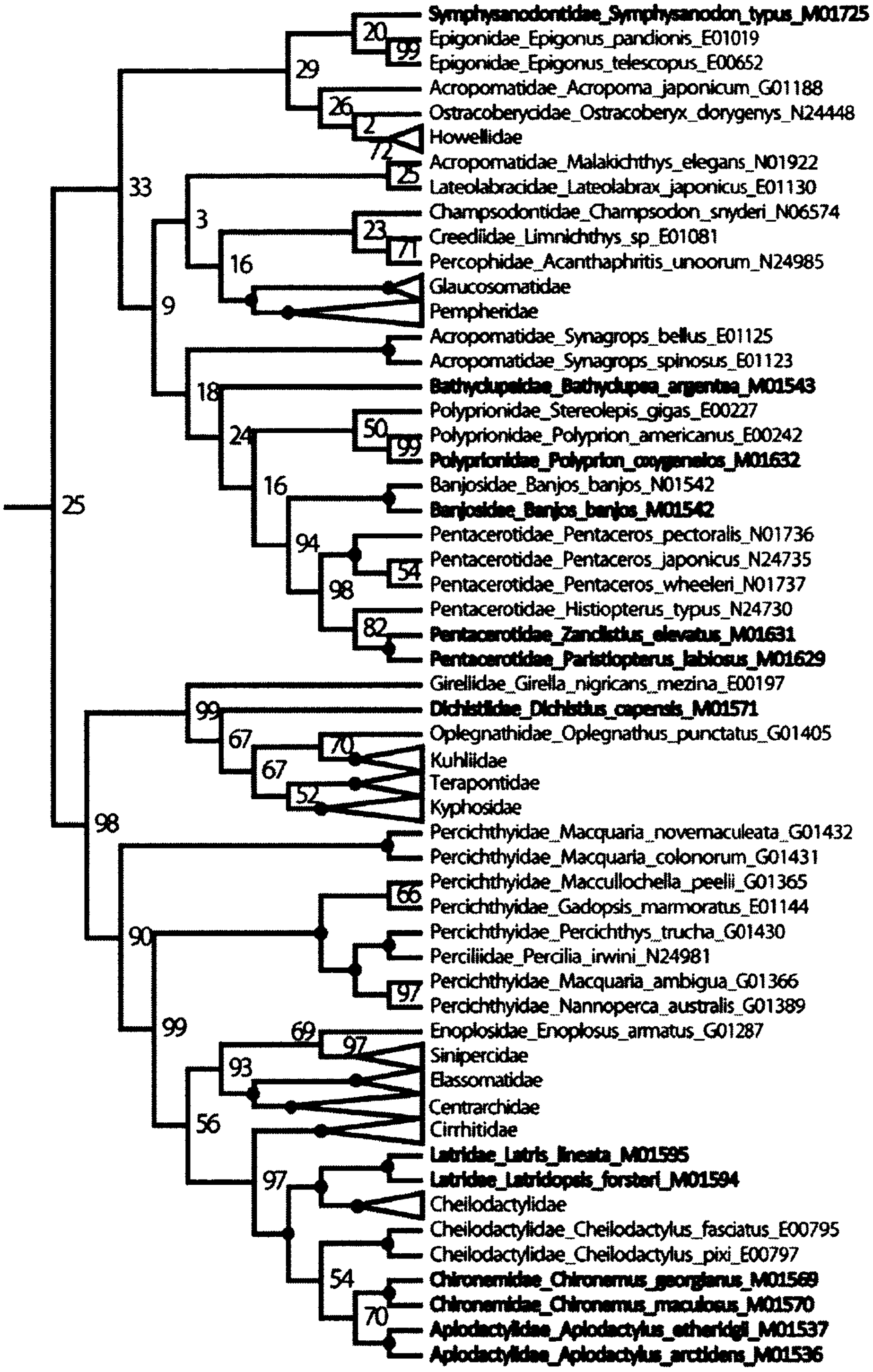


FIGURE 8. Interfamilial relationships of Symphysanodontidae, Bathyclupeidae, Dichistiidae, Latridae, Chironemidae, and Aplodactylidae (see also Appendix E). Values on the nodes represent bootstrap support from RAxML analysis. Filled black circles on the nodes identify the clades supported with a bootstrap score of 100%.

to classify the galjoen fishes in a separate family, Dichistiidae (= Coracinidae), and placed them near the sea chubs, Girellidae and Kyphosidae (Leis and van der Lingen, 1997), a classification which has been followed in subsequent studies. There are several relationships hypothesized for galjoen fishes. Johnson (1984) placed them close to *Drepane,* but regarded them as ephippids, based on the similarity in gill arch characters. Nelson (1994) placed them close to Drepaneidae (sicklefishes), but not close to Ephippidae. Leis and van der Lingen (1997) rejected the placement of galjoen fishes in Sparidae and Sparoidea, noting the absence of diagnostic characters for the two families.

Johnson (1984) and Johnson and Fritzsche (1989) noted that the larval features of the galjoen fishes are distinctive of the larval forms of the microcanthids, scorpidid, girellid, and kyphosids (MSG +K). Johnson and Fritzsche (1989) also suggested that the MSG + K group is also related to Arripidae (Australasian salmon), Kuhliidae (flagtails), Oplegnathidae (knifejaws), Terapontidae (tigerperches), and Stromateiodei. Leis and van der Lingen (1997) provided a thorough discussion on the taxonomic issues and history of Dichistiidae relationships. They tested interrelationships of the group to other fishes by looking at the Freihofer's pattern 10 of the ramus lateralis accessorius nerve (RLA) of larval fishes. They concluded that the MSG + K families, as well as the families Dichistiidae and Arripidae, exhibit the RLA pattern 10. However, they do not have information on the sister groups of those possessing the RLA 10 pattern, and therefore, could not assess the monophyly of the group and resolve its relationships among other perciforms.

Yagishita *et al.* (2009) then examined the RLA pattern 10 of two perciform suborders (*sensu* Nelson 2006) that share this character. These include some members of Percoidei, comprised of members of Arripidae, Dichistiidae, Kyphosidae, Terapontidae, Kuhliidae, and Oplegnathidae, and members of the suborder Stromateoidei. Their results, however, showed two independent origins for the facial nerve pattern, one in the group with Kyphosidae, Terapontidae, Kuhliidae, and Oplegnathidae and another one in the group with Arripidae and Stromateoidei. Interestingly, they recovered Arripidae and Stromateoidei together with Scombridae (mackerels and tunas) and allies, which do not possess the RLA pattern 10. This group corroborates an earlier molecular study that examined the venom evolution in fishes (Smith and Wheeler, 2006). Smith and Wheeler (2006) provided a hypothesis of venom evolution and sampled from a wide selection of spiny-rayed fishes. They indicated that galjoen fishes are close to Kyphosidae and Oplegnathidae, and sister to a group comprising of Kuhliidae, Terapontidae, Creediidae (sandburrowers), and Uranoscopidae (stargazers). My analysis supports Johnson and Fritzsche's (1989), Leis and van der Lingen's (1997), Yagishita *et al.*'s (2009), and Smith and Wheeler's (2006) placement of Dichistiidae close to Kyphosidae, and to Oplegnathidae, Kuhliidae, and Terapontidae (Fig. 8) in the newly circumscribed Order Terapontiformes (*sensu* Betancur-R *et al.* 2013c), which also includes Girrellidae (99% BS).

Latridae, Aplodactylidae, and Chironemidae, Cirrhitiformes: Percomorpharia

The inclusion of three additional families, Latridae (trumpeters), Aplodactylidae (marblefishes), and Chironemidae (kelpfishes) in this study confirmed previous hypothesis regarding relationships within the cirrhitiforms (Fig. 8). These families, together with Cheilodactylidae (morwongs) and Cirrhitidae (hawkfishes), represent the monophyletic superfamily Cirrhitoidei (= Cirrhitiformes, *sensu* Betancur-R *et al.* 2013a), and together encompasses Regan's (1911) natural assemblage, which is collectively termed as the cirrhitoids (*sensu* Greenwood 1995). Although the phylogenetic affinity for the cirrhitiforms has been widely accepted, the relationships within the group remain equivocal (Burridge and Smolenski, 2004; Greenwood, 1995). Greenwood (1966) placed all five families close to each other, without inferring interrelationships, and classified them under the suborder Percoidei. Greenwood (1995) then provided a tentative hypothesis of the relationships within the cirrhitoid family, placing the Cirrhitidae as the most plesiomorphic, followed by Chironemidae, and then by an unresolved trichotomy, which is comprised of Aplodactylidae, Cheilodactylidae, and Latridae.

My results show that the family Cheilodactylidae is not monophyletic, and its members are divided into two clades. The non-monophyly of the family was also recovered in Betancur-R *et al.*'s (2013a) fish phylogeny. One group is comprised of the South African cheilodactylids (*Cheilodactylus fasciatus* and *C. pixi*) together with aplodactylids and chironemids (54% BS), and the other group is comprised of *C. variegatus*, *C. brachydactylus*, and *C. jessicalenorum* together with the latrids (100% BS). This finding was first reported by Burridge and Smolenski (2004). They noted that the South African *Cheilodactylus* can be distinguished from the rest of cheilodactylids by having a higher lateral line scale count and the presence of scales on the postcleithrum (Lamb 1990 in Burridge and Smolenski 2004). Further, they noted that the other members of cheilodactylids do not differ from the latrids. Burridge and Smolenski (2004) proposed to redefine the familial classification of these (non- South African) cheilodactylids, and included them in their "expanded Latridae." They also noted that this expanded group will require new morphological diagnosis and generic and familial reassignment since *Cheilodactylus fasciatus* is the nominal species for the genus and family name, Cheilodactylidae. Their preliminary assessment of the dorsal pterygiophore insertion, for the expanded Latridae, suggests that this group possesses two predorsal bones, both of which are anterior to the first neural spine and located anterior to the first pterygiophore. My results also confirm the Cirrhitiformes as monophyletic (100 BS), with Cirrhitidae as basal to the rest of the group as in Greenwood (1995).

Haemulidae and its closest relatives: Percomorpharia

The inclusion of eight new families (plus six other families that were not examined in Betancur *et al.* 2013a, but were included in Near *et al.* 2013) in the present dataset posed novel hypotheses regarding many sister-group relationships (Appendix E). More importantly, it provided a better framework for determining the sister group of haemulids. The expanded dataset showed a monophyletic Haemulidae as sister to Lutjanidae plus Caesionidae (Fig. 9, Appendix E). Although the bootstrap support for the Haemulidae + (Lutjanidae + Caesionidae) is low, this value is higher compared to previous large-scale studies that did not show any resolution (Betancur-R *et al.*, 2013a; Near *et al.*, 2013). Furthermore, the families Haemulidae and Lutjanidae plus Caesionidae are included in a larger group (Fig. 9, Appendix E) that includes Callanthiidae, Malacanthidae, Pomacanthidae, Emmelichthyidae, Acanthuridae, Zanclidae, Luvaridae, Monodactylidae, Sciaenidae, Chaetodontidae, and Leiognathidae, although support for this is low (31 BS). This group is nested in a bigger assemblage (Fig. 9, Appendix E) that includes the Spariformes, Lobotiformes (including Hapalogenyidae), Siganidae, Scatophagidae, Priacanthidae, Cepolidae, Caproidei, Lophiiformes, Tetraodontiformes, Ephippiformes, Moronidae, and Sillaginidae. This bigger assemblage is highly supported (82 BS), which was also not recovered from previous studies, and shows phylogenetic affinity that deserves further study.

In this study, the addition of two mitochondrial genes, COI and CYT *b*, in addition to Betancur-R *et al.*'s (2013a) 21-gene dataset and the delimitation of the taxonomic sampling to only the Percomorphaceae proved to be useful in improving resolution for some of the more derived clades at different taxonomic levels in the tree. Future efforts should be directed at increasing taxonomic sampling in order to provide a more comprehensive taxonomic framework for determining the close relatives of the haemulids.

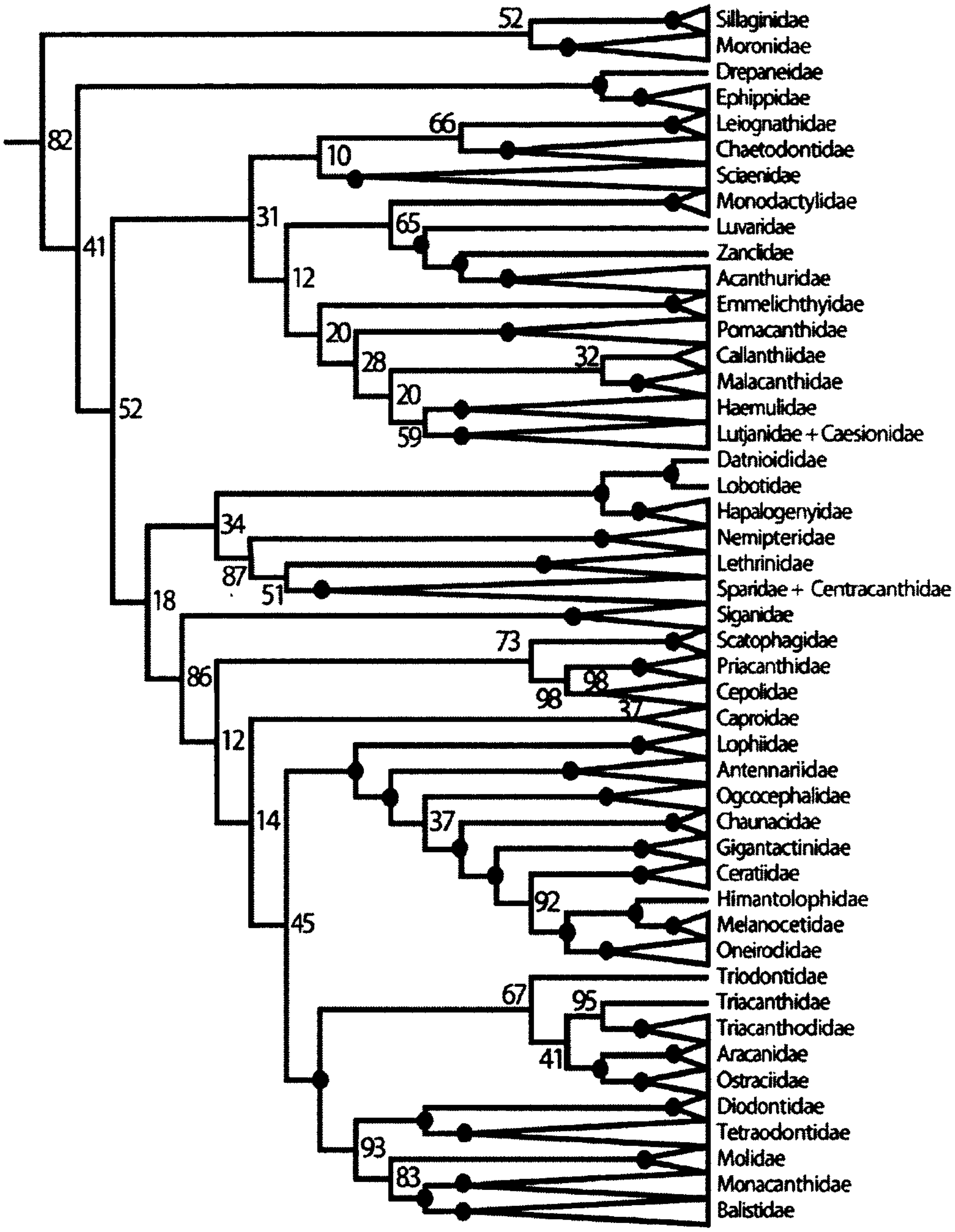


FIGURE 9. Phylogeny of percomorphs inferred from RAxML analysis of the 3+ dataset (1231 taxa) from 23 genes (20 nuclear and three mitochondrial) with eight partitions, showing the closest relatives of the Haemulidae (see also Appendix E). Values on the nodes represent bootstrap support from RAxML analysis. Filled black circles on the nodes identify the clades supported with a bootstrap score of 100%.

CHAPTER IV

THE PHYLOGENY AND BIOGEOGRAPHY OF HAEMULIDAE (SERIES PERCOMORPHARIA) BASED ON COMPLETE MITOGENOMES AND A CONCATENATED DATASET OF 22 GENES

INTRODUCTION

The family Haemulidae (grunts) is one of the largest percoid families and includes 145 putative species belonging to 18 genera in the ill-defined suborder Percoidei (*sensu* Nelson 2006). The systematic classification of the group Percoidei remains unresolved and is classified as *incertae sedis* within the Series Percomorpharia (*sensu* Betancur-R *et al.* 2013c). Within Percomorpharia, there is evidence with moderate support that the haemulids are sister to a group containing snappers (Lutjanidae) and fusiliers (Caesionidae) (Betancur-R *et al.*, 2013a; Sanciangco *et al.*, 2011). A recent molecular study (Sanciangco *et al.*, 2011) supports the monophyly of the family with the inclusion of species of the Inermiidae, which were previously classified with the Haemulidae in the superfamily Haemuloidea (Johnson, 1981; Sanciangco *et al.*, 2011). Similarly, molecular evidence (Sanciangco *et al.*, 2011) corroborates the monophyly of the two well-defined subfamilies, Plectorhinchinae and Haemulinae, diagnosed by several external and anatomical characters (Johnson, 1981; Sanciangco *et al.*, 2011). Several other morphological and molecular studies have examined haemulid relationships based on a limited taxon sampling and using a combination of different markers or morphological characters (Bernardi *et al.*, 2008; Bernardi and Lape, 2005; Betancur-R *et al.*, 2013a; Chen *et al.*, 2007; Dettai and Lecointre, 2005; Li *et al.*, 2009; Liang *et al.*, 2012; Price *et al.*, 2012; Ren and Zhang, 2007; Rocha *et al.*, 2008; Sanciangco *et al.*, 2011; Smith and Craig, 2007; Tavera *et al.*, 2012; Tavera *et al.*, 2011).

Morphological descriptions and molecular data concur on the taxonomic status of several haemulid genera, but also show inconsistencies. These inconsistencies are a result of poor description of several haemulid genera based on superficial characters and are now being realized based on current molecular evidences. For example, a re-examination of 52 morphological characters of all *Anisotremus* and *Genyatremus* species resulted in a reclassification of two former *Anisotremus* species that now belong to the genus *Genyatremus*

(Tavera *et al.*, 2011). This finding is corroborated by a molecular study based on combined mitochondrial and nuclear genes (Sanciangco *et al.*, 2011). The consistent placement of the genus *Xenistius* among the members of the genus *Haemulon* (Price *et al.*, 2012; Sanciangco *et al.*, 2011; Tavera *et al.*, 2012) shows *Xenistius* as ill-defined and has been erected based only on superficial characters. Sanciangco *et al.* (2011) and Rocha *et al.* (2008) considered *Xenistius* as junior synonym of *Haemulon* and treated the former species as *Haemulon chrysargyreum*. Several other genera, including *Boridia*, *Xenichthys*, *Parakuhlia*, and *Xenocys*, were all designated by monotypy (Eschmeyer, 1990) without extensive morphological comparisons, and their placement within the haemulids remains unresolved. In addition, the inter- and intra-generic relationships within the family are also a problem. The genus *Plectorhinchus* is paraphyletic, with the inclusion of *Diagramma* (Sanciangco *et al.*, 2011; Tavera *et al.*, 2012). The genus *Pomadasys* is polyphyletic and its members are scattered in the subfamily Haemulinae in two (Tavera *et al.*, 2012) to three (Sanciangco *et al.*, 2011) clades and nested with other genera. Increased taxonomic sampling and use of additional loci are needed, especially for *Plectorhinchus* and *Pomadasys* genera, to establish more clearly their taxonomic status (Roux, 1981; Sanciangco *et al.*, 2011; Tavera *et al.*, 2012).

In this study, I test the utility of complete mitochondrial genomes to infer the relationships of several representatives of the family Haemulidae. Previous studies have utilized partial mitochondrial genes alone, or in combination with a limited number of nuclear genes, to infer the phylogeny of several haemulids. The complete mitochondrial genome has proven valuable in detecting population structures of species for many organisms and for inferring evolutionary relationships of species in many taxa (Chan *et al.*, 2010; Jacobsen *et al.*, 2012; Jex *et al.*, 2010; Minegishi *et al.*, 2005; Morin *et al.*, 2010; Vilstrup *et al.*, 2011) due to its generally higher rate of substitution, compared to nuclear genes, and its maternal non-recombining inheritance (Avise *et al.*, 1987; Moore, 1995). Further, several studies have illustrated that complete mitogenomes are also valuable, not only in resolving recent divergence within species, but also in inferring deep-level relationships across a broad taxonomic group (Ishiguro *et al.*, 2001, 2003; Kawaguchi *et al.*, 2001; Kawahara *et al.*, 2008; Lavoué *et al.*, 2005; Lavoué *et al.*, 2008; Lavoué *et al.*, 2007; Miya *et al.*, 2001; Miya *et al.*, 2003; Saitoh *et al.*, 2006; Setiamarga *et al.*, 2008; Yamanoue *et al.*, 2008; Yamanoue *et al.*, 2007). The rapid rate of substitution in mitochondrial genes, however, can allow the sequences to reach early saturation, and consequently, suffer from systematic bias, especially when estimating divergences of older lineages, when not accounted for. Mitogenomes, nevertheless, have not been tested to infer intra-familial relationships that can reveal shallow and deep-lineage splits in fishes.

Here, I test the utility of mitogenomes to infer the relationships of several representatives of the family Haemulidae. In a previous study, which included the most comprehensive sampling of haemulids to date, Sanciangco *et al.* (2011) recovered two highly supported distinct clades for the two haemulid subfamilies, but provided no estimates of divergence time for the members of the group. Nevertheless, their phylogenetic hypothesis for most of the haemulids shows sister-species grouping that corroborates the results of earlier studies. In an investigation of the early mechanisms of allopatric speciation of some haemulids, Bernardi and Lape (2005) provided a more recent estimate for the divergence of two pairs of sister-species in *Anisotremus*, which is about 3.5 to 5 Ma and dates the closing of the Isthmus of Panama. This estimate is concordant and falls within the range of speciation dates for the same two pairs of sister-species in a review of divergence of several other marine organisms by Lessios (2008). Based on these findings, I can presume that the present-day distribution of haemulids is likely to have been influenced by at least two major vicariant events, including the more recent closing of the Isthmus, and another major event in the past that allowed sufficient lineage diversification for the two subfamilies to become fixed. In addition, the haemulids are an ideal candidate to test the effects of these vicariant events due to their worldwide distribution spanning the Atlantic, Indian, and Pacific Oceans. Furthermore, haemulids in the fossil record dates back from the Cenozoic, at a time when the Tethys was circumtropical and later divided into smaller oceans (Hobson, 2006). For many marine organisms, the geologic events following the closing of the Tethys have led to independent evolutionary paths for many species now separated by this barrier, and eventually gave rise to a diversity of other localized faunas (Adams, 1981; Hrbek and Meyer, 2003). And about six million years ago, another important biogeographic event subsequently influenced the distribution of many of those marine fauna, particularly at the Central American Isthmus. The formation of the land bridge, known as the Isthmus of Panama, had broken the continuity of the seaway and prevented migration of many marine organisms between Atlantic and Pacific sides of America (Bermingham *et al.*, 1997; Bernardi and Lape, 2005; Duque-Caro, 1990; Knowlton and Weigt, 1998; Pielou, 1979; Rocha and Bowen, 2008). Consequently, the gradual differentiation of these isolated marine fauna could have led to a decrease in population for some species that ultimately became extinct, or could have led to geminate species, as can be explained by the present distribution of many marine fishes, including the two pairs of sister-species of haemulids that we see today.

There are three main goals of this study. First, I test the utility of complete mitochondrial genomes to infer the phylogenetic relationships of several haemulids and compare results with previously published trees. I explore the utility of a high-throughput sequencing platform in generating complete mitogenomes from 26 haemulids. Second, I augment the sampling diversity of the family by adding sequences of species that have not been included in previous phylogenetic study of the group and infer the phylogeny of the haemulids based on available sequences from previous studies. Third, I estimate the dates of divergence for the members of the family using the mitogenome sequences. I hypothesize that the haemulids are Tethyan relicts, with some members subsequently impacted by the closing of the Isthmus of Panama.

MATERIALS AND METHODS

Taxon sampling, DNA isolation, and amplification of mitogenomes using long-PCR

Taxon sampling was limited to 26 unique haemulids, with a single representative for each genus, except for *Pomadasys* (Appendix F). Genomic DNA was isolated from approximately 20 mg of dorsal muscle tissue following the DNeasy® Kit (Qiagen) protocol for all haemulid specimens. A long-PCR technique was adapted to amplify the entire mitogenome sequence for each species in two reactions (Cheng *et al.*, 1994; Kawaguchi *et al.*, 2001; Yamanoue *et al.*, 2007). Each PCR reaction contained 15.25 µl deionized water, 2.5 µl LA Buffer II (provided in kit), 4.0 dNTPs, 1.0 µl of each forward and reverse primers, 0.25 µl of TaKaRa LA Taq® DNA Polymerase (Clontech Laboratories, Inc.), and 1.0 µl of template DNA. The template for the second PCR reaction is a 1:20 dilution of the first PCR product. The volume for the second PCR reaction was doubled (for a total of 50ul per PCR product for each species) in order to comply with volume requirements for the NGS (next-generation sequencing) run using the GS FLX 454 Genome Sequencer (Roche) for quality control purposes. Six fish-versatile long-PCR primers (Table 5) adapted from a previous study (Kawaguchi *et al.*, 2001) were used in various combinations to amplify contiguous, overlapping segments of the entire mitogenome. Samples were amplified using a nested PCR with the following conditions: initial denaturation at 94°C for one minute (to activate the DNA Polymerase), followed by 30 cycles of 98°C for 10 seconds and 68°C for 16 minutes for the first– and second PCR reactions. PCR products were visualized on 1%

agarose gel and quantitated using a NanoDrop (NanoDrop 2000c, Thermo Scientific) to estimate DNA concentration. Undiluted PCR products were sent to GenoSeq (UCLA Genotyping and Sequencing Core) for purification, library preparation, and sequencing, following the manufacturer's protocol using Roche's GS FLX 454 NGS platform.

TABLE 5. Primers used for the long-PCR technique to amplify the complete mitochondrial genomes of the Haemulidae.

Primer	Primer Sequence
L2508	5′-CTC GGC AAA CAT AAG CCT CGC CTG TTT ACC AAA AAC-3′
L12321	5′-GGT CTT AGG AAC CAA AAA CTC TTG GTG CAA-3′
H1065	5′-GGC ATA GTG GGG TAT CTA ATC CCA GTT TGT-3′
H2990	5′-TGC ACC ATT RGG ATG TCC TGA TCC AAC ATC-3′
H12293	5′-TTG CAC CAA GAG TTT TTG GTT CCT AAG ACC-3′
H15149	5′-GGT GGC KCC TCA GAA GGA CAT TTG KCC TCA-3′

Phylogenetic analysis

Raw sequence reads were assembled (with 5X iterations for fine-tuning) and annotated using the Geneious (Biomatters) software. After visual inspection of the assembled reads, a consensus sequence was generated for each species. The resulting consensus sequences were then annotated using the same reference sequence used for assembling reads. Gene annotations from the original reference sequence were then transferred to the consensus sequences. Gene regions were extracted from the newly annotated consensus sequences and exported as separate fasta files for downstream analyses.

Individual gene sequence alignments for coding and non-coding regions were conducted using MACSE (Ranwez *et al.*, 2011) and Clustal X (Thompson *et al.*, 1997), respectively, following default parameters (Hall, 2004; Ranwez *et al.*, 2011). The best-fit model for each of the data partitions was estimated using MrModelTest2 (Nylander, 2004) with models scored in PAUP* version 4.0b10 (Swofford, 2002). Substitution saturation tests for all regions were performed using the graphical exploration tool and statistical tests in DAMBE (Xia, 2013). For the mitogenome dataset, six different partitioning schemes were employed, including **Scheme 1**: no partition; **Scheme 2**: seven partitions = three for each of the three codon positions for 13 CDS (coding regions), one for 22 tRNAs (transfer RNA), two for ribosomal RNAs (12S and 16S rRNAs), and the control region (CR); **Scheme 3**: six partitions = three for each of the three codon positions for the 13 CDS, tRNAs, 12S, and 16S; **Scheme 4**: three partitions = three for each of the three codon positions for the 13 CDS only; **Scheme 5**: tRNA only; **Scheme 6:** two partitions = 12S and 16S (rRNA only); and **Scheme 7**: four partitions = three for each of the codon positions for the 13 CDS and one for tRNA. A concatenated dataset with six partitions, comprising of three codon positions for each exons, plus tRNAs, 12S, and 16S (Scheme 3), was preferred as the final partitioning scheme. For the non-mitogenome dataset (Appendix F), which is a concatenation of 22 partial mitochondrial and nuclear genes that were generated new in the lab or downloaded from Genbank (19 genera, 82 species), sequences were analyzed by each gene and by gene and by codon positions. A concatenated dataset with eight partitions, comprising of three codon positions across all nuclear exons and three codon positions for all mitochondrial exons, plus two separate partitions for the ribosomal S7 and 16S genes, was preferred as the final partitioning scheme for the 22-gene dataset. A rapid bootstrapping algorithm of RAxML (Randomized Axelerated Maximum Likelihood) (Stamatakis, 2014) with 1000 bootstrap replicates was estimated under the GTRCAT model and the collection of sample trees was used to draw the bipartition frequencies on the optimal tree. All RAxML analyses were performed via CIPRES portal.

Divergence time estimates

Divergence times were calculated in BEAST (Drummond *et al.*, 2012) using the uncorrelated lognormal (UCLN) clock-model. The RAxML tree with transformed branch lengths, performed in TreeEdit (v1.0a10), was used as the starting chronogram. The ingroup (Haemulidae) was constrained as monophyletic based on previous studies and a separate non-monophyletic taxon set was designated for all outgroups. The ingroup was assigned a temporal constraint of 50 million years based on secondary calibration (Betancur-R *et al.*, 2013a) and from Cenozoic record for haemulids (Hobson, 2006). The mitogenome dataset included six partitions (three for each of the three codon positions across all exons, tRNA, 12S, and 16S), which was chosen based on the resulting ML topology with the highest number of highly supported nodes. Other parameters included unlinked substitution model using GTR+G with four rates for each partition according to MrModelTest2 (Nylander, 2004) and clock and tree priors linked across partitions. The speciation birth-death process was used as the tree prior. Three replicates of the

Markov chain Monte Carlo (MCMC) analyses were run for 200 million generations. Posterior estimates from MCMC log files were assessed and summarized using Tracer v1.6 (Rambaut and Drummond, 2007) and was considered complete when the effective sample size of each parameter estimate reached >200. All tree files from three MCMC runs were combined in LogCombiner v1.7.5 (Drummond *et al.*, 2012), with the first 10% of trees from each run discarded as burn-in, and re-summarized using Tracer v1.6. The posterior sample of trees were used to produce a maximum clade credibility tree, with means and 95% highest posterior density of divergence times, which was then estimated and summarized using TreeAnnotator v1.7.5 (Drummond *et al.*, 2012). The posterior probabilities were visualized as node annotations in the resulting tree using FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/).

RESULTS AND DISCUSSION

Twenty two of the 26 unique long-PCR products submitted for high-throughput sequencing were successfully amplified and produced overlapping segments to complete the mitochondrial genome sequences. Two additional mitogenome sequences with gaps were also included. Twenty four of the 26 unique samples from long-PCR products successfully generated more than 210,000 individual sequence reads with a 30X coverage and varied from 4,223 to 16,366 reads for each species. Complete mitogenome sequences ranged from 15,920 bp to 16,866 bp in length, with mean read length of 187.2 bp and 99% assembling to a reference sequence. Additional mitogenomes for two haemulid species and five outgroups were downloaded from Genbank and included in the analysis. The final dataset is a concatenation of the annotated 13 protein-coding genes, 22 tRNA, and the two ribosomal RNA genes (12S and 16S).

Figures 10 to 15 show scatter plots of the observed transitions and transversions against genetic distance implemented in DAMBE (Xia, 2013). Results of substitution saturation test for all regions illustrate both transitions and transversions generally increasing with genetic distance. This indicates little to no saturation, except at the third codon positions across all coding regions where some level of saturation is evident (Fig. 12). Substitution saturation refers to the state when sequences are no longer informative about the underlying evolutionary process. Therefore, in the extreme case when sequences have become fully saturated, the phylogenetic signal is lost, allowing gene sequences to cluster based on the similarity in their base composition (nucleotide frequencies) regardless of their true genealogy (Xia, 2013). In a scatter plot, substitution saturation is indicated by the leveling off or curving of data points, as if reaching a plateau, as sequence divergence increases. However, when saturation was assessed using the more quantitative entropy-based index of substitution saturation test (Table 6; also implemented in DAMBE), the third codon positions show little saturation and therefore are still considered phylogenetically informative. The terminology "little saturation" is based on the interpretation of results from Xia *et al.*'s (Xia, 2013; Xia *et al.*, 2003) index of substitution saturation (if $p<0.5$ and $I_{ss}< I_{ss}.c$ = little saturation; if $p<0.5$ and $I_{ss}> I_{ss}.c$ = useless sequences; if $p>0.5$ and $I_{ss}< I_{ss}.c$ = substantial saturation; and if $p>0.5$ and $I_{ss}> I_{ss}.c$ = very poor for phylogenetics). Nevertheless, saturation at third codon position, which is inherent to many markers, can actually improve resolution for many groups (Källersjö *et al.*, 1999). Therefore caution should be observed when treating third codon positions, especially when weighting or removing characters for further analyses.

The results from RAxML analysis for all partitioning strategies for the mitogenome dataset produced largely congruent topologies with similar clade components for major nodes (Table 7). Scheme 3, which had the most number of highly supported nodes, was chosen as the final partitioning strategy and its resultant phylogeny is presented in Figure 16. The results of the RAxML analyses is also congruent with the ML tree from Sanciangco *et al.* (2011), with I_{cong} = 1.37 and p-value = 9.49×10^{-4}). As expected, I recovered the family Haemulidae and the two subfamilies, Plectorhinchinae and Haemulinae, as monophyletic. The support for the subfamilial diversification is high, with 100% bootstrap score. In addition, I recovered *Plectorhinchus* and *Pomadasys* as not monophyletic. Similar to previous findings, *Diagramma* is nested in the *Plectorhinchus*. *Pomadasys* is polyphyletic, appearing in three places in the tree. Clade I is a well-supported clade comprised of *P. perotaei*, *P. maculatus*, and *P. olivaceus*, all of which are restricted to the Old World; Clade II is comprised of *P.argyreus*, *P. kaakan*, *P. macracanthus*, and *P. panamensis*, and close to a clade containing *P. stridens* and *Boridia*, and Clade III includes *P. branickii* and the New World genera *Conodon*, *Xenichthys*, and *Haemulopsis*.

The clade components in my tree are mostly consistent with those of the previously published phylogeny, but with higher support for the nodes using the longer mitogenome sequences. This increase in nodal support can be attributed to the higher number of informative sites and the effectiveness of longer mitochondrial sequences to account for rapid radiations within the family. It is generally accepted that silent substitutions accumulate at a relatively faster rate in mitochondrial genes than in nuclear genes, making them suitable markers for

TABLE 6. Results of the substitution saturation test by Xia *et al.* (2003) conducted for each dataset partition. CDS_1, CDS_2, and CDS_3 refer to the first, second, and third codon positions of the 13 protein coding regions. CR refers to the control region. The resulting I_{ss} values for all partitions are significantly smaller than $I_{ss.c}$, which means that the sequences for each region have only experienced little saturation. I_{ss} refers to the index of substitution saturation and $I_{ss.c}$ refers to the critical Iss value, at which the sequences will begin to fail to recover the true tree.

	CDS_1	**CDS_2**	**CDS_3**	**tRNA**	**12S**	**16S**	**CR**
Proportion of invariant sites	0.2743	0.2132	0.0068	0.0000	0.0000	0.0000	0.0000
I_{ss}	0.1022	0.0397	0.6075	0.1449	0.0936	0.1207	0.2801
$I_{ss.c}$	0.7397	0.7433	0.7007	0.6665	0.7402	0.7683	0.7164
Prob (Two-tailed)	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

***if p<0.5 and Iss < Iss.c = little saturation; if p<0.5 and Iss > Iss.c = useless sequences; if p>0.5 and Iss < Iss.c = substantial saturation; and if p>0.5 and Iss > Iss.c = very poor for phylogenetics.**

TABLE 7. Results of congruence tests between the RAxML trees generated for each partitioning scheme performed using de Vienne *et al.*'s (2007) congruence index. The values refer to the calculated Congruence index Icong and the associated P-value, respectively. All associations show significant congruence (i.e. trees are more congruent than expected by chance).

		1	**2**	**3**	**4**	**5**	**6**
		noPartition	**wPartition**	**wPartition_noCR**	**CDS**	**tRNA**	**rRNA**
1	**noPartition**						
2	**wPartition**	3.69; 1.89e-19					
3	**wPartition_noCR**	3.32; 7.42e-17	3.44; 1.01e-17				
4	**CDS**	2.95; 2.92e-14	3.075; 3.99e-15	2.95; 2.92e-14			
5	**tRNA**	2.21; 4.52e-09	2.21; 4.52e-09	2.58; 1.15e-11	2.34; 6.174e-10		
6	**rRNA**	3.07; 3.99e-15	3.075; 3.99e-15	2.71; 1.57e-12	2.584; 1.15e-11	2.21; 4.52e-09	
7	**CDS+tRNA**	2.95; 2.92e-14	2.83; 2.14e-13	2.71; 1.57e-12	3.20; 5.44e-16	2.46; 8.42e-11	2.71; 1.57e-12

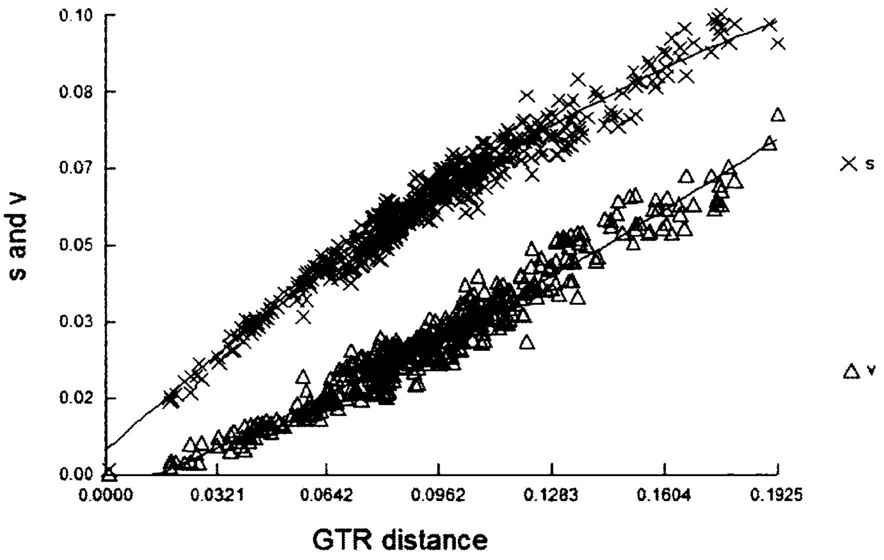


FIGURE 10. Frequency of observed transitions (Xs) and transversions (open triangles) against corrected genetic distance for the first codon positions across all 13 protein-coding regions, as implemented in DAMBE.

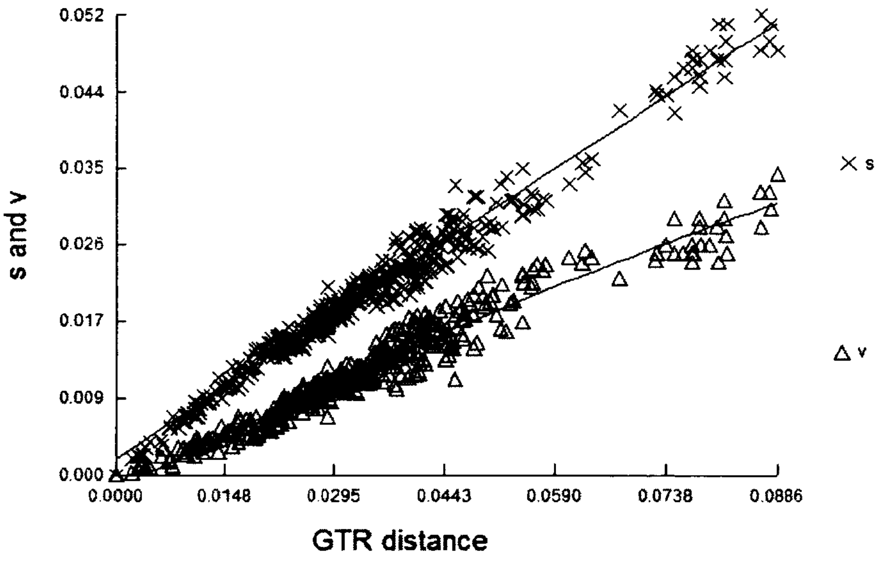


FIGURE 11. Frequency of observed transitions (Xs) and transversions (open triangles) against corrected genetic distance for the second codon positions across all 13 protein-coding regions, as implemented in DAMBE.

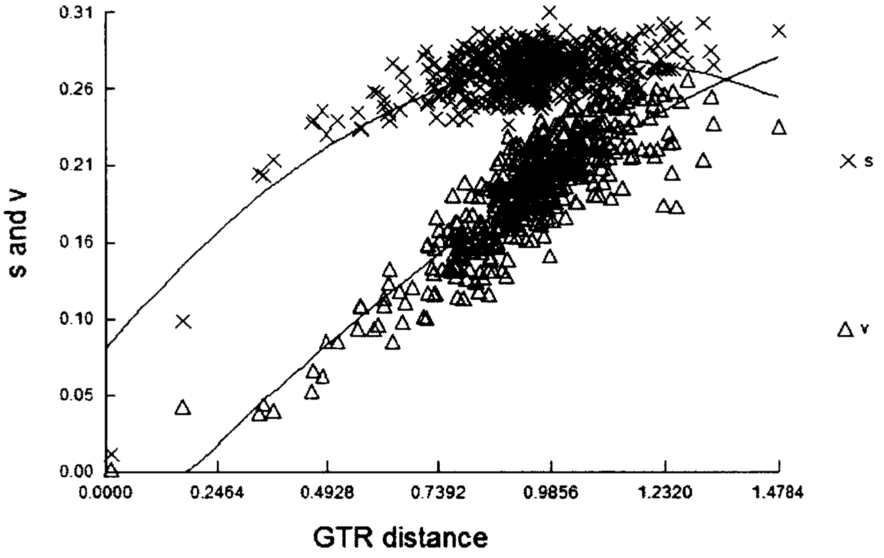


FIGURE 12. Frequency of observed transitions (Xs) and transversions (open triangles) against corrected genetic distance for the third codon positions across all 13 protein-coding regions, as implemented in DAMBE.

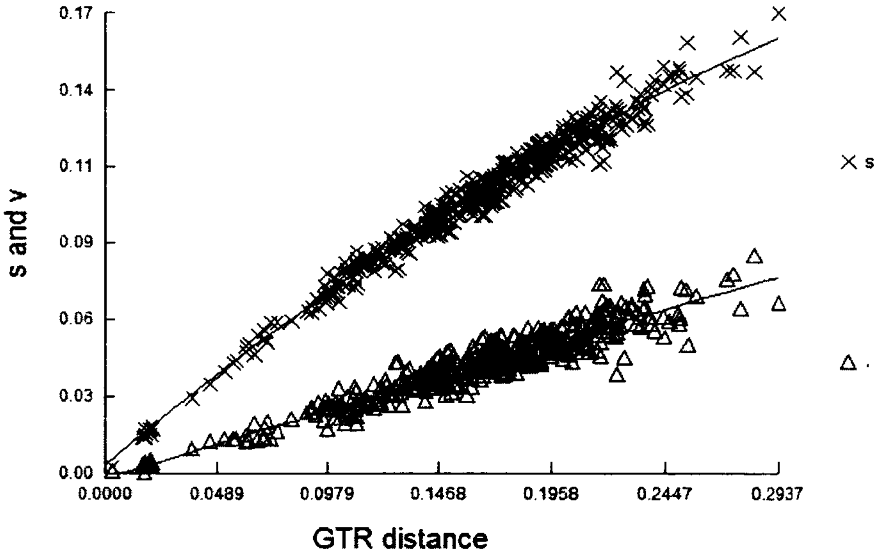


FIGURE 13. Frequency of observed transitions (Xs) and transversions (open triangles) against corrected genetic distance for all 22 tRNAs, as implemented in DAMBE.

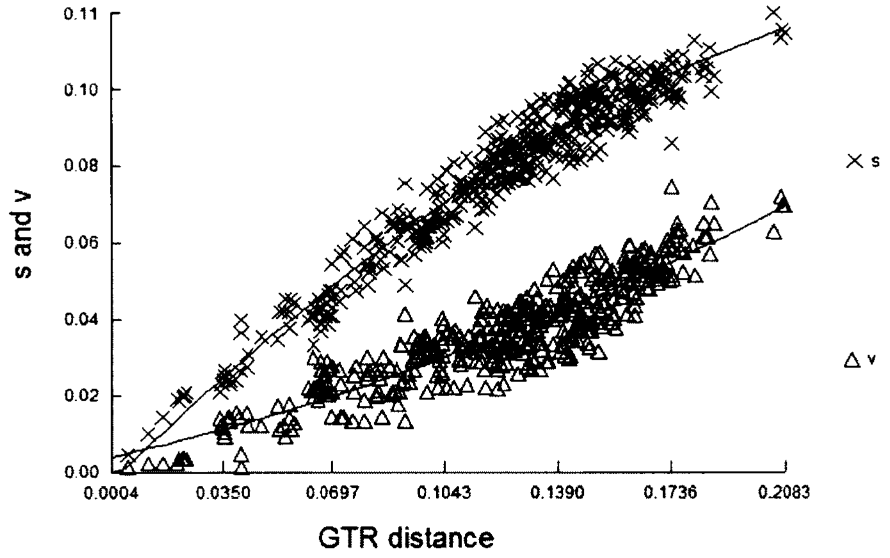


FIGURE 14. Frequency of observed transitions (Xs) and transversions (open triangles) against corrected genetic distance for the 12S region, as implemented in DAMBE.

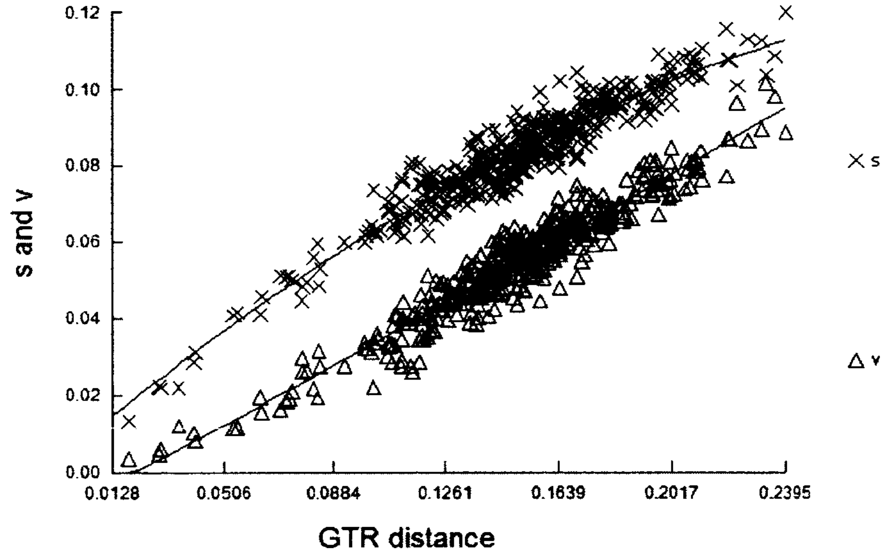


FIGURE 15. Frequency of observed transitions (Xs) and transversions (open triangles) against corrected genetic distance for the 16S region, as implemented in DAMBE.

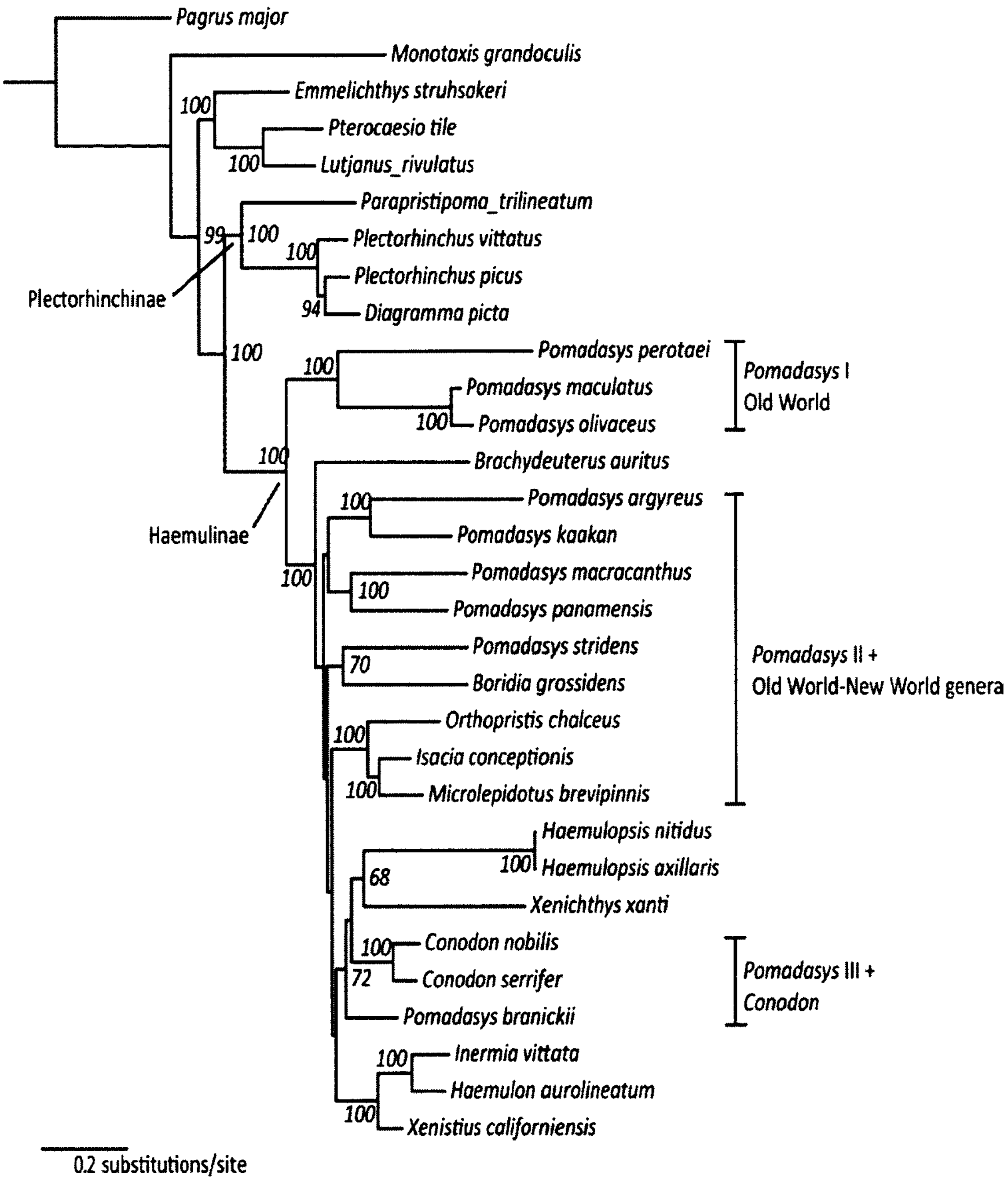


FIGURE 16. Phylogeny of haemulid representatives inferred from RAxML analysis of complete mitochondrial genome sequences. The final dataset is a concatenation of six partitions comprised of three codon positions for each exons, plus tRNAs, 12S, and 16S. Values on the nodes represent bootstrap support from RAxML analysis. Nodes with less than 50% bootstrap score are not shown.

detecting phylogenetic information of species that have recently diverged (Avise *et al.*, 1987; Moore, 1995). However, the results of the mitogenome dataset are only based on a limited taxon sampling of the genus *Pomadasys* and of the family (14 genera, 26 species).

In addition, the results of BEAST analysis (Fig. 17) on the estimated times of divergence gave unexpected insights into the possible biogeographic radiation of haemulid clades of Old World (Indo-Pacific and Eastern Atlantic) and New World (both coasts of the Americas) species, with respect to tectonic movements. All members of the subfamily Plectorhinchinae are Old World, while Haemulinae are mostly New World species. The closing of the Tethys Sea is one possible explanation for the results of the molecular data analysis. The members of the family possibly had a continuous Tethyian distribution when Africa and the Middle East united with Eurasia near the Oligocene-Miocene boundary. Haemulids first evolved during the Cenozoic, a time when the Tethys was circumtropical and later ceased to exist (Hobson, 2006). Haemulids are coastal species and presumably require a more-or-less continuous coastline to become reproductively cohesive. These coastal fishes probably evolved in a continuous distribution during the period of a continuous Tethys Sea. When the Tethys Sea closed and the Atlantic Ocean widened, these haemulids would have continued to evolve in allopatry. The subfamily Plectorhinchinae (*Parapristipoma* and *Plectorhinchus* plus *Diagramma*) has members both in the Indo-Pacific and Eastern Atlantic. Plectorhinchines probably evolved prior to the closing of the Tethys, but after the Atlantic Ocean widened to an extent that prevented transoceanic migration. Conversely, almost all members of the subfamily Haemulinae, with the exception of two genera, *Brachydeuterus* and *Pomadasys*, are restricted to the New World, occurring in the Eastern Pacific or Western Central Atlantic, and presumably evolved prior to the relatively recent closing of the Panamanian Isthmus (Bernardi and Lape, 2005). However, the paraphyletic *Pomadasys* forms a group between Old World and New World haemulid groups as they occur in both the Old– and New Worlds. This can be associated with the separation of the Old World and New World tectonic plates and the widening of the Atlantic Ocean that may have resulted into two separately evolving clades. The intermediate paraphyletic *Pomadasys* group might have evolved when the Old World was separating from the New World and could potentially have been continually evolving as the Atlantic Ocean widened. Consequently, the possible radiation of haemulids is from a basal Old World group leading to a derived (mostly) New World group and places the members of the genus *Pomadasys* in the paraphyletic and intermediate Old

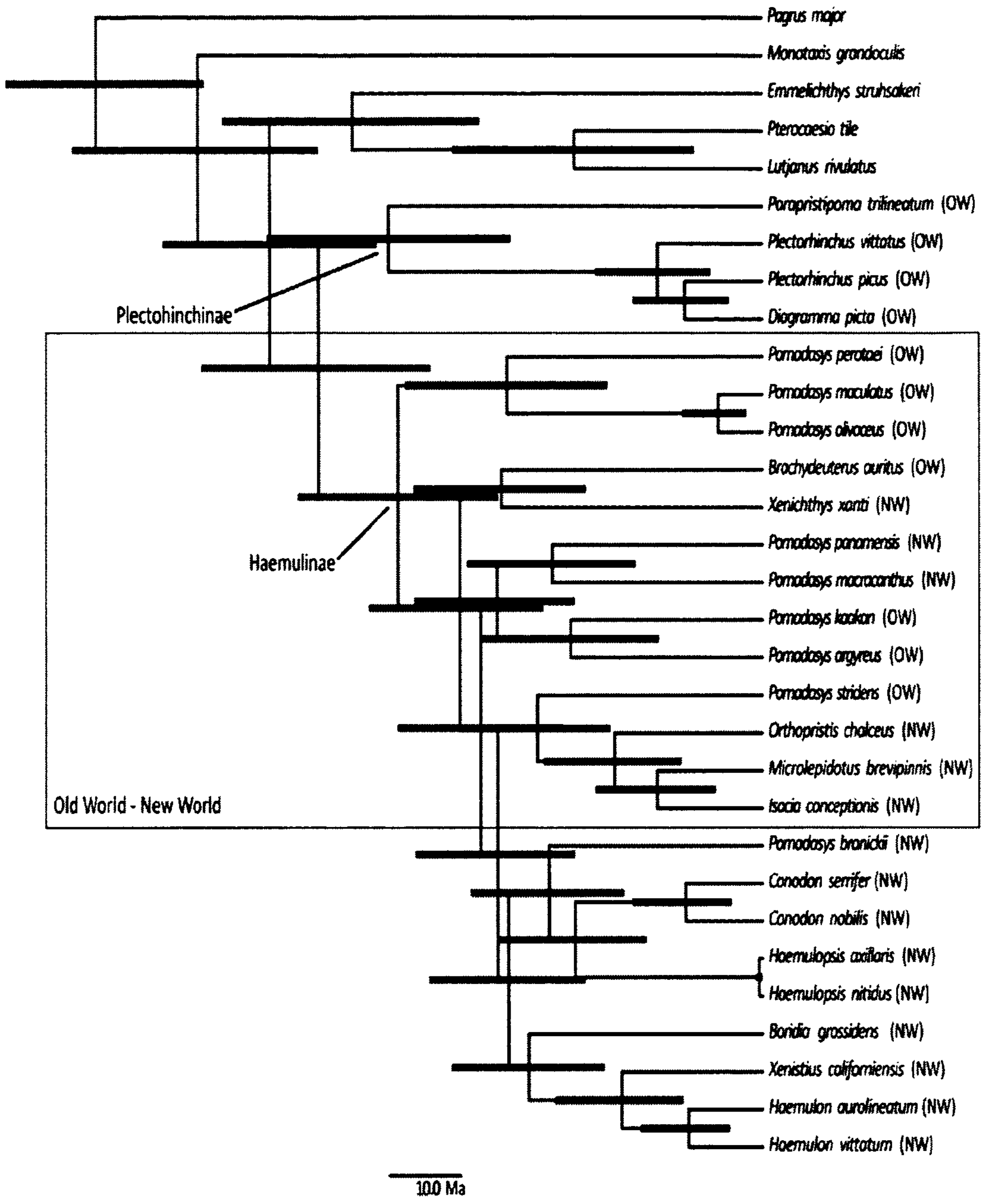


FIGURE 17. Time-calibrated BEAST phylogeny estimated from the complete mitochondrial genome of haemulid representatives. A single calibration is placed on the ingroup (Haemulidae). Bars represent the 95% highest posterior distribution of divergence times. OW – Old World distribution; NW – New World distribution. Ma – million years ago.

World-New World group. Further sampling, including molecular and morphological characterization of all *Pomadasys* species is required to test this hypothesis.

In addition to analyzing the complete mitogenome sequences, I reconstructed a RAxML topology for haemulids (19 genera, 82 species) using a concatenated dataset of 22 genes from all available sequences from Genbank plus some newly generated sequences. Figure 18 shows the RAxML topology for the 22-gene dataset. To date, this is the most inclusive account of sequences included and taxonomic coverage presented for the haemulids and shows resolution for most of the inter-generic relationships that were previously not recovered using a limited taxon sampling and number of genes. The dense taxonomic sampling and using a concatenated dataset of combined mitochondrial and nuclear genes allowed a more accurate estimate of the phylogenetic relationships of the family, particularly for members of *Pomadasys* that has been elusive based on previous molecular studies. Consistent with the results of the mitogenome dataset and from previous studies that have included a limited number of taxa, the monophyly of the family and the two subfamilies are supported (100% BS). Within the subfamily Plectorhinchinae, *Plectorhinchus* is only monophyletic with the inclusion of *Diagramma*. Frequent synonyms and/or species misidentification is a common problem for many *Plectorhinchus*. This is because members of *Plectorhinchus* exhibit diverse coloration throughout their development, with juveniles looking relatively different from adults. I defer reclassification of this clade and recommend further examination of the members of the group using morphological and molecular evidences.

Within Haemulinae, *Anisotremus* is sister to *Genyatremus* (67% BS). *Anisotremus moricandi* is nested within the *Genyatremus*, a finding that contradicts previous phylogenetic hypothesis (Tavera *et al.*, 2011) for the members of this group based on morphological analysis of the oral and pharyngeal jaws. The *Anisotremus-Genyatremus* clade is sister to all *Haemulon* (96% BS). *Haemulon* is monophyletic, including the former *Xenistius californiensis*. The clade comprising of *Isacia*, *Microlepidotus*, *Emmelichthyops* (not sampled in the mitogenome data), and *Orthopristis* is highly supported (99%), and corroborates results of the mitogenome analysis. *Haemulopsis* is monophyletic, including the former *Pomadasys corvinaeformis* (100% BS). This finding was first reported by Tavera *et al.* (2012), and I follow their taxonomic suggestion for this species. *Haemulopsis* is sister to a clade comprised of *Conodon* and *Xenichthys* (99% BS).

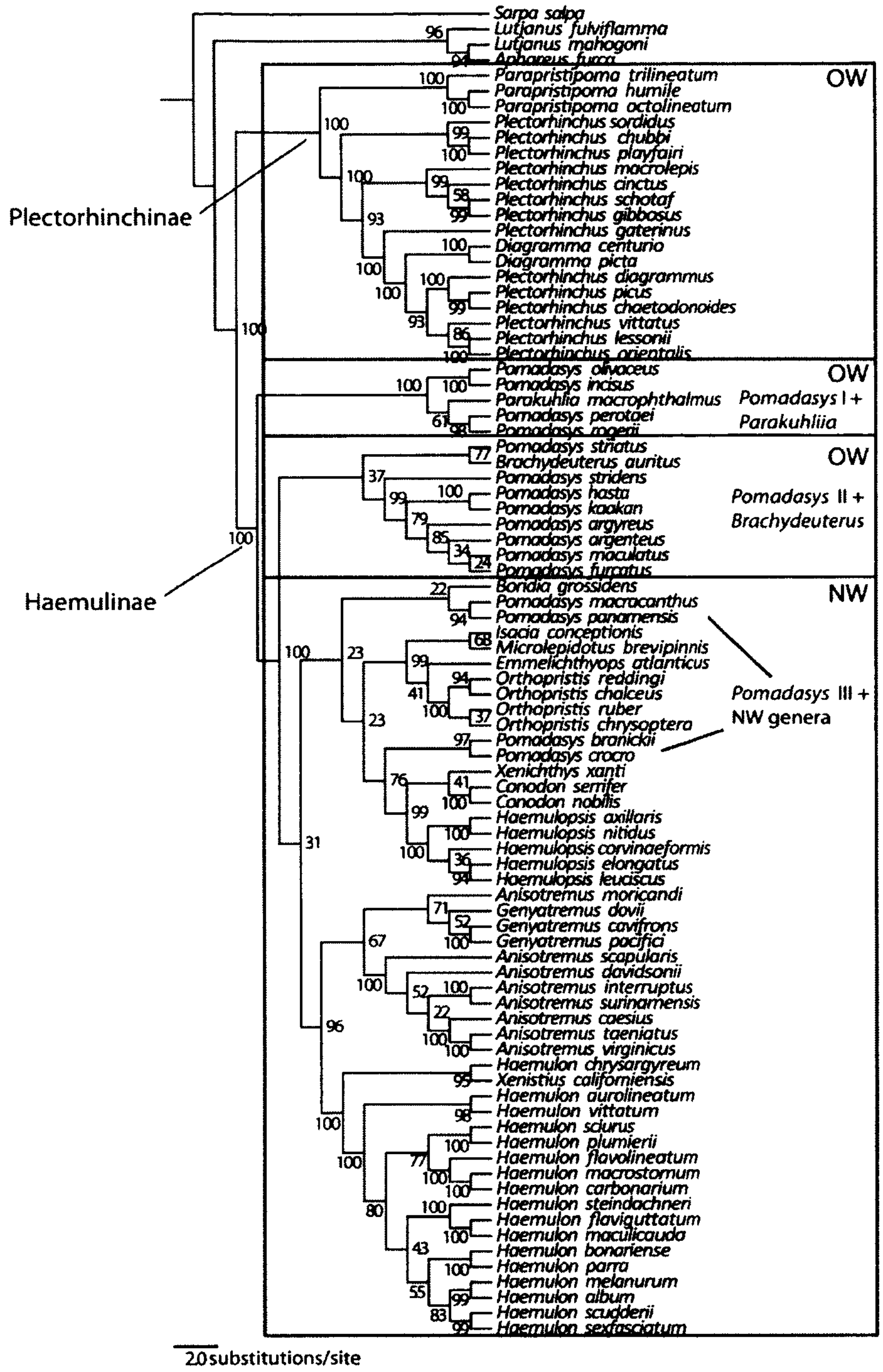


FIGURE 18. Phylogeny of haemulids inferred from RAxML analysis of the 3+ dataset from 22 genes. The final dataset is a concatenation of eight partitions comprised of three codon positions across all nuclear exons, three codon positions for all mitochondrial exons, plus two separate partitions for the ribosomal S7 and 16S genes. Values on the nodes represent bootstrap support from RAxML analysis. OW – Old World distribution; NW – New World distribution.

Members of *Pomadasys* are in three different clades that are consistent with the Old World-New World hypothesis and supported by morphological characters. The New World *Pomadasys* (*P. branickii* and *P. crocro*) is sister to a clade comprised of *Xenicthys*, *Conodon*, and *Haemulopsis* (76% BS). New World *Pomadasys* possess 12-13 dorsal spines, with 11-13 soft rays, and three anal spines, with six to eight soft rays. A secondary clade is comprised of Old World *Pomadasys* (*P. furcatus*, *P. maculatus*, *P. argenteus*, *P. argyreus*, *P. kaakan*, *P. hasta*, *P. stridens*, and *P. striatus*), and includes the monotypic *Brachydeuterus*, but support for this is weak (37% BS). However, the members of this clade are diagnosed by having 12 dorsal spines, with 11-15 soft rays, and three anal spines, with six to nine soft rays (seven common). The third clade, which is basal to all haemulines, is comprised of the rest of the OW *Pomadasys* (*P. olivaceus*, *P. incisus*, *P. perotaei*, and *P. rogerii*), and includes *Parakuhlia* (100% BS). The members of this clade are diagnosed by having 11-13 dorsal spines, with 15-17 soft rays, and three anal spines, with 10 or more soft rays.

The inclusion of the monotypic *Parakuhlia* within the haemulines confirms its placement in the family Haemulidae. Previous studies have suggested close relationships among sunfishes (Centrarchidae) and flagtails (Kuhliidae) (Allen, 1981; Maugé and Desoutter, 1990; Pellegrin, 1913). Nelson (2006), however, suggested that the monotypic species may actually belong in the family Haemulidae (grunts), without providing any explanation. Sanciangco *et al.* (2011) also indicated that *Parakuhlia* might belong in the Haemulidae and suggested a haemuline designation based on morphology. Pellegrin (1913) was the first to establish the genus name, *Parakuhlia*, citing that the species bears striking similarities with *Kuhlia*. The name is from the Greek *para-*, which means "beside or near," and which Pellegrin used to describe the genus and species. Pellegrin noted the similarity between *Parakuhlia* and *Kuhlia* based on external morphology, in particular, by the presence of a developed pseudobranch. He also noted that *Parakuhlia* is discernible from *Kuhlia* by the presence of small scales on the interorbital space, the higher number of spines and soft rays in dorsal and anal fins, and the absence of a separate denticulation palate. According to Pellegrin, this last character is also a synapomorphy shared by the centrarchids (sunfishes), a percoid confined to the fresh waters of North America. Members of *Kuhlia*, on the other hand, are widely distributed in the Indo-Pacific and South Australia and are marine inhabitants, except for one, which inhabits fresh and brackish waters of eastern Africa. Pellegrin commented that it is not reasonable to assign *Parakuhlia* in a group that has no documented reports of occurrence for its members in the region and, therefore, subsumed

Parakuhlia within the sunfishes. This study is the first to include this species in a molecular phylogenetic analysis. My results placed *Parakuhlia* in a clade with members currently assigned to *Pomadasys* that are found in the Old World and share similar meristic characters. My sampling for members of *Pomadasys*, however, is not complete. A comprehensive sampling of the members of the genus *Pomadasys* and further investigation of the interrelationships within the family using morphological characters is necessary for reclassification, and possibly, renaming members of the new group. To date, there are 35 putative species belonging to the genus *Pomadasys* (Eschmeyer, 2013).

In this study, I showed the power of complete mitogenomes in inferring intra-familial relationships, as corroborated by results of previous studies using a combination of nuclear and mitochondrial genes. The complete mitogenomes of haemulid representatives showed improved support for some of the nodes in the topology, and better accounted for the more recent radiation within the family. My results are concordant with previous findings and support the monophyly of the family Haemulidae, as well as the two subfamilies, Plectorhinchinae and Haemulinae. My clade components for some of the major nodes are also concordant regardless of the limited taxon sampling for the mitogenome dataset. However, inclusion of dense taxon sampling and using a concatenated 22 genes of combined mitochondrial and molecular markers provided better resolution for inter-generic relationships and a more accurate phylogenetic hypothesis for Haemulidae. In particular, the molecular evidence shows three separate clades for members of *Pomadasys* that are consistent with Old and New World distributions and are supported by morphological characters such as the number of dorsal and anal fin spines and rays. A more comprehensive examination of the members of *Pomadasys*, as well as for the *Plectorhincus* plus *Diagramma* group, using both molecular and morphological characters will likely result in a revision of generic assignments within the Haemulidae.

CHAPTER V

CONCLUSIONS

The goals of this dissertation were to infer the phylogenetic relationships of the members of the family Haemulidae, to provide a reliable taxonomic framework for the haemulids in the greater percomorph group, and to test the utility of mitochondrial genomes and multi-locus data to better resolve interrelationships within the family.

In Chapter two I presented the first nearly comprehensive phylogenetic hypothesis for the family Haemulidae based on a combined dataset of five genes (mitochondrial and nuclear, 4731 bp) with all sequences present for 56 species representing 18 genera of the expanded haemulids. Results from maximum parsimony, maximum likelihood, and Bayesian analyses show strong support for a monophyletic Haemulidae with the inclusion of former inermiids, *Inermia vittata* and *Emmelichthyops atlanticus*. The former inermiids did not form a clade indicating that the highly protrusible upper jaw specialization to planktivory evolved more than once within the Haemulidae. The subfamilies Haemulinae and Plectorhinchinae, currently diagnosed by eight morphological characters, most notably the number of chin pores and the origin of the retractor dorsalis, are also recovered as monophyletic from these analyses, with the Haemulinae sister to the Plectorhinchinae. However, results of the analyses also call into question the monophyly of a number of genera, including *Plectorhincus*, *Anisotremus*, *Haemulon*, and *Pomadasys*. Furthermore, results show Haemulidae as sister to Lutjanidae and *Hapalogenys* as outside the Haemulidae based on a limited sampling of outgroup taxa. These results suggest that further taxon sampling within the haemulids, as well as an expanded sampling to include other percomorphs, and possibly use of more genes can help define limits and relationships of haemulids.

Perciformes, the order to which the haemulids belong, is a large and diverse group of spiny-finned fishes that has come to be known as the "bush at the top" due to the persistent lack of phylogenetic resolution among its members. Despite significant progress made in accommodating the diversity of percomorph taxa into major clades, there were ca. 49 families, traditionally placed in Perciformes that were not examined in previous studies. In Chapter three I provided evidence for the phylogenetic affinities of 14 of those 49 families, five of which have remained enigmatic. I restricted the taxonomic sampling to 1231 percomorph species, including taxa from more recent studies. Results of maximum likelihood analysis revealed that the new additions, bathyclupeids (Bathyclupeidae), galjoen fishes (Dichistiidae), kelpfishes (Chironemidae), marblefishes (Aplodactyliodae), trumpeters (Latridae), barbeled grunters (Hapalogenyidae), slopefishes (Symphysanodontidae), and picarel porgies (Centracanthidae), are placed within the Percomorpharia ("new bush at the top"). The superfamily Sparoidea was recovered as monophyletic and closely related to tripletails (Lobotidae), barbeled grunters, and sillagos (Sillaginidae), albeit support for this group is low. The picarel porgies and porgies (Sparidae) are now in one clade. None of the newly examined families belongs in the order Perciformes, as previously defined. The results also corroborate placement for the Australasian salmons (Arripidae) within Pelagimorpharia, and the false trevallies (Lactariidae) within Carangimorpharia. Furthermore, the results for this chapter show sister group relationships for the haemulids, previously classified as *incertae sedis* in Percomorpharia. The phylogenetic hypothesis shows haemulids are sister to Lutjanidae plus Caesionidae and in a clade together with Callanthiidae, Malacanthidae, Pomacanthidae, Emmelichthyidae, Acanthuridae, Zanclidae, Luvaridae, Monodactylidae, Sciaenidae, Chaetodontidae, and Leiognathidae, however, support for this group is weak (31 % bootstrap score). Nevertheless, a bigger assemblage comprised of this clade, plus the most recent common ancestor of Lobotiformes (including Hapalogenyidae), Spariformes, Lophiiformes, Tetraodontiformes, Ephippiformes, Sillaginidae, and Moronidae, is now supported (82% bootstrap score), indicating phylogenetic affinity for the members of this group. This study presents the most inclusive dataset for the percomorphs to date, reports novel hypothesis regarding interfamilial relationships of many groups, and provides a framework for delimiting groups for examining morphological characters and investigating intrafamilial relationships.

Chapter four further investigated the phylogenetic relationships within the Haemulidae by testing the utility of complete mitochondrial genome sequences (about 16,000 bp) to infer the relationships among the genera (14 genera with 26 haemulids) in order to address what might have been the limits (e.g. fewer number of characters) in chapter two. The complete mitogenome sequences, comprised of six partitions (three codon positions for each exon, plus tRNAs, 12S, and 16S) were subjected to RAxML analysis. The results are concordant with previous molecular studies that have used a limited number of genes, and with similar clade components for most of the genera, but with higher support for the nodes. Similar to previous findings, the family Haemulidae and the two subfamilies were recovered as monophyletic. The genus *Plectorhinchus* is paraphyletic, with the inclusion of *Diagramma*. *Pomadasys* is polyphyletic, including a restricted Old World *Pomadasys* clade that is basal to all haemulines. Resolution at the species level, however, is not possible due to limited availability of mitogenome sequences for the haemulids. The results of the more inclusive 22-gene dataset (19 genera, 82 species), but which suffers from incomplete or missing data, provided resolution of the interrelationships within the family, including those for the three *Pomadasys* clades that are consistent with biogeographic distribution and are supported by morphological characters.

The results of this dissertation also indicate that dense taxonomic sampling, in combination with an increased number of genes (character sampling), greatly improved the accuracy of inferences regarding phylogenetic relationships within the family, compared to analyzing datasets with a limited number of genes (e.g. 5-gene dataset) or those with limited taxonomic sampling (e.g. mitogenome dataset). This is also true for the percomorph phylogeny, in which no previous information is available regarding the placement and relationships of many taxa. The inclusion of new taxa in this dataset posed novel hypotheses regarding many sister-group relationships. Also, the addition of two mitochondrial genes, though they did not resolve all recalcitrant nodes, provided increased resolution to some of the more derived clades in the percomorph tree. Future studies that will incorporate many more taxa and include a wider subset of genes will help get investigators closer to unraveling the complex phylogenetic relationships within percomorphs. Furthermore, a more comprehensive molecular and morphological examination of the members of *Pomadasys*, as well as for the *Plectorhincus* plus *Diagramma* group, will likely result in a revision of generic assignments within the Haemulidae.

REFERENCES

Adams, C.G. (1981) An outline of tertiary palaeogeography. *In:* Cocks, L.R.M. (Ed), *The evolving earth*, London, UK: British Museum of Natural History, pp. 221–235.

Akazaki, M. (1962) Studies on the spariform fishes — Anatomy, phylogeny, ecology and taxonomy. Misaki Marine Biological Institute, Kyoto University, pp. 1–368.

Alfaro, M.E., Santini, F., Brock, C., Alamillo, H., Dornburg, A., Rabosky, D.L., Carnevale, G. & Harmon, L.J. (2009) Nine exceptional radiations plus high turnover explain species diversity in jawed vertebrates. *Proceedings of the National Academy of Sciences of the United States of America,* 106, 13410–13414.

Allen, G.R. (1981) Kuhliidae. *In:* Fischer, W. & Bianchi, G. (Eds), *FAO species identification sheets for fishery purposes. Eastern Central Atlantic (Fishing areas 34, 47 (in part)),* FAO, Rome.

Anderson, W., Jr., Baranes, A. & Goren, M. (2011) Redescription of the perciform fish *Symphysanodon disii* (Symphysanodontidae) from the Gulf of Aqaba, Red Sea, with comments on *S. pitondelafournaisei* and sexual dimorphism in the genus. *Zootaxa,* 3027, 1–8.

Anderson, W.D., Jr. (2000) Symphysanodontidae. *In:* Carpenter, K.E. & Niem, V.H. (Eds), *FAO Species Identification Guide for Fishery Purposes. The Living Marine Resources of the Western Central Pacific Vol. 4. Bony Fishes Part 2 (Mugilidae to Carangidae),* Food and Agriculture Organization of the United Nations, Rome, pp. 2438–2441.

Anderson, W.D., Jr. (2003) Symphysanodontidae. *In:* Carpenter, K.E. (Ed), *The Living Marine Resources of the Western Central Atlantic. Vol. 2. Bony Fishes Part 1 (Acipenseridae to Grammatidae),* Food and Agriculture Organization of the United Nations, Rome, pp. 1304–1307.

Anderson, W.D., Jr. & Springer, V.G. (2005) Review of the perciform fish genus *Symphysanodon* Bleeker (Symphysanodontidae), with descriptions of three new species, *S. mona, S. parini,* and *S. rhax. Zootaxa,* 996, 1–44.

Apparao, T. (1966) On some aspects of the Biology of *Lactarius lactarius* (Schneider). *Indian Journal of Fisheries,* 13, 334–349.

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. *Annual Review of Ecology and Systematics,* 18, 489–522.

Berendzen, P.B. & Dimmick, W.W. (2002) Phylogenetic relationships of Pleuronectiformes based on molecular evidence. *Copeia,* 642–652.

Bermingham, E., McCafferty, S.S. & Martin, A.P. (1997) Fish biogeography and molecular clocks: perspectives from the Panamanian Isthmus. *In:* Kocher, T.D. & Stepien, C.A. (Eds), *Molecular Systematics of Fishes*. Academic Press, New York, pp. 113–128.

Bernardi, G., Alva-Campbell, Y.R., Gasparini, J.L. & Floeter, S.R. (2008) Molecular ecology, speciation, and evolution of the reef fish genus *Anisotremus. Molecular Phylogenetics and Evolution,* 48, 929–935.

Bernardi, G. & Lape, J. (2005) Tempo and mode of speciation in the Baja California disjunct fish species *Anisotremus davidsonii. Molecular Ecology,* 14, 4085–4096.

Betancur-R, R., Broughton, R.E., Wiley, E.O., Carpenter, K., Lopez, J.A., Li, C., Holcroft, N.I., Arcila, D., Sanciangco, M., Cureton, J.C., II., Zhang, F., Buser, T., Campbell, M.A., Ballesteros, J.A., Roa-Varon, A., Willis, S., Borden, W.C., Rowley, T., Reneau, P.C., Hough, D.J., Lu, G., Grande, T., Arratia, G. & Orti, G. (2013a) The tree of life and a new classification of bony fishes. *PLOS Currents,* 5.

Betancur-R, R., Li, C., Munroe, T.A., Ballesteros, J.A. & Orti, G. (2013b) Addressing gene tree discordance and non-stationarity to resolve a multi-locus phylogeny of the flatfishes (Teleostei: Pleuronectiformes). *Systematic Biology,* 62, 763–785.

Betancur-R, R. & Orti, G. (2014) Molecular evidence for the monophyly of flatfishes (Carangimorpharia: Pleuronectiformes). *Molecular Phylogenetics and Evolution.*

Betancur-R, R., Wiley, E., Miya, M., Lecointre, G., Bailly, N. & Ortí, G. (2013c) *New and Revised Classification of Bony Fishes Version 2* (http://www.deepfin.org/Classification_v2.htm).

Biomatters (2013) Geneious version (6.1.6). Available from http://www.geneious.com/. *In.*

Bloch, M.E. & Schneider, J.G. (1801) *M.E. Blochii Systema Ichthyologiae iconibus cx illustratum.* Berlin.

Brandley, M.C., Schmitz, A. & Reeder, T.W. (2005) Partitioned Bayesian analyses, partition choice, and the phylogenetic relationships of scincid lizards. *Systematic Biology,* 54, 373–390.

Brown, R.W. (1956) *Composition of scientific words: A manual of methods and a lexicon of materials for the practice of logotechnics.* Washington, D.C.: Smithsonian Institution Press.

Burridge, C.P. & Smolenski, A.J. (2004) Molecular phylogeny of the Cheilodactylidae and Latridae (Perciformes: Cirrhitoidea) with notes on taxonomy and biogeography. *Molecular Phylogenetics and Evolution,* 30, 118–127.

Campbell, M.A., Chen, W.-J. & Lopez, J.A. (2013) Are flatfishes (Pleuronectiformes) monophyletic? *Molecular Phylogenetics and Evolution,* 69, 664–673.

Carpenter, K.E. & Johnson, G.D. (2002) A phylogeny of sparoid fishes (Perciformes, Percoidei) based on morphology. *Ichthyological Research,* 49, 114–127.

Chan, Y.-C., Roos, C., Inoue-Murayama, M., Inoue, E., Shih, C., Pei, K.J. & Vigilant, L. (2010) Mitochondrial genome sequences effectively reveal the phylogeny of gibbons. *PLOS One,* 5.

Chapleau, F. (1993) Pleuronectiform relationships: A cladistic reassessment. *Bulletin of Marine Science,* 52, 516–540.

Chen, W.-J., Bonillo, C. & Lecointre, G. (2003) Repeatability of clades as a criterion of reliability: a case study for molecular phylogeny of Acanthomorpha (Teleostei) with larger number of taxa. *Molecular Phylogenetics and Evolution,* 26, 262–288.

Chen, W.J., Ruiz-Carus, R. & Ortí, G. (2007) Relationships among four genera of mojarras (Teleostei: Perciformes: Gerreidae) from the western Atlantic and their tentative placement among percomorph fishes. *Journal of Fish Biology,* 70, 202–218.

Cheng, S., Higuchi, R. & Stoneking, M. (1994) Complete mitochondrial genome amplification. *Nature Genetics,* 7, 350–351.

Chiba, S.N., Iwatsuki, Y., Yoshino, T. & Hanzawa, N. (2009) Comprehensive phylogeny of the family Sparidae (Perciformes: Teleostei) inferred from mitochondrial gene analyses. *Genes & Genetic Systems,* 84, 153–170.

Courtenay, W.R.J. (1961) Western Atlantic fishes of the genus Haemulon (Pomadasyidae): Systematic status and juvenile pigmentation. *Bulletin of Marine Science* 66–149.

Craig, M.T. & Hastings, P.A. (2007) A molecular phylogeny of the groupers of the subfamily Epinephelinae (Serranidae) with a revised classification of the Epinephelini. *Ichthyological Research,* 54, 1–17.

Cuvier, G.L. (1830) *Le Règne Animal Distribué d'Après son Organisation, pour Servir de Base à l'Histoire Naturelle des Animaux et d'Introduction à l'Anatomie Comparée. Nouvelle Edition, Revue et Augmentée par P.A. Latreill* (Vol. 3). Paris: Deterville.

Cuvier, G.L. & Valenciennes, A. (1833) *Histoire Naturelle des Poissons* (Vol. 9). Levrault, Paris.

Day, J.J. (2002) Phylogenetic relationships of the Sparidae (Teleostei: Percoidei) and implications for convergent trophic evolution. *Biological Journal of the Linnean Society,* 76, 269–301.

de Vienne, D.M., Giraud, T. & Martin, O.C. (2007) A congruence index for testing topological similarity between trees. *Bioinformatics,* 23, 3119–3124.

Dettai, A., Bailly, N., Vignes-Lebbe, R. & Lecointre, G. (2004) Metacanthomorpha: essay on a phylogeny-oriented database for morphology--the acanthomorph (Teleostei) example. *Systematic Biology,* 53, 822–834.

Dettai, A. & Lecointre, G. (2005) Further support for the clades obtained by multiple molecular phylogenies in the acanthomorph bush. *Comptes rendus Biologies,* 328 674–689.

Drummond, A.J., Suchard, M.A., Xie, D. & Rambaut, A. (2012) Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Molecular Biology and Evolution.*

Duque-Caro, H. (1990) Neogene stratigraphy, paleocea-nography and paleobiography in northwest SouthAmerica and the evolution of the Panama Seaway. *Palaeogeography, Palaeoclimatology, Palaeoecology,* 77, 203–234.

Eschmeyer, W.N. (1990) *Catalog of the genera of recent fishes* (Vol. VI): Special Publication California Academy of Sciences

Eschmeyer, W.N. (2013) *Genera, species, references. (http://research.calacademy.org/research/ichthyology/catalog/fishcatmain.asp). Electronic version accessed 16 Oct 2013.*

FAO (2014) Global capture production 1950–2012. *In.* Food and Agriculture Organization of the United Nations.

Fowler, H.W. (1934) Fishes obtained by Mr. H. W. Bell-Marley chiefly in Natal and Zululand in 1929 to 1932. *Proceedings of the Academy of Natural Sciences of Philadelphia* 86, 405–514.

Freihofer, W.C. (1963) Patterns of the ramus lateralis accessorius and their systematic significance in teleostean fishes. *Stanford Ichthyological Bulletin,* 8, 80–189.

Friedman, M. (2010) Explosive morphological diversification of spiny-finned teleost fishes in the aftermath of the end-Cretaceous extinction. *Proceedings of the Royal Society B,* 277, 1675–1683.

Gill, T.N. (1861) Catalogue of the fishes of the eastern coast of North America, from Greenland to Georgia. *Proceedings of the Academy of Natural Sciences of Philadelphia,* 13 (Suppl.), 1–63.

Gill, T.N. (1893a) A comparison of antipodal faunas. *Memoirs of the National Academy of Sciences,* 6, 91–124.

Gill, T.N. (1893b) Families and subfamilies of fishes. *Memoirs of the National Academy of Sciences, Washington,* 6, 125–138.

Girard, C.F. (1858) Notes upon various new genera and new species of fishes, in the museum of the Smithsonian Institution, and collected in connection with the United States and Mexican boundary survey: Major William Emory, Commissioner. *Proceedings of the Academy of Natural Sciences of Philadelphia,* 10, 167–171.

Greenwood, P.H. (1964) Patterns of the ramus lateralis accessorius and their systematic significance in teleostean fishes by Warren C. Freihofer. *Copeia,* 1, 248–250.

Greenwood, P.H. (1995) A revised familial classification for certain cirrhitoid genera (Teleostei, Percoidei Cirrhitoidea), with comments on the group's monophyly and taxonomic ranking. *Bulletin of The Natural History Museum Zoology Series*, 61, 1–10.

Greenwood, P.H., Rosen, D.E., Weitzman, S.H. & Myers, G.S. (1966) Phyletic studies of teleostean fishes, with a provisional classification of living forms. *Bulletin of the American Museum of Natural History*, 131, 339–456.

Günther, A. (1860) *Catalogue of the acanthopterygian fishes in the collection of the british museum* (Vol. 2). British Museum.

Hakkimane, S.S. & Rathod, J.L. (2011) Isolation and enumeration of bacterial flora in false trevally, *Lactarius lactarius* of Karwar, central west coast of India. *Indian Journal of Geo-Marine Science*, 40, 583–586.

Hall, B.G. (2004) *Phylogenetic trees made easy: A how-to-manual* (Second ed.): Sinauer Associates, Inc.

Hanel, R. & Sturmbauer, C. (2000) Multiple recurrent evolution of trophic types in northeastern Atlantic and Mediterranean seabreams (Sparidae, Percoidei). *Journal of Molecular Evolution*, 50, 276–283.

Hanel, R. & Tsigenopoulos, C.S. (2011) Phylogeny, evolution, and taxonomy of sparids with some notion their ecology and biology. *In:* Pavlidis, M. & Mylonas, C. (Eds), *Sparidae: Biology and aquaculture of gilthead sea bream and other species (Google eBook)*. John Wiley & Sons, p. 416.

Heemstra, P.C. & Randall, J.E. (1977) A revision of the Emmelichthyidae (Pisces : Perciformes). *Australian Journal of Marine and Freshwater Research*, 28, 361–396.

Hobson, E.S. (2006) Evolution. *In:* Allen, L.G., Pondella, D.J. & Horn, M.H. (Eds), *The ecology of marine fishes: California and adjacent waters*. University of California Press, Berkeley, pp. 55–80.

Hrbek, T. & Meyer, A. (2003) Closing of the Tethys Sea and the phylogeny of Eurasian killifishes (Cyprinodontiformes: Cyprinodontidae). *Journal of Evolutionary Biology*, 16, 17–36.

Huelsenbeck, J.P. & Ronquist, F. (2001) MRBAYES: Bayesian inference of phylogeny. *Bioinformatics*, 17, 754–755.

Ishiguro, N.B., Miya, M. & Nishida, M. (2001) Complete mitochondrial DNA sequence of ayu *Plecoglossus altivelis*. *Fisheries Science*, 67, 474–481.

Ishiguro, N.B., Miya, M. & Nishida, M. (2003) Basal euteleostean relationships: a mitogenomic perspective on the phylogenetic reality of the "Protacanthopterygii". *Molecular Phylogenetics and Evolution*, 27, 476–488.

Iwatsuki, Y., Kohno, H. & Ida, H. (1998) Redescription of a poorly-known haemulid fish, *Pomadasys unimaculatus* Tian, 1982, from Malaysia and comparison with *P. maculatus* (Bloch, 1797) (Perciformes: Haemulidae). *ICHTHYOLOGICAL RESEARCH*, 45, 195–200.

Iwatsuki, Y. & Nakabo, T. (2005) Redescription of *Hapalogenys nigripinnis* (Schlegel in Temminck and Schlegel, 1843), a senior synonym of *H. nitens* Richardson, 1844, and a new species from Japan. *Copeia*, 4, 854–867.

Iwatsuki, Y. & Russell, B.C. (2006) Revision of the genus *Hapalogenys* (Teleostei: Perciformes) with two new species from the Indo-West Pacific. *Memoirs of Museum Victoria*, 63, 29–46.

Iwatsuki, Y., Satapoomin, U. & Amaoka, K. (2000) New Species: *Hapalogenys merguiensis* (Teleostei; Perciformes) from Andaman Sea. *Copeia*, 2000, 129–139.

Jacobsen, M.W., Hansen, M.M., Orlando, L., Bekkevold, D., Bernatchez, L., Willerslev, E. & Gilbert, M.T. (2012) Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish (*Coregonus* spp.). *Molecular Ecology,* 21, 2727–2742.

James, P.S.B.R., Shanbhogue, S.L. & Gupta, T.R.C. (1974) Biology and fishery of *Lactarius lactarius* (Schneider) off Mangalore. *Indian Journal of Marine Sciences,* 3, 72–79.

Jex, A.R., Hall, R.S., Littlewood, D.T. & Gasser, R.B. (2010) An integrated pipeline for next-generation sequencing and annotation of mitochondrial genomes. *Nucleic Acids Research,* 38, 522–533.

Johnson, G.D. (1981) The limits and relationships of the Lutjanidae and associated families. *Bulletin of the Scripps Institution of Oceanography,* 24, 1–114.

Johnson, G.D. (1984) Percoidei: development and relationships. *In:* Moser, H.G., Richards, W.J., Cohen, D.M., Fahay, M.P., Kendall, A.W., Jr. & Richardson, S.L. (Eds). American Society of Ichthyologists and Herpetologists, pp. 464–498.

Johnson, G.D. (1993) Percomorph phylogeny: progress and problems. *Bulletin of Marine Science,* 52, 3–28.

Johnson , G.D. & Fritzsche, R.A. (1989) *Graus nigra*, an omnivorous girellid, with a comparative osteology and comments on relationships of the Girellidae (Pisces: Perciformes). *Proceedings of the Academy of Natural Sciences of Philadelphia,* 141, 1–27.

Johnson, G.D. & Patterson, C. (1993) Percomorph phylogeny: a survey of acanthomorphs and a new proposal. *Bulletin of Marine Science,* 52, 554–626.

Jordan, D.S. (1923) A classification of fishes including families and genera as far as known. *Stanford University publications: University series,* 3, 77–243 + i-x.

Jordan, D.S. & Fesler, B. (1893) A review of the sparoid fishes of American and Europe.

Jordan, D.S. & Gilbert, C.H. (1882) Synopsis of the fishes of North America. *Bulletin of the United States National Museum,* 16, 1–1018.

Kaikini, A.S. (1974) Regional and seasonal abundance of the white fish Lactarius lactarius (Schneider) in the trawling grounds off Bombay — Saurashtra coasts 1957–'63. *Annual Reports of the Central Marine Fisheries Research Institute,* 21.

Källersjö, M., Albert, V.A. & Farris, J.S. (1999) Homoplasy increases phylogenetic structure. *Cladistics,* 15, 91–93.

Kass, R.E. & Raftery, A.E. (1995) Bayes Factors. *Journal of the American Statistical Association,* 90, 773–795.

Kawaguchi, A., Miya, M. & Nishida, M. (2001) Complete mitochondrial DNA sequence of *Aulopus japonicus* (Teleostei: Aulopiformes), a basal Eurypterygii: longer DNA sequences and higher-level relationships. *Ichthyological Research,* 48, 213–223.

Kawahara, R., Miya, M., Mabuchi, K., Lavoue, S., Inoue, J.G., Satoh, T.P., Kawaguchi, A. & Nishida, M. (2008) Interrelationships of the 11 gasterosteiform families (sticklebacks, pipefishes, and their relatives): a new perspective based on whole mitogenome sequences from 75 higher teleosts. *Molecular Phylogenetics and Evolution,* 46, 224–236.

Knowlton, N. & Weigt, L.A. (1998) New dates and new rates for divergence across the Isthmus of Panama. *Proceedings of the Royal Society of London,* 265, 2257–2263.

Konchina, Y.V. (1976) The systematics and distribution of the grunts family (Pomadasyidae). *Japanese Journal of Ichthyology,* 16, 883–900.

Konchina, Y.V. (1977) Some data on the biology of grunts (Family Pomadasyidae). *Japanese Journal of Ichthyology,* 17, 548–558.

Lauder, G.V. & Liem, K.F. (1983) The evolution and interrelationships of the actinopterygian fishes. *Bulletin of The Museum of Comparative Zoology,* 150, 95–197.

Lautredou, A.C., Motomura, H., Gallut, C., Ozouf-Costaz, C., Cruaud, C., Lecointre, G. & Dettai, A. (2013) New nuclear markers and exploration of the relationships among Serraniformes

(Acanthomorpha, Teleostei): the importance of working at multiple scales. *Molecular Phylogenetics and Evolution,* 67, 140–155.

Lavoué, S., Miya, M., Inoue, J.G., Saitoh, K., Ishiguro, N.B. & Nishida, M. (2005) Molecular systematics of the gonorynchiform fishes (Teleostei) based on whole mitogenome sequences: implications for higher-level relationships within the Otocephala. *Molecular Phylogenetics and Evolution,* 37, 165–177.

Lavoué, S., Miya, M., Poulsen, J.Y., Møller, P.R. & Nishida, M. (2008) Monophyly, phylogenetic position and inter-familial relationships of the Alepocephaliformes (Teleostei) based on whole mitogenome sequences. *Molecular Phylogenetics and Evolution,* 47, 1111–1121.

Lavoué, S., Miya, M., Saitoh, K., Ishiguro, N.B. & Nishida, M. (2007) Phylogenetic relationships among anchovies, sardines, herrings and their relatives (Clupeiformes), inferred from whole mitogenome sequences. *Molecular Phylogenetics and Evolution,* 43, 1096–1105.

Leis, J.M. (1994) Larvae, adults and relationships of the monotypic perciform fish family Lactariidae. *Records of the Australian Museum,* 46, 131–143.

Leis, J.M. & Carson-Ewart, B.M. (2000) *The larvae of Indo-Pacific coastal fishes. An identification guide to marine fish larvae. Fauna Malesiana Handbooks 2 (soft cover edition 2004)*: E.J. Brill, Leiden.

Leis, J.M. & van der Lingen, C.D. (1997) Larval development and relationships of the perciform family Dichistiidae (=Coracinidae), the galjoen fishes. *Bulletin of Marine Science,* 60, 100–116.

Lessios, H.A. (2008) The great american schism: Divergence of marine organisms after the rise of the Central American Isthmus. *Annual Review of Ecology, Evolution, and Systematics,* 39, 63–91.

Li, B., Dettaï, A., Cruaud, C., Couloux, A., Desoutter-Meniger, M. & Lecointre, G. (2009) RNF213, a new nuclear marker for acanthomorph phylogeny. *Molecular Phylogenetics and Evolution,* 50, 345–363.

Li, C., Betancur-R, R., Smith, W.L. & Orti, G. (2011) Monophyly and interrelationships of snook and barramundi (Centropomidae *sensu* Greenwood) and five new markers for fish phylogenetics. *Molecular Phylogenetics and Evolution,* 60, 463–471.

Li, C., Lu, G. & Ortí , G. (2008) Optimal data partitioning and a test case for ray-finned fishes (Actinopterygii) based on ten nuclear loci. *Systematic Biology,* 57, 519–539.

Li, C. & Ortí, G. (2007) Molecular phylogeny of Clupeiformes (Actinopterygii) inferred from nuclear and mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution,* 44, 386–398.

Li, C., Ortí, G., Zhang, G. & Lu, G. (2007) A practical approach to phylogenomics: the phylogeny of ray-finned fish (Actinopterygii) as a case study. *BMC Evolutionary Biology,* 7, 44.

Liang, R., Zhuo, X., Yang, G., Luo, D., Zhong, S. & Zou, J. (2012) Molecular phylogenetic relationships of family Haemulidae (Perciformes: Percoidei) and the related species based on mitochondrial and nuclear genes. *Mitochondrial DNA,* 23, 264–277.

Lindeman, K.C. (1986) Development of larvae of the French grunt, *Haemulon flavolineatum*, and comparative development of twelve western Atlantic species of *Haemulon* (Percoidei, Haemulidae). *Bulletin of Marine Science,* 39, 673–716.

Lindeman, K.C. (2006) CHAPTER 141 - Inermiidae: Bonnetmouths. *In:* Richards, W.J. (Ed), *Early Stages of Atlantic Fishes: An Identification Guide for the Western Central North Atlantic, Two Volume Set.* Taylor & Francis, CRC Press, USA, Boca Raton, FL, p. 1341

Lindeman, K.C. & Toxey, C. (2003) Haemulidae – Grunts. *In:* Carpenter, K.E. (Ed), *The living marine resources of the Western Central Atlantic.* FAO species identification guide for fishery purposes and American Society of Ichthyologists and Herpetologists Special Publication No. 5, FAO, Rome, Italy, pp. 1375–2127.

Little, A.G., Lougheed, S.C. & Moyes, C.D. (2010) Evolutionary affinity of billfishes (Xiphiidae and Istiophoridae) and flatfishes (Plueronectiformes): Independent and trans-subordinal origins of endothermy in teleost fishes. *Molecular Phylogenetics and Evolution,* 56, 897–904.

López, J.A., Chen, W.-J. & Ortí, G. (2004) Esociform Phylogeny. *Copeia,* 2004, 449–564.

MacDonald, C.M. (1983) Taxonomic and evolutionary studies on marine fishes of the genus *Arripis* (Perciformes: Arripidae). *Bulletin of Marine Science,* 33, 780.

Maddison, W.P. & Maddison, D.R. (2007) Mesquite: a modular system for evolutionary analysis.

Mahon, A.R. (2007) Molecular phylogenetics of perciform fishes using the nuclear recombination activating gene 1. Unpublished PhD Dissertation. Old Dominion University, Norfolk, Virginia, USA, p. 303.

Maugé, L.A. & Desoutter, M. (1990) Kuhliidae. *In:* Quero, J.C., Hureau, J.C., Karrer, C., Post, A. & Saldanha, L. (Eds), *Check-list of the fishes of the eastern tropical Atlantic (CLOFETA),* JNICT, Lisbon; SEI, Paris; and UNESCO, Paris.

McEachran, J.D. & Fechhelm, J.D. (2005) *Fishes of the Gulf of Mexico: Scorpaeniformes to Tetraodontiformes* (Vol. 2). Austin: University of Texas Press.

McKay, R.J. (1984) Haemulidae. *In:* Fischer, W. & Bianchi, G. (Eds), *FAO species identification sheets for fishery purposes. Western Indian Ocean (Fishing Area 51),* p. pag. var.

McKay, R.J. (2001) Haemulidae (= Pomadasyidae). Grunts (also sweetlips, rubberlips, hotlips, and velvetchins). *In:* Carpenter, K.E.N., V. (Ed), *FAO species identification guide for fishery purposes. The living marine resources of the Western Central Pacific,* FAO, Rome, Italy, p. 589.

McKay, R.J. & Schneider, M. (1995) Haemulidae. Burros, corocoros, chulas, gallinazos, roncos. *In:* Fischer, W., Krupp, F., Schneider, W., Sommer, C., Carpenter, K.E. & Niem, V. (Eds), *Guia FAO para Identification de especies para lo fines de la pesca. Pacifico Centro-Oriental.* Food and Agriculture Organization of the United Nations, Rome, Italy, pp. 1136–1173.

Miles, C. (1953) A new pomadasid fish from the Colombian Caribbean. *Journal of the Linnean Society of London,* 42, 273–275.

Minegishi, Y., Aoyama, J., Inoue, J.G., Miya, M., Nishida, M. & Tsukamoto, K. (2005) Molecular phylogeny and evolution of the freshwater eels genus *Anguilla* based on the whole mitochondrial genome sequences. *Molecular Phylogenetics and Evolution,* 34, 134–146.

Miya, M., Friedman, M., Satoh, T.P., Takeshima, H., Sado, T., Iwasaki, W., Yamanoue, Y., Nakatani, M., Mabuchi, K., Inoue, J.G., Poulsen, J.Y., Fukunaga, T., Sato, Y. & Nishida, M. (2013) Evolutionary origin of the scombridae (tunas and mackerels): members of a paleogene adaptive radiation with 14 other pelagic fish families. *PLOS One,* 8, e73535.

Miya, M., Kawaguchi, A. & Nishida, M. (2001) Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences. *Molecular Biology and Evolution,* 18, 1993–2009.

Miya, M., Satoh, T.P. & Nishida, M. (2005) The phylogenetic position of toadfishes (order Batrachoidiformes) in the higher ray-finned fish as inferred from partitioned Bayesian analysis of 102 whole mitochondrial genome sequences. *Biological Journal of the Linnean Society,* 85, 289–306.

Miya, M., Takeshima, H., Endo, H., Ishiguro, N.B., Inoue, J.G., Mukai, T., Satoh, T.P., Yamaguchi, M., Kawaguchi, A., Mabuchi, K., Shirai, S.M. & Nishida, M. (2003) Major patterns of higher teleostean phylogenies: a new perspective based on 100 complete mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution,* 26, 121–138.

Moore, W.S. (1995) Inferring phylogenies from mtDNA variation: Mitochondrial-gene trees versus nuclear-gene trees. *Evolution,* 49, 718–726.

Morin, P.A., Archer, F.I., Foote, A.D., Vilstrup, J., Allen, E.E., Wade, P., Durban, J., Parsons, K., Pitman, R., Li, L., Bouffard, P., Nielsen, S.C.A., Rasmussen, M., Willerslev, E., Gilbert, M.T. & Harkins, T. (2010) Complete mitochondrial genome phylogeographic analysis of killer whales (*Orcinus orca*) indicates multiple species. *Genome Research,* 20, 908–916.

Near, T.J., Dornburg, A., Eytan, R.I., Keck, B.P., Smith, W.L., Kuhn, K.L., Moore, J.A., Price, S.A., Burbrink, F.T., Friedman, M. & Wainwright, P.C. (2013) Phylogeny and tempo of diversification in the superradiation of spiny-rayed fishes. *Proceedings of the National Academy of Sciences of the United States of America.*

Near, T.J., Eytan, R.I., Dornburg, A., Kuhn, K.L., Moore, J.A., Davis, M.P., Wainwright, P.C., Friedman, M. & Smith, W.L. (2012a) Resolution of ray-finned fish phylogeny and timing of diversification. *Proceedings of the National Academy of Sciences of the United States of America,* 109, 13698–13703.

Near, T.J., Sandel, M., Kuhn, K.L., Unmack, P.J., Wainwright, P.C. & Smith, W.L. (2012b) Nuclear gene-inferred phylogenies resolve the relationships of the enigmatic Pygmy Sunfishes, Elassoma (Teleostei: Percomorpha). *Molecular Phylogenetics and Evolution,* 63, 388–395.

Nelson, G.J. (1989) Phylogeny of major fish groups. *In:* Femholm, B., Bremer, K. & Jomvall, H. (Eds), *The hierarchy of life,* Excerpta Medica, Amsterdam, pp. 325–336.

Nelson, J.S. (1994) *Fishes of the World Third Edition.* Hoboken, New Jersey: John Wiley & Sons, Inc.

Nelson, J.S. (2006) *Fishes of the World Fourth Edition.* Hoboken, New Jersey: John Wiley & Sons, Inc.

Nylander, J.A.A. (2004) MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.

Nylander, J.A.A., Ronquist, F., Huelsenbeck, J.P. & Nieves-Aldrey, J.L. (2004) Bayesian phylogenetic analysis of combined data. *Systematic Biology,* 53, 47–67.

Nylander, J.A.A., Wilgenbusch, J.C., Warren, D.L. & Swofford, D.L. (2008) AWTY (are we there yet?): a system for graphical exploration of MCMC convergence in Bayesian phylogenetics. *Bioinformatics,* 24, 581–583.

Ogden, J.C. & Ehrlich, P.R. (1977) The behavior of heterotypic resting schools of juvenile grunts (Pomadasyidae). *Marine Biology,* 42, 273–280.

Orrell, T.M. & Carpenter, K.E. (2004) A phylogeny of the fish family Sparidae (porgies) inferred from mitochondrial sequence data. *Molecular Phylogenetics and Evolution,* 32, 425–434.

Orrell, T.M., Carpenter, K.E., Musick, J.A. & Graves, J.E. (2002) Phylogenetic and biogeographic analysis of the Sparidae (Perciformes: Percoidei) from cytochrome *b* sequences. *Copeia,* 2002, 618–631.

Pardo, B.G., Machordom, A., Porto-Foresti, F., Sánchez, L., Foresti, F., Azevedo, M.F.C. & Martínez, P. (2005) Phylogenetic analysis of flatfish (Order Pleuronectiformes) based on mitochondrial 16s rDNA sequences. *Scientia Marina,* 69, 531–543.

Paulin, C. (1993) Review of the Australian fish family Arripididae (Percomorpha), with the description of a new species. *Australian Journal of Marine and Freshwater Research,* 44, 459–471.

Pellegrin, J. (1913) Poissons marins de Guinée, de la Côte d'Ivoire, du Dahomey, du Gabon et du Congo. Mission de M. Gruvel. *Bulletin de la Société Zoologique de France,* 38, 151–158.

Pielou, E.C. (1979) *Biogeography*: John Wiley & Sons.

Price, S.A., Tavera, J.J.N., T.J. & Wainwright, P.C. (2012) Elevated rates of morphological and functional diversification in reef-dwelling haemulid fishes. *Evolution,* 674, 417–428.

Rafinesque, C.S. (1810) Indice d'ittiologia siciliana; ossia, catalogo metodico dei nomi latini, italiani, e siciliani dei psci, che si rinvengono in Sicilia disposti secondo un metodo naturale e seguito da un appendice che contiene la descrizione di alcu. ni nuovi pesci siciliani. *In*, Messina, Presso Giovanni del Nobolo, p. 70.

Author (2007) Tracer v1.4. Available from http://beast.bio.ed.ac.uk/Tracer, Available from: http://beast.bio.ed.ac.uk/Tracer

Ranwez, V., Harispe, S., Delsuc, F. & Douzery, E.J. (2011) MACSE: Multiple Alignment of Coding SEquences accounting for frameshifts and stop codons. *PLOS One,* 6, e22594.

Regan, C.T. (1910) The origin and evolution of the teleostean fishes of the order Heterosomata. *Annals and Magazine of Natural History,* 8, 484–496.

Regan, C.T. (1911) On the cirrhitiform percoids. *The Annals and magazine of natural history,* 7, 259–262.

Regan, C.T. (1913) On the classification of the percoid fishes. *Annals and Magazine of Natural History,* 8, 111–145.

Ren, G. & Zhang, Q. (2007) Phylogeny of haemulid with discussion on systematic position of the genus *Hapalogenys*. *Acta Zootaxonomica Sinica,* 32, 835–841.

Reuben, S.K., Vijayakumaran, K. & Sekhar, M.C. (1993) Growth, maturity and mortality of false trevally *Lactarius lactarius* Bloch & Schneider from Andhra Pradesh-Orissa coast. *Indian Journal of Fisheries,* 40, 156–161.

Richardson, J. (1844) Description of a genus of Chinese fish. *Annals and Magazine of Natural History,* 13, 461–462.

Rocha, L.A. & Bowen, B.W. (2008) Speciation in coral-reef fishes. *Journal of Fish Biology,* 72, 1101–1121.

Rocha, L.A., Lindeman, K.C., Rocha, C.R. & Lessios, H.A. (2008) Historical biogeography and speciation in the reef fish genus *Haemulon* (Teleostei: Haemulidae). *Molecular Phylogenetics and Evolution,* 48, 918–928.

Ronquist, F. & Huelsenbeck, J.P. (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics,* 19, 1572–1574.

Roux, C. (1981) Pomadasyidae. *In:* Fischer, W., Bianchi, G. & Scott, W.B. (Eds), *FAO species identification sheets for fishery purposes. Eastern Central Atlantic; fishing areas 34, 47 (in part)*. Department of Fisheries and Oceans Canada and FAO. Vol. 3. Bony fishes (Malacanthidae to Scombridae) FAO, Rome, Italy, p. pag. var.

Saitoh, K., Sado, T., Mayden, R.L., Hanzawa, N., Nakamura, K., Nishida, M. & Miya, M. (2006) Mitogenomic evolution and interrelationships of the Cypriniformes (Actinopterygii: Ostariophysi): The first evidence toward resolution of higher-level relationships of the world's largest freshwater fish clade based on 59 whole mitogenome sequences. *Journal of Molecular Evolution,* 63, 826–841.

Sanciangco, M.D., Rocha, L.A. & Carpenter, K.E. (2011) A molecular phylogeny of the Grunts (Perciformes: Haemulidae) inferred using mitochondrial and nuclear genes. *Zootaxa,* 2966, 37–50.

Santini, F., Carnevale, G. & Sorenson, L. (2014) First multi-locus timetree of seabreams and porgies (Percomorpha: Sparidae). *Italian Journal of Zoology,* 1–17.

Setiamarga, D.H., Miya, M., Yamanoue, Y., Mabuchi, K., Satoh, T.P., Inoue, J.G. & Nishida, M. (2008) Interrelationships of Atherinomorpha (medakas, flyingfishes, killifishes, silversides, and their relatives): The first evidence based on whole mitogenome sequences. *Molecular Phylogenetics and Evolution,* 49, 598–605.

Seutin, G., White, B.N. & Boag, P.T. (1990) Preservation of avian blood and tissue samples for DNA analysis. *Canadian Journal of Zoology,* 69, 82–90.

Smith-Vaniz, W.F. (1984) Carangidae: relationships. *In:* Moser, H.G., Richards, W.J., Cohen, D.M., Fahay, D.M., Kendall, A.W., Jr. & Richardson, S.L. (Eds), *Ontogeny and Systematics of Fishes*, pp. 522–530.

Smith-Vaniz, W.F. (2001) "Cepolidae. Bandfishes" *In:* Carpenter, K.E. & Niem, V. (Eds), *FAO Species Identification Guide for Fishery Purposes. The Living Marine Resources of the Western Central Pacific*, pp. 3331–3332.

Smith, J.L.B. (1935) The "galjoen" fishes of South Africa. *Transactions of the Royal Society of South Africa,* 23, 265–276.

Smith, J.L.B. (1938) The South African fishes of the families Sparidae and Denticidae. *Transactions of the Royal Society of South Africa,* 26, 225–305.

Smith, J.L.B. (1962) Fishes of the Family Gaterinidae of the Western Indian Ocean and the Red Sea with a Resume of all known Indo Pacific Species. *Ichthyological Bulletin,* 25, 469–502.

Smith, M.M. & Heemstra, P.C. (1986) *Smith's sea fishes.* Macmillan South Africa, Johannesburg.

Smith, W.L. (2005) The limits and relationships of mail-cheeked fishes (Teleostei: Percomorpha) and the evolution of venom in fishes. Unpublished PhD Dissertation, Columbia University, New York.

Smith, W.L. & Craig, M. (2007) Casting the percomorph net widely: The importance of broad taxonomic sampling in the search for the placement of serranid and percid fishes. *Copeia,* 2007, 35–55.

Smith, W.L. & Wheeler, W.C. (2006) Venom evolution widespread in fishes: Venom evolution widespread in fishes: A phylogenetic road map for the bioprospecting of piscine venoms. *Journal of Heredity,* 97, 206–217.

Sorenson, M.D. & Franzosa, E.A. (2007) TreeRot, version 3.

Springer, V.G. & Johnson, G.D. (2004) Study of the dorsal gill-arch musculature of teleostome fishes, with special reference to Actinopterygii. *Bulletin of the Biological Society of Washington,* 11, 1–235.

Springer, V.G. & Raasch, M.S. (1995) *Fishes, angling, and finfish fisheries on stamps of the world.* Tucson, Arizona: American Topical Association.

Stamatakis, A. (2014) Raxml version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.*

Steyskal, G.C. (1980) The grammar of family-group names as exemplified by those of fishes. *Proceedings of the Biological Society of Washington,* 93, 168–177.

Swofford, D.L. (2002) PAUP*. Phylogenetic Analysis Using Parsimony (*and Other Methods). Version 4.

Tavera, J.J., Near, T.J., Acero, A., Balart, E.F. & Bernardi, G. (2012) Molecular phylogeny of grunts (Teleostei, Haemulidae), with an emphasis on the ecology, evolution, and speciation history of New World species. *BMC Evolutionary Biology,* 12.

Tavera, J.J., Pizarro, A.A., De la Cruz-Agüero, J. & Balart, E.F. (2011) Phylogeny and reclassification of the species of two neotropical grunt genera, Anisotremus and Genyatremus (Perciformes: Haemulidae), based on morphological evidence. *Journal of Zoological Systematics and Evolutionary Research,* 49, 315–323.

Thacker, C.E. (2009) Phylogeny of Gobioidei and placement within Acanthomorpha, with a new classification and investigation of diversification and character evolution. *Copeia,* 2009, 93–104.

Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F. & Higgins, D.G. (1997) The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research,* 24, 4876–4882.

Tupper, M. & Juanes, F. (1999) Effects of a marine reserve on recruitment of grunts (Pisces: Haemulidae) at Barbados,West Indies. *Environmental Biology of Fishes,* 55, 53–63.

Vaidya, G., Lohman, D.J. & Meier, R. (2011) SequenceMatrix: concatenation software for the fast assembly of multi-gene datasets with character set and codon information. *Cladistics,* 27.

Vilstrup, J.T., Ho, S.Y., Foote, A.D., Morin, P.A., Kreb, D., Krutzen, M., Parra, G.J., Robertson, K.M., de Stephanis, R., Verborgh, P., Willerslev, E., Orlando, L. & Gilbert, M.T. (2011) Mitogenomic phylogenetic analyses of the Delphinidae with an emphasis on the Globicephalinae. *BMC Evolutionary Biology,* 11, 65.

Wainwright, P.C., Smith, W.L., Price, S.A., Tang, K.L., Sparks, J.S., Ferry, L.A., Kuhn, K.L., Eytan, R.I. & Near, T.J. (2012) The evolution of pharyngognathy: a phylogenetic and functional appraisal of the pharyngeal jaw key innovation in labroid fishes and beyond. *Systematic Biology,* 61, 1001–1027.

Ward, R.D., Zemlak, T.S., Innes, B.H., Last, P.R. & Hebert, P.D. (2005) DNA barcoding Australia's fish species. *Philosophical Transactions of the Royal Society B: Biological Sciences* 360, 1847–1857.

Wiley, E.O. & Johnson, G.D. (2010) A teleost classification based on monophyletic groups. *In:* Nelson, J.S., Schultze, H.-P. & Wilson, M.V.H. (Eds), *Origin and phylogenetic interrelationships of teleosts.* Verlag Dr. Friedrich Pfeil, München, Germany, pp. 123–182.

Williams, A., Begg, G., Garrett, R., Larson, H. & Griffiths, S. (2004) Coastal Fishes. *In: National Oceans Office. Description of key species groups in the Northern Planning Area.* National Oceans Office, Hobart, Australia, p. 320.

Xia, X. (2013) DAMBE5: A comprehensive software package for data analysis in molecular biology and evolution. *Molecular Biology and Evolution,* 30, 1720–1728.

Xia, X., Xie, Z., Salemi, M., Chen, L. & Wang, Y. (2003) An index of substitution saturation and its application. *Molecular Phylogenetics and Evolution,* 26, 1–7.

Yagishita, N., Kobayashi, T. & Nakabo, T. (2002) Review of monophyly of the Kyphosidae (*sensu* Nelson, 1994), inferred from the mitochondrial ND2 gene. *Ichthyological Research,* 49, 103–108.

Yagishita, N., Miya, M., Yamanoue, Y., Shirai, S.M., Nakayama, K., Suzuki, N., Satoh, T.P., Mabuchi, K., Nishida, M. & Nakabo, T. (2009) Mitogenomic evaluation of the unique facial nerve pattern as a phylogenetic marker within the percifom fishes (Teleostei: Percomorpha). *Molecular Phylogenetics and Evolution,* 53, 258–266.

Yamanoue, Y., Miya, M., Matsuura, K., Katoh, M., Sakai, H. & Nishida, M. (2008) A new perspective on phylogeny and evolution of tetraodontiform fishes (Pisces: Acanthopterygii) based on whole mitochondrial genome sequences: basal ecological diversification? *BMC Evolutionary Biology,* 8, 212.

Yamanoue, Y., Miya, M., Matsuura, K., Yagishita, N., Mabuchi, K., Sakai, H., Katoh, M. & Nishida, M. (2007) Phylogenetic position of tetraodontiform fishes within the higher teleosts: Bayesian inferences based on 44 whole mitochondrial genome sequences. *Molecular Phylogenetics and Evolution,* 45, 89–101.

Zacharia, P.U. & Jayabalan, N. (2007) Maturation and spawning of the whitefish, *Lactarius lactarius* (Bloch and Schneider, 1801) (Family Lactariidae) along the Karnataka coast, India. *Journal of the Marine Biological Association of India,* 49, 166–176.

Zhang, J. & Hanner, R. (2008) DNA barcoding of fishes in the South China Sea. *Unpublished.*

Zhu, S.H., Zheng, W.J. & Zou, J.X. (2007) Molecular phylogenetic relationship of Carangidae based on sequence of complete mitochondrial cytochrome *b* gene. *Dong Wu Xue Bao.*

Zwickl, D.J. (2006) Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. The University of Texas at

APPENDIX A

LIST OF SPECIES AND THE ACCESSION NUMBER OF HAEMULID SPECIMENS

TABLE A1. List of species and the accession number of haemulid specimens (56), including outgroups (10).

				GenBank Accession Numbers				
Family	**Subfamily**	**Species**	**Accession No.**	**COI**	**CYT *b***	**RAG1**	**SH3PX3**	**PLAGL2**
Haemulidae	Plectorhinchinae	*Diagramma picta*	ODU 3219	HQ676758	HQ676699	HQ676637	HQ667185	HQ667252
Haemulidae	Plectorhinchinae	*Parapristipoma octolineatum*	ODU 3220	HQ676781	HQ676726	HQ676666	HQ667214	HQ667281
Haemulidae	Plectorhinchinae	*Parapristipoma trilineatum*	ODU 3221	HQ676782	HQ676727	HQ676667	HQ667215	HQ667282
Haemulidae	Plectorhinchinae	*Plectorhinchus chaetodonoides*	ODU 3222	HQ676783	HQ676728	HQ676668	HQ667216	HQ667283
Haemulidae	Plectorhinchinae	*Plectorhinchus cinctus*	ODU 3223	HQ676784	HQ676729	HQ676669	HQ667217	HQ667284
Haemulidae	Plectorhinchinae	*Plectorhinchus diagrammus*	ODU 3224	HQ676785	HQ676730	HQ676670	HQ667218	HQ667285
Haemulidae	Plectorhinchinae	*Plectorhinchus gibbosus*	KUT-6832	HQ676786	HQ676731	HQ676671	HQ667219	HQ667286
Haemulidae	Plectorhinchinae	*Plectorhinchus lessonii*	ODU 3225	HQ676787	HQ676732	HQ676672	HQ667220	HQ667287
Haemulidae	Plectorhinchinae	*Plectorhinchus macrolepis*	ODU 3226	HQ676788	HQ676733	166092559	HQ667221	HQ667288
Haemulidae	Plectorhinchinae	*Plectorhinchus schotaf*	ODU 3228	HQ676790	HQ676735	HQ676674	HQ667223	HQ667290
Haemulidae	Plectorhinchinae	*Plectorhinchus sordidus*	ODU 3229	HQ676791	HQ676736	HQ676675	HQ667224	HQ667291
Haemulidae	Plectorhinchinae	*Plectorhinchus vittatus*	KUT-6921	HQ676789	HQ676734	HQ676673	HQ667222	HQ667289
Haemulidae	Haemulinae	*Anisotremus davidsonii*	SIO-04-181	HQ676749	HQ676689	HQ676626	HQ667172	HQ667239
Haemulidae	Haemulinae	*Anisotremus interruptus*	ODU 3232	203282643	HQ676690	HQ676628	HQ667174	HQ667241
Haemulidae	Haemulinae	*Anisotremus scapularis*	ODU 3234	HQ676751	HQ676692	HQ676630	HQ667176	HQ667243
Haemulidae	Haemulinae	*Anisotremus surinamensis*	KUT-2425	HQ676752	203282593	HQ676631	HQ667177	HQ667244
Haemulidae	Haemulinae	*Anisotremus taeniatus*	ODU 3235	203282647	HQ676693	HQ676632	HQ667178	HQ667245
Haemulidae	Haemulinae	*Anisotremus virginicus*	ODU 3236	223366616	189032143	166092457	HQ667179	HQ667246
Haemulidae	Haemulinae	*Boridia grossidens*	ODU 3237	HQ676754	HQ676695	HQ676634	HQ667181	HQ667248
Haemulidae	Haemulinae	*Brachydeuterus auritus*	ODU 3238	HQ676755	HQ676696	166092459	HQ667182	HQ667249
Haemulidae	Haemulinae	*Conodon nobilis*	KUT-5135	HQ676756	HQ676697	HQ676635	HQ667183	HQ667250
Haemulidae	Haemulinae	*Conodon serrifer*	ODU 3239	HQ676757	HQ676698	HQ676636	HQ667184	HQ667251
Haemulidae	Haemulinae	*Emmelichthyops atlanticus*	ODU 3265	HQ676759	HQ676700	HQ676638	HQ667186	HQ667253
Haemulidae	Haemulinae	*Genyatremus cavifrons*	ODU 3240	HQ676760	HQ676701	HQ676639	HQ667187	HQ667254
Haemulidae	Haemulinae	*Genyatremus dovii*	ODU 3231	HQ684719	189032063	HQ676627	HQ667173	HQ667240
Haemulidae	Haemulinae	*Genyatremus pacifici*	ODU 3233	HQ676750	HQ676691	HQ676629	HQ667175	HQ667242
Haemulidae	Haemulinae	*Haemulon aurolineatum*	ODU 3241	HQ676761	HQ676702	HQ676640	HQ667188	HQ667255
Haemulidae	Haemulinae	*Haemulon carbonarium*	NMFS 018	203282675	13183276	HQ676647	HQ667195	HQ667262
Haemulidae	Haemulinae	*Haemulon chrysargyreum*	KUT-232	203282657	HQ676703	HQ676641	HQ667189	HQ667256

Table A1. *Continued*

				GenBank Accession Numbers				
Family	**Subfamily**	**Species**	**Accession No.**	**COI**	**CYT *b***	**RAG1**	**SH3PX3**	**PLAGL2**
Haemulidae	Haemulinae	*Haemulon flaviguttatum*	ODU 3242	203282659	HQ676704	HQ676642	HQ667190	HQ667257
Haemulidae	Haemulinae	*Haemulon flavolineatum*	ODU 3243	203282661	203282607	HQ676643	HQ667191	HQ667258
Haemulidae	Haemulinae	*Haemulon macrostomum*	KUT-235	HQ676762	HQ676705	HQ676644	HQ667192	HQ667259
Haemulidae	Haemulinae	*Haemulon melanurum*	ODU 3244	HQ676763	HQ676706	HQ676645	HQ667193	HQ667260
Haemulidae	Haemulinae	*Haemulon plumierii*	ODU 3245	203282673	HQ676707	HQ676646	HQ667194	HQ667261
Haemulidae	Haemulinae	*Haemulon scudderii*	ODU 3246	203282677	HQ676708	HQ676648	HQ667196	HQ667263
Haemulidae	Haemulinae	*Haemulon steindachneri*	ODU 3247	HQ676764	HQ676709	HQ676649	HQ667197	HQ667264
Haemulidae	Haemulinae	*Haemulon vittatum*	USNM 349224	HQ676771	HQ676716	HQ676656	HQ667204	HQ667271
Haemulidae	Haemulinae	*Haemulopsis axillaris*	ODU 3248	HQ676765	HQ676710	HQ676650	HQ667198	HQ667265
Haemulidae	Haemulinae	*Haemulopsis leuciscus*	ODU 3249	HQ676766	HQ676711	HQ676651	HQ667199	HQ667266
Haemulidae	Haemulinae	*Haemulopsis nitidus*	ODU 3250	HQ676767	HQ676712	HQ676652	HQ667200	HQ667267
Haemulidae	Haemulinae	*Isacia conceptionis*	ODU 3251	HQ676772	HQ676717	HQ676657	HQ667205	HQ667272
Haemulidae	Haemulinae	*Microlepidotus brevipinnis*	ODU 3252	HQ676777	HQ676722	HQ676662	HQ667210	HQ667277
Haemulidae	Haemulinae	*Orthopristis chalceus*	ODU 3253	HQ676779	HQ676724	HQ676664	HQ667212	HQ667279
Haemulidae	Haemulinae	*Orthopristis chrysoptera*	KUT-1195	HQ676780	HQ676725	HQ676665	HQ667213	HQ667280
Haemulidae	Haemulinae	*Pomadasys argyreus*	ODU 3254	HQ676793	HQ676738	HQ676677	HQ667226	HQ667293
Haemulidae	Haemulinae	*Pomadasys branickii*	ODU 3255	HQ676794	HQ676739	HQ676678	HQ667227	HQ667294
Haemulidae	Haemulinae	*Pomadasys incisus*	ODU 3256	HQ676795	133923650	HQ676679	HQ667228	HQ667295
Haemulidae	Haemulinae	*Pomadasys kaakan*	ODU 3257	HQ676796	HQ676740	HQ676680	HQ667229	HQ667296
Haemulidae	Haemulinae	*Pomadasys maculatus*	ODU 3258	HQ676797	13183278	HQ676681	HQ667230	HQ667297
Haemulidae	Haemulinae	*Pomadasys olivaceus*	KUT-6467	HQ676798	HQ676741	164417780	HQ667231	HQ667298
Haemulidae	Haemulinae	*Pomadasys panamensis*	ODU 3259	HQ676799	HQ676742	HQ676682	HQ667232	HQ667299
Haemulidae	Haemulinae	*Pomadasys perotaei*	ODU 3260	HQ676800	HQ676743	HQ676683	HQ667233	HQ667300
Haemulidae	Haemulinae	*Pomadasys striatus*	ODU 3261	HQ676801	HQ676744	HQ676684	HQ667234	HQ667301
Haemulidae	Haemulinae	*Pomadasys stridens*	ODU 3262	HQ676802	HQ676745	HQ676685	HQ667235	HQ667302
Haemulidae	Haemulinae	*Xenichthys xanti*	ODU 3263	HQ676804	HQ676747	HQ676687	HQ667237	HQ667304
Haemulidae	Haemulinae	*Xenistius californiensis*	SIO-02-1	HQ676805	HQ676748	HQ676688	HQ667238	HQ667305
Hapalogenyidae		*Hapalogenys aya*	MUFS 23038	HQ676768	HQ676713	HQ676653	HQ667201	HQ667268
Hapalogenyidae		*Hapalogenys kishinouyei*	MUFS 23603	HQ676769	HQ676714	HQ676654	HQ667202	HQ667269
Hapalogenyidae		*Hapalogenys nigripinnis*	ODU 3264	HQ676770	HQ676715	HQ676655	HQ667203	HQ667270

Table A1. *Continued*

				GenBank Accession Numbers				
Family	**Subfamily**	**Species**	**Accession No.**	**COI**	**CYT *b***	**RAG1**	**SH3PX3**	**PLAGL2**
Lethrinidae		*Lethrinus ornatus*	ODU 3266	HQ676773	HQ676718	HQ676658	HQ667206	HQ667273
Lobotidae		*Lobotes pacificus*	SIO-98-170	HQ676774	HQ676719	HQ676659	HQ667207	HQ667274
Lobotidae		*Lobotes surinamensis*	MUFS 23031	HQ676775	HQ676720	HQ676660	HQ667208	HQ667275
Lutjanidae		*Aphareus furca*	ODU 3267	HQ676753	HQ676694	HQ676633	HQ667180	HQ667247
Lutjanidae		*Lutjanus fulviflamma*	ODU 3268	HQ676776	HQ676721	HQ676661	HQ667209	HQ667276
Nemipteridae		*Nemipterus marginatus*	ODU 3269	HQ676778	HQ676723	HQ676663	HQ667211	HQ667278
Sparidae		*Sarpa salpa*	ODU 3270	HQ676803	HQ676746	HQ676686	HQ667236	HQ667303

* KU - University of Kansas Natural History Museum & Biodiversity Research Center; MUFS – Miyazaki University, Division of Fisheries Sciences, Miyazaki, Japan; NMFS - National Marine Fisheries Services; ODU - Old Dominion University, Norfolk, VA; SIO - Scripps Institution of Oceanography, University of California San Diego, CA; UF-University of Florida; USNM - United States National Museum, Smithsonian, Washington, D.C.

APPENDIX B

CHARACTERISTICS OF THE FIVE MARKERS AMPLIFIED FOR HAEMULIDS

TABLE A2. Characteristics of the five markers amplified for haemulids. Pi: Parsimony-informative sites; ci: Consistency Index on the Maximum Parsimony tree.

Gene	No. of bp	No. of constant sites	No. of PI sites	CI
COI	651	373	245	0.1317
CYT *b*	1140	491	533	0.1698
RAG1	1431	870	385	0.4934
SH3PX3	705	499	144	0.3924
PLAGL2	804	618	112	0.4989

APPENDIX C

THE TEN INDEPENDENT PARAMETERS OF 15 DATA PARTITIONS ESTIMATED IN MRBAYES

TABLE A3. The ten independent parameters of 15 data partitions estimated in MrBayes. Data shows five substitution rates, three base composition proportions, the gamma parameter (alpha), and the rate multiplier for each data block.

	Substitution rates					**Base frequencies**				
Partitions	**AC**	**AG**	**AT**	**CG**	**CT**	**A**	**C**	**G**	**Alpha**	**Multiplier**
COI_1	0.009	0.038	0.011	0.001	0.918	0.256	0.300	0.288	0.153	0.738
COI_2	0.067	0.200	0.055	0.373	0.258	0.152	0.292	0.147	0.051	3.897
COI_3	0.031	0.598	0.024	0.036	0.262	0.261	0.348	0.106	1.704	3.904
CYT*b*_1	0.031	0.259	0.128	0.039	0.470	0.249	0.289	0.260	0.264	0.462
CYT*b*_2	0.063	0.112	0.079	0.306	0.391	0.202	0.234	0.147	0.243	0.117
CYT*b*_3	0.018	0.540	0.029	0.043	0.295	0.301	0.409	0.076	1.596	5.545
RAG1_1	0.247	0.287	0.156	0.061	0.179	0.292	0.197	0.325	0.276	0.072
RAG1_2	0.076	0.351	0.044	0.203	0.289	0.319	0.220	0.191	0.056	0.034
RAG1_3	0.084	0.378	0.062	0.056	0.377	0.200	0.271	0.280	1.081	0.313
SH3PX3_1	0.185	0.065	0.118	0.135	0.429	0.286	0.273	0.261	0.069	0.031
SH3PX3_2	0.039	0.139	0.026	0.265	0.456	0.372	0.208	0.149	0.104	0.216
SH3PX3_3	0.080	0.361	0.082	0.023	0.399	0.125	0.357	0.349	0.815	0.396
PLAGL2_1	0.123	0.248	0.166	0.071	0.354	0.245	0.367	0.222	0.143	0.021
PLAGL2_2	0.194	0.239	0.017	0.403	0.080	0.377	0.260	0.173	50.158	0.511
Pagl2_3	0.068	0.455	0.098	0.019	0.316	0.126	0.326	0.329	0.837	0.216

APPENDIX D

TAXON SAMPLING FOR THE PERCOMORPH DATASET INCLUDED 1231 TAXA AND SEQUENCE DATA FOR 23 GENES

TABLE A4a. Taxon sampling for the percomorph dataset included 1231 taxa and sequence data for 23 genes. The dataset is comprised of sequences for 1180 percomorph species from previous studies (e.g. Li *et al.* 2007; Li *et al.* 2008; Li *et al.* 2010; Li *et al.* 2011; Betancur-R *et al.* 2013b; Broughton *et al.* 2013; Near *et al.* 2013) or public databases, plus newly generated sequences for the 51 additional taxa for this study. The matrix is presented in four parts to show presence of sequence data for the 23 genes. (a.) ENC1, FICD, GLYT, KIAA1239, MYH6, and PANX2; (b.) PLAGL2, PTCHD1, RAG1, RAG2, RH, and RIPK4; (c.) SH3PX3, SIDKEY, SREB2, SVEP1, TBR1, and VCPIP; (d.) ZIC1, COI, CYT *B*, 16S, and HOX.

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Acanthuridae	*Acanthurus bahianus*	E00005	11794	14	657	0	891	0	720	808
Acanthuridae	*Acanthurus guttatus*	E00709	7379	8	657	0	0	0	0	0
Acanthuridae	*Acanthurus leucosternon*	E00880	14819	16	810	645	891	0	744	0
Acanthuridae	*Acanthurus lineatus*	E00889	11234	12	0	645	0	0	0	0
Acanthuridae	*Acanthurus triostegus*	E00711	11027	13	657	654	0	0	744	750
Acanthuridae	*Ctenochaetus striatus*	E00982	6461	8	657	636	0	0	0	713
Acanthuridae	*Ctenochaetus strigosus*	E00050	9642	12	657	0	891	0	645	0
Acanthuridae	*Ctenochaetus truncatus*	E00854	6572	9	0	645	0	0	714	818
Acanthuridae	*Naso brevirostris*	E00918	11979	15	657	657	822	774	744	884
Acanthuridae	*Naso lituratus*	G01514	9769	12	657	0	822	0	744	0
Acanthuridae	*Naso unicornis*	E00701	6934	9	0	654	0	0	719	0
Acanthuridae	*Paracanthurus hepatus*	E00002	9321	11	657	0	0	0	744	843
Acanthuridae	*Zebrasoma flavescens*	E00730	9002	10	0	654	0	0	705	0
Acanthuridae	*Zebrasoma rostratum*	N01742	6780	8	810	0	873	0	744	0
Acanthuridae	*Zebrasoma scopas*	E00859	12917	16	657	636	0	0	684	890
Acanthuridae	*Zebrasoma velifer*	E00029	5029	6	0	0	0	738	681	0
Achiridae	*Achirus lineatus*	E00605	13596	16	759	654	816	915	723	0
Achiridae	*Gymnachirus melas*	E00609	14260	16	750	0	825	729	691	900
Achiridae	*Gymnachirus texae*	E00630	9146	10	0	654	0	738	737	0
Achiridae	*Hypoclinemus sp*	E01162	6483	7	0	0	0	918	0	0
Achiridae	*Trinectes maculatus*	E00046	11078	11	0	0	0	918	708	0
Achiropsettidae	*Mancopsetta maculata*	E01169	6861	8	0	0	0	918	744	0
Achiropsettidae	*Neoachiropsetta milfordi*	E01170	6200	8	0	0	0	915	744	0
Acropomatidae	*Acropoma japonicum*	G01188	12298	14	756	0	852	0	731	0
Acropomatidae	*Malakichthys elegans*	N01922	6894	9	753	0	816	0	675	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Acropomatidae	*Synagrops bellus*	E01125	11059	13	657	0	0	765	744	885
Acropomatidae	*Synagrops spinosus*	E01123	6676	7	0	0	0	0	743	885
Adrianichthyidae	*Oryzias latipes*	G01408	18061	19	657	732	708	930	744	984
Agonidae	*Aspidophoroides monopterygius*	N01986	7472	9	786	0	891	0	744	0
Agonidae	*Bathyagonus alascanus*	E00268	5458	7	0	657	0	0	678	0
Agonidae	*Bathyagonus pentacanthus*	E00430	5127	7	0	0	0	0	692	0
Agonidae	*Hypsagonus quadricornis*	E00269	7151	9	0	696	0	918	0	0
Agonidae	*Sarritor frenatus*	E00264	4738	6	0	684	0	918	0	0
Agonidae	*Sarritor leptorhynchus*	E00254	5516	7	0	657	0	918	710	0
Agonidae	*Stellerina xyosterna*	N02010	6750	8	0	0	891	0	744	0
Agonidae	*Xeneretmus latifrons*	E00278	6400	8	0	0	0	0	710	0
Ambassidae	*Ambassis agrammus*	G01196	8877	9	0	0	0	879	744	0
Ambassidae	*Ambassis interrupta*	E01100	10212	10	0	0	0	930	0	924
Ambassidae	*Ambassis urotaenia*	G01197	8268	10	633	0	873	0	744	0
Ambassidae	*Parambassis ranga*	N01735	7892	10	753	0	834	0	668	0
Ammodytidae	*Ammodytes dubius*	N02375	6015	7	0	0	891	0	0	0
Ammodytidae	*Ammodytes hexapterus*	E00414	15128	17	694	0	879	711	743	0
Anabantidae	*Ctenopoma acutirostre kingsleyae*	E01141	14536	15	657	0	891	918	744	0
Anabantidae	*Microctenopoma nanum*	G01373	12070	13	657	0	846	0	744	0
Anarhichadidae	*Anarhichas denticulatus*	E00787	8620	9	0	0	0	765	0	914
Anarhichadidae	*Anarhichas orientalis lupus*	E00117	15266	17	657	0	873	753	743	850
Anarhichadidae	*Anarrhichthys ocellatus*	E00119	7893	10	0	0	0	765	0	912
Anoplopomatidae	*Anoplopoma fimbria*	E00423	15741	18	657	690	891	774	744	916
Antennariidae	*Antennatus coccineus*	E01092	15457	17	804	606	831	759	728	941
Antennariidae	*Antennatus nummifer*	E00587	9899	13	0	654	0	753	743	793
Antennariidae	*Fowlerichthys radiosus*	E01124	4779	6	0	0	0	753	0	783
Antennariidae	*Histiophryne cryptacanthus*	G01326	9853	12	738	0	873	0	726	0
Antennariidae	*Histrio histrio*	E00643	7964	9	0	0	0	0	0	750
Aphyonidae	*Barathronus maculatus*	N02779	7479	9	678	0	801	0	744	0
Aplocheilidae	*Pachypanchax playfairii*	G01414	7524	9	786	0	819	0	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Aplodactylidae	*Aplodactylus arctidens*	M01536	4728	5	0	0	0	0	0	0
Aplodactylidae	*Aplodactylus etheridgii*	M01537	4710	5	0	0	0	0	0	0
Apogonidae	*Apogon campbelli*	E01069	9380	10	0	0	0	765	730	906
Apogonidae	*Archamia biguttata*	E00522	8166	11	0	657	0	702	728	747
Apogonidae	*Astrapogon puncticulatus*	E00109	7227	9	0	684	0	0	0	925
Apogonidae	*Astrapogon stellatus*	N03004	7517	9	798	0	852	0	626	0
Apogonidae	*Cercamia eremia*	E00546	6660	9	0	0	0	657	410	901
Apogonidae	*Cheilodipterus isostigmus*	E00528	8272	10	0	675	0	741	729	883
Apogonidae	*Cheilodipterus quinquelineatus*	G01247	9762	12	657	0	885	0	738	0
Apogonidae	*Fowleria aurita*	E01090	8780	11	0	675	0	732	743	910
Apogonidae	*Gymnapogon urospilotus*	E00539	5107	7	0	657	0	0	743	897
Apogonidae	*Nectamia bandanensis*	E01040	8860	11	0	0	0	696	743	911
Apogonidae	*Nectamia fusca*	E00732	8861	10	0	0	0	750	723	802
Apogonidae	*Ostorhinchus cookii*	E01087	6400	8	0	675	0	741	730	910
Apogonidae	*Ostorhinchus lateralis*	G01203	8273	10	657	0	855	0	701	0
Apogonidae	*Phaeoptyx pigmentaria*	E00506	12882	15	804	648	0	741	729	866
Apogonidae	*Pristiapogon exostigma*	E00702	8433	11	0	654	0	678	743	798
Apogonidae	*Pseudamia gelatinosa*	E00568	7391	9	0	0	0	0	0	794
Apogonidae	*Pterapogon kauderni*	E00190	6329	8	0	0	0	702	742	740
Apogonidae	*Rhabdamia cypselura*	E01095	6022	7	0	657	0	720	742	906
Apogonidae	*Sphaeramia orbicularis*	N03178	8446	10	810	0	843	0	744	0
Aracanidae	*Anoplocapros lenticularis*	G01533	6886	7	0	0	0	0	744	0
Aracanidae	*Aracana aurita*	G01205	10032	12	810	0	852	0	744	0
Ariommatidae	*Ariomma bondi*	E01126	7867	9	0	0	0	783	743	863
Ariommatidae	*Ariomma melanum*	E00665	9682	12	0	663	0	747	726	896
Arripidae	*Arripis georgianus*	M01539	4794	5	0	0	0	0	0	0
Arripidae	*Arripis trutta*	M01540	3327	4	0	0	0	0	0	0
Arripidae	*Arripis truttacea*	M01541	4659	5	0	0	0	0	0	0
Artedidraconidae	*Artedidraco orianae*	G01525	6898	8	0	0	0	0	676	0
Artedidraconidae	*Pogonophryne barsukovi*	E00158	12842	14	0	0	0	810	744	941

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Atherinidae	*Atherinomorus lacunosus*	E00548	15021	18	657	681	849	702	710	842
Atherinidae	*Atherinomorus stipes*	E00115	13436	16	0	684	0	750	744	906
Atherinidae	*Atherinomorus vaigiensis*	E00181	7813	10	0	684	0	744	744	877
Atherinidae	*Craterocephalus honoriae*	E00180	8597	10	0	684	0	756	0	876
Atherinopsidae	*Atherinopsis californiensis*	E00121	5600	7	0	0	0	771	0	920
Atherinopsidae	*Labidesthes sicculus*	E01112	14372	17	657	0	891	747	744	906
Atherinopsidae	*Membras martinica*	E00170	7275	9	0	0	0	0	657	868
Atherinopsidae	*Menidia beryllina*	E00174	10176	13	789	0	891	0	744	882
Atherinopsidae	*Menidia menidia*	E00167	12560	13	0	0	0	687	0	896
Atherinopsidae	*Menidia peninsulae*	N03847	5694	7	618	0	867	0	744	0
Atherinopsidae	*Odontesthes argentinensis*	E00393	5125	7	0	0	0	756	0	893
Atherinopsidae	*Odontesthes bonariensis*	E00396	9234	11	0	645	0	918	0	830
Atherinopsidae	*Odontesthes humensis*	E00394	5561	7	0	657	0	765	0	842
Atherinopsidae	*Odontesthes retropinnis*	E00395	4826	6	0	681	0	747	0	802
Atherinopsidae	*Poblana ferdebueni*	N01733	5919	7	810	0	858	0	744	0
Aulorhynchidae	*Aulorhynchus flavidus*	G01217	11313	12	657	0	891	0	744	0
Aulostomidae	*Aulostomus chinensis*	E00871	15665	19	810	693	891	726	722	0
Aulostomidae	*Aulostomus maculatus*	E00293	13058	16	657	0	870	915	696	706
Badidae	*Badis pyema*	N03996	7191	9	762	0	813	0	667	0
Badidae	*Dario dario*	N04003	5626	7	762	0	822	0	674	0
Balistidae	*Abalistes stellatus*	E00936	14580	18	759	693	873	714	744	0
Balistidae	*Balistapus undulatus*	E00743	12372	14	809	657	888	0	744	785
Balistidae	*Balistes capriscus*	E00591	13798	17	657	636	876	606	723	879
Balistidae	*Balistes vetula*	E00755	13640	15	810	660	891	0	734	860
Balistidae	*Balistoides conspicillum*	E00373	9468	10	0	648	0	0	708	836
Balistidae	*Canthidermis maculata*	E00378	9887	10	0	645	0	0	729	0
Balistidae	*Melichthys indicus*	E00919	7484	10	0	693	0	0	726	0
Balistidae	*Melichthys niger*	E00922	8652	11	0	693	0	0	722	0
Balistidae	*Pseudobalistes flavimarginatus*	N04225	6715	8	810	0	891	0	734	0
Balistidae	*Pseudobalistes fuscus*	E00524	4607	6	0	0	0	0	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Balistidae	*Rhinecanthus aculeatus*	E00735	9140	10	657	654	0	0	744	817
Balistidae	*Rhinecanthus assasi*	E00381	5259	6	0	0	0	747	712	833
Balistidae	*Rhinecanthus verrucosus*	N04231	7465	9	810	0	891	0	744	0
Balistidae	*Sufflamen chrysopterum*	E00551	11210	14	810	651	891	0	744	777
Balistidae	*Sufflamen fraenatum*	E00935	9148	10	0	693	0	717	714	0
Balistidae	*Xanthichthys auromarginatus*	E00380	11574	12	0	693	0	753	717	857
Balistidae	*Xanthichthys ringens*	N04239	7595	9	810	0	867	0	744	0
Banjosidae	*Banjos banjos*	M01542	4794	5	0	0	0	0	0	0
Banjosidae	*Banjos banjos*	N01542	6206	8	747	0	828	0	674	0
Bathyclupeidae	*Bathyclupea argentea*	M01543	2787	4	0	0	0	0	0	0
Bathydraconidae	*Gymnodraco acuticeps*	E00155	12486	14	0	0	891	0	744	888
Bathydraconidae	*Parachaenichthys charcoti*	E00157	15082	17	648	0	873	0	731	907
Bathymasteridae	*Bathymaster caeruleofasciatus*	E00191	7525	10	0	0	0	0	744	847
Bathymasteridae	*Bathymaster signatus*	E00420	12500	16	810	663	846	723	738	889
Bathymasteridae	*Rathbunella hypoplecta*	E00128	12273	15	804	684	876	729	704	896
Batrachoididae	*Batrachoides pacifici*	N04533	6761	8	753	0	891	0	737	0
Batrachoididae	*Opsanus beta*	E00698	11611	14	810	654	888	0	545	831
Batrachoididae	*Opsanus pardus*	E00513	11301	14	786	654	891	762	744	0
Batrachoididae	*Opsanus tau*	E00040	4773	6	0	0	0	918	0	832
Batrachoididae	*Porichthys notatus*	E00058	13187	16	810	696	891	0	744	0
Batrachoididae	*Porichthys plectrodon*	E00590	13538	16	657	654	891	750	645	0
Batrachoididae	*Sanopus sp*	E00009	4902	6	0	690	0	918	0	849
Bedotiidae	*Rheocles wrightae*	G01467	11051	13	645	0	891	0	744	0
Belonidae	*Ablennes hians*	E00162	11443	13	0	684	0	750	744	915
Belonidae	*Platybelone argalus*	E00114	12856	15	624	0	873	765	744	916
Belonidae	*Strongylura notata*	E00110	15115	19	657	684	891	753	744	906
Belonidae	*Tylosurus crocodilus*	E01051	7580	10	0	675	0	753	0	875
Belonidae	*Xenentodon cancila*	G01508	11377	14	657	0	891	0	744	0
Bembridae	*Bembras japonica*	N01723	6876	9	750	0	825	0	675	0
Bembropidae	*Bembrops anatirostris*	E01120	10273	13	597	0	873	708	743	941

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Bembropidae	*Bembrops gobioides*	E01128	8878	11	657	0	891	780	0	790
Blenniidae	*Alticus arnoldorum*	E00989	2775	4	0	693	0	0	0	0
Blenniidae	*Atrosalarias fuscus*	E00525	2877	4	0	0	0	717	0	906
Blenniidae	*Blenniella chrysospilos paula*	E00986	4186	5	0	0	0	720	0	0
Blenniidae	*Blenniella cyanostigma*	E00715	7419	9	0	0	0	717	707	759
Blenniidae	*Blenniella paula*	E00979	7982	10	0	693	0	717	709	0
Blenniidae	*Cirripectes castaneus*	E00892	8002	10	0	693	0	711	0	0
Blenniidae	*Cirripectes filamentosus*	E00893	5912	7	0	0	0	732	0	0
Blenniidae	*Cirripectes quagga*	E00330	4362	5	0	0	0	915	729	0
Blenniidae	*Cirripectes stigmaticus*	E00520	4037	6	0	0	0	717	690	0
Blenniidae	*Ecsenius bicolor*	E00984	5909	8	0	0	0	720	692	934
Blenniidae	*Ecsenius midas*	E00934	3749	5	0	0	0	726	705	0
Blenniidae	*Ecsenius opsifrontalis*	E00723	5497	7	0	666	0	717	0	799
Blenniidae	*Ecsenius pardus*	E00523	4285	5	0	0	0	717	0	775
Blenniidae	*Enchelyurus flavipes*	N04786	6887	9	750	0	819	0	0	0
Blenniidae	*Entomacrodus nigricans*	E00297	9132	11	801	0	0	915	702	0
Blenniidae	*Entomacrodus niuafoouensis*	E00980	6091	8	0	654	0	723	705	0
Blenniidae	*Entomacrodus striatus*	E00987	5295	7	0	693	0	714	0	0
Blenniidae	*Hypleurochilus sp*	E00298	5653	7	0	693	0	0	0	903
Blenniidae	*Hypsoblennius hentz*	E00289	7330	9	774	0	0	720	0	0
Blenniidae	*Istiblennius dussumieri*	E00556	4755	6	0	0	0	717	0	895
Blenniidae	*Meiacanthus oualanensis grammistes*	E00526	9615	12	657	0	888	0	741	0
Blenniidae	*Nannosalarias nativitatis*	E00521	6717	8	0	0	0	717	0	887
Blenniidae	*Ophioblennius atlanticus*	E00296	11932	15	648	0	871	735	718	734
Blenniidae	*Petroscirtes mitratus*	E00909	5741	8	0	0	0	720	722	0
Blenniidae	*Plagiotremus rhinorhynchos*	E00586	4112	5	0	0	0	0	728	875
Blenniidae	*Plagiotremus tapeinosoma*	E00540	4423	6	0	0	0	717	726	919
Blenniidae	*Praealticus caesius*	E00329	5179	6	0	693	0	915	0	862
Blenniidae	*Salarias fasciatus*	E00988	12606	14	747	693	813	726	0	0
Blenniidae	*Stanulus sp*	E00332	3369	4	0	693	0	0	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Bothidae	*Arnoglossus blachei*	E01160	6253	7	0	0	0	918	0	0
Bothidae	*Arnoglossus imperialis*	E01163	7399	8	0	0	0	912	0	0
Bothidae	*Asterorhombus cocosensis*	E00904	10399	11	0	636	0	0	711	905
Bothidae	*Bothus lunatus*	E00007	8248	9	0	699	819	0	714	856
Bothidae	*Bothus robinsi*	E00038	6724	7	0	675	0	732	660	0
Bothidae	*Chascanopsetta lugubris*	E01181	5982	7	0	0	0	912	0	0
Bothidae	*Laeops kitaharae*	E00082	7794	8	0	678	0	915	721	820
Bothidae	*Monolene sp*	E01172	3326	3	0	0	0	0	0	0
Bothidae	*Psettina tosana*	E00083	7617	8	0	0	0	915	718	0
Bothidae	*Trichopsetta ventralis*	E00599	9704	10	0	654	0	918	731	811
Bovichtidae	*Bovichtus diacanthus*	G01229	12547	13	645	0	891	0	743	0
Bovichtidae	*Cottoperca trigloides*	G01267	5753	6	0	0	0	0	656	0
Bramidae	*Brama brama*	E00970	11377	13	0	0	0	732	690	0
Bramidae	*Brama japonica*	N05217	8586	10	810	0	891	0	744	0
Bramidae	*Pteraclis aesticola*	N05223	7106	9	747	0	816	0	675	0
Bramidae	*Pterycombus brama*	E00996	9728	12	0	0	0	747	0	854
Bramidae	*Taractes asper*	N05227	8588	10	810	0	891	0	744	0
Bramidae	*Taractichthys longipinnis*	E00684	8997	11	0	0	0	0	0	926
Bythitidae	*Bidenichthys capensis*	E00794	7231	9	0	630	0	768	0	0
Bythitidae	*Brosmophyciops pautzkei*	E00717	5948	8	0	690	0	765	0	0
Bythitidae	*Brosmophycis marginata*	N05317	7691	9	717	0	882	0	744	0
Bythitidae	*Cataetyx rubrirostris lepidogenys*	E00261	14883	16	723	699	879	918	717	0
Bythitidae	*Diancistrus sp*	E00236	6903	9	0	657	0	0	717	0
Bythitidae	*Dinematichthys iluocoeteoides*	E00235	4750	6	0	660	0	0	721	0
Bythitidae	*Diplacanthopoma brachysoma*	E00452	8606	9	0	690	0	765	744	0
Bythitidae	*Diplacanthopoma brunnea*	N05377	8280	10	804	0	882	0	742	0
Caesionidae	*Caesio caerulaurea lunaris*	E00920	13727	15	0	630	0	747	0	846
Caesionidae	*Caesio cuning*	N01544	6786	8	810	0	891	0	744	0
Caesionidae	*Caesio teres*	E00951	7741	10	0	630	0	720	0	856
Caesionidae	*Caesio varilineata*	E00949	9671	12	0	630	0	723	0	851

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Caesionidae	*Caesio xanthonota*	E00950	9615	12	0	630	0	693	0	876
Caesionidae	*Pterocaesio pisang*	N01547	8535	10	809	0	890	0	744	0
Caesionidae	*Pterocaesio tile*	E00961	7369	8	0	630	0	741	0	0
Callanthiidae	*Callanthias australis*	M01721	3528	4	0	0	0	0	0	0
Callanthiidae	*Grammatonotus surugaensis*	N05516	4774	6	747	0	822	0	679	0
Callionymidae	*Callionymus sp bairdi*	E00946	14247	16	750	657	891	0	693	916
Callionymidae	*Diplogrammus goramensis*	E00744	3443	4	0	654	0	0	0	896
Callionymidae	*Foetorepus sp*	N01725	7524	9	750	0	891	0	744	0
Callionymidae	*Neosynchiropus ocellatus*	E00030	9857	12	810	0	804	756	708	795
Callionymidae	*Synchiropus agassizii*	E01004	13911	16	750	669	891	702	744	921
Callionymidae	*Synchiropus splendidus*	E00003	7623	9	810	0	891	0	744	0
Callionymidae	*Synchiropus stellatus*	E00925	4153	5	0	0	0	771	0	907
Caproidae	*Antigonia capros*	E01024	15924	18	657	0	858	696	744	904
Caproidae	*Antigonia rubescens*	N05907	8327	10	801	0	849	0	737	0
Caproidae	*Capros aper*	N05913	6917	9	756	0	819	0	673	0
Carangidae	*Alectis ciliaris*	E00469	9715	12	0	690	0	801	712	0
Carangidae	*Atule mate*	E00942	13914	15	0	0	0	735	702	870
Carangidae	*Carangoides ferdau*	E00869	9160	10	0	0	0	738	0	0
Carangidae	*Carangoides plagiotaenia*	E00917	10641	12	0	0	0	747	0	0
Carangidae	*Caranx crysos ruber*	E00510	15973	18	810	0	891	918	744	931
Carangidae	*Caranx ignobilis*	E00574	14220	16	0	690	0	792	702	0
Carangidae	*Caranx sexfasciatus*	E00834	10100	10	0	0	0	753	0	0
Carangidae	*Chloroscombrus chrysurus*	E00763	5515	7	0	0	0	758	0	0
Carangidae	*Decapterus macarellus*	E00212	3266	5	0	0	0	591	0	0
Carangidae	*Decapterus punctatus*	E00671	9777	11	0	690	0	918	0	0
Carangidae	*Elagatis bipinnulata*	E00841	11967	15	0	630	0	768	0	940
Carangidae	*Gnathanodon speciosus*	E00938	13565	15	0	0	0	918	0	917
Carangidae	*Hemicaranx amblyrhynchus*	E00616	11426	13	0	690	0	786	694	838
Carangidae	*Oligoplites saurus*	E00195	16021	19	810	720	883	918	731	0
Carangidae	*Scomberoides lysan*	E00738	10887	13	0	0	0	918	744	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Carangidae	*Selar crumenophthalmus*	E00833	11277	13	0	630	0	765	0	0
Carangidae	*Selene brownii*	E00767	7866	10	0	0	0	711	0	0
Carangidae	*Selene setapinnis*	N01705	6120	8	753	0	891	0	744	0
Carangidae	*Seriola dumerili*	E00623	16521	18	657	0	882	909	732	881
Carangidae	*Seriola rivoliana*	E00467	11164	13	0	0	0	0	729	0
Carangidae	*Trachinotus carolinus*	G01504	11145	13	654	0	882	0	741	0
Carangidae	*Trachinotus falcatus*	E00819	10693	12	0	0	0	756	714	0
Carangidae	*Trachinotus ovatus*	E01145	14822	16	801	0	891	918	744	0
Carangidae	*Trachurus lathami*	E00598	11710	13	657	0	0	798	0	884
Carangidae	*Uraspis secunda*	E00515	11843	13	0	0	0	798	729	917
Carapidae	*Carapus bermudensis*	E00244	3497	5	750	0	0	0	668	0
Carapidae	*Onuxodon parvibrachium*	N06009	5285	7	804	0	882	0	741	0
Carapidae	*Pyramodon ventralis*	N06013	5272	7	801	0	882	0	743	0
Caristiidae	*Caristius macropus*	N06078	5912	8	753	0	813	0	684	0
Caristiidae	*Caristius sp*	E00810	9564	11	0	0	0	774	0	0
Caristiidae	*Platyberyx opalescens*	N06085	7781	10	747	0	822	0	675	0
Centracanthidae	*Centracanthus cirrus*	M01560	2897	3	0	0	0	0	0	0
Centracanthidae	*Spicara alta*	M01561	4032	4	0	0	0	0	0	0
Centracanthidae	*Spicara maena*	M01562	5142	5	0	0	0	0	0	0
Centracanthidae	*Spicara nigricauda*	M01564	4791	5	0	0	0	0	0	0
Centracanthidae	*Spicara smaris*	M01565	5111	5	0	0	0	0	0	0
Centrarchidae	*Acantharchus pomotis*	G01185	10678	10	0	0	0	0	744	0
Centrarchidae	*Ambloplites rupestris*	E00392	18681	20	657	0	891	744	744	863
Centrarchidae	*Archoplites interruptus*	N01722	8586	10	810	0	891	0	744	0
Centrarchidae	*Lepomis cyanellus*	E00132	18334	20	798	684	876	768	732	891
Centrarchidae	*Lepomis macrochirus*	E01113	15647	17	0	660	804	768	743	884
Centrarchidae	*Micropterus salmoides*	E01110	18682	20	798	702	804	735	744	892
Centrarchidae	*Pomoxis nigromaculatus*	E00131	14489	15	0	0	0	699	744	909
Centriscidae	*Aeoliscus strigatus*	G01189	10258	10	657	0	0	0	728	0
Centriscidae	*Macroramphosus gracilis*	E00335	4196	5	0	0	0	915	711	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Centriscidae	*Macroramphosus scolopax*	E00473	10717	12	756	663	0	0	669	0
Centrogenyidae	*Centrogenys vaigiensis*	G01239	9161	11	657	0	891	0	744	0
Centrolophidae	*Icichthys lockingtoni*	E00387	15879	18	810	0	873	717	733	831
Centropomidae	*Centropomus ensiferus*	E00766	14482	15	0	702	0	930	0	902
Centropomidae	*Centropomus medius*	E01158	10458	11	0	702	0	930	0	0
Centropomidae	*Centropomus undecimalis*	E00194	15428	17	657	702	891	918	709	0
Centropomidae	*Centropomus viridis*	E01153	14374	16	810	702	813	801	669	0
Centropomidae	*Lates calcarifer*	E01135	11083	12	0	702	0	930	744	0
Centropomidae	*Lates japonicus*	E01147	10695	11	0	702	0	930	0	0
Centropomidae	*Lates microlepis*	E01149	9785	11	0	702	0	930	0	0
Centropomidae	*Psammoperca waigiensis*	E01148	12243	13	0	702	0	927	744	0
Cepolidae	*Acanthocepola sp*	M01669	4129	4	0	0	0	0	0	0
Cepolidae	*Cepola macrophthalma*	M01566	3339	4	0	0	0	0	0	0
Cepolidae	*Cepola schlegelii*	N06269	6961	9	0	0	822	0	650	0
Cepolidae	*Sphenanthias tosaensis*	N06282	6620	9	750	0	819	0	0	0
Ceratiidae	*Ceratias holboelli*	E00175	8091	11	0	654	861	0	743	0
Ceratiidae	*Ceratias sp*	E00160	6019	7	0	0	0	0	0	903
Ceratiidae	*Cryptopsaras couesii*	E00686	9907	10	0	0	891	750	0	869
Chaenopsidae	*Acanthemblemaria aspera*	E00320	6836	9	0	0	0	915	713	778
Chaenopsidae	*Acanthemblemaria paula*	E00295	6314	8	0	0	0	915	713	891
Chaenopsidae	*Chaenopsis sp alepidota*	E00313	11049	13	0	0	891	915	733	848
Chaenopsidae	*Emblemaria pandionis*	E00310	6208	7	0	0	0	906	717	0
Chaenopsidae	*Lucayablennius zingaro*	E00294	7789	9	0	0	0	915	0	877
Chaenopsidae	*Neoclinus blanchardi*	E00326	6535	8	0	0	0	915	717	0
Chaenopsidae	*Stathmonotus stahli*	E00317	7886	9	0	0	0	915	708	895
Chaetodontidae	*Chaetodon auriga*	E00921	12220	14	0	630	0	747	0	779
Chaetodontidae	*Chaetodon capistratus*	E00205	3871	5	0	720	0	0	740	0
Chaetodontidae	*Chaetodon ocellatus*	E00752	3799	5	0	0	0	0	0	0
Chaetodontidae	*Chaetodon ornatissimus*	G01243	11727	14	657	0	858	0	744	0
Chaetodontidae	*Chaetodon plebeius*	E00573	2874	4	0	690	0	0	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Chaetodontidae	*Chaetodon reticulatus*	E00719	9187	11	0	690	0	0	0	868
Chaetodontidae	*Chaetodon striatus*	E00753	15347	19	657	630	869	708	739	824
Chaetodontidae	*Chelmon rostratus*	G01248	10379	13	810	0	891	0	744	0
Chaetodontidae	*Forcipiger flavissimus*	E00562	14191	17	657	687	891	0	744	925
Chaetodontidae	*Hemitaurichthys polylepis*	E00240	12410	15	810	705	891	0	717	0
Chaetodontidae	*Heniochus chrysostomus*	E00748	14747	18	657	630	0	729	744	0
Chaetodontidae	*Heniochus varius*	E00547	11101	14	0	690	0	786	715	921
Chaetodontidae	*Johnrandallia nigrirostris*	N06546	7594	9	810	0	891	0	734	0
Chaetodontidae	*Prognathodes aya aculeatus*	E00632	16211	20	810	690	888	0	704	905
Champsodontidae	*Champsodon snyderi*	N06574	5798	8	744	0	825	0	675	0
Channichthyidae	*Chionobathyscus dewitti*	G01250	11735	13	657	0	891	0	744	0
Channichthyidae	*Chionodraco rastrospinosus*	E00156	10249	11	0	0	891	0	0	0
Channidae	*Channa lucius*	N06615	7562	9	753	0	0	0	744	0
Channidae	*Channa melasoma*	N06621	8195	10	693	0	891	0	744	0
Channidae	*Channa striata*	E01133	15424	17	657	0	891	918	744	0
Chaunacidae	*Chaunax stigmaeus*	E01121	11544	14	810	0	822	729	742	941
Chaunacidae	*Chaunax suttkusi*	E01117	13670	16	657	675	819	0	743	928
Cheilodactylidae	*Cheilodactylus fasciatus*	E00795	8950	11	0	630	0	759	675	874
Cheilodactylidae	*Cheilodactylus pixi*	E00797	7523	10	753	630	0	711	668	0
Cheilodactylidae	*Cheilodactylus variegatus*	N07699	7481	9	786	0	870	0	744	0
Cheilodactylidae	*Chirodactylus brachydactylus*	E00796	10572	13	690	0	813	0	669	0
Cheilodactylidae	*Chirodactylus jessicalenorum*	E00585	5511	7	0	0	0	0	0	0
Cheimarrichthyidae	*Cheimarrichthys fosteri*	N07713	7400	9	810	0	891	0	705	0
Chiasmodontidae	*Chiasmodon niger*	E01115	6819	8	0	0	0	744	0	897
Chiasmodontidae	*Chiasmodon sp*	N33662	8114	10	735	0	891	0	744	0
Chiasmodontidae	*Kali indica*	E01106	8049	10	0	0	0	720	743	932
Chiasmodontidae	*Kali kerberti*	E00385	8712	11	741	0	879	693	739	857
Chironemidae	*Chironemus georgianus*	M01569	3606	4	0	0	0	0	0	0
Chironemidae	*Chironemus maculosus*	M01570	3605	4	0	0	0	0	0	0
Cichlidae	*Astatotilapia burtoni*	G01518	14530	19	639	712	360	903	648	966

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Cichlidae	*Cichla temensis*	G01256	12888	15	657	0	891	0	744	0
Cichlidae	*Crenicichla lepidota*	E00137	9593	12	0	684	0	753	0	928
Cichlidae	*Etroplus maculatus*	E00133	16104	17	657	0	891	0	744	928
Cichlidae	*Herichthys cyanoguttatus*	G01319	10449	13	657	0	891	0	744	0
Cichlidae	*Heros efasciatus*	G01320	12037	14	657	0	891	0	744	0
Cichlidae	*Heterochromis multidens*	G01321	10659	13	633	0	854	0	744	0
Cichlidae	*Maylandia zebra*	G01519	15105	19	639	711	360	903	744	966
Cichlidae	*Nanochromis parilus*	G01390	2645	4	615	0	0	0	0	0
Cichlidae	*Neolamprologus brichardi*	G01520	18935	21	639	712	360	903	648	966
Cichlidae	*Oreochromis niloticus*	G01407	20724	22	639	732	891	930	744	966
Cichlidae	*Paratilapia polleni*	G01420	11328	12	657	0	891	0	744	0
Cichlidae	*Paretroplus maculatus*	G01423	11220	12	657	0	891	0	744	0
Cichlidae	*Ptychochromis grandidieri*	G01459	9350	12	647	0	819	0	744	0
Cichlidae	*Pundamilia nyererei*	G01521	14440	18	639	712	360	903	648	966
Cichlidae	*Steatocranus gibbiceps*	G01494	2873	4	633	0	0	0	0	0
Cichlidae	*Symphysodon discus*	E00390	10909	13	0	0	0	696	743	879
Cichlidae	*Tilapia louka*	G01503	2873	4	633	0	0	0	0	0
Cirrhitidae	*Amblycirrhitus pinos*	E00314	16355	19	756	657	849	915	711	865
Cirrhitidae	*Cirrhitichthys falco*	N09466	4867	7	0	0	0	0	665	0
Cirrhitidae	*Cirrhitichthys oxycephalus*	E00884	8380	11	0	693	0	735	713	0
Cirrhitidae	*Neocirrhites armatus*	E00725	12592	16	810	651	831	717	714	816
Cirrhitidae	*Paracirrhites forsteri arcatus*	E00924	12505	15	657	693	891	699	744	0
Citharidae	*Citharoides macrolepis*	E00071	12901	15	801	0	849	888	706	875
Citharidae	*Citharus linguatula*	E01174	6850	8	0	0	0	918	0	0
Citharidae	*Lepidoblepharon ophthalmolepis*	E00080	7005	8	0	0	0	750	717	868
Clinidae	*Blennophis striatus*	E00800	3454	4	0	0	0	699	0	884
Clinidae	*Clinus cottoides*	E00804	4782	6	0	0	0	675	0	926
Clinidae	*Clinus superciliosus*	E00803	5297	7	0	0	0	672	0	839
Clinidae	*Gibbonsia metzi*	N09738	6827	8	0	0	0	0	738	0
Clinidae	*Muraenoclinus dorsalis*	E00805	4559	6	0	0	0	708	0	0

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Clinidae	*Pavoclinus profundus*	E00799	3475	4	0	0	0	696	0	907
Coryphaenidae	*Coryphaena hippurus*	E00937	17390	19	810	630	891	918	741	256
Cottidae	*Artediellus uncinatus*	N10447	7522	9	810	0	891	0	744	0
Cottidae	*Chitonotus pugetensis*	E00233	6714	8	0	0	0	918	715	0
Cottidae	*Cottus carolinae*	E00281	10765	13	0	675	864	0	738	0
Cottidae	*Enophrys taurina*	E00234	3576	5	0	660	0	0	0	0
Cottidae	*Gymnocanthus galeatus*	E00259	3095	4	0	0	0	0	0	0
Cottidae	*Hemilepidotus jordani*	E00263	7975	10	0	618	0	0	0	0
Cottidae	*Hemilepidotus zapus*	E00272	5096	6	0	696	0	918	0	0
Cottidae	*Icelinus filamentosus*	E00277	8203	10	0	720	0	918	714	0
Cottidae	*Icelinus quadriseriatus*	E00228	5018	6	0	720	0	918	705	0
Cottidae	*Leptocottus armatus*	E00266	12068	14	0	720	888	918	711	0
Cottidae	*Micrcocottus sellaris*	E00223	2282	3	0	720	0	0	0	0
Cottidae	*Myoxocephalus octodecemspinosus*	E00221	3991	4	0	717	0	0	0	0
Cottidae	*Myoxocephalus polyacanthocephalus*	E00267	4736	5	0	0	0	0	0	0
Cottidae	*Radulinus asprellus*	E00429	6882	9	0	0	0	774	744	904
Cottidae	*Rastrinus scutiger*	E00256	6088	7	0	720	0	918	717	0
Cottidae	*Scorpaenichthys marmoratus*	E00232	10450	13	810	708	891	0	730	0
Cottidae	*Triglops macellus*	E00435	8082	10	0	690	0	777	0	901
Cottidae	*Triglops scepticus*	E00421	5233	7	0	693	0	0	0	851
Creediidae	*Limnichthys sp*	E01081	6256	8	810	0	0	0	734	0
Cryptacanthodidae	*Cryptacanthodes maculatus*	E00116	10532	13	810	0	888	729	744	906
Cyclopteridae	*Cyclopterus lumpus*	E00220	12165	15	657	720	891	0	744	0
Cyclopteridae	*Eumicrotremus orbis*	E00270	12456	15	780	720	891	0	702	868
Cynoglossidae	*Cynoglossus interruptus*	E00076	7900	8	0	0	0	894	0	0
Cynoglossidae	*Symphurus atricaudus*	E00023	10924	12	750	0	891	714	744	804
Cynoglossidae	*Symphurus civitatium*	E00604	7546	8	0	0	0	804	702	919
Cynoglossidae	*Symphurus plagiusa*	E01164	7027	8	0	0	0	744	744	0
Cyprinodontidae	*Cyprinodon variegatus*	E01066	12469	15	780	675	887	747	732	0
Cyprinodontidae	*Floridichthys carpio*	E01063	9295	11	0	675	0	741	732	910

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Cyprinodontidae	*Jordanella floridae*	N14002	5915	7	786	0	0	0	744	0
Dactylopteridae	*Dactyloptena gilberti*	N14051	5845	7	786	0	879	0	736	0
Dactylopteridae	*Dactyloptena orientalis*	E00237	13665	15	792	0	873	918	729	0
Dactylopteridae	*Dactyloptena peterseni*	E00749	14553	15	0	0	873	765	736	928
Dactylopteridae	*Dactylopterus volitans*	E00214	7789	10	0	0	0	918	731	0
Dactyloscopidae	*Gillellus semicinctus*	G01299	6655	8	0	0	0	0	744	0
Dactyloscopidae	*Platygillellus rubrocinctus*	E00319	5427	7	0	0	0	765	723	761
Datnioididae	*Datnioides microlepis*	N14199	7836	10	753	0	819	0	676	0
Dichistiidae	*Dichistius capensis*	M01571	3582	4	0	0	0	0	0	0
Diodontidae	*Chilomycterus schoepfii*	E00517	12554	15	657	0	891	0	744	908
Diodontidae	*Diodon holocanthus*	E00312	13884	15	657	0	867	738	744	826
Drepaneidae	*Drepane punctata*	E00250	13305	15	753	699	825	918	722	0
Echeneidae	*Echeneis naucrates*	E00615	16441	18	810	0	891	795	0	787
Echeneidae	*Echeneis neucratoides*	E00245	7118	7	0	0	0	0	702	0
Echeneidae	*Phtheirichthys lineatus*	G01438	7650	8	0	0	0	0	705	867
Echeneidae	*Remora osteochir australis*	E00503	10993	11	0	0	0	798	699	0
Elassomatidae	*Elassoma evergladei*	E00146	15293	17	0	696	0	771	744	748
Elassomatidae	*Elassoma okefenokee*	G01283	9813	12	795	0	891	0	744	0
Elassomatidae	*Elassoma zonatum*	G01284	14834	15	798	0	888	0	744	0
Eleginopsidae	*Eleginops maclovinus*	G01286	10593	13	645	0	891	0	744	0
Eleotridae	*Dormitator maculatus*	E00169	5763	7	0	0	891	0	662	0
Eleotridae	*Eleotris acanthopoma pisonis*	E00741	12447	14	783	0	870	771	744	750
Eleotridae	*Ophiocara porocephala*	E01101	11395	13	777	0	0	0	744	0
Eleotridae	*Oxyeleotris selheimi*	N01730	5975	7	0	0	0	0	725	0
Embiotocidae	*Amphistichus argenteus*	E00129	8893	12	0	684	0	744	737	891
Embiotocidae	*Cymatogaster aggregata*	E00139	14184	16	657	648	0	744	744	282
Embiotocidae	*Embiotoca jacksoni*	E00120	14177	17	657	639	846	696	744	884
Embiotocidae	*Embiotoca lateralis*	N14635	6883	8	810	0	0	0	731	0
Embiotocidae	*Hyperprosopon anale argenteum*	E00134	14767	18	657	648	810	759	744	862
Embiotocidae	*Phanerodon furcatus*	E00122	11479	14	606	684	0	759	726	933

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Embiotocidae	*Rhacochilus vacca*	E00124	12585	15	657	0	855	756	716	909
Embiotocidae	*Zalembius rosaceus*	E00135	4565	6	0	0	0	747	0	0
Emmelichthyidae	*Erythrocles schlegelii*	E00954	12039	15	657	0	822	747	708	0
Emmelichthyidae	*Erythrocles scintillans*	N14652	6911	9	756	0	828	0	675	0
Enoplosidae	*Enoplosus armatus*	G01287	10134	11	756	0	819	0	673	0
Ephippidae	*Chaetodipterus faber*	E00614	14589	18	657	654	852	735	644	920
Ephippidae	*Platax orbicularis*	E00898	13969	16	657	669	825	0	710	0
Ephippidae	*Platax teira*	E00858	12410	15	657	657	0	747	744	882
Epigonidae	*Epigonus pandionis*	E01019	5505	7	0	0	0	0	0	0
Epigonidae	*Epigonus telescopus*	E00652	10314	12	0	699	0	0	0	0
Exocoetidae	*Cheilopogon dorsomacula*	E00624	11475	14	0	0	0	666	0	876
Exocoetidae	*Cheilopogon melanurus*	N14975	5883	7	687	0	0	0	744	0
Exocoetidae	*Cheilopogon pinnatibarbatus*	E00399	13294	16	567	0	0	681	744	892
Exocoetidae	*Cypselurus callopterus*	E00402	6837	8	0	0	0	0	738	882
Exocoetidae	*Exocoetus monocirrhus*	E00403	10246	13	0	675	0	729	744	648
Exocoetidae	*Hirundichthys marginatus*	E00401	9589	12	0	0	0	666	727	900
Exocoetidae	*Parexocoetus brachypterus*	E00645	4220	5	0	0	0	0	0	741
Exocoetidae	*Prognichthys brevipinnis*	E00400	6286	8	0	0	0	657	744	839
Fistulariidae	*Fistularia commersonii*	E00941	7080	7	753	0	0	0	666	0
Fistulariidae	*Fistularia petimba*	E00602	6969	9	753	0	0	0	666	0
Fundulidae	*Adinia xenica*	E00173	8890	10	0	645	0	726	733	910
Fundulidae	*Fundulus blairae*	E00130	9841	11	0	684	0	702	718	892
Fundulidae	*Fundulus chrysotus*	E00186	8599	9	0	0	0	702	0	916
Fundulidae	*Fundulus heteroclitus*	G01293	12304	13	657	0	891	0	744	0
Fundulidae	*Fundulus parvipinnis*	E00389	11368	13	0	660	0	666	705	0
Fundulidae	*Lucania parva goodei*	E01064	13730	16	657	675	876	747	731	911
Gasterosteidae	*Apeltes quadracus*	E00791	11199	12	657	0	891	0	744	0
Gasterosteidae	*Culaea inconstans*	E00368	12338	14	648	0	0	777	701	744
Gasterosteidae	*Gasterosteus aculeatus*	E01012	20181	21	657	732	891	930	744	984
Gasterosteidae	*Gasterosteus wheatlandi*	N15128	8456	10	795	0	876	0	741	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Gasterosteidae	*Pungitius pungitius*	G01460	10820	11	0	0	0	0	743	0
Gasterosteidae	*Spinachia spinachia*	G01491	10498	11	648	0	0	0	744	0
Gempylidae	*Gempylus serpens*	E00693	9797	13	0	0	0	0	708	917
Gempylidae	*Nealotus tripes*	E00287	6043	8	0	0	0	573	0	871
Gempylidae	*Neoepinnula americana*	E00471	5662	7	0	690	0	804	0	913
Gempylidae	*Neoepinnula orientalis*	E00518	6702	9	0	0	0	810	0	883
Gempylidae	*Paradiplospinus gracilis*	N15143	7281	9	810	0	873	0	733	0
Gempylidae	*Ruvettus pretiosus*	E00226	13794	16	657	0	891	597	744	0
Gerreidae	*Eucinostomus argenteus*	E00575	5749	7	0	0	0	717	736	903
Gerreidae	*Eucinostomus gula*	E00756	7604	9	0	0	0	702	733	920
Gerreidae	*Eugerres plumieri*	G01291	11242	14	655	0	891	0	744	0
Gerreidae	*Gerres cinereus*	E00292	11457	12	0	0	0	738	734	678
Gerreidae	*Gerres longirostris*	E00835	6053	8	0	693	0	690	0	0
Gerreidae	*Gerres oyena*	E00823	6770	8	0	693	0	699	0	0
Gerreidae	*Ulaema lefroyi*	G01507	8309	10	657	0	891	0	728	0
Gigantactinidae	*Gigantactis ios*	E01053	4539	6	0	675	0	750	743	916
Gigantactinidae	*Gigantactis sp*	N34852	6412	8	663	0	885	0	733	0
Gigantactinidae	*Gigantactis vanhoeffeni*	E00177	13239	15	657	684	891	0	744	898
Girellidae	*Girella nigricans mezina*	E00197	11742	13	759	0	822	0	671	0
Glaucosomatidae	*Glaucosoma buergeri*	N15231	7808	10	759	0	825	0	675	0
Glaucosomatidae	*Glaucosoma hebraicum*	G01300	16039	18	810	702	891	930	665	0
Gobiesocidae	*Arcos sp*	E00102	13747	16	759	684	871	765	742	733
Gobiesocidae	*Diademichthys lineatus*	G01276	8298	10	618	0	891	0	732	0
Gobiesocidae	*Gobiesox maeandricus*	G01302	8270	10	657	0	891	0	741	0
Gobiesocidae	*Lepadichthys lineatus*	E01080	3896	5	0	669	0	0	743	0
Gobiidae	*Amblyeleotris guttata*	E01043	8728	11	0	0	0	735	743	930
Gobiidae	*Amblyeleotris gymnocephala*	E00409	6038	8	0	0	0	720	743	907
Gobiidae	*Amblyeleotris wheeleri*	E01073	7397	9	0	0	0	750	710	931
Gobiidae	*Amblygobius decussatus*	E00533	2824	4	0	0	0	0	722	0
Gobiidae	*Amblygobius phalaena*	E00736	7217	10	0	0	0	585	646	0

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Gobiidae	*Asterropteryx semipunctata*	E01089	6719	8	0	0	0	753	741	0
Gobiidae	*Bathygobius mystacium*	E00104	6412	8	0	0	0	0	0	920
Gobiidae	*Bollmannia communis*	E00617	5108	5	0	0	0	0	734	905
Gobiidae	*Cabillus lacertops*	E01093	3915	5	0	0	0	774	742	941
Gobiidae	*Caffrogobius caffer*	E01056	6198	8	0	0	0	774	743	0
Gobiidae	*Caffrogobius saldanha*	E01057	6207	8	0	0	0	756	728	0
Gobiidae	*Coryphopterus glaucofraenum*	E00100	5342	7	0	0	0	726	0	0
Gobiidae	*Coryphopterus personatus*	E00405	4791	7	0	0	0	747	0	0
Gobiidae	*Cryptocentrus sp*	E00407	3883	5	0	663	0	0	0	872
Gobiidae	*Ctenogobiops crocineus*	E01097	5981	7	0	0	0	717	742	941
Gobiidae	*Ctenogobius boleosoma*	E00172	3520	5	0	0	0	0	0	780
Gobiidae	*Elacatinus oceanops*	E00108	11459	12	0	645	0	774	0	777
Gobiidae	*Eviota albolineata*	E01041	6182	8	0	672	0	753	0	932
Gobiidae	*Eviota prasites*	E01044	5506	7	0	0	0	753	743	811
Gobiidae	*Eviota saipanensis*	E00714	4913	6	0	0	0	663	0	801
Gobiidae	*Evorthodus lyricus*	E00171	6129	8	0	648	0	756	0	939
Gobiidae	*Fusigobius duospilus*	E00863	7305	9	0	0	0	0	743	940
Gobiidae	*Fusigobius inframaculatus*	E01076	4985	6	0	0	0	738	743	937
Gobiidae	*Fusigobius neophytus*	E00733	7031	10	0	675	0	753	669	834
Gobiidae	*Gnatholepis anjerensis*	E01075	4977	7	0	0	0	0	737	868
Gobiidae	*Gnatholepis cauerensis*	E00099	3361	5	0	660	0	0	644	0
Gobiidae	*Gobiodon quinquestrigatus*	E01085	6985	9	0	0	0	705	673	937
Gobiidae	*Gobiosoma bosc*	E00097	9910	10	0	591	0	756	0	0
Gobiidae	*Istigobius decoratus*	E01078	9124	11	0	0	0	0	743	937
Gobiidae	*Istigobius ornatus*	E01107	2776	3	0	675	0	0	0	931
Gobiidae	*Lepidogobius lepidus*	G01351	5076	6	0	0	0	0	744	0
Gobiidae	*Lophogobius cyprinoides*	E00508	6153	8	0	0	0	666	720	0
Gobiidae	*Lythrypnus dalli*	E00126	6746	9	0	663	0	723	0	786
Gobiidae	*Oplopomus oplopomus*	E01067	6654	8	0	0	0	759	0	882
Gobiidae	*Paragobiodon modestus*	E01098	8154	11	0	285	0	732	742	930

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Gobiidae	*Periophthalmus kalolo*	E00537	6876	9	0	663	0	762	680	809
Gobiidae	*Priolepis cincta*	E01077	5030	6	0	0	0	0	744	871
Gobiidae	*Priolepis hipoliti*	E00106	5717	7	0	0	0	0	0	893
Gobiidae	*Psammogobius biocellatus*	E00740	5797	8	0	0	0	0	671	751
Gobiidae	*Risor ruber*	E00107	10310	10	0	0	0	762	0	894
Gobiidae	*Stonogobiops nematodes*	N16820	2850	4	0	0	0	0	673	0
Gobiidae	*Trimma caesiura*	E01039	8870	11	0	0	0	750	0	748
Gobiidae	*Trimma haima*	E01084	5533	7	0	0	0	777	743	0
Gobiidae	*Trimma okinawae*	E00726	2759	4	0	0	0	687	0	0
Gobiidae	*Valenciennea puellaris*	E01096	5328	7	0	0	0	768	0	909
Gobiidae	*Valenciennea strigata*	E01094	4256	6	0	0	0	0	743	0
Gobiidae	*Vanderhorstia ornatissima*	E01088	6501	8	0	675	0	0	742	928
Grammatidae	*Gramma loreto*	E00280	14197	16	657	720	891	918	744	0
Grammatidae	*Lipogramma anabantoides*	E00211	6519	8	0	720	0	918	729	0
Grammatidae	*Lipogramma trilineata*	E00210	6532	8	0	720	0	918	720	0
Haemulidae	*Anisotremus surinamensis*	N17175	7479	9	804	0	864	0	715	0
Haemulidae	*Anisotremus virginicus*	E00200	9338	11	0	720	0	918	0	0
Haemulidae	*Conodon nobilis*	E00613	10862	13	0	690	0	804	696	909
Haemulidae	*Haemulon aurolineatum*	E00635	16270	20	798	690	891	798	702	905
Haemulidae	*Haemulon plumierii*	E00279	12545	15	810	720	891	774	717	0
Haemulidae	*Haemulon sciurus*	E00199	14796	18	657	720	891	918	735	0
Haemulidae	*Haemulon vittatum*	E00218	14636	17	657	0	873	918	733	0
Haemulidae	*Orthopristis chrysoptera*	E00607	15170	18	810	690	891	807	709	905
Haemulidae	*Plectorhinchus chaetodonoides*	E00857	12011	14	0	630	0	729	0	0
Haemulidae	*Plectorhinchus vittatus*	E00856	9448	12	0	630	0	729	0	906
Haemulidae	*Pomadasys corvinaeformis*	E00761	10420	14	651	630	0	759	0	0
Haemulidae	*Xenistius californiensis*	E00229	11494	14	0	720	0	918	704	0
Hapalogenyidae	*Hapalogenys aya*	M01722	4098	4	0	0	0	0	0	0
Hapalogenyidae	*Hapalogenys kishinouyei*	M01723	3627	4	0	0	0	0	0	0
Hapalogenyidae	*Hapalogenys nigripinnis*	M01724	4735	5	0	0	0	0	0	0

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Harpagiferidae	*Harpagifer antarcticus*	G01524	10362	11	657	0	891	0	744	0
Helostomatidae	*Helostoma temminkii*	G01315	8144	9	0	0	831	0	669	0
Hemiramphidae	*Arrhamphus sclerolepis*	G01209	7917	10	657	0	0	0	744	0
Hemiramphidae	*Hemiramphus brasiliensis*	E00098	10104	12	0	0	0	0	0	917
Hemiramphidae	*Hyporhamphus affinis*	E01068	5623	7	0	0	0	771	0	937
Hemiramphidae	*Hyporhamphus dussumieri*	E01086	3078	4	0	0	0	756	743	928
Hemiramphidae	*Oxyporhamphus micropterus*	E00397	8076	9	0	0	0	0	733	755
Hexagrammidae	*Hexagrammos decagrammus*	E00348	7318	10	0	657	0	774	699	0
Hexagrammidae	*Hexagrammos lagocephalus otakii*	E00363	13109	16	657	660	891	759	730	0
Hexagrammidae	*Pleurogrammus monopterygius*	E00367	6904	9	0	690	0	774	711	862
Hexagrammidae	*Zaniolepis frenata*	E00353	6326	9	0	666	0	702	709	868
Himantolophidae	*Himantolophus albinares sagamius*	E00656	16540	18	657	666	891	702	744	896
Hoplichthyidae	*Hoplichthys gilberti*	N17743	5272	7	570	0	828	0	679	0
Hoplichthyidae	*Hoplichthys langsdorfii*	N17745	5443	7	750	0	828	0	679	0
Howellidae	*Howella brodiei*	E00816	11083	12	0	702	0	930	0	932
Howellidae	*Howella zina*	N17756	5489	7	759	0	825	0	674	0
Hypoptychidae	*Aulichthys japonicus*	G01216	11602	12	645	0	891	0	744	0
Hypoptychidae	*Hypoptychus dybowskii*	G01335	10399	11	645	0	891	0	744	0
Icosteidae	*Icosteus aenigmaticus*	G01336	7173	9	612	0	0	0	744	0
Indostomidae	*Indostomus crocodilus*	N17863	5047	7	762	0	0	0	733	0
Indostomidae	*Indostomus paradoxus*	E01156	10345	11	810	0	0	0	733	0
Isonidae	*Iso sp*	E00145	8043	10	753	0	840	0	744	0
Istiophoridae	*Istiophorus platypterus*	E00695	12698	12	0	0	0	786	0	877
Istiophoridae	*Kajikia albida*	E00681	7868	10	0	690	0	783	711	905
Istiophoridae	*Makaira nigricans*	E00697	11395	12	0	690	0	777	0	854
Istiophoridae	*Makaira sp*	E00692	8009	9	0	0	0	777	711	912
Istiophoridae	*Tetrapturus angustirostris*	N01741	7787	10	669	0	852	0	668	0
Kuhliidae	*Kuhlia marginata*	G01341	10248	12	654	0	849	0	744	0
Kuhliidae	*Kuhlia mugil*	E00712	16962	18	0	690	0	762	720	883
Kuhliidae	*Kuhlia rupestris*	E00957	12721	15	717	0	828	0	695	0

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Kurtidae	*Kurtus gulliveri*	E00188	16737	18	756	0	816	762	744	931
Kurtidae	*Kurtus indicus*	N17950	5074	7	789	0	816	0	673	0
Kyphosidae	*Kyphosus cinerascens*	N17975	7672	10	717	0	822	0	668	0
Kyphosidae	*Kyphosus elegans*	G01342	9674	11	657	0	891	0	731	0
Kyphosidae	*Kyphosus incisor*	E00202	6684	8	0	0	0	0	744	0
Kyphosidae	*Kyphosus sectatrix*	E00775	12318	14	0	630	0	771	0	928
Labridae	*Anampses lineatus*	E00932	8645	11	0	0	0	762	0	881
Labridae	*Bodianus axillaris*	E00947	9242	11	0	627	0	0	693	0
Labridae	*Bodianus mesothorax*	E00560	14044	17	657	654	891	711	694	0
Labridae	*Cheilinus chlorourus*	E00907	9227	12	0	0	0	756	705	929
Labridae	*Cheilinus fasciatus*	E00876	8639	11	0	669	0	777	0	0
Labridae	*Cheilinus oxycephalus*	E00901	6640	8	0	0	0	0	0	906
Labridae	*Cheilio inermis*	E00906	9477	11	0	0	0	0	709	940
Labridae	*Cirrhilabrus katherinae*	E00728	6057	8	0	654	0	0	693	882
Labridae	*Cirrhilabrus punctatus*	E00553	5794	7	0	0	0	762	681	0
Labridae	*Clepticus parrae*	E00015	14928	18	657	699	0	684	744	923
Labridae	*Coris batuensis*	N18137	4801	6	792	0	0	0	744	0
Labridae	*Coris caudimacula*	E00861	11177	14	0	645	0	0	714	873
Labridae	*Coris formosa*	E00912	8465	11	0	657	0	771	710	940
Labridae	*Coris gaimard*	E00091	11874	15	657	0	891	0	618	807
Labridae	*Decodon puellaris*	E00620	7367	9	0	0	0	729	696	0
Labridae	*Diproctacanthus xanthurus*	G01278	8556	10	657	0	858	0	744	0
Labridae	*Epibulus insidiator*	E00879	16078	19	657	639	861	771	708	794
Labridae	*Gomphosus varius*	E00085	11071	14	651	0	858	0	744	0
Labridae	*Halichoeres bathyphilus bivittatus*	E00637	13256	16	657	654	888	0	732	0
Labridae	*Halichoeres biocellatus*	E00727	5094	7	0	654	0	0	0	0
Labridae	*Halichoeres iridis*	E00928	6442	8	0	0	0	768	0	884
Labridae	*Halichoeres margaritaceus*	N18205	5528	7	774	0	0	0	744	0
Labridae	*Hologymnosus doliatus*	E00567	10593	13	0	654	0	750	711	915
Labridae	*Labrichthys unilineatus*	G01344	10143	12	657	0	858	0	744	0

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Labridae	*Labroides dimidiatus*	E00848	9046	11	0	669	0	0	715	0
Labridae	*Labropsis australis*	G01345	9319	11	657	0	861	0	744	0
Labridae	*Lachnolaimus maximus*	E00014	12305	15	657	0	846	0	744	860
Labridae	*Macropharyngodon bipartitus*	E00895	7503	10	0	669	0	765	714	892
Labridae	*Novaculichthys taeniourus*	E00926	12181	15	0	657	0	768	696	924
Labridae	*Oxycheilinus celebicus*	G01412	8510	10	657	0	861	0	744	0
Labridae	*Oxycheilinus digramma*	E00873	10757	13	0	669	0	765	0	870
Labridae	*Oxycheilinus unifasciatus*	E00721	7878	9	0	0	0	0	0	851
Labridae	*Oxyjulis californica*	G01413	7537	9	657	0	861	0	0	0
Labridae	*Pseudocheilinus evanidus*	E00944	6483	9	0	657	0	0	714	907
Labridae	*Pseudocheilinus hexataenia*	E00945	7019	9	0	660	0	0	693	929
Labridae	*Pteragogus enneacanthus*	G01457	6723	8	645	0	855	0	0	0
Labridae	*Stethojulis balteata*	E00089	4889	6	0	0	0	0	0	843
Labridae	*Stethojulis strigiventer*	E00908	11343	15	0	651	0	753	705	0
Labridae	*Tautoga onitis*	G01499	9257	11	657	0	0	0	744	0
Labridae	*Tautogolabrus adspersus*	G01500	10397	12	657	0	0	0	744	0
Labridae	*Thalassoma amblycephalum*	E00891	10041	13	0	669	0	0	711	915
Labridae	*Thalassoma lunare*	E00902	11967	15	0	645	0	0	693	912
Labridae	*Thalassoma quinquevittatum*	E00092	6872	9	0	0	0	0	720	806
Labridae	*Wetmorella nigropinnata*	E00948	11203	14	0	0	0	762	708	0
Labridae	*Xyrichtys novacula martinicensis*	E00016	18002	21	657	699	861	684	727	932
Labrisomidae	*Labrisomus bucciferus*	E00301	5621	7	0	0	0	915	706	882
Labrisomidae	*Labrisomus guppyi multiporosus*	E00300	8447	10	0	0	891	0	744	0
Labrisomidae	*Labrisomus nigricinctus*	E00302	4582	6	0	0	0	915	703	844
Labrisomidae	*Malacoctenus aurolineatus*	E00299	2229	3	0	669	0	0	0	873
Labrisomidae	*Malacoctenus triangulatus*	E00321	3751	4	0	0	0	0	0	882
Labrisomidae	*Paraclinus marmoratus*	E00309	4124	5	0	0	0	915	0	859
Labrisomidae	*Starksia atlantica*	E00304	5512	7	0	0	0	915	658	677
Labrisomidae	*Starksia fasciata*	E00303	7567	9	0	0	0	915	711	912
Labrisomidae	*Starksia ocellata*	E00318	4469	6	0	0	0	915	0	933

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Lactariidae	*Lactarius lactarius Fiji*	M01673	3453	4	0	0	0	0	0	0
Lactariidae	*Lactarius lactarius Qatar*	M01593	4041	5	0	0	0	0	0	0
Lateolabracidae	*Lateolabrax japonicus*	E01130	12539	12	0	702	0	927	744	0
Latridae	*Latridopsis forsteri*	M01594	4790	5	0	0	0	0	0	0
Latridae	*Latris lineata*	M01595	4794	5	0	0	0	0	0	0
Leiognathidae	*Gazza minuta*	G01298	8150	10	657	0	891	0	711	0
Leiognathidae	*Leiognathus equulus*	G01348	8522	11	657	0	891	0	726	0
Leptobramidae	*Leptobrama muelleri*	E01150	6470	8	0	0	0	777	0	0
Lethrinidae	*Gymnocranius grandoculis*	E00952	7334	9	0	630	0	747	0	0
Lethrinidae	*Lethrinus atkinsoni*	E00750	7416	10	0	630	0	702	0	0
Lethrinidae	*Lethrinus erythropterus*	N18731	7589	9	810	0	870	0	0	0
Lethrinidae	*Lethrinus harak*	E00905	18169	21	657	630	870	567	731	916
Lethrinidae	*Lethrinus obsoletus*	E00910	14297	15	0	630	0	747	720	924
Lethrinidae	*Lethrinus olivaceus*	E00751	11020	13	0	630	0	705	0	788
Lethrinidae	*Monotaxis grandoculis*	G01379	11352	12	657	0	861	0	744	0
Liparidae	*Careproctus melanurus*	E00422	5235	7	0	690	0	765	739	912
Liparidae	*Careproctus rastrinus*	E00255	6920	8	0	0	0	918	717	0
Liparidae	*Liparis gibbus*	E00224	9360	11	0	0	891	0	744	922
Liparidae	*Liparis pulchellus*	E00225	5675	7	0	717	0	0	720	0
Liparidae	*Paraliparis beani*	E00458	3871	5	0	690	0	807	0	895
Liparidae	*Paraliparis copei*	E00453	6908	9	0	690	0	747	737	905
Liparidae	*Paraliparis hystrix*	E00454	8881	11	0	690	891	783	712	883
Liparidae	*Rhinoliparis barbulifer*	E00262	5284	7	0	705	0	0	710	0
Lobotidae	*Lobotes pacificus surinamensis*	G01359	9710	12	801	0	885	0	744	0
Lophiidae	*Lophiodes reticulatus*	E00625	8318	11	0	636	0	0	731	613
Lophiidae	*Lophius americanus*	E00578	16809	19	657	660	891	0	743	875
Lophiidae	*Lophius gastrophysus*	E01119	13495	17	657	675	0	732	743	894
Lutjanidae	*Aphareus furca*	E00563	13687	16	0	690	0	807	723	912
Lutjanidae	*Aprion virescens*	E00828	8178	10	0	0	0	765	0	0
Lutjanidae	*Apsilus dentatus*	E00770	8017	10	0	630	0	0	0	877

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Lutjanidae	*Lutjanus biguttatus*	E00569	10110	12	657	690	848	0	744	866
Lutjanidae	*Lutjanus campechanus*	E00592	9830	12	0	690	0	804	693	906
Lutjanidae	*Lutjanus griseus*	N20115	7237	9	581	0	876	0	744	0
Lutjanidae	*Lutjanus mahogoni*	G01362	10416	12	657	0	891	0	744	0
Lutjanidae	*Macolor niger*	E00939	9071	11	0	0	0	738	0	858
Lutjanidae	*Ocyurus chrysurus*	E00283	13831	16	657	720	891	918	738	0
Lutjanidae	*Pristipomoides aquilonaris*	E00594	10332	13	0	690	0	798	696	931
Lutjanidae	*Pristipomoides auricilla*	E00746	6210	8	0	630	0	765	0	0
Lutjanidae	*Rhomboplites aurorubens*	E00593	13759	16	810	690	884	804	730	902
Luvaridae	*Luvarus imperialis*	E00509	15760	19	657	654	825	756	744	0
Malacanthidae	*Caulolatilus intermedius*	E00595	8981	11	0	690	0	789	699	0
Malacanthidae	*Caulolatilus princeps*	E00231	11865	15	657	708	888	918	717	0
Malacanthidae	*Malacanthus plumieri*	E00774	8060	10	0	0	891	0	735	0
Mastacembelidae	*Macrognathus siamensis*	G01367	8287	10	657	0	891	0	744	0
Mastacembelidae	*Mastacembelus brachyrhinus*	N01727	6948	8	744	0	891	0	744	0
Mastacembelidae	*Mastacembelus cunningtoni*	N20638	7046	8	756	0	891	0	744	0
Mastacembelidae	*Mastacembelus erythrotaenia*	E01157	5328	7	0	0	0	885	744	0
Mastacembelidae	*Mastacembelus niger*	N20658	7640	9	810	0	891	0	744	0
Melanocetidae	*Melanocetus johnsonii*	E00657	12119	14	0	678	0	711	731	885
Melanocetidae	*Melanocetus murrayi*	E00477	8829	10	0	678	0	738	741	905
Melanotaeniidae	*Melanotaenia sp*	N35702	6890	8	810	0	0	0	0	0
Melanotaeniidae	*Melanotaenia splendida*	E00179	10979	13	0	0	0	753	0	929
Melanotaeniidae	*Melanotaenia trifasciata*	E00178	7620	9	0	0	0	768	657	0
Melanotaeniidae	*Rhadinocentrus ornatus*	E00183	8085	9	0	0	0	0	0	0
Menidae	*Mene maculata*	E01131	14538	17	756	0	819	918	744	0
Microdesmidae	*Cerdale floridana*	E00113	5251	7	0	642	0	0	0	0
Microdesmidae	*Gunnellichthys monostigma*	E00545	4244	6	0	657	0	0	0	855
Microdesmidae	*Microdesmus bahianus*	E00112	6294	8	0	0	0	0	0	916
Microdesmidae	*Microdesmus longipinnis*	E00388	7384	9	0	675	0	705	0	891
Microdesmidae	*Nemateleotris magnifica*	N20888	3449	4	0	0	0	0	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Microdesmidae	*Ptereleotris evides*	E00565	10142	12	0	0	0	750	0	819
Microdesmidae	*Ptereleotris microlepis*	E00554	6773	9	0	681	0	681	0	0
Molidae	*Masturus lanceolatus*	E00651	10906	12	657	666	852	0	669	0
Molidae	*Mola mola*	E00683	12859	14	810	0	891	0	732	0
Molidae	*Ranzania laevis*	G01463	10882	12	771	0	828	0	690	0
Monacanthidae	*Acreichthys tomentosus*	N21168	5898	7	810	0	879	0	744	0
Monacanthidae	*Aluterus scriptus*	E00316	8934	9	0	0	0	849	723	0
Monacanthidae	*Amanses scopas*	E00536	7667	7	0	0	0	0	727	796
Monacanthidae	*Cantherhines pardalis pullus*	E00887	13701	14	810	0	870	729	727	0
Monacanthidae	*Oxymonacanthus longirostris*	E00914	7920	8	0	663	0	732	0	0
Monacanthidae	*Paraluteres prionurus*	E00913	10156	10	810	0	882	0	727	0
Monacanthidae	*Pervagor janthinosoma*	N21229	7625	9	810	0	888	0	744	0
Monacanthidae	*Pervagor nigrolineatus*	N21232	5912	7	810	0	842	0	744	0
Monacanthidae	*Stephanolepis hispidus*	E00646	10631	13	657	0	879	0	744	860
Monodactylidae	*Monodactylus argenteus*	E00827	11839	12	0	0	0	840	744	0
Monodactylidae	*Monodactylus sebae*	N21267	8411	10	750	0	867	0	744	0
Moronidae	*Dicentrarchus labrax*	E01132	13167	14	0	699	0	930	744	0
Moronidae	*Morone americana*	E00017	4648	6	0	0	0	0	0	844
Moronidae	*Morone chrysops*	E00992	15777	17	657	0	891	930	738	0
Moronidae	*Morone mississippiensis*	E00087	11851	14	810	0	875	0	741	838
Moronidae	*Morone saxatilis*	G01380	9541	12	756	0	891	0	744	0
Mugilidae	*Chelon macrolepis*	E00845	8599	11	0	0	0	0	0	877
Mugilidae	*Crenimugil crenilabis*	E00846	12826	14	0	645	0	765	719	0
Mugilidae	*Liza richardsonii*	E00808	12339	15	0	0	0	0	690	893
Mugilidae	*Moolgarda engeli*	E00739	6506	8	0	0	0	0	0	435
Mugilidae	*Mugil cephalus*	E00049	13859	15	648	0	891	774	744	0
Mugilidae	*Mugil curema*	E00031	15184	16	657	0	891	753	705	0
Mugilidae	*Mugil trichodon*	E00765	10230	11	0	654	0	0	702	0
Mugilidae	*Myxus capensis*	E00809	9832	10	0	0	0	0	722	912
Mugilidae	*Neomyxus leuciscus*	E00742	10501	12	0	654	0	0	714	760

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Mugilidae	*Valamugil buchanani*	E00847	12275	15	0	669	0	753	706	906
Mullidae	*Mulloidichthys flavolineatus*	E00844	9135	11	714	654	0	0	695	931
Mullidae	*Mullus auratus*	E00634	10617	12	0	654	0	741	723	0
Mullidae	*Parupeneus barberinus*	E00899	8131	10	0	657	734	0	744	941
Mullidae	*Parupeneus ciliatus*	E00840	5965	8	0	645	0	0	0	908
Mullidae	*Parupeneus trifasciatus*	N21710	5845	7	786	0	734	0	744	0
Mullidae	*Pseudupeneus maculatus*	E00773	9043	11	0	654	734	0	671	0
Mullidae	*Upeneus moluccensis*	E00825	7964	10	0	669	0	0	729	788
Mullidae	*Upeneus parvus*	N21732	3287	4	0	0	0	0	668	0
Nandidae	*Nandus andrewi*	N22312	8474	10	810	0	891	0	735	0
Nandidae	*Nandus nandus*	G01388	11524	13	810	0	891	0	672	0
Nandidae	*Nandus nebulosus*	N22314	7688	9	810	0	891	0	744	0
Nematistiidae	*Nematistius pectoralis*	E01146	12623	14	750	0	734	0	744	0
Nemipteridae	*Pentapodus caninus*	G01427	8879	11	657	0	876	0	744	0
Nemipteridae	*Scolopsis bilineata*	E00028	14791	16	657	0	882	0	744	849
Nemipteridae	*Scolopsis frenata*	E00911	6514	8	0	0	0	756	711	881
Nemipteridae	*Scolopsis margaritifera*	G01478	7404	9	657	0	879	0	744	0
Niphonidae	*Niphon spinosus*	G01398	4377	5	753	0	891	0	705	0
Nomeidae	*Cubiceps baxteri*	G01271	9684	12	657	0	891	0	744	0
Nomeidae	*Cubiceps gracilis*	E00672	8634	11	0	630	0	759	0	885
Nomeidae	*Cubiceps pauciradiatus*	E00667	9277	9	0	0	0	723	733	873
Nomeidae	*Psenes cyanophrys*	E00666	6230	6	0	0	0	0	0	0
Nomeidae	*Psenes maculatus*	N23089	7094	9	747	0	828	0	675	0
Nototheniidae	*Aethotaxis mitopteryx*	G01528	7979	9	0	0	0	0	744	0
Nototheniidae	*Dissostichus eleginoides*	G01279	12707	14	597	0	891	0	744	0
Nototheniidae	*Gobionotothen gibberifrons*	G01529	8961	10	657	0	0	0	729	0
Nototheniidae	*Notothenia coriiceps*	G01526	9628	10	657	0	0	0	744	0
Nototheniidae	*Pagothenia borchgrevinki*	G01527	9352	10	0	0	882	0	718	0
Nototheniidae	*Patagonotothen tessellata*	G01530	10915	12	0	0	891	0	744	0
Odacidae	*Haletta semifasciata*	G01312	9038	11	654	0	876	0	744	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Odontobutidae	*Odontobutis potamophila*	E01137	12389	14	654	0	891	0	738	0
Odontobutidae	*Perccottus glenii*	G01429	9285	11	633	0	891	0	744	0
Ogcocephalidae	*Dibranchus tremendus*	E00975	8668	11	0	675	0	735	743	896
Ogcocephalidae	*Halieutichthys aculeatus*	E01122	5969	8	0	0	885	747	703	0
Ogcocephalidae	*Ogcocephalus parvus nasutus*	E00610	11181	14	657	681	891	714	738	886
Ogcocephalidae	*Ogcocephalus radiatus*	E00641	3592	4	0	0	0	0	0	766
Oneirodidae	*Bertella idiomorpha*	E00386	7368	8	0	681	0	0	743	909
Oneirodidae	*Dolopichthys sp*	E00484	3002	4	0	681	0	0	0	854
Oneirodidae	*Oneirodes bulbosus*	E00176	5086	7	0	684	0	0	744	902
Oneirodidae	*Oneirodes macrosteus*	E00655	7815	10	657	0	0	678	744	706
Ophidiidae	*Bassogigas gillii*	E00481	5439	7	0	690	0	0	687	0
Ophidiidae	*Brotula barbata*	E00629	8900	12	0	690	0	0	711	764
Ophidiidae	*Brotula multibarbata*	E00883	12654	16	657	630	891	744	744	0
Ophidiidae	*Brotulotaenia crassa*	E00659	7913	10	0	690	0	0	714	0
Ophidiidae	*Brotulotaenia nigra*	E00817	8794	11	0	630	0	762	0	793
Ophidiidae	*Chilara taylori*	E00260	6335	8	0	720	0	918	744	0
Ophidiidae	*Dicrolene introniger*	E00480	8819	11	651	690	0	0	686	918
Ophidiidae	*Genypterus blacodes*	E00241	3596	4	0	0	0	0	729	0
Ophidiidae	*Lamprogrammus niger*	E00275	11903	13	678	705	882	0	714	0
Ophidiidae	*Lepophidium brevibarbe*	E00758	5469	7	0	630	0	768	0	0
Ophidiidae	*Lepophidium jeannae*	E00621	4709	6	0	0	0	0	694	691
Ophidiidae	*Lepophidium profundorum*	E00248	3341	4	0	0	0	0	0	0
Ophidiidae	*Neobythites gilli*	E00612	7830	10	0	690	0	0	690	0
Ophidiidae	*Ophidion holbrookii*	E01033	7171	9	0	0	0	744	705	919
Ophidiidae	*Ophidion josephi*	E00648	6546	8	0	0	0	798	717	894
Ophidiidae	*Ophidion robinsi*	E01007	6730	8	0	606	0	765	0	871
Ophidiidae	*Petrotyx sanguineus*	E00206	4716	6	0	0	0	0	459	0
Opistognathidae	*Lonchopisthus micrognathus*	E00603	6548	8	0	0	0	723	705	0
Opistognathidae	*Opistognathus aurifrons*	E00216	9008	11	657	0	876	0	744	0
Opistognathidae	*Opistognathus maxillosus*	E00207	6793	8	0	0	0	0	720	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Oplegnathidae	*Oplegnathus punctatus*	G01405	12420	13	780	0	879	0	739	0
Osphronemidae	*Betta splendens*	G01226	9892	10	657	0	891	0	744	0
Osphronemidae	*Trichopodus pectoralis*	N24415	4860	7	750	0	0	0	668	0
Ostraciidae	*Acanthostracion quadricornis*	E00760	5464	6	0	0	0	0	0	0
Ostraciidae	*Ostracion cubicus*	E00588	12421	15	657	633	846	717	744	0
Ostraciidae	*Rhinesomus triqueter*	G01469	10814	13	657	0	863	0	744	0
Ostracoberycidae	*Ostracoberyx dorygenys*	N24448	6883	9	756	0	828	0	671	0
Parabembridae	*Parabembras curtus*	N24483	6893	9	750	0	822	0	675	0
Paralichthyidae	*Ancylopsetta ommata*	E00001	8842	10	0	0	0	699	0	763
Paralichthyidae	*Citharichthys arctifrons*	E00043	6688	8	0	0	0	756	702	823
Paralichthyidae	*Citharichthys sordidus*	E00446	12907	14	810	0	891	774	714	931
Paralichthyidae	*Cyclopsetta chittendeni*	E00597	10244	12	0	654	0	756	708	0
Paralichthyidae	*Etropus crossotus*	E00647	8021	9	0	0	0	909	693	0
Paralichthyidae	*Etropus microstomus*	E00047	5197	5	0	0	0	0	695	0
Paralichthyidae	*Gastropsetta frontalis*	E00640	2345	3	0	0	0	741	485	0
Paralichthyidae	*Paralichthys albigutta*	E01171	8241	9	0	0	0	918	744	0
Paralichthyidae	*Paralichthys californicus*	E00020	8905	10	0	0	0	732	729	909
Paralichthyidae	*Paralichthys dentatus*	N24591	7812	9	810	0	891	0	744	0
Paralichthyidae	*Pseudorhombus pentophthalmus*	E00077	10302	11	0	0	0	765	711	819
Paralichthyidae	*Syacium micrurum*	E00633	9035	11	0	654	0	738	711	0
Paralichthyidae	*Xystreurys liolepis*	E00021	9760	10	0	0	0	744	706	911
Pegasidae	*Eurypegasus draconis*	N24699	2094	3	750	0	0	0	0	0
Pempheridae	*Parapriacanthus ransonneti*	E00923	11086	13	0	630	0	753	0	886
Pempheridae	*Pempheris oualensis*	E00718	9245	11	0	690	0	0	0	887
Pempheridae	*Pempheris schomburgkii*	E00213	10586	12	810	717	891	0	736	0
Pempheridae	*Pempheris schwenkii*	N01628	5322	7	747	0	0	0	654	0
Pempheridae	*Pempheris vanicolensis*	E00886	8350	10	0	630	0	0	0	842
Pentacerotidae	*Histiopterus typus*	N24730	6890	9	747	0	828	0	675	0
Pentacerotidae	*Paristiopterus labiosus*	M01629	3261	4	0	0	0	0	0	0
Pentacerotidae	*Pentaceros japonicus*	N24735	7793	10	747	0	825	0	675	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Pentacerotidae	*Pentaceros pectoralis*	N01736	5434	7	753	0	891	0	744	0
Pentacerotidae	*Pentaceros wheeleri*	N01737	7434	9	750	0	861	0	710	0
Pentacerotidae	*Zanclistius elevatus*	M01631	2901	3	0	0	0	0	0	0
Percichthyidae	*Gadopsis marmoratus*	E01144	13223	14	657	0	891	918	744	0
Percichthyidae	*Maccullochella peelii*	G01365	11015	13	657	0	891	0	744	0
Percichthyidae	*Macquaria ambigua*	G01366	10488	13	762	0	816	0	633	0
Percichthyidae	*Macquaria colonorum*	G01431	10574	13	762	0	825	0	668	0
Percichthyidae	*Macquaria novemaculeata*	G01432	10525	13	759	0	810	0	673	0
Percichthyidae	*Nannoperca australis*	G01389	11969	14	762	0	852	0	668	0
Percichthyidae	*Percichthys trucha*	G01430	9417	9	0	0	0	930	744	0
Percidae	*Ammocrypta beanii*	E00187	8350	10	0	684	0	714	0	930
Percidae	*Ammocrypta meridiana*	E00148	8201	10	0	0	0	0	743	782
Percidae	*Ammocrypta pellucida*	E00149	9339	11	0	0	0	0	743	790
Percidae	*Crystallaria asprella*	E00153	8415	10	0	0	0	699	732	894
Percidae	*Etheostoma atripinne*	G01290	7713	9	810	0	831	0	0	0
Percidae	*Etheostoma juliae*	E00168	11455	14	0	684	0	696	743	911
Percidae	*Etheostoma simoterum*	E00152	12189	15	657	0	831	717	733	909
Percidae	*Etheostoma vitreum*	E00147	11025	13	0	0	0	0	743	901
Percidae	*Etheostoma zonale*	E01111	13171	16	648	675	0	750	0	915
Percidae	*Gymnocephalus cernuus*	E00140	7525	10	657	0	0	0	739	693
Percidae	*Gymnocephalus schraetser*	E00141	6323	8	657	0	0	693	744	920
Percidae	*Perca flavescens*	E00391	14692	16	657	0	840	669	743	858
Percidae	*Perca fluviatilis*	G01428	10413	11	648	0	0	924	744	0
Percidae	*Percina caprodes*	E01054	15273	18	654	675	891	756	0	906
Percidae	*Percina nigrofasciata*	E00154	7519	9	0	0	0	711	743	0
Percidae	*Percina phoxocephala*	E00150	9105	11	0	0	0	717	740	898
Percidae	*Romanichthys valsanicola*	E00143	9564	12	0	657	0	696	0	895
Percidae	*Sander vitreus*	E01109	10398	10	0	675	0	756	0	910
Percidae	*Zingel streber*	E00144	5447	7	657	0	0	0	744	0
Percidae	*Zingel zingel*	E00142	6114	8	0	648	0	0	742	0

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Perciliidae	*Percilia irwini*	N24981	6918	9	762	0	765	0	676	0
Percophidae	*Acanthaphritis unoorum*	N24985	5579	7	750	0	0	0	677	0
Peristediidae	*Peristedion ecuadorense*	E00456	6094	7	0	0	0	696	726	892
Peristediidae	*Peristedion gracile*	E01029	2905	4	0	0	0	0	0	0
Peristediidae	*Peristedion truncatum*	E00450	3441	5	0	642	0	717	0	0
Phallostethidae	*Phenacostethus smithi*	E00398	7945	10	810	0	818	0	743	0
Pholidae	*Pholis crassispina*	G01437	12482	14	657	0	891	0	744	0
Pholidae	*Pholis ornata*	N01732	8528	10	810	0	891	0	734	0
Pholidichthyidae	*Pholidichthys leucotaenia*	E00251	11101	12	657	720	891	0	699	0
Pinguipedidae	*Parapercis clathrata*	E00707	10851	13	0	0	873	678	738	836
Pinguipedidae	*Parapercis hexophtalma*	E01083	11528	14	0	675	810	780	725	910
Pinguipedidae	*Parapercis punctulata*	E01091	7008	9	0	0	0	750	743	871
Platycephalidae	*Platycephalus indicus*	N25405	6719	9	741	0	822	0	528	0
Platycephalidae	*Rogadius asper*	N25418	6352	9	750	0	804	0	671	0
Platycephalidae	*Sunagocia arenicola*	E00708	5403	7	0	666	0	717	0	877
Platycephalidae	*Thysanophrys chiltonae*	E00864	8747	10	0	693	0	711	0	0
Plesiopidae	*Plesiops coeruleolineatus*	E00855	15452	18	753	630	861	753	696	846
Plesiopidae	*Plesiops melas*	G01442	8238	10	609	0	861	0	744	0
Pleuronectidae	*Atheresthes evermanni*	E00055	8437	8	0	0	0	771	0	895
Pleuronectidae	*Embassichthys bathybius*	E00064	11340	12	0	0	0	762	641	825
Pleuronectidae	*Eopsetta jordani*	E00444	14474	17	0	654	0	762	711	890
Pleuronectidae	*Glyptocephalus zachirus*	E00416	10353	12	0	0	0	771	711	0
Pleuronectidae	*Hippoglossoides elassodon*	E00424	12527	13	0	0	0	774	708	0
Pleuronectidae	*Hippoglossus hippoglossus*	E00689	10279	12	0	654	0	0	0	774
Pleuronectidae	*Hypsopsetta guttulata*	E00022	9133	9	0	0	0	753	693	0
Pleuronectidae	*Isopsetta isolepis*	E00018	6603	8	0	0	0	0	708	745
Pleuronectidae	*Lepidopsetta bilineata*	E00438	16335	19	804	654	882	780	691	0
Pleuronectidae	*Limanda limanda*	E00690	7013	8	0	0	0	0	705	0
Pleuronectidae	*Lyopsetta exilis*	E01173	6171	7	0	0	0	0	744	0
Pleuronectidae	*Microstomus pacificus*	E00433	10016	12	0	654	0	780	675	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Pleuronectidae	*Parophrys vetulus*	E00445	12033	14	0	654	0	765	705	0
Pleuronectidae	*Platichthys stellatus*	E00026	7842	9	0	699	0	0	705	788
Pleuronectidae	*Pleuronectes platessa*	E00053	14871	17	0	0	891	756	744	906
Pleuronectidae	*Psettichthys melanostictus*	E00025	9364	11	0	0	0	741	707	913
Pleuronectidae	*Pseudopleuronectes americanus*	E00035	15563	18	657	696	891	750	744	846
Poeciliidae	*Belonesox belizanus*	E01052	10182	11	0	675	0	765	713	861
Poeciliidae	*Gambusia affinis*	G01296	11403	12	657	0	891	0	744	0
Poeciliidae	*Heterandria formosa*	E00185	10113	11	0	684	0	762	0	863
Poeciliidae	*Poecilia latipinna reticulata*	E01065	12149	14	657	675	891	759	0	897
Poeciliidae	*Poeciliopsis elongata*	N01734	6863	8	783	0	876	0	734	0
Poecilopsettidae	*Poecilopsetta beanii*	E00448	5472	7	0	654	0	735	672	0
Poecilopsettidae	*Poecilopsetta plinthus*	E00073	9752	10	0	0	0	753	0	889
Polycentridae	*Monocirrhus polyacanthus*	G01377	8420	10	657	0	852	0	738	0
Polycentridae	*Polycentropsis abbreviata*	N26006	8369	10	810	0	891	0	744	0
Polycentridae	*Polycentrus schomburgkii*	G01444	8382	10	657	0	891	0	729	0
Polynemidae	*Eleutheronema rhadinum*	N26015	7791	10	756	0	819	0	673	0
Polynemidae	*Eleutheronema tetradactylum*	E01154	7961	9	0	0	0	918	0	0
Polynemidae	*Leptomelanosoma indicum*	E00842	11242	14	0	630	0	765	0	864
Polynemidae	*Polydactylus octonemus*	E00606	9992	13	0	627	0	804	717	911
Polynemidae	*Polydactylus sextarius*	N26043	5532	7	0	0	813	0	675	0
Polynemidae	*Polydactylus virginicus*	E00217	11602	13	0	0	0	918	714	0
Polyprionidae	*Polyprion americanus*	E00242	7677	9	0	0	0	0	711	0
Polyprionidae	*Polyprion oxygeneios*	M01632	4716	5	0	0	0	0	0	0
Polyprionidae	*Stereolepis gigas*	E00227	14211	17	651	705	891	918	744	0
Pomacanthidae	*Apolemichthys trimaculatus*	E00839	9202	12	0	630	0	762	0	906
Pomacanthidae	*Centropyge bicolor*	E00550	11381	15	657	687	0	795	660	883
Pomacanthidae	*Centropyge loricula*	E00284	9087	10	0	720	0	0	720	0
Pomacanthidae	*Centropyge nox*	E00542	8384	11	0	0	0	792	699	882
Pomacanthidae	*Chaetodontoplus melanosoma*	G01244	8178	10	657	0	876	0	732	0
Pomacanthidae	*Holacanthus ciliaris*	E00209	6815	8	0	720	0	918	744	0

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Pomacanthidae	*Holacanthus passer*	E00282	12494	15	657	720	873	918	732	0
Pomacanthidae	*Holacanthus tricolor*	E00198	7349	9	0	705	0	0	731	0
Pomacanthidae	*Pomacanthus arcuatus*	E00754	8027	10	0	630	0	777	0	0
Pomacanthidae	*Pomacanthus imperator*	E00710	9192	12	0	690	0	762	711	938
Pomacanthidae	*Pomacanthus semicirculatus*	E00849	10414	14	0	582	0	771	720	814
Pomacanthidae	*Pomacanthus zonipectus*	G01448	9113	11	657	0	891	0	744	0
Pomacanthidae	*Pygoplites diacanthus*	E00534	10507	13	0	0	0	807	740	0
Pomacentridae	*Abudefduf saxatilis*	E00820	14973	18	657	0	870	768	712	0
Pomacentridae	*Abudefduf sexfasciatus*	E00881	12145	15	0	630	0	735	717	891
Pomacentridae	*Abudefduf vaigiensis*	E00890	12132	13	0	0	0	747	714	0
Pomacentridae	*Acanthochromis polyacanthus*	E00466	8743	10	0	690	0	789	0	0
Pomacentridae	*Amblyglyphidodon leucogaster*	E00529	3808	4	0	0	0	0	0	0
Pomacentridae	*Amphiprion clarkii*	E00196	4604	6	0	0	0	0	0	0
Pomacentridae	*Amphiprion ocellaris*	E00193	7717	7	0	0	0	0	0	0
Pomacentridae	*Azurina hirundo*	E00580	9629	12	0	690	0	798	723	886
Pomacentridae	*Chromis atripectoralis*	E00238	9353	11	0	711	0	753	708	0
Pomacentridae	*Chromis cyanea*	E00201	13033	15	657	717	891	918	735	0
Pomacentridae	*Chromis dimidiata*	E00851	9724	12	0	630	0	762	0	930
Pomacentridae	*Chrysiptera taupou*	E00564	9950	13	0	690	0	801	702	747
Pomacentridae	*Dascyllus aruanus*	E00700	11886	14	0	690	0	0	714	885
Pomacentridae	*Dascyllus carneus*	E00862	11899	14	0	630	0	723	0	895
Pomacentridae	*Dascyllus reticulatus*	E00724	8549	10	0	690	0	0	0	882
Pomacentridae	*Dascyllus trimaculatus*	E00865	6439	7	0	0	0	729	0	0
Pomacentridae	*Dischistodus perspicillatus*	E00464	8931	11	0	690	0	804	0	899
Pomacentridae	*Hypsypops rubicundus*	E00459	7285	10	0	690	0	804	684	0
Pomacentridae	*Lepidozygus tapeinosoma*	E00929	7795	10	0	630	0	735	0	0
Pomacentridae	*Microspathodon bairdii*	G01375	8331	10	636	0	891	0	744	0
Pomacentridae	*Microspathodon chrysurus*	E00772	10751	13	0	630	0	771	0	751
Pomacentridae	*Neoglyphidodon melas*	E00465	9828	12	0	0	0	801	0	936
Pomacentridae	*Neoglyphidodon polyacanthus*	E00285	6455	8	0	720	0	918	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Pomacentridae	*Neopomacentrus cyanomos*	E00933	8888	11	0	0	0	741	0	0
Pomacentridae	*Parma microlepis*	E00286	5332	7	0	720	0	918	0	720
Pomacentridae	*Plectroglyphidodon dickii*	E00572	13722	16	0	0	0	0	705	887
Pomacentridae	*Plectroglyphidodon johnstonianus*	E00722	7987	10	0	0	0	0	0	884
Pomacentridae	*Pomacentrus brachialis*	E00239	9865	12	0	0	0	918	708	0
Pomacentridae	*Pomacentrus pavo*	E00729	12503	15	0	690	0	0	670	0
Pomacentridae	*Pomacentrus spilotoceps*	E00557	6421	9	0	690	0	798	714	866
Pomacentridae	*Pomachromis richardsoni*	E00559	8319	11	0	690	0	807	699	902
Pomacentridae	*Stegastes albifasciatus*	E00713	6612	9	0	0	0	765	710	0
Pomacentridae	*Stegastes diencaeus*	E00219	6060	8	0	720	0	918	744	0
Pomacentridae	*Stegastes fuscus*	E00203	12679	15	645	0	872	918	744	881
Pomacentridae	*Stegastes partitus*	E00204	4367	6	0	0	0	0	0	0
Pomatomidae	*Pomatomus saltatrix*	E00516	16569	18	810	0	876	807	709	929
Priacanthidae	*Heteropriacanthus cruentatus*	E00570	14367	17	810	0	882	792	739	893
Priacanthidae	*Priacanthus arenatus*	E00618	14657	18	753	0	822	786	687	909
Priacanthidae	*Pristigenys alta*	E00252	12492	14	753	0	825	930	744	0
Pristolepididae	*Pristolepis fasciata*	N26580	7608	9	753	0	870	0	744	0
Pristolepididae	*Pristolepis sp*	N36627	8543	10	810	0	891	0	744	0
Psettodidae	*Psettodes belcheri*	E01180	6046	7	0	0	0	918	0	0
Psettodidae	*Psettodes erumei*	E01165	12034	14	0	0	819	918	744	0
Pseudaphritidae	*Pseudaphritis urvillii*	G01453	8567	9	657	0	0	0	744	0
Pseudochromidae	*Congrogadus subducens*	G01262	8360	10	621	0	876	0	744	0
Pseudochromidae	*Halidesmus scapularis*	E00793	10231	13	0	630	0	768	705	904
Pseudochromidae	*Labracinus cyclophthalmus*	G01343	11328	12	657	0	891	0	744	0
Pseudochromidae	*Natalichthys sam*	E00589	7891	10	0	690	0	807	717	928
Pseudochromidae	*Ogilbyina novaehollandiae*	G01403	8345	10	609	0	891	0	740	0
Pseudochromidae	*Pholidochromis cerasina*	G01436	8319	10	657	0	879	0	744	0
Pseudochromidae	*Pseudochromis cyanotaenia*	E00706	7668	10	0	690	0	762	660	0
Pseudochromidae	*Pseudochromis fridmani*	N26709	8561	10	810	0	873	0	744	0
Pseudochromidae	*Pseudochromis jamesi*	E00535	6957	9	0	690	0	795	696	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Pseudochromidae	*Pseudoplesiops revellei*	E00745	4311	6	0	0	0	0	684	0
Pseudomugilidae	*Pseudomugil gertrudae*	E00182	14736	18	810	0	819	771	660	720
Pseudomugilidae	*Pseudomugil signifer*	E00184	11998	15	756	684	804	0	744	0
Psychrolutidae	*Cottunculus thomsonii*	E00963	2374	3	0	0	0	0	0	0
Psychrolutidae	*Dasycottus setiger*	E00288	5136	6	0	0	0	0	0	0
Psychrolutidae	*Malacocottus zonurus*	E00253	8212	10	0	720	0	0	717	0
Psychrolutidae	*Psychrolutes phrictus*	E00276	5502	7	0	720	0	0	734	0
Rachycentridae	*Rachycentron canadum*	E00468	15775	17	804	0	891	918	744	888
Rhombosoleidae	*Oncopterus darwinii*	E01184	6659	7	0	0	0	918	0	0
Rhombosoleidae	*Rhombosolea leporina*	E01166	2980	3	0	0	0	0	0	0
Rhombosoleidae	*Rhombosolea plebeia*	E01167	5378	6	0	0	0	720	744	0
Rhombosoleidae	*Rhombosolea tapirina*	E01168	3805	4	0	0	0	0	744	0
Samaridae	*Plagiopsetta glossa*	E00074	7559	8	0	663	0	789	717	0
Samaridae	*Samariscus japonicus*	E00072	7912	8	0	0	0	891	0	855
Samaridae	*Samariscus latus*	N27771	2733	3	0	0	810	0	0	0
Samaridae	*Samariscus xenicus*	E00078	7553	8	0	0	0	786	612	0
Scaridae	*Calotomus carolinus*	N27783	7195	9	753	0	828	0	635	0
Scaridae	*Cetoscarus bicolor*	E00566	14113	17	624	0	882	756	744	0
Scaridae	*Chlorurus gibbus*	E00561	6813	9	0	654	0	762	696	676
Scaridae	*Chlorurus sordidus*	E00837	14642	16	657	0	855	0	671	0
Scaridae	*Cryptotomus roseus*	N27805	7128	9	753	0	810	0	652	0
Scaridae	*Hipposcarus longiceps*	E00737	4541	6	0	0	0	0	0	0
Scaridae	*Leptoscarus vaigiensis*	E00877	8427	11	0	669	0	780	713	0
Scaridae	*Scarus ghobban*	E00878	9678	11	0	657	0	0	716	863
Scaridae	*Scarus globiceps*	N27829	4729	6	711	0	0	0	652	0
Scaridae	*Scarus iseri*	E00013	7345	9	0	696	0	675	711	730
Scaridae	*Scarus niger*	E00875	11274	14	0	0	810	0	705	898
Scaridae	*Scarus quoyi*	E00872	7432	10	0	669	0	762	684	916
Scaridae	*Scarus rubroviolaceus*	E00874	12027	13	0	669	0	0	710	0
Scaridae	*Sparisoma aurofrenatum*	E00008	5465	7	0	0	0	0	0	920

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Scaridae	*Sparisoma chrysopterum*	E00070	2776	4	0	0	0	0	0	0
Scaridae	*Sparisoma viride*	E00004	6443	9	0	0	0	0	730	912
Scatophagidae	*Scatophagus argus*	E00051	13219	16	657	0	849	0	744	902
Scatophagidae	*Selenotoca multifasciata*	G01483	9576	12	657	0	825	0	744	0
Sciaenidae	*Aplodinotus grunniens*	E01108	17827	19	657	0	873	720	743	906
Sciaenidae	*Atractoscion nobilis*	E00125	9878	13	0	684	0	741	741	906
Sciaenidae	*Bairdiella chrysoura*	E00165	7670	10	0	684	0	744	743	933
Sciaenidae	*Cheilotrema saturnum*	E00118	6644	9	0	684	0	759	0	910
Sciaenidae	*Corvula sanctaeluciae*	E01047	5698	7	0	663	0	732	0	883
Sciaenidae	*Cynoscion arenarius*	E00511	11444	13	0	681	0	708	740	862
Sciaenidae	*Cynoscion regalis*	E00164	14880	18	756	684	867	714	744	904
Sciaenidae	*Genyonemus lineatus*	E00138	9138	12	0	684	0	747	0	883
Sciaenidae	*Larimus breviceps*	E01048	4776	7	0	675	0	444	743	905
Sciaenidae	*Leiostomus xanthurus*	G01349	9972	12	657	0	873	0	735	0
Sciaenidae	*Menticirrhus saxatilis*	E00166	7177	9	0	684	0	771	744	895
Sciaenidae	*Menticirrhus undulatus littoralis*	E00127	15027	19	657	684	891	750	744	696
Sciaenidae	*Micropogonias undulatus*	N01637	5789	8	747	0	834	0	671	0
Sciaenidae	*Odontoscion dentex*	E01049	5655	7	0	657	0	0	0	921
Sciaenidae	*Pareques acuminatus*	E01050	3516	4	0	675	0	0	0	930
Sciaenidae	*Pareques umbrosus*	E00639	6228	8	0	678	0	0	0	813
Sciaenidae	*Pogonias cromis*	E00699	8505	11	0	681	0	0	0	915
Sciaenidae	*Sciaenops ocellatus*	E01055	18596	20	810	702	882	768	744	931
Sciaenidae	*Seriphus politus*	E00123	7497	10	0	0	0	756	744	870
Sciaenidae	*Stellifer lanceolatus*	E00608	9278	12	0	681	0	720	743	852
Sciaenidae	*Umbrina coroides*	E00628	8595	11	0	681	0	750	743	871
Scomberesocidae	*Cololabis saira*	E00192	10242	11	0	684	0	756	744	768
Scomberesocidae	*Scomberesox saurus*	E00404	10373	13	657	0	0	738	735	865
Scombridae	*Acanthocybium solandri*	E00927	14337	16	0	0	0	738	0	881
Scombridae	*Auxis rochei*	E00673	14617	18	810	690	834	0	668	0
Scombridae	*Euthynnus affinis*	E00830	9732	12	0	0	0	774	0	903

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Scombridae	*Euthynnus alletteratus*	E00696	7879	11	654	0	0	0	0	0
Scombridae	*Gymnosarda unicolor*	E00832	9359	11	0	0	0	690	0	877
Scombridae	*Katsuwonus pelamis*	E00747	11259	13	0	630	0	750	0	0
Scombridae	*Sarda sarda*	E00243	16203	19	657	0	867	747	702	0
Scombridae	*Scomber japonicus*	E00247	10495	12	0	687	0	756	0	0
Scombridae	*Scomber scombrus*	E00626	19143	20	810	690	891	756	723	931
Scombridae	*Scomberomorus maculatus sp*	E00631	16041	19	747	0	891	798	744	917
Scombridae	*Scomberomorus regalis commerson*	E00694	9863	12	0	0	0	0	0	0
Scombridae	*Thunnus albacares*	E00831	18226	21	810	0	849	687	668	907
Scombrolabracidae	*Scombrolabrax heterolepis*	E00976	11570	14	0	630	0	729	726	798
Scophthalmidae	*Lepidorhombus boscii*	E00462	9162	10	0	0	0	720	0	0
Scophthalmidae	*Scophthalmus aquosus*	E00039	10410	12	657	0	891	0	738	819
Scophthalmidae	*Scophthalmus maximus*	E01161	6280	5	0	0	0	0	0	0
Scorpaenidae	*Caracanthus maculatus*	E00716	8029	10	0	654	0	0	0	882
Scorpaenidae	*Caracanthus unipinna*	E00558	6573	8	0	654	0	762	0	0
Scorpaenidae	*Dendrochirus zebra*	E00897	7402	10	0	669	0	0	687	0
Scorpaenidae	*Iracundus signifer*	E00583	7125	9	0	654	0	753	699	0
Scorpaenidae	*Neomerinthe hemingwayi*	E00619	10221	12	0	654	0	729	715	0
Scorpaenidae	*Pontinus longispinis*	E01010	7126	10	0	693	0	723	528	0
Scorpaenidae	*Pontinus rathbuni*	E00463	6391	8	0	699	0	717	735	893
Scorpaenidae	*Pterois antennata*	E00705	8496	11	0	666	0	717	732	895
Scorpaenidae	*Pterois miles*	E00882	7015	9	0	648	0	726	0	0
Scorpaenidae	*Pterois radiata*	E00850	8182	10	0	693	0	726	0	0
Scorpaenidae	*Scorpaena agassizii*	E01038	2193	3	0	0	0	741	0	0
Scorpaenidae	*Scorpaena brasiliensis*	E00759	4986	7	0	666	0	714	0	857
Scorpaenidae	*Scorpaena dispar*	E00512	3690	5	0	699	0	717	691	869
Scorpaenidae	*Scorpaena guttata*	E00291	8547	10	0	693	0	915	723	788
Scorpaenidae	*Scorpaenodes albaiensis*	E00532	4039	5	0	0	0	0	731	0
Scorpaenidae	*Scorpaenodes guamensis*	E00870	6637	9	0	693	0	720	714	0
Scorpaenidae	*Scorpaenopsis longispina*	E00903	7186	9	0	651	0	726	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Scorpaenidae	*Scorpaenopsis oxycephala*	E00581	5118	7	0	651	0	717	732	912
Scorpaenidae	*Sebastapistes cyanostigma*	E00888	8326	10	0	693	0	729	0	0
Scorpaenidae	*Taenianotus triacanthus*	E00866	8147	10	0	0	0	0	0	0
Sebastidae	*Adelosebastes latens*	E00066	2246	3	0	699	0	0	0	782
Sebastidae	*Helicolenus dactylopterus*	E00044	9920	12	648	0	0	744	744	859
Sebastidae	*Sebastes aurora*	E00349	8679	10	0	0	0	696	714	898
Sebastidae	*Sebastes diploproa*	E00432	6421	8	0	0	0	0	0	897
Sebastidae	*Sebastes fasciatus*	G01482	8330	10	657	0	891	0	738	0
Sebastidae	*Sebastes jordani*	E00350	6619	9	0	0	0	699	702	882
Sebastidae	*Sebastes paucispinis*	E00354	6853	9	0	0	0	702	717	862
Sebastidae	*Sebastes ruberrimus*	N28709	6206	8	810	0	891	0	744	0
Sebastidae	*Sebastolobus alascanus*	E00417	12929	16	654	633	876	660	744	892
Serranidae	*Aethaloperca rogaa*	E01079	6350	8	642	0	0	0	0	912
Serranidae	*Anthias nicholsi*	E00447	6801	6	0	0	0	0	0	0
Serranidae	*Aporops bilinearis*	E00531	7661	10	0	678	0	720	713	817
Serranidae	*Baldwinella aureorubens*	G01220	8097	10	657	678	858	0	744	0
Serranidae	*Baldwinella vivana*	E00338	3660	5	0	693	0	777	723	0
Serranidae	*Centropristis striata*	E00163	8944	11	0	654	0	738	744	861
Serranidae	*Cephalopholis argus*	E00868	14648	18	657	693	891	717	744	0
Serranidae	*Cephalopholis fulva*	E00771	5807	7	0	0	0	0	0	874
Serranidae	*Cephalopholis miniata*	E00838	9601	12	642	693	0	717	0	0
Serranidae	*Diplectrum bivittatum*	E01008	4699	6	0	0	0	708	0	0
Serranidae	*Diplectrum formosum*	E01002	8832	10	0	0	0	738	727	0
Serranidae	*Epinephelus maculatus*	E00549	12180	14	648	702	0	717	717	859
Serranidae	*Epinephelus merra*	E00552	8076	10	0	699	0	717	714	897
Serranidae	*Grammistes sexlineatus*	E00900	15699	17	753	702	822	930	744	0
Serranidae	*Grammistops ocellatus*	E00571	6588	8	0	657	0	717	0	894
Serranidae	*Hypoplectrus puella*	E00505	12795	16	657	651	891	717	732	819
Serranidae	*Hyporthodus flavolimbatus*	E00627	5022	7	0	666	0	717	0	882
Serranidae	*Liopropoma mowbrayi*	E00307	4911	6	0	0	0	915	651	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Serranidae	*Liopropoma rubre*	E00306	13426	14	0	702	0	930	744	858
Serranidae	*Mycteroperca bonaci microlepis*	E00311	14036	17	657	693	879	915	714	874
Serranidae	*Odontanthias chrysostictus*	G01327	10158	10	0	0	0	858	744	0
Serranidae	*Paralabrax nebulifer*	E00325	12094	15	657	693	876	915	732	0
Serranidae	*Pronotogrammus martinicensis*	E00636	3713	4	0	666	0	0	0	0
Serranidae	*Pseudanthias pascalus*	G01452	9024	11	657	0	891	0	705	0
Serranidae	*Pseudanthias squamipinnis*	E00860	6941	8	0	669	0	717	0	0
Serranidae	*Pseudogramma polyacantha*	E00852	7643	10	0	693	0	693	0	0
Serranidae	*Rypticus saponaceus*	E00764	15840	19	657	666	867	0	738	893
Serranidae	*Rypticus subbifrenatus*	E00347	6320	7	0	693	0	780	723	0
Serranidae	*Serranus baldwini*	E00322	14886	16	0	702	0	930	725	768
Serranidae	*Serranus notospilus*	E00337	5719	7	0	684	0	768	729	694
Serranidae	*Serranus phoebe*	E00336	6229	8	0	681	0	717	733	0
Serranidae	*Serranus tigrinus*	G01486	8954	11	657	0	891	0	744	0
Setarchidae	*Setarches guentheri*	E01035	5731	8	0	0	0	723	0	0
Siganidae	*Siganus argenteus*	E00940	7215	10	0	0	0	750	0	836
Siganidae	*Siganus punctatus*	E00958	3704	4	657	0	0	0	0	0
Siganidae	*Siganus spinus*	N29369	8207	10	807	0	828	0	744	0
Siganidae	*Siganus stellatus*	G01488	6854	9	0	0	0	0	0	892
Siganidae	*Siganus vulpinus*	E00090	11306	14	657	0	891	0	744	0
Sillaginidae	*Sillago chondropus*	N29390	6780	9	0	0	822	0	673	0
Sillaginidae	*Sillago sihama*	E00824	13627	15	0	0	834	765	669	0
Sinipercidae	*Coreoperca whiteheadi*	G01264	8180	8	0	0	0	0	744	0
Sinipercidae	*Siniperca chuatsi*	E01136	15198	17	785	702	849	930	744	0
Sinipercidae	*Siniperca scherzeri*	G01489	8368	7	0	0	0	0	0	0
Soleidae	*Aseraggodes heemstrai*	E00582	9255	10	0	654	0	720	0	0
Soleidae	*Aseraggodes kobensis*	E00075	12391	14	801	0	834	753	677	0
Soleidae	*Brachirus annularis*	E01182	5846	7	0	0	0	918	0	0
Soleidae	*Heteromycteris japonicus*	E00079	14809	17	810	666	815	756	666	882
Soleidae	*Microchirus frechkopi*	E01175	5082	6	0	0	0	0	0	0

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Soleidae	*Pegusa lascaris*	E01183	8261	10	0	0	0	918	743	0
Soleidae	*Pseudaesopia japonica*	E00081	10067	11	0	0	0	885	744	802
Soleidae	*Solea solea*	E00054	7675	8	0	0	0	918	0	861
Soleidae	*Soleichthys heterorhinos*	E00943	10673	11	0	0	0	918	708	898
Sparidae	*Acanthopagrus catenula*	E00953	10468	14	0	630	0	747	0	889
Sparidae	*Acanthopagrus latus*	M01638	3048	4	0	0	0	0	0	0
Sparidae	*Archosargus probatocephalus*	E00249	8388	10	0	720	0	0	744	0
Sparidae	*Argyrops spinifer*	M01668	2629	3	0	0	0	0	0	0
Sparidae	*Argyrozona argyrozona*	E00802	9618	12	0	630	0	681	705	937
Sparidae	*Boops boops*	M01640	3246	3	0	0	0	0	0	0
Sparidae	*Boopsoidea inornata*	M01639	3951	4	0	0	0	0	0	0
Sparidae	*Calamus calamus*	N29934	7496	9	810	0	891	0	744	0
Sparidae	*Calamus nodosus*	M01641	3290	4	0	0	0	0	0	0
Sparidae	*Calamus penna*	E00762	7629	10	0	630	0	708	0	0
Sparidae	*Cheimerius nufar*	M01642	3243	3	0	0	0	0	0	0
Sparidae	*Chrysoblephus laticeps*	M01644	3594	4	0	0	0	0	0	0
Sparidae	*Crenidens crenidens*	M01645	4737	5	0	0	0	0	0	0
Sparidae	*Dentex dentex*	M01646	4731	5	0	0	0	0	0	0
Sparidae	*Diplodus annularis*	M01647	4730	5	0	0	0	0	0	0
Sparidae	*Diplodus bermudensis*	M01648	3953	4	0	0	0	0	0	0
Sparidae	*Diplodus capensis*	E00807	5192	7	0	630	0	774	0	896
Sparidae	*Lagodon rhomboides*	G01346	10209	12	657	0	891	0	744	0
Sparidae	*Lithognathus mormyrus*	M01649	4731	5	0	0	0	0	0	0
Sparidae	*Oblada melanura*	M01650	3249	3	0	0	0	0	0	0
Sparidae	*Pachymetopon grande*	M01651	3549	4	0	0	0	0	0	0
Sparidae	*Pagellus affinis*	M01652	3072	4	0	0	0	0	0	0
Sparidae	*Pagellus erythrinus*	M01653	4029	4	0	0	0	0	0	0
Sparidae	*Pagrus pagrus*	E00514	12441	15	657	690	891	0	744	0
Sparidae	*Porcostoma dentata*	M01654	4728	5	0	0	0	0	0	0
Sparidae	*Rhabdosargus haffara*	M01655	2151	3	0	0	0	0	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Sparidae	*Sarpa salpa*	E00806	12445	15	0	630	0	681	714	921
Sparidae	*Sparidentex hasta*	M01657	4746	5	0	0	0	0	0	0
Sparidae	*Sparus aurata*	M01658	3954	4	0	0	0	0	0	0
Sparidae	*Spondyliosoma cantharus*	M01659	3257	4	0	0	0	0	0	0
Sparidae	*Stenotomus chrysops*	E00246	12458	15	657	720	891	0	744	0
Sparidae	*Virididentex acromegalus*	M01660	4676	5	0	0	0	0	0	0
Sphyraenidae	*Sphyraena argentea*	E00230	8319	10	0	0	0	918	717	0
Sphyraenidae	*Sphyraena barracuda*	E00836	19387	22	762	0	891	753	729	876
Sphyraenidae	*Sphyraena japonica*	N30022	5263	7	723	0	825	0	682	0
Sphyraenidae	*Sphyraena jello*	N30023	4747	6	0	0	825	0	682	0
Sphyraenidae	*Sphyraena putnamae*	E00955	13026	14	0	0	0	918	720	868
Sphyraenidae	*Sphyraena sphyraena*	E01143	7520	8	0	0	0	918	0	0
Stichaeidae	*Bryozoichthys marjorius*	E00442	7041	9	0	681	0	702	743	908
Stichaeidae	*Cebidichthys violaceus*	N30217	6500	9	759	0	852	0	669	0
Stichaeidae	*Leptoclinus maculatus*	E00323	5549	7	0	693	0	0	0	0
Stichaeidae	*Lumpenus fabricii*	E00361	3593	5	0	660	0	0	719	0
Stichaeidae	*Lumpenus lampretaeformis*	E00371	5472	7	0	648	0	762	743	0
Stichaeidae	*Poroclinus rothrocki*	E00431	5685	7	0	651	0	717	0	879
Stromateidae	*Peprilus burti*	E00600	5597	7	0	0	0	771	0	794
Stromateidae	*Peprilus paru*	E00622	7448	10	0	678	0	663	0	891
Stromateidae	*Peprilus simillimus*	E00136	10724	12	0	684	0	771	0	937
Stromateidae	*Peprilus triacanthus*	N30548	8492	10	810	0	891	0	744	0
Symphysanodontidae	*Symphysanodon typus*	M01725	1508	2	0	0	0	0	0	0
Synanceiidae	*Synanceia verrucosa*	E00867	10214	13	0	693	0	723	712	0
Synbranchidae	*Monopterus albus*	E01134	14200	15	657	0	891	858	744	0
Syngnathidae	*Corythoichthys intestinalis*	E00734	5411	6	0	0	0	0	0	876
Syngnathidae	*Corythoichthys schultzi*	E00829	4587	5	0	0	0	708	0	0
Syngnathidae	*Doryrhamphus excisus*	E00915	8801	10	0	0	0	735	0	0
Syngnathidae	*Hippocampus erectus*	N30799	2880	4	0	0	0	0	744	0
Syngnathidae	*Syngnathus fuscus*	E00792	6471	8	0	0	849	0	744	910

Table A4a. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2
Syngnathidae	*Syngnathus leptorhynchus*	N30969	2247	3	0	0	861	0	744	0
Syngnathidae	*Syngnathus louisianae*	E00821	4535	5	0	0	0	723	0	0
Syngnathidae	*Syngnathus scovelli*	E00346	4744	6	0	0	0	726	0	886
Telmatherinidae	*Marosatherina ladigesi*	E00406	9346	12	0	678	0	765	737	894
Terapontidae	*Hephaestus fuliginosus*	G01318	10031	11	783	0	852	0	707	0
Terapontidae	*Scortum barcoo*	G01480	10071	11	783	0	852	0	732	0
Terapontidae	*Terapon jarbua*	E00826	14339	16	753	0	822	687	674	0
Tetraodontidae	*Arothron hispidus*	E00985	8771	8	0	0	0	0	0	0
Tetraodontidae	*Arothron nigropunctatus*	N31143	7811	9	810	0	888	0	744	0
Tetraodontidae	*Canthigaster bennetti*	E00530	8390	9	0	0	0	717	0	894
Tetraodontidae	*Canthigaster jactator*	N31165	6260	7	0	0	891	0	0	0
Tetraodontidae	*Canthigaster valentini*	E00853	7767	8	0	0	0	693	0	0
Tetraodontidae	*Lagocephalus laevigatus*	E00601	8160	8	0	0	0	717	743	893
Tetraodontidae	*Sphoeroides maculatus*	E00339	4428	5	0	666	0	786	0	0
Tetraodontidae	*Sphoeroides nephelus*	N01739	6070	7	0	0	891	0	742	0
Tetraodontidae	*Takifugu rubripes*	E00460	20045	21	657	732	891	930	744	984
Tetraodontidae	*Tetractenos hamiltoni*	E00383	2976	4	0	654	0	750	706	866
Tetraodontidae	*Tetraodon fluviatilis*	E00374	4553	5	0	0	0	768	0	0
Tetraodontidae	*Tetraodon miurus*	N01740	8550	10	810	0	885	0	744	0
Tetraodontidae	*Tetraodon nigroviridis*	G01513	17489	18	657	732	891	930	744	984
Tetrarogidae	*Coccotropsis gymnoderma*	E00801	6200	8	0	615	0	0	672	0
Toxotidae	*Toxotes chatareus*	E01139	10242	10	0	0	0	918	744	0
Toxotidae	*Toxotes jaculatrix*	E01155	11428	14	657	0	891	0	744	0
Trachichthyidae	*Hoplostethus occidentalis atlanticus*	E01018	11766	14	657	0	891	759	0	0
Triacanthidae	*Triacanthus biaculeatus*	G01531	11323	12	810	0	891	0	744	0
Triacanthodidae	*Halimochirurgus alcocki*	N31459	6920	9	759	0	816	0	675	0
Triacanthodidae	*Triacanthodes anomalus*	E00382	12061	13	657	0	891	711	744	0
Triacanthodidae	*Triacanthodes ethiops*	G01532	6829	7	0	0	0	0	744	0
Trichiuridae	*Aphanopus carbo*	E00274	5425	7	0	0	0	918	0	0
Trichiuridae	*Assurger anzac*	G01210	9581	12	810	0	891	0	744	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Trichiuridae	*Benthodesmus simonyi*	E00475	4383	6	0	0	0	813	622	0
Trichiuridae	*Evoxymetopon taeniatus*	E00650	3573	5	0	0	0	0	603	0
Trichiuridae	*Lepidopus altifrons*	E00474	6788	9	0	690	0	0	720	929
Trichiuridae	*Trichiurus lepturus*	E00596	12574	14	657	0	866	795	741	908
Trichodontidae	*Trichodon trichodon*	N31563	7181	9	756	0	873	0	704	0
Triglidae	*Bellator militaris*	E01026	4452	6	0	0	0	759	0	0
Triglidae	*Prionotus carolinus*	E00340	7371	9	0	642	0	720	696	703
Triglidae	*Prionotus evolans*	E01021	4575	6	0	0	891	0	744	0
Triglidae	*Prionotus stephanophrys*	E00328	6883	9	0	588	0	0	714	882
Triglidae	*Pterygotrigla hemisticta*	N31939	4770	6	750	0	822	0	0	0
Triodontidae	*Triodon macropterus*	N31959	7201	9	774	0	891	0	692	0
Tripterygiidae	*Enneanectes altivelis*	E00315	5180	7	0	693	0	738	729	917
Tripterygiidae	*Enneanectes boehlkei*	E00305	8688	11	0	0	888	915	739	863
Tripterygiidae	*Enneapterygius abeli*	E00896	2369	3	0	0	0	720	708	941
Tripterygiidae	*Enneapterygius gruschkai*	E00916	3832	5	0	0	0	723	0	0
Tripterygiidae	*Helcogramma ellioti sp*	E00331	9671	11	0	672	0	900	728	903
Tripterygiidae	*Helcogramma fuscopinna*	E00885	2098	3	0	0	0	723	730	0
Uranoscopidae	*Astroscopus ygraecum*	E01028	11671	14	657	0	873	771	742	0
Uranoscopidae	*Kathetostoma albigutta*	E01022	2118	3	0	0	0	0	0	0
Uranoscopidae	*Kathetostoma averruncus*	E00324	11393	14	657	0	876	915	740	870
Uranoscopidae	*Uranoscopus sulphureus*	E00538	5752	7	0	0	0	717	0	883
Xiphiidae	*Xiphias gladius*	E01151	16644	17	807	0	891	0	744	0
Zanclidae	*Zanclus cornutus*	E00894	18204	20	657	669	891	0	731	892
Zaproridae	*Zaprora silenus*	E00362	6043	8	0	0	0	765	727	856
Zenarchopteridae	*Dermogenys collettei*	G01275	6851	8	0	0	891	0	744	0
Zenarchopteridae	*Zenarchopterus dispar*	E00541	5209	6	0	0	0	774	0	809
Zoarcidae	*Bothrocara brunneum*	E00357	6304	8	0	690	0	0	730	852
Zoarcidae	*Bothrocara hollandi*	N01721	4677	6	0	0	891	0	744	0
Zoarcidae	*Eucryphycus californicus*	E00327	5531	7	0	693	0	0	727	902
Zoarcidae	*Lycenchelys crotalinus*	E00425	4583	6	0	696	0	0	0	0

Table A4a. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**
Zoarcidae	*Lycodapus mandibularis*	E00355	8784	11	0	693	0	0	726	862
Zoarcidae	*Lycodes brevipes*	E00413	4381	5	0	0	0	0	0	0
Zoarcidae	*Lycodes diapterus*	G01364	8790	11	753	0	891	0	744	0
Zoarcidae	*Lycodes terraenovae*	E00675	15952	18	657	693	891	738	729	902
Zoarcidae	*Melanostigma pammelas*	E00365	6342	8	0	693	0	0	717	876
Zoarcidae	*Zoarces americanus viviparus*	E00370	5571	8	558	693	0	0	731	0

TABLE A4b. Taxon sampling for the percomorph dataset included 1231 taxa and sequence data for 23 genes. The dataset is comprised of sequences for 1180 percomorph species from previous studies (e.g. Li *et al.* 2007; Li *et al.* 2008; Li *et al.* 2010; Li *et al.* 2011; Betancur-R *et al.* 2013b; Broughton *et al.* 2013; Near *et al.* 2013) or public databases, plus newly generated sequences for the 51 additional taxa for this study. The matrix is presented in four parts to show presence of sequence data for the 23 genes. (a.) ENC1, FICD, GLYT, KIAA1239, MYH6, and PANX2; (b.) PLAGL2, PTCHD1, RAG1, RAG2, RH, and RIPK4; (c.) SH3PX3, SIDKEY, SREB2, SVEP1, TBR1, and VCPIP; (d.) ZIC1, COI, CYT *B*, 16S, and HOX.

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Acanthuridae	*Acanthurus bahianus*	E00005	11794	14	801	765	1368	0	0	0
Acanthuridae	*Acanthurus guttatus*	E00709	7379	8	825	0	1464	0	0	0
Acanthuridae	*Acanthurus leucosternon*	E00880	14819	16	810	750	1398	0	0	0
Acanthuridae	*Acanthurus lineatus*	E00889	11234	12	810	753	0	0	0	0
Acanthuridae	*Acanthurus triostegus*	E00711	11027	13	810	0	1461	0	0	0
Acanthuridae	*Ctenochaetus striatus*	E00982	6461	8	819	0	1464	0	751	0
Acanthuridae	*Ctenochaetus strigosus*	E00050	9642	12	708	765	1398	0	0	0
Acanthuridae	*Ctenochaetus truncatus*	E00854	6572	9	801	753	0	0	0	642
Acanthuridae	*Naso brevirostris*	E00918	11979	15	825	582	1458	0	0	0
Acanthuridae	*Naso lituratus*	G01514	9769	12	825	585	1461	0	852	0
Acanthuridae	*Naso unicornis*	E00701	6934	9	810	0	0	0	0	636
Acanthuridae	*Paracanthurus hepatus*	E00002	9321	11	825	765	1176	0	0	0
Acanthuridae	*Zebrasoma flavescens*	E00730	9002	10	0	0	0	0	0	630
Acanthuridae	*Zebrasoma rostratum*	N01742	6780	8	708	708	1398	0	0	0
Acanthuridae	*Zebrasoma scopas*	E00859	12917	16	825	753	1464	0	0	636
Acanthuridae	*Zebrasoma velifer*	E00029	5029	6	0	0	0	0	0	0
Achiridae	*Achirus lineatus*	E00605	13596	16	636	597	1428	0	762	636
Achiridae	*Gymnachirus melas*	E00609	14260	16	603	591	1311	0	774	645
Achiridae	*Gymnachirus texae*	E00630	9146	10	0	0	1296	0	774	642
Achiridae	*Hypoclinemus sp*	E01162	6483	7	819	0	1446	0	672	645
Achiridae	*Trinectes maculatus*	E00046	11078	11	792	765	1462	1206	852	0
Achiropsettidae	*Mancopsetta maculata*	E01169	6861	8	813	0	0	0	747	645
Achiropsettidae	*Neoachiropsetta milfordi*	E01170	6200	8	813	0	0	0	738	645
Acropomatidae	*Acropoma japonicum*	G01188	12298	14	708	708	1398	0	0	0

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Acropomatidae	*Malakichthys elegans*	N01922	6894	9	651	591	1278	0	0	0
Acropomatidae	*Synagrops bellus*	E01125	11059	13	0	0	1464	0	927	633
Acropomatidae	*Synagrops spinosus*	E01123	6676	7	0	0	0	0	0	624
Adrianichthyidae	*Oryzias latipes*	G01408	18061	19	708	708	1464	1206	927	645
Agonidae	*Aspidophoroides monopterygius*	N01986	7472	9	705	708	1317	0	0	0
Agonidae	*Bathyagonus alascanus*	E00268	5458	7	807	0	0	0	0	630
Agonidae	*Bathyagonus pentacanthus*	E00430	5127	7	810	756	0	0	0	633
Agonidae	*Hypsagonus quadricornis*	E00269	7151	9	810	675	0	0	0	645
Agonidae	*Sarritor frenatus*	E00264	4738	6	810	0	0	0	0	0
Agonidae	*Sarritor leptorhynchus*	E00254	5516	7	0	0	0	0	0	0
Agonidae	*Stellerina xyosterna*	N02010	6750	8	705	708	1398	0	0	0
Agonidae	*Xeneretmus latifrons*	E00278	6400	8	0	756	0	0	852	633
Ambassidae	*Ambassis agrammus*	G01196	8877	9	825	0	1455	0	0	645
Ambassidae	*Ambassis interrupta*	E01100	10212	10	819	0	1464	0	0	645
Ambassidae	*Ambassis urotaenia*	G01197	8268	10	696	708	1377	0	0	0
Ambassidae	*Parambassis ranga*	N01735	7892	10	645	597	1377	0	0	0
Ammodytidae	*Ammodytes dubius*	N02375	6015	7	693	708	1377	0	0	0
Ammodytidae	*Ammodytes hexapterus*	E00414	15128	17	819	755	1266	0	759	630
Anabantidae	*Ctenopoma acutirostre kingsleyae*	E01141	14536	15	696	0	1446	0	758	645
Anabantidae	*Microctenopoma nanum*	G01373	12070	13	672	624	1398	0	0	0
Anarhichadidae	*Anarhichas denticulatus*	E00787	8620	9	810	765	0	0	0	633
Anarhichadidae	*Anarhichas orientalis lupus*	E00117	15266	17	810	756	1398	0	852	645
Anarhichadidae	*Anarrhichthys ocellatus*	E00119	7893	10	810	756	0	0	0	630
Anoplopomatidae	*Anoplopoma fimbria*	E00423	15741	18	810	756	762	0	0	0
Antennariidae	*Antennatus coccineus*	E01092	15457	17	810	765	1398	501	759	0
Antennariidae	*Antennatus nummifer*	E00587	9899	13	810	755	0	489	0	645
Antennariidae	*Fowlerichthys radiosus*	E01124	4779	6	813	0	0	501	0	645
Antennariidae	*Histiophryne cryptacanthus*	G01326	9853	12	705	699	1398	0	0	0
Antennariidae	*Histrio histrio*	E00643	7964	9	0	0	0	519	0	645
Aphyonidae	*Barathronus maculatus*	N02779	7479	9	633	705	1302	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Aplocheilidae	*Pachypanchax playfairii*	G01414	7524	9	0	612	1344	0	0	0
Aplodactylidae	*Aplodactylus arctidens*	M01536	4728	5	792	0	1455	0	0	0
Aplodactylidae	*Aplodactylus etheridgii*	M01537	4710	5	792	0	1455	0	0	0
Apogonidae	*Apogon campbelli*	E01069	9380	10	825	0	0	0	824	633
Apogonidae	*Archamia biguttata*	E00522	8166	11	810	752	0	0	0	633
Apogonidae	*Astrapogon puncticulatus*	E00109	7227	9	0	752	0	0	0	645
Apogonidae	*Astrapogon stellatus*	N03004	7517	9	693	705	1398	0	0	0
Apogonidae	*Cercamia eremia*	E00546	6660	9	810	0	0	0	0	633
Apogonidae	*Cheilodipterus isostigmus*	E00528	8272	10	810	752	0	0	0	0
Apogonidae	*Cheilodipterus quinquelineatus*	G01247	9762	12	690	708	1398	0	0	0
Apogonidae	*Fowleria aurita*	E01090	8780	11	810	765	0	0	0	636
Apogonidae	*Gymnapogon urospilotus*	E00539	5107	7	0	752	0	0	0	0
Apogonidae	*Nectamia bandanensis*	E01040	8860	11	810	0	0	0	0	630
Apogonidae	*Nectamia fusca*	E00732	8861	10	810	752	0	0	0	624
Apogonidae	*Ostorhinchus cookii*	E01087	6400	8	810	765	0	0	0	600
Apogonidae	*Ostorhinchus lateralis*	G01203	8273	10	705	675	1398	0	0	0
Apogonidae	*Phaeoptyx pigmentaria*	E00506	12882	15	810	752	1398	0	0	0
Apogonidae	*Pristiapogon exostigma*	E00702	8433	11	810	752	0	0	0	633
Apogonidae	*Pseudamia gelatinosa*	E00568	7391	9	810	755	0	0	0	612
Apogonidae	*Pterapogon kauderni*	E00190	6329	8	801	752	0	0	0	630
Apogonidae	*Rhabdamia cypselura*	E01095	6022	7	0	0	0	0	0	0
Apogonidae	*Sphaeramia orbicularis*	N03178	8446	10	703	672	1398	0	0	0
Aracanidae	*Anoplocapros lenticularis*	G01533	6886	7	0	0	518	0	771	0
Aracanidae	*Aracana aurita*	G01205	10032	12	705	708	1287	0	0	0
Ariommatidae	*Ariomma bondi*	E01126	7867	9	810	0	1455	0	0	621
Ariommatidae	*Ariomma melanum*	E00665	9682	12	810	756	0	0	0	645
Arripidae	*Arripis georgianus*	M01539	4794	5	792	0	1455	0	0	642
Arripidae	*Arripis trutta*	M01540	3327	4	780	0	0	0	0	642
Arripidae	*Arripis truttacea*	M01541	4659	5	0	0	1455	0	0	639
Artedidraconidae	*Artedidraco orianae*	G01525	6898	8	0	0	0	0	701	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Artedidraconidae	*Pogonophryne barsukovi*	E00158	12842	14	801	756	0	0	738	645
Atherinidae	*Atherinomorus lacunosus*	E00548	15021	18	810	753	1398	0	0	645
Atherinidae	*Atherinomorus stipes*	E00115	13436	16	810	753	1434	0	0	645
Atherinidae	*Atherinomorus vaigiensis*	E00181	7813	10	810	0	0	0	0	630
Atherinidae	*Craterocephalus honoriae*	E00180	8597	10	0	753	0	0	0	0
Atherinopsidae	*Atherinopsis californiensis*	E00121	5600	7	810	756	0	0	0	0
Atherinopsidae	*Labidesthes sicculus*	E01112	14372	17	0	708	1398	0	0	624
Atherinopsidae	*Membras martinica*	E00170	7275	9	0	0	1437	0	0	618
Atherinopsidae	*Menidia beryllina*	E00174	10176	13	0	755	1059	0	0	645
Atherinopsidae	*Menidia menidia*	E00167	12560	13	0	754	1457	0	852	627
Atherinopsidae	*Menidia peninsulae*	N03847	5694	7	0	708	1299	0	0	0
Atherinopsidae	*Odontesthes argentinensis*	E00393	5125	7	0	755	0	0	0	645
Atherinopsidae	*Odontesthes bonariensis*	E00396	9234	11	0	0	0	0	822	645
Atherinopsidae	*Odontesthes humensis*	E00394	5561	7	0	755	0	0	0	645
Atherinopsidae	*Odontesthes retropinnis*	E00395	4826	6	0	755	0	0	0	0
Atherinopsidae	*Poblana ferdebueni*	N01733	5919	7	0	708	1332	0	0	0
Aulorhynchidae	*Aulorhynchus flavidus*	G01217	11313	12	759	708	1341	0	0	0
Aulostomidae	*Aulostomus chinensis*	E00871	15665	19	810	708	1398	0	755	630
Aulostomidae	*Aulostomus maculatus*	E00293	13058	16	810	693	1398	0	0	645
Badidae	*Badis pyema*	N03996	7191	9	0	588	1362	0	0	0
Badidae	*Dario dario*	N04003	5626	7	0	585	1359	0	0	0
Balistidae	*Abalistes stellatus*	E00936	14580	18	708	765	1419	0	360	0
Balistidae	*Balistapus undulatus*	E00743	12372	14	708	708	1333	0	360	0
Balistidae	*Balistes capriscus*	E00591	13798	17	669	708	1419	1206	459	0
Balistidae	*Balistes vetula*	E00755	13640	15	703	708	1419	0	360	0
Balistidae	*Balistoides conspicillum*	E00373	9468	10	0	0	1419	0	360	0
Balistidae	*Canthidermis maculata*	E00378	9887	10	0	0	1404	0	360	0
Balistidae	*Melichthys indicus*	E00919	7484	10	0	765	0	0	0	0
Balistidae	*Melichthys niger*	E00922	8652	11	0	762	1419	0	360	0
Balistidae	*Pseudobalistes flavimarginatus*	N04225	6715	8	705	708	1284	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Balistidae	*Pseudobalistes fuscus*	E00524	4607	6	0	0	1419	0	360	0
Balistidae	*Rhinecanthus aculeatus*	E00735	9140	10	825	0	1464	0	360	0
Balistidae	*Rhinecanthus assasi*	E00381	5259	6	0	0	1419	0	0	0
Balistidae	*Rhinecanthus verrucosus*	N04231	7465	9	701	708	1284	0	0	0
Balistidae	*Sufflamen chrysopterum*	E00551	11210	14	705	696	1332	0	360	0
Balistidae	*Sufflamen fraenatum*	E00935	9148	10	0	765	0	0	0	0
Balistidae	*Xanthichthys auromarginatus*	E00380	11574	12	0	0	1404	0	360	0
Balistidae	*Xanthichthys ringens*	N04239	7595	9	669	708	1296	0	0	0
Banjosidae	*Banjos banjos*	M01542	4794	5	792	0	1455	0	0	642
Banjosidae	*Banjos banjos*	N01542	6206	8	651	591	1281	0	0	0
Bathyclupeidae	*Bathyclupea argentea*	M01543	2787	4	792	0	0	0	0	636
Bathydraconidae	*Gymnodraco acuticeps*	E00155	12486	14	810	756	1332	0	756	645
Bathydraconidae	*Parachaenichthys charcoti*	E00157	15082	17	804	756	1332	0	756	645
Bathymasteridae	*Bathymaster caeruleofasciatus*	E00191	7525	10	747	756	0	0	0	630
Bathymasteridae	*Bathymaster signatus*	E00420	12500	16	810	756	0	0	0	645
Bathymasteridae	*Rathbunella hypoplecta*	E00128	12273	15	654	756	1350	0	0	0
Batrachoididae	*Batrachoides pacifici*	N04533	6761	8	0	708	1275	0	0	0
Batrachoididae	*Opsanus beta*	E00698	11611	14	0	708	1464	0	0	0
Batrachoididae	*Opsanus pardus*	E00513	11301	14	672	708	1314	795	819	0
Batrachoididae	*Opsanus tau*	E00040	4773	6	0	0	0	0	810	642
Batrachoididae	*Porichthys notatus*	E00058	13187	16	705	765	1464	0	819	570
Batrachoididae	*Porichthys plectrodon*	E00590	13538	16	708	708	1284	0	0	0
Batrachoididae	*Sanopus sp*	E00009	4902	6	0	0	0	0	822	0
Bedotiidae	*Rheocles wrightae*	G01467	11051	13	693	708	1464	0	0	0
Belonidae	*Ablennes hians*	E00162	11443	13	810	0	0	999	0	645
Belonidae	*Platybelone argalus*	E00114	12856	15	810	0	1386	1017	0	633
Belonidae	*Strongylura notata*	E00110	15115	19	810	0	1350	998	0	645
Belonidae	*Tylosurus crocodilus*	E01051	7580	10	810	0	0	1001	0	630
Belonidae	*Xenentodon cancila*	G01508	11377	14	708	708	1389	1017	0	0
Bembridae	*Bembras japonica*	N01723	6876	9	645	591	1275	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Bembropidae	*Bembrops anatirostris*	E01120	10273	13	810	762	1365	0	0	645
Bembropidae	*Bembrops gobioides*	E01128	8878	11	708	708	1365	0	0	645
Blenniidae	*Alticus arnoldorum*	E00989	2775	4	0	0	0	0	0	621
Blenniidae	*Atrosalarias fuscus*	E00525	2877	4	0	0	0	0	0	540
Blenniidae	*Blenniella chrysospilos paula*	E00986	4186	5	810	0	0	0	0	0
Blenniidae	*Blenniella cyanostigma*	E00715	7419	9	822	0	0	0	0	645
Blenniidae	*Blenniella paula*	E00979	7982	10	0	765	0	0	0	618
Blenniidae	*Cirripectes castaneus*	E00892	8002	10	810	764	0	0	0	633
Blenniidae	*Cirripectes filamentosus*	E00893	5912	7	810	762	0	0	0	0
Blenniidae	*Cirripectes quagga*	E00330	4362	5	810	0	0	0	0	0
Blenniidae	*Cirripectes stigmaticus*	E00520	4037	6	0	0	0	0	0	573
Blenniidae	*Ecsenius bicolor*	E00984	5909	8	0	0	0	0	0	630
Blenniidae	*Ecsenius midas*	E00934	3749	5	0	765	0	0	0	0
Blenniidae	*Ecsenius opsifrontalis*	E00723	5497	7	810	0	0	0	0	0
Blenniidae	*Ecsenius pardus*	E00523	4285	5	810	0	0	0	0	0
Blenniidae	*Enchelyurus flavipes*	N04786	6887	9	621	588	1380	0	0	0
Blenniidae	*Entomacrodus nigricans*	E00297	9132	11	810	696	1398	0	0	0
Blenniidae	*Entomacrodus niuafoouensis*	E00980	6091	8	0	765	0	0	0	630
Blenniidae	*Entomacrodus striatus*	E00987	5295	7	0	765	0	0	0	633
Blenniidae	*Hypleurochilus sp*	E00298	5653	7	810	0	0	0	759	0
Blenniidae	*Hypsoblennius hentz*	E00289	7330	9	635	696	1272	0	0	0
Blenniidae	*Istiblennius dussumieri*	E00556	4755	6	0	0	0	0	0	597
Blenniidae	*Meiacanthus oualanensis grammistes*	E00526	9615	12	707	699	1398	0	0	0
Blenniidae	*Nannosalarias nativitatis*	E00521	6717	8	0	0	0	0	0	612
Blenniidae	*Ophioblennius atlanticus*	E00296	11932	15	810	704	1398	0	0	0
Blenniidae	*Petroscirtes mitratus*	E00909	5741	8	795	765	0	0	0	633
Blenniidae	*Plagiotremus rhinorhynchos*	E00586	4112	5	0	0	0	0	0	0
Blenniidae	*Plagiotremus tapeinosoma*	E00540	4423	6	0	0	0	0	0	0
Blenniidae	*Praealticus caesius*	E00329	5179	6	810	0	0	0	0	0
Blenniidae	*Salarias fasciatus*	E00988	12606	14	636	744	1368	0	0	633

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Blenniidae	*Stanulus sp*	E00332	3369	4	810	0	0	0	0	609
Bothidae	*Arnoglossus blachei*	E01160	6253	7	813	0	1446	0	795	0
Bothidae	*Arnoglossus imperialis*	E01163	7399	8	0	0	1446	0	756	645
Bothidae	*Asterorhombus cocosensis*	E00904	10399	11	810	752	1446	0	741	645
Bothidae	*Bothus lunatus*	E00007	8248	9	0	696	1374	0	0	0
Bothidae	*Bothus robinsi*	E00038	6724	7	0	765	1377	0	762	0
Bothidae	*Chascanopsetta lugubris*	E01181	5982	7	813	0	0	0	801	0
Bothidae	*Laeops kitaharae*	E00082	7794	8	0	765	1368	0	774	0
Bothidae	*Monolene sp*	E01172	3326	3	0	0	0	0	729	0
Bothidae	*Psettina tosana*	E00083	7617	8	0	765	1428	0	738	637
Bothidae	*Trichopsetta ventralis*	E00599	9704	10	0	0	1344	0	774	0
Bovichtidae	*Bovichtus diacanthus*	G01229	12547	13	708	705	1395	0	745	0
Bovichtidae	*Cottoperca trigloides*	G01267	5753	6	0	0	0	0	741	0
Bramidae	*Brama brama*	E00970	11377	13	810	0	0	0	459	645
Bramidae	*Brama japonica*	N05217	8586	10	703	708	1398	0	0	0
Bramidae	*Pteraclis aesticola*	N05223	7106	9	0	591	1275	0	0	0
Bramidae	*Pterycombus brama*	E00996	9728	12	0	0	0	0	852	636
Bramidae	*Taractes asper*	N05227	8588	10	708	708	1398	0	0	0
Bramidae	*Taractichthys longipinnis*	E00684	8997	11	810	756	0	0	459	0
Bythitidae	*Bidenichthys capensis*	E00794	7231	9	810	0	0	0	0	0
Bythitidae	*Brosmophyciops pautzkei*	E00717	5948	8	810	755	0	0	0	0
Bythitidae	*Brosmophycis marginata*	N05317	7691	9	702	705	1398	0	0	0
Bythitidae	*Cataetyx rubrirostris lepidogenys*	E00261	14883	16	810	753	1290	0	852	0
Bythitidae	*Diancistrus sp*	E00236	6903	9	810	690	0	0	0	537
Bythitidae	*Dinematichthys iluocoeteoides*	E00235	4750	6	810	672	0	0	0	0
Bythitidae	*Diplacanthopoma brachysoma*	E00452	8606	9	798	753	0	0	0	633
Bythitidae	*Diplacanthopoma brunnea*	N05377	8280	10	696	675	1236	0	0	0
Caesionidae	*Caesio caerulaurea lunaris*	E00920	13727	15	813	0	1455	0	738	645
Caesionidae	*Caesio cuning*	N01544	6786	8	708	705	1398	0	0	0
Caesionidae	*Caesio teres*	E00951	7741	10	810	729	0	0	0	645

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Caesionidae	*Caesio varilineata*	E00949	9671	12	810	729	0	0	0	621
Caesionidae	*Caesio xanthonota*	E00950	9615	12	810	729	0	0	0	618
Caesionidae	*Pterocaesio pisang*	N01547	8535	10	702	708	1398	0	0	0
Caesionidae	*Pterocaesio tile*	E00961	7369	8	810	0	0	0	852	0
Callanthiidae	*Callanthias australis*	M01721	3528	4	849	0	1455	0	0	0
Callanthiidae	*Grammatonotus surugaensis*	N05516	4774	6	651	591	1284	0	0	0
Callionymidae	*Callionymus sp bairdi*	E00946	14247	16	825	708	1455	0	758	0
Callionymidae	*Diplogrammus goramensis*	E00744	3443	4	0	0	0	0	0	642
Callionymidae	*Foetorepus sp*	N01725	7524	9	708	708	1347	0	0	0
Callionymidae	*Neosynchiropus ocellatus*	E00030	9857	12	708	708	1455	0	0	0
Callionymidae	*Synchiropus agassizii*	E01004	13911	16	810	752	1335	0	0	0
Callionymidae	*Synchiropus splendidus*	E00003	7623	9	708	708	1329	0	0	0
Callionymidae	*Synchiropus stellatus*	E00925	4153	5	0	0	0	0	0	0
Caproidae	*Antigonia capros*	E01024	15924	18	813	705	1461	0	852	630
Caproidae	*Antigonia rubescens*	N05907	8327	10	705	705	1371	0	0	0
Caproidae	*Capros aper*	N05913	6917	9	623	591	1326	0	0	0
Carangidae	*Alectis ciliaris*	E00469	9715	12	816	0	0	0	699	645
Carangidae	*Atule mate*	E00942	13914	15	798	0	1365	0	750	645
Carangidae	*Carangoides ferdau*	E00869	9160	10	816	0	0	0	768	645
Carangidae	*Carangoides plagiotaenia*	E00917	10641	12	816	0	0	0	759	645
Carangidae	*Caranx crysos ruber*	E00510	15973	18	807	708	1398	0	459	594
Carangidae	*Caranx ignobilis*	E00574	14220	16	804	755	1374	0	753	645
Carangidae	*Caranx sexfasciatus*	E00834	10100	10	0	0	1389	0	753	645
Carangidae	*Chloroscombrus chrysurus*	E00763	5515	7	0	0	0	0	754	636
Carangidae	*Decapterus macarellus*	E00212	3266	5	0	0	0	0	0	636
Carangidae	*Decapterus punctatus*	E00671	9777	11	810	0	1308	0	753	630
Carangidae	*Elagatis bipinnulata*	E00841	11967	15	810	0	0	0	756	645
Carangidae	*Gnathanodon speciosus*	E00938	13565	15	0	755	1365	0	852	645
Carangidae	*Hemicaranx amblyrhynchus*	E00616	11426	13	0	755	1131	0	750	645
Carangidae	*Oligoplites saurus*	E00195	16021	19	0	681	1338	0	753	639

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Carangidae	*Scomberoides lysan*	E00738	10887	13	807	756	1446	0	642	633
Carangidae	*Selar crumenophthalmus*	E00833	11277	13	813	0	0	939	471	645
Carangidae	*Selene brownii*	E00767	7866	10	810	0	0	0	852	645
Carangidae	*Selene setapinnis*	N01705	6120	8	699	708	0	0	0	0
Carangidae	*Seriola dumerili*	E00623	16521	18	813	708	1425	0	459	645
Carangidae	*Seriola rivoliana*	E00467	11164	13	813	756	0	0	459	645
Carangidae	*Trachinotus carolinus*	G01504	11145	13	707	708	1398	0	0	0
Carangidae	*Trachinotus falcatus*	E00819	10693	12	810	0	0	0	714	645
Carangidae	*Trachinotus ovatus*	E01145	14822	16	690	708	1386	0	758	645
Carangidae	*Trachurus lathami*	E00598	11710	13	825	705	0	0	852	645
Carangidae	*Uraspis secunda*	E00515	11843	13	810	0	1122	0	600	645
Carapidae	*Carapus bermudensis*	E00244	3497	5	612	597	0	0	0	0
Carapidae	*Onuxodon parvibrachium*	N06009	5285	7	705	708	0	0	0	0
Carapidae	*Pyramodon ventralis*	N06013	5272	7	705	705	0	0	0	0
Caristiidae	*Caristius macropus*	N06078	5912	8	645	624	0	0	0	0
Caristiidae	*Caristius sp*	E00810	9564	11	825	0	1455	0	774	645
Caristiidae	*Platyberyx opalescens*	N06085	7781	10	651	591	1275	0	0	0
Centracanthidae	*Centracanthus cirrus*	M01560	2897	3	788	0	1455	0	0	0
Centracanthidae	*Spicara alta*	M01561	4032	4	792	0	1455	0	0	0
Centracanthidae	*Spicara maena*	M01562	5142	5	0	0	1455	0	0	642
Centracanthidae	*Spicara nigricauda*	M01564	4791	5	792	0	1455	0	0	642
Centracanthidae	*Spicara smaris*	M01565	5111	5	0	0	1454	0	0	624
Centrarchidae	*Acantharchus pomotis*	G01185	10678	10	689	0	1341	0	852	0
Centrarchidae	*Ambloplites rupestris*	E00392	18681	20	810	756	1341	0	852	645
Centrarchidae	*Archoplites interruptus*	N01722	8586	10	708	708	1392	0	0	0
Centrarchidae	*Lepomis cyanellus*	E00132	18334	20	810	756	1341	0	852	0
Centrarchidae	*Lepomis macrochirus*	E01113	15647	17	810	708	1464	0	852	645
Centrarchidae	*Micropterus salmoides*	E01110	18682	20	825	708	1464	0	852	645
Centrarchidae	*Pomoxis nigromaculatus*	E00131	14489	15	804	756	1341	0	852	645
Centriscidae	*Aeoliscus strigatus*	G01189	10258	10	0	708	1398	0	852	0

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Centriscidae	*Macroramphosus gracilis*	E00335	4196	5	0	0	0	0	0	627
Centriscidae	*Macroramphosus scolopax*	E00473	10717	12	810	591	1275	0	748	0
Centrogenyidae	*Centrogenys vaigiensis*	G01239	9161	11	691	708	1398	0	0	0
Centrolophidae	*Icichthys lockingtoni*	E00387	15879	18	810	756	1398	0	0	645
Centropomidae	*Centropomus ensiferus*	E00766	14482	15	825	0	1464	0	741	645
Centropomidae	*Centropomus medius*	E01158	10458	11	744	0	1464	0	531	645
Centropomidae	*Centropomus undecimalis*	E00194	15428	17	825	612	1398	0	0	645
Centropomidae	*Centropomus viridis*	E01153	14374	16	813	582	1437	0	804	624
Centropomidae	*Lates calcarifer*	E01135	11083	12	729	0	1444	0	690	645
Centropomidae	*Lates japonicus*	E01147	10695	11	822	0	1446	0	771	645
Centropomidae	*Lates microlepis*	E01149	9785	11	822	0	1464	0	741	645
Centropomidae	*Psammoperca waigiensis*	E01148	12243	13	741	0	1464	0	756	644
Cepolidae	*Acanthocepola sp*	M01669	4129	4	783	0	1453	0	0	642
Cepolidae	*Cepola macrophthalma*	M01566	3339	4	792	0	0	0	0	642
Cepolidae	*Cepola schlegelii*	N06269	6961	9	657	591	1278	0	0	0
Cepolidae	*Sphenanthias tosaensis*	N06282	6620	9	654	591	765	0	0	0
Ceratiidae	*Ceratias holboelli*	E00175	8091	11	705	755	0	0	751	0
Ceratiidae	*Ceratias sp*	E00160	6019	7	810	755	0	0	0	645
Ceratiidae	*Cryptopsaras couesii*	E00686	9907	10	810	708	1398	0	0	0
Chaenopsidae	*Acanthemblemaria aspera*	E00320	6836	9	0	0	0	0	735	609
Chaenopsidae	*Acanthemblemaria paula*	E00295	6314	8	0	0	0	0	0	630
Chaenopsidae	*Chaenopsis sp alepidota*	E00313	11049	13	696	708	1464	0	735	0
Chaenopsidae	*Emblemaria pandionis*	E00310	6208	7	0	0	1464	0	735	0
Chaenopsidae	*Lucayablennius zingaro*	E00294	7789	9	0	0	1464	0	735	645
Chaenopsidae	*Neoclinus blanchardi*	E00326	6535	8	0	0	1464	0	735	0
Chaenopsidae	*Stathmonotus stahli*	E00317	7886	9	0	0	1464	0	735	0
Chaetodontidae	*Chaetodon auriga*	E00921	12220	14	813	0	0	849	0	645
Chaetodontidae	*Chaetodon capistratus*	E00205	3871	5	0	0	0	849	0	0
Chaetodontidae	*Chaetodon ocellatus*	E00752	3799	5	0	0	0	849	0	0
Chaetodontidae	*Chaetodon ornatissimus*	G01243	11727	14	708	708	1398	849	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Chaetodontidae	*Chaetodon plebeius*	E00573	2874	4	0	0	0	849	0	627
Chaetodontidae	*Chaetodon reticulatus*	E00719	9187	11	810	756	0	849	0	0
Chaetodontidae	*Chaetodon striatus*	E00753	15347	19	825	693	1341	849	753	0
Chaetodontidae	*Chelmon rostratus*	G01248	10379	13	708	708	1398	0	0	0
Chaetodontidae	*Forcipiger flavissimus*	E00562	14191	17	825	756	1464	849	0	0
Chaetodontidae	*Hemitaurichthys polylepis*	E00240	12410	15	810	756	1455	849	0	636
Chaetodontidae	*Heniochus chrysostomus*	E00748	14747	18	825	756	1464	816	0	645
Chaetodontidae	*Heniochus varius*	E00547	11101	14	810	756	0	849	0	645
Chaetodontidae	*Johnrandallia nigrirostris*	N06546	7594	9	708	708	1398	0	0	0
Chaetodontidae	*Prognathodes aya aculeatus*	E00632	16211	20	695	753	1398	849	0	612
Champsodontidae	*Champsodon snyderi*	N06574	5798	8	648	593	0	0	0	0
Channichthyidae	*Chionobathyscus dewitti*	G01250	11735	13	708	708	1398	0	756	0
Channichthyidae	*Chionodraco rastrospinosus*	E00156	10249	11	810	756	1305	0	756	645
Channidae	*Channa lucius*	N06615	7562	9	639	708	1386	0	0	0
Channidae	*Channa melasoma*	N06621	8195	10	639	609	1374	0	0	0
Channidae	*Channa striata*	E01133	15424	17	801	708	1446	0	759	645
Chaunacidae	*Chaunax stigmaeus*	E01121	11544	14	645	600	1380	0	0	645
Chaunacidae	*Chaunax suttkusi*	E01117	13670	16	786	705	1374	0	0	645
Cheilodactylidae	*Cheilodactylus fasciatus*	E00795	8950	11	813	0	0	0	0	633
Cheilodactylidae	*Cheilodactylus pixi*	E00797	7523	10	636	597	1398	0	0	0
Cheilodactylidae	*Cheilodactylus variegatus*	N07699	7481	9	693	708	1359	0	0	0
Cheilodactylidae	*Chirodactylus brachydactylus*	E00796	10572	13	810	600	1398	0	0	645
Cheilodactylidae	*Chirodactylus jessicalenorum*	E00585	5511	7	810	723	0	0	0	645
Cheimarrichthyidae	*Cheimarrichthys fosteri*	N07713	7400	9	702	708	1116	0	0	0
Chiasmodontidae	*Chiasmodon niger*	E01115	6819	8	801	0	0	0	0	645
Chiasmodontidae	*Chiasmodon sp*	N33662	8114	10	693	693	1104	0	0	0
Chiasmodontidae	*Kali indica*	E01106	8049	10	810	765	0	0	755	0
Chiasmodontidae	*Kali kerberti*	E00385	8712	11	702	753	0	0	0	0
Chironemidae	*Chironemus georgianus*	M01569	3606	4	792	0	1455	0	0	0
Chironemidae	*Chironemus maculosus*	M01570	3605	4	792	0	1454	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Cichlidae	*Astatotilapia burtoni*	G01518	14530	19	825	417	1464	639	462	642
Cichlidae	*Cichla temensis*	G01256	12888	15	708	708	1398	963	0	0
Cichlidae	*Crenicichla lepidota*	E00137	9593	12	810	756	0	0	0	645
Cichlidae	*Etroplus maculatus*	E00133	16104	17	810	756	1464	865	735	0
Cichlidae	*Herichthys cyanoguttatus*	G01319	10449	13	708	708	1038	927	0	0
Cichlidae	*Heros efasciatus*	G01320	12037	14	708	708	1398	902	0	0
Cichlidae	*Heterochromis multidens*	G01321	10659	13	692	693	1368	897	0	0
Cichlidae	*Maylandia zebra*	G01519	15105	19	0	744	1464	855	462	642
Cichlidae	*Nanochromis parilus*	G01390	2645	4	0	693	0	0	0	0
Cichlidae	*Neolamprologus brichardi*	G01520	18935	21	825	744	1464	855	924	642
Cichlidae	*Oreochromis niloticus*	G01407	20724	22	708	693	1464	1206	909	594
Cichlidae	*Paratilapia polleni*	G01420	11328	12	705	708	1398	0	0	0
Cichlidae	*Paretroplus maculatus*	G01423	11220	12	696	708	1347	0	0	0
Cichlidae	*Ptychochromis grandidieri*	G01459	9350	12	705	570	1398	0	0	0
Cichlidae	*Pundamilia nyererei*	G01521	14440	18	825	417	1464	855	924	642
Cichlidae	*Steatocranus gibbiceps*	G01494	2873	4	0	693	0	0	0	0
Cichlidae	*Symphysodon discus*	E00390	10909	13	810	756	1452	908	0	645
Cichlidae	*Tilapia louka*	G01503	2873	4	0	693	0	0	0	0
Cirrhitidae	*Amblycirrhitus pinos*	E00314	16355	19	825	597	1377	0	741	645
Cirrhitidae	*Cirrhitichthys falco*	N09466	4867	7	639	597	0	0	0	0
Cirrhitidae	*Cirrhitichthys oxycephalus*	E00884	8380	11	0	765	0	0	0	645
Cirrhitidae	*Neocirrhites armatus*	E00725	12592	16	639	597	1398	0	0	630
Cirrhitidae	*Paracirrhites forsteri arcatus*	E00924	12505	15	810	765	1422	0	0	0
Citharidae	*Citharoides macrolepis*	E00071	12901	15	0	597	1415	0	744	645
Citharidae	*Citharus linguatula*	E01174	6850	8	0	0	1446	0	755	645
Citharidae	*Lepidoblepharon ophthalmolepis*	E00080	7005	8	0	765	0	0	729	645
Clinidae	*Blennophis striatus*	E00800	3454	4	0	0	0	0	0	0
Clinidae	*Clinus cottoides*	E00804	4782	6	0	0	0	0	429	0
Clinidae	*Clinus superciliosus*	E00803	5297	7	0	0	0	0	429	0
Clinidae	*Gibbonsia metzi*	N09738	6827	8	696	705	1398	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Clinidae	*Muraenoclinus dorsalis*	E00805	4559	6	0	0	0	0	429	0
Clinidae	*Pavoclinus profundus*	E00799	3475	4	0	0	0	0	0	0
Coryphaenidae	*Coryphaena hippurus*	E00937	17390	19	804	708	1437	0	819	645
Cottidae	*Artediellus uncinatus*	N10447	7522	9	704	708	1398	0	0	0
Cottidae	*Chitonotus pugetensis*	E00233	6714	8	810	687	0	0	0	0
Cottidae	*Cottus carolinae*	E00281	10765	13	669	708	1398	0	0	0
Cottidae	*Enophrys taurina*	E00234	3576	5	810	684	0	0	0	0
Cottidae	*Gymnocanthus galeatus*	E00259	3095	4	0	0	0	0	0	0
Cottidae	*Hemilepidotus jordani*	E00263	7975	10	801	756	0	0	0	615
Cottidae	*Hemilepidotus zapus*	E00272	5096	6	810	0	0	0	0	0
Cottidae	*Icelinus filamentosus*	E00277	8203	10	810	684	0	0	0	0
Cottidae	*Icelinus quadriseriatus*	E00228	5018	6	0	0	0	0	0	0
Cottidae	*Leptocottus armatus*	E00266	12068	14	807	708	1398	0	0	621
Cottidae	*Microcottus sellaris*	E00223	2282	3	0	0	0	0	0	0
Cottidae	*Myoxocephalus octodecemspinosus*	E00221	3991	4	0	0	0	0	0	0
Cottidae	*Myoxocephalus polyacanthocephalus*	E00267	4736	5	0	0	0	0	0	0
Cottidae	*Radulinus asprellus*	E00429	6882	9	810	756	0	0	0	630
Cottidae	*Rastrinus scutiger*	E00256	6088	7	0	0	0	0	0	633
Cottidae	*Scorpaenichthys marmoratus*	E00232	10450	13	705	708	1389	0	0	624
Cottidae	*Triglops macellus*	E00435	8082	10	810	756	0	0	0	645
Cottidae	*Triglops scepticus*	E00421	5233	7	810	756	0	0	0	645
Creediidae	*Limnichthys sp*	E01081	6256	8	801	708	0	0	0	579
Cryptacanthodidae	*Cryptacanthodes maculatus*	E00116	10532	13	810	756	1397	0	0	645
Cyclopteridae	*Cyclopterus lumpus*	E00220	12165	15	669	708	1398	0	755	0
Cyclopteridae	*Eumicrotremus orbis*	E00270	12456	15	795	708	1278	0	0	627
Cynoglossidae	*Cynoglossus interruptus*	E00076	7900	8	0	765	1425	0	459	645
Cynoglossidae	*Symphurus atricaudus*	E00023	10924	12	0	708	1383	0	0	558
Cynoglossidae	*Symphurus civitatium*	E00604	7546	8	0	0	0	0	0	645
Cynoglossidae	*Symphurus plagiusa*	E01164	7027	8	0	0	1445	0	600	645
Cyprinodontidae	*Cyprinodon variegatus*	E01066	12469	15	702	612	1302	0	0	0

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Cyprinodontidae	*Floridichthys carpio*	E01063	9295	11	0	758	1464	0	0	645
Cyprinodontidae	*Jordanella floridae*	N14002	5915	7	693	0	1287	0	0	0
Dactylopteridae	*Dactyloptena gilberti*	N14051	5845	7	702	705	1347	0	0	0
Dactylopteridae	*Dactyloptena orientalis*	E00237	13665	15	804	705	1446	0	0	645
Dactylopteridae	*Dactyloptena peterseni*	E00749	14553	15	810	705	1398	0	0	612
Dactylopteridae	*Dactylopterus volitans*	E00214	7789	10	0	0	0	0	750	600
Dactyloscopidae	*Gillellus semicinctus*	G01299	6655	8	693	708	1398	0	0	0
Dactyloscopidae	*Platygillellus rubrocinctus*	E00319	5427	7	0	0	0	0	0	0
Datnioididae	*Datnioides microlepis*	N14199	7836	10	636	588	1377	0	0	0
Dichistiidae	*Dichistius capensis*	M01571	3582	4	792	0	1455	0	0	0
Diodontidae	*Chilomycterus schoepfii*	E00517	12554	15	708	708	1416	0	0	642
Diodontidae	*Diodon holocanthus*	E00312	13884	15	678	708	1419	0	0	0
Drepaneidae	*Drepane punctata*	E00250	13305	15	825	582	1452	0	754	645
Echeneidae	*Echeneis naucrates*	E00615	16441	18	810	708	1398	0	738	591
Echeneidae	*Echeneis neucratoides*	E00245	7118	7	810	0	0	0	0	0
Echeneidae	*Phtheirichthys lineatus*	G01438	7650	8	0	756	0	0	0	0
Echeneidae	*Remora osteochir australis*	E00503	10993	11	810	0	1455	0	750	0
Elassomatidae	*Elassoma evergladei*	E00146	15293	17	807	756	1464	0	926	606
Elassomatidae	*Elassoma okefenokee*	G01283	9813	12	708	708	1389	0	0	0
Elassomatidae	*Elassoma zonatum*	G01284	14834	15	708	708	1464	0	927	0
Eleginopsidae	*Eleginops maclovinus*	G01286	10593	13	708	708	1338	0	747	0
Eleotridae	*Dormitator maculatus*	E00169	5763	7	0	708	1293	0	0	0
Eleotridae	*Eleotris acanthopoma pisonis*	E00741	12447	14	613	708	1398	0	0	576
Eleotridae	*Ophiocara porocephala*	E01101	11395	13	0	705	1290	0	819	645
Eleotridae	*Oxyeleotris selheimi*	N01730	5975	7	636	708	1398	0	0	0
Embiotocidae	*Amphistichus argenteus*	E00129	8893	12	810	756	0	870	0	645
Embiotocidae	*Cymatogaster aggregata*	E00139	14184	16	810	756	1383	0	0	0
Embiotocidae	*Embiotoca jacksoni*	E00120	14177	17	810	756	1464	870	759	0
Embiotocidae	*Embiotoca lateralis*	N14635	6883	8	708	708	1398	0	0	0
Embiotocidae	*Hyperprosopon anale argenteum*	E00134	14767	18	825	708	1398	0	0	645

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Embiotocidae	*Phanerodon furcatus*	E00122	11479	14	810	756	1398	0	0	0
Embiotocidae	*Rhacochilus vacca*	E00124	12585	15	708	756	1398	852	0	0
Embiotocidae	*Zalembius rosaceus*	E00135	4565	6	0	756	0	0	0	0
Emmelichthyidae	*Erythrocles schlegelii*	E00954	12039	15	810	582	1464	0	0	630
Emmelichthyidae	*Erythrocles scintillans*	N14652	6911	9	654	591	1278	0	0	0
Enoplosidae	*Enoplosus armatus*	G01287	10134	11	645	591	1398	0	927	0
Ephippidae	*Chaetodipterus faber*	E00614	14589	18	825	666	1464	846	0	0
Ephippidae	*Platax orbicularis*	E00898	13969	16	708	747	1188	870	0	615
Ephippidae	*Platax teira*	E00858	12410	15	825	750	1464	0	759	0
Epigonidae	*Epigonus pandionis*	E01019	5505	7	810	0	0	0	0	645
Epigonidae	*Epigonus telescopus*	E00652	10314	12	810	0	1455	0	852	618
Exocoetidae	*Cheilopogon dorsomacula*	E00624	11475	14	810	750	0	1002	852	642
Exocoetidae	*Cheilopogon melanurus*	N14975	5883	7	696	708	1368	0	0	0
Exocoetidae	*Cheilopogon pinnatibarbatus*	E00399	13294	16	704	750	1380	933	0	645
Exocoetidae	*Cypselurus callopterus*	E00402	6837	8	0	750	0	933	0	642
Exocoetidae	*Exocoetus monocirrhus*	E00403	10246	13	0	750	0	1002	0	636
Exocoetidae	*Hirundichthys marginatus*	E00401	9589	12	810	750	0	999	0	0
Exocoetidae	*Parexocoetus brachypterus*	E00645	4220	5	0	0	0	933	0	645
Exocoetidae	*Prognichthys brevipinnis*	E00400	6286	8	810	750	0	0	0	0
Fistulariidae	*Fistularia commersonii*	E00941	7080	7	639	591	1287	0	0	0
Fistulariidae	*Fistularia petimba*	E00602	6969	9	636	591	1131	0	0	0
Fundulidae	*Adinia xenica*	E00173	8890	10	0	752	1464	0	0	0
Fundulidae	*Fundulus blairae*	E00130	9841	11	810	752	1464	0	0	0
Fundulidae	*Fundulus chrysotus*	E00186	8599	9	810	0	1464	0	0	0
Fundulidae	*Fundulus heteroclitus*	G01293	12304	13	708	708	1371	0	0	0
Fundulidae	*Fundulus parvipinnis*	E00389	11368	13	810	752	1464	0	0	0
Fundulidae	*Lucania parva goodei*	E01064	13730	16	708	612	1464	0	0	0
Gasterosteidae	*Apeltes quadracus*	E00791	11199	12	789	708	1251	0	0	0
Gasterosteidae	*Culaea inconstans*	E00368	12338	14	780	702	1245	0	0	633
Gasterosteidae	*Gasterosteus aculeatus*	E01012	20181	21	825	765	1464	1206	921	645

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Gasterosteidae	*Gasterosteus wheatlandi*	N15128	8456	10	696	699	1332	0	0	0
Gasterosteidae	*Pungitius pungitius*	G01460	10820	11	798	702	1245	0	0	0
Gasterosteidae	*Spinachia spinachia*	G01491	10498	11	780	708	1326	0	751	0
Gempylidae	*Gempylus serpens*	E00693	9797	13	810	756	0	348	819	633
Gempylidae	*Nealotus tripes*	E00287	6043	8	0	747	0	0	0	630
Gempylidae	*Neoepinnula americana*	E00471	5662	7	0	0	0	0	0	0
Gempylidae	*Neoepinnula orientalis*	E00518	6702	9	810	0	0	0	0	636
Gempylidae	*Paradiplospinus gracilis*	N15143	7281	9	639	708	1284	0	0	0
Gempylidae	*Ruvettus pretiosus*	E00226	13794	16	807	675	1398	1206	819	0
Gerreidae	*Eucinostomus argenteus*	E00575	5749	7	0	0	0	0	0	645
Gerreidae	*Eucinostomus gula*	E00756	7604	9	0	0	1462	0	750	636
Gerreidae	*Eugerres plumieri*	G01291	11242	14	693	708	1464	0	745	0
Gerreidae	*Gerres cinereus*	E00292	11457	12	825	0	1464	0	743	645
Gerreidae	*Gerres longirostris*	E00835	6053	8	0	765	0	0	0	645
Gerreidae	*Gerres oyena*	E00823	6770	8	0	753	1455	0	0	645
Gerreidae	*Ulaema lefroyi*	G01507	8309	10	696	708	1347	0	0	0
Gigantactinidae	*Gigantactis ios*	E01053	4539	6	810	0	0	0	0	645
Gigantactinidae	*Gigantactis sp*	N34852	6412	8	705	705	1293	0	0	0
Gigantactinidae	*Gigantactis vanhoeffeni*	E00177	13239	15	810	755	1329	0	0	645
Girellidae	*Girella nigricans mezina*	E00197	11742	13	810	696	1275	0	0	645
Glaucosomatidae	*Glaucosoma buergeri*	N15231	7808	10	654	591	1278	0	0	0
Glaucosomatidae	*Glaucosoma hebraicum*	G01300	16039	18	741	708	1464	0	759	644
Gobiesocidae	*Arcos sp*	E00102	13747	16	639	0	756	0	0	645
Gobiesocidae	*Diademichthys lineatus*	G01276	8298	10	678	672	1398	0	0	0
Gobiesocidae	*Gobiesox maeandricus*	G01302	8270	10	678	0	1398	0	0	0
Gobiesocidae	*Lepadichthys lineatus*	E01080	3896	5	0	0	0	0	0	0
Gobiidae	*Amblyeleotris guttata*	E01043	8728	11	0	750	0	837	765	630
Gobiidae	*Amblyeleotris gymnocephala*	E00409	6038	8	0	755	0	828	759	645
Gobiidae	*Amblyeleotris wheeleri*	E01073	7397	9	0	765	0	837	759	0
Gobiidae	*Amblygobius decussatus*	E00533	2824	4	0	755	0	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Gobiidae	*Amblygobius phalaena*	E00736	7217	10	0	755	0	837	765	603
Gobiidae	*Asterropteryx semipunctata*	E01089	6719	8	0	765	0	831	756	0
Gobiidae	*Bathygobius mystacium*	E00104	6412	8	0	756	891	0	765	636
Gobiidae	*Bollmannia communis*	E00617	5108	5	0	755	0	0	0	645
Gobiidae	*Cabillus lacertops*	E01093	3915	5	0	0	0	0	750	0
Gobiidae	*Caffrogobius caffer*	E01056	6198	8	0	752	0	0	0	630
Gobiidae	*Caffrogobius saldanha*	E01057	6207	8	0	765	0	813	750	558
Gobiidae	*Coryphopterus glaucofraenum*	E00100	5342	7	0	756	0	0	0	642
Gobiidae	*Coryphopterus personatus*	E00405	4791	7	0	755	0	813	750	0
Gobiidae	*Cryptocentrus sp*	E00407	3883	5	0	755	0	828	765	0
Gobiidae	*Ctenogobiops crocineus*	E01097	5981	7	0	765	0	837	0	0
Gobiidae	*Ctenogobius boleosoma*	E00172	3520	5	0	755	0	0	0	630
Gobiidae	*Elacatinus oceanops*	E00108	11459	12	0	755	1317	813	798	0
Gobiidae	*Eviota albolineata*	E01041	6182	8	0	765	0	0	0	525
Gobiidae	*Eviota prasites*	E01044	5506	7	0	765	0	0	0	555
Gobiidae	*Eviota saipanensis*	E00714	4913	6	0	0	0	813	750	0
Gobiidae	*Evorthodus lyricus*	E00171	6129	8	0	755	0	0	0	0
Gobiidae	*Fusigobius duospilus*	E00863	7305	9	0	765	0	813	750	0
Gobiidae	*Fusigobius inframaculatus*	E01076	4985	6	0	764	0	0	0	0
Gobiidae	*Fusigobius neophytus*	E00733	7031	10	0	754	0	0	750	630
Gobiidae	*Gnatholepis anjerensis*	E01075	4977	7	0	0	0	825	0	645
Gobiidae	*Gnatholepis cauerensis*	E00099	3361	5	0	0	0	0	750	0
Gobiidae	*Gobiodon quinquestrigatus*	E01085	6985	9	0	0	0	813	750	531
Gobiidae	*Gobiosoma bosc*	E00097	9910	10	0	752	1317	0	798	0
Gobiidae	*Istigobius decoratus*	E01078	9124	11	0	765	891	813	750	615
Gobiidae	*Istigobius ornatus*	E01107	2776	3	0	0	0	0	0	0
Gobiidae	*Lepidogobius lepidus*	G01351	5076	6	591	708	1284	0	0	0
Gobiidae	*Lophogobius cyprinoides*	E00508	6153	8	0	0	0	834	765	0
Gobiidae	*Lythrypnus dalli*	E00126	6746	9	0	755	798	810	750	0
Gobiidae	*Oplopomus oplopomus*	E01067	6654	8	0	737	0	837	762	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Gobiidae	*Paragobiodon modestus*	E01098	8154	11	0	765	0	813	750	597
Gobiidae	*Periophthalmus kalolo*	E00537	6876	9	0	0	0	0	852	0
Gobiidae	*Priolepis cincta*	E01077	5030	6	0	0	0	831	765	0
Gobiidae	*Priolepis hipoliti*	E00106	5717	7	0	756	798	747	750	0
Gobiidae	*Psammogobius biocellatus*	E00740	5797	8	0	755	0	813	750	0
Gobiidae	*Risor ruber*	E00107	10310	10	0	756	1317	813	798	0
Gobiidae	*Stonogobiops nematodes*	N16820	2850	4	0	585	0	0	0	0
Gobiidae	*Trimma caesiura*	E01039	8870	11	0	765	0	813	750	630
Gobiidae	*Trimma haima*	E01084	5533	7	0	765	0	0	0	636
Gobiidae	*Trimma okinawae*	E00726	2759	4	0	755	0	0	0	645
Gobiidae	*Valenciennea puellaris*	E01096	5328	7	0	765	0	834	765	636
Gobiidae	*Valenciennea strigata*	E01094	4256	6	0	0	0	837	852	585
Gobiidae	*Vanderhorstia ornatissima*	E01088	6501	8	0	765	0	834	765	621
Grammatidae	*Gramma loreto*	E00280	14197	16	693	624	1434	0	0	630
Grammatidae	*Lipogramma anabantoides*	E00211	6519	8	810	0	0	0	0	0
Grammatidae	*Lipogramma trilineata*	E00210	6532	8	810	678	0	0	0	0
Haemulidae	*Anisotremus surinamensis*	N17175	7479	9	708	708	1353	0	0	0
Haemulidae	*Anisotremus virginicus*	E00200	9338	11	801	0	1455	696	0	633
Haemulidae	*Conodon nobilis*	E00613	10862	13	825	0	1455	696	0	642
Haemulidae	*Haemulon aurolineatum*	E00635	16270	20	825	756	1463	696	756	630
Haemulidae	*Haemulon plumierii*	E00279	12545	15	825	756	1416	696	0	630
Haemulidae	*Haemulon sciurus*	E00199	14796	18	825	708	1437	0	0	645
Haemulidae	*Haemulon vittatum*	E00218	14636	17	813	708	1455	696	702	606
Haemulidae	*Orthopristis chrysoptera*	E00607	15170	18	810	756	1455	696	0	630
Haemulidae	*Plectorhinchus chaetodonoides*	E00857	12011	14	825	0	1455	696	0	645
Haemulidae	*Plectorhinchus vittatus*	E00856	9448	12	810	0	0	696	0	615
Haemulidae	*Pomadasys corvinaeformis*	E00761	10420	14	765	0	0	696	690	645
Haemulidae	*Xenistius californiensis*	E00229	11494	14	825	0	1455	696	0	645
Hapalogenyidae	*Hapalogenys aya*	M01722	4098	4	849	0	1455	0	0	0
Hapalogenyidae	*Hapalogenys kishinouyei*	M01723	3627	4	840	0	1455	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Hapalogenyidae	*Hapalogenys nigripinnis*	M01724	4735	5	846	0	1455	0	0	0
Harpagiferidae	*Harpagifer antarcticus*	G01524	10362	11	711	708	1332	0	758	0
Helostomatidae	*Helostoma temminkii*	G01315	8144	9	645	588	1089	0	0	0
Hemiramphidae	*Arrhamphus sclerolepis*	G01209	7917	10	693	708	1182	0	0	0
Hemiramphidae	*Hemiramphus brasiliensis*	E00098	10104	12	810	0	1434	999	0	642
Hemiramphidae	*Hyporhamphus affinis*	E01068	5623	7	0	0	0	0	0	588
Hemiramphidae	*Hyporhamphus dussumieri*	E01086	3078	4	0	0	0	0	0	0
Hemiramphidae	*Oxyporhamphus micropterus*	E00397	8076	9	0	0	0	965	0	645
Hexagrammidae	*Hexagrammos decagrammus*	E00348	7318	10	825	0	0	0	753	645
Hexagrammidae	*Hexagrammos lagocephalus otakii*	E00363	13109	16	705	708	1398	0	0	633
Hexagrammidae	*Pleurogrammus monopterygius*	E00367	6904	9	810	0	0	0	0	630
Hexagrammidae	*Zaniolepis frenata*	E00353	6326	9	810	0	0	0	0	0
Himantolophidae	*Himantolophus albinares sagamius*	E00656	16540	18	825	755	1464	0	828	645
Hoplichthyidae	*Hoplichthys gilberti*	N17743	5272	7	645	591	1269	0	0	0
Hoplichthyidae	*Hoplichthys langsdorfii*	N17745	5443	7	645	576	1275	0	0	0
Howellidae	*Howella brodiei*	E00816	11083	12	825	0	0	0	852	644
Howellidae	*Howella zina*	N17756	5489	7	657	591	1278	0	0	0
Hypoptychidae	*Aulichthys japonicus*	G01216	11602	12	810	708	1254	0	0	0
Hypoptychidae	*Hypoptychus dybowskii*	G01335	10399	11	651	708	1227	0	0	0
Icosteidae	*Icosteus aenigmaticus*	G01336	7173	9	702	0	1455	0	0	0
Indostomidae	*Indostomus crocodilus*	N17863	5047	7	576	645	765	0	0	0
Indostomidae	*Indostomus paradoxus*	E01156	10345	11	573	708	1353	0	852	645
Isonidae	*Iso sp*	E00145	8043	10	810	591	1464	0	0	645
Istiophoridae	*Istiophorus platypterus*	E00695	12698	12	0	0	1446	1206	819	645
Istiophoridae	*Kajikia albida*	E00681	7868	10	0	0	0	0	0	609
Istiophoridae	*Makaira nigricans*	E00697	11395	12	0	0	1455	1206	813	645
Istiophoridae	*Makaira sp*	E00692	8009	9	0	0	0	810	660	642
Istiophoridae	*Tetrapturus angustirostris*	N01741	7787	10	633	591	1386	0	0	0
Kuhliidae	*Kuhlia marginata*	G01341	10248	12	696	687	1398	0	0	0
Kuhliidae	*Kuhlia mugil*	E00712	16962	18	819	756	1437	954	927	645

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Kuhliidae	*Kuhlia rupestris*	E00957	12721	15	627	597	1437	954	0	0
Kurtidae	*Kurtus gulliveri*	E00188	16737	18	816	752	1455	0	762	0
Kurtidae	*Kurtus indicus*	N17950	5074	7	639	588	0	0	0	0
Kyphosidae	*Kyphosus cinerascens*	N17975	7672	10	636	600	1224	0	0	0
Kyphosidae	*Kyphosus elegans*	G01342	9674	11	708	708	1398	0	0	0
Kyphosidae	*Kyphosus incisor*	E00202	6684	8	810	684	1437	954	0	645
Kyphosidae	*Kyphosus sectatrix*	E00775	12318	14	810	756	0	0	0	645
Labridae	*Anampses lineatus*	E00932	8645	11	0	753	0	0	0	0
Labridae	*Bodianus axillaris*	E00947	9242	11	0	753	0	0	0	645
Labridae	*Bodianus mesothorax*	E00560	14044	17	681	708	1329	876	0	618
Labridae	*Cheilinus chlorourus*	E00907	9227	12	0	0	0	0	0	645
Labridae	*Cheilinus fasciatus*	E00876	8639	11	0	752	0	870	0	0
Labridae	*Cheilinus oxycephalus*	E00901	6640	8	0	0	0	833	0	0
Labridae	*Cheilio inermis*	E00906	9477	11	0	747	0	876	0	621
Labridae	*Cirrhilabrus katherinae*	E00728	6057	8	0	0	0	0	0	645
Labridae	*Cirrhilabrus punctatus*	E00553	5794	7	0	0	0	874	0	0
Labridae	*Clepticus parrae*	E00015	14928	18	696	765	1398	874	0	0
Labridae	*Coris batuensis*	N18137	4801	6	0	708	0	0	0	0
Labridae	*Coris caudimacula*	E00861	11177	14	0	753	0	0	0	618
Labridae	*Coris formosa*	E00912	8465	11	0	753	0	0	0	0
Labridae	*Coris gaimard*	E00091	11874	15	708	708	1398	870	0	582
Labridae	*Decodon puellaris*	E00620	7367	9	810	0	0	0	0	639
Labridae	*Diproctacanthus xanthurus*	G01278	8556	10	0	708	1398	876	0	0
Labridae	*Epibulus insidiator*	E00879	16078	19	666	752	1398	825	0	0
Labridae	*Gomphosus varius*	E00085	11071	14	702	708	1398	872	0	0
Labridae	*Halichoeres bathyphilus bivittatus*	E00637	13256	16	675	708	1389	876	0	639
Labridae	*Halichoeres biocellatus*	E00727	5094	7	0	0	0	0	0	642
Labridae	*Halichoeres iridis*	E00928	6442	8	0	0	0	0	0	630
Labridae	*Halichoeres margaritaceus*	N18205	5528	7	0	708	0	0	0	0
Labridae	*Hologymnosus doliatus*	E00567	10593	13	0	0	0	876	0	630

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Labridae	*Labrichthys unilineatus*	G01344	10143	12	0	708	1398	876	0	0
Labridae	*Labroides dimidiatus*	E00848	9046	11	0	753	0	0	0	0
Labridae	*Labropsis australis*	G01345	9319	11	0	708	1398	876	0	0
Labridae	*Lachnolaimus maximus*	E00014	12305	15	696	708	0	875	0	0
Labridae	*Macropharyngodon bipartitus*	E00895	7503	10	0	0	0	0	0	0
Labridae	*Novaculichthys taeniourus*	E00926	12181	15	0	753	0	876	0	627
Labridae	*Oxycheilinus celebicus*	G01412	8510	10	0	708	1398	0	0	0
Labridae	*Oxycheilinus digramma*	E00873	10757	13	0	752	0	825	0	0
Labridae	*Oxycheilinus unifasciatus*	E00721	7878	9	0	0	0	858	0	642
Labridae	*Oxyjulis californica*	G01413	7537	9	0	708	1398	0	0	0
Labridae	*Pseudocheilinus evanidus*	E00944	6483	9	0	752	0	0	0	561
Labridae	*Pseudocheilinus hexataenia*	E00945	7019	9	0	0	0	0	0	0
Labridae	*Pteragogus enneacanthus*	G01457	6723	8	696	708	1398	0	0	0
Labridae	*Stethojulis balteata*	E00089	4889	6	810	0	0	0	0	0
Labridae	*Stethojulis strigiventer*	E00908	11343	15	0	753	0	0	0	630
Labridae	*Tautoga onitis*	G01499	9257	11	0	708	1398	876	0	0
Labridae	*Tautogolabrus adspersus*	G01500	10397	12	0	708	1398	876	0	0
Labridae	*Thalassoma amblycephalum*	E00891	10041	13	0	753	0	0	0	645
Labridae	*Thalassoma lunare*	E00902	11967	15	0	753	0	861	0	624
Labridae	*Thalassoma quinquevittatum*	E00092	6872	9	0	0	0	0	0	582
Labridae	*Wetmorella nigropinnata*	E00948	11203	14	0	752	0	854	0	591
Labridae	*Xyrichtys novacula martinicensis*	E00016	18002	21	705	708	1398	876	852	597
Labrisomidae	*Labrisomus bucciferus*	E00301	5621	7	0	0	0	0	0	0
Labrisomidae	*Labrisomus guppyi multiporosus*	E00300	8447	10	693	624	1398	0	0	0
Labrisomidae	*Labrisomus nigricinctus*	E00302	4582	6	0	0	0	0	0	0
Labrisomidae	*Malacoctenus aurolineatus*	E00299	2229	3	0	0	0	0	0	0
Labrisomidae	*Malacoctenus triangulatus*	E00321	3751	4	0	0	0	0	0	0
Labrisomidae	*Paraclinus marmoratus*	E00309	4124	5	0	0	0	0	0	0
Labrisomidae	*Starksia atlantica*	E00304	5512	7	0	0	0	0	0	0
Labrisomidae	*Starksia fasciata*	E00303	7567	9	0	0	0	0	0	615

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Labrisomidae	*Starksia ocellata*	E00318	4469	6	0	0	0	0	0	636
Lactariidae	*Lactarius lactarius Fiji*	M01673	3453	4	0	0	1455	0	0	642
Lactariidae	*Lactarius lactarius Qatar*	M01593	4041	5	582	0	1455	0	0	645
Lateolabracidae	*Lateolabrax japonicus*	E01130	12539	12	825	0	1464	0	747	0
Latridae	*Latridopsis forsteri*	M01594	4790	5	792	0	1454	0	0	642
Latridae	*Latris lineata*	M01595	4794	5	792	0	1455	0	0	642
Leiognathidae	*Gazza minuta*	G01298	8150	10	705	672	1398	0	0	0
Leiognathidae	*Leiognathus equulus*	G01348	8522	11	702	633	1356	0	0	0
Leptobramidae	*Leptobrama muelleri*	E01150	6470	8	810	0	0	0	795	645
Lethrinidae	*Gymnocranius grandoculis*	E00952	7334	9	810	714	0	0	0	0
Lethrinidae	*Lethrinus atkinsoni*	E00750	7416	10	0	756	0	0	0	645
Lethrinidae	*Lethrinus erythropterus*	N18731	7589	9	708	696	1398	0	0	0
Lethrinidae	*Lethrinus harak*	E00905	18169	21	822	696	1455	0	705	645
Lethrinidae	*Lethrinus obsoletus*	E00910	14297	15	810	0	1455	0	0	642
Lethrinidae	*Lethrinus olivaceus*	E00751	11020	13	810	0	1455	0	0	645
Lethrinidae	*Monotaxis grandoculis*	G01379	11352	12	708	708	1455	0	0	0
Liparidae	*Careproctus melanurus*	E00422	5235	7	0	756	0	0	0	0
Liparidae	*Careproctus rastrinus*	E00255	6920	8	804	0	0	0	0	0
Liparidae	*Liparis gibbus*	E00224	9360	11	0	756	1398	0	0	0
Liparidae	*Liparis pulchellus*	E00225	5675	7	0	0	0	0	0	0
Liparidae	*Paraliparis beani*	E00458	3871	5	0	756	0	0	0	0
Liparidae	*Paraliparis copei*	E00453	6908	9	0	756	0	0	0	0
Liparidae	*Paraliparis hystrix*	E00454	8881	11	0	756	1344	0	0	645
Liparidae	*Rhinoliparis barbulifer*	E00262	5284	7	789	756	0	0	0	0
Lobotidae	*Lobotes pacificus surinamensis*	G01359	9710	12	825	708	1455	0	0	0
Lophiidae	*Lophiodes reticulatus*	E00625	8318	11	810	746	852	0	0	645
Lophiidae	*Lophius americanus*	E00578	16809	19	819	755	1452	0	759	633
Lophiidae	*Lophius gastrophysus*	E01119	13495	17	708	759	0	0	0	645
Lutjanidae	*Aphareus furca*	E00563	13687	16	810	756	1455	0	0	645
Lutjanidae	*Aprion virescens*	E00828	8178	10	810	0	0	0	0	645

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Lutjanidae	*Apsilus dentatus*	E00770	8017	10	810	0	0	0	0	645
Lutjanidae	*Lutjanus biguttatus*	E00569	10110	12	810	756	1398	0	0	0
Lutjanidae	*Lutjanus campechanus*	E00592	9830	12	807	756	0	0	0	0
Lutjanidae	*Lutjanus griseus*	N20115	7237	9	705	708	1356	0	0	0
Lutjanidae	*Lutjanus mahogoni*	G01362	10416	12	825	708	1464	0	0	0
Lutjanidae	*Macolor niger*	E00939	9071	11	810	0	0	0	0	645
Lutjanidae	*Ocyurus chrysurus*	E00283	13831	16	810	708	1398	0	0	0
Lutjanidae	*Pristipomoides aquilonaris*	E00594	10332	13	810	756	0	0	0	636
Lutjanidae	*Pristipomoides auricilla*	E00746	6210	8	810	0	0	0	0	645
Lutjanidae	*Rhomboplites aurorubens*	E00593	13759	16	810	756	1398	0	0	645
Luvaridae	*Luvarus imperialis*	E00509	15760	19	819	585	1035	0	447	645
Malacanthidae	*Caulolatilus intermedius*	E00595	8981	11	810	0	0	0	0	0
Malacanthidae	*Caulolatilus princeps*	E00231	11865	15	807	708	1398	0	0	621
Malacanthidae	*Malacanthus plumieri*	E00774	8060	10	708	708	1398	0	0	0
Mastacembelidae	*Macrognathus siamensis*	G01367	8287	10	708	708	1376	0	0	0
Mastacembelidae	*Mastacembelus brachyrhinus*	N01727	6948	8	0	708	1350	0	0	0
Mastacembelidae	*Mastacembelus cunningtoni*	N20638	7046	8	0	708	1338	0	0	0
Mastacembelidae	*Mastacembelus erythrotaenia*	E01157	5328	7	813	0	0	0	744	645
Mastacembelidae	*Mastacembelus niger*	N20658	7640	9	693	708	1338	0	0	0
Melanocetidae	*Melanocetus johnsonii*	E00657	12119	14	810	755	0	0	0	645
Melanocetidae	*Melanocetus murrayi*	E00477	8829	10	810	755	0	0	0	645
Melanotaeniidae	*Melanotaenia sp*	N35702	6890	8	696	708	1398	0	0	0
Melanotaeniidae	*Melanotaenia splendida*	E00179	10979	13	810	753	801	0	0	633
Melanotaeniidae	*Melanotaenia trifasciata*	E00178	7620	9	810	753	1464	0	0	630
Melanotaeniidae	*Rhadinocentrus ornatus*	E00183	8085	9	810	752	1464	0	0	576
Menidae	*Mene maculata*	E01131	14538	17	645	267	1464	0	755	645
Microdesmidae	*Cerdale floridana*	E00113	5251	7	0	756	0	0	765	636
Microdesmidae	*Gunnellichthys monostigma*	E00545	4244	6	0	755	0	0	765	561
Microdesmidae	*Microdesmus bahianus*	E00112	6294	8	0	755	0	813	765	558
Microdesmidae	*Microdesmus longipinnis*	E00388	7384	9	0	755	0	0	750	642

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Microdesmidae	*Nemateleotris magnifica*	N20888	3449	4	0	591	1254	0	0	0
Microdesmidae	*Ptereleotris evides*	E00565	10142	12	0	755	1398	0	852	636
Microdesmidae	*Ptereleotris microlepis*	E00554	6773	9	0	755	0	813	765	642
Molidae	*Masturus lanceolatus*	E00651	10906	12	825	582	1464	0	0	0
Molidae	*Mola mola*	E00683	12859	14	708	624	1464	0	843	0
Molidae	*Ranzania laevis*	G01463	10882	12	657	600	1368	0	459	0
Monacanthidae	*Acreichthys tomentosus*	N21168	5898	7	705	696	1359	0	0	0
Monacanthidae	*Aluterus scriptus*	E00316	8934	9	0	0	1419	0	459	0
Monacanthidae	*Amanses scopas*	E00536	7667	7	0	0	1464	0	0	0
Monacanthidae	*Cantherhines pardalis pullus*	E00887	13701	14	0	763	1419	0	0	0
Monacanthidae	*Oxymonacanthus longirostris*	E00914	7920	8	0	765	1419	0	0	0
Monacanthidae	*Paraluteres prionurus*	E00913	10156	10	0	759	1419	0	0	0
Monacanthidae	*Pervagor janthinosoma*	N21229	7625	9	695	687	1398	0	0	0
Monacanthidae	*Pervagor nigrolineatus*	N21232	5912	7	705	708	1398	0	0	0
Monacanthidae	*Stephanolepis hispidus*	E00646	10631	13	810	764	1419	0	459	0
Monodactylidae	*Monodactylus argenteus*	E00827	11839	12	825	753	1464	0	852	636
Monodactylidae	*Monodactylus sebae*	N21267	8411	10	693	696	1350	0	0	0
Moronidae	*Dicentrarchus labrax*	E01132	13167	14	825	0	1458	0	459	645
Moronidae	*Morone americana*	E00017	4648	6	0	765	0	0	0	0
Moronidae	*Morone chrysops*	E00992	15777	17	825	753	1461	0	0	645
Moronidae	*Morone mississippiensis*	E00087	11851	14	810	765	1350	0	0	630
Moronidae	*Morone saxatilis*	G01380	9541	12	693	696	1350	0	852	0
Mugilidae	*Chelon macrolepis*	E00845	8599	11	810	752	0	0	513	0
Mugilidae	*Crenimugil crenilabis*	E00846	12826	14	0	752	0	0	0	0
Mugilidae	*Liza richardsonii*	E00808	12339	15	810	752	0	0	759	0
Mugilidae	*Moolgarda engeli*	E00739	6506	8	810	0	0	0	0	0
Mugilidae	*Mugil cephalus*	E00049	13859	15	705	615	1443	0	759	0
Mugilidae	*Mugil curema*	E00031	15184	16	708	708	1464	0	0	0
Mugilidae	*Mugil trichodon*	E00765	10230	11	0	0	852	0	0	0
Mugilidae	*Myxus capensis*	E00809	9832	10	810	752	0	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Mugilidae	*Neomyxus leuciscus*	E00742	10501	12	810	0	0	0	0	0
Mugilidae	*Valamugil buchanani*	E00847	12275	15	810	752	0	0	0	0
Mullidae	*Mulloidichthys flavolineatus*	E00844	9135	11	645	753	1377	0	0	0
Mullidae	*Mullus auratus*	E00634	10617	12	819	0	0	0	852	645
Mullidae	*Parupeneus barberinus*	E00899	8131	10	708	708	1398	0	0	0
Mullidae	*Parupeneus ciliatus*	E00840	5965	8	810	0	0	0	0	0
Mullidae	*Parupeneus trifasciatus*	N21710	5845	7	708	699	1398	0	0	0
Mullidae	*Pseudupeneus maculatus*	E00773	9043	11	810	696	1398	0	0	0
Mullidae	*Upeneus moluccensis*	E00825	7964	10	801	750	1455	0	0	0
Mullidae	*Upeneus parvus*	N21732	3287	4	645	597	1377	0	0	0
Nandidae	*Nandus andrewi*	N22312	8474	10	639	708	1398	0	0	0
Nandidae	*Nandus nandus*	G01388	11524	13	639	696	1464	0	0	0
Nandidae	*Nandus nebulosus*	N22314	7688	9	0	708	1308	0	0	0
Nematistiidae	*Nematistius pectoralis*	E01146	12623	14	816	708	1455	0	726	645
Nemipteridae	*Pentapodus caninus*	G01427	8879	11	708	708	1398	0	0	0
Nemipteridae	*Scolopsis bilineata*	E00028	14791	16	708	708	1398	0	0	645
Nemipteridae	*Scolopsis frenata*	E00911	6514	8	810	752	0	0	0	0
Nemipteridae	*Scolopsis margaritifera*	G01478	7404	9	708	708	1398	0	0	0
Niphonidae	*Niphon spinosus*	G01398	4377	5	0	0	1338	0	0	0
Nomeidae	*Cubiceps baxteri*	G01271	9684	12	704	708	1380	0	0	0
Nomeidae	*Cubiceps gracilis*	E00672	8634	11	810	756	0	0	852	645
Nomeidae	*Cubiceps pauciradiatus*	E00667	9277	9	810	756	0	0	0	0
Nomeidae	*Psenes cyanophrys*	E00666	6230	6	810	756	0	0	0	618
Nomeidae	*Psenes maculatus*	N23089	7094	9	657	591	1275	0	0	0
Nototheniidae	*Aethotaxis mitopteryx*	G01528	7979	9	0	705	0	0	759	0
Nototheniidae	*Dissostichus eleginoides*	G01279	12707	14	708	708	1398	0	759	0
Nototheniidae	*Gobionotothen gibberifrons*	G01529	8961	10	0	705	0	0	676	0
Nototheniidae	*Notothenia coriiceps*	G01526	9628	10	0	693	1455	0	750	0
Nototheniidae	*Pagothenia borchgrevinki*	G01527	9352	10	711	708	1398	0	750	0
Nototheniidae	*Patagonotothen tessellata*	G01530	10915	12	711	708	1332	0	750	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Odacidae	*Haletta semifasciata*	G01312	9038	11	693	0	1329	897	0	0
Odontobutidae	*Odontobutis potamophila*	E01137	12389	14	693	708	0	0	753	645
Odontobutidae	*Perccottus glenii*	G01429	9285	11	675	708	1398	0	0	0
Ogcocephalidae	*Dibranchus tremendus*	E00975	8668	11	681	765	0	0	0	645
Ogcocephalidae	*Halieutichthys aculeatus*	E01122	5969	8	702	699	0	0	0	0
Ogcocephalidae	*Ogcocephalus parvus nasutus*	E00610	11181	14	825	756	0	0	0	0
Ogcocephalidae	*Ogcocephalus radiatus*	E00641	3592	4	810	756	0	0	0	0
Oneirodidae	*Bertella idiomorpha*	E00386	7368	8	0	755	0	0	0	645
Oneirodidae	*Dolopichthys sp*	E00484	3002	4	810	0	0	0	0	0
Oneirodidae	*Oneirodes bulbosus*	E00176	5086	7	0	755	0	0	0	627
Oneirodidae	*Oneirodes macrosteus*	E00655	7815	10	825	755	1233	0	0	0
Ophidiidae	*Bassogigas gillii*	E00481	5439	7	801	0	0	0	0	639
Ophidiidae	*Brotula barbata*	E00629	8900	12	810	753	0	0	459	630
Ophidiidae	*Brotula multibarbata*	E00883	12654	16	708	708	1398	0	0	642
Ophidiidae	*Brotulotaenia crassa*	E00659	7913	10	810	753	0	0	0	0
Ophidiidae	*Brotulotaenia nigra*	E00817	8794	11	810	0	852	0	0	0
Ophidiidae	*Chilara taylori*	E00260	6335	8	0	0	0	0	0	645
Ophidiidae	*Dicrolene introniger*	E00480	8819	11	810	705	0	0	0	630
Ophidiidae	*Genypterus blacodes*	E00241	3596	4	0	0	1437	0	0	0
Ophidiidae	*Lamprogrammus niger*	E00275	11903	13	810	690	0	0	852	0
Ophidiidae	*Lepophidium brevibarbe*	E00758	5469	7	0	0	0	0	0	642
Ophidiidae	*Lepophidium jeannae*	E00621	4709	6	0	756	0	0	0	633
Ophidiidae	*Lepophidium profundorum*	E00248	3341	4	0	0	0	0	0	645
Ophidiidae	*Neobythites gilli*	E00612	7830	10	810	756	0	0	0	612
Ophidiidae	*Ophidion holbrookii*	E01033	7171	9	0	0	0	0	0	645
Ophidiidae	*Ophidion josephi*	E00648	6546	8	810	756	0	0	0	633
Ophidiidae	*Ophidion robinsi*	E01007	6730	8	0	0	0	0	0	645
Ophidiidae	*Petrotyx sanguineus*	E00206	4716	6	0	756	1464	0	0	645
Opistognathidae	*Lonchopisthus micrognathus*	E00603	6548	8	810	0	0	0	0	639
Opistognathidae	*Opistognathus aurifrons*	E00216	9008	11	810	708	1446	0	0	645

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Opistognathidae	*Opistognathus maxillosus*	E00207	6793	8	813	0	0	0	777	606
Oplegnathidae	*Oplegnathus punctatus*	G01405	12420	13	705	708	1437	954	0	0
Osphronemidae	*Betta splendens*	G01226	9892	10	0	708	1398	0	0	0
Osphronemidae	*Trichopodus pectoralis*	N24415	4860	7	645	585	792	0	0	0
Ostraciidae	*Acanthostracion quadricornis*	E00760	5464	6	810	0	1419	0	0	0
Ostraciidae	*Ostracion cubicus*	E00588	12421	15	810	708	1398	0	0	0
Ostraciidae	*Rhinesomus triqueter*	G01469	10814	13	695	696	1416	0	0	0
Ostracoberycidae	*Ostracoberyx dorygenys*	N24448	6883	9	645	591	1275	0	0	0
Parabembridae	*Parabembras curtus*	N24483	6893	9	645	591	1287	0	0	0
Paralichthyidae	*Ancylopsetta ommata*	E00001	8842	10	0	0	1431	0	741	645
Paralichthyidae	*Citharichthys arctifrons*	E00043	6688	8	0	0	0	0	771	540
Paralichthyidae	*Citharichthys sordidus*	E00446	12907	14	708	708	1398	0	0	0
Paralichthyidae	*Cyclopsetta chittendeni*	E00597	10244	12	819	0	0	0	738	645
Paralichthyidae	*Etropus crossotus*	E00647	8021	9	0	0	0	0	714	645
Paralichthyidae	*Etropus microstomus*	E00047	5197	5	0	0	1368	0	747	0
Paralichthyidae	*Gastropsetta frontalis*	E00640	2345	3	0	0	0	0	0	0
Paralichthyidae	*Paralichthys albigutta*	E01171	8241	9	813	0	0	0	738	645
Paralichthyidae	*Paralichthys californicus*	E00020	8905	10	822	0	0	0	0	645
Paralichthyidae	*Paralichthys dentatus*	N24591	7812	9	705	708	1396	0	0	0
Paralichthyidae	*Pseudorhombus pentophthalmus*	E00077	10302	11	816	765	1446	0	747	645
Paralichthyidae	*Syacium micrurum*	E00633	9035	11	822	0	0	0	431	645
Paralichthyidae	*Xystreurys liolepis*	E00021	9760	10	810	0	1440	0	744	0
Pegasidae	*Eurypegasus draconis*	N24699	2094	3	0	582	762	0	0	0
Pempheridae	*Parapriacanthus ransonneti*	E00923	11086	13	810	0	1455	0	0	645
Pempheridae	*Pempheris oualensis*	E00718	9245	11	810	756	1455	0	0	633
Pempheridae	*Pempheris schomburgkii*	E00213	10586	12	810	756	1398	0	0	645
Pempheridae	*Pempheris schwenkii*	N01628	5322	7	651	591	1275	0	0	0
Pempheridae	*Pempheris vanicolensis*	E00886	8350	10	810	0	0	0	0	618
Pentacerotidae	*Histiopterus typus*	N24730	6890	9	651	591	1278	0	0	0
Pentacerotidae	*Paristiopterus labiosus*	M01629	3261	4	792	0	0	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Pentacerotidae	*Pentaceros japonicus*	N24735	7793	10	648	591	1278	0	0	0
Pentacerotidae	*Pentaceros pectoralis*	N01736	5434	7	0	0	0	0	0	0
Pentacerotidae	*Pentaceros wheeleri*	N01737	7434	9	639	0	1383	0	0	0
Pentacerotidae	*Zanclistius elevatus*	M01631	2901	3	792	0	1455	0	0	0
Percichthyidae	*Gadopsis marmoratus*	E01144	13223	14	822	708	1437	0	927	645
Percichthyidae	*Maccullochella peelii*	G01365	11015	13	708	708	1347	0	0	0
Percichthyidae	*Macquaria ambigua*	G01366	10488	13	627	579	1398	0	0	0
Percichthyidae	*Macquaria colonorum*	G01431	10574	13	627	579	1398	0	0	0
Percichthyidae	*Macquaria novemaculeata*	G01432	10525	13	624	579	1398	0	0	0
Percichthyidae	*Nannoperca australis*	G01389	11969	14	627	579	1398	0	0	0
Percichthyidae	*Percichthys trucha*	G01430	9417	9	825	0	1434	0	0	645
Percidae	*Ammocrypta beanii*	E00187	8350	10	810	756	1341	0	0	0
Percidae	*Ammocrypta meridiana*	E00148	8201	10	810	756	1341	0	0	630
Percidae	*Ammocrypta pellucida*	E00149	9339	11	810	756	1404	0	0	645
Percidae	*Crystallaria asprella*	E00153	8415	10	810	756	1404	0	0	618
Percidae	*Etheostoma atripinne*	G01290	7713	9	705	708	1341	0	0	0
Percidae	*Etheostoma juliae*	E00168	11455	14	810	756	1344	0	0	645
Percidae	*Etheostoma simoterum*	E00152	12189	15	705	756	1308	0	0	630
Percidae	*Etheostoma vitreum*	E00147	11025	13	798	756	1404	0	0	630
Percidae	*Etheostoma zonale*	E01111	13171	16	684	764	1341	0	0	645
Percidae	*Gymnocephalus cernuus*	E00140	7525	10	810	708	0	0	756	0
Percidae	*Gymnocephalus schraetser*	E00141	6323	8	0	708	0	0	0	0
Percidae	*Perca flavescens*	E00391	14692	16	825	756	1464	0	0	546
Percidae	*Perca fluviatilis*	G01428	10413	11	0	666	1464	0	758	634
Percidae	*Percina caprodes*	E01054	15273	18	810	765	1398	0	0	645
Percidae	*Percina nigrofasciata*	E00154	7519	9	810	756	1341	0	0	645
Percidae	*Percina phoxocephala*	E00150	9105	11	810	756	1341	0	0	639
Percidae	*Romanichthys valsanicola*	E00143	9564	12	810	756	0	0	0	645
Percidae	*Sander vitreus*	E01109	10398	10	0	0	1404	0	0	645
Percidae	*Zingel streber*	E00144	5447	7	0	705	0	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Percidae	*Zingel zingel*	E00142	6114	8	810	756	0	0	0	645
Perciliidae	*Percilia irwini*	N24981	6918	9	624	579	1398	0	0	0
Percophidae	*Acanthaphritis unoorum*	N24985	5579	7	648	591	1302	0	0	0
Peristediidae	*Peristedion ecuadorense*	E00456	6094	7	810	0	0	0	0	0
Peristediidae	*Peristedion gracile*	E01029	2905	4	0	0	0	0	0	636
Peristediidae	*Peristedion truncatum*	E00450	3441	5	804	0	0	0	0	621
Phallostethidae	*Phenacostethus smithi*	E00398	7945	10	630	600	1377	0	0	0
Pholidae	*Pholis crassispina*	G01437	12482	14	708	708	1397	0	745	0
Pholidae	*Pholis ornata*	N01732	8528	10	708	708	1398	0	0	0
Pholidichthyidae	*Pholidichthys leucotaenia*	E00251	11101	12	696	672	1398	0	0	0
Pinguipedidae	*Parapercis clathrata*	E00707	10851	13	810	756	1398	0	738	645
Pinguipedidae	*Parapercis hexophtalma*	E01083	11528	14	810	719	1368	0	0	642
Pinguipedidae	*Parapercis punctulata*	E01091	7008	9	0	765	0	0	0	621
Platycephalidae	*Platycephalus indicus*	N25405	6719	9	645	588	1278	0	0	0
Platycephalidae	*Rogadius asper*	N25418	6352	9	645	591	765	0	0	0
Platycephalidae	*Sunagocia arenicola*	E00708	5403	7	0	0	0	0	0	645
Platycephalidae	*Thysanophrys chiltonae*	E00864	8747	10	819	765	0	0	780	645
Plesiopidae	*Plesiops coeruleolineatus*	E00855	15452	18	813	708	1398	0	0	645
Plesiopidae	*Plesiops melas*	G01442	8238	10	687	708	1398	0	0	0
Pleuronectidae	*Atheresthes evermanni*	E00055	8437	8	807	0	1401	837	0	0
Pleuronectidae	*Embassichthys bathybius*	E00064	11340	12	786	0	1368	822	690	642
Pleuronectidae	*Eopsetta jordani*	E00444	14474	17	825	0	1257	849	690	645
Pleuronectidae	*Glyptocephalus zachirus*	E00416	10353	12	816	0	1440	849	459	645
Pleuronectidae	*Hippoglossoides elassodon*	E00424	12527	13	822	0	1422	849	0	645
Pleuronectidae	*Hippoglossus hippoglossus*	E00689	10279	12	825	0	0	0	459	618
Pleuronectidae	*Hypsopsetta guttulata*	E00022	9133	9	819	0	1446	0	0	645
Pleuronectidae	*Isopsetta isolepis*	E00018	6603	8	810	0	0	849	768	0
Pleuronectidae	*Lepidopsetta bilineata*	E00438	16335	19	825	612	1386	849	699	645
Pleuronectidae	*Limanda limanda*	E00690	7013	8	825	0	0	0	459	645
Pleuronectidae	*Lyopsetta exilis*	E01173	6171	7	813	0	0	813	753	645

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Pleuronectidae	*Microstomus pacificus*	E00433	10016	12	825	0	0	807	459	645
Pleuronectidae	*Parophrys vetulus*	E00445	12033	14	825	0	0	822	750	645
Pleuronectidae	*Platichthys stellatus*	E00026	7842	9	807	0	0	849	459	645
Pleuronectidae	*Pleuronectes platessa*	E00053	14871	17	825	708	1446	0	459	645
Pleuronectidae	*Psettichthys melanostictus*	E00025	9364	11	816	0	0	849	717	645
Pleuronectidae	*Pseudopleuronectes americanus*	E00035	15563	18	825	612	1350	849	0	645
Poeciliidae	*Belonesox belizanus*	E01052	10182	11	810	0	1464	0	0	0
Poeciliidae	*Gambusia affinis*	G01296	11403	12	708	708	1464	0	0	0
Poeciliidae	*Heterandria formosa*	E00185	10113	11	810	0	1464	0	0	645
Poeciliidae	*Poecilia latipinna reticulata*	E01065	12149	14	810	764	1459	0	754	0
Poeciliidae	*Poeciliopsis elongata*	N01734	6863	8	705	708	1398	0	0	0
Poecilopsettidae	*Poecilopsetta beanii*	E00448	5472	7	0	0	0	0	771	645
Poecilopsettidae	*Poecilopsetta plinthus*	E00073	9752	10	816	765	1446	0	738	645
Polycentridae	*Monocirrhus polyacanthus*	G01377	8420	10	707	708	1398	0	0	0
Polycentridae	*Polycentropsis abbreviata*	N26006	8369	10	708	708	1344	0	0	0
Polycentridae	*Polycentrus schomburgkii*	G01444	8382	10	705	705	1398	0	0	0
Polynemidae	*Eleutheronema rhadinum*	N26015	7791	10	654	591	1272	0	0	0
Polynemidae	*Eleutheronema tetradactylum*	E01154	7961	9	810	0	1380	0	780	645
Polynemidae	*Leptomelanosoma indicum*	E00842	11242	14	810	0	0	0	735	645
Polynemidae	*Polydactylus octonemus*	E00606	9992	13	813	756	0	0	753	645
Polynemidae	*Polydactylus sextarius*	N26043	5532	7	654	0	1269	0	0	0
Polynemidae	*Polydactylus virginicus*	E00217	11602	13	813	708	0	0	0	645
Polyprionidae	*Polyprion americanus*	E00242	7677	9	822	0	1437	0	753	645
Polyprionidae	*Polyprion oxygeneios*	M01632	4716	5	792	0	1455	0	0	0
Polyprionidae	*Stereolepis gigas*	E00227	14211	17	708	681	1389	0	812	645
Pomacanthidae	*Apolemichthys trimaculatus*	E00839	9202	12	810	0	0	0	0	0
Pomacanthidae	*Centropyge bicolor*	E00550	11381	15	810	0	0	0	0	645
Pomacanthidae	*Centropyge loricula*	E00284	9087	10	810	0	0	0	0	615
Pomacanthidae	*Centropyge nox*	E00542	8384	11	810	0	0	0	0	0
Pomacanthidae	*Chaetodontoplus melanosoma*	G01244	8178	10	708	702	1398	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Pomacanthidae	*Holacanthus ciliaris*	E00209	6815	8	810	0	1452	0	759	0
Pomacanthidae	*Holacanthus passer*	E00282	12494	15	708	708	1398	0	0	0
Pomacanthidae	*Holacanthus tricolor*	E00198	7349	9	810	0	0	0	0	645
Pomacanthidae	*Pomacanthus arcuatus*	E00754	8027	10	804	0	0	849	852	645
Pomacanthidae	*Pomacanthus imperator*	E00710	9192	12	813	0	0	0	0	645
Pomacanthidae	*Pomacanthus semicirculatus*	E00849	10414	14	810	0	0	0	0	645
Pomacanthidae	*Pomacanthus zonipectus*	G01448	9113	11	708	708	1398	0	0	0
Pomacanthidae	*Pygoplites diacanthus*	E00534	10507	13	810	0	1455	849	0	630
Pomacentridae	*Abudefduf saxatilis*	E00820	14973	18	810	693	1464	876	0	633
Pomacentridae	*Abudefduf sexfasciatus*	E00881	12145	15	810	714	1464	0	0	645
Pomacentridae	*Abudefduf vaigiensis*	E00890	12132	13	810	0	0	0	0	645
Pomacentridae	*Acanthochromis polyacanthus*	E00466	8743	10	807	756	1464	0	0	633
Pomacentridae	*Amblyglyphidodon leucogaster*	E00529	3808	4	0	0	1464	876	0	0
Pomacentridae	*Amphiprion clarkii*	E00196	4604	6	804	684	0	0	0	0
Pomacentridae	*Amphiprion ocellaris*	E00193	7717	7	768	0	1464	843	0	0
Pomacentridae	*Azurina hirundo*	E00580	9629	12	810	756	0	0	0	0
Pomacentridae	*Chromis atripectoralis*	E00238	9353	11	810	0	0	0	0	0
Pomacentridae	*Chromis cyanea*	E00201	13033	15	810	678	1464	0	0	0
Pomacentridae	*Chromis dimidiata*	E00851	9724	12	810	0	0	0	0	624
Pomacentridae	*Chrysiptera taupou*	E00564	9950	13	810	756	0	0	0	645
Pomacentridae	*Dascyllus aruanus*	E00700	11886	14	810	0	1463	0	734	642
Pomacentridae	*Dascyllus carneus*	E00862	11899	14	0	756	1464	0	0	633
Pomacentridae	*Dascyllus reticulatus*	E00724	8549	10	0	0	1464	0	0	639
Pomacentridae	*Dascyllus trimaculatus*	E00865	6439	7	0	0	1464	855	852	0
Pomacentridae	*Dischistodus perspicillatus*	E00464	8931	11	804	756	0	0	0	0
Pomacentridae	*Hypsypops rubicundus*	E00459	7285	10	810	756	0	0	0	645
Pomacentridae	*Lepidozygus tapeinosoma*	E00929	7795	10	810	0	0	0	0	645
Pomacentridae	*Microspathodon bairdii*	G01375	8331	10	708	708	1398	0	0	0
Pomacentridae	*Microspathodon chrysurus*	E00772	10751	13	810	0	1464	0	0	645
Pomacentridae	*Neoglyphidodon melas*	E00465	9828	12	810	756	0	0	0	633

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Pomacentridae	*Neoglyphidodon polyacanthus*	E00285	6455	8	810	705	0	0	0	615
Pomacentridae	*Neopomacentrus cyanomos*	E00933	8888	11	810	0	0	0	0	645
Pomacentridae	*Parma microlepis*	E00286	5332	7	807	0	0	0	0	645
Pomacentridae	*Plectroglyphidodon dickii*	E00572	13722	16	810	756	1464	0	927	636
Pomacentridae	*Plectroglyphidodon johnstonianus*	E00722	7987	10	810	756	0	0	0	618
Pomacentridae	*Pomacentrus brachialis*	E00239	9865	12	813	744	0	0	0	633
Pomacentridae	*Pomacentrus pavo*	E00729	12503	15	810	756	1464	0	744	633
Pomacentridae	*Pomacentrus spilotoceps*	E00557	6421	9	0	0	0	0	0	633
Pomacentridae	*Pomachromis richardsoni*	E00559	8319	11	0	756	0	0	0	630
Pomacentridae	*Stegastes albifasciatus*	E00713	6612	9	810	0	0	0	0	645
Pomacentridae	*Stegastes diencaeus*	E00219	6060	8	0	681	0	0	0	0
Pomacentridae	*Stegastes fuscus*	E00203	12679	15	801	693	1398	0	0	630
Pomacentridae	*Stegastes partitus*	E00204	4367	6	810	0	0	0	0	618
Pomatomidae	*Pomatomus saltatrix*	E00516	16569	18	813	708	1443	0	459	645
Priacanthidae	*Heteropriacanthus cruentatus*	E00570	14367	17	810	756	1398	0	459	645
Priacanthidae	*Priacanthus arenatus*	E00618	14657	18	645	756	1389	0	852	645
Priacanthidae	*Pristigenys alta*	E00252	12492	14	825	588	1377	0	0	624
Pristolepididae	*Pristolepis fasciata*	N26580	7608	9	0	708	1332	0	0	0
Pristolepididae	*Pristolepis sp*	N36627	8543	10	705	708	1398	0	0	0
Psettodidae	*Psettodes belcheri*	E01180	6046	7	810	0	0	0	795	645
Psettodidae	*Psettodes erumei*	E01165	12034	14	819	591	1434	0	747	645
Pseudaphritidae	*Pseudaphritis urvillii*	G01453	8567	9	0	708	0	0	744	0
Pseudochromidae	*Congrogadus subducens*	G01262	8360	10	696	708	1398	0	0	0
Pseudochromidae	*Halidesmus scapularis*	E00793	10231	13	819	0	0	0	750	642
Pseudochromidae	*Labracinus cyclophthalmus*	G01343	11328	12	708	708	1398	0	0	0
Pseudochromidae	*Natalichthys sam*	E00589	7891	10	810	0	0	0	0	639
Pseudochromidae	*Ogilbyina novaehollandiae*	G01403	8345	10	690	708	1398	0	0	0
Pseudochromidae	*Pholidochromis cerasina*	G01436	8319	10	693	708	1398	0	0	0
Pseudochromidae	*Pseudochromis cyanotaenia*	E00706	7668	10	0	756	0	0	0	627
Pseudochromidae	*Pseudochromis fridmani*	N26709	8561	10	708	708	1398	0	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Pseudochromidae	*Pseudochromis jamesi*	E00535	6957	9	0	0	0	0	0	0
Pseudochromidae	*Pseudoplesiops revellei*	E00745	4311	6	810	756	0	0	0	645
Pseudomugilidae	*Pseudomugil gertrudae*	E00182	14736	18	810	753	1464	0	0	645
Pseudomugilidae	*Pseudomugil signifer*	E00184	11998	15	810	753	1374	0	0	633
Psychrolutidae	*Cottunculus thomsonii*	E00963	2374	3	0	0	0	0	744	0
Psychrolutidae	*Dasycottus setiger*	E00288	5136	6	810	756	0	0	0	0
Psychrolutidae	*Malacocottus zonurus*	E00253	8212	10	810	756	0	0	0	624
Psychrolutidae	*Psychrolutes phrictus*	E00276	5502	7	810	0	0	0	0	0
Rachycentridae	*Rachycentron canadum*	E00468	15775	17	801	708	1446	0	729	642
Rhombosoleidae	*Oncopterus darwinii*	E01184	6659	7	813	0	1368	0	780	645
Rhombosoleidae	*Rhombosolea leporina*	E01166	2980	3	0	0	0	0	585	642
Rhombosoleidae	*Rhombosolea plebeia*	E01167	5378	6	813	0	0	0	729	618
Rhombosoleidae	*Rhombosolea tapirina*	E01168	3805	4	0	0	0	0	654	0
Samaridae	*Plagiopsetta glossa*	E00074	7559	8	813	0	1431	0	756	645
Samaridae	*Samariscus japonicus*	E00072	7912	8	810	765	1437	0	756	645
Samaridae	*Samariscus latus*	N27771	2733	3	648	0	1275	0	0	0
Samaridae	*Samariscus xenicus*	E00078	7553	8	798	765	1446	0	759	642
Scaridae	*Calotomus carolinus*	N27783	7195	9	708	582	1386	0	0	0
Scaridae	*Cetoscarus bicolor*	E00566	14113	17	690	708	1335	750	0	0
Scaridae	*Chlorurus gibbus*	E00561	6813	9	0	0	0	0	0	621
Scaridae	*Chlorurus sordidus*	E00837	14642	16	0	752	1365	812	0	606
Scaridae	*Cryptotomus roseus*	N27805	7128	9	642	579	1380	0	0	0
Scaridae	*Hipposcarus longiceps*	E00737	4541	6	0	0	0	825	0	612
Scaridae	*Leptoscarus vaigiensis*	E00877	8427	11	0	752	0	750	0	0
Scaridae	*Scarus ghobban*	E00878	9678	11	0	752	0	750	759	0
Scaridae	*Scarus globiceps*	N27829	4729	6	0	582	1350	0	0	0
Scaridae	*Scarus iseri*	E00013	7345	9	0	765	0	0	0	0
Scaridae	*Scarus niger*	E00875	11274	14	630	752	1371	750	0	0
Scaridae	*Scarus quoyi*	E00872	7432	10	0	752	0	0	0	0
Scaridae	*Scarus rubroviolaceus*	E00874	12027	13	0	752	0	750	0	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Scaridae	*Sparisoma aurofrenatum*	E00008	5465	7	0	765	513	750	0	0
Scaridae	*Sparisoma chrysopterum*	E00070	2776	4	0	0	507	869	0	0
Scaridae	*Sparisoma viride*	E00004	6443	9	0	765	513	750	0	0
Scatophagidae	*Scatophagus argus*	E00051	13219	16	825	708	1464	849	753	642
Scatophagidae	*Selenotoca multifasciata*	G01483	9576	12	705	588	1398	0	852	0
Sciaenidae	*Aplodinotus grunniens*	E01108	17827	19	810	762	1380	0	0	645
Sciaenidae	*Atractoscion nobilis*	E00125	9878	13	810	756	0	0	0	573
Sciaenidae	*Bairdiella chrysoura*	E00165	7670	10	810	756	0	0	0	645
Sciaenidae	*Cheilotrema saturnum*	E00118	6644	9	810	756	0	0	0	606
Sciaenidae	*Corvula sanctaeluciae*	E01047	5698	7	810	0	0	0	0	630
Sciaenidae	*Cynoscion arenarius*	E00511	11444	13	810	756	0	0	0	0
Sciaenidae	*Cynoscion regalis*	E00164	14880	18	699	756	1464	0	752	0
Sciaenidae	*Genyonemus lineatus*	E00138	9138	12	810	756	0	0	0	642
Sciaenidae	*Larimus breviceps*	E01048	4776	7	0	0	0	0	0	642
Sciaenidae	*Leiostomus xanthurus*	G01349	9972	12	708	708	1455	0	0	0
Sciaenidae	*Menticirrhus saxatilis*	E00166	7177	9	0	756	0	0	0	0
Sciaenidae	*Menticirrhus undulatus littoralis*	E00127	15027	19	708	756	1398	0	0	606
Sciaenidae	*Micropogonias undulatus*	N01637	5789	8	639	591	0	0	0	0
Sciaenidae	*Odontoscion dentex*	E01049	5655	7	810	0	0	0	0	645
Sciaenidae	*Pareques acuminatus*	E01050	3516	4	0	0	0	0	0	0
Sciaenidae	*Pareques umbrosus*	E00639	6228	8	810	0	0	0	0	645
Sciaenidae	*Pogonias cromis*	E00699	8505	11	810	0	0	0	0	645
Sciaenidae	*Sciaenops ocellatus*	E01055	18596	20	825	708	1464	0	0	645
Sciaenidae	*Seriphus politus*	E00123	7497	10	801	756	0	0	0	645
Sciaenidae	*Stellifer lanceolatus*	E00608	9278	12	807	756	0	0	0	645
Sciaenidae	*Umbrina coroides*	E00628	8595	11	807	756	0	0	0	645
Scomberesocidae	*Cololabis saira*	E00192	10242	11	0	0	0	1001	0	0
Scomberesocidae	*Scomberesox saurus*	E00404	10373	13	0	624	1463	1011	0	645
Scombridae	*Acanthocybium solandri*	E00927	14337	16	810	0	1464	1206	818	630
Scombridae	*Auxis rochei*	E00673	14617	18	810	756	1386	0	510	645

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Scombridae	*Euthynnus affinis*	E00830	9732	12	810	0	0	0	0	627
Scombridae	*Euthynnus alletteratus*	E00696	7879	11	810	756	0	1128	510	633
Scombridae	*Gymnosarda unicolor*	E00832	9359	11	810	0	0	0	0	600
Scombridae	*Katsuwonus pelamis*	E00747	11259	13	810	0	0	1197	459	645
Scombridae	*Sarda sarda*	E00243	16203	19	810	705	1398	1123	819	633
Scombridae	*Scomber japonicus*	E00247	10495	12	0	756	0	0	743	645
Scombridae	*Scomber scombrus*	E00626	19143	20	825	756	1464	1197	819	645
Scombridae	*Scomberomorus maculatus sp*	E00631	16041	19	810	756	1455	1041	819	645
Scombridae	*Scomberomorus regalis commerson*	E00694	9863	12	810	756	1464	1095	819	645
Scombridae	*Thunnus albacares*	E00831	18226	21	810	597	1377	1137	819	633
Scombrolabracidae	*Scombrolabrax heterolepis*	E00976	11570	14	825	0	1455	0	651	645
Scophthalmidae	*Lepidorhombus boscii*	E00462	9162	10	693	0	0	0	753	645
Scophthalmidae	*Scophthalmus aquosus*	E00039	10410	12	810	708	1398	0	852	645
Scophthalmidae	*Scophthalmus maximus*	E01161	6280	5	0	0	1452	0	0	0
Scorpaenidae	*Caracanthus maculatus*	E00716	8029	10	0	0	0	0	0	642
Scorpaenidae	*Caracanthus unipinna*	E00558	6573	8	810	0	0	0	0	0
Scorpaenidae	*Dendrochirus zebra*	E00897	7402	10	810	753	0	0	0	630
Scorpaenidae	*Iracundus signifer*	E00583	7125	9	810	0	0	0	0	0
Scorpaenidae	*Neomerinthe hemingwayi*	E00619	10221	12	810	0	0	1186	819	645
Scorpaenidae	*Pontinus longispinis*	E01010	7126	10	810	764	0	0	852	630
Scorpaenidae	*Pontinus rathbuni*	E00463	6391	8	810	0	0	0	0	633
Scorpaenidae	*Pterois antennata*	E00705	8496	11	810	0	1092	0	0	645
Scorpaenidae	*Pterois miles*	E00882	7015	9	807	0	0	0	0	645
Scorpaenidae	*Pterois radiata*	E00850	8182	10	0	765	0	0	0	633
Scorpaenidae	*Scorpaena agassizii*	E01038	2193	3	810	0	0	0	0	642
Scorpaenidae	*Scorpaena brasiliensis*	E00759	4986	7	0	0	0	0	755	561
Scorpaenidae	*Scorpaena dispar*	E00512	3690	5	0	0	0	0	0	0
Scorpaenidae	*Scorpaena guttata*	E00291	8547	10	810	0	0	0	0	0
Scorpaenidae	*Scorpaenodes albaiensis*	E00532	4039	5	810	0	0	0	0	615
Scorpaenidae	*Scorpaenodes guamensis*	E00870	6637	9	0	765	0	0	0	645

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Scorpaenidae	*Scorpaenopsis longispina*	E00903	7186	9	0	0	0	0	0	645
Scorpaenidae	*Scorpaenopsis oxycephala*	E00581	5118	7	810	0	0	0	0	645
Scorpaenidae	*Sebastapistes cyanostigma*	E00888	8326	10	810	765	0	0	0	624
Scorpaenidae	*Taenianotus triacanthus*	E00866	8147	10	807	765	0	0	0	645
Sebastidae	*Adelosebastes latens*	E00066	2246	3	0	765	0	0	0	0
Sebastidae	*Helicolenus dactylopterus*	E00044	9920	12	0	624	0	0	459	615
Sebastidae	*Sebastes aurora*	E00349	8679	10	822	0	0	0	720	645
Sebastidae	*Sebastes diploproa*	E00432	6421	8	810	0	0	0	720	630
Sebastidae	*Sebastes fasciatus*	G01482	8330	10	708	708	1377	0	0	0
Sebastidae	*Sebastes jordani*	E00350	6619	9	810	0	0	0	0	645
Sebastidae	*Sebastes paucispinis*	E00354	6853	9	810	0	0	0	720	0
Sebastidae	*Sebastes ruberrimus*	N28709	6206	8	708	708	0	0	0	0
Sebastidae	*Sebastolobus alascanus*	E00417	12929	16	810	708	1398	0	0	624
Serranidae	*Aethaloperca rogaa*	E01079	6350	8	810	0	0	0	0	642
Serranidae	*Anthias nicholsi*	E00447	6801	6	816	0	1464	0	0	624
Serranidae	*Aporops bilinearis*	E00531	7661	10	0	756	0	0	0	633
Serranidae	*Baldwinella aureorubens*	G01220	8097	10	693	708	1359	0	0	0
Serranidae	*Baldwinella vivana*	E00338	3660	5	0	0	0	0	0	0
Serranidae	*Centropristis striata*	E00163	8944	11	0	756	1464	0	0	645
Serranidae	*Cephalopholis argus*	E00868	14648	18	810	708	1398	0	0	621
Serranidae	*Cephalopholis fulva*	E00771	5807	7	810	0	0	0	0	555
Serranidae	*Cephalopholis miniata*	E00838	9601	12	0	762	0	0	0	645
Serranidae	*Diplectrum bivittatum*	E01008	4699	6	810	0	0	0	0	0
Serranidae	*Diplectrum formosum*	E01002	8832	10	810	765	0	0	0	0
Serranidae	*Epinephelus maculatus*	E00549	12180	14	810	678	1464	0	746	645
Serranidae	*Epinephelus merra*	E00552	8076	10	810	0	0	0	0	0
Serranidae	*Grammistes sexlineatus*	E00900	15699	17	825	765	1464	0	0	644
Serranidae	*Grammistops ocellatus*	E00571	6588	8	0	0	0	0	0	645
Serranidae	*Hypoplectrus puella*	E00505	12795	16	705	708	1398	0	0	630
Serranidae	*Hyporthodus flavolimbatus*	E00627	5022	7	810	0	0	0	0	618

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Serranidae	*Liopropoma mowbrayi*	E00307	4911	6	810	0	0	0	0	645
Serranidae	*Liopropoma rubre*	E00306	13426	14	825	0	1464	0	0	641
Serranidae	*Mycteroperca bonaci microlepis*	E00311	14036	17	708	696	1398	0	0	636
Serranidae	*Odontanthias chrysostictus*	G01327	10158	10	825	0	1464	0	756	614
Serranidae	*Paralabrax nebulifer*	E00325	12094	15	810	708	1398	0	0	588
Serranidae	*Pronotogrammus martinicensis*	E00636	3713	4	0	0	0	0	0	606
Serranidae	*Pseudanthias pascalus*	G01452	9024	11	705	708	1398	0	0	0
Serranidae	*Pseudanthias squamipinnis*	E00860	6941	8	810	0	0	0	0	0
Serranidae	*Pseudogramma polyacantha*	E00852	7643	10	810	765	0	0	0	645
Serranidae	*Rypticus saponaceus*	E00764	15840	19	810	681	1398	0	444	636
Serranidae	*Rypticus subbifrenatus*	E00347	6320	7	0	0	1436	0	0	0
Serranidae	*Serranus baldwini*	E00322	14886	16	825	0	1464	0	758	642
Serranidae	*Serranus notospilus*	E00337	5719	7	810	0	0	0	0	0
Serranidae	*Serranus phoebe*	E00336	6229	8	810	0	0	0	0	615
Serranidae	*Serranus tigrinus*	G01486	8954	11	702	657	1398	0	0	0
Setarchidae	*Setarches guentheri*	E01035	5731	8	810	765	0	0	0	645
Siganidae	*Siganus argenteus*	E00940	7215	10	810	752	0	0	0	645
Siganidae	*Siganus punctatus*	E00958	3704	4	825	0	1449	0	0	0
Siganidae	*Siganus spinus*	N29369	8207	10	708	588	1398	0	0	0
Siganidae	*Siganus stellatus*	G01488	6854	9	810	752	0	0	0	0
Siganidae	*Siganus vulpinus*	E00090	11306	14	825	708	1464	0	852	0
Sillaginidae	*Sillago chondropus*	N29390	6780	9	645	591	1047	0	0	0
Sillaginidae	*Sillago sihama*	E00824	13627	15	825	597	1455	0	815	636
Sinipercidae	*Coreoperca whiteheadi*	G01264	8180	8	825	0	1464	0	0	0
Sinipercidae	*Siniperca chuatsi*	E01136	15198	17	825	612	1464	0	513	645
Sinipercidae	*Siniperca scherzeri*	G01489	8368	7	825	0	1464	0	0	0
Soleidae	*Aseraggodes heemstrai*	E00582	9255	10	810	0	1287	0	717	645
Soleidae	*Aseraggodes kobensis*	E00075	12391	14	615	765	1377	0	588	645
Soleidae	*Brachirus annularis*	E01182	5846	7	810	0	0	0	741	642
Soleidae	*Heteromycteris japonicus*	E00079	14809	17	627	765	1446	0	741	642

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Soleidae	*Microchirus frechkopi*	E01175	5082	6	813	0	0	0	735	645
Soleidae	*Pegusa lascaris*	E01183	8261	10	789	0	1446	0	783	642
Soleidae	*Pseudaesopia japonica*	E00081	10067	11	792	0	1431	0	738	645
Soleidae	*Solea solea*	E00054	7675	8	0	0	0	0	852	645
Soleidae	*Soleichthys heterorhinos*	E00943	10673	11	813	0	1383	0	753	645
Sparidae	*Acanthopagrus catenula*	E00953	10468	14	810	726	0	0	0	630
Sparidae	*Acanthopagrus latus*	M01638	3048	4	792	0	0	0	0	0
Sparidae	*Archosargus probatocephalus*	E00249	8388	10	810	0	0	0	0	642
Sparidae	*Argyrops spinifer*	M01668	2629	3	781	0	1455	0	0	0
Sparidae	*Argyrozona argyrozona*	E00802	9618	12	810	0	0	0	0	645
Sparidae	*Boops boops*	M01640	3246	3	0	0	1455	0	0	0
Sparidae	*Boopsoidea inornata*	M01639	3951	4	0	0	1455	0	0	0
Sparidae	*Calamus calamus*	N29934	7496	9	708	708	1398	0	0	0
Sparidae	*Calamus nodosus*	M01641	3290	4	791	0	0	0	0	0
Sparidae	*Calamus penna*	E00762	7629	10	798	0	0	0	0	645
Sparidae	*Cheimerius nufar*	M01642	3243	3	0	0	1455	0	0	0
Sparidae	*Chrysoblephus laticeps*	M01644	3594	4	792	0	1452	0	0	0
Sparidae	*Crenidens crenidens*	M01645	4737	5	792	0	1455	0	0	0
Sparidae	*Dentex dentex*	M01646	4731	5	780	0	1454	0	0	0
Sparidae	*Diplodus annularis*	M01647	4730	5	780	0	1454	0	0	0
Sparidae	*Diplodus bermudensis*	M01648	3953	4	0	0	1455	0	0	0
Sparidae	*Diplodus capensis*	E00807	5192	7	810	0	0	0	0	618
Sparidae	*Lagodon rhomboides*	G01346	10209	12	708	708	1455	0	0	0
Sparidae	*Lithognathus mormyrus*	M01649	4731	5	780	0	1455	0	0	0
Sparidae	*Oblada melanura*	M01650	3249	3	0	0	1455	0	0	0
Sparidae	*Pachymetopon grande*	M01651	3549	4	780	0	1455	0	0	0
Sparidae	*Pagellus affinis*	M01652	3072	4	792	0	0	0	0	0
Sparidae	*Pagellus erythrinus*	M01653	4029	4	780	0	1455	0	0	0
Sparidae	*Pagrus pagrus*	E00514	12441	15	825	708	1431	0	459	639
Sparidae	*Porcostoma dentata*	M01654	4728	5	780	0	1455	0	0	0

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Sparidae	*Rhabdosargus haffara*	M01655	2151	3	792	0	0	0	0	0
Sparidae	*Sarpa salpa*	E00806	12445	15	825	0	1455	0	459	645
Sparidae	*Sparidentex hasta*	M01657	4746	5	792	0	1455	0	0	0
Sparidae	*Sparus aurata*	M01658	3954	4	0	0	1455	0	0	0
Sparidae	*Spondyliosoma cantharus*	M01659	3257	4	792	0	0	0	0	0
Sparidae	*Stenotomus chrysops*	E00246	12458	15	801	752	1455	0	0	645
Sparidae	*Virididentex acromegalus*	M01660	4676	5	795	0	1455	0	0	0
Sphyraenidae	*Sphyraena argentea*	E00230	8319	10	786	756	1053	0	0	645
Sphyraenidae	*Sphyraena barracuda*	E00836	19387	22	807	708	1398	1206	750	630
Sphyraenidae	*Sphyraena japonica*	N30022	5263	7	657	591	1266	0	0	0
Sphyraenidae	*Sphyraena jello*	N30023	4747	6	657	591	1287	0	0	0
Sphyraenidae	*Sphyraena putnamae*	E00955	13026	14	810	732	1446	0	732	645
Sphyraenidae	*Sphyraena sphyraena*	E01143	7520	8	819	0	0	0	738	645
Stichaeidae	*Bryozoichthys marjorius*	E00442	7041	9	0	756	0	0	0	645
Stichaeidae	*Cebidichthys violaceus*	N30217	6500	9	642	597	0	0	0	0
Stichaeidae	*Leptoclinus maculatus*	E00323	5549	7	810	0	0	0	0	0
Stichaeidae	*Lumpenus fabricii*	E00361	3593	5	810	0	0	0	0	0
Stichaeidae	*Lumpenus lampretaeformis*	E00371	5472	7	0	0	0	0	0	645
Stichaeidae	*Poroclinus rothrocki*	E00431	5685	7	810	0	0	0	0	0
Stromateidae	*Peprilus burti*	E00600	5597	7	810	0	0	0	0	645
Stromateidae	*Peprilus paru*	E00622	7448	10	810	0	0	0	0	645
Stromateidae	*Peprilus simillimus*	E00136	10724	12	807	756	0	0	0	618
Stromateidae	*Peprilus triacanthus*	N30548	8492	10	639	708	1398	0	0	0
Symphysanodontidae	*Symphysanodon typus*	M01725	1508	2	822	0	0	0	0	0
Synanceiidae	*Synanceia verrucosa*	E00867	10214	13	810	765	0	0	852	645
Synbranchidae	*Monopterus albus*	E01134	14200	15	708	630	1464	0	756	642
Syngnathidae	*Corythoichthys intestinalis*	E00734	5411	6	795	0	0	0	0	0
Syngnathidae	*Corythoichthys schultzi*	E00829	4587	5	0	0	0	0	0	0
Syngnathidae	*Doryrhamphus excisus*	E00915	8801	10	0	756	1464	0	447	0
Syngnathidae	*Hippocampus erectus*	N30799	2880	4	0	708	765	0	0	0

Table A4b. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	PLAGL2	PTCHD1	RAG1	RAG2	RH	RIPK4
Syngnathidae	*Syngnathus fuscus*	E00792	6471	8	0	708	0	0	0	0
Syngnathidae	*Syngnathus leptorhynchus*	N30969	2247	3	0	642	0	0	0	0
Syngnathidae	*Syngnathus louisianae*	E00821	4535	5	0	765	0	0	0	0
Syngnathidae	*Syngnathus scovelli*	E00346	4744	6	0	0	0	0	0	0
Telmatherinidae	*Marosatherina ladigesi*	E00406	9346	12	810	753	0	0	0	642
Terapontidae	*Hephaestus fuliginosus*	G01318	10031	11	654	612	1437	954	0	0
Terapontidae	*Scortum barcoo*	G01480	10071	11	654	612	1437	954	0	0
Terapontidae	*Terapon jarbua*	E00826	14339	16	825	594	1437	954	0	645
Tetraodontidae	*Arothron hispidus*	E00985	8771	8	0	765	1419	0	0	645
Tetraodontidae	*Arothron nigropunctatus*	N31143	7811	9	0	708	1398	0	0	0
Tetraodontidae	*Canthigaster bennetti*	E00530	8390	9	810	0	1419	0	0	0
Tetraodontidae	*Canthigaster jactator*	N31165	6260	7	0	708	1398	0	0	0
Tetraodontidae	*Canthigaster valentini*	E00853	7767	8	0	747	1419	0	0	630
Tetraodontidae	*Lagocephalus laevigatus*	E00601	8160	8	0	0	1419	0	759	0
Tetraodontidae	*Sphoeroides maculatus*	E00339	4428	5	0	0	0	0	0	0
Tetraodontidae	*Sphoeroides nephelus*	N01739	6070	7	0	708	1398	0	0	0
Tetraodontidae	*Takifugu rubripes*	E00460	20045	21	825	708	1464	1206	810	645
Tetraodontidae	*Tetractenos hamiltoni*	E00383	2976	4	0	0	0	0	0	0
Tetraodontidae	*Tetraodon fluviatilis*	E00374	4553	5	0	0	1287	0	0	0
Tetraodontidae	*Tetraodon miurus*	N01740	8550	10	705	708	1398	0	0	0
Tetraodontidae	*Tetraodon nigroviridis*	G01513	17489	18	708	708	1464	1206	927	644
Tetrarogidae	*Coccotropsis gymnoderma*	E00801	6200	8	0	753	0	0	0	0
Toxotidae	*Toxotes chatareus*	E01139	10242	10	813	0	1455	0	747	645
Toxotidae	*Toxotes jaculatrix*	E01155	11428	14	810	708	1416	0	450	645
Trachichthyidae	*Hoplostethus occidentalis atlanticus*	E01018	11766	14	708	705	1395	0	0	645
Triacanthidae	*Triacanthus biaculeatus*	G01531	11323	12	708	708	1287	0	0	0
Triacanthodidae	*Halimochirurgus alcocki*	N31459	6920	9	651	585	1293	0	0	0
Triacanthodidae	*Triacanthodes anomalus*	E00382	12061	13	707	708	1458	0	647	0
Triacanthodidae	*Triacanthodes ethiops*	G01532	6829	7	0	0	645	0	743	0
Trichiuridae	*Aphanopus carbo*	E00274	5425	7	810	0	0	0	510	0

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Trichiuridae	*Assurger anzac*	G01210	9581	12	705	669	1311	0	0	0
Trichiuridae	*Benthodesmus simonyi*	E00475	4383	6	801	756	0	0	0	0
Trichiuridae	*Evoxymetopon taeniatus*	E00650	3573	5	810	756	0	0	0	0
Trichiuridae	*Lepidopus altifrons*	E00474	6788	9	810	756	0	0	0	0
Trichiuridae	*Trichiurus lepturus*	E00596	12574	14	825	756	1455	1129	819	645
Trichodontidae	*Trichodon trichodon*	N31563	7181	9	639	612	1377	0	0	0
Triglidae	*Bellator militaris*	E01026	4452	6	810	765	0	0	0	645
Triglidae	*Prionotus carolinus*	E00340	7371	9	810	0	0	0	0	618
Triglidae	*Prionotus evolans*	E01021	4575	6	693	765	0	0	0	603
Triglidae	*Prionotus stephanophrys*	E00328	6883	9	0	0	0	0	0	585
Triglidae	*Pterygotrigla hemisticta*	N31939	4770	6	639	591	1275	0	0	0
Triodontidae	*Triodon macropterus*	N31959	7201	9	654	612	1374	0	0	0
Tripterygiidae	*Enneanectes altivelis*	E00315	5180	7	0	0	0	0	0	630
Tripterygiidae	*Enneanectes boehlkei*	E00305	8688	11	810	699	0	0	0	0
Tripterygiidae	*Enneapterygius abeli*	E00896	2369	3	0	0	0	0	0	0
Tripterygiidae	*Enneapterygius gruschkai*	E00916	3832	5	0	0	0	0	0	630
Tripterygiidae	*Helcogramma ellioti sp*	E00331	9671	11	0	705	1455	0	0	630
Tripterygiidae	*Helcogramma fuscopinna*	E00885	2098	3	0	0	0	0	0	645
Uranoscopidae	*Astroscopus ygraecum*	E01028	11671	14	810	704	1398	0	0	645
Uranoscopidae	*Kathetostoma albigutta*	E01022	2118	3	0	0	0	0	0	645
Uranoscopidae	*Kathetostoma averruncus*	E00324	11393	14	810	705	1290	0	0	618
Uranoscopidae	*Uranoscopus sulphureus*	E00538	5752	7	810	0	0	0	753	633
Xiphiidae	*Xiphias gladius*	E01151	16644	17	810	708	1446	1206	818	582
Zanclidae	*Zanclus cornutus*	E00894	18204	20	825	749	1398	846	0	639
Zaproridae	*Zaprora silenus*	E00362	6043	8	810	0	0	0	0	0
Zenarchopteridae	*Dermogenys collettei*	G01275	6851	8	0	708	1398	0	0	0
Zenarchopteridae	*Zenarchopterus dispar*	E00541	5209	6	0	0	0	0	0	630
Zoarcidae	*Bothrocara brunneum*	E00357	6304	8	810	0	0	0	0	618
Zoarcidae	*Bothrocara hollandi*	N01721	4677	6	708	708	0	0	0	0
Zoarcidae	*Eucryphycus californicus*	E00327	5531	7	0	0	0	0	0	645

Table A4b. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**PLAGL2**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**
Zoarcidae	*Lycenchelys crotalinus*	E00425	4583	6	0	0	0	0	0	621
Zoarcidae	*Lycodapus mandibularis*	E00355	8784	11	810	0	0	0	852	576
Zoarcidae	*Lycodes brevipes*	E00413	4381	5	0	0	1455	0	0	618
Zoarcidae	*Lycodes diapterus*	G01364	8790	11	681	708	1290	0	0	0
Zoarcidae	*Lycodes terraenovae*	E00675	15952	18	825	765	0	0	927	645
Zoarcidae	*Melanostigma pammelas*	E00365	6342	8	810	0	0	0	0	645
Zoarcidae	*Zoarces americanus viviparus*	E00370	5571	8	0	705	0	0	0	0

TABLE A4c. Taxon sampling for the percomorph dataset included 1231 taxa and sequence data for 23 genes. The dataset is comprised of sequences for 1180 percomorph species from previous studies (e.g. Li *et al.* 2007; Li *et al.* 2008; Li *et al.* 2010; Li *et al.* 2011; Betancur-R *et al.* 2013b; Broughton *et al.* 2013; Near *et al.* 2013) or public databases, plus newly generated sequences for the 51 additional taxa for this study. The matrix is presented in four parts to show presence of sequence data for the 23 genes. (a.) ENC1, FICD, GLYT, KIAA1239, MYH6, and PANX2; (b.) PLAGL2, PTCHD1, RAG1, RAG2, RH, and RIPK4; (c.) SH3PX3, SIDKEY, SREB2, SVEP1, TBR1, and VCPIP; (d.) ZIC1, COI, CYT *B*, 16S, and HOX.

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Acanthuridae	*Acanthurus bahianus*	E00005	11794	14	705	1257	945	0	762	0
Acanthuridae	*Acanthurus guttatus*	E00709	7379	8	0	1257	0	825	0	0
Acanthuridae	*Acanthurus leucosternon*	E00880	14819	16	705	0	972	825	762	765
Acanthuridae	*Acanthurus lineatus*	E00889	11234	12	705	1260	0	825	762	657
Acanthuridae	*Acanthurus triostegus*	E00711	11027	13	705	1257	0	825	0	0
Acanthuridae	*Ctenochaetus striatus*	E00982	6461	8	0	0	0	0	0	0
Acanthuridae	*Ctenochaetus strigosus*	E00050	9642	12	705	0	951	0	762	0
Acanthuridae	*Ctenochaetus truncatus*	E00854	6572	9	669	0	0	0	762	0
Acanthuridae	*Naso brevirostris*	E00918	11979	15	705	0	0	732	690	0
Acanthuridae	*Naso lituratus*	G01514	9769	12	693	0	0	0	681	0
Acanthuridae	*Naso unicornis*	E00701	6934	9	0	1260	0	717	0	0
Acanthuridae	*Paracanthurus hepatus*	E00002	9321	11	0	1257	0	0	762	0
Acanthuridae	*Zebrasoma flavescens*	E00730	9002	10	705	1260	0	825	0	0
Acanthuridae	*Zebrasoma rostratum*	N01742	6780	8	0	0	0	0	762	0
Acanthuridae	*Zebrasoma scopas*	E00859	12917	16	693	0	0	825	762	747
Acanthuridae	*Zebrasoma velifer*	E00029	5029	6	0	1230	0	0	762	0
Achiridae	*Achirus lineatus*	E00605	13596	16	693	0	0	825	0	753
Achiridae	*Gymnachirus melas*	E00609	14260	16	660	1308	879	810	0	0
Achiridae	*Gymnachirus texae*	E00630	9146	10	693	1047	0	813	0	0
Achiridae	*Hypoclinemus sp*	E01162	6483	7	696	1287	0	0	0	0
Achiridae	*Trinectes maculatus*	E00046	11078	11	705	1269	0	0	0	0
Achiropsettidae	*Mancopsetta maculata*	E01169	6861	8	705	0	0	0	0	0
Achiropsettidae	*Neoachiropsetta milfordi*	E01170	6200	8	705	0	0	0	0	0
Acropomatidae	*Acropoma japonicum*	G01188	12298	14	705	1287	960	0	738	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Acropomatidae	*Malakichthys elegans*	N01922	6894	9	705	0	0	0	711	0
Acropomatidae	*Synagrops bellus*	E01125	11059	13	705	1236	0	825	0	0
Acropomatidae	*Synagrops spinosus*	E01123	6676	7	705	1260	0	0	0	0
Adrianichthyidae	*Oryzias latipes*	G01408	18061	19	705	1308	987	0	762	756
Agonidae	*Aspidophoroides monopterygius*	N01986	7472	9	692	0	0	0	762	0
Agonidae	*Bathyagonus alascanus*	E00268	5458	7	0	0	0	0	0	0
Agonidae	*Bathyagonus pentacanthus*	E00430	5127	7	0	0	0	0	0	0
Agonidae	*Hypsagonus quadricornis*	E00269	7151	9	705	1260	0	0	0	0
Agonidae	*Sarritor frenatus*	E00264	4738	6	0	0	0	0	762	0
Agonidae	*Sarritor leptorhynchus*	E00254	5516	7	378	1257	0	819	0	0
Agonidae	*Stellerina xyosterna*	N02010	6750	8	684	0	0	0	741	0
Agonidae	*Xeneretmus latifrons*	E00278	6400	8	0	1233	0	0	0	0
Ambassidae	*Ambassis agrammus*	G01196	8877	9	0	711	978	0	0	0
Ambassidae	*Ambassis interrupta*	E01100	10212	10	0	0	987	0	0	0
Ambassidae	*Ambassis urotaenia*	G01197	8268	10	699	0	897	0	762	0
Ambassidae	*Parambassis ranga*	N01735	7892	10	705	0	882	0	693	0
Ammodytidae	*Ammodytes dubius*	N02375	6015	7	705	0	0	0	762	0
Ammodytidae	*Ammodytes hexapterus*	E00414	15128	17	672	1281	944	0	762	0
Anabantidae	*Ctenopoma acutirostre kingsleyae*	E01141	14536	15	705	1305	966	0	720	0
Anabantidae	*Microctenopoma nanum*	G01373	12070	13	705	0	969	0	750	0
Anarhichadidae	*Anarhichas denticulatus*	E00787	8620	9	0	0	0	0	0	669
Anarhichadidae	*Anarhichas orientalis lupus*	E00117	15266	17	705	0	951	0	762	0
Anarhichadidae	*Anarrhichthys ocellatus*	E00119	7893	10	705	0	0	0	0	0
Anoplopomatidae	*Anoplopoma fimbria*	E00423	15741	18	705	1260	974	687	761	764
Antennariidae	*Antennatus coccineus*	E01092	15457	17	696	1257	0	0	747	723
Antennariidae	*Antennatus nummifer*	E00587	9899	13	672	1257	0	0	0	729
Antennariidae	*Fowlerichthys radiosus*	E01124	4779	6	0	1284	0	0	0	0
Antennariidae	*Histiophryne cryptacanthus*	G01326	9853	12	696	0	876	0	753	0
Antennariidae	*Histrio histrio*	E00643	7964	9	705	1011	0	0	762	0
Aphyonidae	*Barathronus maculatus*	N02779	7479	9	0	0	987	0	750	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Aplocheilidae	*Pachypanchax playfairii*	G01414	7524	9	696	0	945	0	762	0
Aplodactylidae	*Aplodactylus arctidens*	M01536	4728	5	705	0	0	0	0	0
Aplodactylidae	*Aplodactylus etheridgii*	M01537	4710	5	705	0	0	0	0	0
Apogonidae	*Apogon campbelli*	E01069	9380	10	705	1071	0	0	0	0
Apogonidae	*Archamia biguttata*	E00522	8166	11	705	0	0	0	0	0
Apogonidae	*Astrapogon puncticulatus*	E00109	7227	9	0	1257	0	825	762	0
Apogonidae	*Astrapogon stellatus*	N03004	7517	9	681	0	951	0	0	0
Apogonidae	*Cercamia eremia*	E00546	6660	9	0	0	0	0	762	0
Apogonidae	*Cheilodipterus isostigmus*	E00528	8272	10	0	1257	0	0	0	0
Apogonidae	*Cheilodipterus quinquelineatus*	G01247	9762	12	705	0	960	0	762	0
Apogonidae	*Fowleria aurita*	E01090	8780	11	699	0	0	0	0	0
Apogonidae	*Gymnapogon urospilotus*	E00539	5107	7	696	0	0	0	0	0
Apogonidae	*Nectamia bandanensis*	E01040	8860	11	705	1260	0	651	0	0
Apogonidae	*Nectamia fusca*	E00732	8861	10	0	1257	0	0	0	0
Apogonidae	*Ostorhinchus cookii*	E01087	6400	8	0	0	0	0	0	0
Apogonidae	*Ostorhinchus lateralis*	G01203	8273	10	705	0	957	0	762	0
Apogonidae	*Phaeoptyx pigmentaria*	E00506	12882	15	680	1254	951	0	762	0
Apogonidae	*Pristiapogon exostigma*	E00702	8433	11	0	1257	0	0	762	0
Apogonidae	*Pseudamia gelatinosa*	E00568	7391	9	705	1257	0	0	0	0
Apogonidae	*Pterapogon kauderni*	E00190	6329	8	705	1257	0	0	0	0
Apogonidae	*Rhabdamia cypselura*	E01095	6022	7	0	1257	0	0	0	0
Apogonidae	*Sphaeramia orbicularis*	N03178	8446	10	705	0	930	0	762	0
Aracanidae	*Anoplocapros lenticularis*	G01533	6886	7	0	0	0	0	0	0
Aracanidae	*Aracana aurita*	G01205	10032	12	705	0	954	0	762	0
Ariommatidae	*Ariomma bondi*	E01126	7867	9	705	1233	0	0	0	0
Ariommatidae	*Ariomma melanum*	E00665	9682	12	696	1257	0	0	0	744
Arripidae	*Arripis georgianus*	M01539	4794	5	0	1251	0	0	0	0
Arripidae	*Arripis trutta*	M01540	3327	4	0	1251	0	0	0	0
Arripidae	*Arripis truttacea*	M01541	4659	5	705	1251	0	0	0	0
Artedidraconidae	*Artedidraco orianae*	G01525	6898	8	618	0	0	0	699	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Artedidraconidae	*Pogonophryne barsukovi*	E00158	12842	14	657	1308	0	0	762	0
Atherinidae	*Atherinomorus lacunosus*	E00548	15021	18	705	1260	957	0	762	0
Atherinidae	*Atherinomorus stipes*	E00115	13436	16	705	1260	0	813	762	684
Atherinidae	*Atherinomorus vaigiensis*	E00181	7813	10	705	0	0	0	762	0
Atherinidae	*Craterocephalus honoriae*	E00180	8597	10	0	1254	0	804	759	762
Atherinopsidae	*Atherinopsis californiensis*	E00121	5600	7	705	0	0	0	0	0
Atherinopsidae	*Labidesthes sicculus*	E01112	14372	17	705	1242	987	0	762	0
Atherinopsidae	*Membras martinica*	E00170	7275	9	696	0	0	0	0	0
Atherinopsidae	*Menidia beryllina*	E00174	10176	13	705	0	0	0	762	0
Atherinopsidae	*Menidia menidia*	E00167	12560	13	705	0	0	0	762	0
Atherinopsidae	*Menidia peninsulae*	N03847	5694	7	696	0	0	0	762	0
Atherinopsidae	*Odontesthes argentinensis*	E00393	5125	7	0	0	0	0	0	720
Atherinopsidae	*Odontesthes bonariensis*	E00396	9234	11	705	870	0	0	0	0
Atherinopsidae	*Odontesthes humensis*	E00394	5561	7	0	0	0	0	0	0
Atherinopsidae	*Odontesthes retropinnis*	E00395	4826	6	0	0	0	0	0	0
Atherinopsidae	*Poblana ferdebueni*	N01733	5919	7	705	0	0	0	762	0
Aulorhynchidae	*Aulorhynchus flavidus*	G01217	11313	12	705	0	962	0	762	0
Aulostomidae	*Aulostomus chinensis*	E00871	15665	19	705	0	966	780	756	705
Aulostomidae	*Aulostomus maculatus*	E00293	13058	16	679	0	951	0	741	0
Badidae	*Badis pyema*	N03996	7191	9	699	0	879	0	690	0
Badidae	*Dario dario*	N04003	5626	7	0	0	0	0	693	0
Balistidae	*Abalistes stellatus*	E00936	14580	18	705	1257	930	0	762	711
Balistidae	*Balistapus undulatus*	E00743	12372	14	672	0	0	0	0	0
Balistidae	*Balistes capriscus*	E00591	13798	17	690	0	0	0	762	0
Balistidae	*Balistes vetula*	E00755	13640	15	705	1257	947	0	0	0
Balistidae	*Balistoides conspicillum*	E00373	9468	10	657	0	0	0	0	0
Balistidae	*Canthidermis maculata*	E00378	9887	10	705	1257	0	0	0	0
Balistidae	*Melichthys indicus*	E00919	7484	10	696	0	0	825	762	669
Balistidae	*Melichthys niger*	E00922	8652	11	696	0	0	0	762	0
Balistidae	*Pseudobalistes flavimarginatus*	N04225	6715	8	705	0	0	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Balistidae	*Pseudobalistes fuscus*	E00524	4607	6	705	0	0	0	0	0
Balistidae	*Rhinecanthus aculeatus*	E00735	9140	10	0	0	0	0	0	0
Balistidae	*Rhinecanthus assasi*	E00381	5259	6	0	0	0	0	0	0
Balistidae	*Rhinecanthus verrucosus*	N04231	7465	9	705	0	0	0	762	0
Balistidae	*Sufflamen chrysopterum*	E00551	11210	14	703	1245	0	0	0	0
Balistidae	*Sufflamen fraenatum*	E00935	9148	10	705	1239	0	0	753	0
Balistidae	*Xanthichthys auromarginatus*	E00380	11574	12	696	1260	0	0	0	0
Balistidae	*Xanthichthys ringens*	N04239	7595	9	705	0	918	0	0	0
Banjosidae	*Banjos banjos*	M01542	4794	5	0	1251	0	0	0	0
Banjosidae	*Banjos banjos*	N01542	6206	8	0	0	0	0	711	0
Bathyclupeidae	*Bathyclupea argentea*	M01543	2787	4	705	0	0	0	0	0
Bathydraconidae	*Gymnodraco acuticeps*	E00155	12486	14	705	0	0	0	759	0
Bathydraconidae	*Parachaenichthys charcoti*	E00157	15082	17	696	0	0	756	762	762
Bathymasteridae	*Bathymaster caeruleofasciatus*	E00191	7525	10	705	0	0	0	762	669
Bathymasteridae	*Bathymaster signatus*	E00420	12500	16	690	1256	0	0	762	765
Bathymasteridae	*Rathbunella hypoplecta*	E00128	12273	15	705	0	0	0	753	0
Batrachoididae	*Batrachoides pacifici*	N04533	6761	8	693	0	948	0	756	0
Batrachoididae	*Opsanus beta*	E00698	11611	14	705	0	945	0	762	0
Batrachoididae	*Opsanus pardus*	E00513	11301	14	705	0	954	0	762	735
Batrachoididae	*Opsanus tau*	E00040	4773	6	0	861	0	0	0	0
Batrachoididae	*Porichthys notatus*	E00058	13187	16	705	861	950	0	762	0
Batrachoididae	*Porichthys plectrodon*	E00590	13538	16	705	1257	987	792	762	741
Batrachoididae	*Sanopus sp*	E00009	4902	6	0	861	0	0	762	0
Bedotiidae	*Rheocles wrightae*	G01467	11051	13	699	0	978	0	762	0
Belonidae	*Ablennes hians*	E00162	11443	13	705	0	0	0	0	0
Belonidae	*Platybelone argalus*	E00114	12856	15	678	1260	957	0	699	0
Belonidae	*Strongylura notata*	E00110	15115	19	705	0	966	732	761	570
Belonidae	*Tylosurus crocodilus*	E01051	7580	10	705	0	0	0	0	0
Belonidae	*Xenentodon cancila*	G01508	11377	14	705	0	963	0	762	0
Bembridae	*Bembras japonica*	N01723	6876	9	690	0	0	0	711	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Bembropidae	*Bembrops anatirostris*	E01120	10273	13	693	0	0	0	762	0
Bembropidae	*Bembrops gobioides*	E01128	8878	11	693	0	0	0	762	0
Blenniidae	*Alticus arnoldorum*	E00989	2775	4	0	0	0	0	762	0
Blenniidae	*Atrosalarias fuscus*	E00525	2877	4	0	0	0	0	0	0
Blenniidae	*Blenniella chrysospilos paula*	E00986	4186	5	0	0	0	0	762	0
Blenniidae	*Blenniella cyanostigma*	E00715	7419	9	0	1308	0	0	0	0
Blenniidae	*Blenniella paula*	E00979	7982	10	0	1245	0	0	762	0
Blenniidae	*Cirripectes castaneus*	E00892	8002	10	672	1251	0	0	0	0
Blenniidae	*Cirripectes filamentosus*	E00893	5912	7	693	1260	0	0	0	0
Blenniidae	*Cirripectes quagga*	E00330	4362	5	0	1257	0	0	0	0
Blenniidae	*Cirripectes stigmaticus*	E00520	4037	6	705	0	0	0	0	0
Blenniidae	*Ecsenius bicolor*	E00984	5909	8	0	0	0	0	753	0
Blenniidae	*Ecsenius midas*	E00934	3749	5	0	0	0	0	0	0
Blenniidae	*Ecsenius opsifrontalis*	E00723	5497	7	660	0	0	0	0	0
Blenniidae	*Ecsenius pardus*	E00523	4285	5	0	1251	0	0	0	0
Blenniidae	*Enchelyurus flavipes*	N04786	6887	9	459	0	873	0	693	0
Blenniidae	*Entomacrodus nigricans*	E00297	9132	11	684	0	957	0	738	0
Blenniidae	*Entomacrodus niuafoouensis*	E00980	6091	8	0	0	0	0	762	0
Blenniidae	*Entomacrodus striatus*	E00987	5295	7	0	1200	0	0	0	654
Blenniidae	*Hypleurochilus sp*	E00298	5653	7	0	0	0	0	0	0
Blenniidae	*Hypsoblennius hentz*	E00289	7330	9	693	0	0	0	750	0
Blenniidae	*Istiblennius dussumieri*	E00556	4755	6	0	0	0	0	0	0
Blenniidae	*Meiacanthus oualanensis grammistes*	E00526	9615	12	705	0	933	0	756	0
Blenniidae	*Nannosalarias nativitatis*	E00521	6717	8	705	1251	0	0	0	0
Blenniidae	*Ophioblennius atlanticus*	E00296	11932	15	705	0	906	0	755	0
Blenniidae	*Petroscirtes mitratus*	E00909	5741	8	0	0	0	0	762	0
Blenniidae	*Plagiotremus rhinorhynchos*	E00586	4112	5	0	0	0	0	0	0
Blenniidae	*Plagiotremus tapeinosoma*	E00540	4423	6	696	0	0	0	0	0
Blenniidae	*Praealticus caesius*	E00329	5179	6	0	0	0	0	0	0
Blenniidae	*Salarias fasciatus*	E00988	12606	14	684	0	0	0	762	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Blenniidae	*Stanulus sp*	E00332	3369	4	0	1257	0	0	0	0
Bothidae	*Arnoglossus blachei*	E01160	6253	7	681	855	0	0	0	0
Bothidae	*Arnoglossus imperialis*	E01163	7399	8	705	1281	0	0	0	0
Bothidae	*Asterorhombus cocosensis*	E00904	10399	11	705	1308	0	0	0	0
Bothidae	*Bothus lunatus*	E00007	8248	9	684	0	0	0	0	0
Bothidae	*Bothus robinsi*	E00038	6724	7	0	0	0	0	0	0
Bothidae	*Chascanopsetta lugubris*	E01181	5982	7	651	1284	0	0	0	0
Bothidae	*Laeops kitaharae*	E00082	7794	8	0	0	0	0	0	0
Bothidae	*Monolene sp*	E01172	3326	3	0	858	0	0	0	0
Bothidae	*Psettina tosana*	E00083	7617	8	663	0	0	0	0	0
Bothidae	*Trichopsetta ventralis*	E00599	9704	10	693	1308	0	0	0	726
Bovichtidae	*Bovichtus diacanthus*	G01229	12547	13	702	0	987	0	759	0
Bovichtidae	*Cottoperca trigloides*	G01267	5753	6	660	0	0	0	696	0
Bramidae	*Brama brama*	E00970	11377	13	690	1281	0	0	762	765
Bramidae	*Brama japonica*	N05217	8586	10	705	0	987	0	762	0
Bramidae	*Pteraclis aesticola*	N05223	7106	9	672	0	906	0	711	0
Bramidae	*Pterycombus brama*	E00996	9728	12	690	1260	0	801	762	765
Bramidae	*Taractes asper*	N05227	8588	10	705	0	987	0	762	0
Bramidae	*Taractichthys longipinnis*	E00684	8997	11	0	1257	0	0	693	759
Bythitidae	*Bidenichthys capensis*	E00794	7231	9	0	1257	0	825	720	552
Bythitidae	*Brosmophyciops pautzkei*	E00717	5948	8	0	0	0	825	0	732
Bythitidae	*Brosmophycis marginata*	N05317	7691	9	690	0	975	0	0	0
Bythitidae	*Cataetyx rubrirostris lepidogenys*	E00261	14883	16	474	1242	987	0	753	0
Bythitidae	*Diancistrus sp*	E00236	6903	9	705	1257	0	0	762	0
Bythitidae	*Dinematichthys iluocoeteoides*	E00235	4750	6	0	1248	0	0	0	0
Bythitidae	*Diplacanthopoma brachysoma*	E00452	8606	9	0	1257	0	0	0	0
Bythitidae	*Diplacanthopoma brunnea*	N05377	8280	10	678	0	987	0	702	0
Caesionidae	*Caesio caerulaurea lunaris*	E00920	13727	15	0	1215	0	0	762	765
Caesionidae	*Caesio cuning*	N01544	6786	8	0	0	0	0	741	0
Caesionidae	*Caesio teres*	E00951	7741	10	0	1233	0	0	0	765

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Caesionidae	*Caesio varilineata*	E00949	9671	12	0	1236	0	825	762	759
Caesionidae	*Caesio xanthonota*	E00950	9615	12	0	1233	0	0	762	765
Caesionidae	*Pterocaesio pisang*	N01547	8535	10	704	0	939	0	762	0
Caesionidae	*Pterocaesio tile*	E00961	7369	8	0	0	0	0	762	0
Callanthiidae	*Callanthias australis*	M01721	3528	4	672	0	0	0	0	0
Callanthiidae	*Grammatonotus surugaensis*	N05516	4774	6	0	0	0	0	0	0
Callionymidae	*Callionymus sp bairdi*	E00946	14247	16	696	1260	978	801	0	0
Callionymidae	*Diplogrammus goramensis*	E00744	3443	4	0	1251	0	0	0	0
Callionymidae	*Foetorepus sp*	N01725	7524	9	690	0	927	0	0	0
Callionymidae	*Neosynchiropus ocellatus*	E00030	9857	12	690	0	987	0	0	0
Callionymidae	*Synchiropus agassizii*	E01004	13911	16	696	1236	987	825	0	0
Callionymidae	*Synchiropus splendidus*	E00003	7623	9	690	0	981	0	762	0
Callionymidae	*Synchiropus stellatus*	E00925	4153	5	0	0	0	0	0	0
Caproidae	*Antigonia capros*	E01024	15924	18	603	1284	693	0	762	606
Caproidae	*Antigonia rubescens*	N05907	8327	10	690	0	987	0	748	0
Caproidae	*Capros aper*	N05913	6917	9	0	0	693	0	702	0
Carangidae	*Alectis ciliaris*	E00469	9715	12	705	1296	0	0	0	0
Carangidae	*Atule mate*	E00942	13914	15	705	1236	0	0	762	0
Carangidae	*Carangoides ferdau*	E00869	9160	10	0	1281	0	0	762	0
Carangidae	*Carangoides plagiotaenia*	E00917	10641	12	705	1290	0	0	762	765
Carangidae	*Caranx crysos ruber*	E00510	15973	18	705	1230	0	0	762	744
Carangidae	*Caranx ignobilis*	E00574	14220	16	705	1296	0	0	736	750
Carangidae	*Caranx sexfasciatus*	E00834	10100	10	0	1212	0	0	0	0
Carangidae	*Chloroscombrus chrysurus*	E00763	5515	7	0	0	0	0	0	0
Carangidae	*Decapterus macarellus*	E00212	3266	5	0	0	0	0	0	0
Carangidae	*Decapterus punctatus*	E00671	9777	11	705	1290	0	0	0	0
Carangidae	*Elagatis bipinnulata*	E00841	11967	15	705	822	0	825	762	720
Carangidae	*Gnathanodon speciosus*	E00938	13565	15	705	840	0	0	762	765
Carangidae	*Hemicaranx amblyrhynchus*	E00616	11426	13	0	1287	0	0	735	0
Carangidae	*Oligoplites saurus*	E00195	16021	19	705	1287	921	825	762	744

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Carangidae	*Scomberoides lysan*	E00738	10887	13	0	1254	0	825	0	744
Carangidae	*Selar crumenophthalmus*	E00833	11277	13	705	1287	0	0	762	0
Carangidae	*Selene brownii*	E00767	7866	10	705	879	0	0	0	0
Carangidae	*Selene setapinnis*	N01705	6120	8	705	0	0	0	762	0
Carangidae	*Seriola dumerili*	E00623	16521	18	705	1290	927	0	738	0
Carangidae	*Seriola rivoliana*	E00467	11164	13	705	1257	0	825	0	744
Carangidae	*Trachinotus carolinus*	G01504	11145	13	705	0	972	0	762	0
Carangidae	*Trachinotus falcatus*	E00819	10693	12	705	1233	0	825	0	0
Carangidae	*Trachinotus ovatus*	E01145	14822	16	705	0	975	0	762	0
Carangidae	*Trachurus lathami*	E00598	11710	13	0	1308	0	0	762	0
Carangidae	*Uraspis secunda*	E00515	11843	13	705	1287	0	0	0	0
Carapidae	*Carapus bermudensis*	E00244	3497	5	0	0	870	0	0	0
Carapidae	*Onuxodon parvibrachium*	N06009	5285	7	678	0	0	0	0	0
Carapidae	*Pyramodon ventralis*	N06013	5272	7	678	0	0	0	0	0
Caristiidae	*Caristius macropus*	N06078	5912	8	0	0	918	0	744	0
Caristiidae	*Caristius sp*	E00810	9564	11	0	1281	0	786	762	765
Caristiidae	*Platyberyx opalescens*	N06085	7781	10	690	0	906	0	711	0
Centracanthidae	*Centracanthus cirrus*	M01560	2897	3	0	0	0	0	0	0
Centracanthidae	*Spicara alta*	M01561	4032	4	0	0	0	0	0	0
Centracanthidae	*Spicara maena*	M01562	5142	5	0	1251	0	0	0	0
Centracanthidae	*Spicara nigricauda*	M01564	4791	5	0	1251	0	0	0	0
Centracanthidae	*Spicara smaris*	M01565	5111	5	0	1248	0	0	0	0
Centrarchidae	*Acantharchus pomotis*	G01185	10678	10	0	1287	939	0	0	0
Centrarchidae	*Ambloplites rupestris*	E00392	18681	20	705	1287	984	0	762	759
Centrarchidae	*Archoplites interruptus*	N01722	8586	10	705	0	987	0	762	0
Centrarchidae	*Lepomis cyanellus*	E00132	18334	20	687	1203	951	825	762	639
Centrarchidae	*Lepomis macrochirus*	E01113	15647	17	687	0	0	819	0	597
Centrarchidae	*Micropterus salmoides*	E01110	18682	20	687	1266	987	0	759	0
Centrarchidae	*Pomoxis nigromaculatus*	E00131	14489	15	696	1236	0	0	0	0
Centriscidae	*Aeoliscus strigatus*	G01189	10258	10	696	0	960	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Centriscidae	*Macroramphosus gracilis*	E00335	4196	5	0	0	0	0	0	0
Centriscidae	*Macroramphosus scolopax*	E00473	10717	12	690	0	897	0	0	0
Centrogenyidae	*Centrogenys vaigiensis*	G01239	9161	11	705	0	944	0	762	0
Centrolophidae	*Icichthys lockingtoni*	E00387	15879	18	624	1260	957	0	762	0
Centropomidae	*Centropomus ensiferus*	E00766	14482	15	705	1212	975	825	762	0
Centropomidae	*Centropomus medius*	E01158	10458	11	705	1308	789	0	0	0
Centropomidae	*Centropomus undecimalis*	E00194	15428	17	705	1287	903	0	762	0
Centropomidae	*Centropomus viridis*	E01153	14374	16	705	1308	987	0	699	0
Centropomidae	*Lates calcarifer*	E01135	11083	12	0	1260	900	0	0	0
Centropomidae	*Lates japonicus*	E01147	10695	11	657	1284	903	0	0	0
Centropomidae	*Lates microlepis*	E01149	9785	11	654	1272	921	0	0	0
Centropomidae	*Psammoperca waigiensis*	E01148	12243	13	676	1308	987	0	0	0
Cepolidae	*Acanthocepola sp*	M01669	4129	4	0	1251	0	0	0	0
Cepolidae	*Cepola macrophthalma*	M01566	3339	4	0	1251	0	0	0	0
Cepolidae	*Cepola schlegelii*	N06269	6961	9	705	0	825	0	711	0
Cepolidae	*Sphenanthias tosaensis*	N06282	6620	9	705	0	906	0	708	0
Ceratiidae	*Ceratias holboelli*	E00175	8091	11	687	0	0	0	0	0
Ceratiidae	*Ceratias sp*	E00160	6019	7	0	1257	0	0	0	0
Ceratiidae	*Cryptopsaras couesii*	E00686	9907	10	0	0	0	0	762	0
Chaenopsidae	*Acanthemblemaria aspera*	E00320	6836	9	693	0	0	0	0	0
Chaenopsidae	*Acanthemblemaria paula*	E00295	6314	8	693	0	0	0	0	0
Chaenopsidae	*Chaenopsis sp alepidota*	E00313	11049	13	685	0	0	0	762	0
Chaenopsidae	*Emblemaria pandionis*	E00310	6208	7	0	0	0	0	0	0
Chaenopsidae	*Lucayablennius zingaro*	E00294	7789	9	707	0	0	0	0	0
Chaenopsidae	*Neoclinus blanchardi*	E00326	6535	8	0	0	0	0	0	0
Chaenopsidae	*Stathmonotus stahli*	E00317	7886	9	693	0	0	0	0	0
Chaetodontidae	*Chaetodon auriga*	E00921	12220	14	0	996	0	0	762	753
Chaetodontidae	*Chaetodon capistratus*	E00205	3871	5	0	0	0	0	0	0
Chaetodontidae	*Chaetodon ocellatus*	E00752	3799	5	675	0	0	0	0	0
Chaetodontidae	*Chaetodon ornatissimus*	G01243	11727	14	705	0	945	0	762	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Chaetodontidae	*Chaetodon plebeius*	E00573	2874	4	0	0	0	0	0	0
Chaetodontidae	*Chaetodon reticulatus*	E00719	9187	11	705	1260	0	0	0	0
Chaetodontidae	*Chaetodon striatus*	E00753	15347	19	705	1236	825	705	741	753
Chaetodontidae	*Chelmon rostratus*	G01248	10379	13	705	0	936	0	753	0
Chaetodontidae	*Forcipiger flavissimus*	E00562	14191	17	663	1260	966	0	762	0
Chaetodontidae	*Hemitaurichthys polylepis*	E00240	12410	15	705	0	0	0	762	0
Chaetodontidae	*Heniochus chrysostomus*	E00748	14747	18	705	1236	0	822	762	729
Chaetodontidae	*Heniochus varius*	E00547	11101	14	705	1236	0	0	744	0
Chaetodontidae	*Johnrandallia nigrirostris*	N06546	7594	9	705	0	0	0	762	0
Chaetodontidae	*Prognathodes aya aculeatus*	E00632	16211	20	705	1257	945	822	762	762
Champsodontidae	*Champsodon snyderi*	N06574	5798	8	705	0	906	0	702	0
Channichthyidae	*Chionobathyscus dewitti*	G01250	11735	13	705	0	972	0	759	0
Channichthyidae	*Chionodraco rastrospinosus*	E00156	10249	11	696	0	0	0	762	0
Channidae	*Channa lucius*	N06615	7562	9	705	0	987	0	762	0
Channidae	*Channa melasoma*	N06621	8195	10	705	0	966	0	732	0
Channidae	*Channa striata*	E01133	15424	17	705	1308	987	0	762	0
Chaunacidae	*Chaunax stigmaeus*	E01121	11544	14	690	1236	879	0	714	0
Chaunacidae	*Chaunax suttkusi*	E01117	13670	16	705	1260	978	0	762	0
Cheilodactylidae	*Cheilodactylus fasciatus*	E00795	8950	11	693	0	0	0	762	0
Cheilodactylidae	*Cheilodactylus pixi*	E00797	7523	10	0	0	0	0	762	0
Cheilodactylidae	*Cheilodactylus variegatus*	N07699	7481	9	696	0	0	0	762	0
Cheilodactylidae	*Chirodactylus brachydactylus*	E00796	10572	13	705	1236	879	0	762	0
Cheilodactylidae	*Chirodactylus jessicalenorum*	E00585	5511	7	0	1257	0	0	0	750
Cheimarrichthyidae	*Cheimarrichthys fosteri*	N07713	7400	9	0	0	936	0	762	0
Chiasmodontidae	*Chiasmodon niger*	E01115	6819	8	678	1257	0	0	0	0
Chiasmodontidae	*Chiasmodon sp*	N33662	8114	10	696	0	957	0	762	0
Chiasmodontidae	*Kali indica*	E01106	8049	10	0	1248	0	678	0	750
Chiasmodontidae	*Kali kerberti*	E00385	8712	11	687	1257	0	0	750	0
Chironemidae	*Chironemus georgianus*	M01569	3606	4	705	0	0	0	0	0
Chironemidae	*Chironemus maculosus*	M01570	3605	4	705	0	0	0	0	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Cichlidae	*Astatotilapia burtoni*	G01518	14530	19	699	1308	987	459	0	756
Cichlidae	*Cichla temensis*	G01256	12888	15	699	1287	987	0	762	0
Cichlidae	*Crenicichla lepidota*	E00137	9593	12	705	0	0	0	0	0
Cichlidae	*Etroplus maculatus*	E00133	16104	17	705	0	960	0	762	0
Cichlidae	*Herichthys cyanoguttatus*	G01319	10449	13	705	0	987	0	762	0
Cichlidae	*Heros efasciatus*	G01320	12037	14	705	1281	987	0	762	0
Cichlidae	*Heterochromis multidens*	G01321	10659	13	681	0	978	0	762	0
Cichlidae	*Maylandia zebra*	G01519	15105	19	699	1308	987	459	762	756
Cichlidae	*Nanochromis parilus*	G01390	2645	4	681	0	0	0	0	0
Cichlidae	*Neolamprologus brichardi*	G01520	18935	21	699	1308	987	459	762	756
Cichlidae	*Oreochromis niloticus*	G01407	20724	22	705	1308	987	810	762	756
Cichlidae	*Paratilapia polleni*	G01420	11328	12	705	0	978	0	762	0
Cichlidae	*Paretroplus maculatus*	G01423	11220	12	699	0	960	0	762	0
Cichlidae	*Ptychochromis grandidieri*	G01459	9350	12	705	0	891	0	693	0
Cichlidae	*Pundamilia nyererei*	G01521	14440	18	696	1308	987	459	0	756
Cichlidae	*Steatocranus gibbiceps*	G01494	2873	4	681	0	0	0	0	0
Cichlidae	*Symphysodon discus*	E00390	10909	13	0	0	0	0	0	753
Cichlidae	*Tilapia louka*	G01503	2873	4	681	0	0	0	0	0
Cirrhitidae	*Amblycirrhitus pinos*	E00314	16355	19	666	867	882	0	690	0
Cirrhitidae	*Cirrhitichthys falco*	N09466	4867	7	660	0	873	0	702	0
Cirrhitidae	*Cirrhitichthys oxycephalus*	E00884	8380	11	705	1257	0	0	0	322
Cirrhitidae	*Neocirrhites armatus*	E00725	12592	16	663	0	873	0	699	0
Cirrhitidae	*Paracirrhites forsteri arcatus*	E00924	12505	15	705	0	951	0	762	0
Citharidae	*Citharoides macrolepis*	E00071	12901	15	687	0	882	0	702	0
Citharidae	*Citharus linguatula*	E01174	6850	8	705	0	0	0	0	0
Citharidae	*Lepidoblepharon ophthalmolepis*	E00080	7005	8	0	855	0	0	0	0
Clinidae	*Blennophis striatus*	E00800	3454	4	0	0	0	0	0	0
Clinidae	*Clinus cottoides*	E00804	4782	6	0	0	0	0	0	0
Clinidae	*Clinus superciliosus*	E00803	5297	7	0	0	0	0	0	0
Clinidae	*Gibbonsia metzi*	N09738	6827	8	705	0	957	0	762	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Clinidae	*Muraenoclinus dorsalis*	E00805	4559	6	0	0	0	0	0	0
Clinidae	*Pavoclinus profundus*	E00799	3475	4	0	0	0	0	0	0
Coryphaenidae	*Coryphaena hippurus*	E00937	17390	19	693	1281	969	0	0	0
Cottidae	*Artediellus uncinatus*	N10447	7522	9	627	0	0	0	762	0
Cottidae	*Chitonotus pugetensis*	E00233	6714	8	0	1257	0	0	0	0
Cottidae	*Cottus carolinae*	E00281	10765	13	705	0	974	0	762	0
Cottidae	*Enophrys taurina*	E00234	3576	5	0	0	0	0	0	0
Cottidae	*Gymnocanthus galeatus*	E00259	3095	4	0	1215	0	0	0	0
Cottidae	*Hemilepidotus jordani*	E00263	7975	10	0	1260	0	726	0	0
Cottidae	*Hemilepidotus zapus*	E00272	5096	6	0	1233	0	0	0	0
Cottidae	*Icelinus filamentosus*	E00277	8203	10	0	1233	0	0	762	0
Cottidae	*Icelinus quadriseriatus*	E00228	5018	6	0	1257	0	0	0	0
Cottidae	*Leptocottus armatus*	E00266	12068	14	0	0	0	0	738	0
Cottidae	*Micrococttus sellaris*	E00223	2282	3	0	0	0	0	0	0
Cottidae	*Myoxocephalus octodecemspinosus*	E00221	3991	4	0	1254	0	0	0	0
Cottidae	*Myoxocephalus polyacanthocephalus*	E00267	4736	5	0	1233	0	0	0	0
Cottidae	*Radulinus asprellus*	E00429	6882	9	0	0	0	0	0	0
Cottidae	*Rastrinus scutiger*	E00256	6088	7	0	1257	0	0	0	0
Cottidae	*Scorpaenichthys marmoratus*	E00232	10450	13	705	0	0	0	0	0
Cottidae	*Triglops macellus*	E00435	8082	10	0	1263	0	0	0	0
Cottidae	*Triglops scepticus*	E00421	5233	7	0	0	0	0	0	0
Creediidae	*Limnichthys sp*	E01081	6256	8	693	*0*	*0*	*0*	*0*	*0*
Cryptacanthodidae	*Cryptacanthodes maculatus*	E00116	10532	13	705	0	0	0	762	0
Cyclopteridae	*Cyclopterus lumpus*	E00220	12165	15	705	0	870	0	762	0
Cyclopteridae	*Eumicrotremus orbis*	E00270	12456	15	705	1257	0	0	762	0
Cynoglossidae	*Cynoglossus interruptus*	E00076	7900	8	0	1308	0	0	0	0
Cynoglossidae	*Symphurus atricaudus*	E00023	10924	12	705	1284	0	0	0	0
Cynoglossidae	*Symphurus civitatium*	E00604	7546	8	0	1308	0	768	0	0
Cynoglossidae	*Symphurus plagiusa*	E01164	7027	8	0	1287	0	0	0	0
Cyprinodontidae	*Cyprinodon variegatus*	E01066	12469	15	705	1245	954	825	0	630

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Cyprinodontidae	*Floridichthys carpio*	E01063	9295	11	0	1257	0	0	0	411
Cyprinodontidae	*Jordanella floridae*	N14002	5915	7	705	0	936	0	0	0
Dactylopteridae	*Dactyloptena gilberti*	N14051	5845	7	690	0	0	0	0	0
Dactylopteridae	*Dactyloptena orientalis*	E00237	13665	15	705	1254	987	825	0	0
Dactylopteridae	*Dactyloptena peterseni*	E00749	14553	15	681	1259	987	825	0	0
Dactylopteridae	*Dactylopterus volitans*	E00214	7789	10	705	0	0	723	0	0
Dactyloscopidae	*Gillellus semicinctus*	G01299	6655	8	692	0	0	0	762	0
Dactyloscopidae	*Platygillellus rubrocinctus*	E00319	5427	7	711	0	0	0	0	0
Datnioididae	*Datnioides microlepis*	N14199	7836	10	696	0	879	0	693	0
Dichistiidae	*Dichistius capensis*	M01571	3582	4	681	0	0	0	0	0
Diodontidae	*Chilomycterus schoepfii*	E00517	12554	15	705	0	951	0	762	0
Diodontidae	*Diodon holocanthus*	E00312	13884	15	705	0	957	0	762	0
Drepaneidae	*Drepane punctata*	E00250	13305	15	0	1284	0	0	693	0
Echeneidae	*Echeneis naucrates*	E00615	16441	18	705	0	0	810	762	762
Echeneidae	*Echeneis neucratoides*	E00245	7118	7	693	1281	0	0	0	699
Echeneidae	*Phtheirichthys lineatus*	G01438	7650	8	0	0	0	795	0	654
Echeneidae	*Remora osteochir australis*	E00503	10993	11	705	1302	0	0	0	0
Elassomatidae	*Elassoma evergladei*	E00146	15293	17	693	0	0	825	762	747
Elassomatidae	*Elassoma okefenokee*	G01283	9813	12	705	606	975	0	762	0
Elassomatidae	*Elassoma zonatum*	G01284	14834	15	705	1287	933	0	762	0
Eleginopsidae	*Eleginops maclovinus*	G01286	10593	13	705	0	987	0	759	0
Eleotridae	*Dormitator maculatus*	E00169	5763	7	702	0	0	0	0	0
Eleotridae	*Eleotris acanthopoma pisonis*	E00741	12447	14	501	0	948	0	0	0
Eleotridae	*Ophiocara porocephala*	E01101	11395	13	705	1236	0	0	0	0
Eleotridae	*Oxyeleotris selheimi*	N01730	5975	7	705	0	948	0	0	0
Embiotocidae	*Amphistichus argenteus*	E00129	8893	12	705	0	0	0	0	0
Embiotocidae	*Cymatogaster aggregata*	E00139	14184	16	705	0	987	0	762	0
Embiotocidae	*Embiotoca jacksoni*	E00120	14177	17	705	1257	957	0	762	0
Embiotocidae	*Embiotoca lateralis*	N14635	6883	8	705	0	945	0	0	0
Embiotocidae	*Hyperprosopon anale argenteum*	E00134	14767	18	705	1245	966	0	762	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Embiotocidae	*Phanerodon furcatus*	E00122	11479	14	705	0	948	0	762	0
Embiotocidae	*Rhacochilus vacca*	E00124	12585	15	705	0	948	0	0	0
Embiotocidae	*Zalembius rosaceus*	E00135	4565	6	0	0	0	0	0	0
Emmelichthyidae	*Erythrocles schlegelii*	E00954	12039	15	669	1233	879	780	762	0
Emmelichthyidae	*Erythrocles scintillans*	N14652	6911	9	705	0	0	0	711	0
Enoplosidae	*Enoplosus armatus*	G01287	10134	11	0	0	0	0	702	0
Ephippidae	*Chaetodipterus faber*	E00614	14589	18	705	0	972	732	762	744
Ephippidae	*Platax orbicularis*	E00898	13969	16	705	0	0	813	762	0
Ephippidae	*Platax teira*	E00858	12410	15	0	0	0	825	0	735
Epigonidae	*Epigonus pandionis*	E01019	5505	7	690	1236	0	0	762	0
Epigonidae	*Epigonus telescopus*	E00652	10314	12	0	858	0	0	762	708
Exocoetidae	*Cheilopogon dorsomacula*	E00624	11475	14	705	1260	0	0	762	0
Exocoetidae	*Cheilopogon melanurus*	N14975	5883	7	696	0	984	0	0	0
Exocoetidae	*Cheilopogon pinnatibarbatus*	E00399	13294	16	705	0	957	0	0	0
Exocoetidae	*Cypselurus callopterus*	E00402	6837	8	0	0	0	0	0	735
Exocoetidae	*Exocoetus monocirrhus*	E00403	10246	13	0	0	0	0	0	735
Exocoetidae	*Hirundichthys marginatus*	E00401	9589	12	0	0	0	0	762	765
Exocoetidae	*Parexocoetus brachypterus*	E00645	4220	5	0	0	0	0	0	0
Exocoetidae	*Prognichthys brevipinnis*	E00400	6286	8	0	0	0	0	762	0
Fistulariidae	*Fistularia commersonii*	E00941	7080	7	0	0	897	0	0	0
Fistulariidae	*Fistularia petimba*	E00602	6969	9	705	0	894	0	0	0
Fundulidae	*Adinia xenica*	E00173	8890	10	0	1257	0	0	762	0
Fundulidae	*Fundulus blairae*	E00130	9841	11	0	1233	0	0	0	0
Fundulidae	*Fundulus chrysotus*	E00186	8599	9	0	1236	0	0	762	0
Fundulidae	*Fundulus heteroclitus*	G01293	12304	13	705	0	987	0	762	0
Fundulidae	*Fundulus parvipinnis*	E00389	11368	13	0	1245	0	0	762	756
Fundulidae	*Lucania parva goodei*	E01064	13730	16	705	1257	0	813	762	0
Gasterosteidae	*Apeltes quadracus*	E00791	11199	12	696	0	972	0	756	0
Gasterosteidae	*Culaea inconstans*	E00368	12338	14	693	0	984	0	756	0
Gasterosteidae	*Gasterosteus aculeatus*	E01012	20181	21	705	1308	963	0	762	756

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Gasterosteidae	*Gasterosteus wheatlandi*	N15128	8456	10	705	0	972	0	762	0
Gasterosteidae	*Pungitius pungitius*	G01460	10820	11	693	0	963	0	756	0
Gasterosteidae	*Spinachia spinachia*	G01491	10498	11	693	0	963	0	756	0
Gempylidae	*Gempylus serpens*	E00693	9797	13	0	1248	0	0	762	759
Gempylidae	*Nealotus tripes*	E00287	6043	8	705	1233	0	0	0	0
Gempylidae	*Neoepinnula americana*	E00471	5662	7	669	1257	0	0	0	0
Gempylidae	*Neoepinnula orientalis*	E00518	6702	9	0	0	0	0	762	648
Gempylidae	*Paradiplospinus gracilis*	N15143	7281	9	705	0	0	0	762	0
Gempylidae	*Ruvettus pretiosus*	E00226	13794	16	705	0	987	0	762	0
Gerreidae	*Eucinostomus argenteus*	E00575	5749	7	0	0	0	0	0	0
Gerreidae	*Eucinostomus gula*	E00756	7604	9	0	0	0	0	0	0
Gerreidae	*Eugerres plumieri*	G01291	11242	14	695	0	969	0	762	0
Gerreidae	*Gerres cinereus*	E00292	11457	12	0	1281	0	0	0	0
Gerreidae	*Gerres longirostris*	E00835	6053	8	0	0	0	825	0	0
Gerreidae	*Gerres oyena*	E00823	6770	8	0	0	0	0	0	714
Gerreidae	*Ulaema lefroyi*	G01507	8309	10	696	0	954	0	762	0
Gigantactinidae	*Gigantactis ios*	E01053	4539	6	0	0	0	0	0	0
Gigantactinidae	*Gigantactis sp*	N34852	6412	8	675	0	0	0	753	0
Gigantactinidae	*Gigantactis vanhoeffeni*	E00177	13239	15	648	0	0	819	762	729
Girellidae	*Girella nigricans mezina*	E00197	11742	13	705	1236	0	0	711	0
Glaucosomatidae	*Glaucosoma buergeri*	N15231	7808	10	690	0	906	0	708	0
Glaucosomatidae	*Glaucosoma hebraicum*	G01300	16039	18	705	1308	975	0	762	0
Gobiesocidae	*Arcos sp*	E00102	13747	16	678	873	960	0	702	0
Gobiesocidae	*Diademichthys lineatus*	G01276	8298	10	705	0	963	0	762	0
Gobiesocidae	*Gobiesox maeandricus*	G01302	8270	10	705	0	981	0	0	0
Gobiesocidae	*Lepadichthys lineatus*	E01080	3896	5	0	0	0	0	0	669
Gobiidae	*Amblyeleotris guttata*	E01043	8728	11	0	0	0	792	0	0
Gobiidae	*Amblyeleotris gymnocephala*	E00409	6038	8	0	0	0	0	0	0
Gobiidae	*Amblyeleotris wheeleri*	E01073	7397	9	0	0	0	810	0	0
Gobiidae	*Amblygobius decussatus*	E00533	2824	4	0	0	0	0	0	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Gobiidae	*Amblygobius phalaena*	E00736	7217	10	0	0	0	0	0	0
Gobiidae	*Asterropteryx semipunctata*	E01089	6719	8	0	0	0	0	0	0
Gobiidae	*Bathygobius mystacium*	E00104	6412	8	0	0	0	0	0	0
Gobiidae	*Bollmannia communis*	E00617	5108	5	0	0	0	0	0	0
Gobiidae	*Cabillus lacertops*	E01093	3915	5	0	0	0	0	0	0
Gobiidae	*Caffrogobius caffer*	E01056	6198	8	696	0	0	810	0	0
Gobiidae	*Caffrogobius saldanha*	E01057	6207	8	666	0	0	0	0	0
Gobiidae	*Coryphopterus glaucofraenum*	E00100	5342	7	0	0	0	810	0	0
Gobiidae	*Coryphopterus personatus*	E00405	4791	7	0	0	0	0	0	0
Gobiidae	*Cryptocentrus sp*	E00407	3883	5	0	0	0	0	0	0
Gobiidae	*Ctenogobiops crocineus*	E01097	5981	7	0	0	0	810	0	0
Gobiidae	*Ctenogobius boleosoma*	E00172	3520	5	0	0	0	0	0	0
Gobiidae	*Elacatinus oceanops*	E00108	11459	12	0	0	0	0	0	0
Gobiidae	*Eviota albolineata*	E01041	6182	8	0	0	0	0	0	0
Gobiidae	*Eviota prasites*	E01044	5506	7	0	0	0	0	0	0
Gobiidae	*Eviota saipanensis*	E00714	4913	6	0	0	0	0	0	0
Gobiidae	*Evorthodus lyricus*	E00171	6129	8	705	0	0	0	0	0
Gobiidae	*Fusigobius duospilus*	E00863	7305	9	692	0	0	807	0	0
Gobiidae	*Fusigobius inframaculatus*	E01076	4985	6	0	0	0	0	0	0
Gobiidae	*Fusigobius neophytus*	E00733	7031	10	663	0	0	0	0	0
Gobiidae	*Gnatholepis anjerensis*	E01075	4977	7	0	0	0	0	0	0
Gobiidae	*Gnatholepis cauerensis*	E00099	3361	5	0	0	0	0	0	0
Gobiidae	*Gobiodon quinquestrigatus*	E01085	6985	9	0	0	0	0	0	0
Gobiidae	*Gobiosoma bosc*	E00097	9910	10	0	0	0	711	0	0
Gobiidae	*Istigobius decoratus*	E01078	9124	11	0	0	0	0	0	0
Gobiidae	*Istigobius ornatus*	E01107	2776	3	0	0	0	0	0	0
Gobiidae	*Lepidogobius lepidus*	G01351	5076	6	0	0	981	0	0	0
Gobiidae	*Lophogobius cyprinoides*	E00508	6153	8	706	0	0	0	0	0
Gobiidae	*Lythrypnus dalli*	E00126	6746	9	0	0	0	0	0	0
Gobiidae	*Oplopomus oplopomus*	E01067	6654	8	0	0	0	801	0	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Gobiidae	*Paragobiodon modestus*	E01098	8154	11	0	0	0	732	0	0
Gobiidae	*Periophthalmus kalolo*	E00537	6876	9	705	0	0	0	0	0
Gobiidae	*Priolepis cincta*	E01077	5030	6	0	0	0	0	0	0
Gobiidae	*Priolepis hipoliti*	E00106	5717	7	0	0	0	0	0	0
Gobiidae	*Psammogobius biocellatus*	E00740	5797	8	705	0	0	0	0	0
Gobiidae	*Risor ruber*	E00107	10310	10	0	0	0	0	0	0
Gobiidae	*Stonogobiops nematodes*	N16820	2850	4	0	0	879	0	0	0
Gobiidae	*Trimma caesiura*	E01039	8870	11	0	0	0	786	0	0
Gobiidae	*Trimma haima*	E01084	5533	7	0	0	0	714	0	0
Gobiidae	*Trimma okinawae*	E00726	2759	4	0	0	0	0	0	0
Gobiidae	*Valenciennea puellaris*	E01096	5328	7	0	0	0	0	0	0
Gobiidae	*Valenciennea strigata*	E01094	4256	6	0	0	0	0	0	0
Gobiidae	*Vanderhorstia ornatissima*	E01088	6501	8	0	0	0	0	0	0
Grammatidae	*Gramma loreto*	E00280	14197	16	696	1287	978	0	762	0
Grammatidae	*Lipogramma anabantoides*	E00211	6519	8	0	1233	0	0	762	693
Grammatidae	*Lipogramma trilineata*	E00210	6532	8	0	1257	0	0	0	0
Haemulidae	*Anisotremus surinamensis*	N17175	7479	9	693	0	0	0	762	0
Haemulidae	*Anisotremus virginicus*	E00200	9338	11	705	1260	0	0	0	0
Haemulidae	*Conodon nobilis*	E00613	10862	13	705	1260	0	0	0	0
Haemulidae	*Haemulon aurolineatum*	E00635	16270	20	705	1242	0	0	762	723
Haemulidae	*Haemulon plumierii*	E00279	12545	15	705	1254	0	0	762	0
Haemulidae	*Haemulon sciurus*	E00199	14796	18	705	1257	796	0	759	684
Haemulidae	*Haemulon vittatum*	E00218	14636	17	684	1278	0	0	762	0
Haemulidae	*Orthopristis chrysoptera*	E00607	15170	18	705	1260	0	0	762	0
Haemulidae	*Plectorhinchus chaetodonoides*	E00857	12011	14	693	1236	0	795	762	0
Haemulidae	*Plectorhinchus vittatus*	E00856	9448	12	705	1236	0	0	0	0
Haemulidae	*Pomadasys corvinaeformis*	E00761	10420	14	696	1257	0	741	0	0
Haemulidae	*Xenistius californiensis*	E00229	11494	14	705	1236	0	0	0	609
Hapalogenyidae	*Hapalogenys aya*	M01722	4098	4	705	0	0	0	0	0
Hapalogenyidae	*Hapalogenys kishinouyei*	M01723	3627	4	681	0	0	0	0	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Hapalogenyidae	*Hapalogenys nigripinnis*	M01724	4735	5	705	0	0	0	0	0
Harpagiferidae	*Harpagifer antarcticus*	G01524	10362	11	660	0	0	0	759	0
Helostomatidae	*Helostoma temminkii*	G01315	8144	9	693	0	0	0	702	0
Hemiramphidae	*Arrhamphus sclerolepis*	G01209	7917	10	696	0	972	0	762	0
Hemiramphidae	*Hemiramphus brasiliensis*	E00098	10104	12	705	1233	0	0	0	708
Hemiramphidae	*Hyporhamphus affinis*	E01068	5623	7	696	0	0	825	0	0
Hemiramphidae	*Hyporhamphus dussumieri*	E01086	3078	4	0	0	0	0	0	0
Hemiramphidae	*Oxyporhamphus micropterus*	E00397	8076	9	0	1260	0	0	0	0
Hexagrammidae	*Hexagrammos decagrammus*	E00348	7318	10	702	867	0	0	0	0
Hexagrammidae	*Hexagrammos lagocephalus otakii*	E00363	13109	16	699	0	867	0	762	0
Hexagrammidae	*Pleurogrammus monopterygius*	E00367	6904	9	633	0	0	0	0	0
Hexagrammidae	*Zaniolepis frenata*	E00353	6326	9	648	0	0	0	0	0
Himantolophidae	*Himantolophus albinares sagamius*	E00656	16540	18	705	1254	0	0	762	759
Hoplichthyidae	*Hoplichthys gilberti*	N17743	5272	7	690	0	0	0	0	0
Hoplichthyidae	*Hoplichthys langsdorfii*	N17745	5443	7	690	0	0	0	0	0
Howellidae	*Howella brodiei*	E00816	11083	12	0	1308	0	825	0	765
Howellidae	*Howella zina*	N17756	5489	7	705	0	0	0	0	0
Hypoptychidae	*Aulichthys japonicus*	G01216	11602	12	690	0	963	0	0	0
Hypoptychidae	*Hypoptychus dybowskii*	G01335	10399	11	696	0	960	0	756	0
Icosteidae	*Icosteus aenigmaticus*	G01336	7173	9	705	0	0	0	762	0
Indostomidae	*Indostomus crocodilus*	N17863	5047	7	693	0	873	0	0	0
Indostomidae	*Indostomus paradoxus*	E01156	10345	11	693	861	861	0	0	0
Isonidae	*Iso sp*	E00145	8043	10	705	0	0	0	762	0
Istiophoridae	*Istiophorus platypterus*	E00695	12698	12	0	1299	0	825	0	0
Istiophoridae	*Kajikia albida*	E00681	7868	10	0	1236	0	795	0	729
Istiophoridae	*Makaira nigricans*	E00697	11395	12	0	0	0	825	0	732
Istiophoridae	*Makaira sp*	E00692	8009	9	0	1011	0	0	0	0
Istiophoridae	*Tetrapturus angustirostris*	N01741	7787	10	696	0	882	0	690	0
Kuhliidae	*Kuhlia marginata*	G01341	10248	12	705	1287	957	0	744	0
Kuhliidae	*Kuhlia mugil*	E00712	16962	18	705	1281	0	825	762	759

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Kuhliidae	*Kuhlia rupestris*	E00957	12721	15	705	1287	882	0	699	0
Kurtidae	*Kurtus gulliveri*	E00188	16737	18	645	1308	906	0	762	0
Kurtidae	*Kurtus indicus*	N17950	5074	7	687	0	882	0	0	0
Kyphosidae	*Kyphosus cinerascens*	N17975	7672	10	705	0	882	0	693	0
Kyphosidae	*Kyphosus elegans*	G01342	9674	11	705	1287	948	0	762	0
Kyphosidae	*Kyphosus incisor*	E00202	6684	8	0	0	0	0	756	0
Kyphosidae	*Kyphosus sectatrix*	E00775	12318	14	705	1281	0	825	0	765
Labridae	*Anampses lineatus*	E00932	8645	11	693	0	0	798	762	681
Labridae	*Bodianus axillaris*	E00947	9242	11	0	1257	0	825	0	0
Labridae	*Bodianus mesothorax*	E00560	14044	17	0	1257	984	0	762	0
Labridae	*Cheilinus chlorourus*	E00907	9227	12	696	0	0	816	762	600
Labridae	*Cheilinus fasciatus*	E00876	8639	11	678	0	0	819	762	0
Labridae	*Cheilinus oxycephalus*	E00901	6640	8	0	0	0	825	762	0
Labridae	*Cheilio inermis*	E00906	9477	11	678	1215	0	0	0	0
Labridae	*Cirrhilabrus katherinae*	E00728	6057	8	693	0	0	807	0	0
Labridae	*Cirrhilabrus punctatus*	E00553	5794	7	705	1257	0	0	0	0
Labridae	*Clepticus parrae*	E00015	14928	18	705	1239	984	0	762	513
Labridae	*Coris batuensis*	N18137	4801	6	705	0	974	0	0	0
Labridae	*Coris caudimacula*	E00861	11177	14	696	1257	0	825	762	720
Labridae	*Coris formosa*	E00912	8465	11	705	0	0	723	0	756
Labridae	*Coris gaimard*	E00091	11874	15	705	0	966	0	762	0
Labridae	*Decodon puellaris*	E00620	7367	9	705	1257	0	753	0	0
Labridae	*Diproctacanthus xanthurus*	G01278	8556	10	678	0	962	0	0	0
Labridae	*Epibulus insidiator*	E00879	16078	19	705	1257	960	0	762	0
Labridae	*Gomphosus varius*	E00085	11071	14	705	0	927	0	762	0
Labridae	*Halichoeres bathyphilus bivittatus*	E00637	13256	16	705	0	987	0	762	0
Labridae	*Halichoeres biocellatus*	E00727	5094	7	705	0	0	825	0	0
Labridae	*Halichoeres iridis*	E00928	6442	8	0	1257	0	0	762	720
Labridae	*Halichoeres margaritaceus*	N18205	5528	7	705	0	957	0	762	0
Labridae	*Hologymnosus doliatus*	E00567	10593	13	696	1257	0	681	0	711

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Labridae	*Labrichthys unilineatus*	G01344	10143	12	705	0	972	0	762	0
Labridae	*Labroides dimidiatus*	E00848	9046	11	0	1257	0	825	762	762
Labridae	*Labropsis australis*	G01345	9319	11	705	0	912	0	762	0
Labridae	*Lachnolaimus maximus*	E00014	12305	15	696	1245	933	0	762	0
Labridae	*Macropharyngodon bipartitus*	E00895	7503	10	690	0	0	765	762	0
Labridae	*Novaculichthys taeniourus*	E00926	12181	15	696	1257	0	783	0	747
Labridae	*Oxycheilinus celebicus*	G01412	8510	10	705	0	972	0	762	0
Labridae	*Oxycheilinus digramma*	E00873	10757	13	693	1245	0	0	762	0
Labridae	*Oxycheilinus unifasciatus*	E00721	7878	9	705	1257	0	0	0	0
Labridae	*Oxyjulis californica*	G01413	7537	9	705	0	984	0	0	0
Labridae	*Pseudocheilinus evanidus*	E00944	6483	9	654	0	0	0	0	0
Labridae	*Pseudocheilinus hexataenia*	E00945	7019	9	0	0	0	0	762	702
Labridae	*Pteragogus enneacanthus*	G01457	6723	8	705	0	954	0	762	0
Labridae	*Stethojulis balteata*	E00089	4889	6	0	0	0	0	0	0
Labridae	*Stethojulis strigiventer*	E00908	11343	15	705	1257	0	825	762	609
Labridae	*Tautoga onitis*	G01499	9257	11	705	0	975	0	762	0
Labridae	*Tautogolabrus adspersus*	G01500	10397	12	705	0	972	0	762	0
Labridae	*Thalassoma amblycephalum*	E00891	10041	13	705	1251	0	825	762	0
Labridae	*Thalassoma lunare*	E00902	11967	15	696	1251	0	825	762	0
Labridae	*Thalassoma quinquevittatum*	E00092	6872	9	0	1251	0	0	762	0
Labridae	*Wetmorella nigropinnata*	E00948	11203	14	705	1245	0	825	762	696
Labridae	*Xyrichtys novacula martinicensis*	E00016	18002	21	703	1257	966	0	762	0
Labrisomidae	*Labrisomus bucciferus*	E00301	5621	7	678	0	0	0	0	0
Labrisomidae	*Labrisomus guppyi multiporosus*	E00300	8447	10	699	0	978	0	762	0
Labrisomidae	*Labrisomus nigricinctus*	E00302	4582	6	696	0	0	0	0	0
Labrisomidae	*Malacoctenus aurolineatus*	E00299	2229	3	0	0	0	0	0	0
Labrisomidae	*Malacoctenus triangulatus*	E00321	3751	4	0	1182	0	0	0	0
Labrisomidae	*Paraclinus marmoratus*	E00309	4124	5	0	0	0	0	0	0
Labrisomidae	*Starksia atlantica*	E00304	5512	7	706	0	0	0	0	0
Labrisomidae	*Starksia fasciata*	E00303	7567	9	707	1257	0	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Labrisomidae	*Starksia ocellata*	E00318	4469	6	621	0	0	0	0	0
Lactariidae	*Lactarius lactarius Fiji*	M01673	3453	4	705	0	0	0	0	0
Lactariidae	*Lactarius lactarius Qatar*	M01593	4041	5	705	0	0	0	0	0
Lateolabracidae	*Lateolabrax japonicus*	E01130	12539	12	0	1281	984	0	0	0
Latridae	*Latridopsis forsteri*	M01594	4790	5	0	1251	0	0	0	0
Latridae	*Latris lineata*	M01595	4794	5	0	1251	0	0	0	0
Leiognathidae	*Gazza minuta*	G01298	8150	10	693	0	0	0	0	0
Leiognathidae	*Leiognathus equulus*	G01348	8522	11	693	0	0	0	0	0
Leptobramidae	*Leptobrama muelleri*	E01150	6470	8	669	1287	0	0	0	0
Lethrinidae	*Gymnocranius grandoculis*	E00952	7334	9	705	1260	0	0	0	0
Lethrinidae	*Lethrinus atkinsoni*	E00750	7416	10	681	0	0	0	762	759
Lethrinidae	*Lethrinus erythropterus*	N18731	7589	9	534	0	951	0	762	0
Lethrinidae	*Lethrinus harak*	E00905	18169	21	693	1281	950	813	762	759
Lethrinidae	*Lethrinus obsoletus*	E00910	14297	15	705	1257	0	813	762	723
Lethrinidae	*Lethrinus olivaceus*	E00751	11020	13	687	1260	0	765	762	0
Lethrinidae	*Monotaxis grandoculis*	G01379	11352	12	705	0	969	0	762	0
Liparidae	*Careproctus melanurus*	E00422	5235	7	0	0	0	0	0	0
Liparidae	*Careproctus rastrinus*	E00255	6920	8	705	0	0	0	0	0
Liparidae	*Liparis gibbus*	E00224	9360	11	705	0	0	0	744	0
Liparidae	*Liparis pulchellus*	E00225	5675	7	0	0	0	0	762	0
Liparidae	*Paraliparis beani*	E00458	3871	5	0	0	0	0	0	0
Liparidae	*Paraliparis copei*	E00453	6908	9	690	0	0	0	762	0
Liparidae	*Paraliparis hystrix*	E00454	8881	11	705	0	0	0	762	0
Liparidae	*Rhinoliparis barbulifer*	E00262	5284	7	0	0	0	0	762	0
Lobotidae	*Lobotes pacificus surinamensis*	G01359	9710	12	705	0	0	0	762	0
Lophiidae	*Lophiodes reticulatus*	E00625	8318	11	696	1260	0	0	0	0
Lophiidae	*Lophius americanus*	E00578	16809	19	705	1260	966	0	762	747
Lophiidae	*Lophius gastrophysus*	E01119	13495	17	705	1257	987	0	762	744
Lutjanidae	*Aphareus furca*	E00563	13687	16	705	1236	0	0	762	747
Lutjanidae	*Aprion virescens*	E00828	8178	10	651	1251	0	825	0	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Lutjanidae	*Apsilus dentatus*	E00770	8017	10	705	1257	0	0	762	0
Lutjanidae	*Lutjanus biguttatus*	E00569	10110	12	672	1257	0	0	762	0
Lutjanidae	*Lutjanus campechanus*	E00592	9830	12	0	1260	0	0	762	0
Lutjanidae	*Lutjanus griseus*	N20115	7237	9	690	0	0	0	762	0
Lutjanidae	*Lutjanus mahogoni*	G01362	10416	12	705	0	987	0	762	0
Lutjanidae	*Macolor niger*	E00939	9071	11	0	1236	0	813	0	765
Lutjanidae	*Ocyurus chrysurus*	E00283	13831	16	680	1233	951	0	762	0
Lutjanidae	*Pristipomoides aquilonaris*	E00594	10332	13	0	1233	0	0	0	684
Lutjanidae	*Pristipomoides auricilla*	E00746	6210	8	0	1257	0	717	762	0
Lutjanidae	*Rhomboplites aurorubens*	E00593	13759	16	696	1236	0	0	0	0
Luvaridae	*Luvarus imperialis*	E00509	15760	19	636	0	885	825	693	726
Malacanthidae	*Caulolatilus intermedius*	E00595	8981	11	705	1260	0	825	0	729
Malacanthidae	*Caulolatilus princeps*	E00231	11865	15	654	0	894	0	762	0
Malacanthidae	*Malacanthus plumieri*	E00774	8060	10	705	0	0	0	762	0
Mastacembelidae	*Macrognathus siamensis*	G01367	8287	10	0	0	947	0	756	0
Mastacembelidae	*Mastacembelus brachyrhinus*	N01727	6948	8	0	0	963	0	762	0
Mastacembelidae	*Mastacembelus cunningtoni*	N20638	7046	8	0	0	969	0	762	0
Mastacembelidae	*Mastacembelus erythrotaenia*	E01157	5328	7	0	0	0	0	0	0
Mastacembelidae	*Mastacembelus niger*	N20658	7640	9	690	0	966	0	0	0
Melanocetidae	*Melanocetus johnsonii*	E00657	12119	14	669	0	0	0	762	732
Melanocetidae	*Melanocetus murrayi*	E00477	8829	10	0	0	0	0	0	645
Melanotaeniidae	*Melanotaenia sp*	N35702	6890	8	660	0	987	0	762	0
Melanotaeniidae	*Melanotaenia splendida*	E00179	10979	13	0	1257	987	807	0	741
Melanotaeniidae	*Melanotaenia trifasciata*	E00178	7620	9	705	0	0	0	0	0
Melanotaeniidae	*Rhadinocentrus ornatus*	E00183	8085	9	0	1260	0	0	0	0
Menidae	*Mene maculata*	E01131	14538	17	705	1281	906	0	708	0
Microdesmidae	*Cerdale floridana*	E00113	5251	7	0	0	0	0	0	0
Microdesmidae	*Gunnellichthys monostigma*	E00545	4244	6	0	0	0	0	0	0
Microdesmidae	*Microdesmus bahianus*	E00112	6294	8	0	0	0	0	0	0
Microdesmidae	*Microdesmus longipinnis*	E00388	7384	9	0	0	0	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Microdesmidae	*Nemateleotris magnifica*	N20888	3449	4	0	0	882	0	0	0
Microdesmidae	*Ptereleotris evides*	E00565	10142	12	705	0	954	0	750	0
Microdesmidae	*Ptereleotris microlepis*	E00554	6773	9	0	0	0	0	0	0
Molidae	*Masturus lanceolatus*	E00651	10906	12	669	0	0	0	696	0
Molidae	*Mola mola*	E00683	12859	14	705	0	957	0	753	0
Molidae	*Ranzania laevis*	G01463	10882	12	699	0	0	0	0	0
Monacanthidae	*Acreichthys tomentosus*	N21168	5898	7	705	0	0	0	0	0
Monacanthidae	*Aluterus scriptus*	E00316	8934	9	672	0	0	0	0	0
Monacanthidae	*Amanses scopas*	E00536	7667	7	636	0	0	0	0	0
Monacanthidae	*Cantherhines pardalis pullus*	E00887	13701	14	675	1257	939	804	0	0
Monacanthidae	*Oxymonacanthus longirostris*	E00914	7920	8	693	0	0	0	0	747
Monacanthidae	*Paraluteres prionurus*	E00913	10156	10	690	1215	0	0	762	0
Monacanthidae	*Pervagor janthinosoma*	N21229	7625	9	705	0	957	0	741	0
Monacanthidae	*Pervagor nigrolineatus*	N21232	5912	7	705	0	0	0	0	0
Monacanthidae	*Stephanolepis hispidus*	E00646	10631	13	705	0	0	0	0	0
Monodactylidae	*Monodactylus argenteus*	E00827	11839	12	0	1308	0	0	762	0
Monodactylidae	*Monodactylus sebae*	N21267	8411	10	705	0	969	0	759	0
Moronidae	*Dicentrarchus labrax*	E01132	13167	14	705	1287	975	0	0	0
Moronidae	*Morone americana*	E00017	4648	6	0	0	0	0	747	0
Moronidae	*Morone chrysops*	E00992	15777	17	705	1269	987	825	762	0
Moronidae	*Morone mississippiensis*	E00087	11851	14	705	0	0	0	762	0
Moronidae	*Morone saxatilis*	G01380	9541	12	705	0	903	0	762	0
Mugilidae	*Chelon macrolepis*	E00845	8599	11	705	0	0	0	762	0
Mugilidae	*Crenimugil crenilabis*	E00846	12826	14	705	1257	0	825	762	765
Mugilidae	*Liza richardsonii*	E00808	12339	15	705	1257	0	825	762	756
Mugilidae	*Moolgarda engeli*	E00739	6506	8	696	1254	0	810	0	0
Mugilidae	*Mugil cephalus*	E00049	13859	15	705	0	888	0	762	0
Mugilidae	*Mugil curema*	E00031	15184	16	705	1188	987	0	762	0
Mugilidae	*Mugil trichodon*	E00765	10230	11	684	1257	0	819	0	0
Mugilidae	*Myxus capensis*	E00809	9832	10	0	1257	0	0	762	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Mugilidae	*Neomyxus leuciscus*	E00742	10501	12	678	1257	0	660	0	0
Mugilidae	*Valamugil buchanani*	E00847	12275	15	703	1257	0	822	762	0
Mullidae	*Mulloidichthys flavolineatus*	E00844	9135	11	705	1257	0	0	0	0
Mullidae	*Mullus auratus*	E00634	10617	12	693	1254	0	825	0	0
Mullidae	*Parupeneus barberinus*	E00899	8131	10	0	0	0	819	0	0
Mullidae	*Parupeneus ciliatus*	E00840	5965	8	680	0	0	819	0	684
Mullidae	*Parupeneus trifasciatus*	N21710	5845	7	0	0	0	0	0	0
Mullidae	*Pseudupeneus maculatus*	E00773	9043	11	0	0	0	825	0	0
Mullidae	*Upeneus moluccensis*	E00825	7964	10	705	0	0	0	0	651
Mullidae	*Upeneus parvus*	N21732	3287	4	0	0	0	0	0	0
Nandidae	*Nandus andrewi*	N22312	8474	10	705	0	957	0	759	0
Nandidae	*Nandus nandus*	G01388	11524	13	705	1284	981	0	762	0
Nandidae	*Nandus nebulosus*	N22314	7688	9	705	0	939	0	762	0
Nematistiidae	*Nematistius pectoralis*	E01146	12623	14	705	0	900	0	762	0
Nemipteridae	*Pentapodus caninus*	G01427	8879	11	705	0	0	0	762	0
Nemipteridae	*Scolopsis bilineata*	E00028	14791	16	669	1098	906	0	762	0
Nemipteridae	*Scolopsis frenata*	E00911	6514	8	0	0	0	825	0	0
Nemipteridae	*Scolopsis margaritifera*	G01478	7404	9	669	0	0	0	762	0
Niphonidae	*Niphon spinosus*	G01398	4377	5	690	0	0	0	0	0
Nomeidae	*Cubiceps baxteri*	G01271	9684	12	705	0	912	0	762	0
Nomeidae	*Cubiceps gracilis*	E00672	8634	11	696	1254	0	0	0	0
Nomeidae	*Cubiceps pauciradiatus*	E00667	9277	9	705	1257	0	0	0	0
Nomeidae	*Psenes cyanophrys*	E00666	6230	6	0	0	0	0	0	0
Nomeidae	*Psenes maculatus*	N23089	7094	9	0	0	906	0	702	0
Nototheniidae	*Aethotaxis mitopteryx*	G01528	7979	9	705	0	0	0	759	0
Nototheniidae	*Dissostichus eleginoides*	G01279	12707	14	705	0	987	0	759	0
Nototheniidae	*Gobionotothen gibberifrons*	G01529	8961	10	681	0	0	0	762	0
Nototheniidae	*Notothenia coriiceps*	G01526	9628	10	705	0	0	0	759	0
Nototheniidae	*Pagothenia borchgrevinki*	G01527	9352	10	696	0	0	0	0	0
Nototheniidae	*Patagonotothen tessellata*	G01530	10915	12	705	0	0	0	759	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Odacidae	*Haletta semifasciata*	G01312	9038	11	699	0	969	0	762	0
Odontobutidae	*Odontobutis potamophila*	E01137	12389	14	693	1287	978	0	0	0
Odontobutidae	*Perccottus glenii*	G01429	9285	11	705	0	933	0	0	0
Ogcocephalidae	*Dibranchus tremendus*	E00975	8668	11	0	1236	0	813	762	717
Ogcocephalidae	*Halieutichthys aculeatus*	E01122	5969	8	696	0	0	825	0	0
Ogcocephalidae	*Ogcocephalus parvus nasutus*	E00610	11181	14	705	1260	0	822	762	696
Ogcocephalidae	*Ogcocephalus radiatus*	E00641	3592	4	0	1260	0	0	0	0
Oneirodidae	*Bertella idiomorpha*	E00386	7368	8	0	0	0	0	0	732
Oneirodidae	*Dolopichthys sp*	E00484	3002	4	0	0	0	0	0	0
Oneirodidae	*Oneirodes bulbosus*	E00176	5086	7	0	0	0	0	0	0
Oneirodidae	*Oneirodes macrosteus*	E00655	7815	10	0	0	0	0	762	759
Ophidiidae	*Bassogigas gillii*	E00481	5439	7	669	1257	0	0	0	0
Ophidiidae	*Brotula barbata*	E00629	8900	12	690	0	0	0	762	765
Ophidiidae	*Brotula multibarbata*	E00883	12654	16	705	0	963	825	759	750
Ophidiidae	*Brotulotaenia crassa*	E00659	7913	10	0	1245	0	825	762	744
Ophidiidae	*Brotulotaenia nigra*	E00817	8794	11	0	1251	0	825	762	765
Ophidiidae	*Chilara taylori*	E00260	6335	8	0	0	0	0	0	0
Ophidiidae	*Dicrolene introniger*	E00480	8819	11	678	1236	0	0	0	0
Ophidiidae	*Genypterus blacodes*	E00241	3596	4	0	0	0	0	0	0
Ophidiidae	*Lamprogrammus niger*	E00275	11903	13	693	1236	975	0	0	0
Ophidiidae	*Lepophidium brevibarbe*	E00758	5469	7	0	1257	0	825	0	0
Ophidiidae	*Lepophidium jeannae*	E00621	4709	6	0	1257	0	0	0	0
Ophidiidae	*Lepophidium profundorum*	E00248	3341	4	0	1257	0	0	0	0
Ophidiidae	*Neobythites gilli*	E00612	7830	10	705	1257	0	825	0	765
Ophidiidae	*Ophidion holbrookii*	E01033	7171	9	0	1257	0	825	762	0
Ophidiidae	*Ophidion josephi*	E00648	6546	8	0	1233	0	0	0	0
Ophidiidae	*Ophidion robinsi*	E01007	6730	8	0	1215	0	0	762	0
Ophidiidae	*Petrotyx sanguineus*	E00206	4716	6	0	0	0	0	0	0
Opistognathidae	*Lonchopisthus micrognathus*	E00603	6548	8	0	1257	0	780	0	0
Opistognathidae	*Opistognathus aurifrons*	E00216	9008	11	699	0	981	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Opistognathidae	*Opistognathus maxillosus*	E00207	6793	8	693	0	0	0	0	0
Oplegnathidae	*Oplegnathus punctatus*	G01405	12420	13	696	0	987	0	750	0
Osphronemidae	*Betta splendens*	G01226	9892	10	0	0	0	0	762	0
Osphronemidae	*Trichopodus pectoralis*	N24415	4860	7	0	0	0	0	692	0
Ostraciidae	*Acanthostracion quadricornis*	E00760	5464	6	0	0	0	0	0	0
Ostraciidae	*Ostracion cubicus*	E00588	12421	15	705	0	0	0	756	0
Ostraciidae	*Rhinesomus triqueter*	G01469	10814	13	669	0	954	0	738	0
Ostracoberycidae	*Ostracoberyx dorygenys*	N24448	6883	9	705	0	0	0	699	0
Parabembridae	*Parabembras curtus*	N24483	6893	9	690	0	0	0	711	0
Paralichthyidae	*Ancylopsetta ommata*	E00001	8842	10	705	1305	0	0	0	0
Paralichthyidae	*Citharichthys arctifrons*	E00043	6688	8	693	0	0	0	0	0
Paralichthyidae	*Citharichthys sordidus*	E00446	12907	14	693	1284	0	756	762	745
Paralichthyidae	*Cyclopsetta chittendeni*	E00597	10244	12	693	1281	0	807	0	747
Paralichthyidae	*Etropus crossotus*	E00647	8021	9	693	1191	0	780	0	0
Paralichthyidae	*Etropus microstomus*	E00047	5197	5	0	0	0	0	0	0
Paralichthyidae	*Gastropsetta frontalis*	E00640	2345	3	0	0	0	0	0	0
Paralichthyidae	*Paralichthys albigutta*	E01171	8241	9	705	1308	0	0	0	0
Paralichthyidae	*Paralichthys californicus*	E00020	8905	10	0	1260	0	0	0	0
Paralichthyidae	*Paralichthys dentatus*	N24591	7812	9	705	0	975	0	0	0
Paralichthyidae	*Pseudorhombus pentophthalmus*	E00077	10302	11	0	0	0	0	0	0
Paralichthyidae	*Syacium micrurum*	E00633	9035	11	693	1281	0	0	0	654
Paralichthyidae	*Xystreurys liolepis*	E00021	9760	10	693	1308	0	0	0	0
Pegasidae	*Eurypegasus draconis*	N24699	2094	3	0	0	0	0	0	0
Pempheridae	*Parapriacanthus ransonneti*	E00923	11086	13	705	1245	0	747	762	0
Pempheridae	*Pempheris oualensis*	E00718	9245	11	705	1185	0	0	762	0
Pempheridae	*Pempheris schomburgkii*	E00213	10586	12	702	0	0	0	0	0
Pempheridae	*Pempheris schwenkii*	N01628	5322	7	705	0	0	0	699	0
Pempheridae	*Pempheris vanicolensis*	E00886	8350	10	0	1260	0	825	0	0
Pentacerotidae	*Histiopterus typus*	N24730	6890	9	705	0	0	0	702	0
Pentacerotidae	*Paristiopterus labiosus*	M01629	3261	4	705	0	0	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Pentacerotidae	*Pentaceros japonicus*	N24735	7793	10	705	0	906	0	705	0
Pentacerotidae	*Pentaceros pectoralis*	N01736	5434	7	666	0	879	0	762	0
Pentacerotidae	*Pentaceros wheeleri*	N01737	7434	9	706	0	882	0	744	0
Pentacerotidae	*Zanclistius elevatus*	M01631	2901	3	0	0	0	0	0	0
Percichthyidae	*Gadopsis marmoratus*	E01144	13223	14	705	1287	975	0	762	0
Percichthyidae	*Maccullochella peelii*	G01365	11015	13	705	1287	954	0	762	0
Percichthyidae	*Macquaria ambigua*	G01366	10488	13	696	1287	864	0	702	0
Percichthyidae	*Macquaria colonorum*	G01431	10574	13	696	1287	879	0	696	0
Percichthyidae	*Macquaria novemaculeata*	G01432	10525	13	696	1287	864	0	702	0
Percichthyidae	*Nannoperca australis*	G01389	11969	14	696	1287	627	0	669	0
Percichthyidae	*Percichthys trucha*	G01430	9417	9	0	1287	906	0	0	0
Percidae	*Ammocrypta beanii*	E00187	8350	10	705	0	0	0	0	0
Percidae	*Ammocrypta meridiana*	E00148	8201	10	705	0	0	0	0	0
Percidae	*Ammocrypta pellucida*	E00149	9339	11	705	0	0	0	0	0
Percidae	*Crystallaria asprella*	E00153	8415	10	0	0	0	0	0	0
Percidae	*Etheostoma atripinne*	G01290	7713	9	705	0	975	0	759	0
Percidae	*Etheostoma juliae*	E00168	11455	14	0	0	0	825	762	765
Percidae	*Etheostoma simoterum*	E00152	12189	15	705	0	978	0	758	0
Percidae	*Etheostoma vitreum*	E00147	11025	13	705	0	0	0	762	759
Percidae	*Etheostoma zonale*	E01111	13171	16	705	0	0	822	762	765
Percidae	*Gymnocephalus cernuus*	E00140	7525	10	0	0	0	0	762	0
Percidae	*Gymnocephalus schraetser*	E00141	6323	8	0	0	0	0	750	0
Percidae	*Perca flavescens*	E00391	14692	16	0	0	903	0	759	759
Percidae	*Perca fluviatilis*	G01428	10413	11	0	0	0	0	744	0
Percidae	*Percina caprodes*	E01054	15273	18	705	0	975	0	744	750
Percidae	*Percina nigrofasciata*	E00154	7519	9	0	0	0	0	0	0
Percidae	*Percina phoxocephala*	E00150	9105	11	705	0	0	0	0	0
Percidae	*Romanichthys valsanicola*	E00143	9564	12	690	0	0	819	762	738
Percidae	*Sander vitreus*	E01109	10398	10	696	1236	0	0	0	0
Percidae	*Zingel streber*	E00144	5447	7	0	0	0	0	762	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Percidae	*Zingel zingel*	E00142	6114	8	0	0	0	0	0	0
Perciliidae	*Percilia irwini*	N24981	6918	9	696	0	0	0	687	0
Percophidae	*Acanthaphritis unoorum*	N24985	5579	7	705	0	906	0	0	0
Peristediidae	*Peristedion ecuadorense*	E00456	6094	7	0	1245	0	0	0	0
Peristediidae	*Peristedion gracile*	E01029	2905	4	0	0	0	0	762	0
Peristediidae	*Peristedion truncatum*	E00450	3441	5	0	0	0	0	0	0
Phallostethidae	*Phenacostethus smithi*	E00398	7945	10	678	0	873	0	693	0
Pholidae	*Pholis crassispina*	G01437	12482	14	693	0	942	0	762	0
Pholidae	*Pholis ornata*	N01732	8528	10	690	0	954	0	756	0
Pholidichthyidae	*Pholidichthys leucotaenia*	E00251	11101	12	693	1287	987	0	0	0
Pinguipedidae	*Parapercis clathrata*	E00707	10851	13	693	1234	0	0	762	0
Pinguipedidae	*Parapercis hexophtalma*	E01083	11528	14	696	1260	0	0	0	753
Pinguipedidae	*Parapercis punctulata*	E01091	7008	9	0	0	0	0	0	741
Platycephalidae	*Platycephalus indicus*	N25405	6719	9	690	0	0	0	714	0
Platycephalidae	*Rogadius asper*	N25418	6352	9	693	0	0	0	711	0
Platycephalidae	*Sunagocia arenicola*	E00708	5403	7	0	0	0	0	0	0
Platycephalidae	*Thysanophrys chiltonae*	E00864	8747	10	0	0	0	813	0	0
Plesiopidae	*Plesiops coeruleolineatus*	E00855	15452	18	705	1308	906	0	762	765
Plesiopidae	*Plesiops melas*	G01442	8238	10	699	0	912	0	762	0
Pleuronectidae	*Atheresthes evermanni*	E00055	8437	8	0	1308	0	0	0	0
Pleuronectidae	*Embassichthys bathybius*	E00064	11340	12	0	1281	0	0	0	0
Pleuronectidae	*Eopsetta jordani*	E00444	14474	17	705	840	0	717	762	753
Pleuronectidae	*Glyptocephalus zachirus*	E00416	10353	12	0	0	0	753	762	744
Pleuronectidae	*Hippoglossoides elassodon*	E00424	12527	13	693	1278	0	0	762	0
Pleuronectidae	*Hippoglossus hippoglossus*	E00689	10279	12	693	867	0	807	0	0
Pleuronectidae	*Hypsopsetta guttulata*	E00022	9133	9	0	1308	0	0	0	0
Pleuronectidae	*Isopsetta isolepis*	E00018	6603	8	0	1308	0	0	0	0
Pleuronectidae	*Lepidopsetta bilineata*	E00438	16335	19	696	0	981	0	762	765
Pleuronectidae	*Limanda limanda*	E00690	7013	8	0	834	0	0	0	0
Pleuronectidae	*Lyopsetta exilis*	E01173	6171	7	0	0	0	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Pleuronectidae	*Microstomus pacificus*	E00433	10016	12	681	1011	0	0	0	0
Pleuronectidae	*Parophrys vetulus*	E00445	12033	14	693	1245	0	0	762	744
Pleuronectidae	*Platichthys stellatus*	E00026	7842	9	0	0	0	0	0	0
Pleuronectidae	*Pleuronectes platessa*	E00053	14871	17	705	861	975	0	762	0
Pleuronectidae	*Psettichthys melanostictus*	E00025	9364	11	0	879	0	0	0	0
Pleuronectidae	*Pseudopleuronectes americanus*	E00035	15563	18	705	1215	921	0	741	0
Poeciliidae	*Belonesox belizanus*	E01052	10182	11	0	1260	0	825	0	0
Poeciliidae	*Gambusia affinis*	G01296	11403	12	705	0	987	0	762	0
Poeciliidae	*Heterandria formosa*	E00185	10113	11	0	1257	0	0	762	0
Poeciliidae	*Poecilia latipinna reticulata*	E01065	12149	14	705	1248	0	0	0	720
Poeciliidae	*Poeciliopsis elongata*	N01734	6863	8	705	0	954	0	0	0
Poecilopsettidae	*Poecilopsetta beanii*	E00448	5472	7	0	1233	0	0	762	0
Poecilopsettidae	*Poecilopsetta plinthus*	E00073	9752	10	0	1305	0	0	0	0
Polycentridae	*Monocirrhus polyacanthus*	G01377	8420	10	0	0	957	0	762	0
Polycentridae	*Polycentropsis abbreviata*	N26006	8369	10	705	0	951	0	762	0
Polycentridae	*Polycentrus schomburgkii*	G01444	8382	10	705	0	951	0	762	0
Polynemidae	*Eleutheronema rhadinum*	N26015	7791	10	708	0	906	0	702	0
Polynemidae	*Eleutheronema tetradactylum*	E01154	7961	9	705	1287	0	0	0	0
Polynemidae	*Leptomelanosoma indicum*	E00842	11242	14	0	1287	0	825	762	750
Polynemidae	*Polydactylus octonemus*	E00606	9992	13	561	1284	0	696	0	714
Polynemidae	*Polydactylus sextarius*	N26043	5532	7	706	0	0	0	702	0
Polynemidae	*Polydactylus virginicus*	E00217	11602	13	705	1284	0	0	762	696
Polyprionidae	*Polyprion americanus*	E00242	7677	9	0	0	0	0	762	0
Polyprionidae	*Polyprion oxygeneios*	M01632	4716	5	705	0	0	0	0	0
Polyprionidae	*Stereolepis gigas*	E00227	14211	17	705	1260	912	0	762	0
Pomacanthidae	*Apolemichthys trimaculatus*	E00839	9202	12	654	1257	0	825	759	0
Pomacanthidae	*Centropyge bicolor*	E00550	11381	15	705	1257	0	0	762	750
Pomacanthidae	*Centropyge loricula*	E00284	9087	10	705	1236	0	0	0	0
Pomacanthidae	*Centropyge nox*	E00542	8384	11	696	1257	0	786	0	729
Pomacanthidae	*Chaetodontoplus melanosoma*	G01244	8178	10	705	0	954	0	0	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Pomacanthidae	*Holacanthus ciliaris*	E00209	6815	8	0	0	0	0	0	0
Pomacanthidae	*Holacanthus passer*	E00282	12494	15	657	0	978	0	0	0
Pomacanthidae	*Holacanthus tricolor*	E00198	7349	9	705	1233	0	0	0	0
Pomacanthidae	*Pomacanthus arcuatus*	E00754	8027	10	0	1203	0	0	0	0
Pomacanthidae	*Pomacanthus imperator*	E00710	9192	12	693	1281	0	0	0	0
Pomacanthidae	*Pomacanthus semicirculatus*	E00849	10414	14	705	1236	0	0	762	759
Pomacanthidae	*Pomacanthus zonipectus*	G01448	9113	11	705	0	975	0	0	0
Pomacanthidae	*Pygoplites diacanthus*	E00534	10507	13	696	1257	0	0	0	612
Pomacentridae	*Abudefduf saxatilis*	E00820	14973	18	687	1260	0	825	762	765
Pomacentridae	*Abudefduf sexfasciatus*	E00881	12145	15	0	0	0	825	762	711
Pomacentridae	*Abudefduf vaigiensis*	E00890	12132	13	690	1215	0	825	0	765
Pomacentridae	*Acanthochromis polyacanthus*	E00466	8743	10	0	1260	0	822	0	0
Pomacentridae	*Amblyglyphidodon leucogaster*	E00529	3808	4	0	0	0	0	0	0
Pomacentridae	*Amphiprion clarkii*	E00196	4604	6	705	0	0	0	0	0
Pomacentridae	*Amphiprion ocellaris*	E00193	7717	7	0	0	0	0	762	0
Pomacentridae	*Azurina hirundo*	E00580	9629	12	0	1257	0	0	762	765
Pomacentridae	*Chromis atripectoralis*	E00238	9353	11	705	1260	0	0	0	0
Pomacentridae	*Chromis cyanea*	E00201	13033	15	705	1260	909	0	762	0
Pomacentridae	*Chromis dimidiata*	E00851	9724	12	705	1236	0	0	762	0
Pomacentridae	*Chrysiptera taupou*	E00564	9950	13	0	1260	0	825	720	639
Pomacentridae	*Dascyllus aruanus*	E00700	11886	14	698	1260	0	0	0	741
Pomacentridae	*Dascyllus carneus*	E00862	11899	14	705	1260	0	810	0	765
Pomacentridae	*Dascyllus reticulatus*	E00724	8549	10	700	1260	0	0	726	0
Pomacentridae	*Dascyllus trimaculatus*	E00865	6439	7	0	0	0	0	0	0
Pomacentridae	*Dischistodus perspicillatus*	E00464	8931	11	0	1260	0	783	762	645
Pomacentridae	*Hypsypops rubicundus*	E00459	7285	10	0	0	0	0	762	0
Pomacentridae	*Lepidozygus tapeinosoma*	E00929	7795	10	0	1245	0	819	762	0
Pomacentridae	*Microspathodon bairdii*	G01375	8331	10	696	0	909	0	762	0
Pomacentridae	*Microspathodon chrysurus*	E00772	10751	13	696	1260	0	825	0	750
Pomacentridae	*Neoglyphidodon melas*	E00465	9828	12	0	1260	0	0	735	642

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Pomacentridae	*Neoglyphidodon polyacanthus*	E00285	6455	8	0	1260	0	0	0	0
Pomacentridae	*Neopomacentrus cyanomos*	E00933	8888	11	696	1260	0	753	0	738
Pomacentridae	*Parma microlepis*	E00286	5332	7	705	0	0	0	0	0
Pomacentridae	*Plectroglyphidodon dickii*	E00572	13722	16	693	1260	0	822	761	750
Pomacentridae	*Plectroglyphidodon johnstonianus*	E00722	7987	10	0	1260	0	0	762	729
Pomacentridae	*Pomacentrus brachialis*	E00239	9865	12	693	1284	0	804	0	645
Pomacentridae	*Pomacentrus pavo*	E00729	12503	15	696	1257	0	825	0	708
Pomacentridae	*Pomacentrus spilotoceps*	E00557	6421	9	0	0	0	0	762	636
Pomacentridae	*Pomachromis richardsoni*	E00559	8319	11	0	0	0	825	762	726
Pomacentridae	*Stegastes albifasciatus*	E00713	6612	9	0	0	0	735	762	0
Pomacentridae	*Stegastes diencaeus*	E00219	6060	8	0	0	0	0	762	0
Pomacentridae	*Stegastes fuscus*	E00203	12679	15	686	0	960	0	744	0
Pomacentridae	*Stegastes partitus*	E00204	4367	6	705	0	0	0	0	0
Pomatomidae	*Pomatomus saltatrix*	E00516	16569	18	705	1284	951	0	762	0
Priacanthidae	*Heteropriacanthus cruentatus*	E00570	14367	17	702	1257	957	0	762	0
Priacanthidae	*Priacanthus arenatus*	E00618	14657	18	705	1224	885	0	693	765
Priacanthidae	*Pristigenys alta*	E00252	12492	14	534	1095	861	0	699	0
Pristolepididae	*Pristolepis fasciata*	N26580	7608	9	658	0	963	0	762	0
Pristolepididae	*Pristolepis sp*	N36627	8543	10	690	0	957	0	762	0
Psettodidae	*Psettodes belcheri*	E01180	6046	7	705	1302	0	0	0	0
Psettodidae	*Psettodes erumei*	E01165	12034	14	705	1308	906	0	0	0
Pseudaphritidae	*Pseudaphritis urvillii*	G01453	8567	9	705	0	0	0	759	0
Pseudochromidae	*Congrogadus subducens*	G01262	8360	10	699	0	987	0	762	0
Pseudochromidae	*Halidesmus scapularis*	E00793	10231	13	705	1284	0	0	756	0
Pseudochromidae	*Labracinus cyclophthalmus*	G01343	11328	12	705	0	963	0	762	0
Pseudochromidae	*Natalichthys sam*	E00589	7891	10	0	1233	0	0	762	0
Pseudochromidae	*Ogilbyina novaehollandiae*	G01403	8345	10	699	0	978	0	762	0
Pseudochromidae	*Pholidochromis cerasina*	G01436	8319	10	699	0	987	0	678	0
Pseudochromidae	*Pseudochromis cyanotaenia*	E00706	7668	10	705	1260	0	0	762	738
Pseudochromidae	*Pseudochromis fridmani*	N26709	8561	10	705	0	975	0	762	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Pseudochromidae	*Pseudochromis jamesi*	E00535	6957	9	705	1260	0	0	762	726
Pseudochromidae	*Pseudoplesiops revellei*	E00745	4311	6	0	0	0	0	762	0
Pseudomugilidae	*Pseudomugil gertrudae*	E00182	14736	18	705	1248	873	798	762	747
Pseudomugilidae	*Pseudomugil signifer*	E00184	11998	15	0	1254	870	0	702	0
Psychrolutidae	*Cottunculus thomsonii*	E00963	2374	3	0	0	0	0	0	0
Psychrolutidae	*Dasycottus setiger*	E00288	5136	6	0	1236	0	744	0	0
Psychrolutidae	*Malacocottus zonurus*	E00253	8212	10	0	1236	0	0	0	0
Psychrolutidae	*Psychrolutes phrictus*	E00276	5502	7	0	1233	0	0	0	0
Rachycentridae	*Rachycentron canadum*	E00468	15775	17	693	0	984	0	762	0
Rhombosoleidae	*Oncopterus darwinii*	E01184	6659	7	0	1263	0	0	0	0
Rhombosoleidae	*Rhombosolea leporina*	E01166	2980	3	0	0	0	0	0	0
Rhombosoleidae	*Rhombosolea plebeia*	E01167	5378	6	0	0	0	0	0	0
Rhombosoleidae	*Rhombosolea tapirina*	E01168	3805	4	0	0	0	0	0	0
Samaridae	*Plagiopsetta glossa*	E00074	7559	8	0	0	0	0	0	0
Samaridae	*Samariscus japonicus*	E00072	7912	8	0	0	0	0	0	0
Samaridae	*Samariscus latus*	N27771	2733	3	0	0	0	0	0	0
Samaridae	*Samariscus xenicus*	E00078	7553	8	0	0	0	0	0	0
Scaridae	*Calotomus carolinus*	N27783	7195	9	627	0	918	0	0	0
Scaridae	*Cetoscarus bicolor*	E00566	14113	17	695	1251	972	0	762	723
Scaridae	*Chlorurus gibbus*	E00561	6813	9	0	0	0	783	0	0
Scaridae	*Chlorurus sordidus*	E00837	14642	16	696	1251	974	825	762	747
Scaridae	*Cryptotomus roseus*	N27805	7128	9	678	0	909	0	0	0
Scaridae	*Hipposcarus longiceps*	E00737	4541	6	0	0	0	0	0	720
Scaridae	*Leptoscarus vaigiensis*	E00877	8427	11	0	0	0	825	762	765
Scaridae	*Scarus ghobban*	E00878	9678	11	696	0	0	825	0	0
Scaridae	*Scarus globiceps*	N27829	4729	6	552	0	882	0	0	0
Scaridae	*Scarus iseri*	E00013	7345	9	0	1251	0	0	762	0
Scaridae	*Scarus niger*	E00875	11274	14	706	0	873	738	744	714
Scaridae	*Scarus quoyi*	E00872	7432	10	705	0	0	741	762	624
Scaridae	*Scarus rubroviolaceus*	E00874	12027	13	705	1251	0	825	762	765

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Scaridae	*Sparisoma aurofrenatum*	E00008	5465	7	0	0	0	0	0	0
Scaridae	*Sparisoma chrysopterum*	E00070	2776	4	0	0	0	0	0	0
Scaridae	*Sparisoma viride*	E00004	6443	9	705	0	0	0	0	0
Scatophagidae	*Scatophagus argus*	E00051	13219	16	654	0	969	0	762	0
Scatophagidae	*Selenotoca multifasciata*	G01483	9576	12	705	0	879	0	693	0
Sciaenidae	*Aplodinotus grunniens*	E01108	17827	19	705	1236	954	732	756	0
Sciaenidae	*Atractoscion nobilis*	E00125	9878	13	705	0	0	0	0	0
Sciaenidae	*Bairdiella chrysoura*	E00165	7670	10	0	0	0	0	762	0
Sciaenidae	*Cheilotrema saturnum*	E00118	6644	9	0	0	0	0	0	0
Sciaenidae	*Corvula sanctaeluciae*	E01047	5698	7	0	1257	0	0	0	0
Sciaenidae	*Cynoscion arenarius*	E00511	11444	13	696	1257	0	0	762	0
Sciaenidae	*Cynoscion regalis*	E00164	14880	18	705	0	942	0	762	0
Sciaenidae	*Genyonemus lineatus*	E00138	9138	12	705	1260	0	0	0	0
Sciaenidae	*Larimus breviceps*	E01048	4776	7	0	0	0	0	0	0
Sciaenidae	*Leiostomus xanthurus*	G01349	9972	12	705	0	926	0	762	0
Sciaenidae	*Menticirrhus saxatilis*	E00166	7177	9	705	1257	0	0	0	0
Sciaenidae	*Menticirrhus undulatus littoralis*	E00127	15027	19	705	0	963	813	762	690
Sciaenidae	*Micropogonias undulatus*	N01637	5789	8	0	0	879	0	693	0
Sciaenidae	*Odontoscion dentex*	E01049	5655	7	0	1257	0	0	0	0
Sciaenidae	*Pareques acuminatus*	E01050	3516	4	0	1257	0	0	0	0
Sciaenidae	*Pareques umbrosus*	E00639	6228	8	705	1257	0	0	0	0
Sciaenidae	*Pogonias cromis*	E00699	8505	11	705	1257	0	0	762	0
Sciaenidae	*Sciaenops ocellatus*	E01055	18596	20	705	1278	903	816	762	0
Sciaenidae	*Seriphus politus*	E00123	7497	10	705	0	0	0	762	0
Sciaenidae	*Stellifer lanceolatus*	E00608	9278	12	705	1257	0	0	762	0
Sciaenidae	*Umbrina coroides*	E00628	8595	11	0	1257	0	0	0	744
Scomberesocidae	*Cololabis saira*	E00192	10242	11	705	1236	0	0	0	0
Scomberesocidae	*Scomberesox saurus*	E00404	10373	13	705	0	987	0	0	0
Scombridae	*Acanthocybium solandri*	E00927	14337	16	705	1236	0	0	762	675
Scombridae	*Auxis rochei*	E00673	14617	18	705	1233	879	0	762	756

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Scombridae	*Euthynnus affinis*	E00830	9732	12	0	1260	0	813	762	765
Scombridae	*Euthynnus alletteratus*	E00696	7879	11	0	0	0	723	762	738
Scombridae	*Gymnosarda unicolor*	E00832	9359	11	0	1233	0	810	762	0
Scombridae	*Katsuwonus pelamis*	E00747	11259	13	684	1233	0	0	762	0
Scombridae	*Sarda sarda*	E00243	16203	19	705	1260	957	0	756	642
Scombridae	*Scomber japonicus*	E00247	10495	12	705	1257	0	0	762	0
Scombridae	*Scomber scombrus*	E00626	19143	20	705	1308	954	0	762	0
Scombridae	*Scomberomorus maculatus sp*	E00631	16041	19	705	1260	966	774	762	723
Scombridae	*Scomberomorus regalis commerson*	E00694	9863	12	0	0	0	759	747	720
Scombridae	*Thunnus albacares*	E00831	18226	21	705	1233	885	786	762	540
Scombrolabracidae	*Scombrolabrax heterolepis*	E00976	11570	14	657	1308	0	0	762	762
Scophthalmidae	*Lepidorhombus boscii*	E00462	9162	10	693	1308	0	0	0	699
Scophthalmidae	*Scophthalmus aquosus*	E00039	10410	12	0	1281	960	0	0	0
Scophthalmidae	*Scophthalmus maximus*	E01161	6280	5	0	1281	0	0	0	0
Scorpaenidae	*Caracanthus maculatus*	E00716	8029	10	687	1251	0	825	0	0
Scorpaenidae	*Caracanthus unipinna*	E00558	6573	8	705	1257	0	0	0	0
Scorpaenidae	*Dendrochirus zebra*	E00897	7402	10	0	0	0	0	762	0
Scorpaenidae	*Iracundus signifer*	E00583	7125	9	0	1257	0	825	0	747
Scorpaenidae	*Neomerinthe hemingwayi*	E00619	10221	12	0	1257	0	813	0	0
Scorpaenidae	*Pontinus longispinis*	E01010	7126	10	0	0	0	0	762	0
Scorpaenidae	*Pontinus rathbuni*	E00463	6391	8	0	0	0	0	0	0
Scorpaenidae	*Pterois antennata*	E00705	8496	11	0	0	0	0	0	0
Scorpaenidae	*Pterois miles*	E00882	7015	9	0	0	0	0	0	0
Scorpaenidae	*Pterois radiata*	E00850	8182	10	0	1200	0	0	0	0
Scorpaenidae	*Scorpaena agassizii*	E01038	2193	3	0	0	0	0	0	0
Scorpaenidae	*Scorpaena brasiliensis*	E00759	4986	7	0	0	0	0	0	0
Scorpaenidae	*Scorpaena dispar*	E00512	3690	5	0	0	0	0	0	0
Scorpaenidae	*Scorpaena guttata*	E00291	8547	10	0	1260	0	0	0	0
Scorpaenidae	*Scorpaenodes albaiensis*	E00532	4039	5	0	0	0	0	0	0
Scorpaenidae	*Scorpaenodes guamensis*	E00870	6637	9	0	0	0	0	0	696

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Scorpaenidae	*Scorpaenopsis longispina*	E00903	7186	9	0	1257	0	0	762	699
Scorpaenidae	*Scorpaenopsis oxycephala*	E00581	5118	7	0	0	0	0	0	0
Scorpaenidae	*Sebastapistes cyanostigma*	E00888	8326	10	0	1260	0	819	0	723
Scorpaenidae	*Taenianotus triacanthus*	E00866	8147	10	0	1257	0	777	0	720
Sebastidae	*Adelosebastes latens*	E00066	2246	3	0	0	0	0	0	0
Sebastidae	*Helicolenus dactylopterus*	E00044	9920	12	0	1257	0	0	0	0
Sebastidae	*Sebastes aurora*	E00349	8679	10	651	1308	0	0	0	0
Sebastidae	*Sebastes diploproa*	E00432	6421	8	0	1257	0	0	0	0
Sebastidae	*Sebastes fasciatus*	G01482	8330	10	705	0	0	0	753	0
Sebastidae	*Sebastes jordani*	E00350	6619	9	705	0	0	0	0	0
Sebastidae	*Sebastes paucispinis*	E00354	6853	9	672	0	0	0	0	0
Sebastidae	*Sebastes ruberrimus*	N28709	6206	8	705	0	0	0	762	0
Sebastidae	*Sebastolobus alascanus*	E00417	12929	16	705	0	0	0	729	0
Serranidae	*Aethaloperca rogaa*	E01079	6350	8	0	0	0	690	0	0
Serranidae	*Anthias nicholsi*	E00447	6801	6	0	1257	0	0	0	0
Serranidae	*Aporops bilinearis*	E00531	7661	10	0	1260	0	0	0	741
Serranidae	*Baldwinella aureorubens*	G01220	8097	10	705	0	957	0	0	0
Serranidae	*Baldwinella vivana*	E00338	3660	5	696	0	0	0	0	0
Serranidae	*Centropristis striata*	E00163	8944	11	0	0	0	0	762	0
Serranidae	*Cephalopholis argus*	E00868	14648	18	696	0	948	0	762	702
Serranidae	*Cephalopholis fulva*	E00771	5807	7	0	1236	0	0	0	0
Serranidae	*Cephalopholis miniata*	E00838	9601	12	696	1257	0	0	0	750
Serranidae	*Diplectrum bivittatum*	E01008	4699	6	0	0	0	0	762	702
Serranidae	*Diplectrum formosum*	E01002	8832	10	0	0	0	0	762	531
Serranidae	*Epinephelus maculatus*	E00549	12180	14	0	0	903	0	0	0
Serranidae	*Epinephelus merra*	E00552	8076	10	0	0	0	0	0	0
Serranidae	*Grammistes sexlineatus*	E00900	15699	17	666	1308	987	0	762	0
Serranidae	*Grammistops ocellatus*	E00571	6588	8	0	1203	0	0	0	0
Serranidae	*Hypoplectrus puella*	E00505	12795	16	663	1257	0	0	756	0
Serranidae	*Hyporthodus flavolimbatus*	E00627	5022	7	696	0	0	0	0	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Serranidae	*Liopropoma mowbrayi*	E00307	4911	6	0	1236	0	0	0	0
Serranidae	*Liopropoma rubre*	E00306	13426	14	705	1278	900	0	0	0
Serranidae	*Mycteroperca bonaci microlepis*	E00311	14036	17	712	0	951	0	762	0
Serranidae	*Odontanthias chrysostictus*	G01327	10158	10	0	1287	975	0	0	0
Serranidae	*Paralabrax nebulifer*	E00325	12094	15	705	0	948	0	741	0
Serranidae	*Pronotogrammus martinicensis*	E00636	3713	4	0	1257	0	0	0	0
Serranidae	*Pseudanthias pascalus*	G01452	9024	11	705	0	963	0	762	0
Serranidae	*Pseudanthias squamipinnis*	E00860	6941	8	705	0	0	0	711	0
Serranidae	*Pseudogramma polyacantha*	E00852	7643	10	0	0	0	0	759	759
Serranidae	*Rypticus saponaceus*	E00764	15840	19	687	1245	957	0	744	0
Serranidae	*Rypticus subbifrenatus*	E00347	6320	7	0	1257	0	0	0	0
Serranidae	*Serranus baldwini*	E00322	14886	16	650	1275	900	0	0	0
Serranidae	*Serranus notospilus*	E00337	5719	7	0	1257	0	0	0	0
Serranidae	*Serranus phoebe*	E00336	6229	8	0	1236	0	0	0	0
Serranidae	*Serranus tigrinus*	G01486	8954	11	0	0	905	0	762	0
Setarchidae	*Setarches guentheri*	E01035	5731	8	0	0	0	0	762	0
Siganidae	*Siganus argenteus*	E00940	7215	10	705	0	0	0	0	0
Siganidae	*Siganus punctatus*	E00958	3704	4	0	0	0	0	0	0
Siganidae	*Siganus spinus*	N29369	8207	10	684	0	879	0	693	0
Siganidae	*Siganus stellatus*	G01488	6854	9	696	0	0	0	762	735
Siganidae	*Siganus vulpinus*	E00090	11306	14	705	0	888	0	762	0
Sillaginidae	*Sillago chondropus*	N29390	6780	9	657	0	918	0	702	0
Sillaginidae	*Sillago sihama*	E00824	13627	15	663	1281	0	0	762	0
Sinipercidae	*Coreoperca whiteheadi*	G01264	8180	8	0	1269	981	0	0	0
Sinipercidae	*Siniperca chuatsi*	E01136	15198	17	522	840	900	0	732	0
Sinipercidae	*Siniperca scherzeri*	G01489	8368	7	0	846	975	0	0	0
Soleidae	*Aseraggodes heemstrai*	E00582	9255	10	588	1281	0	807	0	0
Soleidae	*Aseraggodes kobensis*	E00075	12391	14	690	1293	929	0	0	0
Soleidae	*Brachirus annularis*	E01182	5846	7	705	1284	0	0	0	0
Soleidae	*Heteromycteris japonicus*	E00079	14809	17	705	1308	873	0	0	0

Table 4Ac. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	SH3PX3	SIDKEY	SREB2	SVEP1	TBR1	VCPIP
Soleidae	*Microchirus frechkopi*	E01175	5082	6	705	1284	0	0	0	0
Soleidae	*Pegusa lascaris*	E01183	8261	10	705	0	0	0	0	0
Soleidae	*Pseudaesopia japonica*	E00081	10067	11	705	864	0	0	0	0
Soleidae	*Solea solea*	E00054	7675	8	0	864	0	0	0	0
Soleidae	*Soleichthys heterorhinos*	E00943	10673	11	693	1284	0	825	0	0
Sparidae	*Acanthopagrus catenula*	E00953	10468	14	696	1233	0	822	762	765
Sparidae	*Acanthopagrus latus*	M01638	3048	4	705	0	0	0	0	0
Sparidae	*Archosargus probatocephalus*	E00249	8388	10	0	1233	0	0	762	0
Sparidae	*Argyrops spinifer*	M01668	2629	3	0	0	0	0	0	0
Sparidae	*Argyrozona argyrozona*	E00802	9618	12	705	1260	0	0	762	0
Sparidae	*Boops boops*	M01640	3246	3	0	0	0	0	0	0
Sparidae	*Boopsoidea inornata*	M01639	3951	4	705	0	0	0	0	0
Sparidae	*Calamus calamus*	N29934	7496	9	705	0	0	0	762	0
Sparidae	*Calamus nodosus*	M01641	3290	4	705	0	0	0	0	0
Sparidae	*Calamus penna*	E00762	7629	10	705	1257	0	0	762	0
Sparidae	*Cheimerius nufar*	M01642	3243	3	0	0	0	0	0	0
Sparidae	*Chrysoblephus laticeps*	M01644	3594	4	705	0	0	0	0	0
Sparidae	*Crenidens crenidens*	M01645	4737	5	705	0	0	0	0	0
Sparidae	*Dentex dentex*	M01646	4731	5	703	0	0	0	0	0
Sparidae	*Diplodus annularis*	M01647	4730	5	705	0	0	0	0	0
Sparidae	*Diplodus bermudensis*	M01648	3953	4	704	0	0	0	0	0
Sparidae	*Diplodus capensis*	E00807	5192	7	0	0	0	0	759	0
Sparidae	*Lagodon rhomboides*	G01346	10209	12	705	0	0	0	762	0
Sparidae	*Lithognathus mormyrus*	M01649	4731	5	705	0	0	0	0	0
Sparidae	*Oblada melanura*	M01650	3249	3	0	0	0	0	0	0
Sparidae	*Pachymetopon grande*	M01651	3549	4	705	0	0	0	0	0
Sparidae	*Pagellus affinis*	M01652	3072	4	705	0	0	0	0	0
Sparidae	*Pagellus erythrinus*	M01653	4029	4	0	0	0	0	0	0
Sparidae	*Pagrus pagrus*	E00514	12441	15	705	1257	0	0	762	0
Sparidae	*Porcostoma dentata*	M01654	4728	5	705	0	0	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Sparidae	*Rhabdosargus haffara*	M01655	2151	3	705	0	0	0	0	0
Sparidae	*Sarpa salpa*	E00806	12445	15	693	1287	0	0	762	0
Sparidae	*Sparidentex hasta*	M01657	4746	5	705	0	0	0	0	0
Sparidae	*Sparus aurata*	M01658	3954	4	705	0	0	0	0	0
Sparidae	*Spondyliosoma cantharus*	M01659	3257	4	674	0	0	0	0	0
Sparidae	*Stenotomus chrysops*	E00246	12458	15	705	0	0	0	762	744
Sparidae	*Virididentex acromegalus*	M01660	4676	5	705	0	0	0	0	0
Sphyraenidae	*Sphyraena argentea*	E00230	8319	10	702	1260	0	0	0	0
Sphyraenidae	*Sphyraena barracuda*	E00836	19387	22	705	1287	969	816	720	762
Sphyraenidae	*Sphyraena japonica*	N30022	5263	7	519	0	0	0	0	0
Sphyraenidae	*Sphyraena jello*	N30023	4747	6	705	0	0	0	0	0
Sphyraenidae	*Sphyraena putnamae*	E00955	13026	14	705	1281	0	0	0	741
Sphyraenidae	*Sphyraena sphyraena*	E01143	7520	8	0	861	0	0	0	0
Stichaeidae	*Bryozoichthys marjorius*	E00442	7041	9	0	1256	0	0	0	657
Stichaeidae	*Cebidichthys violaceus*	N30217	6500	9	672	0	882	0	702	0
Stichaeidae	*Leptoclinus maculatus*	E00323	5549	7	0	0	0	0	0	0
Stichaeidae	*Lumpenus fabricii*	E00361	3593	5	0	0	0	0	0	0
Stichaeidae	*Lumpenus lampretaeformis*	E00371	5472	7	0	1256	0	0	0	0
Stichaeidae	*Poroclinus rothrocki*	E00431	5685	7	0	1260	0	0	0	0
Stromateidae	*Peprilus burti*	E00600	5597	7	660	1245	0	0	0	0
Stromateidae	*Peprilus paru*	E00622	7448	10	705	1257	0	0	0	0
Stromateidae	*Peprilus simillimus*	E00136	10724	12	693	1281	0	0	0	0
Stromateidae	*Peprilus triacanthus*	N30548	8492	10	705	0	975	0	753	0
Symphysanodontidae	*Symphysanodon typus*	M01725	1508	2	686	0	0	0	0	0
Synanceiidae	*Synanceia verrucosa*	E00867	10214	13	0	1260	0	0	0	732
Synbranchidae	*Monopterus albus*	E01134	14200	15	705	1269	978	0	762	0
Syngnathidae	*Corythoichthys intestinalis*	E00734	5411	6	0	0	0	0	0	0
Syngnathidae	*Corythoichthys schultzi*	E00829	4587	5	696	1245	0	768	0	0
Syngnathidae	*Doryrhamphus excisus*	E00915	8801	10	0	1260	0	804	0	732
Syngnathidae	*Hippocampus erectus*	N30799	2880	4	663	0	0	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Syngnathidae	*Syngnathus fuscus*	E00792	6471	8	705	0	0	0	0	0
Syngnathidae	*Syngnathus leptorhynchus*	N30969	2247	3	0	0	0	0	0	0
Syngnathidae	*Syngnathus louisianae*	E00821	4535	5	0	0	0	0	0	0
Syngnathidae	*Syngnathus scovelli*	E00346	4744	6	621	0	0	0	0	0
Telmatherinidae	*Marosatherina ladigesi*	E00406	9346	12	0	1251	0	0	0	717
Terapontidae	*Hephaestus fuliginosus*	G01318	10031	11	705	1287	906	0	0	0
Terapontidae	*Scortum barcoo*	G01480	10071	11	705	1287	921	0	0	0
Terapontidae	*Terapon jarbua*	E00826	14339	16	0	1281	0	654	762	762
Tetraodontidae	*Arothron hispidus*	E00985	8771	8	669	1248	0	0	0	0
Tetraodontidae	*Arothron nigropunctatus*	N31143	7811	9	705	0	957	0	756	0
Tetraodontidae	*Canthigaster bennetti*	E00530	8390	9	0	1248	0	0	0	0
Tetraodontidae	*Canthigaster jactator*	N31165	6260	7	705	0	951	0	762	0
Tetraodontidae	*Canthigaster valentini*	E00853	7767	8	678	0	0	0	0	0
Tetraodontidae	*Lagocephalus laevigatus*	E00601	8160	8	0	0	0	0	0	0
Tetraodontidae	*Sphoeroides maculatus*	E00339	4428	5	0	1251	0	0	0	0
Tetraodontidae	*Sphoeroides nephelus*	N01739	6070	7	705	0	0	0	762	0
Tetraodontidae	*Takifugu rubripes*	E00460	20045	21	705	1308	987	0	762	753
Tetraodontidae	*Tetractenos hamiltoni*	E00383	2976	4	0	0	0	0	0	0
Tetraodontidae	*Tetraodon fluviatilis*	E00374	4553	5	702	0	0	0	0	0
Tetraodontidae	*Tetraodon miurus*	N01740	8550	10	705	0	954	0	762	0
Tetraodontidae	*Tetraodon nigroviridis*	G01513	17489	18	705	1308	987	0	762	0
Tetrarogidae	*Coccotropsis gymnoderma*	E00801	6200	8	0	0	0	813	762	678
Toxotidae	*Toxotes chatareus*	E01139	10242	10	705	1308	0	0	0	0
Toxotidae	*Toxotes jaculatrix*	E01155	11428	14	705	1287	0	0	756	0
Trachichthyidae	*Hoplostethus occidentalis atlanticus*	E01018	11766	14	705	1248	978	810	783	0
Triacanthidae	*Triacanthus biaculeatus*	G01531	11323	12	705	0	954	0	762	0
Triacanthodidae	*Halimochirurgus alcocki*	N31459	6920	9	693	0	0	0	702	0
Triacanthodidae	*Triacanthodes anomalus*	E00382	12061	13	705	0	978	0	756	0
Triacanthodidae	*Triacanthodes ethiops*	G01532	6829	7	0	0	0	0	0	0
Trichiuridae	*Aphanopus carbo*	E00274	5425	7	0	0	0	0	762	0

Table 4Ac. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Trichiuridae	*Assurger anzac*	G01210	9581	12	705	0	942	0	735	0
Trichiuridae	*Benthodesmus simonyi*	E00475	4383	6	0	0	0	0	0	0
Trichiuridae	*Evoxymetopon taeniatus*	E00650	3573	5	0	0	0	0	0	0
Trichiuridae	*Lepidopus altifrons*	E00474	6788	9	666	0	0	807	0	0
Trichiuridae	*Trichiurus lepturus*	E00596	12574	14	0	0	0	0	0	0
Trichodontidae	*Trichodon trichodon*	N31563	7181	9	706	0	0	0	744	0
Triglidae	*Bellator militaris*	E01026	4452	6	0	0	0	0	762	0
Triglidae	*Prionotus carolinus*	E00340	7371	9	0	1233	0	0	0	0
Triglidae	*Prionotus evolans*	E01021	4575	6	0	0	0	0	0	0
Triglidae	*Prionotus stephanophrys*	E00328	6883	9	705	1212	0	0	0	0
Triglidae	*Pterygotrigla hemisticta*	N31939	4770	6	693	0	0	0	0	0
Triodontidae	*Triodon macropterus*	N31959	7201	9	705	0	0	0	750	0
Tripterygiidae	*Enneanectes altivelis*	E00315	5180	7	696	0	0	0	0	0
Tripterygiidae	*Enneanectes boehlkei*	E00305	8688	11	705	0	942	0	690	0
Tripterygiidae	*Enneapterygius abeli*	E00896	2369	3	0	0	0	0	0	0
Tripterygiidae	*Enneapterygius gruschkai*	E00916	3832	5	0	0	0	0	756	0
Tripterygiidae	*Helcogramma ellioti sp*	E00331	9671	11	705	1257	948	0	0	0
Tripterygiidae	*Helcogramma fuscopinna*	E00885	2098	3	0	0	0	0	0	0
Uranoscopidae	*Astroscopus ygraecum*	E01028	11671	14	690	1257	975	0	755	693
Uranoscopidae	*Kathetostoma albigutta*	E01022	2118	3	0	0	0	0	762	0
Uranoscopidae	*Kathetostoma averruncus*	E00324	11393	14	705	0	0	0	747	0
Uranoscopidae	*Uranoscopus sulphureus*	E00538	5752	7	0	1233	0	0	0	0
Xiphiidae	*Xiphias gladius*	E01151	16644	17	705	1287	951	0	762	0
Zanclidae	*Zanclus cornutus*	E00894	18204	20	705	1308	954	825	762	657
Zaproridae	*Zaprora silenus*	E00362	6043	8	0	0	0	0	0	0
Zenarchopteridae	*Dermogenys collettei*	G01275	6851	8	699	0	0	0	762	0
Zenarchopteridae	*Zenarchopterus dispar*	E00541	5209	6	0	1236	0	0	0	0
Zoarcidae	*Bothrocara brunneum*	E00357	6304	8	0	0	0	0	0	0
Zoarcidae	*Bothrocara hollandi*	N01721	4677	6	0	0	0	0	762	0
Zoarcidae	*Eucryphycus californicus*	E00327	5531	7	0	0	0	0	0	0

Table 4Ac. *Continued*

Family	**Genus Species**	***ETOL_ID***	***Length (bp)***	***charset***	**SH3PX3**	**SIDKEY**	**SREB2**	**SVEP1**	**TBR1**	**VCPIP**
Zoarcidae	*Lycenchelys crotalinus*	E00425	4583	6	0	0	0	0	0	0
Zoarcidae	*Lycodapus mandibularis*	E00355	8784	11	705	1256	0	0	0	0
Zoarcidae	*Lycodes brevipes*	E00413	4381	5	0	0	0	0	0	0
Zoarcidae	*Lycodes diapterus*	G01364	8790	11	705	0	0	0	756	0
Zoarcidae	*Lycodes terraenovae*	E00675	15952	18	705	1245	987	0	762	711
Zoarcidae	*Melanostigma pammelas*	E00365	6342	8	0	0	0	0	0	0
Zoarcidae	*Zoarces americanus viviparus*	E00370	5571	8	0	0	0	0	711	0

TABLE A4d. Taxon sampling for the percomorph dataset included 1231 taxa and sequence data for 23 genes. The dataset is comprised of sequences for 1180 percomorph species from previous studies (e.g. Li *et al.* 2007; Li *et al.* 2008; Li *et al.* 2010; Li *et al.* 2011; Betancur-R *et al.* 2013b; Broughton *et al.* 2013; Near *et al.* 2013) or public databases, plus newly generated sequences for the 51 additional taxa for this study. The matrix is presented in four parts to show presence of sequence data for the 23 genes. (a.) ENC1, FICD, GLYT, KIAA1239, MYH6, and PANX2; (b.) PLAGL2, PTCHD1, RAG1, RAG2, RH, and RIPK4; (c.) SH3PX3, SIDKEY, SREB2, SVEP1, TBR1, and VCPIP; (d.) ZIC1, COI, CYT *B*, 16S, and HOX.

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Acanthuridae	*Acanthurus bahianus*	E00005	11794	14	858	651	606	0	0
Acanthuridae	*Acanthurus guttatus*	E00709	7379	8	717	645	0	0	989
Acanthuridae	*Acanthurus leucosternon*	E00880	14819	16	774	651	0	2252	1065
Acanthuridae	*Acanthurus lineatus*	E00889	11234	12	768	645	0	2252	1152
Acanthuridae	*Acanthurus triostegus*	E00711	11027	13	717	645	0	773	1029
Acanthuridae	*Ctenochaetus striatus*	E00982	6461	8	0	648	0	773	0
Acanthuridae	*Ctenochaetus strigosus*	E00050	9642	12	879	651	630	0	0
Acanthuridae	*Ctenochaetus truncatus*	E00854	6572	9	768	0	0	0	0
Acanthuridae	*Naso brevirostris*	E00918	11979	15	879	648	0	922	0
Acanthuridae	*Naso lituratus*	G01514	9769	12	879	648	0	922	0
Acanthuridae	*Naso unicornis*	E00701	6934	9	720	645	0	773	0
Acanthuridae	*Paracanthurus hepatus*	E00002	9321	11	722	648	0	922	0
Acanthuridae	*Zebrasoma flavescens*	E00730	9002	10	720	654	597	2252	0
Acanthuridae	*Zebrasoma rostratum*	N01742	6780	8	777	0	0	0	0
Acanthuridae	*Zebrasoma scopas*	E00859	12917	16	767	648	0	922	1008
Acanthuridae	*Zebrasoma velifer*	E00029	5029	6	696	0	0	922	0
Achiridae	*Achirus lineatus*	E00605	13596	16	0	651	0	1699	1049
Achiridae	*Gymnachirus melas*	E00609	14260	16	0	0	0	1749	1035
Achiridae	*Gymnachirus texae*	E00630	9146	10	0	0	0	1752	0
Achiridae	*Hypoclinemus sp*	E01162	6483	7	0	0	0	0	0
Achiridae	*Trinectes maculatus*	E00046	11078	11	0	648	0	1753	0
Achiropsettidae	*Mancopsetta maculata*	E01169	6861	8	0	544	0	1745	0
Achiropsettidae	*Neoachiropsetta milfordi*	E01170	6200	8	0	653	0	987	0
Acropomatidae	*Acropoma japonicum*	G01188	12298	14	750	654	1140	911	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Acropomatidae	*Malakichthys elegans*	N01922	6894	9	714	0	0	0	0
Acropomatidae	*Synagrops bellus*	E01125	11059	13	776	654	0	788	0
Acropomatidae	*Synagrops spinosus*	E01123	6676	7	706	0	0	1753	0
Adrianichthyidae	*Oryzias latipes*	G01408	18061	19	879	0	0	2251	0
Agonidae	*Aspidophoroides monopterygius*	N01986	7472	9	867	0	0	0	0
Agonidae	*Bathyagonus alascanus*	E00268	5458	7	0	647	0	934	1105
Agonidae	*Bathyagonus pentacanthus*	E00430	5127	7	648	654	0	934	0
Agonidae	*Hypsagonus quadricornis*	E00269	7151	9	0	654	0	788	0
Agonidae	*Sarritor frenatus*	E00264	4738	6	776	0	0	788	0
Agonidae	*Sarritor leptorhynchus*	E00254	5516	7	777	0	0	0	0
Agonidae	*Stellerina xyosterna*	N02010	6750	8	879	0	0	0	0
Agonidae	*Xeneretmus latifrons*	E00278	6400	8	777	651	0	788	0
Ambassidae	*Ambassis agrammus*	G01196	8877	9	867	0	0	1773	0
Ambassidae	*Ambassis interrupta*	E01100	10212	10	867	654	0	1759	1163
Ambassidae	*Ambassis urotaenia*	G01197	8268	10	879	0	0	0	0
Ambassidae	*Parambassis ranga*	N01735	7892	10	738	0	0	0	0
Ammodytidae	*Ammodytes dubius*	N02375	6015	7	879	0	0	0	0
Ammodytidae	*Ammodytes hexapterus*	E00414	15128	17	687	654	0	1753	1119
Anabantidae	*Ctenopoma acutirostre kingsleyae*	E01141	14536	15	876	0	1140	2069	0
Anabantidae	*Microctenopoma nanum*	G01373	12070	13	879	631	1128	2067	0
Anarhichadidae	*Anarhichas denticulatus*	E00787	8620	9	0	654	0	2252	1158
Anarhichadidae	*Anarhichas orientalis lupus*	E00117	15266	17	723	647	0	2252	889
Anarhichadidae	*Anarrhichthys ocellatus*	E00119	7893	10	722	654	0	935	1004
Anoplopomatidae	*Anoplopoma fimbria*	E00423	15741	18	723	615	0	2252	0
Antennariidae	*Antennatus coccineus*	E01092	15457	17	879	0	0	2253	0
Antennariidae	*Antennatus nummifer*	E00587	9899	13	678	0	0	921	0
Antennariidae	*Fowlerichthys radiosus*	E01124	4779	6	0	0	0	0	0
Antennariidae	*Histiophryne cryptacanthus*	G01326	9853	12	801	654	0	934	0
Antennariidae	*Histrio histrio*	E00643	7964	9	669	648	0	2255	0
Aphyonidae	*Barathronus maculatus*	N02779	7479	9	879	0	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Aplocheilidae	*Pachypanchax playfairii*	G01414	7524	9	852	0	0	708	0
Aplodactylidae	*Aplodactylus arctidens*	M01536	4728	5	0	654	1122	0	0
Aplodactylidae	*Aplodactylus etheridgii*	M01537	4710	5	0	654	1104	0	0
Apogonidae	*Apogon campbelli*	E01069	9380	10	0	0	0	1753	1168
Apogonidae	*Archamia biguttata*	E00522	8166	11	696	632	1104	0	0
Apogonidae	*Astrapogon puncticulatus*	E00109	7227	9	723	654	0	0	0
Apogonidae	*Astrapogon stellatus*	N03004	7517	9	813	0	0	0	0
Apogonidae	*Cercamia eremia*	E00546	6660	9	663	654	0	0	1170
Apogonidae	*Cheilodipterus isostigmus*	E00528	8272	10	684	654	0	0	1087
Apogonidae	*Cheilodipterus quinquelineatus*	G01247	9762	12	840	651	0	768	0
Apogonidae	*Fowleria aurita*	E01090	8780	11	0	654	1104	0	1052
Apogonidae	*Gymnapogon urospilotus*	E00539	5107	7	708	654	0	0	0
Apogonidae	*Nectamia bandanensis*	E01040	8860	11	722	651	0	0	1081
Apogonidae	*Nectamia fusca*	E00732	8861	10	672	650	0	1821	0
Apogonidae	*Ostorhinchus cookii*	E01087	6400	8	0	0	0	0	1169
Apogonidae	*Ostorhinchus lateralis*	G01203	8273	10	858	0	0	0	0
Apogonidae	*Phaeoptyx pigmentaria*	E00506	12882	15	666	654	0	0	1167
Apogonidae	*Pristiapogon exostigma*	E00702	8433	11	696	650	0	0	0
Apogonidae	*Pseudamia gelatinosa*	E00568	7391	9	666	654	0	0	1138
Apogonidae	*Pterapogon kauderni*	E00190	6329	8	0	0	0	0	0
Apogonidae	*Rhabdamia cypselura*	E01095	6022	7	0	654	0	0	1086
Apogonidae	*Sphaeramia orbicularis*	N03178	8446	10	879	0	0	0	0
Aracanidae	*Anoplocapros lenticularis*	G01533	6886	7	846	654	1089	2264	0
Aracanidae	*Aracana aurita*	G01205	10032	12	762	654	1089	0	0
Ariommatidae	*Ariomma bondi*	E01126	7867	9	0	654	0	0	0
Ariommatidae	*Ariomma melanum*	E00665	9682	12	699	0	0	0	1043
Arripidae	*Arripis georgianus*	M01539	4794	5	0	654	0	0	0
Arripidae	*Arripis trutta*	M01540	3327	4	0	654	0	0	0
Arripidae	*Arripis truttacea*	M01541	4659	5	0	609	0	0	0
Artedidraconidae	*Artedidraco orianae*	G01525	6898	8	737	651	561	2255	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Artedidraconidae	*Pogonophryne barsukovi*	E00158	12842	14	719	651	0	2252	1058
Atherinidae	*Atherinomorus lacunosus*	E00548	15021	18	687	651	1140	812	0
Atherinidae	*Atherinomorus stipes*	E00115	13436	16	711	654	1121	0	0
Atherinidae	*Atherinomorus vaigiensis*	E00181	7813	10	717	0	1140	0	0
Atherinidae	*Craterocephalus honoriae*	E00180	8597	10	0	0	1140	809	0
Atherinopsidae	*Atherinopsis californiensis*	E00121	5600	7	723	0	0	0	915
Atherinopsidae	*Labidesthes sicculus*	E01112	14372	17	879	644	500	809	1169
Atherinopsidae	*Membras martinica*	E00170	7275	9	0	606	500	828	1065
Atherinopsidae	*Menidia beryllina*	E00174	10176	13	723	651	500	0	1070
Atherinopsidae	*Menidia menidia*	E00167	12560	13	723	651	1121	2253	1072
Atherinopsidae	*Menidia peninsulae*	N03847	5694	7	0	0	0	0	0
Atherinopsidae	*Odontesthes argentinensis*	E00393	5125	7	705	651	0	0	0
Atherinopsidae	*Odontesthes bonariensis*	E00396	9234	11	699	651	702	1747	0
Atherinopsidae	*Odontesthes humensis*	E00394	5561	7	717	0	0	0	1180
Atherinopsidae	*Odontesthes retropinnis*	E00395	4826	6	687	0	0	0	1154
Atherinopsidae	*Poblana ferdebueni*	N01733	5919	7	0	0	0	0	0
Aulorhynchidae	*Aulorhynchus flavidus*	G01217	11313	12	879	654	0	2251	0
Aulostomidae	*Aulostomus chinensis*	E00871	15665	19	705	600	1140	0	1165
Aulostomidae	*Aulostomus maculatus*	E00293	13058	16	879	588	0	659	1171
Badidae	*Badis pyema*	N03996	7191	9	731	0	0	0	0
Badidae	*Dario dario*	N04003	5626	7	731	0	0	0	0
Balistidae	*Abalistes stellatus*	E00936	14580	18	720	645	0	777	1038
Balistidae	*Balistapus undulatus*	E00743	12372	14	720	654	1089	2245	0
Balistidae	*Balistes capriscus*	E00591	13798	17	710	651	1140	1007	0
Balistidae	*Balistes vetula*	E00755	13640	15	723	618	0	2245	0
Balistidae	*Balistoides conspicillum*	E00373	9468	10	777	651	0	2245	1167
Balistidae	*Canthidermis maculata*	E00378	9887	10	771	651	0	2245	1120
Balistidae	*Melichthys indicus*	E00919	7484	10	576	645	0	0	1127
Balistidae	*Melichthys niger*	E00922	8652	11	711	606	0	784	1137
Balistidae	*Pseudobalistes flavimarginatus*	N04225	6715	8	878	0	0	0	0

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Balistidae	*Pseudobalistes fuscus*	E00524	4607	6	720	630	0	773	0
Balistidae	*Rhinecanthus aculeatus*	E00735	9140	10	723	651	0	2245	0
Balistidae	*Rhinecanthus assasi*	E00381	5259	6	771	0	0	777	0
Balistidae	*Rhinecanthus verrucosus*	N04231	7465	9	860	0	0	0	0
Balistidae	*Sufflamen chrysopterum*	E00551	11210	14	879	639	0	778	0
Balistidae	*Sufflamen fraenatum*	E00935	9148	10	705	612	0	2245	0
Balistidae	*Xanthichthys auromarginatus*	E00380	11574	12	771	651	0	2245	1167
Balistidae	*Xanthichthys ringens*	N04239	7595	9	878	0	0	0	0
Banjosidae	*Banjos banjos*	M01542	4794	5	0	654	0	0	0
Banjosidae	*Banjos banjos*	N01542	6206	8	723	0	0	0	0
Bathyclupeidae	*Bathyclupea argentea*	M01543	2787	4	0	654	0	0	0
Bathydraconidae	*Gymnodraco acuticeps*	E00155	12486	14	722	651	576	2251	0
Bathydraconidae	*Parachaenichthys charcoti*	E00157	15082	17	717	606	1081	2250	0
Bathymasteridae	*Bathymaster caeruleofasciatus*	E00191	7525	10	722	0	0	0	943
Bathymasteridae	*Bathymaster signatus*	E00420	12500	16	705	654	0	788	0
Bathymasteridae	*Rathbunella hypoplecta*	E00128	12273	15	879	654	0	780	1049
Batrachoididae	*Batrachoides pacifici*	N04533	6761	8	0	0	0	0	0
Batrachoididae	*Opsanus beta*	E00698	11611	14	879	651	0	788	981
Batrachoididae	*Opsanus pardus*	E00513	11301	14	0	0	0	0	0
Batrachoididae	*Opsanus tau*	E00040	4773	6	0	0	0	710	0
Batrachoididae	*Porichthys notatus*	E00058	13187	16	861	651	0	933	0
Batrachoididae	*Porichthys plectrodon*	E00590	13538	16	879	0	0	0	1118
Batrachoididae	*Sanopus sp*	E00009	4902	6	0	0	0	0	0
Bedotiidae	*Rheocles wrightae*	G01467	11051	13	873	645	1140	809	0
Belonidae	*Ablennes hians*	E00162	11443	13	708	635	541	2252	1055
Belonidae	*Platybelone argalus*	E00114	12856	15	723	0	0	771	0
Belonidae	*Strongylura notata*	E00110	15115	19	723	647	800	773	0
Belonidae	*Tylosurus crocodilus*	E01051	7580	10	0	560	800	771	0
Belonidae	*Xenentodon cancila*	G01508	11377	14	879	654	531	769	0
Bembridae	*Bembras japonica*	N01723	6876	9	714	0	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Bembropidae	*Bembrops anatirostris*	E01120	10273	13	723	651	0	0	0
Bembropidae	*Bembrops gobioides*	E01128	8878	11	879	0	0	0	0
Blenniidae	*Alticus arnoldorum*	E00989	2775	4	699	0	0	0	0
Blenniidae	*Atrosalarias fuscus*	E00525	2877	4	714	0	0	0	0
Blenniidae	*Blenniella chrysospilos paula*	E00986	4186	5	710	0	0	0	1184
Blenniidae	*Blenniella cyanostigma*	E00715	7419	9	710	567	0	0	1184
Blenniidae	*Blenniella paula*	E00979	7982	10	713	636	0	0	1124
Blenniidae	*Cirripectes castaneus*	E00892	8002	10	717	638	0	0	1113
Blenniidae	*Cirripectes filamentosus*	E00893	5912	7	714	0	0	0	941
Blenniidae	*Cirripectes quagga*	E00330	4362	5	0	651	0	0	0
Blenniidae	*Cirripectes stigmaticus*	E00520	4037	6	714	638	0	0	0
Blenniidae	*Ecsenius bicolor*	E00984	5909	8	696	573	0	911	0
Blenniidae	*Ecsenius midas*	E00934	3749	5	0	642	0	911	0
Blenniidae	*Ecsenius opsifrontalis*	E00723	5497	7	722	0	0	0	1123
Blenniidae	*Ecsenius pardus*	E00523	4285	5	732	0	0	0	0
Blenniidae	*Enchelyurus flavipes*	N04786	6887	9	704	0	0	0	0
Blenniidae	*Entomacrodus nigricans*	E00297	9132	11	777	654	0	0	0
Blenniidae	*Entomacrodus niuafoouensis*	E00980	6091	8	680	0	0	0	1172
Blenniidae	*Entomacrodus striatus*	E00987	5295	7	0	636	0	0	0
Blenniidae	*Hypleurochilus sp*	E00298	5653	7	0	651	0	739	1098
Blenniidae	*Hypsoblennius hentz*	E00289	7330	9	879	0	0	911	0
Blenniidae	*Istiblennius dussumieri*	E00556	4755	6	711	651	0	0	1184
Blenniidae	*Meiacanthus oualanensis grammistes*	E00526	9615	12	720	623	0	788	0
Blenniidae	*Nannosalarias nativitatis*	E00521	6717	8	710	651	0	0	1184
Blenniidae	*Ophioblennius atlanticus*	E00296	11932	15	776	631	630	911	0
Blenniidae	*Petroscirtes mitratus*	E00909	5741	8	708	636	0	0	0
Blenniidae	*Plagiotremus rhinorhynchos*	E00586	4112	5	726	635	0	0	1148
Blenniidae	*Plagiotremus tapeinosoma*	E00540	4423	6	714	651	0	0	0
Blenniidae	*Praealticus caesius*	E00329	5179	6	741	0	0	0	1158
Blenniidae	*Salarias fasciatus*	E00988	12606	14	710	651	0	2255	1184

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Blenniidae	*Stanulus sp*	E00332	3369	4	0	0	0	0	0
Bothidae	*Arnoglossus blachei*	E01160	6253	7	0	0	0	745	0
Bothidae	*Arnoglossus imperialis*	E01163	7399	8	0	651	0	1003	0
Bothidae	*Asterorhombus cocosensis*	E00904	10399	11	0	0	0	1740	0
Bothidae	*Bothus lunatus*	E00007	8248	9	0	654	0	1752	0
Bothidae	*Bothus robinsi*	E00038	6724	7	0	0	0	1753	0
Bothidae	*Chascanopsetta lugubris*	E01181	5982	7	0	650	0	871	0
Bothidae	*Laeops kitaharae*	E00082	7794	8	0	0	0	1753	0
Bothidae	*Monolene sp*	E01172	3326	3	0	0	0	1739	0
Bothidae	*Psettina tosana*	E00083	7617	8	0	0	0	1753	0
Bothidae	*Trichopsetta ventralis*	E00599	9704	10	0	0	0	1745	0
Bovichtidae	*Bovichtus diacanthus*	G01229	12547	13	879	0	1134	2254	0
Bovichtidae	*Cottoperca trigloides*	G01267	5753	6	744	0	0	2256	0
Bramidae	*Brama brama*	E00970	11377	13	0	654	1140	1753	996
Bramidae	*Brama japonica*	N05217	8586	10	878	0	0	0	0
Bramidae	*Pteraclis aesticola*	N05223	7106	9	713	0	0	0	0
Bramidae	*Pterycombus brama*	E00996	9728	12	648	647	0	0	1066
Bramidae	*Taractes asper*	N05227	8588	10	875	0	0	0	0
Bramidae	*Taractichthys longipinnis*	E00684	8997	11	708	654	1140	835	0
Bythitidae	*Bidenichthys capensis*	E00794	7231	9	720	0	0	0	949
Bythitidae	*Brosmophyciops pautzkei*	E00717	5948	8	720	651	0	0	0
Bythitidae	*Brosmophycis marginata*	N05317	7691	9	878	0	0	0	0
Bythitidae	*Cataetyx rubrirostris lepidogenys*	E00261	14883	16	879	654	0	2253	0
Bythitidae	*Diancistrus sp*	E00236	6903	9	768	0	0	0	0
Bythitidae	*Dinematichthys iluocoeteoides*	E00235	4750	6	0	639	0	0	0
Bythitidae	*Diplacanthopoma brachysoma*	E00452	8606	9	713	0	0	2253	0
Bythitidae	*Diplacanthopoma brunnea*	N05377	8280	10	878	0	0	0	0
Caesionidae	*Caesio caerulaurea lunaris*	E00920	13727	15	708	651	879	1744	1129
Caesionidae	*Caesio cuning*	N01544	6786	8	789	0	0	0	0
Caesionidae	*Caesio teres*	E00951	7741	10	702	651	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Caesionidae	*Caesio varilineata*	E00949	9671	12	705	0	0	0	1020
Caesionidae	*Caesio xanthonota*	E00950	9615	12	698	651	0	0	1150
Caesionidae	*Pterocaesio pisang*	N01547	8535	10	879	0	0	0	0
Caesionidae	*Pterocaesio tile*	E00961	7369	8	671	651	0	2252	0
Callanthiidae	*Callanthias australis*	M01721	3528	4	0	552	0	0	0
Callanthiidae	*Grammatonotus surugaensis*	N05516	4774	6	0	0	0	0	0
Callionymidae	*Callionymus sp bairdi*	E00946	14247	16	773	0	0	903	1183
Callionymidae	*Diplogrammus goramensis*	E00744	3443	4	0	0	0	0	0
Callionymidae	*Foetorepus sp*	N01725	7524	9	759	0	0	0	0
Callionymidae	*Neosynchiropus ocellatus*	E00030	9857	12	0	648	0	788	0
Callionymidae	*Synchiropus agassizii*	E01004	13911	16	768	642	0	0	1183
Callionymidae	*Synchiropus splendidus*	E00003	7623	9	0	0	0	0	0
Callionymidae	*Synchiropus stellatus*	E00925	4153	5	771	651	0	0	1053
Caproidae	*Antigonia capros*	E01024	15924	18	768	636	0	2252	0
Caproidae	*Antigonia rubescens*	N05907	8327	10	734	0	0	0	0
Caproidae	*Capros aper*	N05913	6917	9	734	0	0	0	0
Carangidae	*Alectis ciliaris*	E00469	9715	12	711	648	1140	852	0
Carangidae	*Atule mate*	E00942	13914	15	710	651	1088	1752	1145
Carangidae	*Carangoides ferdau*	E00869	9160	10	738	654	1016	1742	0
Carangidae	*Carangoides plagiotaenia*	E00917	10641	12	714	651	0	1746	1041
Carangidae	*Caranx crysos ruber*	E00510	15973	18	728	651	1140	1753	0
Carangidae	*Caranx ignobilis*	E00574	14220	16	708	651	1107	1752	0
Carangidae	*Caranx sexfasciatus*	E00834	10100	10	711	627	1126	1753	1131
Carangidae	*Chloroscombrus chrysurus*	E00763	5515	7	708	654	1115	890	0
Carangidae	*Decapterus macarellus*	E00212	3266	5	0	651	511	877	0
Carangidae	*Decapterus punctatus*	E00671	9777	11	0	654	1140	879	0
Carangidae	*Elagatis bipinnulata*	E00841	11967	15	717	651	1140	1076	0
Carangidae	*Gnathanodon speciosus*	E00938	13565	15	702	648	942	1753	996
Carangidae	*Hemicaranx amblyrhynchus*	E00616	11426	13	711	651	0	1753	0
Carangidae	*Oligoplites saurus*	E00195	16021	19	777	654	1117	756	0

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Carangidae	*Scomberoides lysan*	E00738	10887	13	708	654	0	756	0
Carangidae	*Selar crumenophthalmus*	E00833	11277	13	717	651	1140	1752	0
Carangidae	*Selene brownii*	E00767	7866	10	729	651	1135	749	0
Carangidae	*Selene setapinnis*	N01705	6120	8	858	0	0	0	0
Carangidae	*Seriola dumerili*	E00623	16521	18	705	651	1140	2254	0
Carangidae	*Seriola rivoliana*	E00467	11164	13	708	651	1140	1732	0
Carangidae	*Trachinotus carolinus*	G01504	11145	13	879	651	1116	970	0
Carangidae	*Trachinotus falcatus*	E00819	10693	12	762	654	1122	1753	0
Carangidae	*Trachinotus ovatus*	E01145	14822	16	813	654	1116	2256	0
Carangidae	*Trachurus lathami*	E00598	11710	13	735	654	1140	1745	0
Carangidae	*Uraspis secunda*	E00515	11843	13	711	651	1115	1753	0
Carapidae	*Carapus bermudensis*	E00244	3497	5	0	0	0	0	0
Carapidae	*Onuxodon parvibrachium*	N06009	5285	7	767	0	0	0	0
Carapidae	*Pyramodon ventralis*	N06013	5272	7	758	0	0	0	0
Caristiidae	*Caristius macropus*	N06078	5912	8	731	0	0	0	0
Caristiidae	*Caristius sp*	E00810	9564	11	711	0	0	786	0
Caristiidae	*Platyberyx opalescens*	N06085	7781	10	713	0	0	0	0
Centracanthidae	*Centracanthus cirrus*	M01560	2897	3	0	654	0	0	0
Centracanthidae	*Spicara alta*	M01561	4032	4	0	654	1131	0	0
Centracanthidae	*Spicara maena*	M01562	5142	5	0	654	1140	0	0
Centracanthidae	*Spicara nigricauda*	M01564	4791	5	0	651	0	0	0
Centracanthidae	*Spicara smaris*	M01565	5111	5	0	645	1140	0	0
Centrarchidae	*Acantharchus pomotis*	G01185	10678	10	879	561	1134	2252	0
Centrarchidae	*Ambloplites rupestris*	E00392	18681	20	678	654	1134	2252	1163
Centrarchidae	*Archoplites interruptus*	N01722	8586	10	879	0	0	0	0
Centrarchidae	*Lepomis cyanellus*	E00132	18334	20	723	651	1134	2251	0
Centrarchidae	*Lepomis macrochirus*	E01113	15647	17	0	651	1134	2252	1169
Centrarchidae	*Micropterus salmoides*	E01110	18682	20	741	651	1134	2252	1036
Centrarchidae	*Pomoxis nigromaculatus*	E00131	14489	15	723	651	1134	2252	1047
Centriscidae	*Aeoliscus strigatus*	G01189	10258	10	867	0	1140	2252	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Centriscidae	*Macroramphosus gracilis*	E00335	4196	5	774	0	0	0	1169
Centriscidae	*Macroramphosus scolopax*	E00473	10717	12	714	651	0	2253	0
Centrogenyidae	*Centrogenys vaigiensis*	G01239	9161	11	873	0	0	788	0
Centrolophidae	*Icichthys lockingtoni*	E00387	15879	18	825	654	1140	921	1163
Centropomidae	*Centropomus ensiferus*	E00766	14482	15	867	0	0	1773	1154
Centropomidae	*Centropomus medius*	E01158	10458	11	867	0	0	1773	0
Centropomidae	*Centropomus undecimalis*	E00194	15428	17	867	654	1140	1753	0
Centropomidae	*Centropomus viridis*	E01153	14374	16	867	0	0	1753	0
Centropomidae	*Lates calcarifer*	E01135	11083	12	627	654	0	1758	0
Centropomidae	*Lates japonicus*	E01147	10695	11	762	0	0	1773	0
Centropomidae	*Lates microlepis*	E01149	9785	11	759	0	0	875	0
Centropomidae	*Psammoperca waigiensis*	E01148	12243	13	867	654	0	1773	0
Cepolidae	*Acanthocepola sp*	M01669	4129	4	0	0	0	0	0
Cepolidae	*Cepola macrophthalma*	M01566	3339	4	0	654	0	0	0
Cepolidae	*Cepola schlegelii*	N06269	6961	9	722	0	0	0	0
Cepolidae	*Sphenanthias tosaensis*	N06282	6620	9	722	0	0	0	0
Ceratiidae	*Ceratias holboelli*	E00175	8091	11	722	651	0	610	952
Ceratiidae	*Ceratias sp*	E00160	6019	7	722	0	0	0	927
Ceratiidae	*Cryptopsaras couesii*	E00686	9907	10	830	651	0	2238	0
Chaenopsidae	*Acanthemblemaria aspera*	E00320	6836	9	696	654	0	0	1043
Chaenopsidae	*Acanthemblemaria paula*	E00295	6314	8	774	654	0	0	1044
Chaenopsidae	*Chaenopsis sp alepidota*	E00313	11049	13	777	0	0	782	1053
Chaenopsidae	*Emblemaria pandionis*	E00310	6208	7	777	570	0	0	1039
Chaenopsidae	*Lucayablennius zingaro*	E00294	7789	9	777	651	0	0	1018
Chaenopsidae	*Neoclinus blanchardi*	E00326	6535	8	774	651	528	751	0
Chaenopsidae	*Stathmonotus stahli*	E00317	7886	9	771	570	0	0	1135
Chaetodontidae	*Chaetodon auriga*	E00921	12220	14	714	651	1067	1753	1061
Chaetodontidae	*Chaetodon capistratus*	E00205	3871	5	0	651	0	911	0
Chaetodontidae	*Chaetodon ocellatus*	E00752	3799	5	716	648	0	911	0
Chaetodontidae	*Chaetodon ornatissimus*	G01243	11727	14	879	651	1038	825	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Chaetodontidae	*Chaetodon plebeius*	E00573	2874	4	708	0	0	0	0
Chaetodontidae	*Chaetodon reticulatus*	E00719	9187	11	705	651	1068	825	0
Chaetodontidae	*Chaetodon striatus*	E00753	15347	19	879	615	0	0	0
Chaetodontidae	*Chelmon rostratus*	G01248	10379	13	777	648	390	911	0
Chaetodontidae	*Forcipiger flavissimus*	E00562	14191	17	879	648	390	825	0
Chaetodontidae	*Hemitaurichthys polylepis*	E00240	12410	15	770	651	1068	825	0
Chaetodontidae	*Heniochus chrysostomus*	E00748	14747	18	683	651	1068	825	0
Chaetodontidae	*Heniochus varius*	E00547	11101	14	711	622	0	911	0
Chaetodontidae	*Johnrandallia nigrirostris*	N06546	7594	9	878	0	0	0	0
Chaetodontidae	*Prognathodes aya aculeatus*	E00632	16211	20	711	621	411	911	0
Champsodontidae	*Champsodon snyderi*	N06574	5798	8	0	0	0	0	0
Channichthyidae	*Chionobathyscus dewitti*	G01250	11735	13	879	651	0	1907	0
Channichthyidae	*Chionodraco rastrospinosus*	E00156	10249	11	722	654	0	2252	0
Channidae	*Channa lucius*	N06615	7562	9	878	0	0	0	0
Channidae	*Channa melasoma*	N06621	8195	10	842	0	0	0	0
Channidae	*Channa striata*	E01133	15424	17	879	654	807	1753	0
Chaunacidae	*Chaunax stigmaeus*	E01121	11544	14	711	0	0	0	0
Chaunacidae	*Chaunax suttkusi*	E01117	13670	16	711	0	1134	788	0
Cheilodactylidae	*Cheilodactylus fasciatus*	E00795	8950	11	711	654	0	1746	0
Cheilodactylidae	*Cheilodactylus pixi*	E00797	7523	10	717	651	0	0	0
Cheilodactylidae	*Cheilodactylus variegatus*	N07699	7481	9	863	0	0	0	0
Cheilodactylidae	*Chirodactylus brachydactylus*	E00796	10572	13	714	651	0	0	0
Cheilodactylidae	*Chirodactylus jessicalenorum*	E00585	5511	7	675	651	0	0	0
Cheimarrichthyidae	*Cheimarrichthys fosteri*	N07713	7400	9	770	0	0	0	0
Chiasmodontidae	*Chiasmodon niger*	E01115	6819	8	0	654	0	0	1143
Chiasmodontidae	*Chiasmodon sp*	N33662	8114	10	839	0	0	0	0
Chiasmodontidae	*Kali indica*	E01106	8049	10	0	648	0	0	0
Chiasmodontidae	*Kali kerberti*	E00385	8712	11	0	654	0	0	0
Chironemidae	*Chironemus georgianus*	M01569	3606	4	0	654	0	0	0
Chironemidae	*Chironemus maculosus*	M01570	3605	4	0	654	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Cichlidae	*Astatotilapia burtoni*	G01518	14530	19	879	0	0	765	0
Cichlidae	*Cichla temensis*	G01256	12888	15	858	645	670	911	0
Cichlidae	*Crenicichla lepidota*	E00137	9593	12	723	654	1128	752	1055
Cichlidae	*Etroplus maculatus*	E00133	16104	17	879	586	1115	2253	994
Cichlidae	*Herichthys cyanoguttatus*	G01319	10449	13	879	651	0	792	0
Cichlidae	*Heros efasciatus*	G01320	12037	14	879	623	0	792	0
Cichlidae	*Heterochromis multidens*	G01321	10659	13	879	649	829	0	0
Cichlidae	*Maylandia zebra*	G01519	15105	19	879	0	0	765	0
Cichlidae	*Nanochromis parilus*	G01390	2645	4	0	0	0	656	0
Cichlidae	*Neolamprologus brichardi*	G01520	18935	21	879	0	1140	2263	0
Cichlidae	*Oreochromis niloticus*	G01407	20724	22	879	645	1140	2256	0
Cichlidae	*Paratilapia polleni*	G01420	11328	12	879	648	0	2253	0
Cichlidae	*Paretroplus maculatus*	G01423	11220	12	855	648	0	2253	0
Cichlidae	*Ptychochromis grandidieri*	G01459	9350	12	765	648	0	765	0
Cichlidae	*Pundamilia nyererei*	G01521	14440	18	879	0	0	0	0
Cichlidae	*Steatocranus gibbiceps*	G01494	2873	4	0	0	0	866	0
Cichlidae	*Symphysodon discus*	E00390	10909	13	693	651	0	765	1158
Cichlidae	*Tilapia louka*	G01503	2873	4	0	0	0	866	0
Cirrhitidae	*Amblycirrhitus pinos*	E00314	16355	19	777	651	0	1728	1156
Cirrhitidae	*Cirrhitichthys falco*	N09466	4867	7	731	0	0	0	0
Cirrhitidae	*Cirrhitichthys oxycephalus*	E00884	8380	11	717	654	0	0	1174
Cirrhitidae	*Neocirrhites armatus*	E00725	12592	16	729	654	0	0	1171
Cirrhitidae	*Paracirrhites forsteri arcatus*	E00924	12505	15	711	613	0	911	1171
Citharidae	*Citharoides macrolepis*	E00071	12901	15	717	651	0	1742	0
Citharidae	*Citharus linguatula*	E01174	6850	8	0	654	826	901	0
Citharidae	*Lepidoblepharon ophthalmolepis*	E00080	7005	8	0	0	0	1676	0
Clinidae	*Blennophis striatus*	E00800	3454	4	720	0	0	0	1151
Clinidae	*Clinus cottoides*	E00804	4782	6	0	654	0	957	1141
Clinidae	*Clinus superciliosus*	E00803	5297	7	744	651	0	814	1148
Clinidae	*Gibbonsia metzi*	N09738	6827	8	866	0	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Clinidae	*Muraenoclinus dorsalis*	E00805	4559	6	720	651	0	962	1089
Clinidae	*Pavoclinus profundus*	E00799	3475	4	720	0	0	0	1152
Coryphaenidae	*Coryphaena hippurus*	E00937	17390	19	861	654	1128	2169	976
Cottidae	*Artediellus uncinatus*	N10447	7522	9	878	0	0	0	0
Cottidae	*Chitonotus pugetensis*	E00233	6714	8	756	635	0	936	0
Cottidae	*Cottus carolinae*	E00281	10765	13	879	651	1077	665	0
Cottidae	*Enophrys taurina*	E00234	3576	5	777	645	0	0	0
Cottidae	*Gymnocanthus galeatus*	E00259	3095	4	777	651	0	452	0
Cottidae	*Hemilepidotus jordani*	E00263	7975	10	0	597	1071	427	1104
Cottidae	*Hemilepidotus zapus*	E00272	5096	6	0	651	0	788	0
Cottidae	*Icelinus filamentosus*	E00277	8203	10	777	651	0	934	0
Cottidae	*Icelinus quadriseriatus*	E00228	5018	6	0	651	0	767	0
Cottidae	*Leptocottus armatus*	E00266	12068	14	777	654	1083	935	1110
Cottidae	*Microcottus sellaris*	E00223	2282	3	774	0	0	788	0
Cottidae	*Myoxocephalus octodecemspinosus*	E00221	3991	4	0	0	1140	880	0
Cottidae	*Myoxocephalus polyacanthocephalus*	E00267	4736	5	777	651	1140	935	0
Cottidae	*Radulinus asprellus*	E00429	6882	9	696	639	0	929	0
Cottidae	*Rastrinus scutiger*	E00256	6088	7	776	0	0	0	1067
Cottidae	*Scorpaenichthys marmoratus*	E00232	10450	13	750	651	1083	696	0
Cottidae	*Triglops macellus*	E00435	8082	10	651	654	0	935	0
Cottidae	*Triglops scepticus*	E00421	5233	7	690	0	0	788	0
Creediidae	*Limnichthys sp*	E01081	6256	8	765	0	0	0	1166
Cryptacanthodidae	*Cryptacanthodes maculatus*	E00116	10532	13	726	654	0	0	0
Cyclopteridae	*Cyclopterus lumpus*	E00220	12165	15	879	654	1140	613	0
Cyclopteridae	*Eumicrotremus orbis*	E00270	12456	15	777	651	0	935	0
Cynoglossidae	*Cynoglossus interruptus*	E00076	7900	8	0	651	0	1753	0
Cynoglossidae	*Symphurus atricaudus*	E00023	10924	12	0	651	0	1732	0
Cynoglossidae	*Symphurus civitatium*	E00604	7546	8	0	647	0	1753	0
Cynoglossidae	*Symphurus plagiusa*	E01164	7027	8	0	651	0	911	0
Cyprinodontidae	*Cyprinodon variegatus*	E01066	12469	15	0	645	0	0	1028

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Cyprinodontidae	*Floridichthys carpio*	E01063	9295	11	0	651	0	0	1051
Cyprinodontidae	*Jordanella floridae*	N14002	5915	7	764	0	0	0	0
Dactylopteridae	*Dactyloptena gilberti*	N14051	5845	7	0	0	0	0	0
Dactylopteridae	*Dactyloptena orientalis*	E00237	13665	15	774	654	0	1554	0
Dactylopteridae	*Dactyloptena peterseni*	E00749	14553	15	680	0	0	2261	1033
Dactylopteridae	*Dactylopterus volitans*	E00214	7789	10	759	651	1140	812	0
Dactyloscopidae	*Gillellus semicinctus*	G01299	6655	8	870	0	0	788	0
Dactyloscopidae	*Platygillellus rubrocinctus*	E00319	5427	7	774	654	0	0	1039
Datnioididae	*Datnioides microlepis*	N14199	7836	10	719	0	0	0	0
Dichistiidae	*Dichistius capensis*	M01571	3582	4	0	654	0	0	0
Diodontidae	*Chilomycterus schoepfii*	E00517	12554	15	879	654	0	778	1151
Diodontidae	*Diodon holocanthus*	E00312	13884	15	777	624	0	2251	1171
Drepaneidae	*Drepane punctata*	E00250	13305	15	774	654	0	1725	0
Echeneidae	*Echeneis naucrates*	E00615	16441	18	879	654	1134	2159	1048
Echeneidae	*Echeneis neucratoides*	E00245	7118	7	774	0	0	2159	0
Echeneidae	*Phtheirichthys lineatus*	G01438	7650	8	0	651	1063	2159	0
Echeneidae	*Remora osteochir australis*	E00503	10993	11	705	651	959	2159	0
Elassomatidae	*Elassoma evergladei*	E00146	15293	17	717	654	1125	2252	0
Elassomatidae	*Elassoma okefenokee*	G01283	9813	12	879	651	0	0	0
Elassomatidae	*Elassoma zonatum*	G01284	14834	15	879	650	1128	2253	0
Eleginopsidae	*Eleginops maclovinus*	G01286	10593	13	879	651	831	0	0
Eleotridae	*Dormitator maculatus*	E00169	5763	7	768	0	0	739	0
Eleotridae	*Eleotris acanthopoma pisonis*	E00741	12447	14	879	654	0	2252	0
Eleotridae	*Ophiocara porocephala*	E01101	11395	13	768	606	1107	911	1082
Eleotridae	*Oxyeleotris selheimi*	N01730	5975	7	855	0	0	0	0
Embiotocidae	*Amphistichus argenteus*	E00129	8893	12	693	654	0	704	0
Embiotocidae	*Cymatogaster aggregata*	E00139	14184	16	711	654	1114	2255	972
Embiotocidae	*Embiotoca jacksoni*	E00120	14177	17	717	654	0	0	0
Embiotocidae	*Embiotoca lateralis*	N14635	6883	8	878	0	0	0	0
Embiotocidae	*Hyperprosopon anale argenteum*	E00134	14767	18	711	651	0	763	908

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Embiotocidae	*Phanerodon furcatus*	E00122	11479	14	717	0	0	704	971
Embiotocidae	*Rhacochilus vacca*	E00124	12585	15	720	654	0	920	1031
Embiotocidae	*Zalembius rosaceus*	E00135	4565	6	702	654	0	704	1002
Emmelichthyidae	*Erythrocles schlegelii*	E00954	12039	15	642	654	0	0	0
Emmelichthyidae	*Erythrocles scintillans*	N14652	6911	9	713	0	0	0	0
Enoplosidae	*Enoplosus armatus*	G01287	10134	11	720	651	0	2252	0
Ephippidae	*Chaetodipterus faber*	E00614	14589	18	729	651	0	0	1031
Ephippidae	*Platax orbicularis*	E00898	13969	16	771	654	0	2252	1023
Ephippidae	*Platax teira*	E00858	12410	15	768	648	0	903	1046
Epigonidae	*Epigonus pandionis*	E01019	5505	7	708	654	0	0	0
Epigonidae	*Epigonus telescopus*	E00652	10314	12	711	653	1131	1057	0
Exocoetidae	*Cheilopogon dorsomacula*	E00624	11475	14	699	0	636	774	1041
Exocoetidae	*Cheilopogon melanurus*	N14975	5883	7	0	0	0	0	0
Exocoetidae	*Cheilopogon pinnatibarbatus*	E00399	13294	16	699	651	1131	779	1076
Exocoetidae	*Cypselurus callopterus*	E00402	6837	8	0	0	1131	0	1026
Exocoetidae	*Exocoetus monocirrhus*	E00403	10246	13	675	647	1131	774	1100
Exocoetidae	*Hirundichthys marginatus*	E00401	9589	12	687	0	631	774	1118
Exocoetidae	*Parexocoetus brachypterus*	E00645	4220	5	0	0	1131	770	0
Exocoetidae	*Prognichthys brevipinnis*	E00400	6286	8	675	0	0	0	1049
Fistulariidae	*Fistularia commersonii*	E00941	7080	7	0	0	0	2247	0
Fistulariidae	*Fistularia petimba*	E00602	6969	9	0	651	0	942	0
Fundulidae	*Adinia xenica*	E00173	8890	10	0	651	990	0	0
Fundulidae	*Fundulus blairae*	E00130	9841	11	0	651	990	0	945
Fundulidae	*Fundulus chrysotus*	E00186	8599	9	0	637	990	0	1082
Fundulidae	*Fundulus heteroclitus*	G01293	12304	13	879	650	990	2252	0
Fundulidae	*Fundulus parvipinnis*	E00389	11368	13	0	651	990	743	1164
Fundulidae	*Lucania parva goodei*	E01064	13730	16	0	651	990	0	1171
Gasterosteidae	*Apeltes quadracus*	E00791	11199	12	870	615	0	2250	0
Gasterosteidae	*Culaea inconstans*	E00368	12338	14	777	648	0	2250	0
Gasterosteidae	*Gasterosteus aculeatus*	E01012	20181	21	879	654	1140	2250	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Gasterosteidae	*Gasterosteus wheatlandi*	N15128	8456	10	878	0	0	0	0
Gasterosteidae	*Pungitius pungitius*	G01460	10820	11	879	651	1140	2250	0
Gasterosteidae	*Spinachia spinachia*	G01491	10498	11	879	0	0	2250	0
Gempylidae	*Gempylus serpens*	E00693	9797	13	747	508	0	782	0
Gempylidae	*Nealotus tripes*	E00287	6043	8	776	508	0	0	0
Gempylidae	*Neoepinnula americana*	E00471	5662	7	675	654	0	0	0
Gempylidae	*Neoepinnula orientalis*	E00518	6702	9	720	651	0	782	0
Gempylidae	*Paradiplospinus gracilis*	N15143	7281	9	767	0	0	0	0
Gempylidae	*Ruvettus pretiosus*	E00226	13794	16	879	651	1140	876	0
Gerreidae	*Eucinostomus argenteus*	E00575	5749	7	0	654	0	911	1183
Gerreidae	*Eucinostomus gula*	E00756	7604	9	0	654	0	613	1134
Gerreidae	*Eugerres plumieri*	G01291	11242	14	870	513	720	813	0
Gerreidae	*Gerres cinereus*	E00292	11457	12	777	654	0	1753	1165
Gerreidae	*Gerres longirostris*	E00835	6053	8	705	568	0	0	1162
Gerreidae	*Gerres oyena*	E00823	6770	8	0	648	0	0	1163
Gerreidae	*Ulaema lefroyi*	G01507	8309	10	870	0	0	0	0
Gigantactinidae	*Gigantactis ios*	E01053	4539	6	0	0	0	0	0
Gigantactinidae	*Gigantactis sp*	N34852	6412	8	0	0	0	0	0
Gigantactinidae	*Gigantactis vanhoeffeni*	E00177	13239	15	0	618	0	2250	0
Girellidae	*Girella nigricans mezina*	E00197	11742	13	777	654	0	1981	0
Glaucosomatidae	*Glaucosoma buergeri*	N15231	7808	10	722	0	0	0	0
Glaucosomatidae	*Glaucosoma hebraicum*	G01300	16039	18	843	651	708	1773	0
Gobiesocidae	*Arcos sp*	E00102	13747	16	716	0	0	2256	968
Gobiesocidae	*Diademichthys lineatus*	G01276	8298	10	879	0	0	0	0
Gobiesocidae	*Gobiesox maeandricus*	G01302	8270	10	879	650	0	690	0
Gobiesocidae	*Lepadichthys lineatus*	E01080	3896	5	0	654	0	0	1161
Gobiidae	*Amblyeleotris guttata*	E01043	8728	11	723	654	0	0	1169
Gobiidae	*Amblyeleotris gymnocephala*	E00409	6038	8	681	0	0	0	0
Gobiidae	*Amblyeleotris wheeleri*	E01073	7397	9	0	651	0	0	1184
Gobiidae	*Amblygobius decussatus*	E00533	2824	4	696	651	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Gobiidae	*Amblygobius phalaena*	E00736	7217	10	652	651	556	0	1167
Gobiidae	*Asterropteryx semipunctata*	E01089	6719	8	0	641	1097	0	1135
Gobiidae	*Bathygobius mystacium*	E00104	6412	8	708	651	1085	0	0
Gobiidae	*Bollmannia communis*	E00617	5108	5	0	0	0	2069	0
Gobiidae	*Cabillus lacertops*	E01093	3915	5	708	0	0	0	0
Gobiidae	*Caffrogobius caffer*	E01056	6198	8	0	651	0	0	1142
Gobiidae	*Caffrogobius saldanha*	E01057	6207	8	0	0	0	0	1171
Gobiidae	*Coryphopterus glaucofraenum*	E00100	5342	7	708	651	0	0	1049
Gobiidae	*Coryphopterus personatus*	E00405	4791	7	549	652	525	0	0
Gobiidae	*Cryptocentrus sp*	E00407	3883	5	0	0	0	0	0
Gobiidae	*Ctenogobiops crocineus*	E01097	5981	7	0	0	0	0	1169
Gobiidae	*Ctenogobius boleosoma*	E00172	3520	5	708	647	0	0	0
Gobiidae	*Elacatinus oceanops*	E00108	11459	12	708	634	1140	2069	1029
Gobiidae	*Eviota albolineata*	E01041	6182	8	711	651	0	0	1173
Gobiidae	*Eviota prasites*	E01044	5506	7	708	0	0	0	1171
Gobiidae	*Eviota saipanensis*	E00714	4913	6	702	0	0	0	1184
Gobiidae	*Evorthodus lyricus*	E00171	6129	8	708	622	0	0	996
Gobiidae	*Fusigobius duospilus*	E00863	7305	9	0	613	0	0	1182
Gobiidae	*Fusigobius inframaculatus*	E01076	4985	6	0	619	0	0	1184
Gobiidae	*Fusigobius neophytus*	E00733	7031	10	675	628	0	0	0
Gobiidae	*Gnatholepis anjerensis*	E01075	4977	7	708	651	543	0	0
Gobiidae	*Gnatholepis cauerensis*	E00099	3361	5	656	651	0	0	0
Gobiidae	*Gobiodon quinquestrigatus*	E01085	6985	9	0	651	0	756	1169
Gobiidae	*Gobiosoma bosc*	E00097	9910	10	707	0	1140	2069	1069
Gobiidae	*Istigobius decoratus*	E01078	9124	11	708	647	1085	0	1170
Gobiidae	*Istigobius ornatus*	E01107	2776	3	0	0	0	0	1170
Gobiidae	*Lepidogobius lepidus*	G01351	5076	6	768	0	0	0	0
Gobiidae	*Lophogobius cyprinoides*	E00508	6153	8	639	654	0	0	1169
Gobiidae	*Lythrypnus dalli*	E00126	6746	9	0	651	0	810	0
Gobiidae	*Oplopomus oplopomus*	E01067	6654	8	708	0	0	0	1168

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Gobiidae	*Paragobiodon modestus*	E01098	8154	11	0	638	0	0	1170
Gobiidae	*Periophthalmus kalolo*	E00537	6876	9	696	0	0	706	1003
Gobiidae	*Priolepis cincta*	E01077	5030	6	0	650	0	0	1169
Gobiidae	*Priolepis hipoliti*	E00106	5717	7	708	0	0	0	1065
Gobiidae	*Psammogobius biocellatus*	E00740	5797	8	701	651	0	0	0
Gobiidae	*Risor ruber*	E00107	10310	10	723	0	1140	2069	1038
Gobiidae	*Stonogobiops nematodes*	N16820	2850	4	713	0	0	0	0
Gobiidae	*Trimma caesiura*	E01039	8870	11	720	621	1104	0	1183
Gobiidae	*Trimma haima*	E01084	5533	7	729	0	0	0	1169
Gobiidae	*Trimma okinawae*	E00726	2759	4	672	0	0	0	0
Gobiidae	*Valenciennea puellaris*	E01096	5328	7	0	651	0	0	0
Gobiidae	*Valenciennea strigata*	E01094	4256	6	0	651	588	0	0
Gobiidae	*Vanderhorstia ornatissima*	E01088	6501	8	0	0	0	0	1171
Grammatidae	*Gramma loreto*	E00280	14197	16	869	597	0	1697	0
Grammatidae	*Lipogramma anabantoides*	E00211	6519	8	0	654	0	0	0
Grammatidae	*Lipogramma trilineata*	E00210	6532	8	775	654	0	0	0
Haemulidae	*Anisotremus surinamensis*	N17175	7479	9	872	0	0	0	0
Haemulidae	*Anisotremus virginicus*	E00200	9338	11	0	654	684	812	0
Haemulidae	*Conodon nobilis*	E00613	10862	13	717	651	0	812	0
Haemulidae	*Haemulon aurolineatum*	E00635	16270	20	718	651	747	812	0
Haemulidae	*Haemulon plumierii*	E00279	12545	15	777	0	0	812	0
Haemulidae	*Haemulon sciurus*	E00199	14796	18	861	639	747	812	0
Haemulidae	*Haemulon vittatum*	E00218	14636	17	776	513	720	1742	0
Haemulidae	*Orthopristis chrysoptera*	E00607	15170	18	708	642	1122	812	0
Haemulidae	*Plectorhinchus chaetodonoides*	E00857	12011	14	0	651	1047	813	1034
Haemulidae	*Plectorhinchus vittatus*	E00856	9448	12	0	513	720	812	1076
Haemulidae	*Pomadasys corvinaeformis*	E00761	10420	14	708	651	720	811	0
Haemulidae	*Xenistius californiensis*	E00229	11494	14	772	651	746	812	0
Hapalogenyidae	*Hapalogenys aya*	M01722	4098	4	0	0	1089	0	0
Hapalogenyidae	*Hapalogenys kishinouyei*	M01723	3627	4	0	651	0	0	0

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Hapalogenyidae	*Hapalogenys nigripinnis*	M01724	4735	5	0	651	1078	0	0
Harpagiferidae	*Harpagifer antarcticus*	G01524	10362	11	879	0	0	2263	0
Helostomatidae	*Helostoma temminkii*	G01315	8144	9	858	0	0	2069	0
Hemiramphidae	*Arrhamphus sclerolepis*	G01209	7917	10	867	0	636	0	0
Hemiramphidae	*Hemiramphus brasiliensis*	E00098	10104	12	715	632	541	768	0
Hemiramphidae	*Hyporhamphus affinis*	E01068	5623	7	0	636	0	0	1170
Hemiramphidae	*Hyporhamphus dussumieri*	E01086	3078	4	0	651	0	0	0
Hemiramphidae	*Oxyporhamphus micropterus*	E00397	8076	9	0	651	1127	774	1166
Hexagrammidae	*Hexagrammos decagrammus*	E00348	7318	10	776	620	0	0	0
Hexagrammidae	*Hexagrammos lagocephalus otakii*	E00363	13109	16	777	651	1140	1072	0
Hexagrammidae	*Pleurogrammus monopterygius*	E00367	6904	9	0	654	1140	0	0
Hexagrammidae	*Zaniolepis frenata*	E00353	6326	9	777	654	0	492	0
Himantolophidae	*Himantolophus albinares sagamius*	E00656	16540	18	695	0	0	2252	1040
Hoplichthyidae	*Hoplichthys gilberti*	N17743	5272	7	0	0	0	0	0
Hoplichthyidae	*Hoplichthys langsdorfii*	N17745	5443	7	0	0	0	0	0
Howellidae	*Howella brodiei*	E00816	11083	12	873	654	0	1773	0
Howellidae	*Howella zina*	N17756	5489	7	0	0	0	0	0
Hypoptychidae	*Aulichthys japonicus*	G01216	11602	12	879	647	1119	2252	0
Hypoptychidae	*Hypoptychus dybowskii*	G01335	10399	11	870	0	0	2251	0
Icosteidae	*Icosteus aenigmaticus*	G01336	7173	9	774	651	0	768	0
Indostomidae	*Indostomus crocodilus*	N17863	5047	7	0	0	0	0	0
Indostomidae	*Indostomus paradoxus*	E01156	10345	11	0	0	0	2256	0
Isonidae	*Iso sp*	E00145	8043	10	729	0	0	0	0
Istiophoridae	*Istiophorus platypterus*	E00695	12698	12	747	654	1140	2254	0
Istiophoridae	*Kajikia albida*	E00681	7868	10	756	654	0	0	0
Istiophoridae	*Makaira nigricans*	E00697	11395	12	0	654	1140	1604	0
Istiophoridae	*Makaira sp*	E00692	8009	9	741	0	0	1745	0
Istiophoridae	*Tetrapturus angustirostris*	N01741	7787	10	720	0	0	0	0
Kuhliidae	*Kuhlia marginata*	G01341	10248	12	879	648	0	0	0
Kuhliidae	*Kuhlia mugil*	E00712	16962	18	0	651	1134	2252	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Kuhliidae	*Kuhlia rupestris*	E00957	12721	15	729	654	1122	788	0
Kurtidae	*Kurtus gulliveri*	E00188	16737	18	705	654	1101	1743	1119
Kurtidae	*Kurtus indicus*	N17950	5074	7	0	0	0	0	0
Kyphosidae	*Kyphosus cinerascens*	N17975	7672	10	725	0	0	0	0
Kyphosidae	*Kyphosus elegans*	G01342	9674	11	879	0	0	0	0
Kyphosidae	*Kyphosus incisor*	E00202	6684	8	0	654	0	0	0
Kyphosidae	*Kyphosus sectatrix*	E00775	12318	14	696	654	1122	1730	0
Labridae	*Anampses lineatus*	E00932	8645	11	771	651	1068	825	0
Labridae	*Bodianus axillaris*	E00947	9242	11	750	654	1068	825	1145
Labridae	*Bodianus mesothorax*	E00560	14044	17	711	651	0	817	1043
Labridae	*Cheilinus chlorourus*	E00907	9227	12	774	651	1068	825	0
Labridae	*Cheilinus fasciatus*	E00876	8639	11	768	651	1068	825	0
Labridae	*Cheilinus oxycephalus*	E00901	6640	8	770	651	1068	825	0
Labridae	*Cheilio inermis*	E00906	9477	11	0	645	1053	825	1168
Labridae	*Cirrhilabrus katherinae*	E00728	6057	8	720	0	0	0	963
Labridae	*Cirrhilabrus punctatus*	E00553	5794	7	698	0	0	817	0
Labridae	*Clepticus parrae*	E00015	14928	18	720	648	0	817	1100
Labridae	*Coris batuensis*	N18137	4801	6	878	0	0	0	0
Labridae	*Coris caudimacula*	E00861	11177	14	770	651	1068	825	0
Labridae	*Coris formosa*	E00912	8465	11	771	651	0	0	1028
Labridae	*Coris gaimard*	E00091	11874	15	726	651	0	825	0
Labridae	*Decodon puellaris*	E00620	7367	9	0	651	0	0	1127
Labridae	*Diproctacanthus xanthurus*	G01278	8556	10	858	0	0	817	0
Labridae	*Epibulus insidiator*	E00879	16078	19	768	651	1068	825	1011
Labridae	*Gomphosus varius*	E00085	11071	14	713	648	558	825	0
Labridae	*Halichoeres bathyphilus bivittatus*	E00637	13256	16	879	651	0	942	1112
Labridae	*Halichoeres biocellatus*	E00727	5094	7	675	651	0	942	0
Labridae	*Halichoeres iridis*	E00928	6442	8	771	650	0	0	0
Labridae	*Halichoeres margaritaceus*	N18205	5528	7	878	0	0	0	0
Labridae	*Hologymnosus doliatus*	E00567	10593	13	0	645	0	942	1125

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Labridae	*Labrichthys unilineatus*	G01344	10143	12	879	645	0	939	0
Labridae	*Labroides dimidiatus*	E00848	9046	11	759	651	1068	825	0
Labridae	*Labropsis australis*	G01345	9319	11	879	0	0	817	0
Labridae	*Lachnolaimus maximus*	E00014	12305	15	695	654	0	817	1117
Labridae	*Macropharyngodon bipartitus*	E00895	7503	10	770	651	0	825	0
Labridae	*Novaculichthys taeniourus*	E00926	12181	15	777	651	0	825	1144
Labridae	*Oxycheilinus celebicus*	G01412	8510	10	879	0	0	824	0
Labridae	*Oxycheilinus digramma*	E00873	10757	13	771	651	1068	825	861
Labridae	*Oxycheilinus unifasciatus*	E00721	7878	9	0	651	1041	825	1048
Labridae	*Oxyjulis californica*	G01413	7537	9	879	654	0	691	0
Labridae	*Pseudocheilinus evanidus*	E00944	6483	9	764	651	0	823	0
Labridae	*Pseudocheilinus hexataenia*	E00945	7019	9	768	609	0	824	1072
Labridae	*Pteragogus enneacanthus*	G01457	6723	8	0	0	0	0	0
Labridae	*Stethojulis balteata*	E00089	4889	6	717	651	0	927	941
Labridae	*Stethojulis strigiventer*	E00908	11343	15	768	651	498	825	951
Labridae	*Tautoga onitis*	G01499	9257	11	879	648	0	905	0
Labridae	*Tautogolabrus adspersus*	G01500	10397	12	879	651	1140	905	0
Labridae	*Thalassoma amblycephalum*	E00891	10041	13	771	651	558	825	0
Labridae	*Thalassoma lunare*	E00902	11967	15	771	651	558	825	1140
Labridae	*Thalassoma quinquevittatum*	E00092	6872	9	717	651	558	825	0
Labridae	*Wetmorella nigropinnata*	E00948	11203	14	768	651	1059	825	0
Labridae	*Xyrichtys novacula martinicensis*	E00016	18002	21	879	654	1140	772	1173
Labrisomidae	*Labrisomus bucciferus*	E00301	5621	7	777	641	0	0	1022
Labrisomidae	*Labrisomus guppyi multiporosus*	E00300	8447	10	870	0	0	788	0
Labrisomidae	*Labrisomus nigricinctus*	E00302	4582	6	777	647	0	0	0
Labrisomidae	*Malacoctenus aurolineatus*	E00299	2229	3	687	0	0	0	0
Labrisomidae	*Malacoctenus triangulatus*	E00321	3751	4	776	0	0	911	0
Labrisomidae	*Paraclinus marmoratus*	E00309	4124	5	777	651	0	0	922
Labrisomidae	*Starksia atlantica*	E00304	5512	7	777	654	0	0	1125
Labrisomidae	*Starksia fasciata*	E00303	7567	9	776	633	0	0	1041

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Labrisomidae	*Starksia ocellata*	E00318	4469	6	777	587	0	0	0
Lactariidae	*Lactarius lactarius Fiji*	M01673	3453	4	0	651	0	0	0
Lactariidae	*Lactarius lactarius Qatar*	M01593	4041	5	0	654	0	0	0
Lateolabracidae	*Lateolabrax japonicus*	E01130	12539	12	873	606	1134	2252	0
Latridae	*Latridopsis forsteri*	M01594	4790	5	0	651	0	0	0
Latridae	*Latris lineata*	M01595	4794	5	0	654	0	0	0
Leiognathidae	*Gazza minuta*	G01298	8150	10	858	654	0	911	0
Leiognathidae	*Leiognathus equulus*	G01348	8522	11	726	645	582	911	0
Leptobramidae	*Leptobrama muelleri*	E01150	6470	8	0	615	0	872	0
Lethrinidae	*Gymnocranius grandoculis*	E00952	7334	9	677	651	1140	0	0
Lethrinidae	*Lethrinus atkinsoni*	E00750	7416	10	687	654	1140	0	0
Lethrinidae	*Lethrinus erythropterus*	N18731	7589	9	860	0	0	0	0
Lethrinidae	*Lethrinus harak*	E00905	18169	21	708	651	1140	1718	0
Lethrinidae	*Lethrinus obsoletus*	E00910	14297	15	705	0	1140	2264	0
Lethrinidae	*Lethrinus olivaceus*	E00751	11020	13	722	651	1140	0	0
Lethrinidae	*Monotaxis grandoculis*	G01379	11352	12	879	651	0	2253	0
Liparidae	*Careproctus melanurus*	E00422	5235	7	0	654	0	719	0
Liparidae	*Careproctus rastrinus*	E00255	6920	8	773	651	741	1611	0
Liparidae	*Liparis gibbus*	E00224	9360	11	846	651	768	935	0
Liparidae	*Liparis pulchellus*	E00225	5675	7	777	654	0	935	1110
Liparidae	*Paraliparis beani*	E00458	3871	5	723	0	0	0	0
Liparidae	*Paraliparis copei*	E00453	6908	9	711	0	0	910	0
Liparidae	*Paraliparis hystrix*	E00454	8881	11	710	0	0	0	0
Liparidae	*Rhinoliparis barbulifer*	E00262	5284	7	0	651	0	911	0
Lobotidae	*Lobotes pacificus surinamensis*	G01359	9710	12	638	651	723	813	0
Lophiidae	*Lophiodes reticulatus*	E00625	8318	11	705	624	0	0	0
Lophiidae	*Lophius americanus*	E00578	16809	19	690	654	525	2256	0
Lophiidae	*Lophius gastrophysus*	E01119	13495	17	879	654	525	0	1169
Lutjanidae	*Aphareus furca*	E00563	13687	16	702	654	1140	943	0
Lutjanidae	*Aprion virescens*	E00828	8178	10	714	654	918	945	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Lutjanidae	*Apsilus dentatus*	E00770	8017	10	714	654	963	0	0
Lutjanidae	*Lutjanus biguttatus*	E00569	10110	12	650	0	0	0	0
Lutjanidae	*Lutjanus campechanus*	E00592	9830	12	729	651	801	971	0
Lutjanidae	*Lutjanus griseus*	N20115	7237	9	815	0	0	0	0
Lutjanidae	*Lutjanus mahogoni*	G01362	10416	12	879	654	1140	0	0
Lutjanidae	*Macolor niger*	E00939	9071	11	711	654	894	947	0
Lutjanidae	*Ocyurus chrysurus*	E00283	13831	16	777	654	963	971	0
Lutjanidae	*Pristipomoides aquilonaris*	E00594	10332	13	693	654	963	788	0
Lutjanidae	*Pristipomoides auricilla*	E00746	6210	8	0	624	0	0	0
Lutjanidae	*Rhomboplites aurorubens*	E00593	13759	16	711	654	1062	971	0
Luvaridae	*Luvarus imperialis*	E00509	15760	19	879	654	0	2252	1043
Malacanthidae	*Caulolatilus intermedius*	E00595	8981	11	696	654	1124	0	0
Malacanthidae	*Caulolatilus princeps*	E00231	11865	15	768	627	0	738	0
Malacanthidae	*Malacanthus plumieri*	E00774	8060	10	642	639	0	872	0
Mastacembelidae	*Macrognathus siamensis*	G01367	8287	10	879	621	0	0	0
Mastacembelidae	*Mastacembelus brachyrhinus*	N01727	6948	8	786	0	0	0	0
Mastacembelidae	*Mastacembelus cunningtoni*	N20638	7046	8	878	0	0	0	0
Mastacembelidae	*Mastacembelus erythrotaenia*	E01157	5328	7	0	627	0	870	0
Mastacembelidae	*Mastacembelus niger*	N20658	7640	9	800	0	0	0	0
Melanocetidae	*Melanocetus johnsonii*	E00657	12119	14	698	651	1140	2252	0
Melanocetidae	*Melanocetus murrayi*	E00477	8829	10	660	0	0	2252	0
Melanotaeniidae	*Melanotaenia sp*	N35702	6890	8	869	0	0	0	0
Melanotaeniidae	*Melanotaenia splendida*	E00179	10979	13	729	651	1128	0	0
Melanotaeniidae	*Melanotaenia trifasciata*	E00178	7620	9	705	0	1128	0	0
Melanotaeniidae	*Rhadinocentrus ornatus*	E00183	8085	9	720	602	1128	773	0
Menidae	*Mene maculata*	E01131	14538	17	714	654	828	1729	0
Microdesmidae	*Cerdale floridana*	E00113	5251	7	729	620	1103	0	0
Microdesmidae	*Gunnellichthys monostigma*	E00545	4244	6	0	651	0	0	0
Microdesmidae	*Microdesmus bahianus*	E00112	6294	8	729	654	1104	0	0
Microdesmidae	*Microdesmus longipinnis*	E00388	7384	9	699	0	1104	0	1163

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Microdesmidae	*Nemateleotris magnifica*	N20888	3449	4	722	0	0	0	0
Microdesmidae	*Ptereleotris evides*	E00565	10142	12	699	650	0	0	1174
Microdesmidae	*Ptereleotris microlepis*	E00554	6773	9	681	0	581	0	1174
Molidae	*Masturus lanceolatus*	E00651	10906	12	879	0	693	2254	0
Molidae	*Mola mola*	E00683	12859	14	771	651	696	2254	0
Molidae	*Ranzania laevis*	G01463	10882	12	765	651	1140	2254	0
Monacanthidae	*Acreichthys tomentosus*	N21168	5898	7	0	0	0	0	0
Monacanthidae	*Aluterus scriptus*	E00316	8934	9	771	648	1140	2253	0
Monacanthidae	*Amanses scopas*	E00536	7667	7	0	651	0	2253	1140
Monacanthidae	*Cantherhines pardalis pullus*	E00887	13701	14	714	650	0	2253	1091
Monacanthidae	*Oxymonacanthus longirostris*	E00914	7920	8	0	648	0	2253	0
Monacanthidae	*Paraluteres prionurus*	E00913	10156	10	0	639	0	2253	0
Monacanthidae	*Pervagor janthinosoma*	N21229	7625	9	0	0	0	0	0
Monacanthidae	*Pervagor nigrolineatus*	N21232	5912	7	0	0	0	0	0
Monacanthidae	*Stephanolepis hispidus*	E00646	10631	13	780	654	1128	772	0
Monodactylidae	*Monodactylus argenteus*	E00827	11839	12	764	639	0	2252	0
Monodactylidae	*Monodactylus sebae*	N21267	8411	10	878	0	0	0	0
Moronidae	*Dicentrarchus labrax*	E01132	13167	14	873	654	1140	1773	0
Moronidae	*Morone americana*	E00017	4648	6	732	651	0	909	0
Moronidae	*Morone chrysops*	E00992	15777	17	765	651	1140	1773	0
Moronidae	*Morone mississippiensis*	E00087	11851	14	684	612	1140	0	1129
Moronidae	*Morone saxatilis*	G01380	9541	12	843	0	0	346	0
Mugilidae	*Chelon macrolepis*	E00845	8599	11	771	598	784	908	1119
Mugilidae	*Crenimugil crenilabis*	E00846	12826	14	771	586	912	2255	1107
Mugilidae	*Liza richardsonii*	E00808	12339	15	771	598	784	810	1167
Mugilidae	*Moolgarda engeli*	E00739	6506	8	0	598	784	0	1119
Mugilidae	*Mugil cephalus*	E00049	13859	15	879	651	1140	2255	0
Mugilidae	*Mugil curema*	E00031	15184	16	879	651	702	2253	1171
Mugilidae	*Mugil trichodon*	E00765	10230	11	717	619	1044	1841	1041
Mugilidae	*Myxus capensis*	E00809	9832	10	762	556	1044	2255	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Mugilidae	*Neomyxus leuciscus*	E00742	10501	12	708	602	784	1821	1053
Mugilidae	*Valamugil buchanani*	E00847	12275	15	768	651	784	810	1122
Mullidae	*Mulloidichthys flavolineatus*	E00844	9135	11	750	654	0	0	0
Mullidae	*Mullus auratus*	E00634	10617	12	0	654	0	1726	1031
Mullidae	*Parupeneus barberinus*	E00899	8131	10	768	654	0	0	0
Mullidae	*Parupeneus ciliatus*	E00840	5965	8	768	651	0	0	0
Mullidae	*Parupeneus trifasciatus*	N21710	5845	7	776	0	0	0	0
Mullidae	*Pseudupeneus maculatus*	E00773	9043	11	789	640	0	788	1038
Mullidae	*Upeneus moluccensis*	E00825	7964	10	762	654	0	0	0
Mullidae	*Upeneus parvus*	N21732	3287	4	0	0	0	0	0
Nandidae	*Nandus andrewi*	N22312	8474	10	872	0	0	0	0
Nandidae	*Nandus nandus*	G01388	11524	13	861	631	1128	0	0
Nandidae	*Nandus nebulosus*	N22314	7688	9	821	0	0	0	0
Nematistiidae	*Nematistius pectoralis*	E01146	12623	14	879	634	0	2165	0
Nemipteridae	*Pentapodus caninus*	G01427	8879	11	879	654	0	788	0
Nemipteridae	*Scolopsis bilineata*	E00028	14791	16	879	0	1116	1718	1052
Nemipteridae	*Scolopsis frenata*	E00911	6514	8	768	0	0	0	1011
Nemipteridae	*Scolopsis margaritifera*	G01478	7404	9	879	0	0	0	0
Niphonidae	*Niphon spinosus*	G01398	4377	5	0	0	0	0	0
Nomeidae	*Cubiceps baxteri*	G01271	9684	12	765	651	0	805	0
Nomeidae	*Cubiceps gracilis*	E00672	8634	11	693	654	0	0	0
Nomeidae	*Cubiceps pauciradiatus*	E00667	9277	9	0	0	0	2255	1165
Nomeidae	*Psenes cyanophrys*	E00666	6230	6	0	651	1140	2255	0
Nomeidae	*Psenes maculatus*	N23089	7094	9	713	0	0	0	0
Nototheniidae	*Aethotaxis mitopteryx*	G01528	7979	9	879	648	517	2263	0
Nototheniidae	*Dissostichus eleginoides*	G01279	12707	14	879	642	678	2252	0
Nototheniidae	*Gobionotothen gibberifrons*	G01529	8961	10	759	654	1075	2263	0
Nototheniidae	*Notothenia coriiceps*	G01526	9628	10	0	513	1089	2263	0
Nototheniidae	*Pagothenia borchgrevinki*	G01527	9352	10	0	651	575	2263	0
Nototheniidae	*Patagonotothen tessellata*	G01530	10915	12	879	648	525	2263	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Odacidae	*Haletta semifasciata*	G01312	9038	11	0	654	0	761	0
Odontobutidae	*Odontobutis potamophila*	E01137	12389	14	879	621	1104	1745	0
Odontobutidae	*Perccottus glenii*	G01429	9285	11	837	654	1107	0	0
Ogcocephalidae	*Dibranchus tremendus*	E00975	8668	11	0	0	0	0	0
Ogcocephalidae	*Halieutichthys aculeatus*	E01122	5969	8	0	0	0	712	0
Ogcocephalidae	*Ogcocephalus parvus nasutus*	E00610	11181	14	0	0	0	788	0
Ogcocephalidae	*Ogcocephalus radiatus*	E00641	3592	4	0	0	0	0	0
Oneirodidae	*Bertella idiomorpha*	E00386	7368	8	0	651	0	2252	0
Oneirodidae	*Dolopichthys sp*	E00484	3002	4	657	0	0	0	0
Oneirodidae	*Oneirodes bulbosus*	E00176	5086	7	720	654	0	0	0
Oneirodidae	*Oneirodes macrosteus*	E00655	7815	10	696	0	0	0	0
Ophidiidae	*Bassogigas gillii*	E00481	5439	7	696	0	0	0	0
Ophidiidae	*Brotula barbata*	E00629	8900	12	726	0	1140	0	0
Ophidiidae	*Brotula multibarbata*	E00883	12654	16	879	651	0	0	0
Ophidiidae	*Brotulotaenia crassa*	E00659	7913	10	716	654	0	0	0
Ophidiidae	*Brotulotaenia nigra*	E00817	8794	11	720	624	0	0	0
Ophidiidae	*Chilara taylori*	E00260	6335	8	777	650	0	743	1138
Ophidiidae	*Dicrolene introniger*	E00480	8819	11	675	0	1140	0	0
Ophidiidae	*Genypterus blacodes*	E00241	3596	4	0	648	0	782	0
Ophidiidae	*Lamprogrammus niger*	E00275	11903	13	762	654	0	2252	0
Ophidiidae	*Lepophidium brevibarbe*	E00758	5469	7	699	648	0	0	0
Ophidiidae	*Lepophidium jeannae*	E00621	4709	6	678	0	0	0	0
Ophidiidae	*Lepophidium profundorum*	E00248	3341	4	0	651	0	788	0
Ophidiidae	*Neobythites gilli*	E00612	7830	10	720	0	0	0	0
Ophidiidae	*Ophidion holbrookii*	E01033	7171	9	663	651	0	0	0
Ophidiidae	*Ophidion josephi*	E00648	6546	8	705	0	0	0	0
Ophidiidae	*Ophidion robinsi*	E01007	6730	8	705	0	0	0	1161
Ophidiidae	*Petrotyx sanguineus*	E00206	4716	6	768	624	0	0	0
Opistognathidae	*Lonchopisthus micrognathus*	E00603	6548	8	0	605	0	0	1029
Opistognathidae	*Opistognathus aurifrons*	E00216	9008	11	0	654	0	788	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Opistognathidae	*Opistognathus maxillosus*	E00207	6793	8	777	654	0	1753	0
Oplegnathidae	*Oplegnathus punctatus*	G01405	12420	13	879	654	0	2252	0
Osphronemidae	*Betta splendens*	G01226	9892	10	873	651	1137	2071	0
Osphronemidae	*Trichopodus pectoralis*	N24415	4860	7	728	0	0	0	0
Ostraciidae	*Acanthostracion quadricornis*	E00760	5464	6	717	651	1089	778	0
Ostraciidae	*Ostracion cubicus*	E00588	12421	15	714	654	1140	788	1151
Ostraciidae	*Rhinesomus triqueter*	G01469	10814	13	861	654	1089	778	0
Ostracoberycidae	*Ostracoberyx dorygenys*	N24448	6883	9	713	0	0	0	0
Parabembridae	*Parabembras curtus*	N24483	6893	9	722	0	0	0	0
Paralichthyidae	*Ancylopsetta ommata*	E00001	8842	10	705	0	0	773	1075
Paralichthyidae	*Citharichthys arctifrons*	E00043	6688	8	0	651	0	1752	0
Paralichthyidae	*Citharichthys sordidus*	E00446	12907	14	0	0	0	1733	0
Paralichthyidae	*Cyclopsetta chittendeni*	E00597	10244	12	0	651	0	1745	0
Paralichthyidae	*Etropus crossotus*	E00647	8021	9	0	651	0	1745	0
Paralichthyidae	*Etropus microstomus*	E00047	5197	5	0	651	0	1736	0
Paralichthyidae	*Gastropsetta frontalis*	E00640	2345	3	0	0	0	0	1119
Paralichthyidae	*Paralichthys albigutta*	E01171	8241	9	0	617	0	1753	0
Paralichthyidae	*Paralichthys californicus*	E00020	8905	10	723	651	681	1753	0
Paralichthyidae	*Paralichthys dentatus*	N24591	7812	9	878	0	0	0	0
Paralichthyidae	*Pseudorhombus pentophthalmus*	E00077	10302	11	0	651	0	1753	1184
Paralichthyidae	*Syacium micrurum*	E00633	9035	11	0	653	0	1753	0
Paralichthyidae	*Xystreurys liolepis*	E00021	9760	10	0	651	0	1753	0
Pegasidae	*Eurypegasus draconis*	N24699	2094	3	0	0	0	0	0
Pempheridae	*Parapriacanthus ransonneti*	E00923	11086	13	717	654	0	0	1077
Pempheridae	*Pempheris oualensis*	E00718	9245	11	714	648	0	0	0
Pempheridae	*Pempheris schomburgkii*	E00213	10586	12	777	627	0	1717	0
Pempheridae	*Pempheris schwenkii*	N01628	5322	7	0	0	0	0	0
Pempheridae	*Pempheris vanicolensis*	E00886	8350	10	708	653	0	972	1032
Pentacerotidae	*Histiopterus typus*	N24730	6890	9	713	0	0	0	0
Pentacerotidae	*Paristiopterus labiosus*	M01629	3261	4	0	654	1110	0	0

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Pentacerotidae	*Pentaceros japonicus*	N24735	7793	10	713	0	0	0	0
Pentacerotidae	*Pentaceros pectoralis*	N01736	5434	7	739	0	0	0	0
Pentacerotidae	*Pentaceros wheeleri*	N01737	7434	9	759	0	0	0	0
Pentacerotidae	*Zanclistius elevatus*	M01631	2901	3	0	654	0	0	0
Percichthyidae	*Gadopsis marmoratus*	E01144	13223	14	0	0	0	1745	0
Percichthyidae	*Maccullochella peelii*	G01365	11015	13	858	654	0	740	0
Percichthyidae	*Macquaria ambigua*	G01366	10488	13	723	654	0	747	0
Percichthyidae	*Macquaria colonorum*	G01431	10574	13	756	654	0	747	0
Percichthyidae	*Macquaria novemaculeata*	G01432	10525	13	732	654	0	747	0
Percichthyidae	*Nannoperca australis*	G01389	11969	14	732	600	1140	1332	0
Percichthyidae	*Percichthys trucha*	G01430	9417	9	873	0	0	1773	0
Percidae	*Ammocrypta beanii*	E00187	8350	10	722	639	0	0	1049
Percidae	*Ammocrypta meridiana*	E00148	8201	10	717	645	0	0	1072
Percidae	*Ammocrypta pellucida*	E00149	9339	11	714	651	1077	0	1044
Percidae	*Crystallaria asprella*	E00153	8415	10	723	639	1140	0	0
Percidae	*Etheostoma atripinne*	G01290	7713	9	879	0	0	0	0
Percidae	*Etheostoma juliae*	E00168	11455	14	723	651	1140	0	0
Percidae	*Etheostoma simoterum*	E00152	12189	15	711	651	1140	0	0
Percidae	*Etheostoma vitreum*	E00147	11025	13	716	651	1119	0	1081
Percidae	*Etheostoma zonale*	E01111	13171	16	735	651	1140	0	1169
Percidae	*Gymnocephalus cernuus*	E00140	7525	10	0	651	1140	609	0
Percidae	*Gymnocephalus schraetser*	E00141	6323	8	711	0	1140	0	0
Percidae	*Perca flavescens*	E00391	14692	16	873	654	1134	2252	0
Percidae	*Perca fluviatilis*	G01428	10413	11	0	651	1134	2046	0
Percidae	*Percina caprodes*	E01054	15273	18	861	651	1140	788	1159
Percidae	*Percina nigrofasciata*	E00154	7519	9	722	651	1140	0	0
Percidae	*Percina phoxocephala*	E00150	9105	11	741	651	1107	0	0
Percidae	*Romanichthys valsanicola*	E00143	9564	12	0	0	1140	0	956
Percidae	*Sander vitreus*	E01109	10398	10	0	651	0	2251	1174
Percidae	*Zingel streber*	E00144	5447	7	0	651	1140	788	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Percidae	*Zingel zingel*	E00142	6114	8	723	650	1140	0	0
Perciliidae	*Percilia irwini*	N24981	6918	9	731	0	0	0	0
Percophidae	*Acanthaphritis unoorum*	N24985	5579	7	0	0	0	0	0
Peristediidae	*Peristedion ecuadorense*	E00456	6094	7	687	0	0	0	1038
Peristediidae	*Peristedion gracile*	E01029	2905	4	719	0	0	788	0
Peristediidae	*Peristedion truncatum*	E00450	3441	5	657	0	0	0	0
Phallostethidae	*Phenacostethus smithi*	E00398	7945	10	723	0	0	0	0
Pholidae	*Pholis crassispina*	G01437	12482	14	879	585	519	2252	0
Pholidae	*Pholis ornata*	N01732	8528	10	879	0	0	0	0
Pholidichthyidae	*Pholidichthys leucotaenia*	E00251	11101	12	0	648	0	1753	0
Pinguipedidae	*Parapercis clathrata*	E00707	10851	13	690	0	0	0	0
Pinguipedidae	*Parapercis hexophtalma*	E01083	11528	14	729	651	0	0	0
Pinguipedidae	*Parapercis punctulata*	E01091	7008	9	723	621	0	0	1173
Platycephalidae	*Platycephalus indicus*	N25405	6719	9	713	0	0	0	0
Platycephalidae	*Rogadius asper*	N25418	6352	9	722	0	0	0	0
Platycephalidae	*Sunagocia arenicola*	E00708	5403	7	714	650	0	0	1134
Platycephalidae	*Thysanophrys chiltonae*	E00864	8747	10	0	602	0	1751	1168
Plesiopidae	*Plesiops coeruleolineatus*	E00855	15452	18	720	654	0	1529	0
Plesiopidae	*Plesiops melas*	G01442	8238	10	858	0	0	0	0
Pleuronectidae	*Atheresthes evermanni*	E00055	8437	8	0	0	665	1753	0
Pleuronectidae	*Embassichthys bathybius*	E00064	11340	12	0	654	0	1742	1127
Pleuronectidae	*Eopsetta jordani*	E00444	14474	17	0	651	0	1732	1031
Pleuronectidae	*Glyptocephalus zachirus*	E00416	10353	12	0	650	0	1753	0
Pleuronectidae	*Hippoglossoides elassodon*	E00424	12527	13	0	651	1140	1752	1031
Pleuronectidae	*Hippoglossus hippoglossus*	E00689	10279	12	0	654	1140	1750	1038
Pleuronectidae	*Hypsopsetta guttulata*	E00022	9133	9	0	651	0	1753	1065
Pleuronectidae	*Isopsetta isolepis*	E00018	6603	8	0	654	0	761	0
Pleuronectidae	*Lepidopsetta bilineata*	E00438	16335	19	879	654	0	1721	1050
Pleuronectidae	*Limanda limanda*	E00690	7013	8	0	654	1140	1751	0
Pleuronectidae	*Lyopsetta exilis*	E01173	6171	7	0	651	0	1752	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Pleuronectidae	*Microstomus pacificus*	E00433	10016	12	0	654	0	1751	1074
Pleuronectidae	*Parophrys vetulus*	E00445	12033	14	0	651	0	1731	1041
Pleuronectidae	*Platichthys stellatus*	E00026	7842	9	0	636	0	2254	0
Pleuronectidae	*Pleuronectes platessa*	E00053	14871	17	879	651	906	1752	0
Pleuronectidae	*Psettichthys melanostictus*	E00025	9364	11	717	651	0	1729	0
Pleuronectidae	*Pseudopleuronectes americanus*	E00035	15563	18	717	651	0	1748	0
Poeciliidae	*Belonesox belizanus*	E01052	10182	11	0	654	1128	0	1027
Poeciliidae	*Gambusia affinis*	G01296	11403	12	879	651	0	2247	0
Poeciliidae	*Heterandria formosa*	E00185	10113	11	0	647	1128	0	1091
Poeciliidae	*Poecilia latipinna reticulata*	E01065	12149	14	0	641	0	0	1169
Poeciliidae	*Poeciliopsis elongata*	N01734	6863	8	0	0	0	0	0
Poecilopsettidae	*Poecilopsetta beanii*	E00448	5472	7	0	0	0	0	0
Poecilopsettidae	*Poecilopsetta plinthus*	E00073	9752	10	642	0	0	1753	0
Polycentridae	*Monocirrhus polyacanthus*	G01377	8420	10	876	0	0	765	0
Polycentridae	*Polycentropsis abbreviata*	N26006	8369	10	746	0	0	0	0
Polycentridae	*Polycentrus schomburgkii*	G01444	8382	10	879	0	0	0	0
Polynemidae	*Eleutheronema rhadinum*	N26015	7791	10	710	0	0	0	0
Polynemidae	*Eleutheronema tetradactylum*	E01154	7961	9	0	654	0	782	0
Polynemidae	*Leptomelanosoma indicum*	E00842	11242	14	711	654	0	755	1049
Polynemidae	*Polydactylus octonemus*	E00606	9992	13	711	0	0	0	0
Polynemidae	*Polydactylus sextarius*	N26043	5532	7	713	0	0	0	0
Polynemidae	*Polydactylus virginicus*	E00217	11602	13	777	654	0	1753	1173
Polyprionidae	*Polyprion americanus*	E00242	7677	9	771	654	1122	0	0
Polyprionidae	*Polyprion oxygeneios*	M01632	4716	5	0	654	1110	0	0
Polyprionidae	*Stereolepis gigas*	E00227	14211	17	858	654	0	916	0
Pomacanthidae	*Apolemichthys trimaculatus*	E00839	9202	12	708	651	387	853	0
Pomacanthidae	*Centropyge bicolor*	E00550	11381	15	708	651	594	817	0
Pomacanthidae	*Centropyge loricula*	E00284	9087	10	768	623	639	2251	0
Pomacanthidae	*Centropyge nox*	E00542	8384	11	710	636	387	0	0
Pomacanthidae	*Chaetodontoplus melanosoma*	G01244	8178	10	801	645	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Pomacanthidae	*Holacanthus ciliaris*	E00209	6815	8	777	635	0	0	0
Pomacanthidae	*Holacanthus passer*	E00282	12494	15	861	654	696	813	1121
Pomacanthidae	*Holacanthus tricolor*	E00198	7349	9	0	654	0	847	1019
Pomacanthidae	*Pomacanthus arcuatus*	E00754	8027	10	702	654	0	911	0
Pomacanthidae	*Pomacanthus imperator*	E00710	9192	12	708	651	393	907	0
Pomacanthidae	*Pomacanthus semicirculatus*	E00849	10414	14	711	648	393	858	0
Pomacanthidae	*Pomacanthus zonipectus*	G01448	9113	11	879	651	0	797	0
Pomacanthidae	*Pygoplites diacanthus*	E00534	10507	13	702	651	387	911	0
Pomacentridae	*Abudefduf saxatilis*	E00820	14973	18	879	654	0	817	841
Pomacentridae	*Abudefduf sexfasciatus*	E00881	12145	15	696	651	1069	825	0
Pomacentridae	*Abudefduf vaigiensis*	E00890	12132	13	708	654	1071	2253	1035
Pomacentridae	*Acanthochromis polyacanthus*	E00466	8743	10	705	0	0	817	0
Pomacentridae	*Amblyglyphidodon leucogaster*	E00529	3808	4	0	651	0	817	0
Pomacentridae	*Amphiprion clarkii*	E00196	4604	6	0	582	1031	798	0
Pomacentridae	*Amphiprion ocellaris*	E00193	7717	7	0	599	1031	2250	0
Pomacentridae	*Azurina hirundo*	E00580	9629	12	714	651	0	817	0
Pomacentridae	*Chromis atripectoralis*	E00238	9353	11	770	651	1071	825	1089
Pomacentridae	*Chromis cyanea*	E00201	13033	15	774	629	0	0	1124
Pomacentridae	*Chromis dimidiata*	E00851	9724	12	720	649	1071	825	0
Pomacentridae	*Chrysiptera taupou*	E00564	9950	13	705	650	0	0	0
Pomacentridae	*Dascyllus aruanus*	E00700	11886	14	702	651	1071	825	0
Pomacentridae	*Dascyllus carneus*	E00862	11899	14	711	651	1071	825	0
Pomacentridae	*Dascyllus reticulatus*	E00724	8549	10	720	651	0	817	0
Pomacentridae	*Dascyllus trimaculatus*	E00865	6439	7	0	651	1071	817	0
Pomacentridae	*Dischistodus perspicillatus*	E00464	8931	11	711	0	0	817	0
Pomacentridae	*Hypsypops rubicundus*	E00459	7285	10	693	654	0	787	0
Pomacentridae	*Lepidozygus tapeinosoma*	E00929	7795	10	681	651	0	817	0
Pomacentridae	*Microspathodon bairdii*	G01375	8331	10	879	0	0	0	0
Pomacentridae	*Microspathodon chrysurus*	E00772	10751	13	678	654	0	817	0
Pomacentridae	*Neoglyphidodon melas*	E00465	9828	12	708	651	1071	825	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Pomacentridae	*Neoglyphidodon polyacanthus*	E00285	6455	8	777	650	0	0	0
Pomacentridae	*Neopomacentrus cyanomos*	E00933	8888	11	699	650	1071	825	0
Pomacentridae	*Parma microlepis*	E00286	5332	7	0	0	0	817	0
Pomacentridae	*Plectroglyphidodon dickii*	E00572	13722	16	705	650	1071	825	0
Pomacentridae	*Plectroglyphidodon johnstonianus*	E00722	7987	10	702	641	0	825	0
Pomacentridae	*Pomacentrus brachialis*	E00239	9865	12	768	0	0	897	958
Pomacentridae	*Pomacentrus pavo*	E00729	12503	15	705	650	1070	825	0
Pomacentridae	*Pomacentrus spilotoceps*	E00557	6421	9	705	617	0	0	0
Pomacentridae	*Pomachromis richardsoni*	E00559	8319	11	705	0	0	817	0
Pomacentridae	*Stegastes albifasciatus*	E00713	6612	9	710	650	0	825	0
Pomacentridae	*Stegastes diencaeus*	E00219	6060	8	768	650	0	817	0
Pomacentridae	*Stegastes fuscus*	E00203	12679	15	768	0	0	817	1122
Pomacentridae	*Stegastes partitus*	E00204	4367	6	768	650	0	816	0
Pomatomidae	*Pomatomus saltatrix*	E00516	16569	18	710	654	1140	2164	0
Priacanthidae	*Heteropriacanthus cruentatus*	E00570	14367	17	711	654	1140	0	0
Priacanthidae	*Priacanthus arenatus*	E00618	14657	18	705	648	0	788	0
Priacanthidae	*Pristigenys alta*	E00252	12492	14	864	0	0	1773	0
Pristolepididae	*Pristolepis fasciata*	N26580	7608	9	818	0	0	0	0
Pristolepididae	*Pristolepis sp*	N36627	8543	10	878	0	0	0	0
Psettodidae	*Psettodes belcheri*	E01180	6046	7	0	0	0	871	0
Psettodidae	*Psettodes erumei*	E01165	12034	14	738	654	0	1006	0
Pseudaphritidae	*Pseudaphritis urvillii*	G01453	8567	9	879	0	1119	2252	0
Pseudochromidae	*Congrogadus subducens*	G01262	8360	10	869	0	0	0	0
Pseudochromidae	*Halidesmus scapularis*	E00793	10231	13	711	654	0	903	0
Pseudochromidae	*Labracinus cyclophthalmus*	G01343	11328	12	879	651	0	2262	0
Pseudochromidae	*Natalichthys sam*	E00589	7891	10	654	651	0	0	0
Pseudochromidae	*Ogilbyina novaehollandiae*	G01403	8345	10	870	0	0	0	0
Pseudochromidae	*Pholidochromis cerasina*	G01436	8319	10	876	0	0	0	0
Pseudochromidae	*Pseudochromis cyanotaenia*	E00706	7668	10	708	0	0	0	0
Pseudochromidae	*Pseudochromis fridmani*	N26709	8561	10	878	0	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Pseudochromidae	*Pseudochromis jamesi*	E00535	6957	9	669	654	0	0	0
Pseudochromidae	*Pseudoplesiops revellei*	E00745	4311	6	0	654	0	0	0
Pseudomugilidae	*Pseudomugil gertrudae*	E00182	14736	18	720	622	0	809	0
Pseudomugilidae	*Pseudomugil signifer*	E00184	11998	15	699	602	504	809	0
Psychrolutidae	*Cottunculus thomsonii*	E00963	2374	3	0	0	0	613	1017
Psychrolutidae	*Dasycottus setiger*	E00288	5136	6	0	654	0	936	0
Psychrolutidae	*Malacocottus zonurus*	E00253	8212	10	771	651	1139	788	0
Psychrolutidae	*Psychrolutes phrictus*	E00276	5502	7	777	582	0	646	0
Rachycentridae	*Rachycentron canadum*	E00468	15775	17	723	654	1128	2260	0
Rhombosoleidae	*Oncopterus darwinii*	E01184	6659	7	0	0	0	872	0
Rhombosoleidae	*Rhombosolea leporina*	E01166	2980	3	0	0	0	1753	0
Rhombosoleidae	*Rhombosolea plebeia*	E01167	5378	6	0	0	0	1754	0
Rhombosoleidae	*Rhombosolea tapirina*	E01168	3805	4	0	654	0	1753	0
Samaridae	*Plagiopsetta glossa*	E00074	7559	8	0	0	0	1745	0
Samaridae	*Samariscus japonicus*	E00072	7912	8	0	0	0	1753	0
Samaridae	*Samariscus latus*	N27771	2733	3	0	0	0	0	0
Samaridae	*Samariscus xenicus*	E00078	7553	8	0	0	0	1745	0
Scaridae	*Calotomus carolinus*	N27783	7195	9	758	0	0	0	0
Scaridae	*Cetoscarus bicolor*	E00566	14113	17	762	651	0	770	1038
Scaridae	*Chlorurus gibbus*	E00561	6813	9	0	636	0	943	1042
Scaridae	*Chlorurus sordidus*	E00837	14642	16	768	648	0	2253	0
Scaridae	*Cryptotomus roseus*	N27805	7128	9	725	0	0	0	0
Scaridae	*Hipposcarus longiceps*	E00737	4541	6	0	0	579	770	1035
Scaridae	*Leptoscarus vaigiensis*	E00877	8427	11	0	627	0	770	1014
Scaridae	*Scarus ghobban*	E00878	9678	11	759	648	0	2253	0
Scaridae	*Scarus globiceps*	N27829	4729	6	0	0	0	0	0
Scaridae	*Scarus iseri*	E00013	7345	9	0	654	0	0	1101
Scaridae	*Scarus niger*	E00875	11274	14	766	0	0	817	0
Scaridae	*Scarus quoyi*	E00872	7432	10	0	0	0	817	0
Scaridae	*Scarus rubroviolaceus*	E00874	12027	13	764	650	0	2253	1171

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Scaridae	*Sparisoma aurofrenatum*	E00008	5465	7	0	589	0	770	1158
Scaridae	*Sparisoma chrysopterum*	E00070	2776	4	0	630	0	770	0
Scaridae	*Sparisoma viride*	E00004	6443	9	644	654	0	770	0
Scatophagidae	*Scatophagus argus*	E00051	13219	16	720	651	0	0	1070
Scatophagidae	*Selenotoca multifasciata*	G01483	9576	12	879	651	0	0	0
Sciaenidae	*Aplodinotus grunniens*	E01108	17827	19	879	654	1134	2255	1026
Sciaenidae	*Atractoscion nobilis*	E00125	9878	13	717	654	717	813	1061
Sciaenidae	*Bairdiella chrysoura*	E00165	7670	10	0	654	0	939	0
Sciaenidae	*Cheilotrema saturnum*	E00118	6644	9	717	651	0	751	0
Sciaenidae	*Corvula sanctaeluciae*	E01047	5698	7	723	0	0	0	0
Sciaenidae	*Cynoscion arenarius*	E00511	11444	13	699	654	741	2078	0
Sciaenidae	*Cynoscion regalis*	E00164	14880	18	723	654	741	971	1042
Sciaenidae	*Genyonemus lineatus*	E00138	9138	12	711	639	0	346	955
Sciaenidae	*Larimus breviceps*	E01048	4776	7	716	651	0	0	0
Sciaenidae	*Leiostomus xanthurus*	G01349	9972	12	879	621	0	943	0
Sciaenidae	*Menticirrhus saxatilis*	E00166	7177	9	711	654	0	0	0
Sciaenidae	*Menticirrhus undulatus littoralis*	E00127	15027	19	710	651	0	814	1029
Sciaenidae	*Micropogonias undulatus*	N01637	5789	8	735	0	0	0	0
Sciaenidae	*Odontoscion dentex*	E01049	5655	7	711	654	0	0	0
Sciaenidae	*Pareques acuminatus*	E01050	3516	4	0	654	0	0	0
Sciaenidae	*Pareques umbrosus*	E00639	6228	8	693	627	0	0	0
Sciaenidae	*Pogonias cromis*	E00699	8505	11	659	651	601	819	0
Sciaenidae	*Sciaenops ocellatus*	E01055	18596	20	873	654	705	2255	1166
Sciaenidae	*Seriphus politus*	E00123	7497	10	717	0	741	0	0
Sciaenidae	*Stellifer lanceolatus*	E00608	9278	12	696	654	0	0	0
Sciaenidae	*Umbrina coroides*	E00628	8595	11	687	654	0	0	0
Scomberesocidae	*Cololabis saira*	E00192	10242	11	0	654	541	2239	914
Scomberesocidae	*Scomberesox saurus*	E00404	10373	13	0	651	541	751	0
Scombridae	*Acanthocybium solandri*	E00927	14337	16	743	654	1140	835	1040
Scombridae	*Auxis rochei*	E00673	14617	18	764	518	511	1380	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Scombridae	*Euthynnus affinis*	E00830	9732	12	737	651	511	0	1119
Scombridae	*Euthynnus alletteratus*	E00696	7879	11	0	654	511	0	0
Scombridae	*Gymnosarda unicolor*	E00832	9359	11	752	651	1140	0	1034
Scombridae	*Katsuwonus pelamis*	E00747	11259	13	723	508	604	2254	0
Scombridae	*Sarda sarda*	E00243	16203	19	768	507	1140	1007	0
Scombridae	*Scomber japonicus*	E00247	10495	12	767	654	511	2252	0
Scombridae	*Scomber scombrus*	E00626	19143	20	861	654	1140	2252	0
Scombridae	*Scomberomorus maculatus sp*	E00631	16041	19	717	0	511	0	0
Scombridae	*Scomberomorus regalis commerson*	E00694	9863	12	0	651	511	886	0
Scombridae	*Thunnus albacares*	E00831	18226	21	738	518	511	2254	0
Scombrolabracidae	*Scombrolabrax heterolepis*	E00976	11570	14	0	654	0	968	0
Scophthalmidae	*Lepidorhombus boscii*	E00462	9162	10	0	654	1140	1857	0
Scophthalmidae	*Scophthalmus aquosus*	E00039	10410	12	0	651	0	0	0
Scophthalmidae	*Scophthalmus maximus*	E01161	6280	5	0	654	1140	1753	0
Scorpaenidae	*Caracanthus maculatus*	E00716	8029	10	711	552	0	788	1037
Scorpaenidae	*Caracanthus unipinna*	E00558	6573	8	723	651	0	0	1011
Scorpaenidae	*Dendrochirus zebra*	E00897	7402	10	768	650	888	785	0
Scorpaenidae	*Iracundus signifer*	E00583	7125	9	720	0	0	660	0
Scorpaenidae	*Neomerinthe hemingwayi*	E00619	10221	12	642	0	0	1007	944
Scorpaenidae	*Pontinus longispinis*	E01010	7126	10	704	0	0	660	0
Scorpaenidae	*Pontinus rathbuni*	E00463	6391	8	723	0	0	0	1181
Scorpaenidae	*Pterois antennata*	E00705	8496	11	732	648	774	785	0
Scorpaenidae	*Pterois miles*	E00882	7015	9	711	651	876	785	1166
Scorpaenidae	*Pterois radiata*	E00850	8182	10	720	651	888	785	1121
Scorpaenidae	*Scorpaena agassizii*	E01038	2193	3	0	0	0	0	0
Scorpaenidae	*Scorpaena brasiliensis*	E00759	4986	7	0	645	0	788	0
Scorpaenidae	*Scorpaena dispar*	E00512	3690	5	714	0	0	0	0
Scorpaenidae	*Scorpaena guttata*	E00291	8547	10	777	651	0	760	1170
Scorpaenidae	*Scorpaenodes albaiensis*	E00532	4039	5	699	0	0	0	1184
Scorpaenidae	*Scorpaenodes guamensis*	E00870	6637	9	588	651	0	0	1165

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Scorpaenidae	*Scorpaenopsis longispina*	E00903	7186	9	696	648	0	0	1102
Scorpaenidae	*Scorpaenopsis oxycephala*	E00581	5118	7	0	651	0	0	0
Scorpaenidae	*Sebastapistes cyanostigma*	E00888	8326	10	720	0	0	0	1183
Scorpaenidae	*Taenianotus triacanthus*	E00866	8147	10	704	642	0	658	1172
Sebastidae	*Adelosebastes latens*	E00066	2246	3	0	0	0	0	0
Sebastidae	*Helicolenus dactylopterus*	E00044	9920	12	717	645	1140	1468	0
Sebastidae	*Sebastes aurora*	E00349	8679	10	0	480	0	1745	0
Sebastidae	*Sebastes diploproa*	E00432	6421	8	711	456	0	940	0
Sebastidae	*Sebastes fasciatus*	G01482	8330	10	858	0	0	935	0
Sebastidae	*Sebastes jordani*	E00350	6619	9	0	456	780	940	0
Sebastidae	*Sebastes paucispinis*	E00354	6853	9	777	654	0	939	0
Sebastidae	*Sebastes ruberrimus*	N28709	6206	8	878	0	0	0	0
Sebastidae	*Sebastolobus alascanus*	E00417	12929	16	726	654	0	935	1181
Serranidae	*Aethaloperca rogaa*	E01079	6350	8	0	654	0	911	1089
Serranidae	*Anthias nicholsi*	E00447	6801	6	867	0	0	1773	0
Serranidae	*Aporops bilinearis*	E00531	7661	10	723	620	0	0	0
Serranidae	*Baldwinella aureorubens*	G01220	8097	10	738	0	0	0	0
Serranidae	*Baldwinella vivana*	E00338	3660	5	771	0	0	0	0
Serranidae	*Centropristis striata*	E00163	8944	11	701	654	0	965	0
Serranidae	*Cephalopholis argus*	E00868	14648	18	870	654	726	955	1096
Serranidae	*Cephalopholis fulva*	E00771	5807	7	711	654	0	967	0
Serranidae	*Cephalopholis miniata*	E00838	9601	12	720	651	0	946	1122
Serranidae	*Diplectrum bivittatum*	E01008	4699	6	687	0	0	0	1030
Serranidae	*Diplectrum formosum*	E01002	8832	10	717	0	768	1983	1031
Serranidae	*Epinephelus maculatus*	E00549	12180	14	867	651	0	1773	0
Serranidae	*Epinephelus merra*	E00552	8076	10	723	648	807	940	1121
Serranidae	*Grammistes sexlineatus*	E00900	15699	17	867	645	0	1773	1042
Serranidae	*Grammistops ocellatus*	E00571	6588	8	726	588	0	0	1158
Serranidae	*Hypoplectrus puella*	E00505	12795	16	879	651	681	0	0
Serranidae	*Hyporthodus flavolimbatus*	E00627	5022	7	633	0	0	0	0

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Serranidae	*Liopropoma mowbrayi*	E00307	4911	6	0	654	0	0	0
Serranidae	*Liopropoma rubre*	E00306	13426	14	777	654	0	1773	1175
Serranidae	*Mycteroperca bonaci microlepis*	E00311	14036	17	777	654	0	939	1071
Serranidae	*Odontanthias chrysostictus*	G01327	10158	10	873	0	0	1762	0
Serranidae	*Paralabrax nebulifer*	E00325	12094	15	771	600	0	952	0
Serranidae	*Pronotogrammus martinicensis*	E00636	3713	4	0	0	0	0	1184
Serranidae	*Pseudanthias pascalus*	G01452	9024	11	879	651	0	0	0
Serranidae	*Pseudanthias squamipinnis*	E00860	6941	8	711	624	0	1994	0
Serranidae	*Pseudogramma polyacantha*	E00852	7643	10	711	0	0	818	990
Serranidae	*Rypticus saponaceus*	E00764	15840	19	864	651	780	970	1152
Serranidae	*Rypticus subbifrenatus*	E00347	6320	7	777	654	0	0	0
Serranidae	*Serranus baldwini*	E00322	14886	16	867	654	789	1773	1164
Serranidae	*Serranus notospilus*	E00337	5719	7	777	0	0	0	0
Serranidae	*Serranus phoebe*	E00336	6229	8	756	0	681	0	0
Serranidae	*Serranus tigrinus*	G01486	8954	11	879	570	789	0	0
Setarchidae	*Setarches guentheri*	E01035	5731	8	715	651	0	660	0
Siganidae	*Siganus argenteus*	E00940	7215	10	768	654	522	773	0
Siganidae	*Siganus punctatus*	E00958	3704	4	0	0	0	773	0
Siganidae	*Siganus spinus*	N29369	8207	10	878	0	0	0	0
Siganidae	*Siganus stellatus*	G01488	6854	9	771	648	0	788	0
Siganidae	*Siganus vulpinus*	E00090	11306	14	864	651	522	773	0
Sillaginidae	*Sillago chondropus*	N29390	6780	9	725	0	0	0	0
Sillaginidae	*Sillago sihama*	E00824	13627	15	0	651	393	2263	1018
Sinipercidae	*Coreoperca whiteheadi*	G01264	8180	8	873	0	1134	890	0
Sinipercidae	*Siniperca chuatsi*	E01136	15198	17	750	0	1134	2251	0
Sinipercidae	*Siniperca scherzeri*	G01489	8368	7	873	0	1134	2251	0
Soleidae	*Aseraggodes heemstrai*	E00582	9255	10	0	0	0	1746	0
Soleidae	*Aseraggodes kobensis*	E00075	12391	14	687	0	0	1737	0
Soleidae	*Brachirus annularis*	E01182	5846	7	0	0	0	746	0
Soleidae	*Heteromycteris japonicus*	E00079	14809	17	720	650	0	1737	0

Table A4d. *Continued*

Family	Genus Species	ETOL_ID	Length (bp)	charset	ZIC1	COI	CYT *b*	16s	HOX
Soleidae	*Microchirus frechkopi*	E01175	5082	6	0	0	0	900	0
Soleidae	*Pegusa lascaris*	E01183	8261	10	0	654	711	870	0
Soleidae	*Pseudaesopia japonica*	E00081	10067	11	714	0	0	1747	0
Soleidae	*Solea solea*	E00054	7675	8	0	651	1140	1744	0
Soleidae	*Soleichthys heterorhinos*	E00943	10673	11	0	0	0	1753	0
Sparidae	*Acanthopagrus catenula*	E00953	10468	14	708	654	396	0	0
Sparidae	*Acanthopagrus latus*	M01638	3048	4	0	654	897	0	0
Sparidae	*Archosargus probatocephalus*	E00249	8388	10	777	651	1140	909	0
Sparidae	*Argyrops spinifer*	M01668	2629	3	0	0	393	0	0
Sparidae	*Argyrozona argyrozona*	E00802	9618	12	707	645	1131	0	0
Sparidae	*Boops boops*	M01640	3246	3	0	651	1140	0	0
Sparidae	*Boopsoidea inornata*	M01639	3951	4	0	651	1140	0	0
Sparidae	*Calamus calamus*	N29934	7496	9	770	0	0	0	0
Sparidae	*Calamus nodosus*	M01641	3290	4	0	654	1140	0	0
Sparidae	*Calamus penna*	E00762	7629	10	705	654	0	765	0
Sparidae	*Cheimerius nufar*	M01642	3243	3	0	648	1140	0	0
Sparidae	*Chrysoblephus laticeps*	M01644	3594	4	0	645	0	0	0
Sparidae	*Crenidens crenidens*	M01645	4737	5	0	645	1140	0	0
Sparidae	*Dentex dentex*	M01646	4731	5	0	654	1140	0	0
Sparidae	*Diplodus annularis*	M01647	4730	5	0	651	1140	0	0
Sparidae	*Diplodus bermudensis*	M01648	3953	4	0	654	1140	0	0
Sparidae	*Diplodus capensis*	E00807	5192	7	705	0	0	0	0
Sparidae	*Lagodon rhomboides*	G01346	10209	12	879	651	1140	909	0
Sparidae	*Lithognathus mormyrus*	M01649	4731	5	0	651	1140	0	0
Sparidae	*Oblada melanura*	M01650	3249	3	0	654	1140	0	0
Sparidae	*Pachymetopon grande*	M01651	3549	4	0	609	0	0	0
Sparidae	*Pagellus affinis*	M01652	3072	4	0	654	921	0	0
Sparidae	*Pagellus erythrinus*	M01653	4029	4	0	654	1140	0	0
Sparidae	*Pagrus pagrus*	E00514	12441	15	879	654	1140	0	0
Sparidae	*Porcostoma dentata*	M01654	4728	5	0	648	1140	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Sparidae	*Rhabdosargus haffara*	M01655	2151	3	0	654	0	0	0
Sparidae	*Sarpa salpa*	E00806	12445	15	714	651	1140	868	0
Sparidae	*Sparidentex hasta*	M01657	4746	5	0	654	1140	0	0
Sparidae	*Sparus aurata*	M01658	3954	4	0	654	1140	0	0
Sparidae	*Spondyliosoma cantharus*	M01659	3257	4	0	651	1140	0	0
Sparidae	*Stenotomus chrysops*	E00246	12458	15	879	654	1140	909	0
Sparidae	*Virididentex acromegalus*	M01660	4676	5	0	654	1067	0	0
Sphyraenidae	*Sphyraena argentea*	E00230	8319	10	0	651	0	831	0
Sphyraenidae	*Sphyraena barracuda*	E00836	19387	22	720	555	629	1753	961
Sphyraenidae	*Sphyraena japonica*	N30022	5263	7	0	0	0	0	0
Sphyraenidae	*Sphyraena jello*	N30023	4747	6	0	0	0	0	0
Sphyraenidae	*Sphyraena putnamae*	E00955	13026	14	0	651	0	1745	1032
Sphyraenidae	*Sphyraena sphyraena*	E01143	7520	8	0	654	1140	1745	0
Stichaeidae	*Bryozoichthys marjorius*	E00442	7041	9	693	0	0	0	0
Stichaeidae	*Cebidichthys violaceus*	N30217	6500	9	725	0	0	0	0
Stichaeidae	*Leptoclinus maculatus*	E00323	5549	7	765	651	519	942	1169
Stichaeidae	*Lumpenus fabricii*	E00361	3593	5	765	639	0	0	0
Stichaeidae	*Lumpenus lampretaeformis*	E00371	5472	7	764	654	0	0	0
Stichaeidae	*Poroclinus rothrocki*	E00431	5685	7	723	645	0	0	0
Stromateidae	*Peprilus burti*	E00600	5597	7	672	0	0	0	0
Stromateidae	*Peprilus paru*	E00622	7448	10	357	654	0	788	0
Stromateidae	*Peprilus simillimus*	E00136	10724	12	716	654	0	1753	1054
Stromateidae	*Peprilus triacanthus*	N30548	8492	10	869	0	0	0	0
Symphysanodontidae	*Symphysanodon typus*	M01725	1508	2	0	0	0	0	0
Synanceiidae	*Synanceia verrucosa*	E00867	10214	13	711	645	0	493	1173
Synbranchidae	*Monopterus albus*	E01134	14200	15	879	0	0	2257	0
Syngnathidae	*Corythoichthys intestinalis*	E00734	5411	6	0	651	1135	770	1184
Syngnathidae	*Corythoichthys schultzi*	E00829	4587	5	0	0	0	0	1170
Syngnathidae	*Doryrhamphus excisus*	E00915	8801	10	0	603	1125	875	0
Syngnathidae	*Hippocampus erectus*	N30799	2880	4	0	0	0	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Syngnathidae	*Syngnathus fuscus*	E00792	6471	8	0	648	1138	769	0
Syngnathidae	*Syngnathus leptorhynchus*	N30969	2247	3	0	0	0	0	0
Syngnathidae	*Syngnathus louisianae*	E00821	4535	5	0	0	1140	739	1168
Syngnathidae	*Syngnathus scovelli*	E00346	4744	6	0	632	1140	739	0
Telmatherinidae	*Marosatherina ladigesi*	E00406	9346	12	648	642	0	809	0
Terapontidae	*Hephaestus fuliginosus*	G01318	10031	11	0	0	1134	0	0
Terapontidae	*Scortum barcoo*	G01480	10071	11	0	0	1134	0	0
Terapontidae	*Terapon jarbua*	E00826	14339	16	0	618	1119	1752	0
Tetraodontidae	*Arothron hispidus*	E00985	8771	8	0	645	1128	2252	0
Tetraodontidae	*Arothron nigropunctatus*	N31143	7811	9	845	0	0	0	0
Tetraodontidae	*Canthigaster bennetti*	E00530	8390	9	753	651	0	774	1124
Tetraodontidae	*Canthigaster jactator*	N31165	6260	7	845	0	0	0	0
Tetraodontidae	*Canthigaster valentini*	E00853	7767	8	696	651	0	2253	0
Tetraodontidae	*Lagocephalus laevigatus*	E00601	8160	8	726	651	0	2252	0
Tetraodontidae	*Sphoeroides maculatus*	E00339	4428	5	777	0	0	948	0
Tetraodontidae	*Sphoeroides nephelus*	N01739	6070	7	864	0	0	0	0
Tetraodontidae	*Takifugu rubripes*	E00460	20045	21	879	621	0	2250	1184
Tetraodontidae	*Tetractenos hamiltoni*	E00383	2976	4	0	0	0	0	0
Tetraodontidae	*Tetraodon fluviatilis*	E00374	4553	5	777	0	0	1019	0
Tetraodontidae	*Tetraodon miurus*	N01740	8550	10	879	0	0	0	0
Tetraodontidae	*Tetraodon nigroviridis*	G01513	17489	18	879	0	0	2253	0
Tetrarogidae	*Coccotropsis gymnoderma*	E00801	6200	8	771	0	0	0	1136
Toxotidae	*Toxotes chatareus*	E01139	10242	10	0	654	0	2253	0
Toxotidae	*Toxotes jaculatrix*	E01155	11428	14	837	651	0	871	0
Trachichthyidae	*Hoplostethus occidentalis atlanticus*	E01018	11766	14	701	0	0	781	0
Triacanthidae	*Triacanthus biaculeatus*	G01531	11323	12	837	651	0	2266	0
Triacanthodidae	*Halimochirurgus alcocki*	N31459	6920	9	746	0	0	0	0
Triacanthodidae	*Triacanthodes anomalus*	E00382	12061	13	846	0	0	2253	0
Triacanthodidae	*Triacanthodes ethiops*	G01532	6829	7	846	499	1089	2263	0
Trichiuridae	*Aphanopus carbo*	E00274	5425	7	777	508	1140	0	0

Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Trichiuridae	*Assurger anzac*	G01210	9581	12	765	508	0	796	0
Trichiuridae	*Benthodesmus simonyi*	E00475	4383	6	741	650	0	0	0
Trichiuridae	*Evoxymetopon taeniatus*	E00650	3573	5	750	654	0	0	0
Trichiuridae	*Lepidopus altifrons*	E00474	6788	9	759	651	0	0	0
Trichiuridae	*Trichiurus lepturus*	E00596	12574	14	0	624	601	1753	0
Trichodontidae	*Trichodon trichodon*	N31563	7181	9	770	0	0	0	0
Triglidae	*Bellator militaris*	E01026	4452	6	711	0	0	0	0
Triglidae	*Prionotus carolinus*	E00340	7371	9	777	0	0	0	1172
Triglidae	*Prionotus evolans*	E01021	4575	6	879	0	0	0	0
Triglidae	*Prionotus stephanophrys*	E00328	6883	9	762	651	0	784	0
Triglidae	*Pterygotrigla hemisticta*	N31939	4770	6	0	0	0	0	0
Triodontidae	*Triodon macropterus*	N31959	7201	9	749	0	0	0	0
Tripterygiidae	*Enneanectes altivelis*	E00315	5180	7	777	0	0	0	0
Tripterygiidae	*Enneanectes boehlkei*	E00305	8688	11	786	651	0	0	0
Tripterygiidae	*Enneapterygius abeli*	E00896	2369	3	0	0	0	0	0
Tripterygiidae	*Enneapterygius gruschkai*	E00916	3832	5	698	0	0	0	1025
Tripterygiidae	*Helcogramma ellioti sp*	E00331	9671	11	768	0	0	0	0
Tripterygiidae	*Helcogramma fuscopinna*	E00885	2098	3	0	0	0	0	0
Uranoscopidae	*Astroscopus ygraecum*	E01028	11671	14	701	0	0	0	0
Uranoscopidae	*Kathetostoma albigutta*	E01022	2118	3	711	0	0	0	0
Uranoscopidae	*Kathetostoma averruncus*	E00324	11393	14	777	651	0	0	1032
Uranoscopidae	*Uranoscopus sulphureus*	E00538	5752	7	723	0	0	0	0
Xiphiidae	*Xiphias gladius*	E01151	16644	17	879	654	1140	2254	0
Zanclidae	*Zanclus cornutus*	E00894	18204	20	771	636	0	2254	1035
Zaproridae	*Zaprora silenus*	E00362	6043	8	777	654	519	935	0
Zenarchopteridae	*Dermogenys collettei*	G01275	6851	8	861	0	0	788	0
Zenarchopteridae	*Zenarchopterus dispar*	E00541	5209	6	669	0	0	0	1091
Zoarcidae	*Bothrocara brunneum*	E00357	6304	8	777	651	0	0	1176
Zoarcidae	*Bothrocara hollandi*	N01721	4677	6	864	0	0	0	0
Zoarcidae	*Eucryphycus californicus*	E00327	5531	7	766	654	0	0	1144

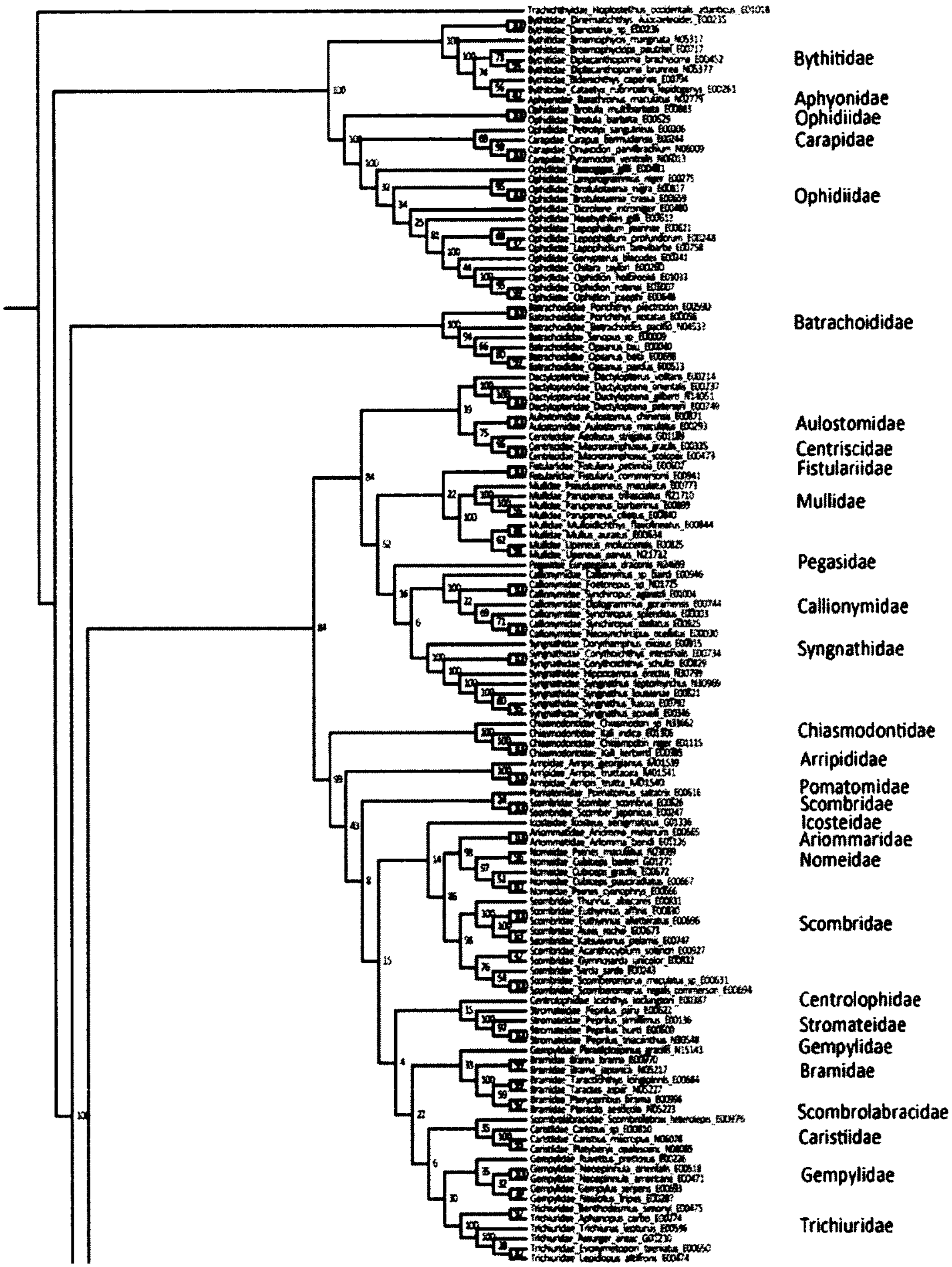
Table A4d. *Continued*

Family	**Genus Species**	**ETOL_ID**	**Length (bp)**	**charset**	**ZIC1**	**COI**	**CYT *b***	**16s**	**HOX**
Zoarcidae	*Lycenchelys crotalinus*	E00425	4583	6	714	651	0	767	1134
Zoarcidae	*Lycodapus mandibularis*	E00355	8784	11	777	585	0	942	0
Zoarcidae	*Lycodes brevipes*	E00413	4381	5	720	654	0	934	0
Zoarcidae	*Lycodes diapterus*	G01364	8790	11	819	651	0	792	0
Zoarcidae	*Lycodes terraenovae*	E00675	15952	18	879	0	0	1745	1146
Zoarcidae	*Melanostigma pammelas*	E00365	6342	8	777	654	0	0	1170
Zoarcidae	*Zoarces americanus viviparus*	E00370	5571	8	0	647	584	942	0

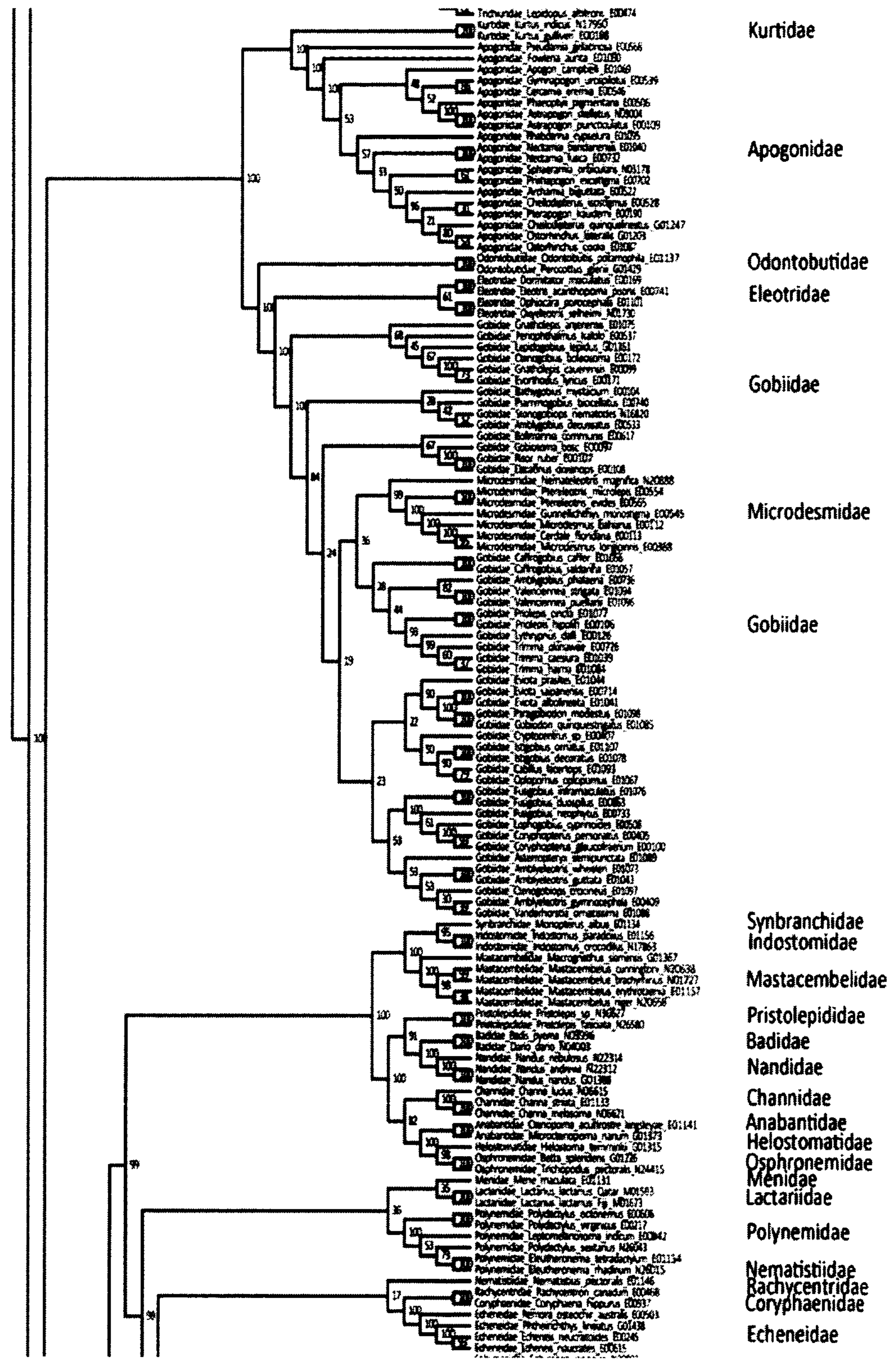
APPENDIX E

PHYLOGENY OF PERCOMORPHS INFERRED FROM RAXML ANALYSIS OF THE 3+ DATASET (1231 TAXA) FROM 23 GENES (20 NUCLEAR AND THREE MITOCHONDRIAL) WITH EIGHT PARTITIONS

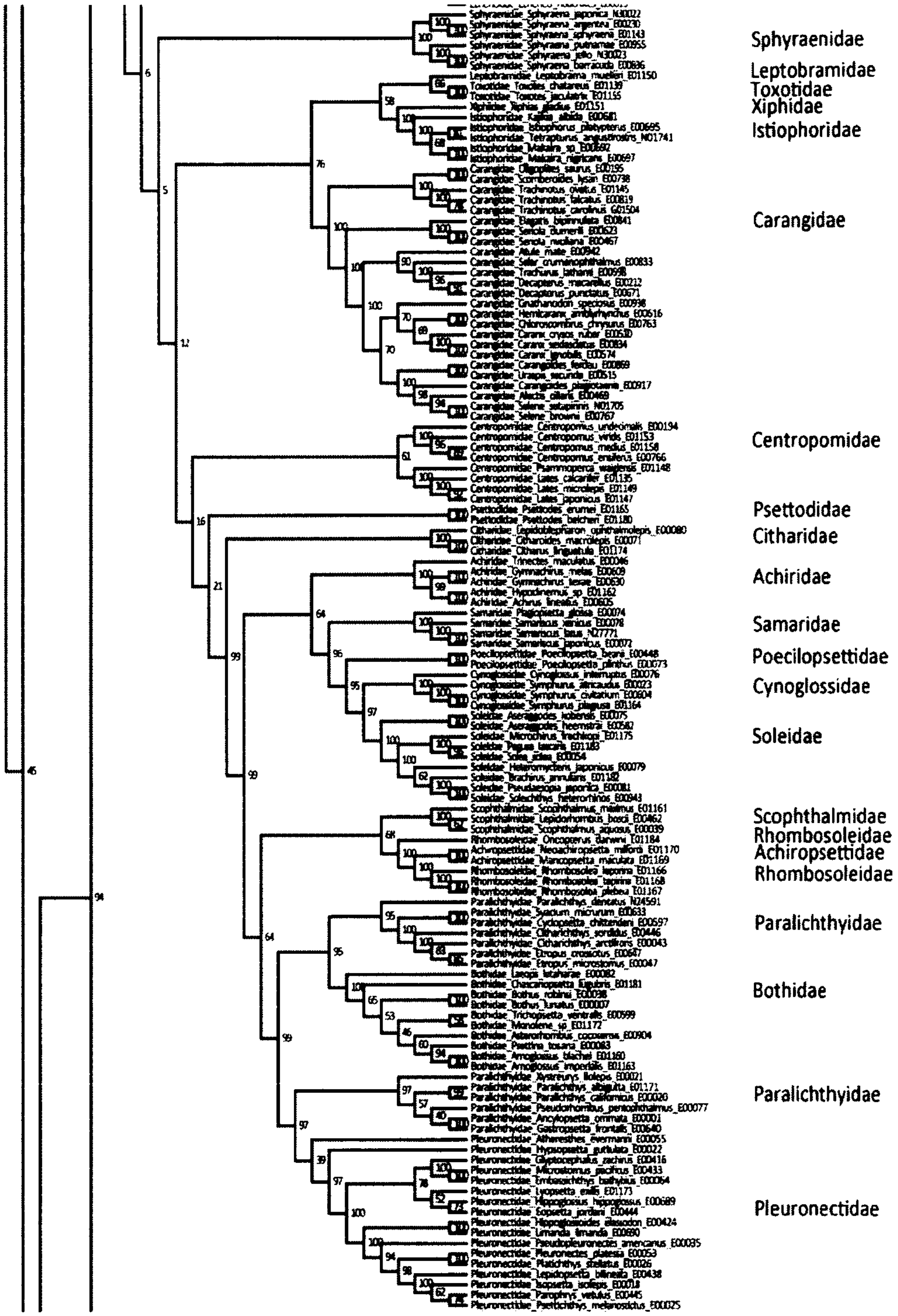
(a)


Bythitidae
Aphyonidae
Ophidiidae
Carapidae
Ophidiidae
Batrachoididae
Aulostomidae
Centriscidae
Fistulariidae
Mullidae
Pegasidae
Callionymidae
Syngnathidae
Chiasmodontidae
Arripididae
Pomatomidae
Scombridae
Icosteidae
Ariommaridae
Nomeidae
Scombridae
Centrolophidae
Stromateidae
Gempylidae
Bramidae
Scombrolabracidae
Caristiidae
Gempylidae
Trichiuridae

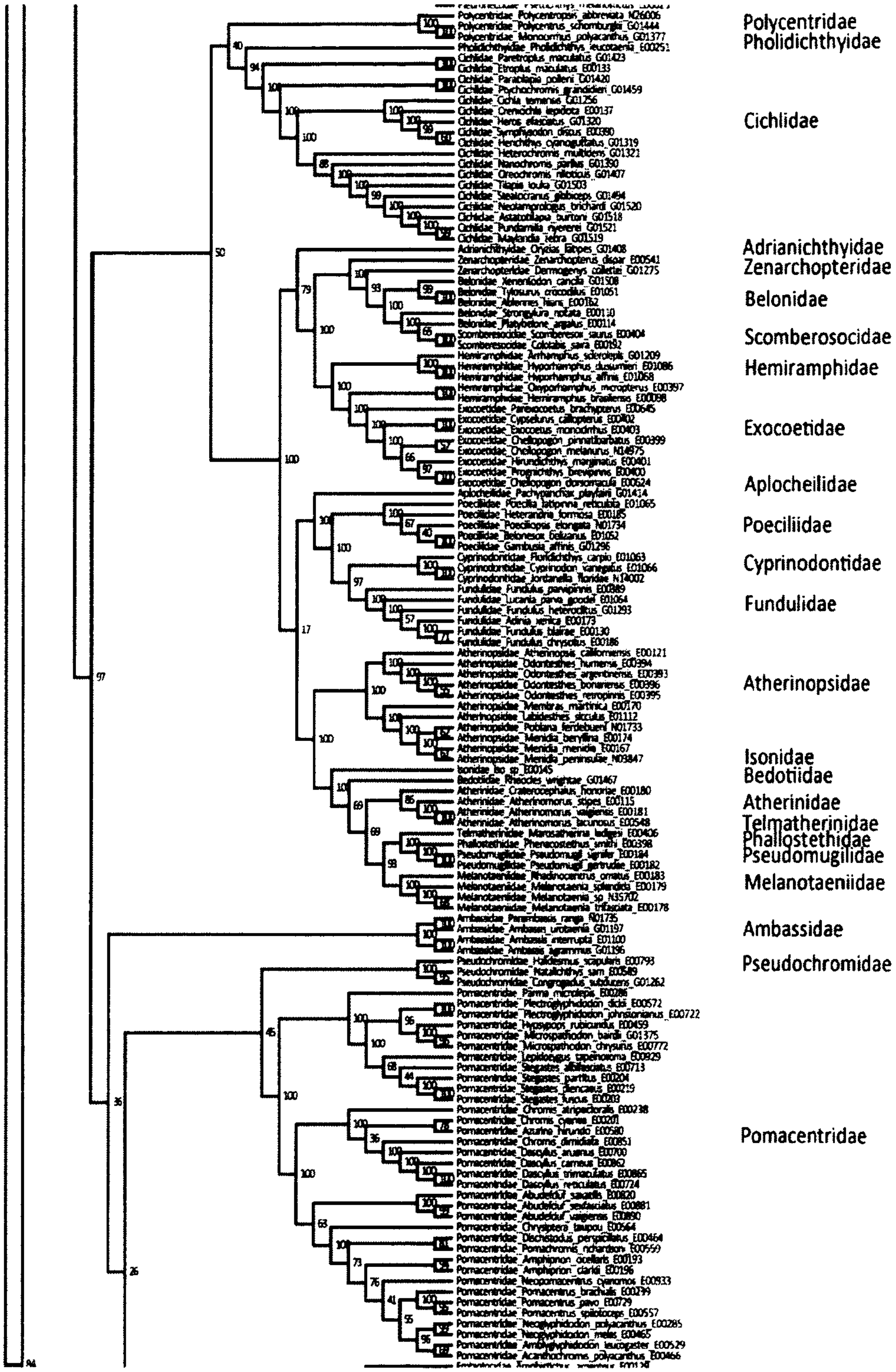
(b)


Kurtidae
Apogonidae
Odontobutidae
Eleotridae
Gobiidae
Microdesmidae
Gobiidae
Synbranchidae
Indostomidae
Mastacembelidae
Pristolepididae
Badidae
Nandidae
Channidae
Anabantidae
Helostomatidae
Osphronemidae
Menidae
Lactariidae
Polynemidae
Nematistiidae
Rachycentridae
Coryphaenidae
Echeneidae

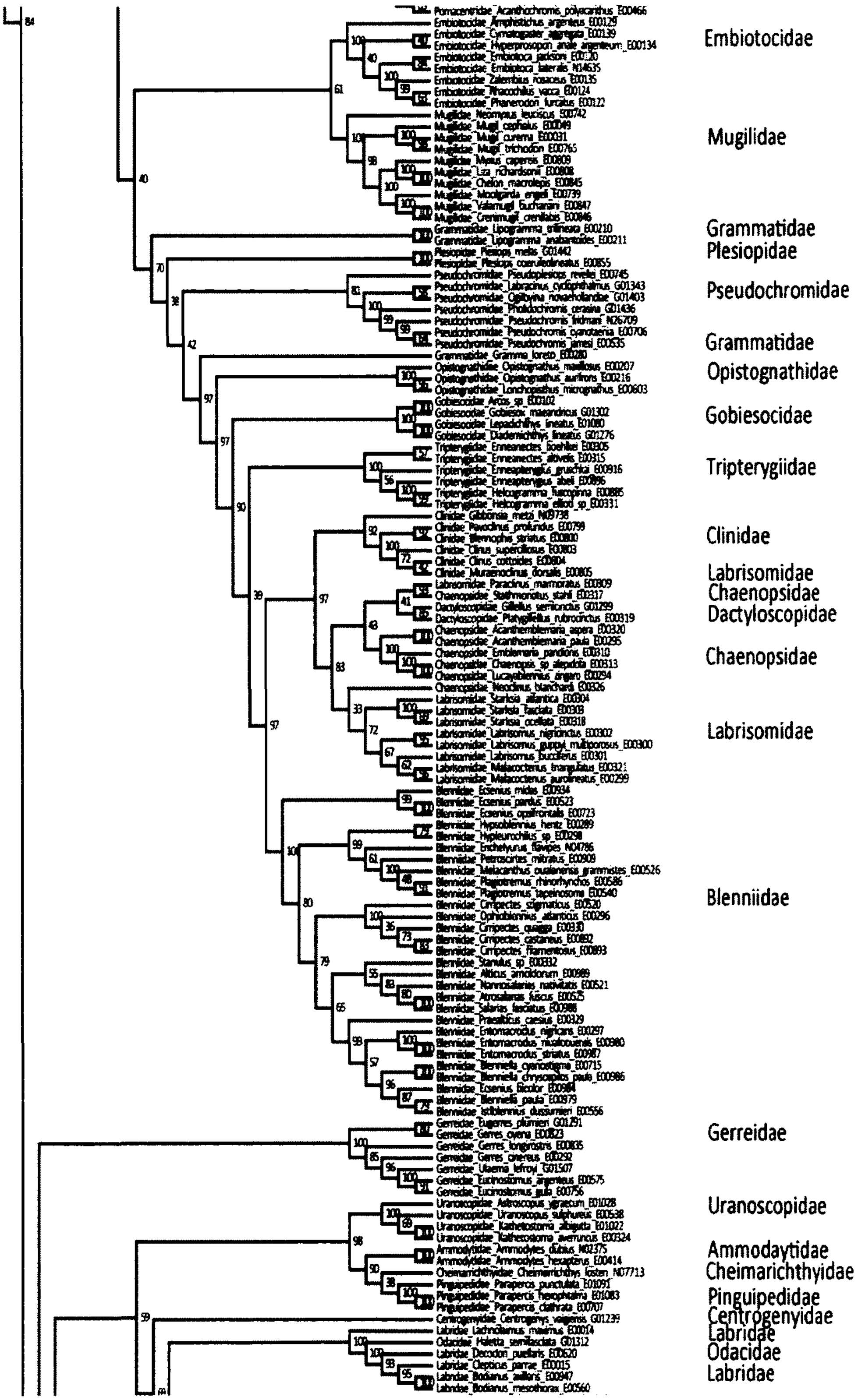
(c)


Sphyraenidae
Leptobramidae
Toxotidae
Xiphidae
Istiophoridae
Carangidae
Centropomidae
Psettodidae
Citharidae
Achiridae
Samaridae
Poecilopsettidae
Cynoglossidae
Soleidae
Scophthalmidae
Rhombosoleidae
Achiropsettidae
Rhombosoleidae
Paralichthyidae
Bothidae
Paralichthyidae
Pleuronectidae

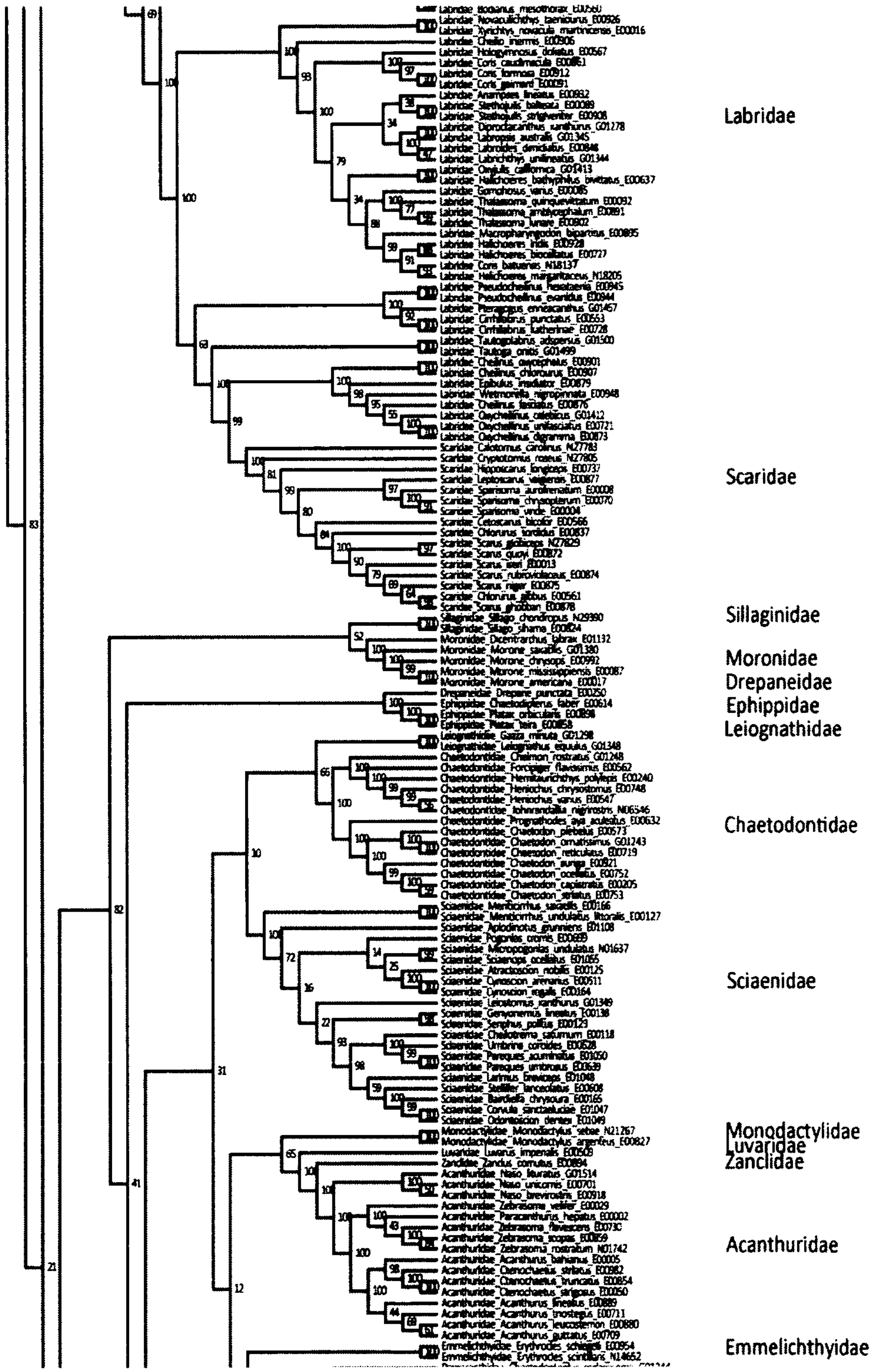
(d)


Polycentridae
Pholidichthyidae
Cichlidae
Adrianichthyidae
Zenarchopteridae
Belonidae
Scomberosocidae
Hemiramphidae
Exocoetidae
Aplocheilidae
Poeciliidae
Cyprinodontidae
Fundulidae
Atherinopsidae
Isonidae
Bedotiidae
Atherinidae
Telmatherinidae
Phallostethidae
Pseudomugilidae
Melanotaeniidae
Ambassidae
Pseudochromidae
Pomacentridae

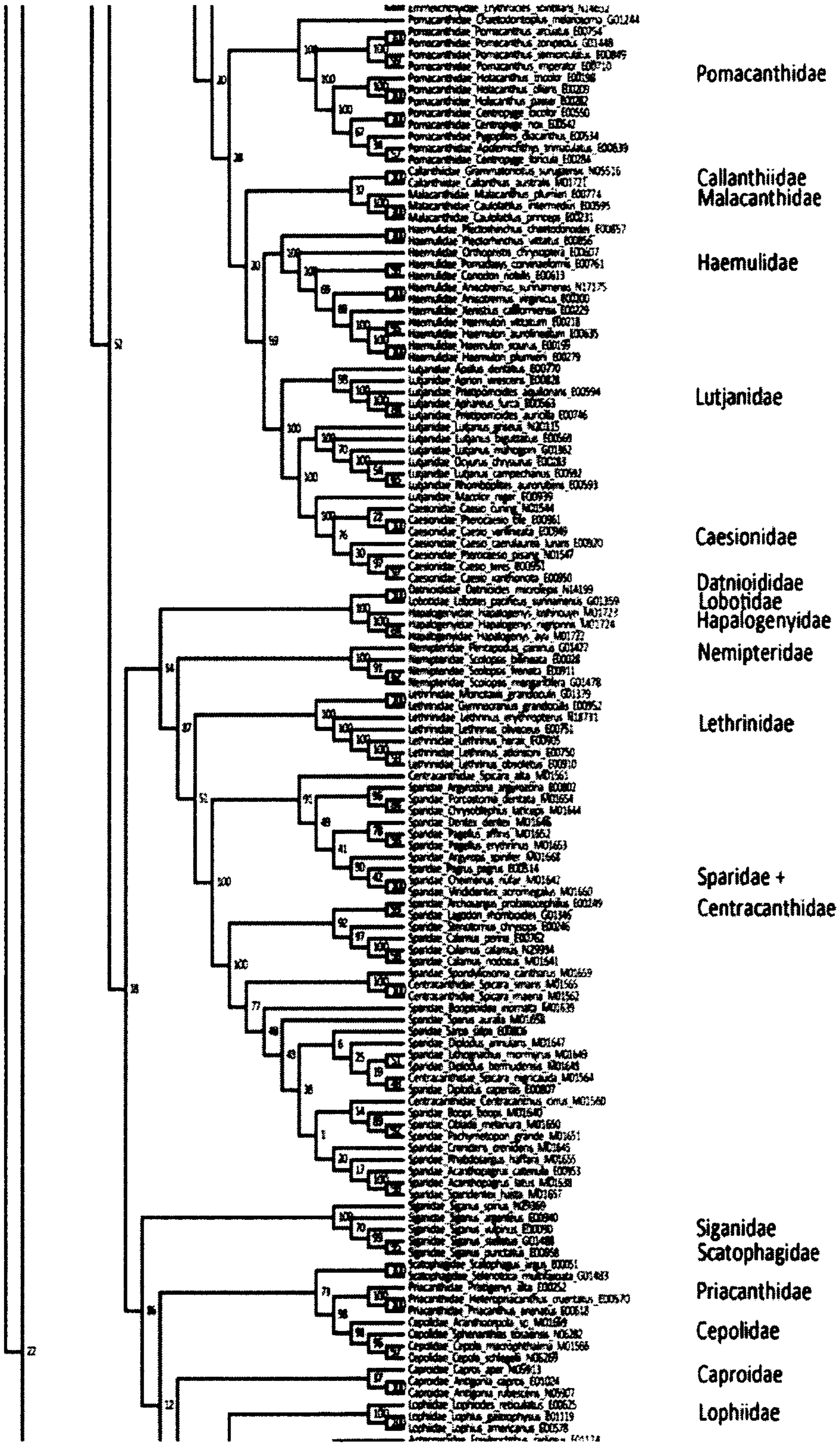
(e)


Pomacentridae_Acanthochromis_polyacanthus_E00466
Embiotocidae_Amphistichus_argenteus_E00129
Embiotocidae_Cymatogaster_aggregata_E00139
Embiotocidae_Hyperprosopon_anale_argenteum_E00134
Embiotocidae_Embiotoca_jacksoni_E00120
Embiotocidae_Embiotoca_lateralis_N14635
Embiotocidae_Zalembius_rosaceus_E00135
Embiotocidae_Rhacochilus_vacca_E00124
Embiotocidae_Phanerodon_furcatus_E00122
Mugilidae_Neomyxus_leuciscus_E00742
Mugilidae_Mugil_cephalus_E00049
Mugilidae_Mugil_curema_E00031
Mugilidae_Mugil_trichodon_E00765
Mugilidae_Myxus_capensis_E00809
Mugilidae_Liza_richardsonii_E00808
Mugilidae_Chelon_macrolepis_E00845
Mugilidae_Moolgarda_engeli_E00739
Mugilidae_Valamugil_buchanani_E00847
Mugilidae_Crenimugil_crenilabis_E00846
Grammatidae_Lipogramma_trilineata_E00210
Grammatidae_Lipogramma_anabantoides_E00211
Plesiopidae_Plesiops_melas_G01442
Plesiopidae_Plesiops_coeruleolineatus_E00855
Pseudochromidae_Pseudoplesiops_revellei_E00745
Pseudochromidae_Labracinus_cyclophthalmus_G01343
Pseudochromidae_Ogilbyina_novaehollandiae_G01403
Pseudochromidae_Pholidochromis_cerasina_G01436
Pseudochromidae_Pseudochromis_fridmani_N26709
Pseudochromidae_Pseudochromis_cyanotaenia_E00706
Pseudochromidae_Pseudochromis_jamesi_E00635
Grammatidae_Gramma_loreto_E00280
Opistognathidae_Opistognathus_maxillosus_E00207
Opistognathidae_Opistognathus_aurifrons_E00216
Opistognathidae_Lonchopisthus_micrognathus_E00603
Gobiesocidae_Arcos_sp_E00102
Gobiesocidae_Gobiesox_maeandricus_G01302
Gobiesocidae_Lepadichthys_lineatus_E01080
Gobiesocidae_Diademichthys_lineatus_G01276
Tripterygiidae_Enneanectes_boehlkei_E00305
Tripterygiidae_Enneanectes_altivelis_E00315
Tripterygiidae_Enneapterygius_gruschkai_E00916
Tripterygiidae_Enneapterygius_abeli_E00896
Tripterygiidae_Helcogramma_fuscopinna_E00885
Tripterygiidae_Helcogramma_ellioti_sp_E00331
Clinidae_Gibbonsia_metzi_N09738
Clinidae_Pavoclinus_profundus_E00799
Clinidae_Blennophis_striatus_E00800
Clinidae_Clinus_superciliosus_E00803
Clinidae_Clinus_cottoides_E00804
Clinidae_Muraenoclinus_dorsalis_E00805
Labrisomidae_Paraclinus_marmoratus_E00309
Chaenopsidae_Stathmonotus_stahli_E00317
Dactyloscopidae_Gillellus_semicinctus_G01299
Dactyloscopidae_Platygillellus_rubrocinctus_E00319
Chaenopsidae_Acanthemblemaria_aspera_E00320
Chaenopsidae_Acanthemblemaria_paula_E00295
Chaenopsidae_Emblemaria_pandionis_E00310
Chaenopsidae_Chaenopsis_sp_alepidota_E00313
Chaenopsidae_Lucayablennius_zingaro_E00294
Chaenopsidae_Neoclinus_blanchardi_E00326
Labrisomidae_Starksia_atlantica_E00304
Labrisomidae_Starksia_fasciata_E00303
Labrisomidae_Starksia_ocellata_E00318
Labrisomidae_Labrisomus_nigricinctus_E00302
Labrisomidae_Labrisomus_guppyi_multiporosus_E00300
Labrisomidae_Labrisomus_bucciferus_E00301
Labrisomidae_Malacoctenus_triangulatus_E00321
Labrisomidae_Malacoctenus_aurolineatus_E00299
Blenniidae_Ecsenius_midas_E00934
Blenniidae_Ecsenius_pardus_E00523
Blenniidae_Ecsenius_opsifrontalis_E00723
Blenniidae_Hypsoblennius_hentz_E00289
Blenniidae_Hypleurochilus_sp_E00298
Blenniidae_Enchelyurus_flavipes_N04786
Blenniidae_Petroscirtes_mitratus_E00909
Blenniidae_Meiacanthus_oualanensis_grammistes_E00526
Blenniidae_Plagiotremus_rhinorhynchos_E00586
Blenniidae_Plagiotremus_tapeinosoma_E00540
Blenniidae_Cirripectes_stigmaticus_E00520
Blenniidae_Ophioblennius_atlanticus_E00296
Blenniidae_Cirripectes_quagga_E00330
Blenniidae_Cirripectes_castaneus_E00892
Blenniidae_Cirripectes_filamentosus_E00893
Blenniidae_Stanulus_sp_E00332
Blenniidae_Alticus_arnoldorum_E00989
Blenniidae_Nannosalarias_nativitatis_E00521
Blenniidae_Atrosalarias_fuscus_E00525
Blenniidae_Salarias_fasciatus_E00988
Blenniidae_Praealticus_caesius_E00329
Blenniidae_Entomacrodus_nigricans_E00297
Blenniidae_Entomacrodus_niuafoouensis_E00980
Blenniidae_Entomacrodus_striatus_E00987
Blenniidae_Blenniella_cyanostigma_E00715
Blenniidae_Blenniella_chrysospilos_paula_E00986
Blenniidae_Ecsenius_bicolor_E00984
Blenniidae_Blenniella_paula_E00879
Blenniidae_Istiblennius_dussumieri_E00556
Gerreidae_Eugerres_plumieri_G01291
Gerreidae_Gerres_oyena_E00823
Gerreidae_Gerres_longirostris_E00835
Gerreidae_Gerres_cinereus_E00292
Gerreidae_Ulaema_lefroyi_G01507
Gerreidae_Eucinostomus_argenteus_E00575
Gerreidae_Eucinostomus_gula_E00756
Uranoscopidae_Astroscopus_y-graecum_E01028
Uranoscopidae_Uranoscopus_sulphureus_E00538
Uranoscopidae_Kathetostoma_albigutta_E01022
Uranoscopidae_Kathetostoma_averruncus_E00324
Ammodytidae_Ammodytes_dubius_N02375
Ammodytidae_Ammodytes_hexapterus_E00414
Cheimarrichthyidae_Cheimarrichthys_fosteri_N07713
Pinguipedidae_Parapercis_punctulata_E01091
Pinguipedidae_Parapercis_hexophtalma_E01083
Pinguipedidae_Parapercis_clathrata_E00707
Centrogenyidae_Centrogenys_vaigiensis_G01239
Labridae_Lachnolaimus_maximus_E00014
Odacidae_Haletta_semifasciata_G01312
Labridae_Decodon_puellaris_E00620
Labridae_Clepticus_parrae_E00015
Labridae_Bodianus_axillaris_E00947
Labridae_Bodianus_mesothorax_E00560
Embiotocidae
Mugilidae
Grammatidae
Plesiopidae
Pseudochromidae
Grammatidae
Opistognathidae
Gobiesocidae
Tripterygiidae
Clinidae
Labrisomidae
Chaenopsidae
Dactyloscopidae
Chaenopsidae
Labrisomidae
Blenniidae
Gerreidae
Uranoscopidae
Ammodaytidae
Cheimarichthyidae
Pinguipedidae
Centrogenyidae
Labridae
Odacidae
Labridae

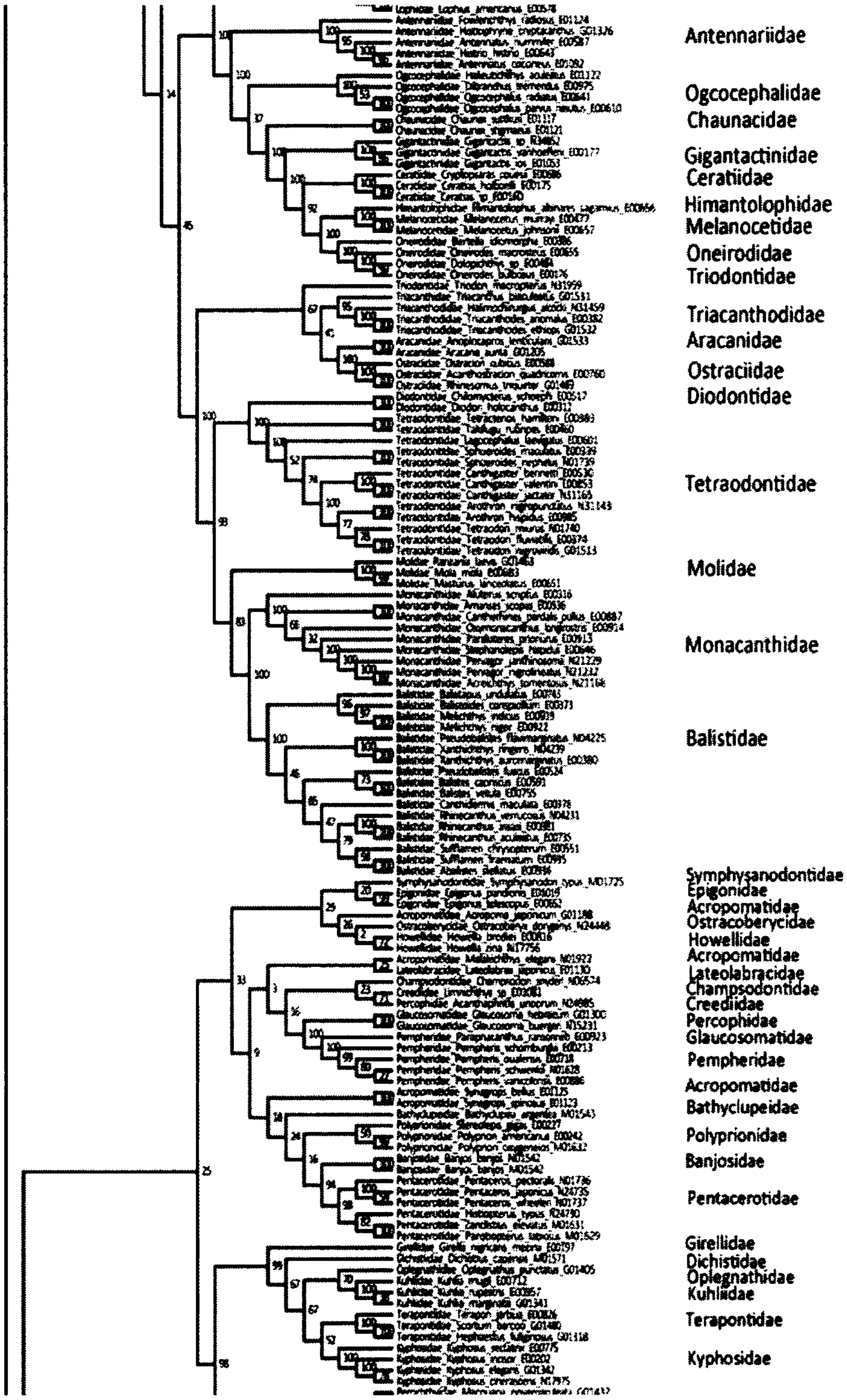
(f)


Labridae
Scaridae
Sillaginidae
Moronidae
Drepaneidae
Ephippidae
Leiognathidae
Chaetodontidae
Sciaenidae
Monodactylidae
Luvaridae
Zanclidae
Acanthuridae
Emmelichthyidae

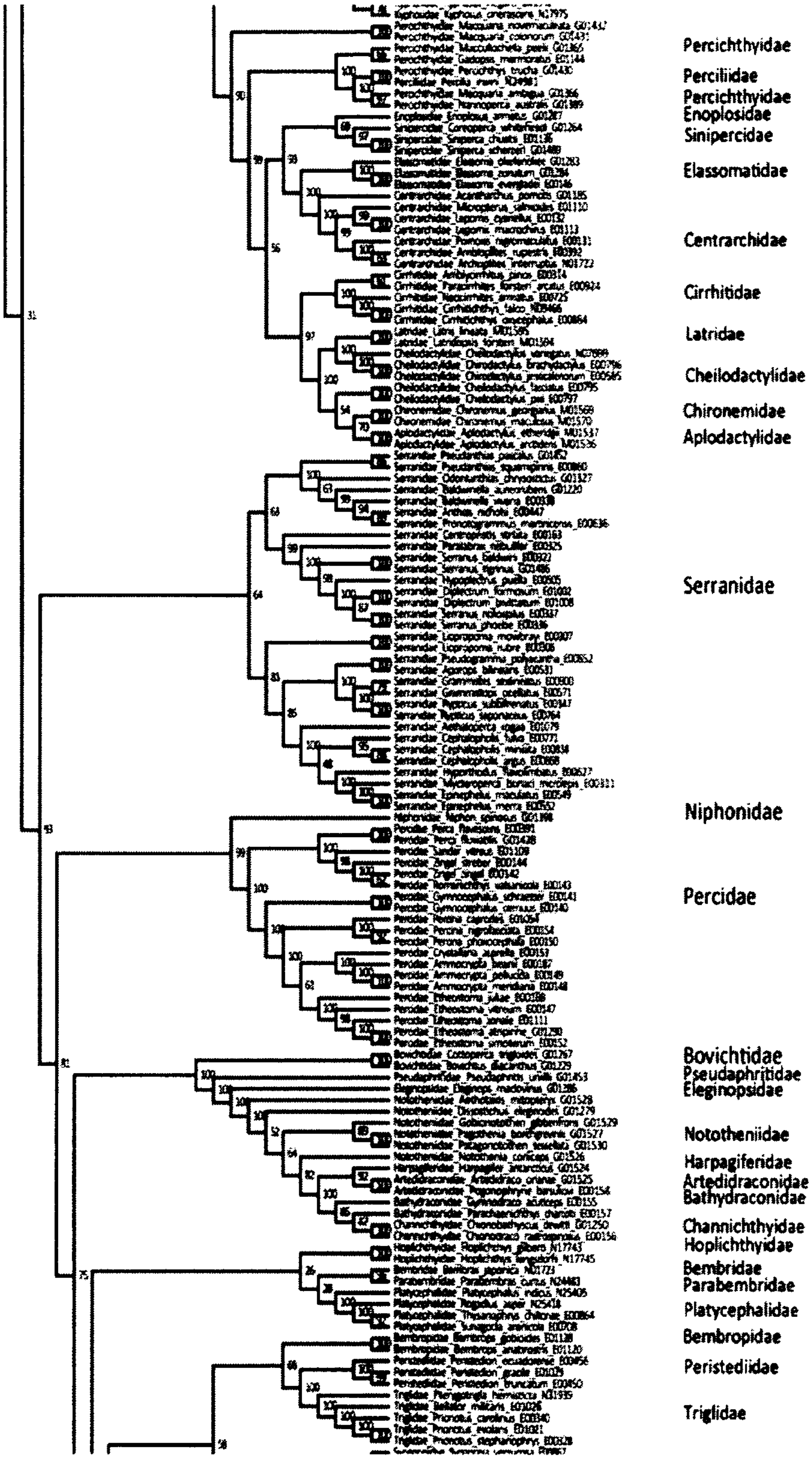
(g)


Pomacanthidae
Callanthiidae
Malacanthidae
Haemulidae
Lutjanidae
Caesionidae
Datnioididae
Lobotidae
Hapalogenyidae
Nemipteridae
Lethrinidae
Sparidae +
Centracanthidae
Siganidae
Scatophagidae
Priacanthidae
Cepolidae
Caproidae
Lophiidae

(h)


Antennariidae
Ogcocephalidae
Chaunacidae
Gigantactinidae
Ceratiidae
Himantolophidae
Melanocetidae
Oneirodidae
Triodontidae
Triacanthodidae
Aracanidae
Ostraciidae
Diodontidae
Tetraodontidae
Molidae
Monacanthidae
Balistidae
Symphysanodontidae
Epigonidae
Acropomatidae
Ostracoberycidae
Howellidae
Acropomatidae
Lateolabracidae
Champsodontidae
Creediidae
Percophidae
Glaucosomatidae
Pempheridae
Acropomatidae
Bathyclupeidae
Polyprionidae
Banjosidae
Pentacerotidae
Girellidae
Dichistidae
Oplegnathidae
Kuhliidae
Terapontidae
Kyphosidae

(i)


Percichthyidae
Perciliidae
Percichthyidae
Enoplosidae
Sinipercidae
Elassomatidae
Centrarchidae
Cirrhitidae
Latridae
Cheilodactylidae
Chironemidae
Aplodactylidae
Serranidae
Niphonidae
Percidae
Bovichtidae
Pseudaphritidae
Eleginopsidae
Nototheniidae
Harpagiferidae
Artedidraconidae
Bathydraconidae
Channichthyidae
Hoplichthyidae
Bembridae
Parabembridae
Platycephalidae
Bembropidae
Peristediidae
Triglidae

(j)

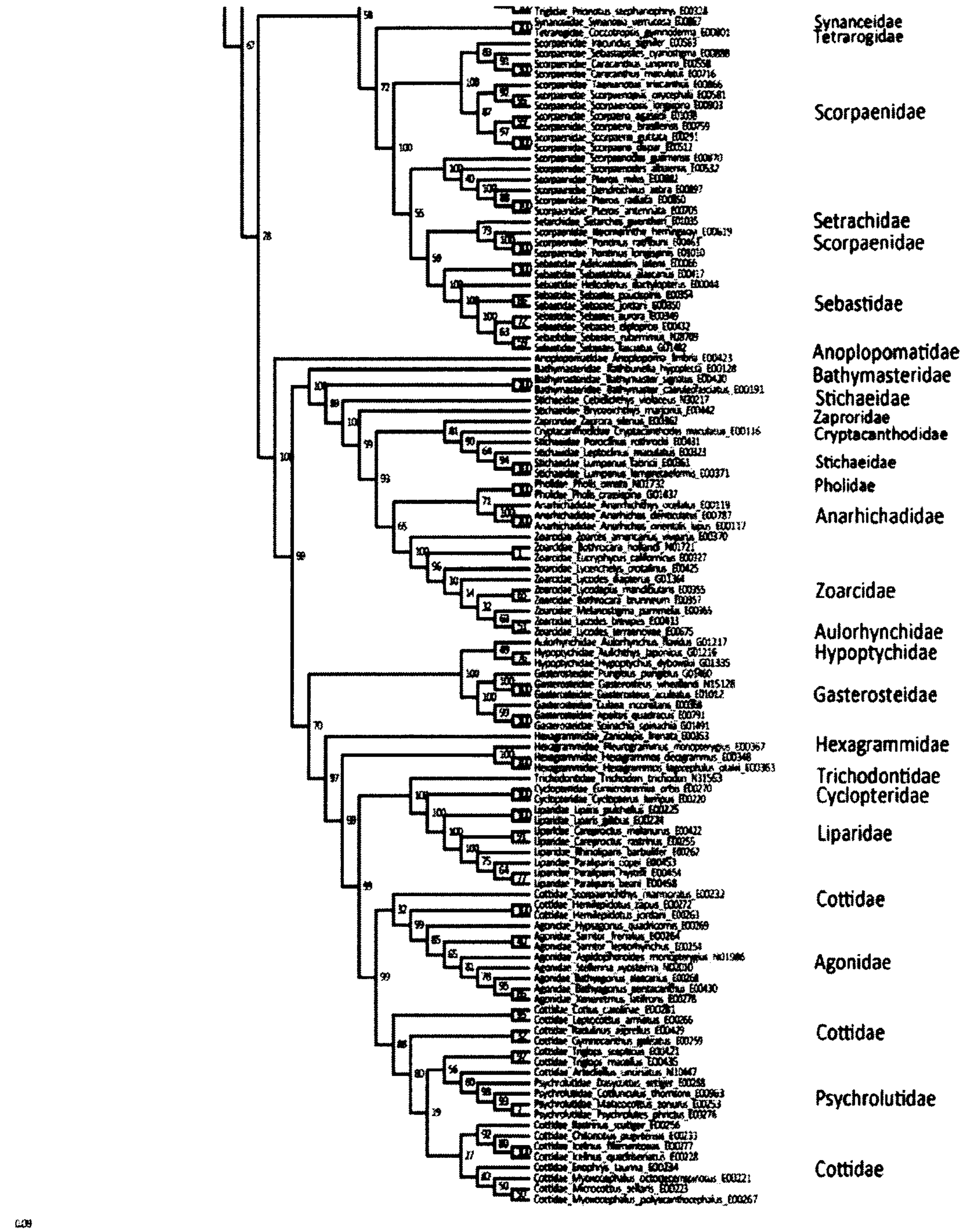


FIGURE A1. Phylogeny of percomorphs inferred from RAxML analysis of the 3+ dataset (1231 taxa) from 23 genes (20 nuclear and three mitochondrial) with eight partitions. The phylogeny is illustrated in ten parts, labeled a-j. See also Figures 3 to 8 for higher resolution versions of the tree for the additional taxa.

APPENDIX F

LIST OF SPECIES FOR THE MITOGENOME DATASET INCLUDING 26 HAEMULIDS PLUS FIVE OUTGROUPS

TABLE A5. List of species for the mitogenome dataset including 26 haemulids plus five outgroups. The last three columns show the percentage of sequences with phred (quality) scores of at least Q20, Q30, and Q40, respectively. Seven sequences were obtained from Genbank and the rest were newly generated from amplicon sequencing using Roche GS Flx 454 genome sequencer.

Family	Genus	Species	Voucher	Genbank	Reads	Used reads	Length	Mean read length	≤ Q20	≤ Q30	≤ Q40
Caesionidae	*Pterocaesio*	*tile*		AP004447							
Emmelichthyidae	*Emmelichthys*	*struhsakeri*		AP004446							
Haemulidae	*Boridia*	*grossidens*	ODU 3237		6022	6019	16666	131	81	54	16
Haemulidae	*Brachydeuterus*	*auritus*	ODU 3290		4771	4707	16569	120	81	51	13
Haemulidae	*Conodon*	*nobilis*	KU 30150		5661	5659	16722	123	83	55	17
Haemulidae	*Conodon*	*serrifer*	ODU 3239		6709	6703	16708	157	82	54	15
Haemulidae	*Diagramma*	*picta*		AP009167							
Haemulidae	*Haemulon*	*aurolineatum*	USNM 349060		7055	7048	16663	165	82	54	15
Haemulidae	*Haemulon*	*vittatum*	USNM 349224		6925	6919	16676	170	83	55	16
Haemulidae	*Haemulopsis*	*axillaris*	ODU 3291		8614	8588	15920	181	82	53	15
Haemulidae	*Haemulopsis*	*nitidus*	ODU 3250		7440	7436	16777	161	82	54	15
Haemulidae	*Isacia*	*conceptionis*	ODU 3251		9315	9309	16738	231	83	55	17
Haemulidae	*Microlepidotus*	*brevipinnis*	ODU 3252		7407	7404	16749	169	83	55	17
Haemulidae	*Orthopristis*	*chalceus*	ODU 3253		6941	6937	16758	170	82	53	14
Haemulidae	*Parapristipoma*	*trilineatum*		AP009168							
Haemulidae	*Plectorhinchus*	*picus*	KU 32545		10263	10254	16556	228	82	54	16
Haemulidae	*Plectorhinchus*	*vittatus*	SAIAB 78102		9854	9851	16512	219	83	56	18
Haemulidae	*Pomadasys*	*argyreus*	ODU 3292		5037	5034	16626	108	82	54	16
Haemulidae	*Pomadasys*	*branickii*	ODU 3255		8861	8853	16766	202	83	55	16
Haemulidae	*Pomadasys*	*kaakan*	ODU 3293		7862	7860	16002	196	82	53	14
Haemulidae	*Pomadasys*	*macracanthus*	ODU 3294		6880	6643	17193	156	80	50	11
Haemulidae	*Pomadasys*	*maculatus*	ODU 3090		13100	13088	16492	342	82	55	17
Haemulidae	*Pomadasys*	*olivaceus*	SAIAB		9238	9224	16452	222	83	55	15
Haemulidae	*Pomadasys*	*panamensis*	ODU 3259		5693	5691	16865	125	81	53	15
Haemulidae	*Pomadasys*	*perotaei*	ODU 3295		6068	6062	13678	42	74	41	0
Haemulidae	*Pomadasys*	*stridens*	ODU 3262		4223	4219	16729	93	82	54	16

Table A5. *Continued*

Family	**Genus**	**Species**	**Voucher**	**Genbank**	**Reads**	**Used reads**	**Length**	**Mean read length**	**≤ Q20**	**≤ Q30**	**≤ Q40**
Haemulidae	*Xenichthys*	*xanti*	ODU 3263		10615	10580	16866	382	82	55	17
Haemulidae	*Xenistius*	*californiensis*	KU 28128		16366	16352	16713	406	81	54	16
Lethrinidae	*Monotaxis*	*grandoculis*		AP009166							
Lutjanidae	*Lutjanus*	*rivulatus*		AP006000							
Sparidae	*Pagrus*	*major*		AP002949							

* KU - University of Kansas Natural History Museum & Biodiversity Research Center; ODU - Old Dominion University, Norfolk, VA; SAIAB - South African Institute for Aquatic Biodiversity; USNM - United States National Museum (now National Museum of Natural History; Smithsonian Institution; Washington, DC

APPENDIX G

TAXON SAMPLING FOR THE 22-GENE DATASET, INCLUDING 82 UNIQUE HAEMULID TAXA AND FOUR OUTGROUPS

TABLE A6a. Taxon sampling for the 22-gene dataset, including 82 unique haemulid taxa and four outgroups. Sequences were obtained from previous studies, public databases, or generated new in the lab. The matrix is presented in three parts to show presence of sequence data for the 22 genes. (a.) ENC1, FICD, GLYT, KIAA1239, MYH6, PANX2, and PLAGL2; (b.) PTCHD1, RAG1, RAG2, RH, RIPK4, SH3PX3, and SIDKEY; (C.) TBR, VCPIP, ZIC1, TMO-4C4, COI, CYT *B*, S7, and 16S.

Family	Taxon	Total length	No. of charsets	ENC1	FICD	GLYT	KIAA1239	MYH6	PANX2	PLAGL2
Haemulidae	*Anisotremus caesius*	2418 bp	4	0	0	0	0	0	0	0
Haemulidae	*Anisotremus davidsonii*	5415 bp	7	0	0	0	0	0	0	804
Haemulidae	*Anisotremus interruptus*	5883 bp	7	0	0	0	0	0	0	804
Haemulidae	*Anisotremus moricandi*	2504 bp	4	0	0	0	0	0	0	0
Haemulidae	*Anisotremus scapularis*	5874 bp	7	0	0	0	0	0	0	804
Haemulidae	*Anisotremus surinamensis*	10416 bp	14	804	0	843	0	699	0	801
Haemulidae	*Anisotremus taeniatus*	6023 bp	7	0	0	0	0	0	0	804
Haemulidae	*Anisotremus virginicus*	9977 bp	13	0	720	0	918	0	0	780
Haemulidae	*Boridia grossidens*	4419 bp	5	0	0	0	0	0	0	552
Haemulidae	*Brachydeuterus auritus*	4596 bp	5	0	0	0	0	0	0	690
Haemulidae	*Conodon nobilis*	12303 bp	16	0	690	0	804	681	705	804
Haemulidae	*Conodon serrifer*	5910 bp	7	0	0	0	0	0	0	804
Haemulidae	*Diagramma centurio*	1710 bp	3	0	0	0	0	0	0	0
Haemulidae	*Diagramma picta*	5684 bp	7	0	0	0	0	0	0	804
Haemulidae	*Emmelichthyops atlanticus*	4596 bp	5	0	0	0	0	0	0	717
Haemulidae	*Genyatremus cavifrons*	5901 bp	7	0	0	0	0	0	0	792
Haemulidae	*Genyatremus dovii*	5580 bp	7	0	0	0	0	0	0	804
Haemulidae	*Genyatremus pacifici*	6002 bp	7	0	0	0	0	0	0	804
Haemulidae	*Haemulon album*	2603 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulon aurolineatum*	16494 bp	22	798	690	870	798	687	702	669
Haemulidae	*Haemulon bonariense*	2613 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulon carbonarium*	2613 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulon chrysargyreum*	6309 bp	8	0	0	0	0	0	0	786
Haemulidae	*Haemulon flaviguttatum*	5817 bp	7	0	0	0	0	0	0	804
Haemulidae	*Haemulon flavolineatum*	5991 bp	8	0	0	0	0	0	0	804
Haemulidae	*Haemulon macrostomum*	6372 bp	8	0	0	0	0	0	0	804

Table A6a. *Continued*

Family	**Taxon**	**Total length**	**No. of charsets**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**	**PLAGL2**
Haemulidae	*Haemulon maculicauda*	1866 bp	3	0	0	0	0	0	0	0
Haemulidae	*Haemulon melanurum*	5931 bp	7	0	0	0	0	0	0	804
Haemulidae	*Haemulon parra*	2002 bp	3	0	0	0	0	0	0	0
Haemulidae	*Haemulon plumierii*	14496 bp	19	810	720	870	774	702	0	672
Haemulidae	*Haemulon sciurus*	14196 bp	19	657	720	870	918	720	0	804
Haemulidae	*Haemulon scudderii*	5798 bp	7	0	0	0	0	0	0	804
Haemulidae	*Haemulon sexfasciatum*	2613 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulon steindachneri*	5928 bp	7	0	0	0	0	0	0	804
Haemulidae	*Haemulon vittatum*	14232 bp	19	657	0	852	918	717	0	804
Haemulidae	*Haemulopsis axillaris*	5444 bp	7	0	0	0	0	0	0	804
Haemulidae	*Haemulopsis elongatus*	2448 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulopsis leuciscus*	5958 bp	8	0	0	0	0	0	0	789
Haemulidae	*Haemulopsis nitidus*	5214 bp	7	0	0	0	0	0	0	801
Haemulidae	*Isacia conceptionis*	5922 bp	7	0	0	0	0	0	0	804
Haemulidae	*Microlepidotus brevipinnis*	5859 bp	7	0	0	0	0	0	0	804
Haemulidae	*Orthopristis chalceus*	5217 bp	6	0	0	0	0	0	0	798
Haemulidae	*Orthopristis chrysoptera*	14625 bp	19	810	690	870	807	693	702	804
Haemulidae	*Orthopristis reddingi*	2448 bp	4	0	0	0	0	0	0	0
Haemulidae	*Orthopristis ruber*	2465 bp	4	0	0	0	0	0	0	0
Haemulidae	*Parakuhlia macrophthalmus*	4662 bp	5	0	0	0	0	0	0	747
Haemulidae	*Parapristipoma humile*	2835 bp	3	0	0	0	0	0	0	756
Haemulidae	*Parapristipoma octolineatum*	4692 bp	5	0	0	0	0	0	0	804
Haemulidae	*Parapristipoma trilineatum*	5740 bp	7	0	0	0	0	0	0	792
Haemulidae	*Plectorhinchus chaetodonoides*	10650 bp	14	0	630	0	729	0	0	804
Haemulidae	*Plectorhinchus chubbi*	1707 bp	3	0	0	0	0	0	0	0
Haemulidae	*Plectorhinchus cinctus*	5668 bp	7	0	0	0	0	0	0	804
Haemulidae	*Plectorhinchus diagrammus*	5038 bp	7	0	0	0	0	0	0	804
Haemulidae	*Plectorhinchus gaterinus*	5706 bp	7	0	0	0	0	0	0	756
Haemulidae	*Plectorhinchus gibbosus*	5666 bp	7	0	0	0	0	0	0	783
Haemulidae	*Plectorhinchus lessonii*	5868 bp	7	0	0	0	0	0	0	804

Table A6a. *Continued*

Family	**Taxon**	**Total length**	**No. of charsets**	**ENC1**	**FICD**	**GLYT**	**KIAA1239**	**MYH6**	**PANX2**	**PLAGL2**
Haemulidae	*Plectorhinchus macrolepis*	4023 bp	4	0	0	0	0	0	0	804
Haemulidae	*Plectorhinchus orientalis*	4647 bp	6	0	0	0	0	0	0	804
Haemulidae	*Plectorhinchus picus*	2850 bp	4	0	0	0	0	0	0	0
Haemulidae	*Plectorhinchus playfairi*	1710 bp	3	0	0	0	0	0	0	0
Haemulidae	*Plectorhinchus schotaf*	5661 bp	7	0	0	0	0	0	0	804
Haemulidae	*Plectorhinchus sordidus*	5775 bp	7	0	0	0	0	0	0	801
Haemulidae	*Plectorhinchus vittatus*	9273 bp	13	0	630	0	729	0	705	765
Haemulidae	*Pomadasys argenteus*	2823 bp	5	0	0	0	0	0	0	0
Haemulidae	*Pomadasys argyreus*	4710 bp	5	0	0	0	0	0	0	804
Haemulidae	*Pomadasys branickii*	5923 bp	7	0	0	0	0	0	0	804
Haemulidae	*Pomadasys corvinaeformis*	10182 bp	15	651	630	0	759	0	0	699
Haemulidae	*Pomadasys crocro*	2448 bp	4	0	0	0	0	0	0	0
Haemulidae	*Pomadasys furcatus*	1710 bp	3	0	0	0	0	0	0	0
Haemulidae	*Pomadasys hasta*	1225 bp	2	0	0	0	0	0	0	0
Haemulidae	*Pomadasys incisus*	5297 bp	6	0	0	0	0	0	0	804
Haemulidae	*Pomadasys kaakan*	5035 bp	7	0	0	0	0	0	0	804
Haemulidae	*Pomadasys macracanthus*	3036 bp	5	0	0	0	0	0	0	0
Haemulidae	*Pomadasys maculatus*	5752 bp	7	0	0	0	0	0	0	804
Haemulidae	*Pomadasys olivaceus*	5730 bp	7	0	0	0	0	0	0	780
Haemulidae	*Pomadasys panamensis*	5919 bp	7	0	0	0	0	0	0	789
Haemulidae	*Pomadasys perotaei*	5567 bp	7	0	0	0	0	0	0	804
Haemulidae	*Pomadasys rogerii*	1383 bp	2	0	0	0	0	0	0	732
Haemulidae	*Pomadasys striatus*	5052 bp	7	0	0	0	0	0	0	786
Haemulidae	*Pomadasys stridens*	6300 bp	8	0	0	0	0	0	0	780
Haemulidae	*Xenichthys xanti*	5190 bp	7	0	0	0	0	0	0	792
Haemulidae	*Xenistius californiensis*	11730 bp	16	0	720	0	918	687	0	795
Lutjanidae	*Aphareus furca*	10257 bp	13	0	690	0	807	708	711	792
Lutjanidae	*Lutjanus fulviflamma*	3219 bp	3	0	0	0	0	0	0	0
Lutjanidae	*Lutjanus mahogoni*	4332 bp	6	657	0	870	0	729	0	0
Sparidae	*Sarpa salpa*	10941 bp	14	0	630	0	681	699	714	804

TABLE A6b. Taxon sampling for the 22-gene dataset, including 82 unique haemulid taxa and four outgroups. Sequences were obtained from previous studies, public databases, or generated new in the lab. The matrix is presented in three parts to show presence of sequence data for the 22 genes. (a.) ENC1, FICD, GLYT, KIAA1239, MYH6, PANX2, and PLAGL2; (b.) PTCHD1, RAG1, RAG2, RH, RIPK4, SH3PX3, and SIDKEY; (C.) TBR, VCPIP, ZIC1, TMO-4C4, COI, CYT *B*, S7, and 16S.

Family	Taxon	Total length	No. of charsets	PTCHD1	RAG1	RAG2	RH	RIPK4	SH3PX3	SIDKEY
Haemulidae	*Anisotremus caesius*	2418 bp	4	0	0	0	0	0	0	0
Haemulidae	*Anisotremus davidsonii*	5415 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Anisotremus interruptus*	5883 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Anisotremus moricandi*	2504 bp	4	0	0	0	0	0	0	0
Haemulidae	*Anisotremus scapularis*	5874 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Anisotremus surinamensis*	10416 bp	14	705	1428	0	0	0	702	0
Haemulidae	*Anisotremus taeniatus*	6023 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Anisotremus virginicus*	9977 bp	13	0	1428	660	0	633	705	1041
Haemulidae	*Boridia grossidens*	4419 bp	5	0	1428	0	0	0	678	0
Haemulidae	*Brachydeuterus auritus*	4596 bp	5	0	1428	0	0	0	705	0
Haemulidae	*Conodon nobilis*	12303 bp	16	0	1428	660	0	642	705	1041
Haemulidae	*Conodon serrifer*	5910 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Diagramma centurio*	1710 bp	3	0	0	0	0	0	0	0
Haemulidae	*Diagramma picta*	5684 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Emmelichthyops atlanticus*	4596 bp	5	0	1428	0	0	0	705	0
Haemulidae	*Genyatremus cavifrons*	5901 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Genyatremus dovii*	5580 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Genyatremus pacifici*	6002 bp	7	0	1428	0	0	0	696	0
Haemulidae	*Haemulon album*	2603 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulon aurolineatum*	16494 bp	22	741	1428	660	756	630	696	1023
Haemulidae	*Haemulon bonariense*	2613 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulon carbonarium*	2613 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulon chrysargyreum*	6309 bp	8	0	1428	0	0	0	705	0
Haemulidae	*Haemulon flaviguttatum*	5817 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Haemulon flavolineatum*	5991 bp	8	0	1428	0	0	0	696	0

Table A6b. *Continued*

Family	Taxon	Total length	No. of charsets	PTCHD1	RAG1	RAG2	RH	RIPK4	SH3PX3	SIDKEY
Haemulidae	*Haemulon macrostomum*	6372 bp	8	0	1428	0	0	0	702	0
Haemulidae	*Haemulon maculicauda*	1866 bp	3	0	0	0	0	0	0	0
Haemulidae	*Haemulon melanurum*	5931 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Haemulon parra*	2002 bp	3	0	0	0	0	0	0	0
Haemulidae	*Haemulon plumierii*	14496 bp	19	741	1389	660	0	630	705	1035
Haemulidae	*Haemulon sciurus*	14196 bp	19	705	1371	0	0	645	705	1038
Haemulidae	*Haemulon scudderii*	5798 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Haemulon sexfasciatum*	2613 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulon steindachneri*	5928 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Haemulon vittatum*	14232 bp	19	705	1428	660	702	606	705	1059
Haemulidae	*Haemulopsis axillaris*	5444 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Haemulopsis elongatus*	2448 bp	4	0	0	0	0	0	0	0
Haemulidae	*Haemulopsis leuciscus*	5958 bp	8	0	1428	0	0	0	705	0
Haemulidae	*Haemulopsis nitidus*	5214 bp	7	0	1428	0	0	0	696	0
Haemulidae	*Isacia conceptionis*	5922 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Microlepidotus brevipinnis*	5859 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Orthopristis chalceus*	5217 bp	6	0	1428	0	0	0	0	0
Haemulidae	*Orthopristis chrysoptera*	14625 bp	19	741	1428	660	0	630	0	1041
Haemulidae	*Orthopristis reddingi*	2448 bp	4	0	0	0	0	0	0	0
Haemulidae	*Orthopristis ruber*	2465 bp	4	0	0	0	0	0	0	0
Haemulidae	*Parakuhlia macrophthalmus*	4662 bp	5	0	1425	0	0	0	705	0
Haemulidae	*Parapristipoma humile*	2835 bp	3	0	1428	0	0	0	0	0
Haemulidae	*Parapristipoma octolineatum*	4692 bp	5	0	1428	0	0	0	705	0
Haemulidae	*Parapristipoma trilineatum*	5740 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus chaetodonoides*	10650 bp	14	0	1428	660	0	645	693	1023
Haemulidae	*Plectorhinchus chubbi*	1707 bp	3	0	0	0	0	0	0	0
Haemulidae	*Plectorhinchus cinctus*	5668 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus diagrammus*	5038 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus gaterinus*	5706 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus gibbosus*	5666 bp	7	0	1428	0	0	0	705	0

Table A6b. *Continued*

Family	**Taxon**	**Total length**	**No. of charsets**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**	**SH3PX3**	**SIDKEY**
Haemulidae	*Plectorhinchus lessonii*	5868 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus macrolepis*	4023 bp	4	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus orientalis*	4647 bp	6	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus picus*	2850 bp	4	0	0	0	0	0	0	0
Haemulidae	*Plectorhinchus playfairi*	1710 bp	3	0	0	0	0	0	0	0
Haemulidae	*Plectorhinchus schotaf*	5661 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus sordidus*	5775 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Plectorhinchus vittatus*	9273 bp	13	0	0	660	0	615	693	1023
Haemulidae	*Pomadasys argenteus*	2823 bp	5	0	0	0	0	0	0	0
Haemulidae	*Pomadasys argyreus*	4710 bp	5	0	1428	0	0	0	702	0
Haemulidae	*Pomadasys branickii*	5923 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Pomadasys corvinaeformis*	10182 bp	15	0	0	660	690	645	696	1038
Haemulidae	*Pomadasys crocro*	2448 bp	4	0	0	0	0	0	0	0
Haemulidae	*Pomadasys furcatus*	1710 bp	3	0	0	0	0	0	0	0
Haemulidae	*Pomadasys hasta*	1225 bp	2	0	0	0	0	0	0	0
Haemulidae	*Pomadasys incisus*	5297 bp	6	0	1428	0	0	0	705	0
Haemulidae	*Pomadasys kaakan*	5035 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Pomadasys macracanthus*	3036 bp	5	0	0	0	0	0	0	0
Haemulidae	*Pomadasys maculatus*	5752 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Pomadasys olivaceus*	5730 bp	7	0	1428	0	0	0	702	0
Haemulidae	*Pomadasys panamensis*	5919 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Pomadasys perotaei*	5567 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Pomadasys rogerii*	1383 bp	2	0	0	0	0	0	0	0
Haemulidae	*Pomadasys striatus*	5052 bp	7	0	1428	0	0	0	705	0
Haemulidae	*Pomadasys stridens*	6300 bp	8	0	1428	0	0	0	705	0
Haemulidae	*Xenichthys xanti*	5190 bp	7	0	1428	0	0	0	681	0
Haemulidae	*Xenistius californiensis*	11730 bp	16	0	1428	660	0	645	666	1023
Lutjanidae	*Aphareus furca*	10257 bp	13	741	1428	0	0	645	0	1023
Lutjanidae	*Lutjanus fulviflamma*	3219 bp	3	0	1428	0	0	0	0	0
Lutjanidae	*Lutjanus mahogoni*	4332 bp	6	705	0	0	0	0	0	0

Table A6b. *Continued*

Family	**Taxon**	**Total length**	**No. of charsets**	**PTCHD1**	**RAG1**	**RAG2**	**RH**	**RIPK4**	**SH3PX3**	**SIDKEY**
Sparidae	*Sarpa salpa*	10941 bp	14	0	1428	0	459	645	705	1068

TABLE A6c. Taxon sampling for the 22-gene dataset, including 82 unique haemulid taxa and four outgroups. Sequences were obtained from previous studies, public databases, or generated new in the lab. The matrix is presented in three parts to show presence of sequence data for the 22 genes. (a.) ENC1, FICD, GLYT, KIAA1239, MYH6, PANX2, and PLAGL2; (b.) PTCHD1, RAG1, RAG2, RH, RIPK4, SH3PX3, and SIDKEY; (C.) TBR, VCPIP, ZIC1, TMO-4C4, COI, CYT *B*, S7, and 16S.

Family	Taxon	Total length	No. of charsets	TBR	VCPIP	ZIC1	TMO-4c4	COI	CYT *b*	S7	16S
Haemulidae	*Anisotremus caesius*	2418 bp	4	0	0	0	0	513	690	604	611
Haemulidae	*Anisotremus davidsonii*	5415 bp	7	0	0	0	0	567	738	562	611
Haemulidae	*Anisotremus interruptus*	5883 bp	7	0	0	0	0	651	1122	562	611
Haemulidae	*Anisotremus moricandi*	2504 bp	4	0	0	0	0	513	690	690	611
Haemulidae	*Anisotremus scapularis*	5874 bp	7	0	0	0	0	645	1119	562	611
Haemulidae	*Anisotremus surinamensis*	10416 bp	14	642	0	729	450	651	747	604	611
Haemulidae	*Anisotremus taeniatus*	6023 bp	7	0	0	0	0	651	1134	690	611
Haemulidae	*Anisotremus virginicus*	9977 bp	13	0	0	0	450	651	690	690	611
Haemulidae	*Boridia grossidens*	4419 bp	5	0	0	0	0	651	1110	0	0
Haemulidae	*Brachydeuterus auritus*	4596 bp	5	0	0	0	0	651	1122	0	0
Haemulidae	*Conodon nobilis*	12303 bp	16	0	0	687	450	651	1140	604	611
Haemulidae	*Conodon serrifer*	5910 bp	7	0	0	0	0	651	1107	604	611
Haemulidae	*Diagramma centurio*	1710 bp	3	0	0	0	450	651	0	0	609
Haemulidae	*Diagramma picta*	5684 bp	7	0	0	0	450	651	1035	0	611
Haemulidae	*Emmelichthyops atlanticus*	4596 bp	5	0	0	0	0	651	1095	0	0
Haemulidae	*Genyatremus cavifrons*	5901 bp	7	0	0	0	0	642	1119	604	611
Haemulidae	*Genyatremus dovii*	5580 bp	7	0	0	0	0	651	690	691	611
Haemulidae	*Genyatremus pacifici*	6002 bp	7	0	0	0	0	651	1122	690	611
Haemulidae	*Haemulon album*	2603 bp	4	0	0	0	0	651	747	594	611
Haemulidae	*Haemulon aurolineatum*	16494 bp	22	642	720	687	450	651	1026	559	611
Haemulidae	*Haemulon bonariense*	2613 bp	4	0	0	0	0	651	747	604	611
Haemulidae	*Haemulon carbonarium*	2613 bp	4	0	0	0	0	651	747	604	611
Haemulidae	*Haemulon chrysargyreum*	6309 bp	8	0	0	0	450	651	1074	604	611
Haemulidae	*Haemulon flaviguttatum*	5817 bp	7	0	0	0	0	651	1014	604	611
Haemulidae	*Haemulon flavolineatum*	5991 bp	8	0	0	0	450	651	747	604	611

Table A6c. *Continued*

Family	**Taxon**	**Total length**	**No. of charsets**	**TBR**	**VCPIP**	**ZIC1**	**TMO-4c4**	**COI**	**CYT *b***	**S7**	**16S**
Haemulidae	*Haemulon macrostomum*	6372 bp	8	0	0	0	450	651	1122	604	611
Haemulidae	*Haemulon maculicauda*	1866 bp	3	0	0	0	0	651	0	604	611
Haemulidae	*Haemulon melanurum*	5931 bp	7	0	0	0	0	651	1128	604	611
Haemulidae	*Haemulon parra*	2002 bp	3	0	0	0	0	651	747	604	0
Haemulidae	*Haemulon plumierii*	14496 bp	19	642	0	720	450	651	1110	604	611
Haemulidae	*Haemulon sciurus*	14196 bp	19	639	684	729	450	651	690	589	611
Haemulidae	*Haemulon scudderii*	5798 bp	7	0	0	0	0	651	909	690	611
Haemulidae	*Haemulon sexfasciatum*	2613 bp	4	0	0	0	0	651	747	604	611
Haemulidae	*Haemulon steindachneri*	5928 bp	7	0	0	0	0	651	1125	604	611
Haemulidae	*Haemulon vittatum*	14232 bp	19	642	0	714	450	651	747	604	611
Haemulidae	*Haemulopsis axillaris*	5444 bp	7	0	0	0	0	651	720	525	611
Haemulidae	*Haemulopsis elongatus*	2448 bp	4	0	0	0	0	513	720	604	611
Haemulidae	*Haemulopsis leuciscus*	5958 bp	8	0	0	0	450	651	720	604	611
Haemulidae	*Haemulopsis nitidus*	5214 bp	7	0	0	0	0	651	423	604	611
Haemulidae	*Isacia conceptionis*	5922 bp	7	0	0	0	0	651	1119	604	611
Haemulidae	*Microlepidotus brevipinnis*	5859 bp	7	0	0	0	0	597	1110	604	611
Haemulidae	*Orthopristis chalceus*	5217 bp	6	0	0	0	0	651	1125	604	611
Haemulidae	*Orthopristis chrysoptera*	14625 bp	19	642	0	678	450	642	1122	604	611
Haemulidae	*Orthopristis reddingi*	2448 bp	4	0	0	0	0	513	720	604	611
Haemulidae	*Orthopristis ruber*	2465 bp	4	0	0	0	0	651	720	483	611
Haemulidae	*Parakuhlia macrophthalmus*	4662 bp	5	0	0	0	0	651	1134	0	0
Haemulidae	*Parapristipoma humile*	2835 bp	3	0	0	0	0	651	0	0	0
Haemulidae	*Parapristipoma octolineatum*	4692 bp	5	0	0	0	0	642	1113	0	0
Haemulidae	*Parapristipoma trilineatum*	5740 bp	7	0	0	0	450	651	1140	0	574
Haemulidae	*Plectorhinchus chaetodonoides*	10650 bp	14	642	0	0	450	651	1047	639	609
Haemulidae	*Plectorhinchus chubbi*	1707 bp	3	0	0	0	450	648	0	0	609
Haemulidae	*Plectorhinchus cinctus*	5668 bp	7	0	0	0	450	651	1056	0	574
Haemulidae	*Plectorhinchus diagrammus*	5038 bp	7	0	0	0	450	651	426	0	574
Haemulidae	*Plectorhinchus gaterinus*	5706 bp	7	0	0	0	450	651	1107	0	609
Haemulidae	*Plectorhinchus gibbosus*	5666 bp	7	0	0	0	450	651	1038	0	611

Table A6c. *Continued*

Family	**Taxon**	**Total length**	**No. of charsets**	**TBR**	**VCPIP**	**ZIC1**	**TMO-4c4**	**COI**	**CYT *b***	**S7**	**16S**
Haemulidae	*Plectorhinchus lessonii*	5868 bp	7	0	0	0	0	513	1068	739	611
Haemulidae	*Plectorhinchus macrolepis*	4023 bp	4	0	0	0	0	0	1086	0	0
Haemulidae	*Plectorhinchus orientalis*	4647 bp	6	0	0	0	450	651	0	0	609
Haemulidae	*Plectorhinchus picus*	2850 bp	4	0	0	0	450	651	1140	0	609
Haemulidae	*Plectorhinchus playfairi*	1710 bp	3	0	0	0	450	651	0	0	609
Haemulidae	*Plectorhinchus schotaf*	5661 bp	7	0	0	0	450	648	1017	0	609
Haemulidae	*Plectorhinchus sordidus*	5775 bp	7	0	0	0	450	651	1131	0	609
Haemulidae	*Plectorhinchus vittatus*	9273 bp	13	0	0	0	450	513	1140	739	611
Haemulidae	*Pomadasys argenteus*	2823 bp	5	0	0	0	450	513	645	604	611
Haemulidae	*Pomadasys argyreus*	4710 bp	5	0	0	0	0	651	1125	0	0
Haemulidae	*Pomadasys branickii*	5923 bp	7	0	0	0	0	651	1119	605	611
Haemulidae	*Pomadasys corvinaeformis*	10182 bp	15	0	0	678	450	651	720	604	611
Haemulidae	*Pomadasys crocro*	2448 bp	4	0	0	0	0	513	720	604	611
Haemulidae	*Pomadasys furcatus*	1710 bp	3	0	0	0	450	651	0	0	609
Haemulidae	*Pomadasys hasta*	1225 bp	2	0	0	0	0	651	0	0	574
Haemulidae	*Pomadasys incisus*	5297 bp	6	0	0	0	0	609	1140	0	611
Haemulidae	*Pomadasys kaakan*	5035 bp	7	0	0	0	450	651	423	0	574
Haemulidae	*Pomadasys macracanthus*	3036 bp	5	0	0	0	450	651	720	604	611
Haemulidae	*Pomadasys maculatus*	5752 bp	7	0	0	0	450	651	1140	0	574
Haemulidae	*Pomadasys olivaceus*	5730 bp	7	0	0	0	450	651	1110	0	609
Haemulidae	*Pomadasys panamensis*	5919 bp	7	0	0	0	0	651	1131	604	611
Haemulidae	*Pomadasys perotaei*	5567 bp	7	0	0	0	450	651	1083	0	446
Haemulidae	*Pomadasys rogerii*	1383 bp	2	0	0	0	0	651	0	0	0
Haemulidae	*Pomadasys striatus*	5052 bp	7	0	0	0	450	651	423	0	609
Haemulidae	*Pomadasys stridens*	6300 bp	8	0	0	0	450	651	1071	604	611
Haemulidae	*Xenichthys xanti*	5190 bp	7	0	0	0	0	651	423	604	611
Haemulidae	*Xenistius californiensis*	11730 bp	16	0	609	711	450	651	597	591	579
Lutjanidae	*Aphareus furca*	10257 bp	13	642	747	672	0	651	0	0	0
Lutjanidae	*Lutjanus fulviflamma*	3219 bp	3	0	0	0	0	651	1140	0	0
Lutjanidae	*Lutjanus mahogoni*	4332 bp	6	642	0	729	0	0	0	0	0

Table A6c. *Continued*

Family	**Taxon**	**Total length**	**No. of charsets**	**TBR**	**VCPIP**	**ZIC1**	**TMO-4c4**	**COI**	**CYT *b***	**S7**	**16S**
Sparidae	*Sarpa salpa*	10941 bp	14	642	0	684	0	642	1140	0	0

VITA

MILLICENT D. SANCIANGCO

EDUCATION

- PhD in Ecological Sciences, Candidate, Old Dominion University. Department of Biological Sciences, Norfolk, Virginia, USA. Faculty Mentor: Dr. Kent Carpenter. 2014
- Master of Science in Biology. Old Dominion University. Department of Biological Sciences, Norfolk, Virginia, USA. Faculty Mentor: Dr. Kent Carpenter. 2007
- Bachelor of Science in Zoology. University of the Philippines Los Baños, College, Laguna, Philippines. 2002

PROFESSIONAL EXPERIENCE

- **Research Assistant.** Old Dominion University, Department of Biological Sciences. Fall 2005 to December 2006 and January 2008 to August 2013
- **Assistant Scientist.** International Rice Research Institute, Genetic Resources Center, International Rice Research Institute, Los Baños, Laguna. July 2007 to December 2007
- **Researcher.** WorldFish Center – Philippine Office, Khush Hall, IRRI, Los Baños, Laguna, Philippines. June 2002 to December 2004
- **Research Assistant.** Animal Biology Division, Institute of Biological Sciences, College of Arts and Sciences, University of the Philippines Los Baños, College, Laguna, Philippines. AY 2001-2002

AWARDS/SCHOLARSHIPS

- Collection Study Grant Program, Richard Gilder Graduate School, American Museum of Natural History (proposal accepted, but declined award due to conflict of schedule)
- College of Sciences University Fellowship, Fall 2011-Spring 2012
- Outstanding Leadership Award, AY 2010-2011, Office of Student Activities & Leadership, Old Dominion University
- Deepfin Student Exchange Awardee. June 21–July 3, 2010
- BGSO (Biology Graduate Student Organization) Spring Symposium - 1st place, PhD Category Paper presentation, March 20, 2010
- BGSO Travel Award, Old Dominion University, March, 2009
- Fulbright Award, Fulbright-Philippine Agriculture Scholarship Program, (Granted August 2004) January 2005- December 2006

PUBLICATIONS

- Betancur-R, R., Broughton, R.E., Wiley, E.O., Carpenter, K., Lopez, J.A., Li, C., Holcroft, N.I., Arcila, D., **Sanciangco, M.,** Cureton, J.C., II., Zhang, F., Buser, T., Campbell, M.A., Ballesteros, J.A., Roa-Varon, A., Willis, S., Borden, W.C., Rowley, T., Reneau, P.C., Hough, D.J., Lu, G., Grande, T., Arratia, G. & Orti, G. (2013) The tree of life and a new classification of bony fishes. *PLOS Currents,* 5.
- **Sanciangco, M.D.**, Rocha, L.A. & Carpenter, K.E. (2011) A molecular phylogeny of the Grunts (Perciformes: Haemulidae) inferred using mitochondrial and nuclear genes. *Zootaxa,* 2966, 37–50.