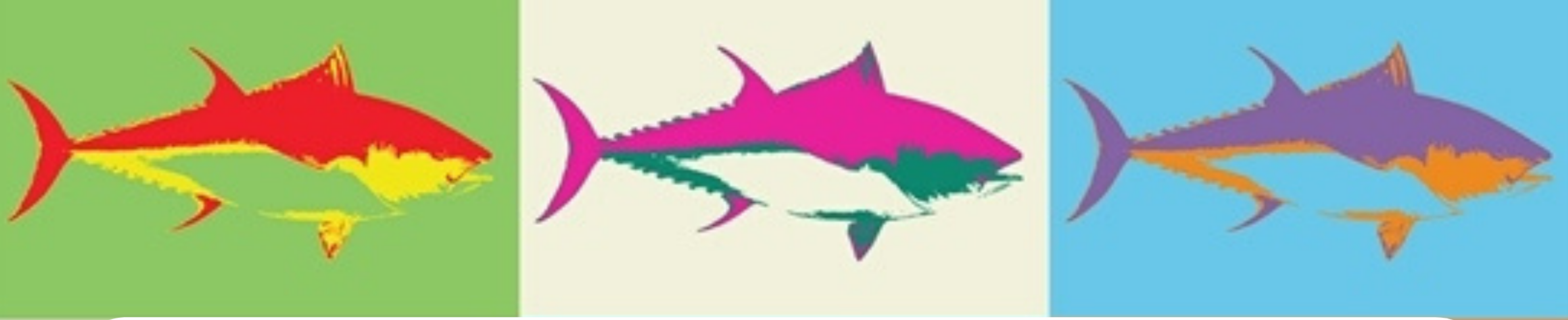

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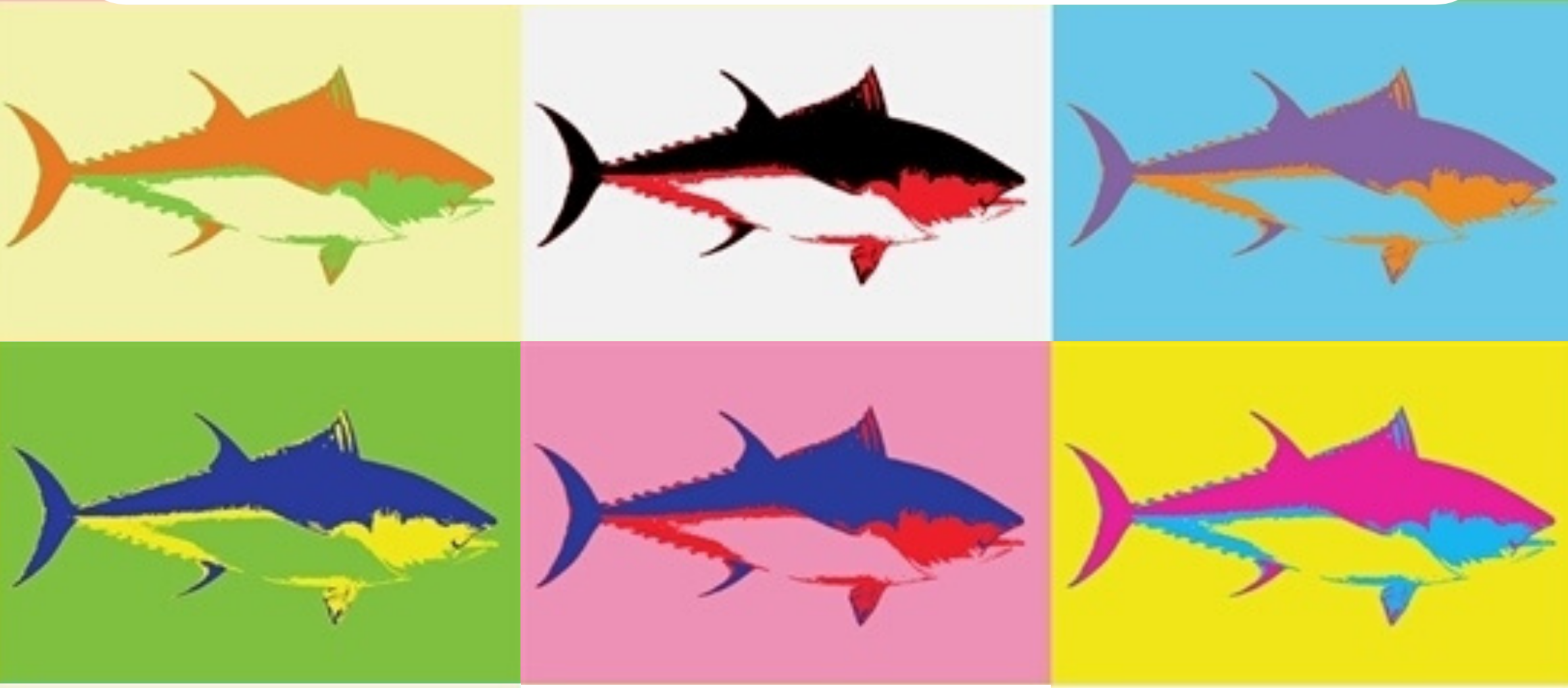

Natalia Díaz Arce

PhD Thesis 2020

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Universidad del País Vasco

Euskal Herriko Unibertsitatea

Zooming into the evolution of Atlantic bluefin tuna (*Thunnus thynnus*) using high-throughput sequencing: towards a phylogenomics and population dynamics informed management

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MEMBER OF
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& TECHNOLOGY ALLIANCE

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Cover picture was adapted from an image courtesy of FAO.

"A scientist is a child confronting natural phenomena that
impress him as though they were fairy tales. "

Marie Curie

Contents

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General Introduction

1. Fisheries management and the relevance of species and stock identification

Fish are globally an essential source of food supply of high economic value for which there is a growing demand: global fish production has nearly quintupled during the last six decades reaching 171 million tonnes in 2016 with an estimated value of USD 362 billion and involving 59.6 million employments (FAO 2018). Fish are considered a self-renewable limited resource so that theoretically, for each fishing activity there is a certain maximum amount of fish that can be harvested ensuring continued production. Yet, if harvesting surpasses that amount, the resource is then said to be overfished, involving negative consequences which may range from resource depletion to marine ecosystems destabilization (Murawski 2000; Coleman, Williams 2002; Hilborn et al. 2003; Hutchings 2005; Scheffer, Carpenter, Young 2005). Unfortunately, as the result of centuries of fishing activity, numerous fisheries globally have been and are heavily overfished and several are heading towards depletion (Hilborn et al. 2003; Coll et al. 2008). Indeed, many marine exploited fish species are considered to be at serious risk of extinction (Rice, Legacè 2007), and ecosystem regime shifts have been reported in different ecosystems around the world (Daskalov et al. 2007; Coll et al. 2008; Möllmann, Diekmann 2012).

In order to avoid or mitigate overfishing and ensure continued profitable and sustainable exploitation rates, fishing needs to be regulated through fisheries management. Fisheries management involves evaluating the status of the resources (assessment) to estimate sustainable catchable quotas. Assessment relies on integration of information about different aspects of the biology of the fish species, population dynamics, abundance or productive capacity and their impact on total recruitment (Cochrane 2002). Therefore, fisheries are assessed according to self-sustainable management units called fish stocks for which aspects such as vital rates or dynamics are or should be uniform, and from which catches are not expected to influence to other management units, even from the same species. Stock delimitation is therefore a key issue for a correct evaluation and management of fisheries. However, in practice fish management units often oversimplify true populations dynamics and connectivity patterns as well as their ecology, resulting in a discrepancy between fish populations and management units, which leads to mismanagement (Begg, Waldman 1999; Stephenson 1999; Reiss et al. 2009). This discrepancy may be caused by different reasons, such as lack of information about the populations or the complexity of reconciling different factors such as biological, economic, social or political factors which concern management plans (Reiss et al. 2009). Nevertheless, ignoring the populations dynamic patterns and oversimplification of their complexity could lead to incorrect management of the fisheries having negative effects on the resource, due to overexploitation or erosion of spawning components (Stephenson 1999; Ying et al. 2011; Cao, Truesdell, Chen 2014; Kerr et al. 2016). On the other hand, fish stock identification can be a particularly challenging objective when some fish species show complex dynamics and migratory patterns or when stocks vary both spatially and temporally (Figure 1). For example, fish stock trait variation between cohorts has been reported for salmon (Blouw, Saxon, Chadwick 1988) and cod (Kraus et al. 2000; Michio, Peter 2004). Furthermore, fish from different stocks of origin can intermingle in the same geographic region, as it has been recorded for overwintering Atlantic cod (Campana et al. 1999) or Atlantic herring feeding aggregates (Bekkevold et al. 2011), mixing at temporally varying stock proportions (Ruzzante et al. 2006; Hüssy et al. 2015). Fish stocks’ mixing can therefore be particularly challenging for fisheries management (Goethel, Quinn, Cadrin 2011).

The success of fisheries management in maintaining sustainable fish stocks is hampered by illegal, unreported and unregulated (IUU) fishing, which prevents accurate records of fish catch as well as potentially leading to overfishing. IUU is a mayor global issue (Metuzals et al. 2010; Liddick 2014) which has large biological (Ye, Valbo-Jørgensen 2012) and economic (Gallic, Cox 2006) negative effects on fisheries and consequently, different organisms responsible of fisheries management strive to combat it (Song 2009; Doulman 2010; Leroy, Galletti, Chaboud 2016). Fish product origin traceability, which can aid to detect IUU, is often difficult or rather impossible for morphologically similar species or stocks and specially for fish products modified from their original shape.

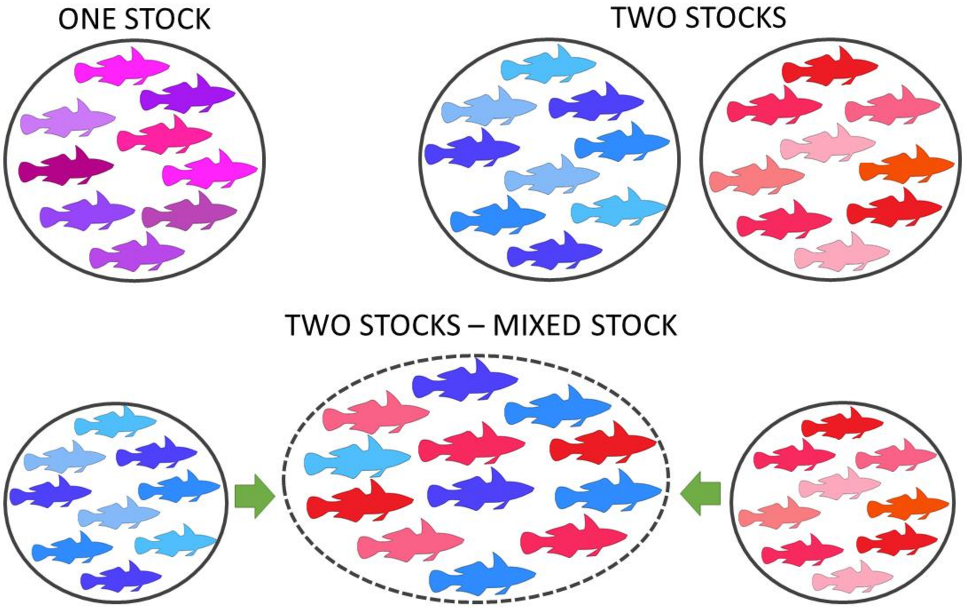

Figure 1. *Top left circle represents one stock corresponding to a panmictic population. Top right circle pair indicate two genetically differentiated stocks that remain reproductively isolated. Bottom circles represent a case of a mixed-stock fishery where two different stocks remain reproductively isolated but mix during a given period of time.*

2. Types of genetic markers and the advent of high-throughput sequencing techniques

The use of genetic tools applied to fisheries science has increased significantly during the last 50 years, hand-in-hand with continuous advances in the field of genetic techniques and data analysis (Ovenden et al. 2015). Indeed, since the first study of population structure of a fish species using molecular tools was published more than 50 years ago, molecular methods have gained popularity in fisheries science (Mariani, Bekkevold 2014; Cuéllar-Pinzón et al. 2016). Estimation of genetic diversity is based on the use of genetic markers which represent variations in the genome among individuals. Laboratory and computational techniques to obtain genetic markers have considerably progressed during the last decades, increasing the variety of available genetic marker types. From more classic, such as restriction fragment length polymorphism (RFLP) or amplified fragment length polymorphisms (AFLP), microsatellites and mitochondrial polymorphisms to more modern genetic markers such as single nucleotide polymorphisms (SNPs) have been successfully applied to population structure studies of commercial fish species (Cuéllar-Pinzón et al. 2016). For example, allozyme markers revealed structure between populations of Atlantic salmon (Bourke et al. 1997), RFLP markers allowed detection of genetic population structure of Atlantic cod (Pogson, Mesa, Boutilier 1995) and albacore tuna (Chow, Ushiama 1995) and more recently developed AFLP markers have been used to differentiate five populations of Japanese Spanish mackerel (Shui et al. 2008). Likewise, microsatellite markers have been proved useful for population differentiation and measure of genetic diversity in fish (McConnell et al. 1995; Pérez-Lezaun et al. 1996; Schlötterer, Pemberton 1998; Shaw et al. 1999; Hauser et al. 2002; Melon Barroso et al. 2005) and their use drastically increased from 2004 to 2011 (Cuéllar-Pinzón et al. 2016). The development of techniques to obtain SNP markers during the last two decades induced different studies comparing results based on microsatellites and SNPs, proving equal or better power of the latter to detect genetic variability between populations (Rengmark et al. 2006) or population structure (Liu et al. 2005). In contrast, microsatellites show higher mutation rates compared to SNPs and in general lower number of microsatellite markers are needed to detect genetic differentiation (Schlötterer 2004). The relatively reduced cost and availability of greater number of markers have led into a shift towards the use of SNPs (Helyar et al. 2011).

Since the emergence of high-throughput sequencing (HTS) techniques and during the last fifteen years (Reuter, Spacek, Snyder 2015), the use of nuclear SNP markers proved to have high discriminative power for genetic variation studies (Novembre et al. 2008), including those addressing marine fish populations (Helyar et al. 2012) significantly increasing the resolution power of detection of the genetic signal (Mariani, Bekkevold 2014). SNPs are based on single nucleotide substitutions in the DNA originating polymorphism, which may be inherited and transmitted through generations and provide with information of features such as species evolutionary origin or evolutionary processes at different taxonomic levels. HTS is a term generally used to encompass different sequencing techniques that enable generating large amount of high-quality sequence data at relatively low costs, thanks to the development of HTS platforms (Mardis 2013; Mariani, Bekkevold 2014; Kumar, Kocour 2017). Instead of sequencing the whole genome, the use of HTS coupled with the use of restriction enzymes allows the obtention of reduced representation of genomes for both model and non-model organisms, which can be useful to answer many biological questions at lower economic costs (Davey et al. 2011). Restriction Site Associated sequencing (RAD-seq) is a reduced representation sequencing technique which allows to genotype short individual orthologous loci in both model and non-model species (Davey et al. 2011; Etter et al. 2012). The use of individual barcodes coupled to restriction enzyme cut-sites, which reduces labour and costs compared to other reduced representation genome sequencing techniques, together with the high density of genome-wide obtained markers providing with high resolution population genomic data, have made RAD-seq gain popularity as a promising powerful technique for different genomic studies (Davey et al. 2011), and for population genomics studies in particular (Davey, Blaxter 2011). However, since their emergence the processing of RAD-seq as well as HTS data in general are been eased by the development of specific bioinformatic software. This type of data and particularly when used on non-model species, require making assumptions for read assembly along a challenging data analysis process, whose effects on obtained results remain unexplored (Rodríguez-Ezpeleta et al. 2016).

3. Genetic markers at service of fisheries management

Different genetics tools have been proved useful in fisheries science to address different key questions arisen at different stages of the management process (Ovenden et al. 2015). The use of genetic markers can be used to identify harvested species, identify fisheries stocks' structure and resolve mixed-stock fisheries where other techniques may not be useful. Large SNP datasets accessible today have been applied and proved useful in numerous population genetic structure studies of marine exploited fish species at different levels of genetic divergence, providing with substantially increased resolution compared to other methodologies (Bernatchez et al. 2017; Kumar, Kocour 2017). Likewise, genetic stock characterization allows the selection of genetic markers to perform traceability that can be used to identify species or assign an individual back to its population of origin in species where other types of markers may not be informative even for fish products modified from their original form (Nielsen et al. 2012; Bernatchez et al. 2017; Hosch, Blaha 2017; Kumar, Kocour 2017). Fish products traceability by the use of genetic markers is a valuable approach to detect and confront IUU fishing (Hauser, Carvalho 2008; Ogden 2008).

3.1. Species Identification

Correct species identification is required for accurate estimation of total stock catches and detect illegal fishing or food fraud. Indeed, species misidentification between very morphologically similar fish species (Beerkircher et al. 2009; Garcia-Vazquez et al. 2012) and unawareness of the existence of cryptic species (Griffiths et al. 2010) has led into overexploitation. Genetic species identification may be conclusive in cases where distinctive morphological features are not known or do not exist for example in case of cryptic species (Griffiths et al. 2010) allowing for posterior identification of morphological distinctive features, or when fish products have been modified from their original form (Teletchea 2009). Genetic identification relies on characterization of species discriminating genetic markers, such as AFLPs (Maldini et al. 2006), or typically using mitochondrial markers that are compared against reference databases such as GenBank (Benson et al. 2007) using an approach called DNA barcoding (Ward et al. 2005). The use of genetic markers if of particular interest for seafood products species traceability (Sotelo et al. 1993) and detection of commercial frauds (Cutarelli et al. 2014). Indeed, although genetic species identification requires relatively non degraded DNA samples it can be applied to industrially processed products such as canned or cooked products (Mackie et al. 1999; Galimberti et al. 2013). Indeed, the use of genetic markers has proved existing fraud in certification labelling of origin of fish products (Helyar et al. 2014) allowing not only for detection of IUU but also for consumers protection (Hauser, Carvalho 2008; Bernatchez et al. 2017). Genetic species identification presents some limitations, like the need for well documented and costly reference databases.

3.1. Fish stocks identification

Multiple approaches exist that can be used for assessment of fish stock delimitation and connectivity. Methods that provide with information about the physical individuals movements and dynamics such as mark-recapture of tagged animals and electronic tagging can help differentiate stocks (Metcalfe 2006). For example, stock differentiation can be inferred if individuals from the same stock are detected to migrate homogeneously to particular spawning grounds (Block et al. 2005) or from behavioural differences in dynamics (Lindley et al. 2011). However, integration of physical tagging derived data can be complex to incorporate into stock assessment (Sippel et al. 2015) and often depend on catching the same individual twice. Other methods rely on the printing of chemical and biological characteristics of the environment on the individuals. Fish otolith is a calcium carbonate structure whose chemical composition can reflect environmental chemical and physical conditions. Otolith chemical composition (Campana et al. 2000; Rooker et al. 2003) and shape (DeVries, Grimes, Prager 2002; Burke, Brophy, King 2008) have been successfully used as environmental tags for stock delimitation and identification. However, analysis of otolith chemical composition requires undamaged samples and involves killing the individual, which may be a constraint when analysing fish products or endangered species. Moreover, otolith chemical composition printing of one location may vary temporally, for example between different years (Gillanders 2002) or seasonally (Reis-Santos et al. 2012). Parasites can also be used as biological tags providing information of the fish migration movements and stock structure information. Some limitations on the use of parasites for stock identification are that parasitic composition between different stocks may not be different or that it requires good knowledge of the ecology of the parasites and the expected composition as well as possible variation over time (Lester 1990; MacKenzie, Abaunza 2014).

Fish stock structure could also be assessed by measuring genetic diversity between individuals. The use of genetic markers allows to detect long-term reproductive isolation between populations through genetic differentiation without necessarily sacrificing the specimen. Many marine fish species typically show large population sizes, high rates of dispersal and wide-ranging distributions which results on weak differentiation genetic signal. Nevertheless, plentiful genetic studies have successfully determined fine-scale fish population subdivision at unprecedented resolution (Hauser, Carvalho 2008; Ovenden et al. 2015; Cuéllar-Pinzón et al. 2016). For example two different local populations of Atlantic cod were found within the same fjord despite low levels of genetic divergence (Knutsen et al. 2011) and temporal and spatial structure was found between chinook salmon subpopulations (Banks et al. 2000). Furthermore, genetic markers can be used to detect local adaptation despite high gene-flow, which could be helpful to identify evolutionary significant units and relevant for fisheries management to ensure sustainability of the stocks (Mariani, Bekkevold 2014; Gagnaire et al. 2015). At this low level of divergence, the use of techniques which allow the obtention of thousands of SNPs which provides with high resolution may be of great relevance. HTS techniques, such as RAD-seq have been successfully applied to detect genetic differentiation between fish populations (Larson et al. 2014; Rodríguez-Ezpeleta et al. 2016; Leone et al. 2019). Constant methodology evolution allows fisheries science benefiting from incorporating up-to-date refined methodologies (Begg, Waldman 1999).

3.2. Resolving mixed-stocks fisheries

Fish stocks distribution may vary both spatially and temporally, which could be problematic for fisheries management if stocks' dynamics are ignored. For example, different fish populations corresponding to separated spawning components (areas or seasons for example) may intermingle in foraging grounds, implying that captures in this area would come from two or more stocks. To correctly manage each stock separately it is therefore important to know proportions of each individual stock in these captures. In general, all the techniques useful for stock identification such as otolith chemic composition can help to understand stocks dynamics. Particularly those that can be efficiently used to assess stock or origin of individuals could be used to estimate population or species contribution proportions in mixed stock assemblages (Hauser, Carvalho 2008). For example, genetic markers have provided with information about stock composition of salmonid stock mixtures (Utter, Ryman 1993), identify mixing of different populations of Atlantic herring (Bekkevold et al. 2011) and a reduced panel of 27 SNPs was used to estimate origin stock proportions of Atlantic cod on the local market (Jorde et al. 2018).

4. The potential of genetics for improving fisheries management of tuna species

Tuna is a term which encompass species from five different genus (*Thunnus, Allothunnus, Auxis, Euthynnus* and *Katsuwonus*). Tuna species are highly commercially demanded in the international market and some stocks suffer from overfishing (ie. total catches in 2016 reached 7.5 million tonnes, while 43% of the stocks of the seven most traded tunas were fished at biologically unsustainable levels in 2015 (FAO 2018)). From the 8 species that are included within the genus *Thunnus*, 6 of them present decreasing population trends and are catalogued in the IUCN Red list from near threatened to critically endangered. The Atlantic bluefin tuna (*Thunnus thynnus*, Linnaeus, 1758) is an emblematic tuna species included among the seven principal market tuna species (FAO 2018). It is the largest member of the genus and inhabits temperate waters of the North Atlantic and adjacent seas including the Mediterranean Sea, where is capable of performing long trans-Atlantic movements (Block et al. 2005).

4.1. Phylogeny of the genus *Thunnus* and species identification

Despite the importance of tuna species, phylogenetic relationships between species of the genus *Thunnus* are not yet well known. Some members of this genus are tolerant to colder waters through the development of a heat exchanger system, reason why members of this genus have been conventionally classified into two groups for temperate and tropical waters inhabiting species (Collette, Reeb, Block 2001). Typically, phylogenetic relationships between species are studied using mitochondrial markers. However, previous studies based on mitochondrial markers found paraphyletic origin of bluefin tuna mitochondrial haplotypes, sharing haplotypes present at different proportions in Atlantic and Pacific bluefin tunas which clusters bluefin tuna carriers closer to albacore tuna (*Thunnus alalunga*) than their conspecifics. Further studies of nuclear derived markers were congruent with taxonomy based on morphological traits, revealing mito-nuclear discordance and leading to the hypothesis of mitochondrial introgression from albacore into bluefin tuna (Takeyama et al. 2001; Viñas et al. 2003; Alvarado Bremer et al. 2005; Chow et al. 2006; Viñas, Tudela 2009). Species identification using mitochondrial markers is therefore susceptible to misidentification due to this introgression phenomenon. Species misidentification of *Thunnus* species has indeed been reported during larvae stages when morphological characteristics have not been developed yet (Puncher et al. 2015), which may bias estimates of recruitment of the species. The unknown extent of the potential introgression effects on the phylogenetic relationships within the genus *Thunnus* together with the need of a reliable tool for genetic species identification call for further exploration of the evolutionary context of this clade.

4.2. Atlantic bluefin tuna

The Atlantic bluefin tuna is currently managed by the International Commission for the Conservation of Atlantic Tunas (ICCAT) considering two stocks spatially separated by the 45˚W meridian, defined since 1980 and associated with the only two main spawning grounds known for the species located in the Gulf of Mexico and in the Mediterranean Sea (Fromentin, Powers 2005). Although both stocks are not considered to be subject to overfishing right now (ICCAT 2019), the western stock collapsed (Safina, Klinger 2008) without significant increase in the estimated biomass since the 1980's despite the imposition of management quotas (Figure 2) (ICCAT 2018) and the Eastern stock was considered at serious risk of collapse (MacKenzie, Mosegaard, Rosenberg 2009) following decades of overfishing. This highlights the need to give more weight to scientific advice in management plans elaboration for Atlantic bluefin tuna (Fromentin et al. 2014).

Despite evidence from both electronic tagging data (Block et al. 2005) and otolith chemistry composition (Rooker et al. 2014) for spawning site fidelity which would support the two-stock theory, frequent trans-Atlantic movements registered from tagging data and formation of mixed-stock feeding aggregates in the Atlantic Ocean can potentially bias estimates of catches for each stock. Furthermore, the recent discovery of a new spawning ground in the Slope Sea close to the North-east coast of America has open debate about their potential stock composition (Safina 2016), their implication in the behaviour (Walter et al. 2016) and the migratory strategies of the species, calling into question hypothesis about age-related migratory behaviour of the different stocks

(Richardson et al. 2016a). The uncertainties around the migratory behaviour and mixing proportions of the different spawning grounds and the origin of samples found in the newly discovered spawning ground call for the development of a tool for assignment of individuals to stock of origin. While differentiation based on otolith microchemistry find limitations regarding identification of larvae and juvenile individuals and require sacrificing samples, genetic marker-based identification may be informative and useful to answer open questions required for correct management of ABFT fisheries. Nevertheless, results on genetic differentiation from previous studies were contradictory (Ely et al. 2002; Carlsson et al. 2006; Boustany, Reeb, Block 2008; Albaina et al. 2013) potentially due to the use of limited number of genetic markers.

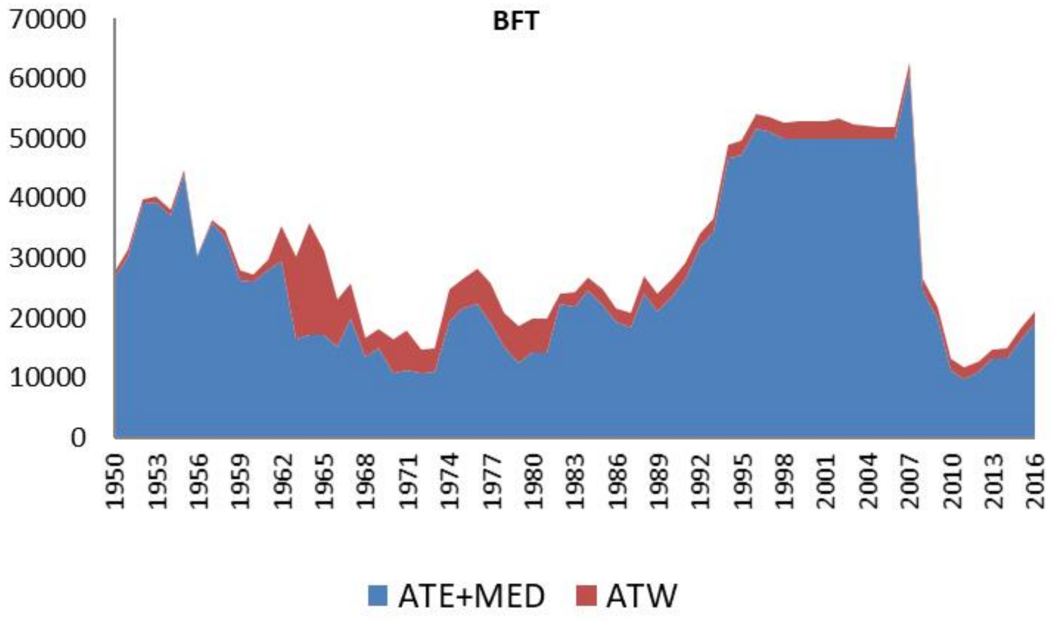

Figure 2. *Total cumulative catches of Atlantic bluefin tuna per year and area. ATE+MED denotes Eastern Atlantic Ocean plus Mediterranean Sea and ATW, Western Atlantic. (Source: https://www.iccat.int/sbull/SB45-2019/s3.html; Figure 17)*

Hypothesis and Objectives

Hypothesis

Information relevant for Atlantic bluefin tuna (*Thunnus thynnus*) conservation and management can be obtained through the study of the evolutionary context of the species and through the understanding of its population dynamics using Single Nucleotide Polymorphisms (SNPs) discovered and genotyped through high-throughput sequencing.

Objectives

1. Assess the effect of RAD-seq data *de novo* assembly parameters and SNP selection procedures on population structure and phylogenetic inferences (Chapters I, II, III & IV)

2. Determine the phylogeny of the genus *Thunnus* using nuclear SNP markers and mitochondrial sequences to understand the evolutionary context of Atlantic Bluefin tuna (Chapters II & IV)

3. Assess if the Atlantic Bluefin tuna spawning components belong to genetically differentiated populations (Chapters III & IV)

4. Determine spawning component of Atlantic Bluefin tuna mixing aggregates through a genetic stock of origin traceability tool (Chapter III)

5. Understanding the role of a recently discovered spawning ground on the population dynamics of Atlantic Bluefin tuna (Chapter IV)

Chapter 1

Selecting RAD-seq data analysis parameters for population genetics: the more the better?

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All the Supplementary Information of this manuscript can be found in **Appendix A**.

Abstract

Restriction site Associated DNA sequencing (RAD-seq) has become a powerful and widely used tool in molecular ecology studies as it allows to cost-effectively recover thousands of polymorphic sites across individuals of non-model organisms. However, its successful implementation in population genetics relies on correct data processing that would minimize potential loci-assembly biases and consequent genotyping error rates. RAD-seq data processing when no reference genome is available involves the assembly of hundreds of thousands high-throughput sequencing reads into orthologous loci, for which various key parameter values need to be selected by the researcher. Previous studies exploring the effect of these parameter values found or assumed that a larger number of recovered polymorphic loci is associated with a better assembly. Here, using three RAD-seq datasets from different species, we explore the effect of read filtering, loci assembly and polymorphic site selection on number of markers obtained and genetic differentiation inferred using the Stacks software. We find i) that recovery of higher numbers of polymorphic loci is not necessarily associated with higher genetic differentiation, ii) that the presence of PCR duplicates, selected loci assembly parameters and selected SNP filtering parameters affect the number of recovered polymorphic loci and degree of genetic differentiation, and iii) that this effect is different in each dataset, meaning that defining a systematic universal protocol for RAD-seq data analysis may lead to missing relevant information about population differentiation.

1. Introduction

Restriction site Associated DNA sequencing (RAD-seq) (Baird et al. 2008) and related methods (Davey et al. 2011) are revolutionizing the fields of ecological and evolutionary genomics (Davey, Blaxter 2011; Andrews et al. 2016). These approaches consist in subsampling putative homologous regions from the genome of several individuals with the aim of discovering and genotyping thousands of variable genetic markers that can be used for evolutionary, phylogenomic and population structure studies among others (Andrews et al. 2016). RAD-seq is particularly relevant for studies focused on species for which no genomic resources are available as it allows to cost-effectively discover thousands of genome-wide SNPs while genotyping them in hundreds of individuals performing *de novo* alignment of the reads (Davey et al. 2011). Thus, the number of studies relying on RAD-seq or related approaches for assessing population differentiation is increasing exponentially (Davey, Blaxter 2011; Andrews et al. 2016).

As for other approaches relying on high-throughput sequencing, data processing is one of the major challenges of reduced representation sequencing studies. The hundreds of thousands short reads need to be assembled into putative alleles and then into putative orthologous loci, for which some assumptions need to be made (Catchen et al. 2013; Davey et al. 2013; Eaton 2014; Sovic, Fries, Gibbs 2015). Several software packages for assembling orthologous loci and typing variant positions from reduced representation sequencing data have been developed (i.e. PyRAD (Eaton 2014), AftrRAD (Sovic, Fries, Gibbs 2015), Rainbow (Chong, Ruan, Wu 2012), RADtools (Baxter et al. 2011), RADProc (Nadukkalam Ravindran et al. 2019) and Stacks (Catchen et al. 2013)). Among them, Stacks is one of the most widely used programs and for which procedures for several applications have been established (Rochette, Catchen 2017). The program comprises several modules for read preprocessing (*process_radtags*), read merging into loci within individuals (*ustacks* for *de novo* merging and *pstacks* for reference-based merging), merging loci between individuals (*cstacks*) and loci and variant selection for further analysis (*genotypes* and *populations*). Read merging into loci within individuals relies on two main parameters: the minimum required read coverage depth to form a stack or group of identical reads (*m*), the maximum number of mismatches allowed between stacks or groups of identical reads to be considered as different alleles of the same locus (*M*). Loci merging between individuals relies on one main parameter: the maximum number of mismatches between loci from different individuals to be considered homologs (*n*). Additional pipelines are available to complement Stacks data processing steps, such as *clone_filter*, for filtering PCR clones, that is, identical sequence fragments generated during the amplification process required for RAD-seq library generation, when paired-ends are available.

How to properly select the read processing parameters for obtaining a meaningful set of markers from RAD-seq data is a largely discussed issue, and several studies have examined the effect of different parameters on the number of obtained loci (Catchen et al. 2013; Paris, Stevens, Catchen 2017), SNP call and genotyping error rate (Mastretta-Yanes et al. 2015; O'Leary et al. 2018), resolution power of derived phylogeny (Cruaud et al. 2014; Harvey et al. 2015; Díaz-Arce et al. 2016) and population genetic and evolutionary inferences (Puebla, Bermingham, McMillan 2014; Rodríguez-Ezpeleta et al. 2016; Rodriguez-Ezpeleta, Álvarez, Irigoien 2017; Shafer et al. 2017). From a theoretical point of view and from results obtained by these studies, the anticipated effect of under or over estimating each of the above mentioned Stacks parameters can be inferred: for example, setting too low or too high *m* values might result in an under or an over-merging of reads, respectively (Catchen et al. 2013). There are additional biases inherent to RAD-seq data that have been discussed, such as allele dropout (Arnold et al. 2013; Gautier et al. 2013; O'Leary et al. 2018) and false genotypes due to the presence of PCR clones (Davey et al. 2013; Andrews et al. 2014; Tin et al. 2015; O'Leary et al. 2018). These biases could potentially lead into high genotyping error rates, which could be reduced by a correct data assembly and filtering (Hendricks et al. 2018).

In search of a consensus for parameter selection, two studies applied systematic iterations of the main parameters within Stacks and defined the optimal parameter set as that which minimizes genotyping errors and maximizes number of shared loci (Mastretta-Yanes et al. 2015) or only the latter (Paris, Stevens, Catchen 2017). Yet, obtaining the maximum number of shared loci among individuals included in our study is not indicative of the accuracy of orthology assignment or SNP calling, neither of the meaningful genetic information contained in the dataset. Indeed, none of these studies tested the effect of the different parameter combinations on the derived population genetics analyses, which can also be affected by the subsequent SNP filtering steps (Roesti, Salzburger, Berner 2012; De la Cruz, Raska 2014). For example, population structure inferences based on SNPs filtered by different minimum allele frequency (MAF) threshold values by De la Cruz, Raska (2014) derived into different patterns of differentiation.

Here we have, used data from three published studies to explore the effect of removing PCR clones and of using alternative values of the main Stacks parameters and of MAF thresholds for SNP selection on the number of obtained shared markers and on population genetic inferences. The aim of the study is to analyze the importance of parameter setting during the de novo RAD-seq data analysis, and to test the derived effects on population differentiation inferences. Our results show that maximizing the number of obtained shared polymorphic loci in the dataset does not necessarily provide the strongest genetic differentiation signal and suggest that a systematic Stacks parameter selection method might limit population differentiation power of the dataset.

2. Materials and Methods

2.1. Datasets

We selected a subset of individuals of European green crab (*Carcinus maenas*), Atlantic mackerel (*Scomber scombrus*) and Atlantic deep-sea scallop (*Placopecten magellanicus*) from three previous studies (Rodríguez-Ezpeleta et al. 2016; Jeffery et al. 2017; Van Wyngaarden et al. 2017) for which RAD-seq data are publicly available (Table 1). Libraries for all three datasets were prepared following the same protocol (Etter et al. 2012) using the *SbfI* restriction enzyme, but with a variable number of PCR cycles for RAD-tag amplification (Table 1). The Atlantic mackerel dataset consists of individuals from four locations of which all pairs show genetic differentiation: larger F_{ST} values are observed between Atlantic Ocean and Mediterranean Sea locations. The green crab and scallop datasets include individuals from, respectively, four and five locations along the

East coast of North America (latitude 39-49º N). In both species, northern and southern locations (separated at latitude 45º N) are genetically differentiated. No differentiation is found within green crab northern or southern, nor within scallop southern locations. However, genetic differentiation is observed within northern scallop locations.

Table 1. *For each species, number of individuals analyzed per location and population, number of PCR-cycles used for library building, average number and standard deviation (SD) of forward reads retained per individual and average depth coverage per locus when applying m =2, M = 2 parameters, before (above) and after (below) removing PCR clones.*

Species	**Location**	**Population**	**n**	**PCR-cycles**	**Average number of reads**	**Average depth coverage per locus (*m*=3 *M*=2)**	**NCBI SRA BioProject**
European green crab (*Carcinus maenas*)	Brudenell River	North	22	14	6,750,558 (SD. 2,594,048) 2,389,818 (SD. 767,861)	221x 93.6x	PRJNA377723
	Cole Harbour	North	22	14			
	Campobello Island	South	22	14			
	Tuckerton	South	22	14			
Atlantic mackerel (*Scomber scombrus*)	East Canada	West Atlantic	29	14	3,161,222 (SD. 1,630,037) 1,905,752 (SD. 902,165)	43x 33x	PRJNA310297
	Bay of Biscay	East Atlantic	22	14			
	Adriatic Sea	East Mediterranean	20	14			
	Western Mediterranean	West Mediterranean	16	14			
Deep sea scallop (*Placopecten magellanicus*)	Sunnyside	North	20	13	7,198,343 (SD. 1,807,699) 1,924,472 (SD. 1,433,721)	171x 58.3x	PRJNA340326
	Little Bay	North	21	18			
	Magdalen Islands	North	21	18			
	Gulf of Main	South	20	18			
	Browns Bank	South	22	13			

2.2. RAD-seq data preprocessing

Raw reads were processed with Stacks v1.44 (Catchen et al. 2013). Quality filtering and demultiplexing was performed using *process_radtags* truncating all reads to 90 nucleotides to avoid the lower quality bases at the end of the read. PCR clones were removed applying *clone_filter* to reads whose forward and reverse pairs passed quality filtering. Using separately non clone-filtered data (i.e., all forward reads passing quality filtering, even if their reverse pair failed) and clone-filtered data (i.e., single representatives of each PCR clone), putative orthologous loci (RAD tags) per individual were assembled using *ustacks*. The minimum number of identical cleaned sequence reads used to form a stack (*m*) was set iteratively from 2 to 5, and the maximum number of nucleotide mismatches allowed between stacks before merging two or more stacks into a locus (*M*) set to 2 or 4. Reads not included in primary stacks during individual RAD loci formation (secondary reads) were subsequently incorporated to increase primary stack depth allowing a maximum nucleotide mismatch (*N*) of *M*+2 (default).

Catalogs of RAD loci were assembled using *cstacks* with a maximum number of nucleotide mismatches allowed between loci while merging them into the catalog (*n*) of 3 (for *M*=2) or 6 (for *M*=4). In sum, for each species, 16 catalogs were generated combining the use or not of PCR clones, the use of 4 different *m* values and the use of two different combinations of *M* and *n* values. Matches of individual RAD loci to the catalog were searched using *sstacks* and SNPs present in RAD loci found in at least 75% of the individuals under study were selected using *populations*. One additional catalog was generated per species following the 'r80 rule' (Paris, Stevens, Catchen 2017), which consists in selecting the *m*, *M* and *n* parameter values that provide the maximum number of polymorphic loci present in at least the 80% of the individuals; the process consists in i) selecting the optimal *m* value (among values ranging from 2 to 7) for *M* = 2 *n* = 0, ii) selecting the optimal *M* value (among values ranging from 1 to 5) for the *m* value optimized previously and *N* = 0 and iii) selecting the optimal *n* value (among *M* – 1, *M* and *M* + 1) for the *m* and *M* values optimized previously. Optimum Stacks parameters following the 'r80 rule' were *m*=3 *M*=4 *n*=4 for mackerel, *m*=6 *M*=1 *n*=1 for scallop and *m*=7 *M*=2 *n*=2 for the green crab datasets.

2.3. SNP genotype table generation and calculations of population differentiation

Using PLINK version 1.07 (Purcell et al. 2007), individuals with a genotyping rate smaller than 0.4 where removed, and SNPs with a genotyping rate smaller than 0.99 (for mackerel) and 0.85 (for scallop and green crab) were removed. SNPs were filtered according to a minimum minor allele frequency (MAF) of 0.01, 0.05 or 0.10. The resulting 153 genotype datasets (three per catalog) were generated and exported to GENEPOP

(ROUSSET 2008) format using PGDSpider version 2.0.8.3 (Lischer, Excoffier 2011). Overall fixation index (F_{ST}) per population pair was calculated following the Weir, Cockerham (1984) formulation as implemented in *Genepop 4.3* (ROUSSET 2008). In addition, F_{ST} was calculated for each catalog and pair using a subset of 2000 SNPs to test the possible effect of the number of SNPs included in the calculation.

3. Results and discussion

3.1. Effect of PCR clones on RAD-loci assembly

Average percentage of PCR clones per species differ (Figure 1A), being 27.1% for mackerel, 57.2% for green crab and 58.1% for scallop. Whereas in mackerel and green crab the number of PCR clones is similar across individuals, in scallop, groups of samples processed using 13 or 18 PCR cycles can be distinguished (23% and 82% of clone reads respectively, Fig 1A). Thus, average PCR clone percentages increase with number of PCR cycles, as expected (Andrews et al. 2016). Yet, although both mackerel and green crab datasets were generated using 14 PCR cycles, mackerel shows a lower percentage of clonal reads. The use of different amounts of starting material could have an effect on presence proportions of these PCR clones (Davey et al. 2011; Andrews et al. 2016), but here we reject this hypothesis as green crab libraries were generated from more starting DNA than the mackerel libraries. Instead, this could be explained by the larger number of reads for green crab (Table 1) combined with a lower number of *SbfI* cut sites, inferred from a lowest number of loci (Figure 1B), which makes presence of PCR clones more likely.

The maximum possible number of correct RAD loci per individual depends on the number of cut sites for the restriction enzyme of choice present in the genome of the species under study. Reaching this maximum number depends on the number of reads sequenced, so that a minimum coverage per loci is ensured. Here, although the average number of loci obtained per individual differs per species, in all cases the number of loci increases with sequencing depth until a certain value of convergence (Figure 1C). This convergence suggests that this maximum number is reached for each species. After removing PCR clones the number of loci per individual is less variable and the maximum total number of RAD loci is more clearly identified (Figure 1B, C), suggesting that when PCR clones are included artefactual loci might appear. Indeed, average number of assembled loci per individual is lower when removing PCR clones, a difference that is less pronounced in mackerel (lower average percentage of PCR clones per individual). Interestingly, in scallop, numbers of loci per individual follow the same bimodal distribution observed for percentages of PCR clones, suggesting that the clone percentage affects the number of inferred loci, and that removing clone reads only partially corrects this effect (Figure 1B, S1). The PCR clone percentages found in our three examples are in the range of what it is found in other reduced-representation library sequencing datasets (Andrews et al. 2014; Andrews et al. 2016), suggesting that the effects we observe can be extrapolated to other studies.

3.2. Effect of RAD-loci assembly parameters and MAF thresholds on number of selected loci and SNPs

As expected (Paris, Stevens, Catchen 2017), increasing values of *m* result in lower and more homogeneous numbers of individual loci recovered across individuals, particularly before filtering PCR clones (Figure S2, S3 and S4). This is because lower values of *m* result in loci assembled from low coverage haplotypes, which could be generated from PCR or sequencing errors. In all cases, the number of shared loci is higher when increasing *m* from 2 to 3, although this effect is less pronounced in clone filtered catalogs, where PCR derived erroneous reads have been likely removed (Figures 2 and S5). As shown, allowing a minimum stack depth parameter of *m*=2 results in highest number of loci per individual (Figures S2, S3 and S4), which would increase the chance between individual loci to match. At the same time, this would increase the chance for more than one individual locus to collapse into the same catalog locus and vice versa, consequently, decreasing the number of shared loci. Yet, when increasing *m* from 3 to 4 and 5, the number of shared loci decreases or increases depending on the dataset, and on the removal or not of PCR clones (Figure 2, S5). In their study, Paris, Stevens, Catchen (2017) also found that the number of polymorphic loci increased from *m*=2 to *m*=3 and decreased when using higher values of *m*. Here, in the mackerel catalogs and the PCR clone filtered scallop catalogs, for which also number of shared polymorphic loci decrease with high values of *m*, show average coverages per locus similar to those included in Paris, Stevens, Catchen (2017) (Table 1). Therefore, one possible explanation for the decrease in the number of shared loci after peaking at certain value of *m* could be missing loci (being harder for a locus to be shared among individuals) and/or haplotypes (being harder to find orthologous loci with lower number of alleles recovered) with lowest coverages. Interestingly, in the mackerel dataset before removing clones, while the number of polymorphic loci decreases with values of *m* higher than 3 (Figure 2), the total number of shared loci (both monomorphic and polymorphic) still increases (Figure S5), which could be explained by skewed haplotype coverages due to the presence of PCR clones, which would lead into heterozygotes to appear as homozygotes (Andrews et al. 2016). None of these two measures (number of shared total or polymorphic loci) alone does necessarily indicate a more realistic assemblage. Besides, in this case, the values of the *m* parameter that provides the highest number of polymorphic loci and the highest number of total shared loci is not the same in all datasets.

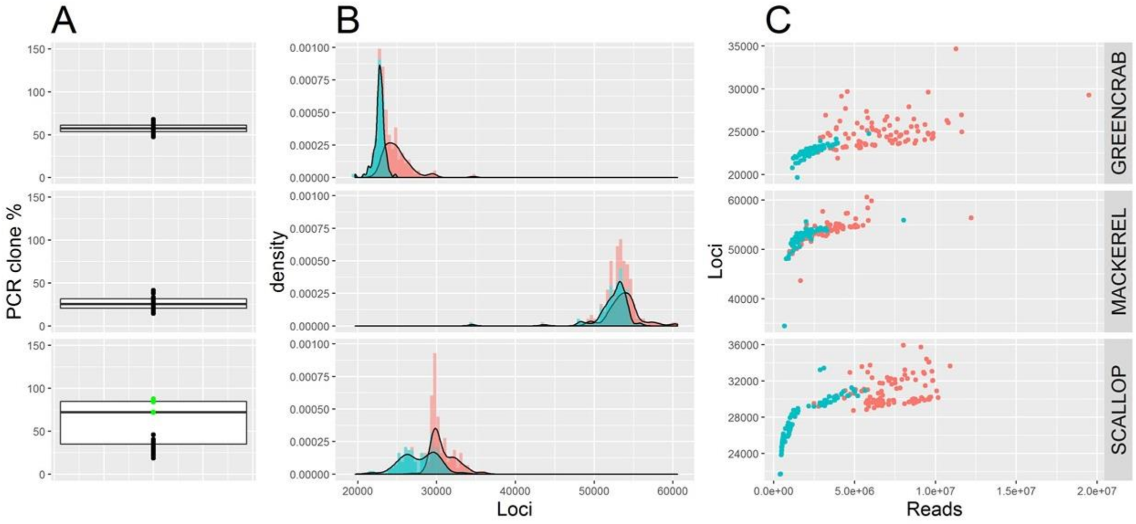

Figure 1. A. *Boxplots showing percentage of PCR clones per individual. Green dots represent scallop individuals whose libraries were generated using 18 PCR cycles.* ***B.*** *Frequency distribution of the number of loci per individual before (red) and after (blue) removing PCR clones.* ***C.*** *Number of retained reads and assembled loci per individual before (red) and after (blue) removing PCR clones. Note that figures* ***B*** *and* ***C*** *show*

*number of loci estimated using m = 5 M = 4; alternative parameter combinations produce equivalent results (see **Supplementary Figures S2**, **S3** and **S4**).*

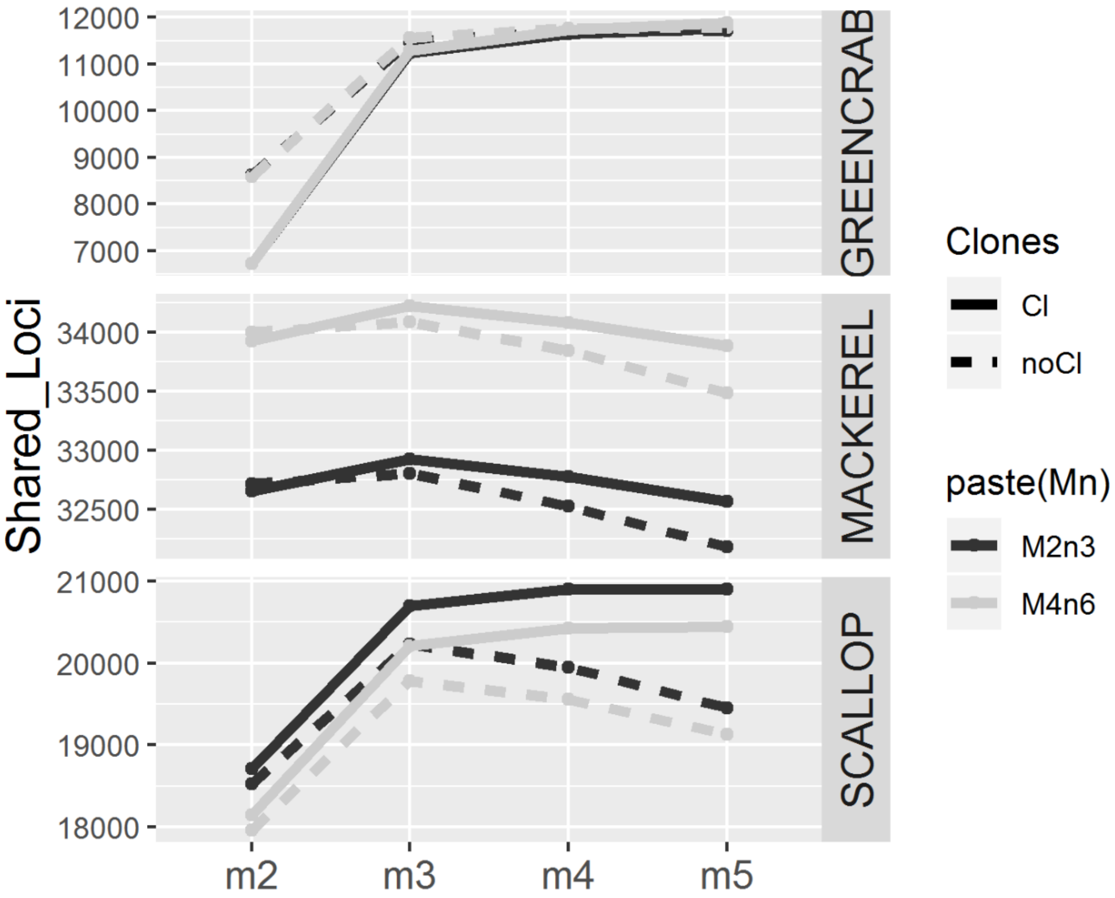

***Figure 2.** Number of polymorphic loci present in at least 75% of the individuals for different values of m (x axis), using different combinations of M and n parameters (M=2 n=3 in black and M=4 n=6 in grey), before (solid line) and after (dotted line) removing PCR clones.*

Changing *M* and *n* parameters from *M*=2 *n*=3 to *M*=4 *n*=6 makes the number of shared loci increase and decrease in mackerel and scallop datasets respectively, while we observed almost no differences in the green crab dataset. In mackerel, it has been shown that while increasing *n* from 3 to 6 would make more RAD loci merge in the same catalog locus reducing the number of common loci found, increasing *M* from 2 to 4 increases the number of shared loci, as common loci would be more easily found with higher number of alleles per locus (Rodríguez-Ezpeleta et al. 2016). The separated effect of *M* and *n* parameters has not been tested in this study and there may be different causes for variation.

The number of shared SNPs in general increased with increasing number of shared polymorphic loci, regardless the different *m* values and the use or exclusion of PCR clones. When increasing the *M* and *n* parameters from *M*=2 *n*=3 to *M*=4 *n*=6, both the total number of SNPs and average number of SNPs per shared polymorphic locus always increases (Figure 3), including the scallop and green crab catalogs, for which the number of shared polymorphic loci respectively decreases and remains nearly identical. On the other hand, the green crab dataset shows the lowest number of SNPs per locus, followed by the mackerel and scallop datasets (Figure 3). Low polymorphism values could explain a lower variation in the number of loci in the green crab catalogs when varying *M* and *n* parameters, as only few polymorphic loci or haplotypes would be excluded by allowing a too low number of heterozygous positions per locus (*M*) or SNPs per catalog locus (*n*) and the risk of over merging individual or catalog loci at the tested combinations would be low. Scallop and mackerel datasets instead, show higher levels of polymorphism and variation in the number of SNPs per locus between the two different tested combinations of *M* and *n*. In these cases, testing different parameter combinations could become of major importance.

Between datasets, proportions of SNPs with MAF values ranging between 0-0.01, 0.01-0.05, 0.05-0.10 and >0.10 vary: proportions of SNPs with MAF values below 0.01 are <17% in the green crab dataset catalogs, 45-51% in the mackerel catalogs and 58-67% in the scallop catalogs. Between catalogs within the same dataset, although proportions of SNPs relying within these MAF range categories are very similar, some differences can be observed (Figure 4). In general, with higher values of *m* and *M*/*n*, numbers of SNPs with MAF higher than 0.10 increase, while those with MAF lower than 0.01 decrease. The exception is the scallop dataset where proportion of SNPs with MAF lower than 0.01 increase in catalogs with higher values of *m* (Figure 4). The filtering of PCR clones, particularly with low values of *m*, also provided with proportionally slightly more SNPs with MAF >0.10 in green crab and mackerel datasets. The presence of clonal reads may lead into PCR errors considered as true alleles (Andrews et al. 2016), which would not be shared among individuals, and therefore would show very low allele frequencies. Besides, their presence would be enhanced when setting low values of *m*. MAF proportions could vary due to the dataset individual compositions and their genetic distances, because of what De la Cruz, Raska (2014) call “scale” effect: rare variants would be shared at an smaller scale. They concluded that looking at structure inferred from rarer variants (lower MAF values) will show differences at a smaller scale, shared by closer located individuals, while common variants (higher MAF values) will be shared by individuals from longer distances. Therefore, the exploration of population structure at different MAF values could be informative.

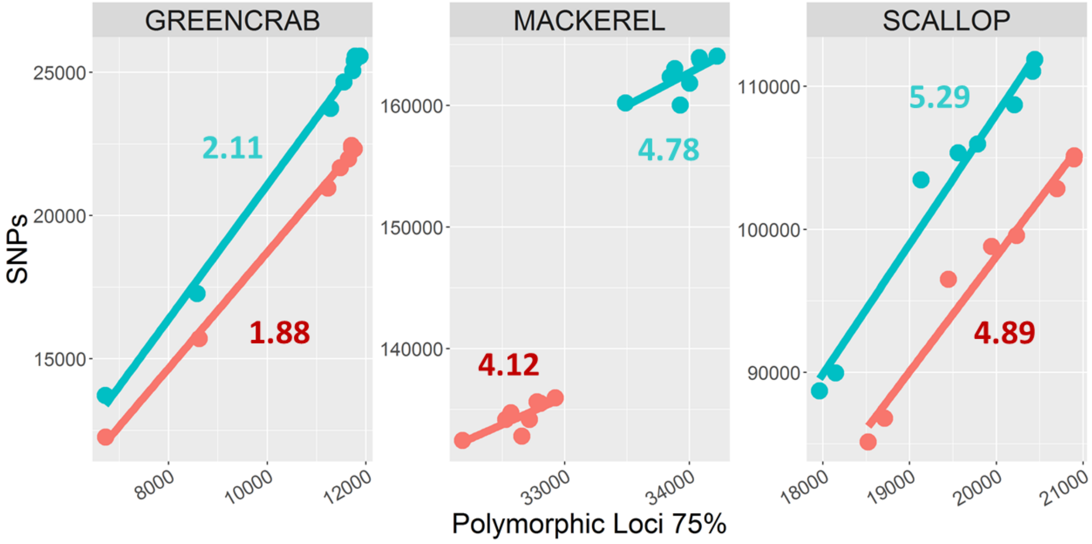

Figure 3. *Numbers of shared polymorphic loci and derived SNPs. Dots represent catalogs built using M=2 n=3 (blue), and M=4 n=6 (red) combinations. Each color includes 8 dots, corresponding to m=2, m=3, m=4 and m=5, and PCR clone filtered/non-filtered catalogs. Numbers represent average number of SNPs per shared polymorphic loci in M=2 n=3 (blue) and M=4 n=6 (red) catalogs.*

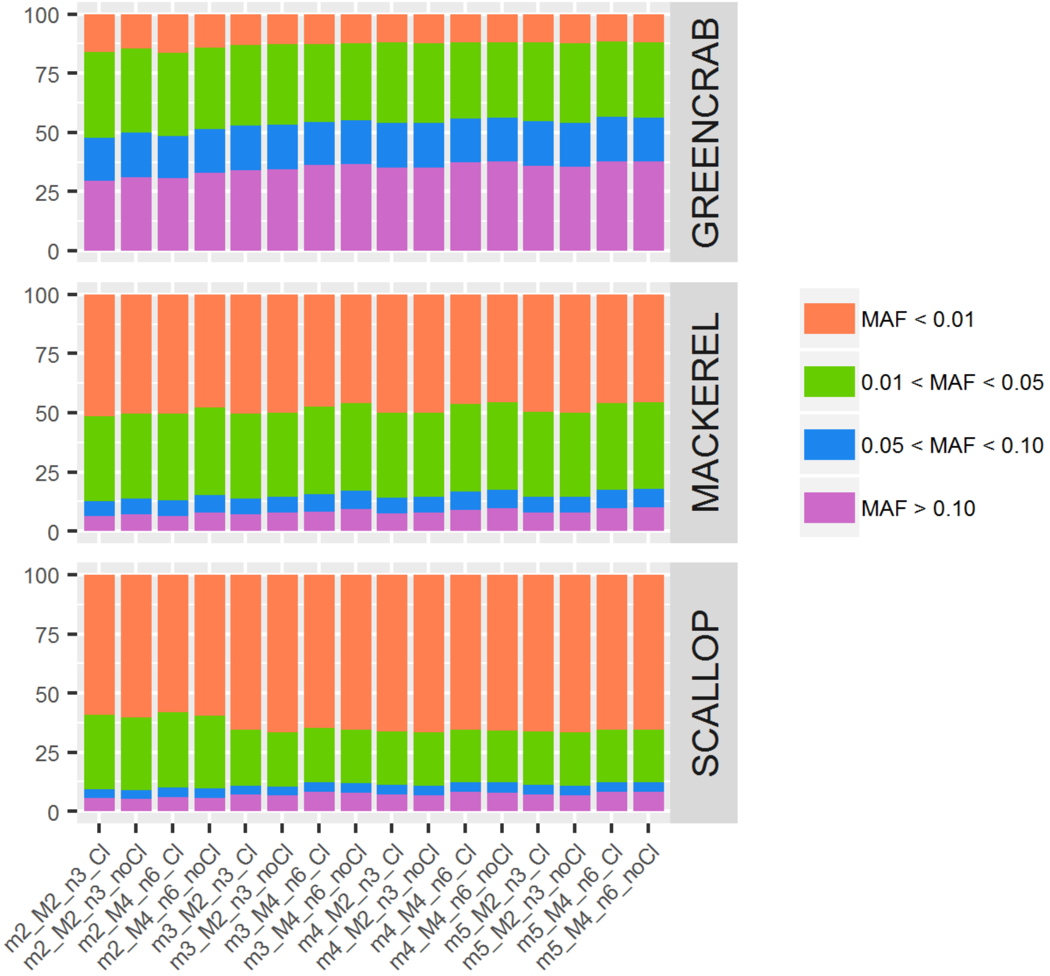

Figure 4. *Percentage of SNPs for each MAF value range. Colored bars represent percentages of SNPs per MAF value range: orange bars indicate MAF below 0.01; green bars, MAF between 0.01 and 0.05; blue bars, MAF between 0.05 and 0.10; and purple bars, MAF higher than 0.10. Each column represents a different catalog, obtained with different values of m, M and n, before (Cl) and after (noCl) filtering PCR clones.*

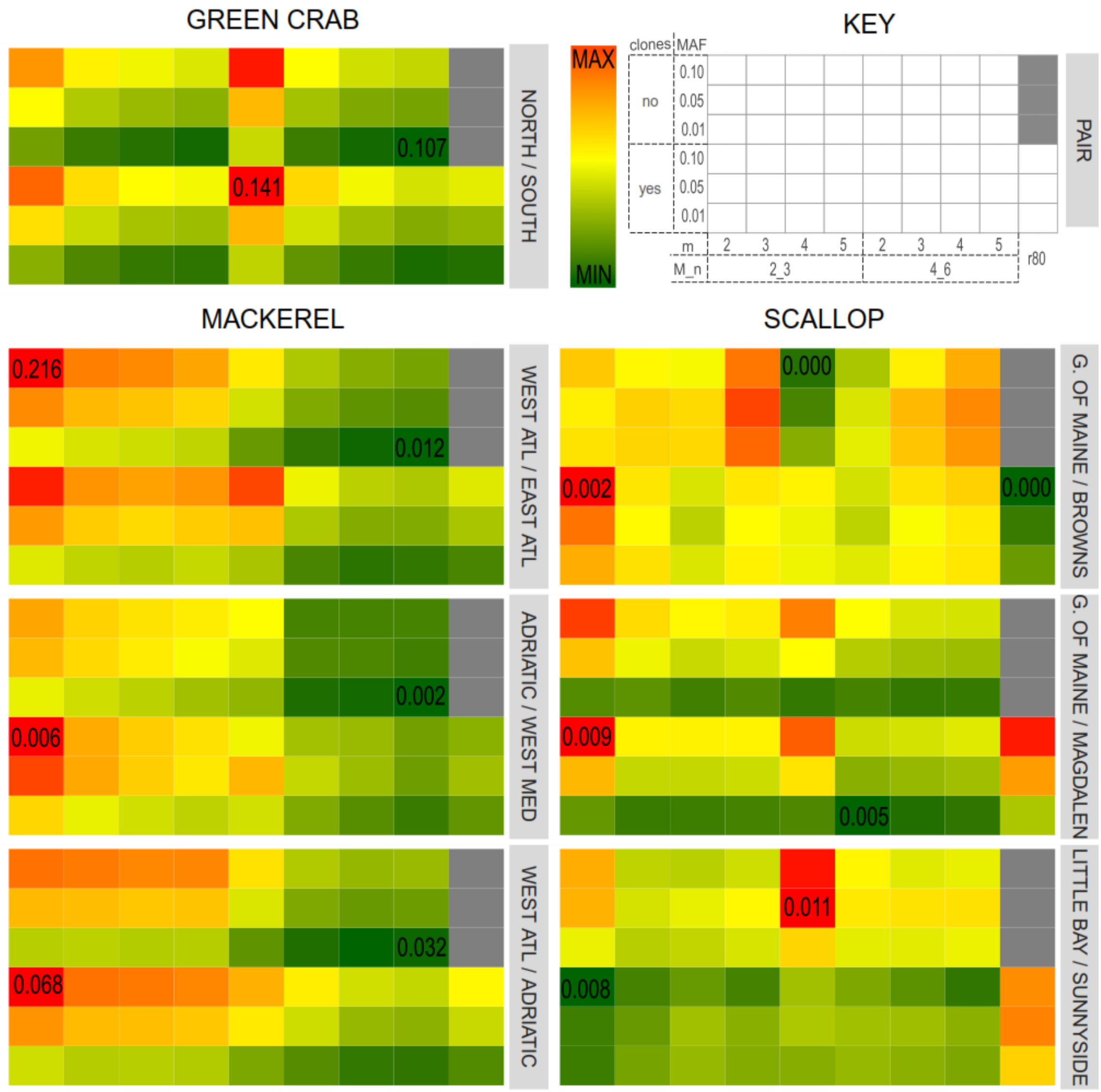

Figure 5. *Average pairwise F_{ST} values for each catalog and population pairs for the three datasets: Northern/Southern green crab locations; Western/Eastern Atlantic Ocean, Adriatic Sea/Western Mediterranean Sea (intra-Mediterranean) and Western Atlantic/Adriatic Sea mackerel populations; Gulf of Maine/Magdalen Islands (northern/southern locations), Little Bay/Sunnyside (intra-North) and Gulf of Maine/ Browns Bank (intra-South) scallop locations. Color gradients represent F_{ST} values, from lowest (dark green) to highest (dark red). Minimum and maximum F_{ST} values for each pair are indicated in the corresponding cell.*

3.3. RAD-loci assembly and SNP selection parameters affect population differentiation inferences

For all the green crab and mackerel population pairs and for the north vs. south scallop populations pairs, highest F_{ST} values were obtained when *m*=2. In general, F_{ST} values decreased with higher values of *m* (Figure 5). This also agrees with Mastretta-Yanes et al. (2015) where catalogs with lower values of *m* resulted in higher F_{ST} values. Variation in *M/n* combinations had a noticeable effect in the mackerel dataset, where setting *M*=2 *n*=3 provided with higher F_{ST} values, while having little effect in the other two datasets. Besides, in the scallop intra-south and intra-north population pairs, variation of *m*, *M* and *n* do not show a clear pattern in the effect on F_{ST} values.

The presence of PCR clones also affected differently each dataset and population pair. Catalogs where PCR clones were kept provided with higher (in the green crab dataset and in the mackerel dataset for the Adriatic Sea/Western Mediterranean Sea and Adriatic Sea/Western Atlantic population pairs), lower (in the scallop dataset Gulf of Main/Magdalen Island and Little Bay/Sunnyside populations pairs) or more heterogeneous (in the mackerel dataset Bay of Biscay/East Canada and in the Scallop Gulf of Main/ Browns Bank population pairs) F_{ST} values compared to their clone-filtered relatives (Figure 5).

For each dataset, those parameters that resulted in a higher variation in the number of shared polymorphic loci, are also those with a higher effect on the estimated F_{ST} values. Thus, major differences were found among green crab catalogs when varying *m*, and among mackerel and scallop catalogs when varying *M* and *n*. Nevertheless, while the inferred F_{ST} values varied affected by the different combination of Stacks parameters tested in this study or by the filtering of PCR clones, this variation does not follow the same patterns as the number of shared polymorphic loci, nor as the number of SNPs.

Besides, the F_{ST} values estimated from the SNP sets from the 'optimum catalogs' obtained following the 'r80 rule' (Paris, Stevens, Catchen 2017), were not the highest if compared with the rest of the catalogs which include PCR clones, except for the scallop north vs. south and intra-south population pairs (Figure 5). Mastretta-Yanes et al. (2015)

found that highest mean pairwise F_{ST} values were obtained from the catalogs with the smallest SNP error rate (estimated by comparing sample replicates) and larger number of loci. In our datasets, we did not find any correlation between F_{ST} values and number of loci, which means that if minimum SNP error rates were associated with highest F_{ST} values, they would not be necessarily always associated with larger numbers of loci. Higher filtering thresholds for MAF values provide with larger F_{ST} values for the across Atlantic mackerel and scallop and green crab north vs. south population pairs (population pairs with previous evidence of genetic differentiation). Hendricks et al. (2018) also found a general trend towards increasing F_{ST} values with increasing MAF filtering thresholds. However, for intra-south or intra-north scallop pairs and the intra-Mediterranean Sea mackerel populations pairs it is not always the case (Figure 5). In these latter pairs, MAF values have less effect on F_{ST} value variation than other parameters, whereas in the former pairs, the MAF filtering threshold is the main factor affecting F_{ST}. This agrees with De la Cruz, Raska (2014), who obtained different F_{ST} values when using different MAF filtering thresholds over the same SNP set. They concluded that using higher MAF thresholds (common variants) more distantly shared variants would be addressed, and therefore population structural signal could be better observed. However, for those more recently coalesced population pairs, genetic differentiation would be more likely represented by rarer variants with lower MAF values. In order to test if the obtained F_{ST} values were affected by the number of filtered SNPs, F_{ST} values estimated using subsets of 2,000 SNPs from each dataset and were found to vary following the same pattern (Figure S6).

4. Conclusions

Here we show that inferences of population differentiation based on RAD-seq derived SNPs are affected by the presence of PCR clones, RAD-loci assembly parameters and MAF threshold used for SNP selection. Importantly, different species, geographic scales and group pairs are differently affected by these factors, suggesting that the use of a systematic method based on common criteria for parameter selection might lead to limited information about genetic differentiation. Here, we show that the systematic protocol developed by Paris, Stevens, Catchen (2017) to maximize the number of shared polymorphic loci does not necessarily imply maximizing the number of population differentiation informative markers. Yet, neither higher number of shared loci between individual, nor higher F_{ST} values or estimated genetic distances between a priori differentiated populations indicate a more realistic assemblage of RAD-seq data. For that reason, the most appropriate set of loci assembly parameters will depend on the aim of the study and different combinations should be checked for consistency (Díaz-Arce et al. 2016; Rodríguez-Ezpeleta et al. 2016) and/or be based on particular characteristics of each dataset (Rochette, Catchen 2017). Our results suggest that those Stacks assembly parameters with highest effect on numbers of recovered shared polymorphic loci and SNPs also provide with highest variation in inferred population differentiation values. We recommend testing for different combinations of loci assembly parameters emphasizing variation of those parameters. In our study we used the Stacks software (Catchen et al. 2013), but our recommendations can be extrapolated to the use of other pipelines, such as pyRAD (Eaton 2014) which allow the user to modulate analogous parameters.

Chapter 2

RAD-seq derived genome-wide nuclear markers resolve the phylogeny of tunas

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All the Supplementary Information of this manuscript can be found in **Appendix B**.

Abstract

Although species from the genus *Thunnus* include some of the most commercially important and most severely overexploited fishes, the phylogeny of this genus is still unresolved, hampering evolutionary and traceability studies that could help improve conservation and management strategies for these species. Previous attempts based on mitochondrial and nuclear markers were unsuccessful in inferring a congruent and reliable phylogeny, probably due to mitochondrial introgression events and lack of enough phylogenetically informative markers. Here we infer the first genome-wide nuclear marker-based phylogeny of tunas using restriction site associated DNA sequencing (RAD-seq) data. Our results, derived from phylogenomic inferences obtained from 128 nucleotide matrices constructed using alternative data assembly procedures, support a single *Thunnus* evolutionary history that challenges previous assumptions based on morphological and molecular data.

1. Introduction

Species of the genus *Thunnus* include some of the most economically important, but also most severely overexploited fish on the planet. Yet, despite its relevance for enabling more efficient management plans and avoiding masked trade of mislabeled tuna species by providing tools for DNA-based species identification, the phylogeny of the genus *Thunnus* remains unresolved. According to morphological features, this genus was divided into two subgenera: the temperate *Thunnus* (bluefin tuna group), comprising the albacore (*Thunnus alalunga*) and the Atlantic (*Thunnus thynnus*), Pacific (*Thunnus orientalis*) and Southern (*Thunnus maccoyii*) bluefin tunas, and the tropical *Neothunnus* (yellowfin tuna group), comprising the blackfin (*Thunnus atlanticus*), longtail (*Thunnus tonggol*) and yellowfin (*Thunnus albacares*) tunas. Although sharing a similar number of morphological features with both groups, the bigeye tuna (*Thunnus obesus*) has been included into the subgenus *Thunnus* due to its adaptation to cooler waters (Collette, Reeb, Block 2001).

Most of molecular phylogenies aimed at solving the relationships among tuna species are based on mitochondrial markers (Chow, Ushiama 1995; Alvarado Bremer, Naseri, Ely 1997; Chow et al. 2006; Viñas, Tudela 2009; Tseng et al. 2012) and/or do not include all the species of the genus *Thunnus* (Orrell, Collette, Johnson 2006; Miya et al. 2013; Santini, Carnevale, Sorenson 2013). These studies consistently recover the *Neothunnus* subgenus and a close relationship between the albacore and the Pacific bluefin tuna. Yet, evidence of mitochondrial introgression in *T. orientalis* with *T. thynnus* or *T. alalunga* (Chow, Inoue 1993; Chow, Ushiama 1995; Chow et al. 2006), and in *T. thynnus* with *T. alalunga* or *T. orientalis* (Takeyama et al. 2001; Viñas et al. 2003; Alvarado Bremer et al. 2005; Chow et al. 2006; Viñas, Tudela 2009) makes mitochondrial-based inferences of the relationships between these three species ambiguous. The only nuclear based phylogenetic studies that include all eight species of *Thunnus* (Chow et al. 2006; Viñas, Tudela 2009) group the Atlantic and Pacific bluefin tunas in a well-supported clade. Thus, overall, the analyses published to date support the monophyly of the *Neothunnus* subgenus, but do not provide resolution for the relationships within this clade nor congruence or support for the relationships within *Neothunnus* or among *T. maccoyii, T. obesus, T. alalunga* and the *T. orientalis+T. thynnus* group. Besides preventing accurate inferences of their evolutionary history, this lack of congruence or resolution is translated into a lack of suitable DNA-based tools for tuna species discrimination. The few genetic markers in use for this purpose (*e.g*. Bartlett and Davidson, 1991; Chow et al., 2003; Pardo and Pérez-Villareal, 2004; Takeyama et al., 2001; Tseng et al., 2011; Viñas and Tudela, 2009) are mitochondrial, and the sole contrasted nuclear marker, the ribosomal internal transcribed spacer (ITS1), can only be used as a complement to mitochondrial markers when introgression is suspected (Viñas, Tudela 2009), as it does not discriminate between all eight *Thunnus* species (Chow et al. 2006; Viñas, Tudela 2009). Thus, overcoming the lack of congruence and/or resolution associated to the published *Thunnus* evolutionary relationships requires evolutionary inferences based on genome-wide phylogenetically informative positions of nuclear origin.

Recently, the restriction site-associated DNA sequencing (RAD-seq) method, which, allows to rapidly and cost-efficiently sequence thousands of homologous regions in hundreds of individuals both, with and without available reference genomes, has been applied to resolve phylogenetic relationships (*e.g*. Cruaud et al., 2014; Herrera and Shank, 2015; Leaché et al., 2015) . Yet some studies have shown that gathering a suitable set of phylogenetically informative markers from RAD-seq data relies on the ability to discover enough orthologous loci among the species under study, which largely depends on divergence times between lineages and filtering and assembly parameters applied for orthology inference (Rubin, Ree, Moreau 2012; Jones et al. 2013; Wagner et al. 2013; Leaché et al. 2015). It is therefore recommended to explore the results applying different parameter combinations (Rubin, Ree, Moreau 2012; Ree, Hipp 2015). Here, we infer the evolutionary history of tunas based on phylogenomic analyses of RAD-seq derived nuclear markers. With the final aim of building a robust phylogenetic tree, we have explored alternative procedures for selecting phylogenetically informative sites and built 128 RAD-seq derived nucleotide matrices obtained by i) using different parameters for putative orthologous loci identification, ii) including different sets of species, iii) selecting variable or fixed sites iv) within individuals or within species and v) allowing different thresholds of missing individuals or species to select a locus. Our analyses highlight the influence of RAD-seq data analyses procedures in derived nucleotide matrices and phylogenetic inferences, and provide the first genome-wide resolved evolutionary tree of the *Thunnus* genus. The inferred relationships restructure the *Neothunnus* subgenus including *T. obesus* within this group, and clarify the relationships between the Altantic and Pacific bluefin tunas and albacore, setting the root of the genus within the latter. Our results establish the basics for future evolutionary studies of these species and provide valuable data for developing species identification and traceability tools that will assist better management and conservation of tunas.

2. Materials and Methods

2.1. Sampling and genomic DNA extraction

Samples from *T. thynnus* (nine individuals), *T. albacares*, *T. atlanticus*, *T. orientalis, T. tonggol* (five individuals), *T. alalunga*, *T. maccoyii* and *T. obesus* (four individuals) and from three other Scombridae species included as outgroup (*Katsuwonus pelamis* – four individuals, *Euthynnus alletteratus* – five individuals, and *Auxis rochei* – three individuals) were obtained from scientific surveys and commercial fisheries. From each fish, about 1 cm^3 of muscle tissue was resected and immediately stored in 96% molecular grade ethanol at -20ºC. Genomic DNA was extracted from about 20 mg of muscle tissue using the Wizard® Genomic DNA Purification kit (Promega, WI, USA) following manufacturer’s instructions for “Isolating Genomic DNA from Tissue Culture Cells and Animal Tissue”. Extracted DNA was suspended in Milli-Q water and concentration was determined with the Quant-iT dsDNA HS assay kit using a Qubit® 2.0 Fluorometer (Life Technologies). DNA integrity was assessed by electrophoresis, migrating about 100 ng of GelRed™-stained DNA on an agarose 1.0% gel.

2.2. Restriction Site Associated DNA sequencing library preparation and analysis

Restriction-site-associated DNA libraries were prepared following the methods of Etter et al. (2012). Briefly, about 300 ng of genomic DNA were digested with the *SbfI* restriction enzyme and ligated to modified Illumina P1 adapters containing 5bp unique barcodes. Pools of 33 individuals were sheared using the Covaris® M220 Focused-ultrasonicator™ Instrument (Life Technologies) and size selected to 300-500 pb by cutting agarose migrated DNA. After Illumina P2 adaptor ligation, library was amplified using 14 PCR cycles. Each pool was sequenced (100 pb) on an Illumina HiSeq2000 lane. RAD sequencing data were processed with Stacks version 1.27 (Catchen et al. 2013) with default parameters unless otherwise specified. Raw sequences were demultiplexed and filtered for low quality using the *process_radtags* module; for each individual, putative loci were identified using *ustacks* allowing a minimum stack depth parameter of 5 (parameter *m*) and 1 or 2 mismatches (parameter *M*). Catalogs of loci were built based on two different subsets of individuals (all individuals and only *Thunnus* individuals) using *cstacks* allowing 4 or 8 mismatches (parameter *n*). A total of 8 different catalogs were produced. Individual sets of loci were matched against the catalog using *sstacks*. From the 8 catalogs built, the *populations* program was used to select phylogenetically informative markers based on all possible combinations of i) considering individuals or species for informative marker selection, ii) considering fixed (within individuals or species) or IUPAC encoded variable sites (can include heterozygous sites when using individuals), and iii) allowing different thresholds (0%, 25%, 50% or 75%) of missing individuals or species for marker selection. A total of 128 matrices (16 per catalog) including only the phylogenetically informative sites within each locus were produced for phylogenetic analyses. Maximum Likelihood phylogenetic trees were built using the unpartitioned GTRCAT model as implemented in RAxML version 8.1.21 (Stamatakis 2014) and branch support was assessed by a 100 replicate rapid-bootstrap analysis.

3. Results and Discussion

3.1. RAD-seq data preprocessing

The number of reads per individual that met the quality requirements ranges from 1,529,640 to 6,645,450, with an average of 3,266,093, of which from 92% to 99% per individual were used for stacks (RAD loci) formation. As expected, higher M values increase coverage (53x vs 50x) and produce fewer RAD loci per individual (Figure 1). The number of estimated *SbfI* cut sites (about 30,000 to 32,000 restriction sites for *Thunnus* species and slightly higher for outgroup species) show that the RAD-seq approach using this restriction enzyme allows to cost-effectively produce high coverage orthologous markers in these species, which is relevant for future population genetics studies on these taxa.

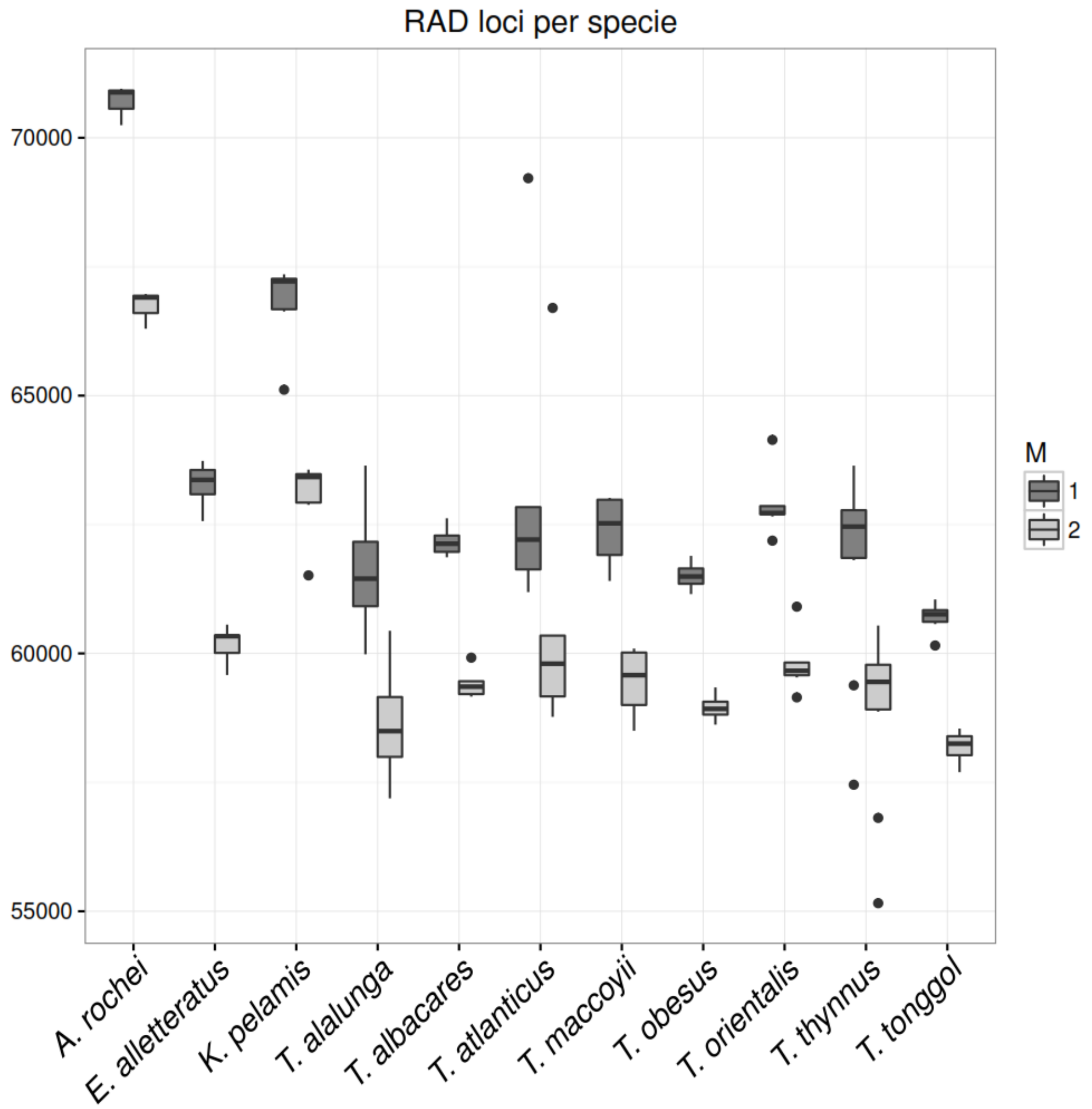

Figure 1. *Boxplots depicting median, first and third quartile and standard deviation of number of inferred RAD loci per species when allowing a maximum of 1 (dark grey) or 2 (light grey) mismatches between stacks to create a locus (parameter M).*

3.2. Assembly of phylogenetically informative nucleotide matrices

The number of nucleotide positions included in the matrices ranges from 2,625 to 426,052 varying substantially depending on the catalog building and filtering parameters applied (Table 1). In general, allowing more missing positions, using IUPAC encoded sites instead of fixed positions and using individuals instead of species to select positions results in larger matrices. When missing data are allowed, individual-based site selection results in larger matrices both for IUPAC encoded and fixed positions, which is due to the fact that even when missing data are allowed, markers present in all individuals within the same species are scarcer. However, when no missing data are allowed, the number of markers is similar whether using individuals or species, particularly when IUPAC encoded sites are selected. When IUPAC encoded sites are used, M=2 always results in larger matrices than M=1, and the observed differences are higher the lower the missing data threshold (factors of 1.34, 1.45, 1.62 and 2.29 for missing data of 75, 50, 25 and 0% respectively); when fixed positions are used, differences of matrix sizes produced with different M values are lower, but still more pronounced when less missing data are allowed. When building each individual locus, higher values of M will allow higher heterozygosity within loci. Thus, putative loci presenting more than one heterozygous positions that would otherwise be split when M=1, cluster together when M=2. This increases the probability of alignment of those loci among individuals when building the catalog, and thus, the probability of finding these loci in a higher number of individuals also increases. This added variability information will be represented only when IUPAC encoded sites are used, explaining why the differences between matrix sizes using M=1 and M=2 are bigger. When all species are considered, n=8 results in larger matrices than n=4 (by an average factor of 1.3 and 1.7 for fixed and IUPAC encoded sites respectively), whereas almost no difference is observed when using different n values when only *Thunnus* species are considered. The outgroup species are expected to be more divergent with respect to the rest the species. Higher values of n allow recovering more divergent orthologous loci, providing more informative positions resulting from the relatively high genetic distance of the outgroup species. When fixed positions are considered, matrices including all species are always larger than those including only *Thunnus* individuals (by an average factor of 1.6 and 2.8 when using individuals or species respectively); when IUPAC encoded sites are used, including all or only *Thunnus* species results in similar size matrices when high thresholds of missing data are used (75 and 50%), but on smaller matrices when all species are considered when small missing data thresholds are used (factors of 0.6 and 0.5 when 25 and 0% of missing data are allowed). More positions fixed within but variable between species are found if the outgroup is included, which is expected given that these positions are product of fixation process during speciation, and the greater the evolutionary time, the greater the allele fixation probability. IUPAC encoding of polymorphic sites allows for retention of heterozygous positions within individuals and species, which may be valuable in resolving recent divergences. However, when low percentages of missing data are allowed and the outgroup is included, positions resulting from recent speciation events may not be included in the analysis and thus prevent resolution of close relationships. On the other hand, high percentages of missing data allow positions present in only a subset of individuals to be included in the analysis.

Table 1. *Matrix sizes and supported topologies according to bootstrap value thresholds of 95% (BV > 95) and 80% (BV > 80) for all the 128 analyses produced from the 8 catalogs, using both fixed and IUPAC encoded positions filtered per individual or per species and allowing different percentages of missing data (represented in black in the ''missing" column). Topology 1 stands for the one supported by the majority of the analyses and topologies 2 and 3 for the alternative ones (corresponding to trees 60, 31 and 105 in Appendix A, respectively). When the outgroup is included, the genus was either rooted by T. alalunga (ala) or the T. thynnus and T. orientalis (thyori) clade. The asterisks indicate analyses for which the either monophyly of T. thynnus or of T. orientalis is not supported.*

					only *Thunnus*			all species				
						TOPOLOGY			TOPOLOGY		ROOT	
M	n	positions	sp/ind	missing	matrix size	BV>95	BV>80	matrix size	BV>95	BV>80	BV>95	BV>80
1	4	IUPAC	ind	◕	279084	1	1	303886	1	1	-	ala
				◑	218133	1	1	223175	1*	1	-	-
				◔	151770	1	1	98594	1*	1	-	-
				○	25107	1*	1*	10957	-*	-*	-	-
			sps	◕	146462	1	1	173859	1	1	-	ala
				◑	114492	1	1	110185	1	1	-	ala
				◔	75737	1	1	37361	1	1	-	-
				○	25112	-	-	10957	-	-	-	-
		fixed	ind	◕	106321	1	1	125843	1	1	-	-
				◑	64379	1	1	75907	1*	1*	-	-
				◔	32334	1*	1	36210	1*	1*	-	thyori
				○	3435	-*	-*	5006	-*	-*	-	-
			sps	◕	19618	1	1	46740	1	1	ala	ala
				◑	14132	1	1	31424	-	-	-	-
				◔	8480	1	1	16344	-	-	-	-
				○	2653	-	-	4793	-	-	-	-
	8	IUPAC	ind	◕	297574	1	1	370270	1	1	-	ala
				◑	228350	1	1	274984	1*	1*	-	ala
				◔	154610	1	1	146512	1*	1	ala	ala
				○	24079	1*	1*	14483	-*	-*	-	-
			sps	◕	147745	1	1	208048	1	1	-	-
				◑	114556	1	1	139795	1	1	-	ala
				◔	75067	-	-	57151	1	1	-	-
				○	24083	-	-	14483	-	-	-	-
		fixed	ind	◕	127019	1	1	191582	1	1	-	-
				◑	75110	1	1	124622	1*	1*	-	-
				◔	35738	1*	1	71968	1*	1	-	-
				○	3404	-*	-*	7508	-*	2*	-	-
			sps	◕	21759	1	1	78371	1	1	ala	ala
				◑	15254	1	1	56389	-	1	-	-
				◔	8944	-	1	29274	-	2	-	-
				○	2625	-	-	7230	-	-	-	-
2	4	IUPAC	ind	◕	328966	1	1	357395	1	1	-	-
				◑	271503	1	1	283198	1	1	-	-
				◔	214363	1	1	153249	1*	1	-	-
				○	64492	1*	1	20808	-*	-*	-	-
			sps	◕	223772	1	1	263424	1	1	-	ala
				◑	190082	1	1	185416	1	1	ala	ala
				◔	144305	1	1	58529	1	1	-	ala
				○	64497	-	1	20808	-	-	-	-
		fixed	ind	◕	83906	1	1	104393	1	1	-	-
				◑	51918	1	1	68202	1*	1*	-	-
				◔	30471	1*	1*	39151	1*	1*	-	thyori
				○	6478	-*	3*	8142	-*	2*	-	-
			sps	◕	18482	1	1	50093	1	1	ala	ala
				◑	14705	1	1	35243	-	1	-	-
				◔	10350	-	-	21090	-	-	-	-
				○	4441	-	3	7694	-	-	-	-
	8	IUPAC	ind	◕	346583	1	1	426052	1	1	-	ala
				◑	283161	1	1	339603	1*	1	-	ala
				◔	218996	1	1	207223	1*	1	ala	ala
				○	61359	1*	1	30851	-*	-*	-	ala
			sps	◕	224582	1	1	305538	1	1	ala	ala
				◑	189662	1	1	224042	1	1	-	ala
				◔	143035	1	1	98675	1	1	ala	ala
				○	61363	1	1	30851	-	-	-	-
		fixed	ind	◕	103893	1	1	168757	1	1	-	-
				◑	63489	1	1	117399	1*	1	-	-
				◔	35285	1*	1*	77852	1*	1*	-	thyori
				○	6444	-*	-*	13950	-*	2*	-	-
			sps	◕	21092	1	1	87287	1	1	ala	ala
				◑	16230	1	1	66299	1	1	-	ala
				◔	11139	-	-	42688	-	2	-	-
				○	4438	-	-	13304	-	-	-	-

3.3. Phylogeny of the genus Thunnus

Taking all analyses into account, a single topology (Figure 2) is supported (all branches with BV>95%) by 90 out of the 128 analyses, whereas no alternative topology is supported at that BV level (Table 1). Only when lowering the BV threshold down to 80%, two new topologies, supported by a few analyses based on the smallest matrices, arose. As for the position of the root, 9 or 22 (for BV>95% or 80% respectively) of the 64 analyses that include all species support the position of the root on the branch of *T. alalunga*, whereas an alternative rooting in the *T. orientalis/T. thynnus* branch is supported by 3 analyses only when lowering the BV to 80% (Table 1). As reported by other studies (Rubin, Ree, Moreau 2012; Jones et al. 2013; Wagner et al. 2013; Cruaud et al. 2014; Hipp et al. 2014; Hou et al. 2015; Leaché et al. 2015), the use of IUPAC encoded sites and allowing higher missing data percentages not only produces larger matrices, but also results in better resolved trees (Table 1). Yet, although high bootstrap alone is not evidence of tree accuracy (Rodríguez-Ezpeleta et al. 2007), the congruence obtained among our different analyses is considered a good indicator of true evolutionary signal in the data (Hillis 1995; Rubin, Ree, Moreau 2012). Additionally, the fact that the trees with the highest support are the ones that have relatively the longest internal and shortest external branches suggests that the increased support is obtained by the use of more common and less independently acquired substitutions among lineages. In sum, our analyses support an alternative evolutionary history of *Thunnus* species that challenges previous definitions of the *Neothunnus* subgenus (Alvarado Bremer, Naseri, Ely 1997) and sets the root of the *Thunnus* genus within the *T. alalunga* branch. According to our results, *T. obesus* should be included within the *Neothunnus* subgenus. This implies that either this species lost the central heat exchanger and adapted to colder waters independently from the rest of temperate tunas by developing the lateral heat exchanger, as well as visceral and cranial retia mirabilia as it has been reported before for different lineages of Scombridae (Block et al. 1993) or that tropical tunas developed their central heat exchanger *a posteriori* independently from other lineages of Scombridae (Collette, Reeb, Block 2001).

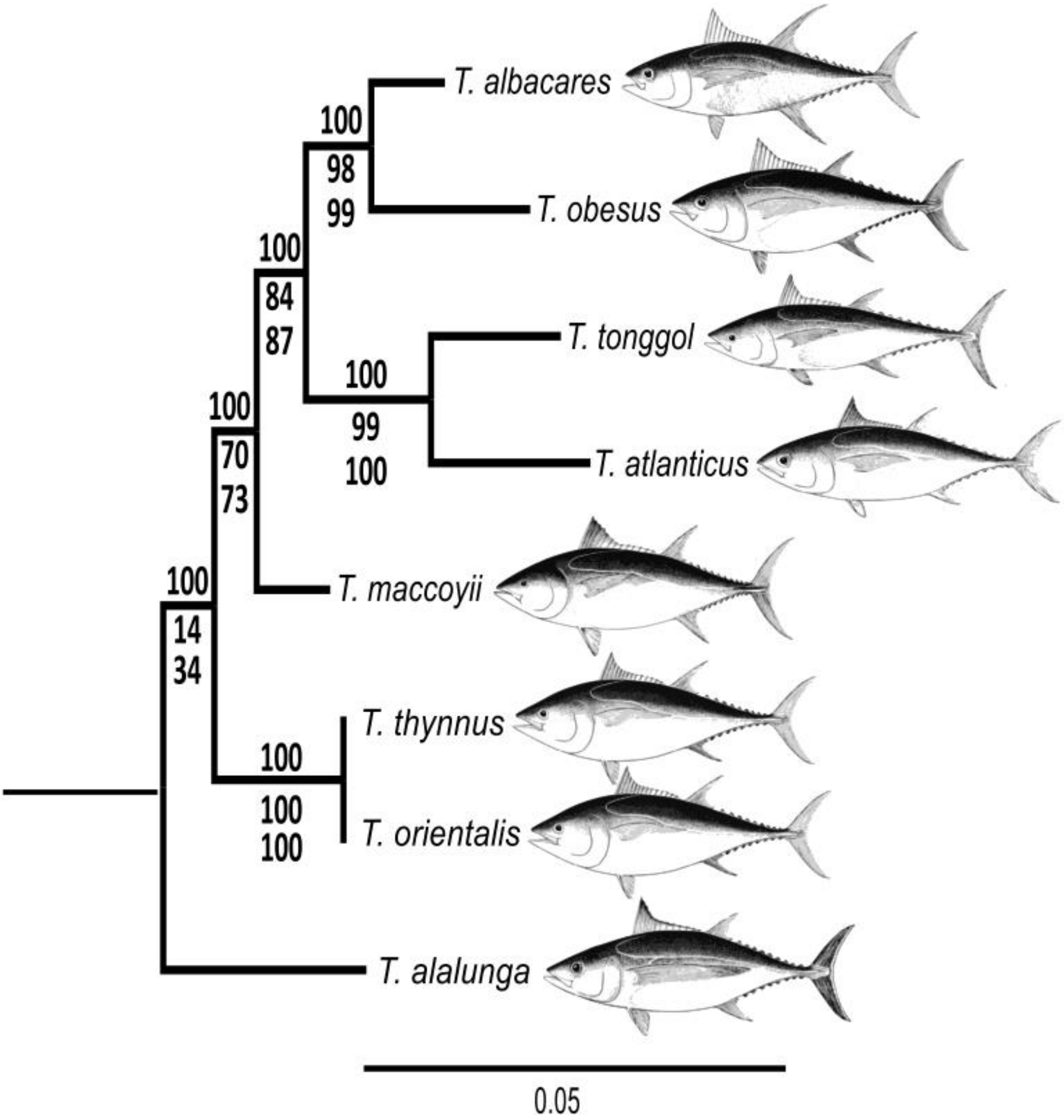

Figure 2. *Tree obtained from the analysis corresponding to M=2, n=8, IUPAC encoded sites selected per species allowing 75% of missing data that represents topology 1, supported by the majority of the analyses (outgroup has been removed to improve visibility; see Tree 60 in Appendix I). Values above branches indicate bootstrap values and below, percentage of analyses that support that branch at BV > 95 % (above) or BV > 80% (below). The scale bar indicates number of estimated substitutions per site. Images are courtesy of FAO.*

3.4. Relationships between the Atlantic and Pacific bluefin tunas

All species- and individual-based phylogenetic trees (see Appendix I) strongly support, with bootstrap values (BV) of 100%, the sister group of *T. thynnus* and *T. orientalis*, and contradict previous mtDNA-based studies where Atlantic and Pacific bluefin tunas did not cluster as sister species (Chow, Inoue 1993; Chow, Kishino 1995; Takeyama et al. 2001; Alvarado Bremer et al. 2005; Viñas, Tudela 2009). Some authors have hypothesized mitochondrial introgression events between different *Thunnus* species as the main reason for discordances between mtDNA and nuclear DNA-based inferred relationships (Chow et al. 2006; Viñas, Tudela 2009). This is supported by our analyses as the comparative study of the COI sequences revealed two *T. thynnus* individuals with introgressed mitochondrial DNA (Supplementary Figure 1) that had no phylogenetic relationships with *T. alalunga* or *T. orientalis* in the nuclear DNA-based phylogenetic trees. Attending to morphological features (Gibbs Jr, ColleTTE 1967) and allozyme and mitochondrial molecular markers (Collette, Reeb, Block 2001), the Atlantic and Pacific bluefin tunas have been considered as two different subspecies; yet, this has been questioned after their ITS1 nuclear marker sequences were found nearly identical (Chow et al. 2006). In our study, most analyses support the respective monophylies of *T. thynnus* and *T. orientalis*, with only some trees based on the smallest matrices not providing support for either of the two monophylies (Table 1). The fact that these analyses do not provide support for any other alternative grouping and that these two species constitute closely related lineages (Chow et al. 2006; Viñas, Tudela 2009), suggest that finding enough phylogenetic signal to resolve their relationship requires not including distant groups, such as the outgroup, allowing high percentages of missing data in order to allow markers not present in other taxa, and using positions that are heterozygous within individuals and/or variable among species. Additionally, events such as incomplete lineage sorting, introgression or hybridization may hamper phylogenetic inferences (Hou et al. 2015). Resolving the recent evolutionary history of Pacific and Atlantic Bluefin tuna will require further analyses based on more individuals.

4. Conclusions

Our study corroborates RAD-seq as an efficient tool to gather enough phylogenetically informative nuclear markers to resolve relationships among closely related species.

Testing different strategies to select markers to be used for phylogenetic inference, we have observed that, generally, despite including more missing data, bigger matrixes based on variable sites provide higher phylogenetic resolution. Applied to the resolution of the phylogeny of the genus *Thunnus*, our study based on RAD-seq derived genome-wide nuclear markers, redefine the *Neothunnus* group, which should now include *T. obesus*, raising new questions about the evolutionary history and adaptation processes to temperate or tropical waters within the genus *Thunnus*. Additionally, we found markers that support the differentiation of Atlantic and Pacific bluefin tunas, although their classification as two distinct species remains unclear and needs further review. Importantly, the analyses performed and data generated within this study represent a valuable resource for the development of nuclear genetic markers for species identification that, unlike previously developed markers, are valid for both, closely related (*T. thynnus* and *T. orientalis*) or more distantly related species and are not affected by mitochondrial introgression events. Yet, in order to be applicable for fish product traceability and thus assist implementation and enforcement of conservation and management plans these markers should be validated in an alternative set of samples of known origin.

Chapter 3

Determining natal origin for improved management of Atlantic bluefin tuna

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All the Supplementary Information of this manuscript can be found in **Appendix C**.

Abstract

Successful sustainable management of marine fish populations requires that assessed management units (stocks) correspond to biological populations. This issue has long been discussed in the context of Atlantic bluefin tuna (ABFT) management, which currently considers two unmixed stocks while not incorporating that individuals born at each of the two main spawning grounds (Gulf of Mexico and Mediterranean Sea) mix in feeding aggregations throughout the Atlantic. Here, using thousands of highly informative genome-wide markers obtained from larvae and young of the year collected at the main spawning grounds of the species, we provide the first direct genetic evidence for “natal homing” in ABFT. This has facilitated the development of an accurate, cost-effective and non-invasive genetic origin traceability tool that allows for the assignment of catches to population of origin, which is crucial for ensuring an ABFT management based on biologically meaningful stock units rather than simply on catch location.

1. Main text

The fishing industry makes important contributions to the economy, social health and well-being in many countries, but has led to an overexploitation of several fish species (FAO 2016). In order to ensure a sustainable use of these valuable resources, fisheries management strategies need to be formulated and implemented, for which the status (i.e, abundance, levels of mortality, etc.) of fish stocks (management units) needs to be assessed (Musick, Bonfil 2005). Developing successful fisheries management measures requires reproductively isolated populations be assessed as independent stocks (Reiss et al. 2009). Yet, marine fish stock definition is not trivial, as intermediate scenarios that lie between full random mating (panmixia) and no genetic exchange among populations are frequent and not easy to discern. This seems to be the case of the iconic Atlantic bluefin tuna (ABFT), *Thunnus thynnus*, a highly migratory large pelagic fish that inhabits the North Atlantic Ocean and adjacent seas (Mather, Mason, Jones 1995; Fromentin, Powers 2005), and whose sustainable management is a priority due to high demand in the growing globalized fish market (Sissenwine, Pearce 2017).

Since the early 1980s, management of ABFT has considered two stocks separated at the 45°W meridian. The division was based on the recognition of two main spawning grounds, the Gulf of Mexico and the Mediterranean Sea (Fromentin, Powers 2005), and on the assumption of no or low levels of mixing between the two. Yet, tagging surveys (Lutcavage et al. 1999; Galuardi et al. 2010; Arregui et al. 2018) and ear stone (otolith) chemistry analyses (Rooker et al. 2008; Rooker et al. 2014) have challenged this management delineation by demonstrating regular and frequent trans-Atlantic migrations of ABFT adults while also suggesting that individuals return to their birth place to spawn (Block et al. 2005; Rooker et al. 2014). This process, termed "natal homing" would imply that ABFT should be managed as a mixed stock fishery (*i.e.*, that composed by spatio-temporally defined aggregations of individuals from different biological populations), which would require individuals caught in the mixing areas be assigned to their birth location.

Genetic analyses could provide the decisive line of evidence of natal homing in ABFT, but studies performed so far have been based on a few number of markers that do not allow developing a traceability panel (Alvarado Bremer et al. 2005; Carlsson et al. 2007; Boustany, Reeb, Block 2008), and have not considered a recently discovered potential alternative spawning location within the Northwest Atlantic Ocean (Richardson et al. 2016a). This lack of genome-wide based evidence for the homing hypothesis has prevented the development of the standardized, reliable and cost-effective origin traceability tool needed for implementing a mixed-stock management approach in ABFT.

Here, we have performed population genetic analyses based on hundreds of reference samples (*i.e.* larvae and young of the year, assumed to be found at or close to the area where they were spawned) and thousands of genome-wide Single Nucleotide Polymorphism (SNP) markers. Our analyses provide solid direct genetic evidence of natal homing in ABFT. From this, we have derived a genetic traceability tool that we have used to map the natal origin of one thousand ABFT individuals caught in the mixing areas throughout the Atlantic Ocean as well as of larvae and young of the year from outside the Gulf of Mexico and Mediterranean Sea, including recently found larvae from the Slope Sea (Richardson et al. 2016a). The accurate and cost-effective genetic stock assignment tool developed here allows separating ABFT catches into two biologically meaningful units so that accurate stock assessments can be performed on each of them, allowing an efficient sustainable management strategy.

2. Materials and Methods

A detailed description of the methodological procedures as well as schematic representation of the samples used, and approach followed throughout the study are provided as WebPanel 1.

Larvae, young of the year, juveniles and medium to large adult ABFT (*Thunnus thynnus*) samples were obtained from scientific surveys and commercial fisheries operating throughout the species distribution range, including spawning grounds (WebTables 1-5). Genomic DNA was extracted from tissue or larvae samples and used for generation and sequencing of Restriction-site-associated DNA (RAD-seq) libraries. Generated RAD-tags were quality filtered and used for SNP discovery and genotyping. About ten thousand SNPs passing quality filters and 204 samples (26 from the Gulf of Mexico, 13 from the Slope Sea, and 68, 48 and 49 from the Western, Central and Eastern Mediterranean respectively) were used for deciphering ABFT population structure based on principal component analyses (PCA) and Bayesian clustering of individuals into potential ancestral populations. Based on the populations identified in the PCA and Bayesian clustering analyses, SNPs were ranked according to their differentiation level among populations, and the 230 most discriminant (WebTable 6) were genotyped in a new set of samples for technical and biological validation. From them, the 96 most discriminant (WebTable 7) were genotyped in an additional set of known-origin reference samples for assessing their assignment power as percentage of correctly assigned samples. All reference samples of known origin genotyped for this final set of 96 SNPs constituted a baseline of 646 samples that was used for assignment of 940 adults of unknown origin collected at feeding aggregates and of 21 larvae and young of the year collected at or near potential spawning grounds.

3. Results

3.1. First direct genetic evidence of natal homing in ABFT

Our population genetics analyses, based on thousands of genome-wide markers discovered and genotyped through RAD-seq (see WebPanel 2 for details) from more than 200 ABFT larvae and small young of the year, show differentiation among Northwest Atlantic (including Gulf of Mexico and Slope Sea) and Mediterranean Sea locations (Figure 1). In the Bayesian analysis, despite all individuals displaying admixed representation of each of the two hypothetical ancestral populations, samples generally cluster by assumed stock, and probability of belonging to one of the two hypothetical ancestral populations is significantly different between the Northwest Atlantic and the Mediterranean Sea (p value = 2.2×10^{-16}). This genetic differentiation between the two main spawning grounds coupled with the reported extensive trans-Atlantic migrations of ABFT supports the natal homing hypothesis. On each side of the Atlantic Ocean, distinct patterns of genetic differentiation emerged. The Mediterranean Sea samples appear genetically indistinguishable, supporting current paradigms (Arrizabalaga, et al.

2018) and contradicting previous findings based on a few markers (Carlsson et al. 2007; Boustany, Reeb, Block 2008; Riccioni et al. 2010). In contrast, the Gulf of Mexico larvae and the Slope Sea young of the year show genetic differentiation in both the Bayesian analyses (their distributions of belonging to one of the two hypothetical ancestral populations differ; p value=0.047) and the principal component analyses (some Slope Sea samples overlap with the Mediterranean Sea ones), highlighting the need for further studies to decipher the western, eastern or mixed population of origin of Slope Sea larvae.

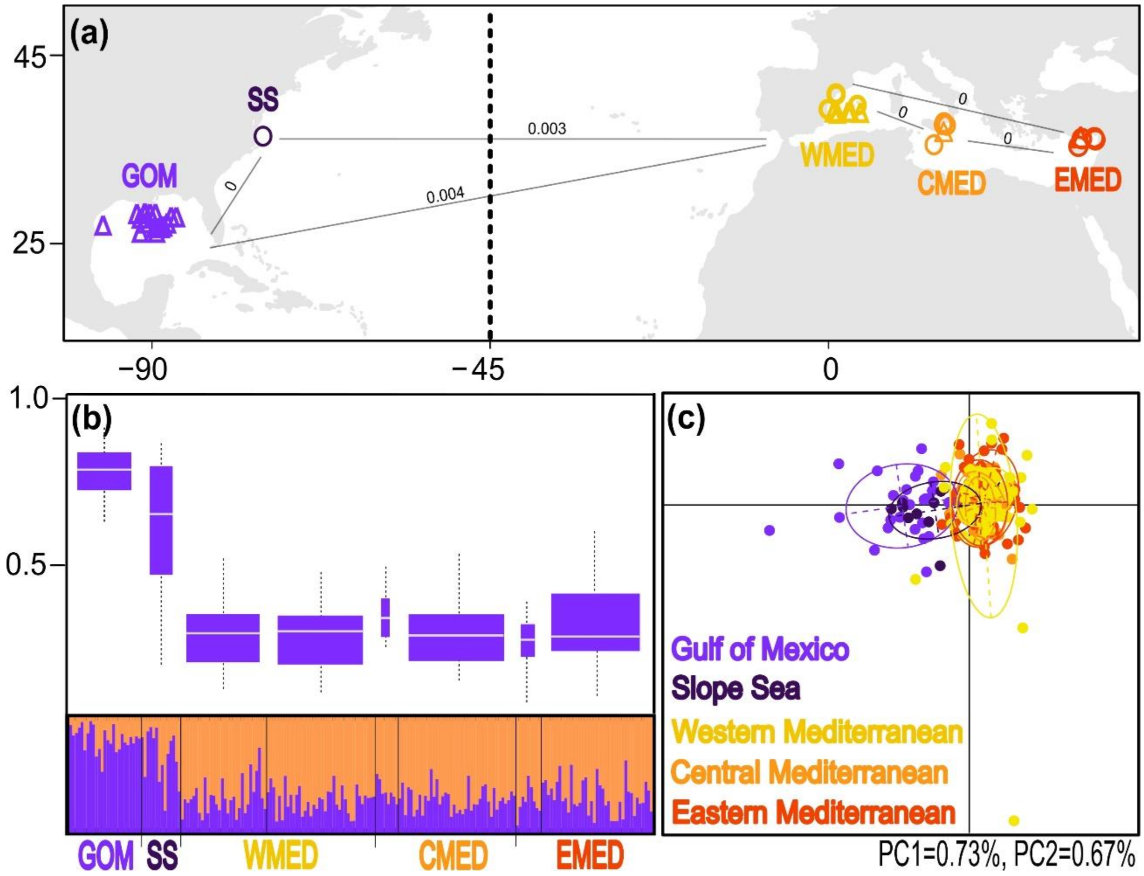


Figure 1. Genetic differentiation among main spawning grounds. *a) Map showing the stock delimitation meridian and depicting the locations where reference samples used for population genetics analyses were collected;* F_{ST} *values (rounded to three decimals) among each pair are indicated; triangles denote larvae and circles, young of the year. b) Graphical representation of the Bayesian clustering approach, where each bar represents an individual and each color, its inferred membership to each of two potential ancestral populations (K=2); boxplots, sized proportionally to number of individuals, illustrate assignment of individuals from each location to one of two hypothetical*

ancestral populations; for the different Mediterranean locations, larvae and young of the year are situated left and right of the black line respectively. c) Principal Component Analysis (PCA) of allele frequencies; the first two principal components are shown; each dot represents one sample colored according to its area of origin. Ovals represent 95% inertia ellipses. Based on catalog 1 (see WebFigures 1 and 2 and WebTable 8 for all catalogs).

3.2. Development of an origin traceability tool for improving ABFT management

The confirmation of natal homing by our population genetics study allowed us to develop an accurate and operational origin traceability tool. For that aim, we selected and validated a subset of stock differentiating SNPs (see WebPanel 3 for details) and included the 96 most discriminant in a genetic stock identification panel. SNP panel validation conducted on a reference set of samples excluded from SNP discovery or selection resulted in 81% and 83% of the Gulf of Mexico and Mediterranean Sea origin samples being correctly assigned, 10% and 2% incorrectly assigned and 9% and 15% unassigned respectively (Figure 2A). Despite the good performance of our assignment panel (89 and 98% of the samples with assignment score higher than 80% are correctly assigned to the Gulf of Mexico or Mediterranean Sea respectively) compared to previous endeavors (Puncher et al. 2018), there are samples that indicate a different origin from the region from where they were collected, consistent with the pattern observed in the principal component analysis (PCA) of allele frequencies of our baseline samples (Figure 2B). Interestingly, the 95% confidence ellipses of each spawning component showed low overlap compared to that observed using otolith chemistry (Rooker et al. 2008; Rooker et al. 2014), suggesting higher discriminant power of SNP markers for origin assignment of ABFT.

Similar to otolith chemistry analyses, SNPs based traceability is better for samples collected in the Mediterranean Sea *versus* the western Atlantic and is not 100% in either case. This could be compatible with a fraction of individuals spawning in a different area from which where they were born, which, due to the larger biomass of the eastern stock (estimated to be ten times larger than that of the western stock), would mean more

Mediterranean origin individuals not returning to their birth area. Another explanation could be the limited number of Gulf of Mexico and Slope Sea samples used for the first SNP selection, which could have not been enough to capture the whole diversity of this area. Finally, we could also argue that our SNP panel is not able to capture the entire genetic diversity to perform a perfect assignment due to a limited number of markers, which could be possible if allele fixation is still incomplete due to a recent separation among stocks (Alvarado Bremer, et al. 2005). If this were the case, increasing the SNP number would lead to an increased assignment power, while we observe that the maximum assignment power was attained with as low as 36 SNPs markers if the most discriminant among the 96 were chosen (Figure 2C).

3.3. Mapping the origin of ABFT mixing aggregates

Origin assignments using the newly developed 96 SNP panel suggest that most individuals caught in each area originate from their closest spawning ground (Figure 3). The proportion of western origin ABFT in eastern fishing grounds varied between 0 and 9% (average of 4%), and proportion of eastern origin ABFT in western fishing grounds varied between 23 and 56% (average of 37%). Individuals caught in Norway (close to the northern distribution limit of the species) and Mauritania (where ABFT observations are very rare), whose stock of origin has never been studied before, seem to be mostly of Mediterranean Sea origin. The proportion of western origin fish in other Eastern regions (Central Atlantic, Bay of Biscay, Gulf of Cadiz, Strait of Gibraltar, Morocco and Canary Islands) is comparable with previous estimates using otolith chemistry (Rooker et al. 2014). The origin of individuals caught west of the 45°W meridian is more variable between regions, and the proportion of Mediterranean Sea origin is highest in the Central Atlantic and lowest in the Newfoundland-Labrador area. Strikingly, the Gulf of St. Lawrence shows a surprisingly high proportion of Mediterranean Sea origin ABFT individuals, which can be due to the greater abundance of the eastern population, such that even relatively low migration rates can result in a high proportion of Mediterranean Sea origin fish in this area.

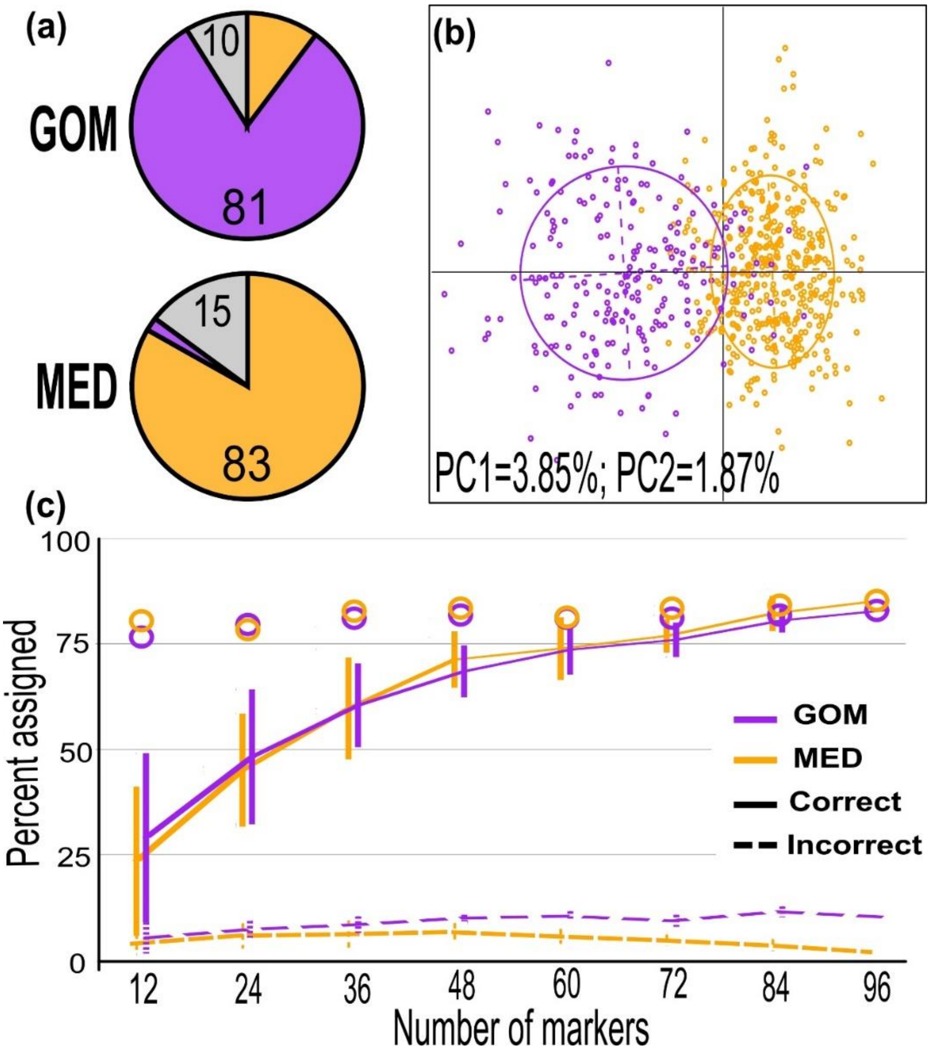


Figure 2. Composition of the genetic baseline and origin assignment success rates. *a) Percentages of correct or incorrectly assigned samples for reference samples captured in the Gulf of Mexico (GOM) and the Mediterranean (MED); purple indicates Gulf of Mexico origin, orange, Mediterranean origin, and grey, unassigned samples. b) Principal Component Analysis (PCA) of allele frequencies of the Gulf of Mexico (purple) and Mediterranean (orange) individuals included in the baseline; the first two principal components of the PCA are shown; each dot represents one sample, and ovals represent 95% inertia ellipses. c) Evolution of the percentage of correctly or incorrectly assigned Gulf of Mexico (purple) and Mediterranean (orange) origin samples as number of SNPs used increases; vertical bars indicate standard deviation and dots, correct assignment rates for the most discriminant subsets of SNPs. Panels A and C are calculated for an 80% assignment score threshold; see WebFigure 3 for 70 and 90% assignments scores as well as for sensitivity and specificity analyses of each threshold.*

For the first time, larvae and young of the year caught in two potential spawning areas outside the Mediterranean Sea and Gulf of Mexico have been genetically analyzed. All confidently assigned Canary Island individuals have similar genetic signals as fish of Mediterranean Sea origin. These islands have already been suggested as a potential spawning area (Mather, Mason, Jones 1995); however, it is unclear if the young of the year found here are from natal sites in the eastern Atlantic Ocean or migrants from the Mediterranean Sea. On the other hand, the larvae caught in the Slope Sea were assigned to both main spawning areas. Given the distance to the two main spawning grounds and estimated larval age (less than four days), it is not possible that these larvae were spawned in the Gulf of Mexico or the Mediterranean Sea. Instead, these results suggest more complex scenarios: i) the Slope Sea spawners are part of a single population that includes fish born in the Mediterranean Sea; ii) the Slope Sea spawners are part of a single population that includes fish born in the Gulf of Mexico; iii) the Slope Sea spawners form an independent population; iv) individuals from the Gulf of Mexico and Mediterranean Sea use this area independently as an alternative spawning site or v) individuals from the Gulf of Mexico and Mediterranean Sea interbreed in this area. Further targeted genetic studies are needed to test these hypotheses and shed light on the contribution of the Slope Sea and other Atlantic Ocean spawning areas.

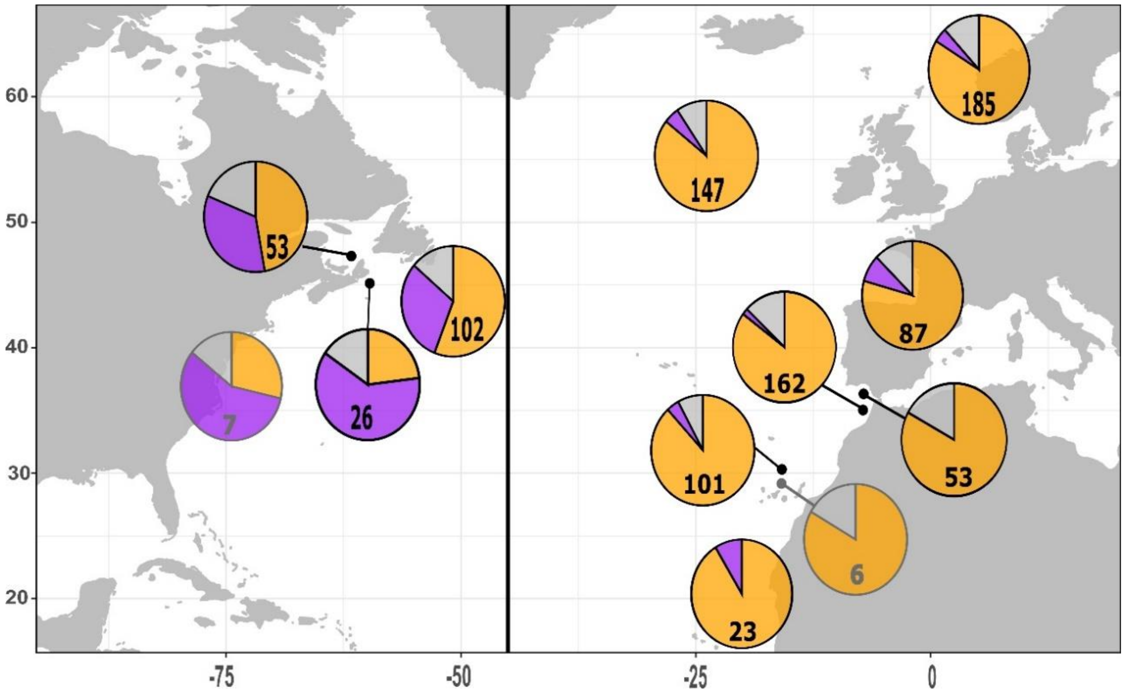


Figure 3. Origin assignment of mixing aggregates and reference samples from outside main spawning grounds. *Proportion of samples assigned to the Mediterranean (orange) or Gulf of Mexico (purple). Black outline indicates mixing aggregates; grey outline indicates Slope Sea larvae and Canary island young of the year. Number of samples analyzed per location are indicated.*

4. Discussion

The assessment and management of ABFT have been hindered for decades due to an incomplete understanding of the species' complex migratory patterns. Spatial dynamics is especially important for the assessment and management of the western stock (Morse et al. 2018), which is estimated to be an order of magnitude smaller than the eastern stock. Given the extensive and interannually variable mixing across the Atlantic (Galuardi et al. 2010; Arregui et al. 2018; Arrizabalaga et al. 2018), the hypothesis behind the current management approach, where fish caught west of the 45°W meridian are assigned as western origin and *vice versa* is not valid. Instead, an appropriate management approach should rely on a tool that accurately and cost-effectively assigns

ABFT catches to a given stock based on where they were spawned and not on where they were caught.

The SNP panel presented here allows the annual assignment of catches to population of origin within the same turn-around time at which ICCAT currently provides annual catch estimates, allowing for timely catch reporting in terms of biologically meaningful stock units rather than broad spatial areas. Our SNP panel is based on a solid sample baseline, provides accurate origin assignment and is cost-effective (less than US$10 per sample (Campbell Nathan, Harmon Stephanie, Narum Shawn 2014)). Moreover, this non-invasive tool can be operationalized to screen the origin of international catches following an easy sampling protocol and without affecting the market value of the fish. This facilitates mixing based assessment approaches (Taylor et al. 2011) that can capture stock specific productivity dynamics and tailor management advice for each stock. Additionally, while the current management regime only allows for area-based quotas to be implemented, which is ineffective for ensuring sustainable population harvesting, an operational implementation of the genetic tool developed here would allow for population specific quotas, which is critical for effective management of ABFT. This new genetic tool comes at an opportune time as alternative management strategies are under consideration by ICCAT (Carruthers et al. 2016), that could include management approaches based on monitoring of population-specific exploitation rates (Bradbury et al. 2014). This scientific achievement is relevant for ABFT fishery managers, who will now see their management actions have the expected impacts on ABFT populations.

Additionally, our research also represents a promising avenue for all other mixed stock fisheries around the world. Unfortunately, it is very common that stock boundaries do not correspond to true biological populations (Reiss et al. 2009). Consequently, management actions do not have the expected impacts (e.g. on recovery of overfished stocks) and mismanaged populations remain at risk. Developing genetic tools to assign the catch to the correct population will allow for a more effective fisheries management worldwide.

Chapter 4

Contemporary unidirectional trans-Atlantic gene flow and a recently originated mixed spawning area shape the genetic connectivity of Atlantic Bluefin tuna

This chapter is in preparation for submission to a scientific journal:

Diaz-Arce, N., *et al.* Contemporary unidirectional trans-Atlantic gene Flow and a recently originated mixed spawning area shape the genetic connectivity of Atlantic bluefin tuna.

All the Supplementary Information of this manuscript can be found in **Appendix D**.

Abstract

The Atlantic bluefin tuna (ABFT, *Thunnus thynnus*) is considered as two demographically independent populations for the purpose of management: East and West, separated by the 45°W meridian and assumed to spawn respectively in the Mediterranean Sea and the Gulf of Mexico. However, evidence of regular and frequent trans-Atlantic movements involving stock-mixing in the North Atlantic and the unknown origin of a newly discovered spawning ground in the Slope Sea (between the Gulf Stream and the northeast U.S. continental shelf) challenge the current two-stocks based management strategy. Using thousands of single nucleotide polymorphisms (SNPs) discovered through Restriction Associated DNA sequencing (RAD-seq) of five hundred larvae, young of the year and spawning adult ABFT samples covering the three spawning grounds and including individuals of other *Thunnus* species, we have studied the population structure and genetic connectivity of Atlantic bluefin tuna, integrating information of possible signs of inter-species introgression. We found i) Mediterranean-like individuals in the Gulf of Mexico, ii) that the Slope Sea is a genetically intermediate population between the genetically differentiated Mediterranean and Gulf of Mexico populations, iii) signatures of introgression from albacore tuna (*Thunnus alalunga*) in the ABFT nuclear genome occurring at different intensities between populations, and iv) genomic signatures of natural selection in a chromosomal inversion of albacore tuna origin present at highest proportions in the Mediterranean population. Altogether, these results support strongly asymmetric trans-Atlantic gene-flow from the Mediterranean to the Atlantic spawning grounds. Our findings highlight the need to revisit ABFT management strategies integrating a comprehensive view of population mixing dynamics.

1. Introduction

The Atlantic bluefin tuna (ABFT, *Thunnus thynnus*) is a large and highly migratory species that inhabits waters of the North Atlantic Ocean and adjacent seas (Fromentin, Powers 2005). Decades of fishing activity have led to the overexploitation of this great commercial pelagic species, which, as recently as 2011 was considered endangered (Collette et al. 2011) but has during the last years experienced signs of substantial population increase at least in some population components (ICCAT 2017). ABFT is currently managed by the International Commission for the Conservation of Atlantic Tunas (ICCAT) as two separated management units: the Western and Eastern stocks which are separated by the 45°W meridian boundary and are assumed to originate from the two main spawning areas located in the Gulf of Mexico and the Mediterranean Sea, respectively (ICCAT 2019). Several studies on the population structure and dynamics of the species using different techniques such as electronic tagging (Block et al. 2005), otolith chemical signature (Rooker et al. 2014) or genetic markers (Puncher et al. 2015; Rodríguez-Ezpeleta et al. 2019) support the demographic uncoupling of the two spawning components (Gulf of Mexico and the Mediterranean Sea) . No individuals have been recorded to visit both spawning areas (Block et al. 2005), and otolith chemistry signatures (Rooker et al. 2014) and genetic differentiation support natal homing behaviour (Rodríguez-Ezpeleta et al. 2019). However, all these studies and past ones as well, found evidence for regular events of trans-Atlantic movements crossing the 45°W meridian boundary line between the two assumed stocks and mixing in foraging grounds along the North Atlantic. Nonetheless, the extent of stock mixing and connectivity at odd with current stock management remains unknown.

In the midst of this uncertainty about the stock dynamics, the implications of a new recently found larvae of ABFT in the Slope Sea (Richardson et al. 2016a) generated great debate and controversy (Safina 2016; Walter et al. 2016) with one of the key unknowns being the origin of the Slope Sea larvae. Although subsequent work has documented that young of the year (YoY) captured in the mid-Atlantic areas were born at times consistent only with Gulf of Mexico birth origin (Arai, Graves, Secor 2020), the finding of these larvae in the Slope Sea which clearly indicated spawning activity in this area (Richardson et al. 2016b), coupled with satellite tagging indicating usage of this area by spawning size fish (Galuardi et al. 2010), inspired an hypothesis of age-structured spawning of the Western stock individuals which would use the Slope Sea spawning area at younger ages, which remains untested.

In addition to this, previous studies based on mitochondrial genetic markers detected mitochondrial introgression from albacore tuna (*Thunnus alalunga*) in a small percentage of Atlantic Bluefin tuna individuals (Alvarado Bremer et al. 2005; Viñas et al. 2011; Díaz-Arce et al. 2016), but the exact origin and the potential influence of this introgression on the evolution of the species is unknown. It is known that introgression between species can lead to different phenomena relevant to understand species structure and connectivity such as triggering genomic evolution (Jay et al. 2018) or the incorporation of adaptive traits (Taylor, Larson 2019).

In order to disentangle the population structure and connectivity of ABFT, here we genotyped thousands of SNPs discovered thought Restriction Associated DNA sequencing (RAD-seq) of five hundred ABFT, including larvae, young of the year (YoY) and adult samples covering the three spawning grounds. We also analysed individuals of other *Thunnus* species to test for and quantify inter-species introgression. We detected ongoing asymmetric migration occurring from the Mediterranean to the Atlantic spawning grounds and determined that the intermediate genetic composition of the Slope Sea samples results from admixture between the Mediterranean and Gulf of Mexico ancestral populations. We reported a signal of nuclear introgression from albacore into the Atlantic bluefin tuna and identified a chromosomal inversion of albacore origin containing genomic signature of natural selection. We hypothesized that the observed genetic differentiation between the Mediterranean and the Atlantic populations despite evidence for ongoing gene-flow could be due to genetic isolation followed by a recent intensification of migration rates towards the Atlantic spawning grounds, exposing this populations to a risk of genetic erosion. Our study improves knowledge on the population dynamics of the species and calls for reappraisal of ABFT fisheries management strategy.

2. Material and Methods

A summarized schematic view of samples used and methods applied is included in Figure S1.

2.1. Tissue sampling and DNA extraction

Larvae, young of the year and adult samples from ABFT were obtained from scientific surveys and commercial fisheries (Table S1) from the three known spawning grounds of the species (Figure S2). From each fish, a ~1cm^3 piece of muscle or fin tissue sample was excised and immediately stored in RNA-later or 96% molecular grade ethanol at -20ºC until DNA extraction. Larvae were collected with a 60 cm diameter bongo net or a 2 x 1 meter frame net and immediately preserved in molecular grade ethanol 96%. Genomic DNA was extracted from about 20 mg of tissue or from whole or partial larvae (eyeballs or tails) using the Wizard® Genomic DNA Purification kit (Promega, WI, USA), following manufacturer's instructions for "Isolating Genomic DNA from Tissue Culture Cells and Animal Tissue". Extracted DNA was suspended in Milli-Q water and concentration was determined with the Quant-iT dsDNA HS assay kit using a Qubit® 2.0 Fluorometer (Life Technologies). DNA integrity was assessed by electrophoresis, migrating about 100 ng of GelRed™-stained DNA on an agarose 1.0% gel.

2.2. COI sequence amplification

A fragment of the cytochrome oxidase subunit I (COI) gene was amplified from 86 *T. thynnus* individuals (37 from the Mediterranean Sea, 16 from the Slope Sea and 33 from the Gulf of Mexico; see Table S1) using the FishF1 (5ˈ-244 TCAACCAACCACAAAGACATTGGCAC-3ˈ) and FishR1 (5ˈ-TAGACTTCTGGGTGGCCAAAGAATCA-3ˈ) primers (Ward et al. 2005). Amplification was performed in a total volume of 20 µl with 0.2 µl of Dream Taq Polymerase (Thermo Fisher Scientific), 2 µl of Dream Taq Buffer 10X (Thermo Fisher Scientific), 0.4 µl of each primer and 50 ng of total DNA using the following profile: an initial denaturation step at 95°C during 3 min, 35 cycles of 30 sec at 98°C, 30 sec at 54°C and 60 sec at 72°C, and a final extension of 72°C for 10 minutes. Products were visualized on 1.7% agarose gels, purified with GE Healthcare Illustra ExoProStar™ (ref. US77705) and Sanger sequenced.

The newly generated 86 sequences were edited using SeqTrace 0.9.0, submitted to Genbank (Accession numbers MT037084- MT037149, MT037151-MT037170) and aligned with BioEdit (v7.2.5) together with other publicly available COI sequences of albacore (accession numbers KT074094-KT074102, KP975846-KP975848, KJ709651, KC501673- KC501692, KC015952, KC015953, DQ835818-DQ835824, LN908908, LN908909, KY984977, KY656479, KU945044, EU752221-EU752223, HM007772-HM007774, KU168615-KU168617, HQ167713, GQ414571, GQ414565, FJ605767, FJ605798, FJ605804, FJ605808, JQ624006, KP330355- KP330357, KM055416, JN007752-JN007761, KF544951, KF597027, DQ107645-DQ107647, DQ107658, DQ107659, MT037065-MT037069), Pacific bluefin tuna (accession numbers DQ107581, DQ107590-DQ107592, DQ107631, MT037070-MT037074) and ABFT (accession number NC004901, DQ107585-DQ107587, DQ107589, GQ414568, GQ414569 , MT037075-MT037081), including the alalunga-like (accession number GQ414567, GQ414572, MT037082, MT037083) and the Pacific-like (accession number GQ414573) haplotypes. Diagnostic positions indicating mitochondrial introgression from albacore were identified as those that cluster some of the ABFT samples with albacore or Pacific bluefin and not with the rest of the ABFT.

2.3. RAD-seq libraries preparation and sequencing

Restriction-site-associated DNA libraries of 527 ABFT individuals (Table S1) were prepared following Etter et al. (2012). Starting DNA (ranging from 50 to 500ng) was digested with the *SbfI* restriction enzyme and ligated to modified Illumina P1 adapters containing 5bp unique barcodes. Pooled DNA of 32 individuals was sheared using the Covaris® M220 Focused-ultrasonicator™ Instrument (Life Technologies) and size selected to 300-500 pb by cutting agarose migrated DNA. After Illumina P2 adaptor ligation, each library was amplified using 14 PCR cycles. Each pool was paired-end sequenced (100 pb) on an Illumina HiSeq2000.

2.4. RAD-tag assembly and SNP calling

Generated RAD-tags were analyzed using *Stacks* version 2.3e (Catchen et al. 2013). Demultiplexing and quality filtering were performed using *process_radtags* truncating all reads to 90 nucleotides to remove low-quality bases at the end of reads. Only those reads whose forward and reverse pairs passed quality filtering were kept, and PCR duplicates were removed applying *clone_filter*. Reference based assembly was performed by mapping the passing-filter reads of Atlantic bluefin tuna generated here as well as those of 4 Southern bluefin tuna (*Thunnus maccoyii*), 4 albacore (*Thunnus alalunga*) and 5 Pacific bluefin tuna (*Thunnus orientalis*) available from (Díaz-Arce et al. 2016) (Table S1) to the least fragmented available reference genome of Pacific bluefin tuna (Suda et al. 2019) and to the ABFT mitochondrial genome (accession number NC_014052) using the BWA-MEM algorithm (Li 2013). Using SAMTOOLS (Li et al. 2009), the resulting SAM files were converted to BAM format, sorted and indexed. Mapped reads were filtered to include only primary alignments and correctly mate mapped reads, and SNPs from the nuclear genome were called using *gstacks* generating two catalogs, including and excluding individuals from the other *Thunnus* species. To ensure that population structure inferences were not biased by the use of a reference genome from a different species, de novo assembly was performed for result comparison including only samples from ABFT. Only forward reads were used to build loci with *ustacks,* setting a minimum coverage depth (m) of 3 reads per allele and a maximum number of 2 nucleotide mismatches (M) between two alleles at a same locus. A catalog of RAD loci was generated using *cstacks,* allowing a maximum number of 6 mismatches between two individuals homozygous for different alleles (n). Individual RAD loci were matched against the catalog using *sstacks*, data were stored by locus and SNPs were called using information from paired-end reads using *tsv2bam* and *gstacks*. Stacks parameters (m, M and n) were selected based on previous analyses from (Rodríguez-Ezpeleta et al. 2019). The following steps were applied to both mapped and de novo catalogs. Only samples with more than 25,000 RAD loci were kept (Table S1) and only SNPs contained in RAD-loci present in at least 75% of the bluefin tuna (mapped and de novo) or in 75% of the individuals from each of the species included (mapped) were kept and exported into PLINK (Purcell et al. 2007) using *populations*. To avoid potential erroneous SNPs derived from read 2, only SNPs located in the first 90 bp of each contig were considered. Increasing threshold values for minimum genotyping rate for individuals and SNPs were applied to obtain a final genotype table with a minimum genotyping rate of 0.90 and 0.80 per SNP and individual respectively. SNPs with a minimum allele frequency smaller than 0.05 within ABFT (except when the minor allele had a minimum allele frequency over 0.25 in at least one of the other species for the catalog including the other species) and which failed Hardy Weinberg equilibrium test at $p < 0.05$ in the group composed by Mediterranean larvae and young of the year or in that composed by Gulf of Mexico larvae were removed. Resulting genotype tables including all SNPs or only the first SNP per tag were converted to *genepop*, *structure*, PLINK, *BayeScan*, *immanc*, VCF and treemix formats using populations and PGDSpider version 2.0.8.3 (Lischer, Excoffier 2011). Variant calling from the bam files obtained after mapping RAD-seq reads to the reference mtDNA genome was performed with *gstacks* and *populations*. Mitochondrial introgression diagnostic positions were extracted using PLINK (Purcell et al. 2007).

Finally, one extra catalog was generated including only larvae of ABFT from the three different locations and the 4 available individuals of albacore. This catalog was built to maximize the number of variants to generate an unfolded site frequency spectrum of genetic variation between the three different locations of ABFT, and infer their joint demographic history. We used albacore as an outgroup species to polarize variants. Only sites that were not variable within albacore were kept to determine the most parsimonious ancestral alleles. Polymorphic positions not failing H-W equilibrium test in any ABFT location, with a minimum allele count of two, and derived from RAD loci present in at least the 80% of the samples of each group were selected using PLINK and VCFtools and saved in a variant calling format (VCF) file.

2.5. Genetic diversity and population structure estimates

The following analyses were performed on the mapped and de novo RAD-seq ABFT nuclear datasets including only the first SNP per tag. Differentiation was first assessed estimating total and per SNP pairwise F_{ST} values were calculated using GENEPOP (Raymond 1995) both including and excluding adult individuals. Significance ($p < 0.05$) of F_{ST} values was estimated by performing 10,000 permutations. Principal Component Analysis (PCA) were then performed using the *adegenet* R package (Jombart, Ahmed 2011) to illustrate the segregation of individuals. The number and nature of distinct genetic clusters was investigated using the model based clustering method implemented in ADMIXTURE (Alexander, Novembre, Lange 2009) assuming from 2 to 5 ancestral populations (K) and setting 5000 bootstrap runs. A first ADMIXTURE run was launched for each value of K to check the number of steps necessary to reach the default 0.001 likelihood value during the first run. This information was used to set the "-c" parameter (steps to be fulfilled in each bootstrapped run) that would assure convergence for each analysis (from 20 to 100 steps) for the bootstrapped runs. The value of K with lowest associated error value was identified using ADMIXTURE's cross-validation procedure. The convertf function from ADMIXTOOLS software (Patterson et al. 2012) was used to convert from PLINK to eigenstrat format and then the qp3Pop function was used to calculate F3 statistic and Z-score associated values (Patterson et al. 2012), testing for all possible admixture scenarios grouping samples per location and considering adults in separated groups.

2.6. Estimation of recent migration rates

Migration rates between the Mediterranean Sea, Slope Sea and the Gulf of Mexico locations as well as individual ancestries were estimated considering only Larvae and YoY samples using BayesAss v3.04 (Wilson, Rannala 2003) and the reference mapped RAD catalog. Mixing parameters were adjusted by running tests following manual recommendations and the mixing parameters for the allele frequencies, inbreeding coefficients and migration rates were set to 0.2, 0.01 and 0.1 respectively. BayesAss was run executing 10,000,000 iterations and discarding the first 3,000,000 iterations as burn-in and setting the interval between samples of the MCMC to 100. The program was run three times using different subsets of 5,000 randomly selected SNPs.

2.7. Demographic History

The unfolded Site Frequency Spectrum (SFS) for each ABFT location pair was estimated using the allele counts included in the VCF file obtained from the fourth catalog, including only of ABFT larvae and the 4 albacore samples for variant polarization for inference of the demographic history of ABFT.. Allele counts were averaged over all possible resampling of 20 genotypes within each ABFT location and singletons were excluded. Expected joint multi-populations allele frequency spectrum of biallelic variants and model parameters were estimated for 5 different candidate models (Table

S5) using a diffusion approximation approach implemented in δaδi v1.7.0 (Gutenkunst et al. 2009). We adapted some of the available models and applied the optimization routine based on consecutive rounds of optimizations from Portik et al. (2017) to include the three different possible dichotomic origin of the three populations involving two splits, split of the ancestral population simultaneously originating the three populations and a first split originating the Mediterranean and Gulf of Mexico populations and admixed origin of the SS. We tested all models suppressing or allowing inter-population constant migration rates since the time at which all the three populations were originated. All the models include a parameter which reflects the percentage of the variable sites correctly orientated with respect to the ancestral state. Best fit model was assessed using the Akaike information criterion and goodness of fit was analyzed by comparing our empirical SFS against a Poisson's distribution of 100 simulated SFS log-likelihood and log transformed chi-squared test values (Portik et al. 2017).

2.8. Loci under selection

Loci under selection were screened from the mapped and de novo RAD-seq ABFT nuclear datasets using two approaches. The reversible jump Markov chain Monte Carlo approach implemented in BAYESCAN 2.1 (Foll, Gaggiotti 2008) was applied by grouping samples per location setting default parameters of 50000 burn-in steps, 5000 iterations 10 thinning interval size and 20 pilot runs of size 5000. Candidate loci under selection with a posterior probability higher than 0.76 (considered as strong according to the Jeffery's interpretation in the software manual) and a false discovery rate (FDR) lower than 0.05 were selected. The multivariate analysis method, which does not require a prior grouping of the samples, implemented in the pcadapt R package was applied following Luu, Bazin, Blum (2017) recommendations and outlier SNPs were selected following the Benjamini-Hochberg procedure. Contigs built by *gstacks* from de novo catalog in which outlier SNPs were located were mapped to the nuclear reference genome of the Pacific bluefin tuna to identify their positions along the genome. Pairwise linkage disequilibria between all filtered SNPs obtained from the mapped catalog and from those scaffolds which contained SNPs under selection was measured using the R package LDheatmap.

2.9. Tests for nuclear introgression

Nuclear introgression from albacore to ABFT was tested by estimating historical relationships among species and populations using TreeMix (Prickell 2012), which estimates the maximum likelihood tree for a set of populations allowing historical gene flow events. This was completed by the *ABBA/BABA* test (Kulathinal, Stevison, Noor 2009; Green et al. 2010; Durand et al. 2011), which measures the excess of derived alleles shared by the outgroup and one tested group (in this case, one ABFT group) compared with the derived alleles shared by the outgroup and another group taken as a reference (a different ABFT group). For both analyses (Treemix and ABBA/BABA), the first SNP in each tag of the mapped nuclear dataset including other tuna species was used. TreeMix was run allowing from 0 to 10 migration events, obtaining increasing number of possible gene flow events and associated likelihood values. The *ABBA/BABA* test was performed on the allele frequencies of the derived allele in albacore and ABFT locations, based on the ancestral state defined by the outgroup species Southern bluefin tuna. Patterson’s D statistic was calculated using R for all possible combinations of target and reference groups of ABFT, always considering albacore as the donor species.

3. Results and discussion

3.1. RAD-seq read assembly and SNP calling

Five catalogs were constructed from the RAD-seq data (see Figure S1). For the de novo catalog, an average of 87% (SD. 14.1) of the total reads that passed pre-processing filters per sample were clustered into loci, which had an average coverage of 15.5X; the catalog resulted in 411 individuals and a total of 10,208 common loci and 16,369 SNPs. For the ABFT reference mapped catalog, 95.6 % of the reads mapped to the nuclear reference genome and an average of 90.7 % (SD. 2.6) of the mapped reads per sample were clustered into loci, which had an average coverage of 11.4X; the catalog resulted in 463 individuals and a total of 19,291 common loci and 34,919 SNPs. For the reference mapped catalog including all ABFT individuals and other *Thunnus* species, 95.6 % of the reads mapped to the nuclear reference genome and an average of 90.7 % (SD. 2.6) of the mapped reads per sample were clustered into loci, which had an average coverage of 11.0X; the catalog resulted in 486 individuals and a total of 26,080 common loci and

61,393 SNPs. For the reference mapped catalog specifically generated for demographic history inference, 79.6 % (SD. 11) of the reads mapped to the nuclear reference genome and were clustered into loci, which had an average coverage of 16.9X; the catalog resulted in 84 ABFT individuals and a total of 13,238 common loci and selected SNPs. For the catalog mapped to the mitochondrial reference genome, 0.14% of the reads were mapped and an average of 28.18 % (SD. 7.3) were clustered into loci, which had an average coverage of 37.2X; only two tags covered three of the identified position diagnostic for introgression from albacore. Size of each final dataset and steps followed during data analysis are summarized in Figure S1.

3.2. Population structure and contemporary migratory behaviour of ABFT

Principal Component and ADMIXTURE analyses of ABFT populations based on RAD-seq datasets showed the existence of two genetically differentiated groups corresponding to Mediterranean and Gulf of Mexico samples (Figures 1 and S3). Increasing the number of assumed ancestral populations above two (Figure S3 and S4) did not provide with additional sub-structuring, supporting that genetic backgrounds of current ABFT populations derive from two ancestral populations. All pairwise F_{ST} values were very low (lower than 0.004) but significantly different from 0 ($p<0.05$), thus rejecting the hypothesis of panmixia. (Table S3). Consistently with the existence of two main genetic clusters, pairwise F_{ST} values were the highest between Mediterranean Sea and the Gulf of Mexico locations. However, F_{ST} values involving the Gulf of Mexico always decreased if adult individuals were included (Table S3). This was explained by the presence of Mediterranean-like adult individuals within the group of Gulf of Mexico samples, as revealed by both PCA and ADMIXTURE results (Figures 1, S3 and S4). Frequency distribution of the ancestry values of Gulf of Mexico and Mediterranean Sea locations estimated by ADMIXTURE (using the reference mapped catalog and assuming 2 ancestral populations) were statistically different (Kolmogorov-Smirnov D=0.90765, p<2.2e-16). However, both distributions overlapped due to a secondary bump in the right tail of Gulf of Mexico distribution, due to the presence of Mediterranean-like genotypes (Figure 1B). In addition, some adult samples from the Gulf of Mexico were genetically intermediate, possibly reflecting mixed ancestries. Indeed, F3-admixture tests indicate an admixed origin of the Gulf of Mexico adults, but not of Gulf of Mexico larvae (Figure 2A, Table S4). These results thus indicate contrasting ancestries between adults and larvae from Gulf of Mexico.

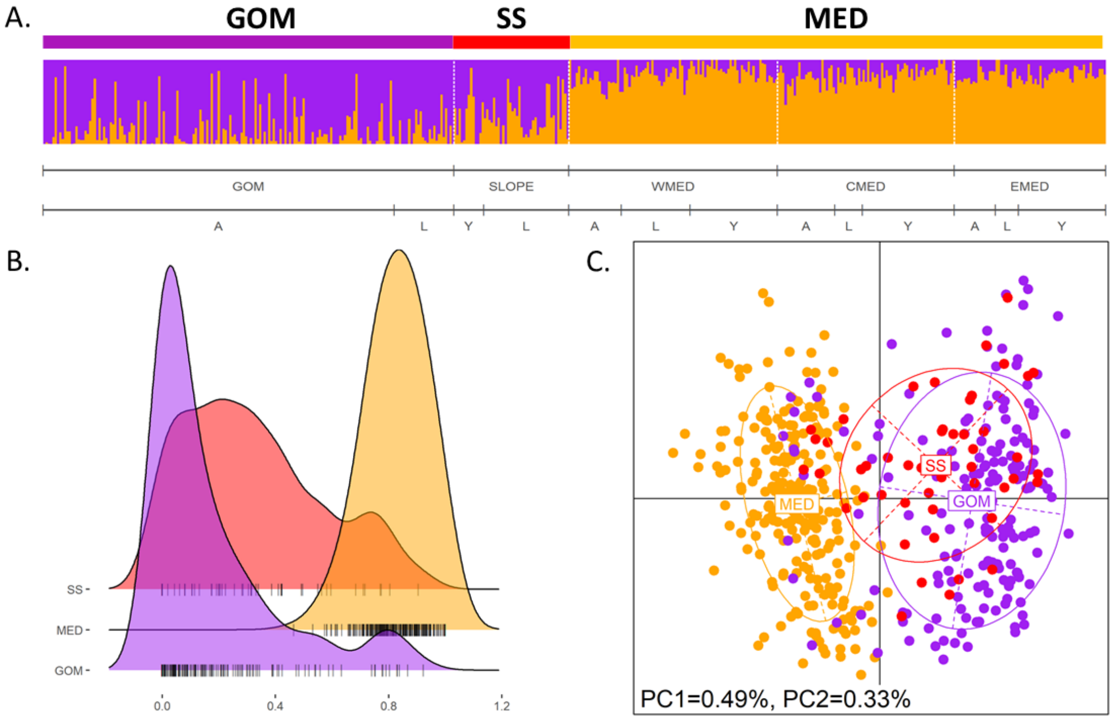


Figure 1. *Population structure of ABFT estimated from the nuclear SNPs mapped to the reference nuclear genome. A. Individual ancestry proportions estimated by ADMIXTURE when assuming two ancestral populations. B. Per location density distribution of individual ancestry proportions shown in A. C. Principal Component Analysis where individuals from the Gulf of Mexico (GOM), the Slope Sea (SS) and the Mediterranean Sea (MED) are represented in purple, red and orange respectively*.

In total, there were 12 adults (and no larvae) samples captured in the Gulf of Mexico for which their membership to the Mediterranean Sea distribution could not be rejected ($p < 0.05$) (see “MED-like” in Table S1). The likely migrant nature of those individuals was also supported by the BayesAss analysis, which provides evidence for contemporary migration from the Mediterranean Sea (Figure 2B, Figure S6). All these individuals were capture inside the Gulf of Mexico (not in Fl keys), and gonad histologic inspection of these 12 individuals revealed that all were spawning capable. Moreover, the only female Mediterranean-like individual caught in the Gulf of Mexico was at vitellogenesis stage 3 and thus assumed to have ovulated within the last 24 hours (postovulatory follicle complexes were observed, which are assumed to degrade within 24-48 h hours, although the exact time is unknown (McPherson 1991; Schaefer 1996; Aranda et al. 2011)) (see Table S2 for reproductive stage of adult samples captured in the Gulf of Mexico). While no ABFT individual has been recorded from tagging data to visit both the Mediterranean Sea and Gulf of Mexico spawning grounds (Block et al. 2005), adult individuals found in the Gulf of Mexico which show a Mediterranean-like genetic profile suggest that migration into the Gulf of Mexico exists. Moreover, the finding of admixed genotypes suggests that this likely results in effective gene flow. In previous studies, genetic assignment of reference samples using a developed SNP panel for differentiation between the Gulf of Mexico and Mediterranean Sea populations was less effective when assigning samples of Gulf of Mexico origin (Puncher et al. 2018; Rodríguez-Ezpeleta et al. 2019). Percentage of fish captured in the Gulf of Mexico that was assigned as Mediterranean using the developed SNP panels were consistent with the proportion of Gulf of Mexico adults with Mediterranean ancestry that we observed in this study, meaning that rather than being incorrectly assigned, these percentages may reflect the presence of incoming migrants to the Gulf of Mexico. Otolith microchemistry measurements available for some individuals included in this study, were compared with the available baseline for measurements of $\delta^{18}O$ and $\delta^{13}C$ for Gulf of Mexico and Mediterranean Sea populations (Rooker et al. 2014) (Figure S7). However, baseline otolith microchemistry composition of both populations overlaps, and measurements available for 5 out of the 12 genetically Mediterranean-like adult individuals caught in the Gulf of Mexico show values within or near this overlap (Figure S7), suggesting that they may belong to a sub-group within ABFT populations of different origin, or characterized by particular migratory patterns during the first months of life. Indeed, the area of the North Atlantic Ocean with predicted values for otolith isotopic composition of oxygen ($\delta^{18}O$) intermediate between the Gulf of Mexico and the Mediterranean Sea spawning areas, reflecting a vast geographical area which includes the Slope Sea spawning area (Trueman, MacKenzie, Palmer 2012).

3.3. Origin and role of the Slope Sea in the ABFT populations connectivity

Individuals collected in the Slope Sea displayed an intermediate genetic composition to Gulf of Mexico and Mediterranean Sea, and a particularly large variance in ancestry ranging from Mediterranean Sea to Gulf of Mexico like profiles (Figure 1, Table S3). Admixed genotypes covered a wide range of ancestry proportions that were consistently assessed by ADMIXTURE and the PCA (Figure S5). Accordingly, F3-admixture tests support an admixed composition of the Slope Sea from the Mediterranean Sea and Gulf of Mexico individuals (Figure 2A, Table S4). Moreover, the inferred proportions of individuals that are migrants from other source locations estimated by BayesAss support a strong contribution of contemporary migration from the Mdediterranean Sea, and to a lesser extent from the Gulf of Mexico (Figure 2B, Figure S6). Therefore, the observed variance in ancestry in Slope Sea likely reflects continuous influx and admixture.

Likewise, all tested versions of the demographic scenarii including migration between locations were better ranked than those that did not include migration (Table S5). The best fit model includes a first split between Mediterranean and Atlantic populations and a second split between the current Gulf of Mexico and Slope Sea populations, allowing for inter-population migration since the second split event. The log-likelihood and log-transformed chi-square's values obtained after fitting the best model to the empirical data fall within the distribution of values obtained from simulated data optimization (Figure S8), indicating that the empirical data fits well within the expected values under the tested demographic model. Divergence time since the second split represents about 6,7% of the divergence since the first split, supporting a relative recent origin of the Slope Sea population within the evolutionary history of the species. The best run for this model supports strong migration rates from the Mediterranean Sea into the two Atlantic populations, relatively high migration rates from the Gulf of Mexico into the Slope Sea, but moderate from the Slope Sea into the Gulf of Mexico, and relatively very weak migration towards the Mediterranean Sea (Figure 2C, Table S5). In general, for all the models the percentage of correctly orientated variants was above 98% (Table S5), suggesting that uncertainties in ancestral state estimation did not affect the inferred direction of asymmetric gene-flow.

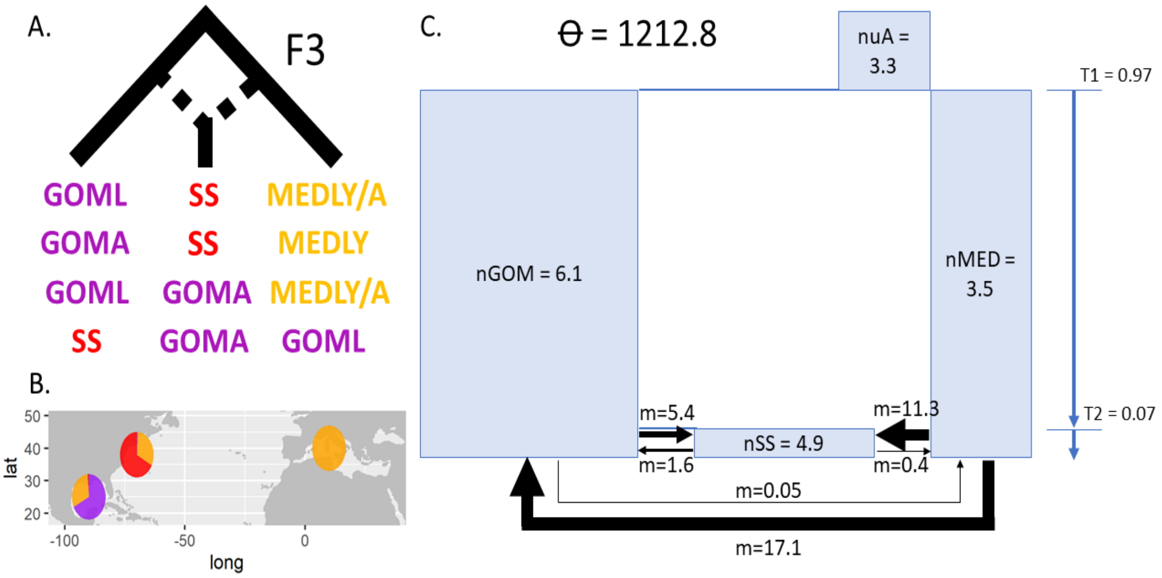


Figure 2. *Genetic and demographic connectivity between the three ABFT spawning grounds. A. Combination tests for which F3-statistic provided with statistically significant (Z< -1.96) negative values, indicating genetic admixture origin of a target population (central branch) from other two source populations (side branches). B. Per-location recent in-migration rates measured as proportion of individuals at each location that are migrants from the other two source locations (pie-charts) estimated by BayesAss. C. Visual representation of the best fit model (split_MED_mig) selected after comparison with the other nine demographic models tested in this study following the Aikaike information criteria. Values for effective populations sizes, migration rates and time estimates since splits are scaled to ϴ (theta).*

The heterogeneous ancestry profile of the Slope Sea, compatible with the three possible F1 parental pair combinations between Mediterranean and Gulf of Mexico individuals, suggest significantly strong contemporary influx of migrants which prevents genetic variation from stabilization. Results from electronic tagging revealed how some adult individuals visiting either the Gulf of Mexico or the Mediterranean spawning grounds routinely visit the recently discovered Slope Sea spawning area (Block et al. 2005), supporting the capability of adult individuals from both populations of spawning in the Slope Sea.

3.4. Genomic signatures of natural selection

Our results that suggest relatively high ongoing migration rates between ABFT populations question how the observed genetic differences can be maintained despite gene flow. Beyond a few dozen migrants exchanged per generation gene-flow readily dilutes genetic differentiation between populations (Lowe, Allendorf 2010; Gagnaire et al. 2015). Although the low F_{ST} values between ABFT populations are common among marine fish species with large population sizes, high rates of dispersal and wide-ranging distributions, the number of migrants detected here should lead to genetic homogeneity. It is thus possible that genetic differentiation observed among samples exists because gene flow is relatively recent relative to mean generation times between 17 and 20 years (ICCAT 2017) nor giving enough time for genetic homogenization. Given the population size of the Mediterranean population, we could be on the cusp of a process of genetic homogenization in Atlantic Bluefin tuna that will not be realized in the spawning population for several more years. As local adaptation can also help maintain genetic differentiation despite high gene-flow (Dionne et al. 2008; Tigano, Friesen 2016), we screened for signatures of natural selection in the genome of ABFT.

PCA performed using only neutral markers still show genetic differentiation and produced a similar pattern to that obtained with the whole dataset (Figure S9). Therefore, while the role of local adaptation mechanisms contributing to population structuring is unknown, this result confirms that the genetic differentiation between the two distinct genetic backgrounds observed in ABFT populations is not only driven by selection.

Regardless of the approach used to seek for outlier loci, candidate SNPs potentially under selection consistently revealed strong structuring that pulls the data towards location or other grouping that does not correspond to the three sampled locations (Figure 3A, Figure S10). Coordinates of the first two PC's from the PCAs performed using the SNP subsets obtained from the different analyses were highly correlated (Figure S10), all analyses showing strong grouping along the first PC (Figure 3A, Figure S10). No library or phenotypic sex effect (Benestan et al. 2017) was related to this grouping (Figures S11 and S12). In all the analyses, the 10% with the highest loadings to the first and second PC consistently mapped to the same two (BKCK01000075 and BKCK01000111) and four (BKCK01000076, BKCK01000100, BKCK01000161 and BKCK01000173) reference scaffolds, respectively, with few exceptions (Table S6). The PCA performed using SNPs selected using PCAdapt from the de novo catalog, showed a different grouping pattern of three differentiated clusters observed along the second PC, whose highest 10% loading SNPs mapped to three reference scaffolds that were exclusive to this analysis (Figure S10, Table S6).

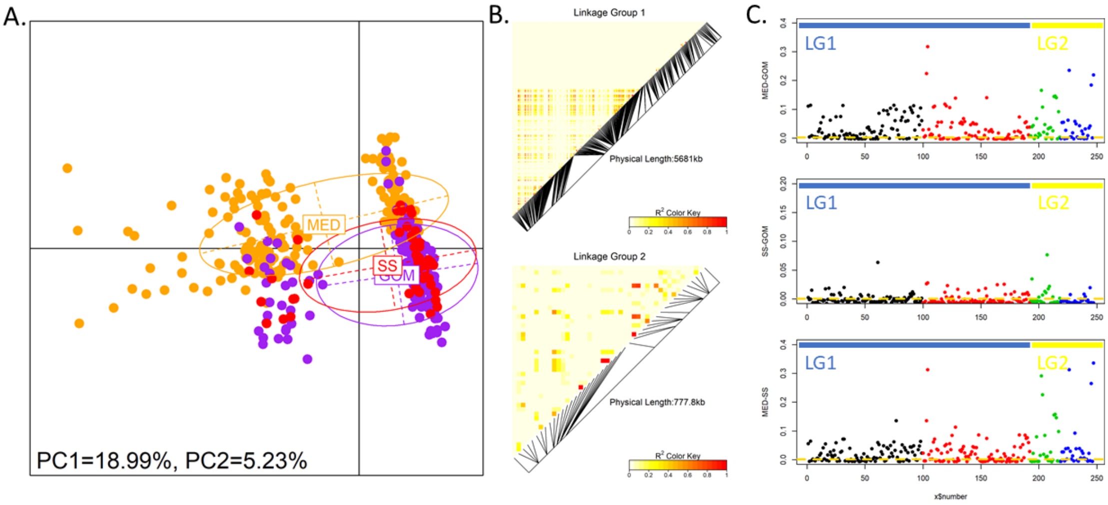
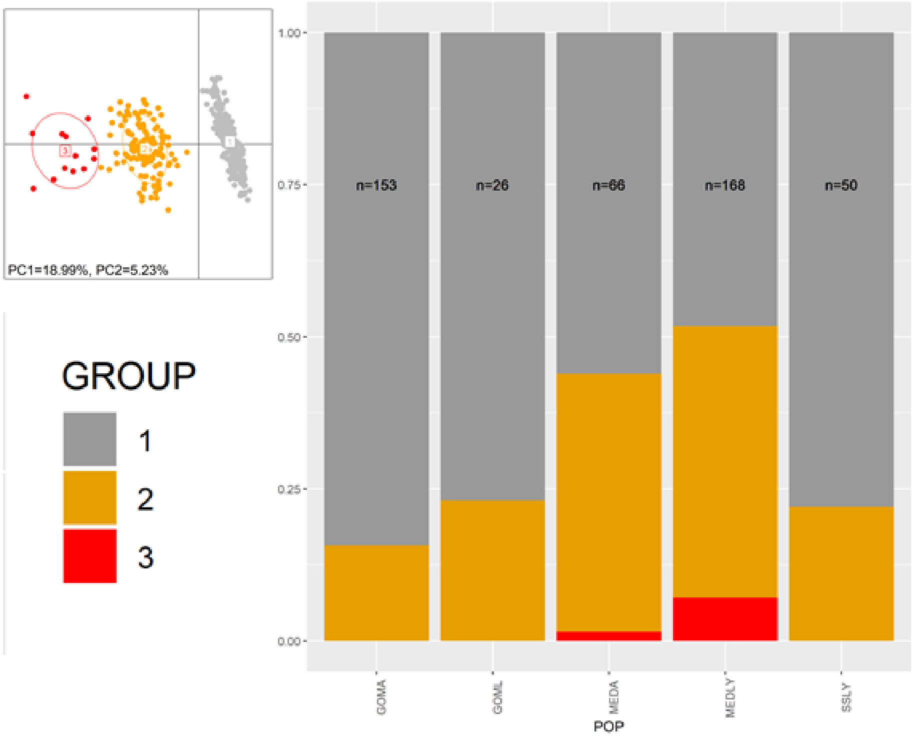
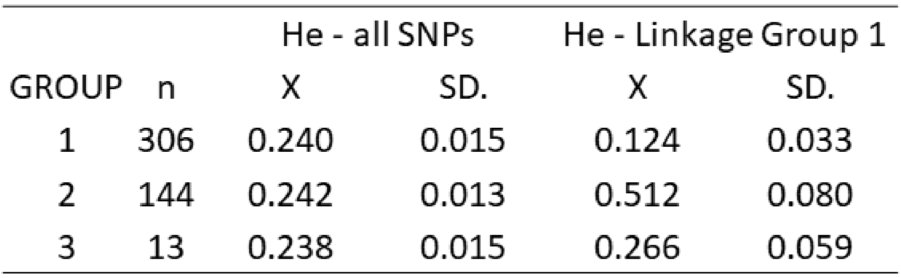


Figure 3. A. *PCA performed using the 226 candidate outlier SNPs selected using the approach implemented in PCAdapt on the mapped ABFT catalog dataset.* ***B.*** *Pairwise linkage disequilibrium between SNPs from linkage groups 1 and 2.* ***C.*** *Pairwise* F_{ST} *values between all filtered SNPs located in the two linkage groups composed by two genome scaffolds each. Dashed line represents average* F_{ST} *for each pairwise comparison.*

Among all scaffolds containing outlier SNPs detected with either method or catalog, two scaffold pairs were found to be under high linkage-disequilibrium when including all SNPs: the first 750Kb region of scaffold BKCK01000075 (where the SNP under selection are located) and scaffold BKCK01000111 (hereafter called linkage group 1), and scaffolds BKCK01000161 and BKCK01000173 (linkage group 2) (Figures 3B). Expectedly, the grouping pattern observed along the first PC is maintained when using all filtered SNPs derived from the linkage group 1 (Figure S13A), while PCA performed using all filtered SNPs from linkage group 2 (scaffolds BKCK01000161 and BKCK01000173) show a pattern more similar to that observed when using all SNPs (Figure S13B). Nevertheless, despite outlier SNPs revealed a cryptic sample grouping pattern that contrasts with location-based identification, SNPs derived from scaffolds which repetitively contained outlier SNPs also showed increased pairwise F_{ST} values per SNP between locations (Figure 3C), suggesting that both patterns may not be completely unrelated.





		He - all SNPs		He - Linkage Group 1	
GROUP	n	X	SD.	X	SD.
1	306	0.240	0.015	0.124	0.033
2	144	0.242	0.013	0.512	0.080
3	13	0.238	0.015	0.266	0.059

Figure 4. *A. Proportion of individuals from each location and age class that belong to the three different clusters differentiated by SNPs derived from linkage group 1 along the first axis of the PCA performed using outlier loci detected by PCAdapt in the mapped catalog as shown in the legend. B. Average and standard deviation of heterozygosity values within each defined ground when using all filtered SNPs or only SNPs from linkage group 1.*

Samples within clusters along the PC1, which are those driven by the linkage group 1 identified based on x axis coordinate (Figure 4) exhibited different average heterozygosity values for SNPs derived from the linkage group 1. Individuals from the most represented group (group 1 in Figure 4) and from the central group (group 2 in Figure 4) were about half and twice as heterozygous, respectively, compared to the genome-wide average (Figure 4). The observed clear-cut clustering pattern, the high measures of linkage disequilibrium, and the different heterozygosity proportions between groups suggest that the linkage group 1 is consistent with features found within chromosomal inversions (Barth et al. 2019; Puncher et al. 2019). Instead, we found no evidences suggesting that linkage group 2 could represent a chromosomal inversion. Alternatively, recombination rates can drop within certain chromosomic regions such as centro-chromosomal regions, causing high linkage-disequilibrium. The proportions of samples within each group segregated by haplotypes of the linkage group 1, presumably carrying different genotypes for the inversion, differed between locations (Figure 4).

3.5. Introgression from albacore

Using ancestry-informative sites from the mitochondrial genome (Table S7), we found 3 individuals containing albacore mitochondrial DNA (2 from the Mediterranean Sea, 1 from the Slope Sea and 0 from the Gulf of Mexico, Table S8). Higher percentages of introgression in the Mediterranean Sea (4.2 %) and the Slope Sea (5.8 %) than in the Gulf of Mexico (0.9 %) were also found based on haplotype frequencies derived from the RAD-seq datasets (Table S8). Previous studies analyzing mitochondrial sequences found introgressed haplotypes in Atlantic samples of ABFT, but they did not include reference samples such as larvae or spawning adults from the Gulf of Mexico (Alvarado Bremer et al. 2005). Here, based on samples from three different spawning grounds we consistently found higher proportions of introgressed mitochondrial haplotypes in the Mediterranean Sea and Slope Sea populations (Figure 5A).

The phylogenetic tree estimated by TreeMix based on the RAD mapped catalog dataset (Figure 5A) was coherent with the expected topology (Díaz-Arce et al. 2016):the two most likely estimated gene flow events occurred between albacore and the

Mediterranean ABFT groups (Figure 5A, for successive migration events and associated likelihood values see Figure S14). Accordingly, ABBA/BABA tests reveal an excess of albacore alleles shared with the Slope Sea and the Mediterranean Sea, and to a lesser extent with the Gulf of Mexico (Figure 5B). These results show the footprinting of nuclear introgression from albacore into ABFT. Considering Treemix and ABBA/BABA test results together, signature of introgression is stronger in the Mediterranean Sea, lower in the Slope Sea and the least in the Gulf of Mexico. Therefore, most likely, introgression likely occurred in the Mediterranean Sea, where spawning areas for ABFT and albacore tuna overlap.

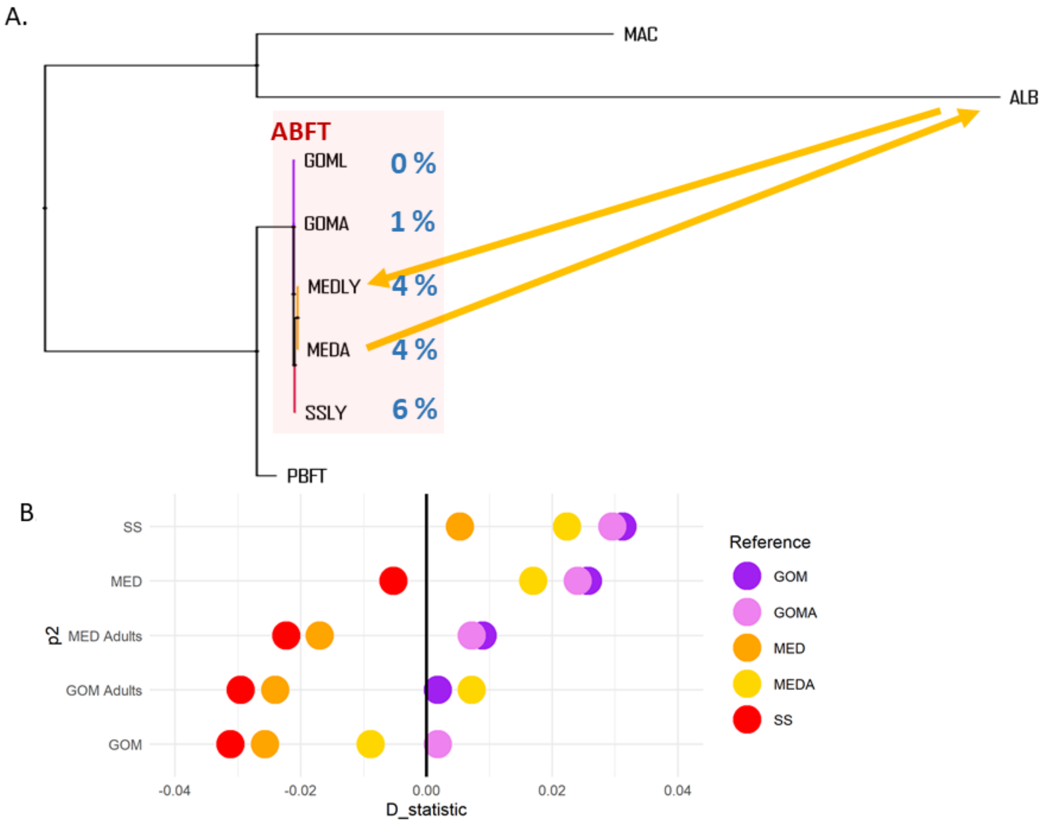


Figure 5. *Nuclear and mitochondrial introgression from albacore into ABFT. A. Phylogenetic tree estimated by Treemix allowing two migration events (yellow arrow). Numbers in blue represent percentages of mitochondrial introgression detected based on three markerss (using the RAD-seq data). B. D statistic values estimated from the ABBA/BABA test used to detect introgression from albacore to different target (rows) using different reference (colors) locations (adults in separated groups) of ABFT. Southern bluefin tuna allele frequencies were used to define the ancestral state of each SNP.*

Contemplating the results on demographic history and connectivity patterns presented in this work, introgressed haplotypes may either have been incorporated into the

Mediterranean Sea population and subsequently transmitted to the Slope Sea, discarding the possibility of introgression into a common ancestral population and present contemporary different proportions in the different lineages due to incomplete lineage sorting. Nevertheless, the nearly complete absence of both nuclear and mitochondrial introgression in Gulf of Mexico individuals (except for two Gulf of Mexico adult individuals showing introgressed mitochondrial haplotypes) suggests that introgression happened after Mediterranean and Gulf of Mexico ancestral populations lineages split. The heterogeneous strength of signature of introgression in the different populations on one hand may contribute to differentiation between Mediterranean Sea and Gulf of Mexico ancestral population and on the other hand provides another lead to understand genetic connectivity between ABFT populations.

3.6. Origin of the linkage groups

PCA performed using all filtered SNPs from the catalog including the other *Thunnus* species expectedly clustered together all the ABFT populations with the Pacific bluefin tuna individuals, while albacore and Southern bluefin tuna samples cluster together respectively and approximately equidistant between them and other bluefin tunas group (Figure S15). PCA performed using 291 SNPs and 83 SNPs extracted from the linkage group 1 and linkage group 2 respectively from the catalog including the other *Thunnus* species (Figure 6) showed the same previously observed grouping among ABFT samples (Figure S13). When using linkage group 1 SNPs Pacific bluefin tuna samples cluster with the majoritarian ABFT group while albacore samples are grouped near to the minoritarian ABFT group. When using linkage group 2 SNPs albacore individuals are more variable but closer to the Mediterranean Sea samples, while Pacific bluefin tuna does not clearly cluster with any ABFT population. Southern bluefin tuna, included in this catalog as an outgroup appears in general as genetically more distant (Figure 6). Likewise, ABBA/BABA test performed using these SNPs provides with much higher D-statistic values indicating introgression from albacore into the Mediterranean Sea and Slope Sea populations in these regions of the genome (Figure 6) compared to values obtained when using the whole dataset (Figure 5). These results show that the identified linkage groups detected by searching for genomic signatures of natural selection in ABFT populations are related to a past introgression event from albacore tuna. ABBA/BABA test performed removing all SNPs from those scaffolds in which highest 10% loading plots for the first two PC were much lower but still show higher levels of introgression in the Slope Sea and Mediterranean Sea compared to the Gulf of Mexico (Figure S16).

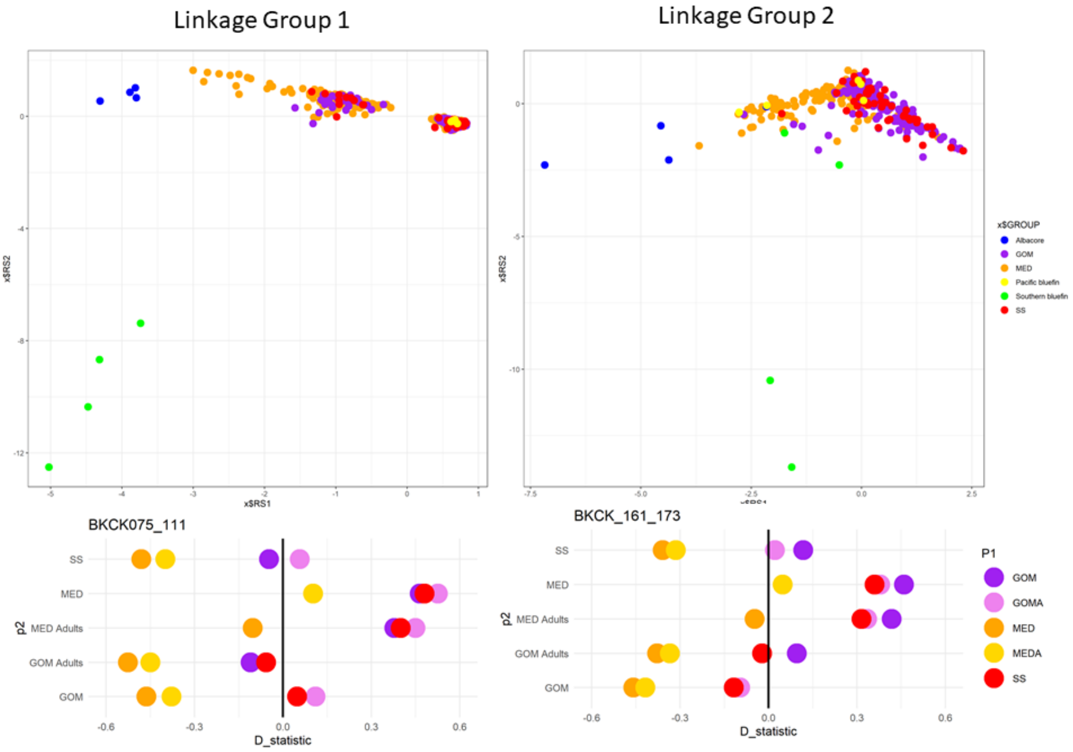


Figure 6. *Analysis performed using 291 SNPs from linkage group 1 (left) and 83 SNPs from linkage group 2 extracted from the reference mapped catalog dataset which includes other Thunnus species. A. PCA. B. Results of ABBA/BABA test: along the y axis are target groups and colors represent reference groups. The higher the D-statistic, the more introgressed is the target group respect to the reference group. In all the tests Southern bluefin tuna and albacore tuna were used as outgroup and donor respectively.*

3.7. Introgression helps to disentangle genetic connectivity

In the introgressive hybridization process, after hybridization between two distinct lineages haplotype blocks inherited from each parental group are broken down through recombination along generations. Thus, in relatively few generations (ca. 400-5000 generations), some introgressed tracts may become fixed or lost in the population through a process called genome stabilization (Runemark, Vallejo-Marin, Meier 2019).

Dispersion of detectable admixed or introgressed tracts can provide a unique source of information about recent or contemporary connectivity. For example, length of admixture tracts have been used to estimate populations connectivity of Mediterranean sea bass (Duranton, Bonhomme, Gagnaire 2019). Here we were not able to detect and measure length of the tracts, but we found a signature of introgression of variable intensity among spawning components. If we assume that introgressive hybridization occurred in the Mediterranean Sea where the introgression signature is strongest and which consists on a shared spawning ground area between albacore and ABFT, as supported by TreeMix (Figure 5A), introgressed albacore alleles detected in the Slope Sea could have been indirectly transmitted through gene-flow from the Mediterranean Sea. Likewise, the weaker signal of introgression found in the Gulf of Mexico is compatible with direct but reduced gene-flow from the Mediterranean Sea and/or indirect gene-flow through the Slope Sea spawning component which would dilute introgressed alleles.

However, high proportions of Mediterranean genetically shaped adult individuals found in the Gulf of Mexico suggest significantly strong ongoing migration. Introgression and/or presence of structural variants may induce reproductive isolation which could explain how genetic differentiation between Gulf of Mexico and Mediterranean Sea would be maintained through reduced fitness or incompatibilities between individuals carrying different versions of the structural variant (Faria et al. 2019) despite high migration. However, genome-wide genetic differentiation between Mediterranean Sea and Gulf of Mexico at neutral alleles reflects that differentiation is not primarily driven by introgression or adaptation but by remains of ancient genetic structure between Mediterranean and Atlantic populations as indicated by the demographic history. Moreover, the Slope Sea where both components presumably interbreed, would be directly affected by a reduced fitness. Alternatively, in the absence of barriers to gene-flow, another possible explanation to the currently observed ancestry patterns is contemporary secondary contact following genetic divergence of both ancestral populations during long-term restricted gene-flow period. Strong and rapid decline of the western stock over the last decades due to overfishing and oceanographic changes (Fromentin et al. 2014) could have intensified the impact of immigration from the Mediterranean population which is currently of one order of magnitude bigger than the

Gulf of Mexico population (ICCAT 2017). This may potentially lead to genetic erosion of the Gulf of Mexico genetic component. In this case, introgressed alleles and alternatives of the inversion would be transmitted neutrally following (and revealing) the connectivity patterns of the species.

While mitochondrial introgressed haplotypes are majoritarian in the Pacific bluefin tuna species (Alvarado Bremer et al. 2005), we did not detect signs of introgression in the nuclear genome, which would be compatible with indirect transmission of introgressed mitochondrial haplotype through Atlantic bluefin tuna that would become nearly fixed in the Pacific bluefin tuna through stochastic processes or mediated by selection. Nevertheless, we only included 5 individuals of Pacific bluefin tuna in this study which may not be enough representation of the species genetic pool as to detect ancient introgression tracts. Therefore, further exploration of the introgression signal is needed to better understand the historical gene-flow events between these species.

3.8. Introgression and inversions as potential source of genetic variation and local adaptation

Introgression represents an important source of genetic variation playing an

important role favouring speciation through processes such as adaptive introgression or reproductive isolation (Abbott et al. 2013). For example, introgressed tracts have been related with population reproductive isolation between Atlantic and Mediterranean populations of European sea bass (Duranton et al. 2019) and adaptive introgression of favoured alleles have been proved in several taxa (Arnold, Martin 2009; Clarkson et al. 2014). Likewise, different studies found that chromosomic structural variants can be linked to different evolutionary mechanisms. For example, structural chromosomic rearrangements have been related to local adaptation to different environments in Atlantic cod (Barth et al. 2017) and European plaice (Le Moan, Bekkevold, Hemmer-Hansen 2020), or linked to different ecotypes in Atlantic cod (Berg et al. 2016). To study possible connections between linkage groups or introgressed alleles with adaptation to environmental or ecological variables we would need further information about samples environmental variables or ecological traits that are not available for this study, we could not explore. However, biological differences between Gulf of Mexico and Mediterranean populations suggest that introgressed alleles from albacore tuna could confer characteristic adaptive traits to the latter population. For example, Atlantic bluefin tuna estimated age of maturity in the Gulf of Mexico and Mediterranean is 8-12 years and 3-5 years respectively; the finding of the spawning ground in the Slope Sea where adults of unknown origin spawn at the age of ≥5 (Corriero et al. 2020) may reflect the mixed genetic origin of fish in this area (Rodríguez-Ezpeleta et al. 2019). Similarly, age of maturity of albacore tuna in the Indian, Atlantic and Pacific oceans is 5-6 years, while albacore in the Mediterranean becomes sexually mature at the age of 2 years (Nikolic et al. 2017). Further studies of association of introgressed alleles, or those within the found linkage groups with environmental adaptations or biological traits would unveil their potential source of adaptation in ABFT which remains so far speculative.

4. Conclusions

Contrary to previous assumptions based on a potential homing behaviour of Atlantic Bluefin tuna, our study demonstrates ongoing trans-Atlantic gene-flow from the Mediterranean to the Gulf of Mexico and the Slope Sea spawning grounds. The spawning ground located in the Slope Sea is used by the western and eastern populations as a mixed-stock spawning ground. Moreover, the discovery of a chromosomal inversion recently introduced from the albacore into the Mediterranean Atlantic Bluefin tuna population, which seems to be propagating into the Slope sea (and to a lesser extent in the Gulf of Mexico) further confirm this unidirectional trans-Atlantic gene-flow. The lack of genetic homogeneity between the western and eastern populations despite gene-flow could be explained by long-term relative isolation between Atlantic and Mediterranean ancestral populations followed by very recent intensification of the effect of migration in the Atlantic spawning grounds. This intensification could potentially be due to the sharp decrease in the western stock size during the last decades, the recent increase meaning the presumed recovery of the eastern stock, an increase of the migration rates as a result of oceanographic changes which could attract eastern fish to the Atlantic spawning grounds, or a joint action of more than one of these factors. In sum, the increased gene-flow effect in the Atlantic spawning grounds could imply that the western spawning grounds are at risk of genetic erosion. We also hypothesized that here found traces of introgression and the chromosomal inversion could play a role in adaptation of the Mediterranean population reproductive features. These findings have strong implications relevant for fisheries management and conservation of Atlantic Bluefin tuna and therefore need to be further understood.

General Discussion

An increasing number of studies are successfully applying genetic tools to produce information that is relevant to fisheries management, especially during the last decades since the advent of HTS techniques. One of the applications that is being benefiting from the accessibility to HTS is stock delimitation based on thousands of informative genomic markers, such as SNPs. Together with laboratory protocols and sequencing techniques developing, bioinformatic tools are also needed to develop and adjust to specific data characteristics, implying in most of the cases laborious data analysis. The results presented in this thesis help to understand the effect of parameter setting during data analysis of population structure employing a commonly used sequencing technique to obtain SNP datasets, showing that simply applying an standard assembly and filtering protocol for every case study may lead into result bias. The increased genetic resolution obtained using SNPs through HTS also allows to answer many different evolutionary questions at different taxonomic scales which can be relevant to meet management and conservation informative demands. Results on the evolutionary context and stock structure and dynamics of an emblematic fish species explored using SNP datasets confirm that fisheries management can be enriched by information about evolutionary history of the species. Thus, our findings show that fisheries management strategy of Atlantic bluefin tuna needs to be revisited.

1. Challenges in the analysis of RAD-seq data

The increase in the number of studies using RAD-seq data during the last decade is partly due to the possibility of performing de novo assembly of the sequences, permitting to obtain genotypes of thousands of SNPs from species for which no reference genome is available. This is particularly valuable when working with exploited fish species, for which reference genomes are rarely available. However, this useful attribute is accompanied by challenges in the data analysis. As shown in chapters 1 and 2, assumptions made for sequence assembly parameter selection and thresholds applied for SNP filtering affect the power of the dataset to infer population structure and phylogenetic relationships. Procedures for RAD-seq read assembly have been proposed to maximize the number of shared polymorphic loci (Paris, Stevens, Catchen 2017) or minimize erroneously merging of paralog loci (McCartney-Melstad, Gidiş, Shaffer 2019).

Applying similar thresholds of missing data than in Paris, Stevens, Catchen (2017), assembly parameter combinations that derived into larger datasets did not provide better phylogenetic or population structure resolution. Furthermore, SNPs datasets from RAD catalogs obtained following the procedures described by the authors missed genetic differentiation between populations that was detected with an alternative set of parameters. While studies reporting effects of the assumptions made during data analysis are highly useful, development and application of universal standardized protocols may be risky. Instead, it is advisable to test for different parameter combinations, adapting decisions to the dataset and the objective of the study. Thus, in chapter 3 we tested different assembly parameter combinations to generate four different de novo catalogs. We individually sequenced 215 tag sequences inferred from assembly of these catalogs obtaining very similar amplification rate between them. Individual sequences of these tags at 32 Atlantic bluefin tuna individuals that were already included in the RAD catalogs, allowed to confirm high genotyping and correct assembly validation rate (98%). Additionally, in chapter 4 we used an extended dataset combining samples included in chapter 3 and newly sequenced samples to generate two comparable de novo and mapped catalog (for the latter, RAD-seq reads were previously mapped to a reference genome of a close species). We compared population structure inference results, obtaining very similar conclusions. In sum, these results prove the suitability of the de novo assemblage of the Atlantic bluefin tuna reads and to address questions at different evolutionary levels: from phylogenetic relationships within the genus *Thunnus* to population structure and detection of loci under selection of a species with very low values of genetic diversity.

2. Evolutionary context of the genus *Thunnus* and the Atlantic bluefin tuna

Phylogeny of the genus *Thunnus* was resolved using nuclear SNP markers clarifying relationships within the group of tropical and temperate tunas. Despite inhabiting colder waters, the bigeye tuna (*Thunnus obesus*) clearly clusters within the warm-water tunas' clade, supporting that bigeye and other cold-water tuna species are paraphyletic as results based on phylotranscriptomic data have confirmed later (Ciezarek et al. 2018).

This result sheds light into the evolutionary history of the endothermic mechanisms of tunas. Signs of mitochondrial but no nuclear introgression had been found between albacore, Pacific and Atlantic bluefin tunas (Chow et al. 2006; Viñas, Tudela 2009; Ciezarek et al. 2018). As shown in these studies, phylogenetic analysis using nuclear SNPs clustered Atlantic and Pacific bluefin tunas in a monophyletic group, regardless of the presence of albacore-like mitochondrial haplotypes. The results presented in this work, reveal that proportions of individuals of Atlantic bluefin tuna showing an introgressed mitochondrial haplotype are different between the three known spawning grounds. Moreover, printing of nuclear introgression was also found in those spawning components where highest percentages of inrogressed mitochondrial haplotypes were found. In Alvarado Bremer et al. (2005) comparison of sequences of the mitochondrial control region I showed that introgression was present in both the Mediterranean and Atlantic components. However, results on the population structure and mixing-dynamic of Atlantic bluefin tuna included in this work, suggest that the samples included in Alvarado Bremer et al. (2005) could belong to the Mediterranean or Slope Sea spawning components, where similar percentages of mitochondrial introgression were found in this study. Stronger signal of introgression in the Mediterranean Sea samples and weaker in the Gulf of Mexico helps to decipher genetic connectivity of Atlantic bluefin tuna between spawning grounds. Support for the presence of a structural variant present at different haplotype proportions between Atlantic bluefin tuna spawning grounds was found. This phenomenon has been observed in other species, such as between cod populations with weak genetic differentiation (Barth et al. 2019) or between lesser sandeel sampled locations without background genetic differentiation (Jiménez-Mena et al. 2020) suggesting that structural variant polymorphisms could be related to partial reproductive isolation. The role that structural variants play on speciation is still unknown, although it has been shown how they can affect adaptation and reproductive isolation (Feulner, De-Kayne 2017). Moreover, polymorphism of the potential structural variant found in Atlantic bluefin tuna seems to be the result of introgression from albacore. Previous studies have found that introgression from a different species can be a source for adaptive variation (Pardo-Diaz et al. 2012; Jones et al. 2018).

3. Implications for management of Atlantic bluefin tuna

The results presented in this work highlight the need to revisit current management strategies of Atlantic bluefin tuna. Although two ancestral genetic components have been detected, which seems to correspond to the Mediterranean and Gulf of Mexico spawning grounds, the evidence of the newly discovered spawning ground in the Slope sea receiving incoming gene-flow from the Mediterranean and the Gulf of Mexico genetic components and playing an important role on the global genetic connectivity of the species, suggests that the current two-stock definition of populations of Atlantic bluefin tuna underestimates the natural structuring complexity of the species. Demographic connectivity dependant on migration rates between populations is a relevant issue for fisheries management and assurance of sustainability of stocks. Genetic connectivity helps to understand migration dynamics between populations of the species, but high genetic connectivity does not necessarily imply high demographic connectivity (Lowe, Allendorf 2010). Demographic connectivity between populations of Atlantic bluefin tuna needs further research to understand populations demographic interdependency and potential effects of overexploitation of each spawning component.

Evidence of overlap of western and eastern stocks in foraging grounds in the North Atlantic from electronic tagging (Block et al. 2005) and otolith chemistry (Rooker et al. 2014) highlight the need for an efficient assignment technique to estimate stock of origin proportions of these feeding aggregates. Samples from western and eastern stocks can be discriminated using otolith chemical data, although the origin specific distributions of isotopic values overlap, affecting the assignment rates. Results of otolith chemistry analysis of individuals from different foraging grounds along the North Atlantic support mixing of western and eastern stocks at different proportions (Rooker et al. 2014). Here we developed a panel of SNP markers of high assignment rate to assign origin of fish from feeding aggregates along the North Atlantic, confirming mixing of western and eastern genetic background components. Similar to what was observed from otolith (Rooker et al. 2014) and electronic tagging (Block et al. 2005) data, individuals from the Mediterranean Sea seem to perform longer westward migrations while individuals with western genetic background are found in higher proportions closer to the west Atlantic coast. Further knowledge of the observed asymmetrical migration flow would help to better understand demographic connectivity between populations which needs to be considered for the correct management of the stocks. Moreover, this SNP panel is a useful, cost-effective and no invasive tool for fisheries management to estimate population of origin proportions of total catches from fisheries.

Study of the genetic diversity of all Atlantic bluefin tuna populations revealed the presence of a group of markers under linkage disequilibrium which behave as a chromosomal inversion originating a cryptic subpopulation structure. The inverted haplotype version was potentially introduced in Atlantic bluefin tuna from an introgression event from the albacore tuna. Both chromosomal inversions and introgressed alleles have been proposed as sources of variation permitting local adaptation and speciation (Pardo-Diaz et al. 2012; Berg et al. 2016; Jones et al. 2018; Barth et al. 2019). Further research on the possible effects of chromosomal rearrangement on adaptation as well as on local recruitment of Atlantic bluefin tuna is needed to explore its relevance for fisheries management of the species.

Conclusions and Thesis

Conclusions

Taking into account the objectives of this Thesis we conclude that:

1. Sequencing read filtering criteria, *de novo* read assembly parameter values and SNP filtering thresholds applied during Restriction site Associated DNA sequencing (RAD-seq) data analysis affect population structure inferences, having variable impacts among datasets. Thus, adopting a common analysing strategy for all RAD-seq datasets as suggested by previous studies might prevent capturing population structure informative markers and therefore, testing alternative analysis procedures for each dataset is advised.

2. RAD-seq read assembly parameters and marker filtering and encoding criteria affect size, amount of missing data and informativeness of the resulting nucleotide alignments. Thus, procedures for mining RAD-seq data for phylogenetic inference need to be tailored to the evolutionary scale of the relationships to be resolved.

3. Nuclear genome-wide single nucleotide polymorphisms (SNPs) are more suitable than mitochondrial markers to resolve the phylogenetic relationships among the genus *Thunnus* as they are not or less affected by introgression events among species. Thus, assays for species identification used for traceability should be based on nuclear genome markers.

4. Phylogenetic analyses based on thousands of nuclear SNP markers confirm that Atlantic and Pacific bluefin tunas are different, although very closely related, species and that, as previously proposed based on morphological features, the bigeye tuna (*Thunnus obesus*) is more closely related to the tropical tunas than to temperate tunas, suggesting parallel adaptation to cold-waters.

5. Genome-wide genetic differentiation between Atlantic bluefin tuna from the Mediterranean Sea and the Gulf of Mexico supports reproductive isolation between these two spawning areas. The newly discovered spawning activity of individuals of Mediterranean and Gulf of Mexico origin in the Slope Sea has started recently in the evolutionary history of the species, resulting in genetic profiles of the individuals

captured in this area covering the whole diversity range of the species. This, together with presence of genetically Mediterranean-like individuals in the Gulf of Mexico, supports on-going westwards trans-Atlantic gene-flow in Atlantic bluefin tuna.

6. The Atlantic bluefin tuna genome contains variant positions that could be potential sources of local adaptation resulting from an inter-species introgression event.

7. Traces of an introgression event from albacore tuna detectable in the Atlantic bluefin tuna genome, at highest intensity in the Mediterranean Sea, lower in the Slope Sea and lowest in the Gulf of Mexico, suggest that this introgression event happened in the Mediterranean Sea, where both species spawn, and support that the genetic homogenizer effect of westward trans-Atlantic gene-flow has been stronger in the Slope Sea.

8. A newly developed SNP traceability tool allows to assign Atlantic bluefin tuna specimens as Mediterranean or Gulf of Mexico origin at an unprecedented rate. Assignment of individuals captured in feeding grounds along the North Atlantic Ocean confirms higher mixing in the Western Atlantic, which defies the assumed Western-Eastern stock delimitation boundary placed at the 45°W meridian.

9. The current management strategy of Atlantic bluefin tuna, based on two spatially delimited stocks, needs to be revisited to consider the existence of a newly originated mixed-stock spawning ground in the Slope Sea, the extent of asymmetric inter-stock genetic and demographic exchange and the geographic distribution of stock mixing proportions on feeding grounds along the North Atlantic.

10. Future conservation measures for Atlantic bluefin tuna should consider that the recently intensified trans-Atlantic gene-flow could result in the genetic erosion between the Atlantic and Mediterranean spawning grounds, which has important and imminent implications in the adaptation capacities and resilience of the species.

Thesis

Existence of contemporary unidirectional trans-Atlantic gene flow, establishment of a recently originated mixed spawning area, and estimation of stock mixing proportions on feeding grounds in the Atlantic bluefin tuna (*Thunnus thynnus*), all relevant for the conservation and management of the species, are revealed from the study of the phylogenetic relationships within the genus *Thunnus* and the species' population structure using Single Nucleotide Polymorphisms (SNPs) discovered and genotyped through high-throughput sequencing.

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Appendix A

Selecting RAD-seq data analysis parameters for population genetics: the more the better?

Natalia Díaz-Arce, Naiara Rodríguez-Ezpeleta

Supplementary Figures

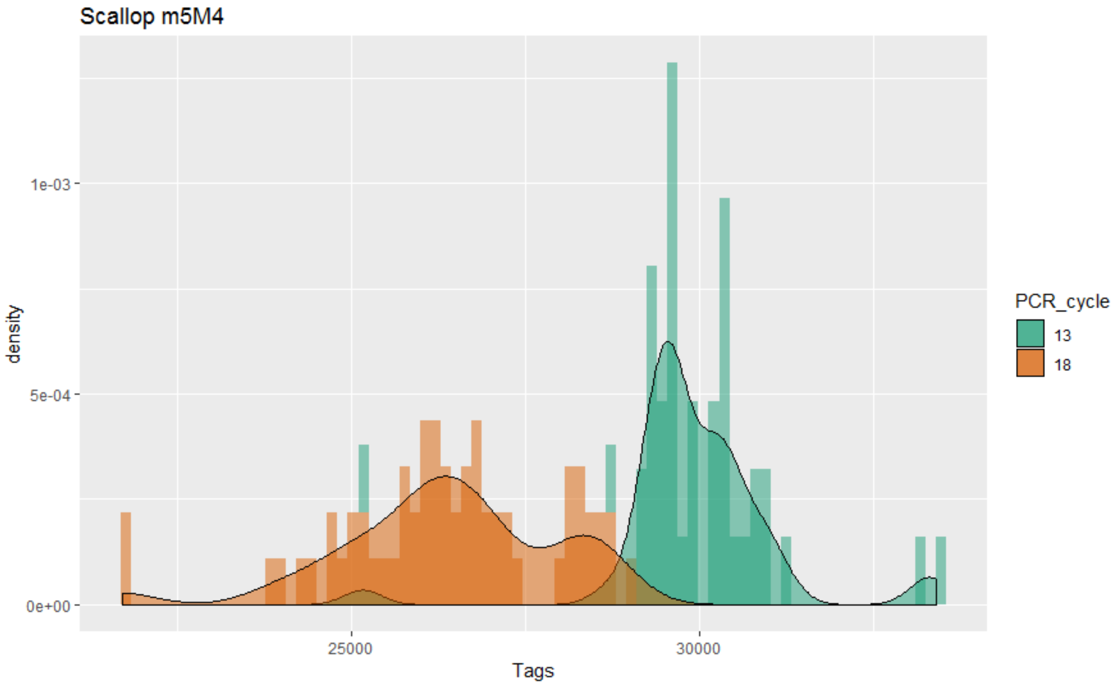


Figure S1. Frequency distribution of the number of assembled loci per individual in the Scallop dataset after applying the following parameters: *m*=5, *M*=4, and PCR clones filtered. The graph shows distribution for those samples for which 13 (green) and 18 (orange) PCR cycles were applied for library building.

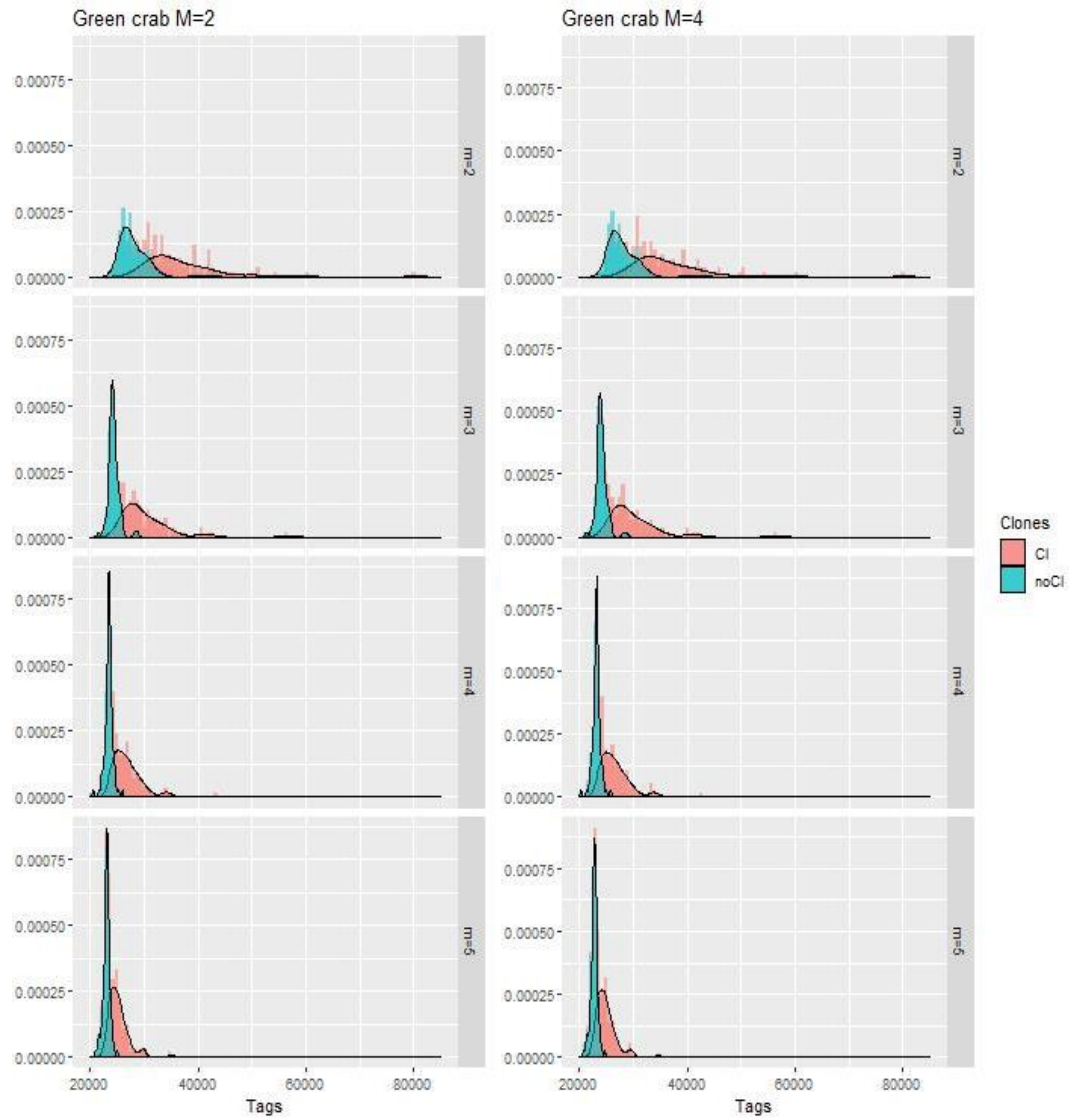


Figure S2. Frequency distribution of the number of tags per individual before (red) and after (blue) removing PCR clones for the different *m* and *M* combinations for the Green crab dataset.

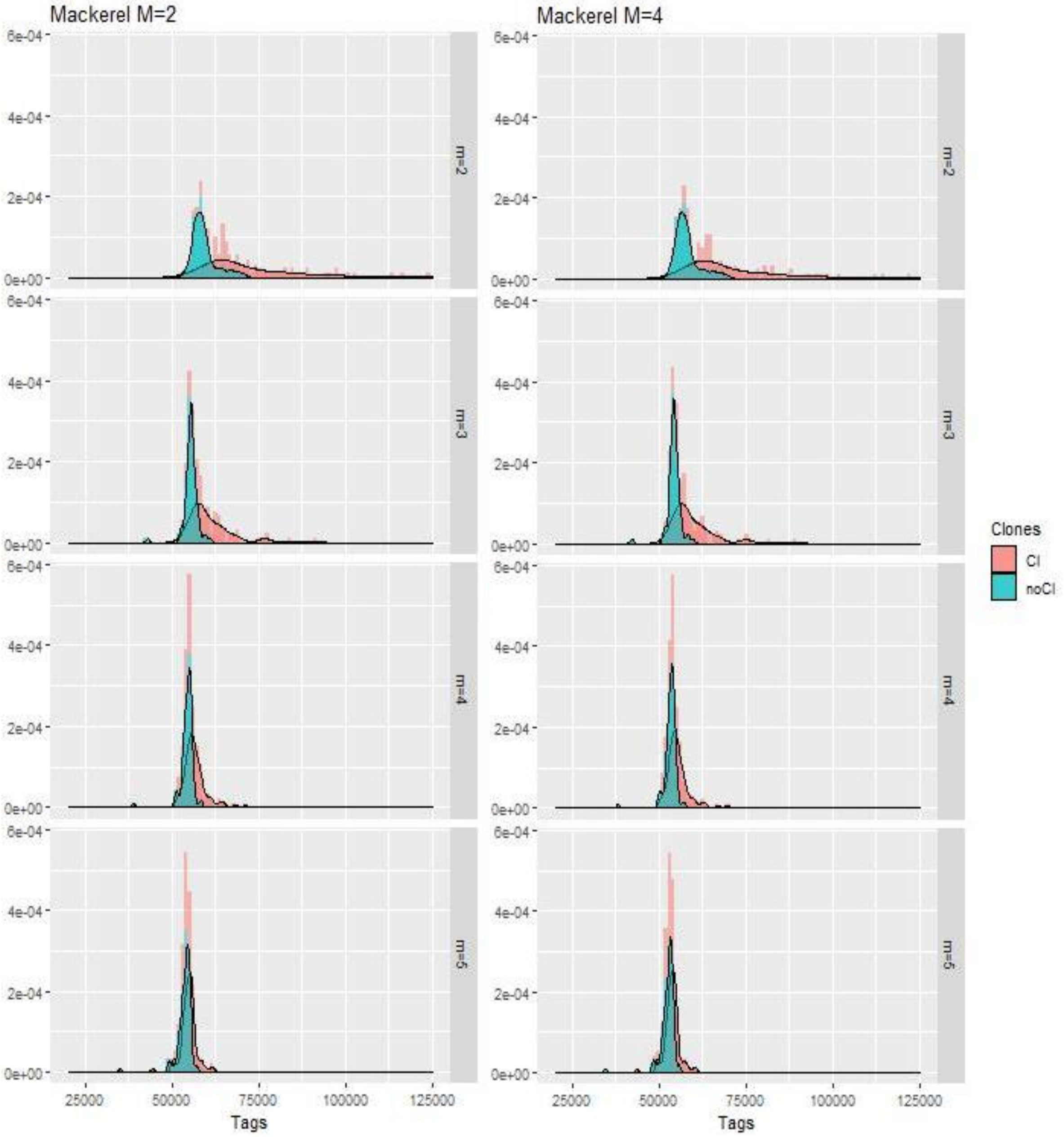


Figure S3. Frequency distribution of the number of tags per individual before (red) and after (blue) removing PCR clones for the different *m* and *M* combinations for the mackerel dataset.

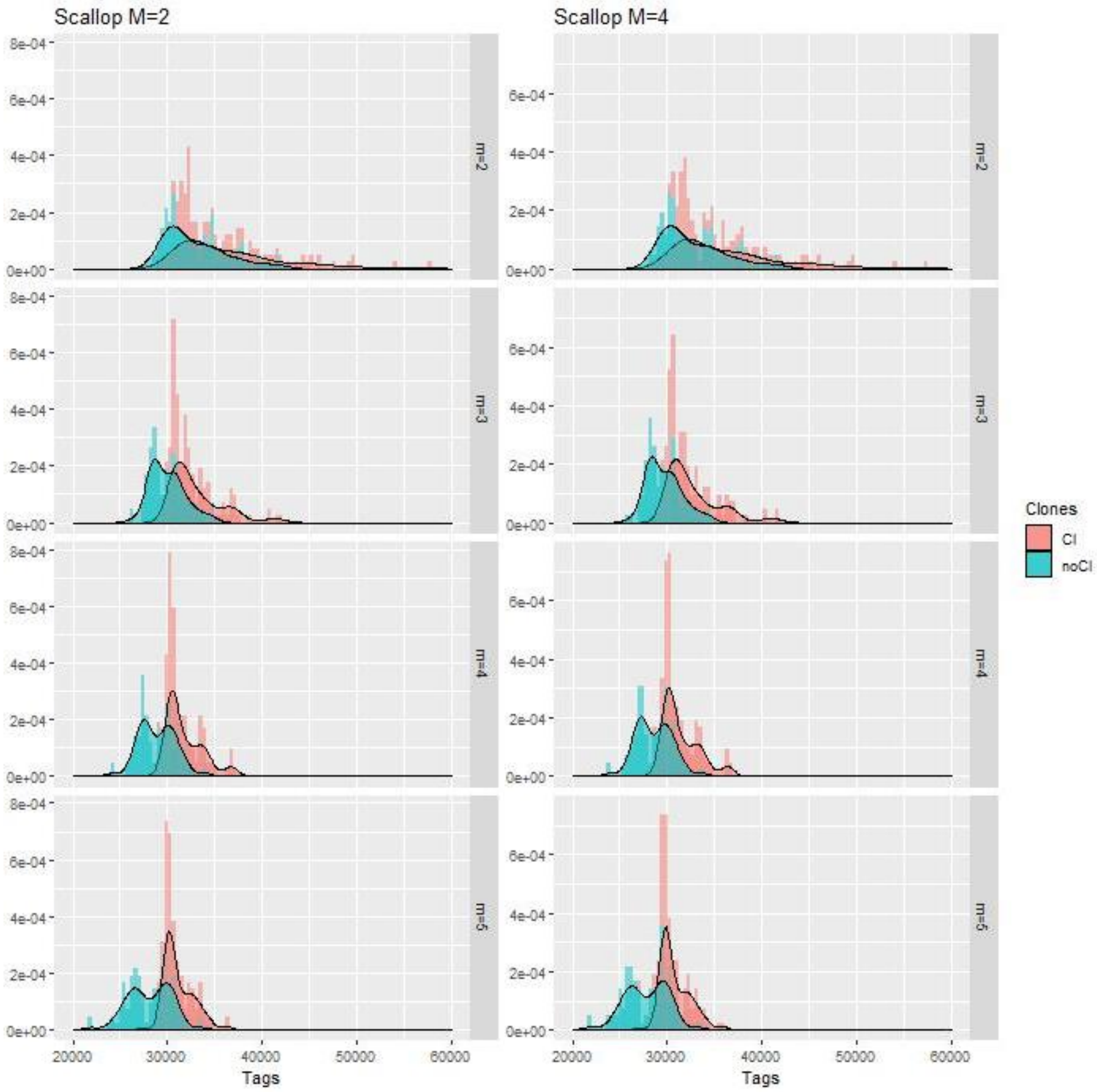


Figure S4. Frequency distribution of the number of tags per individual before (red) and after (blue) removing PCR clones for the different *m* and *M* combinations for the scallop dataset.

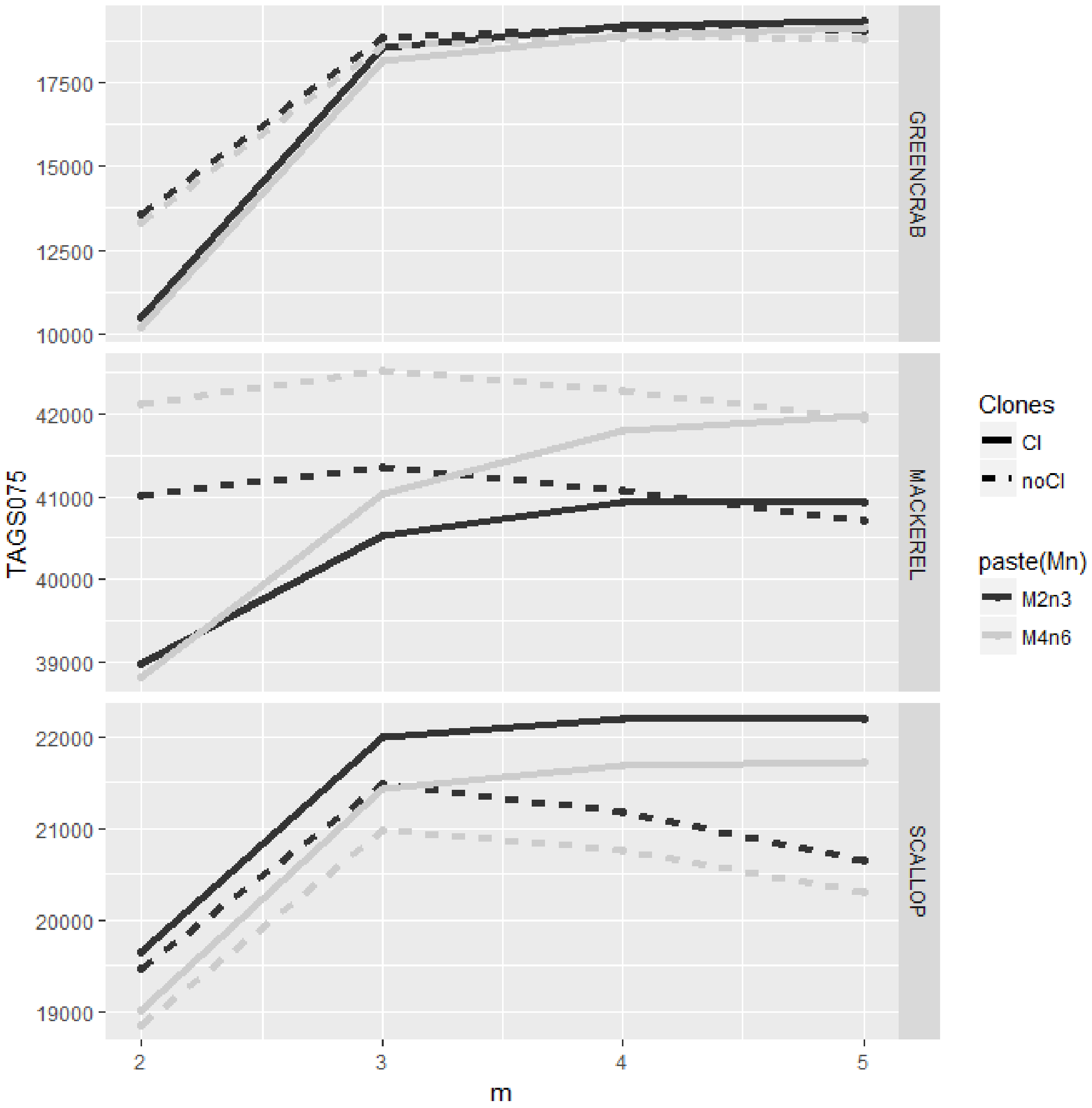


Figure S5. Total number of tags present in at least 75% of the individuals in all catalogs for different values of m (x axis), different combinations of M and n parameters (M=2 and n=3 in black and M=4 and n=6 in grey) and before (solid line) and after (dotted line) removing PCR clones.

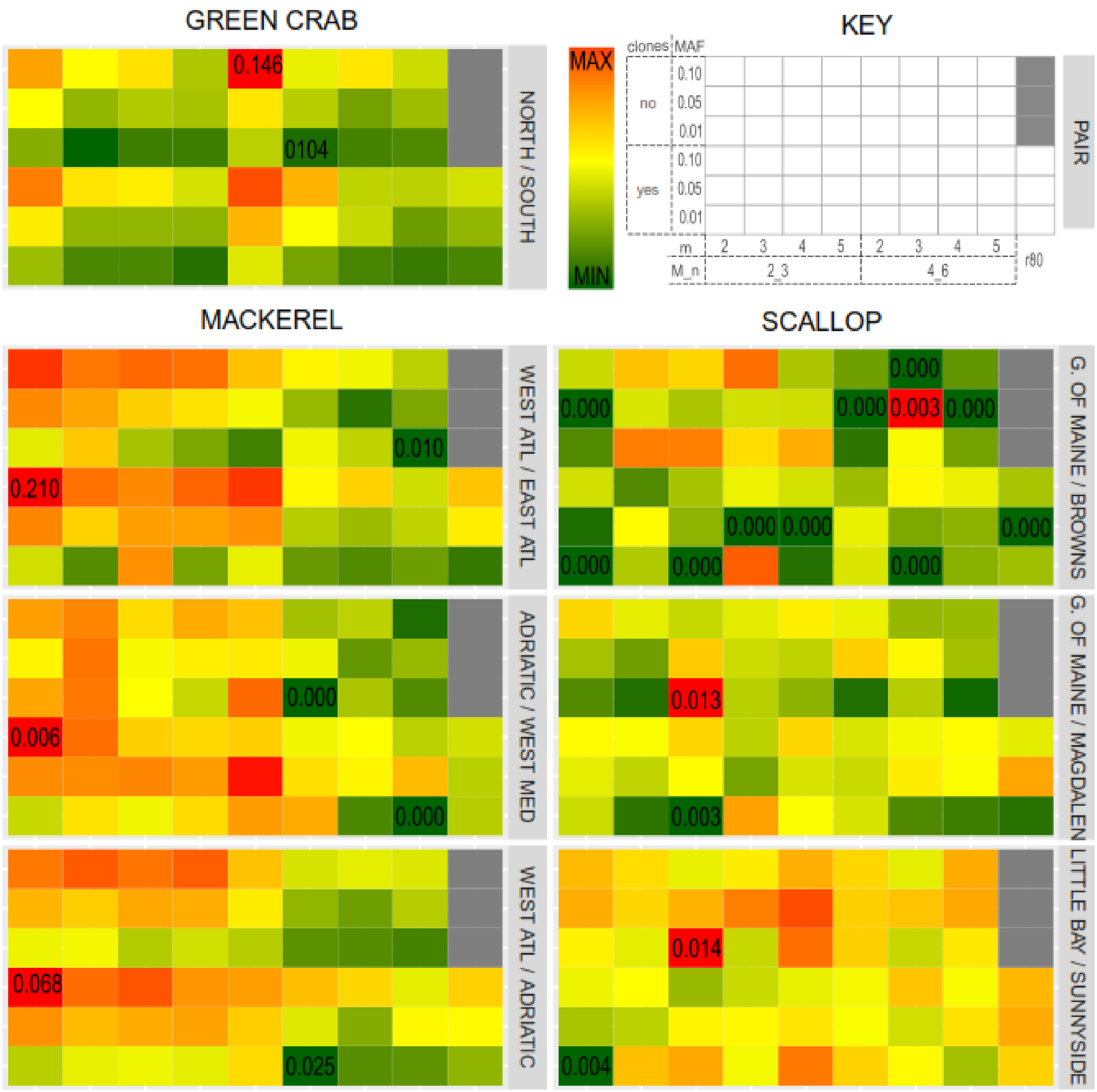


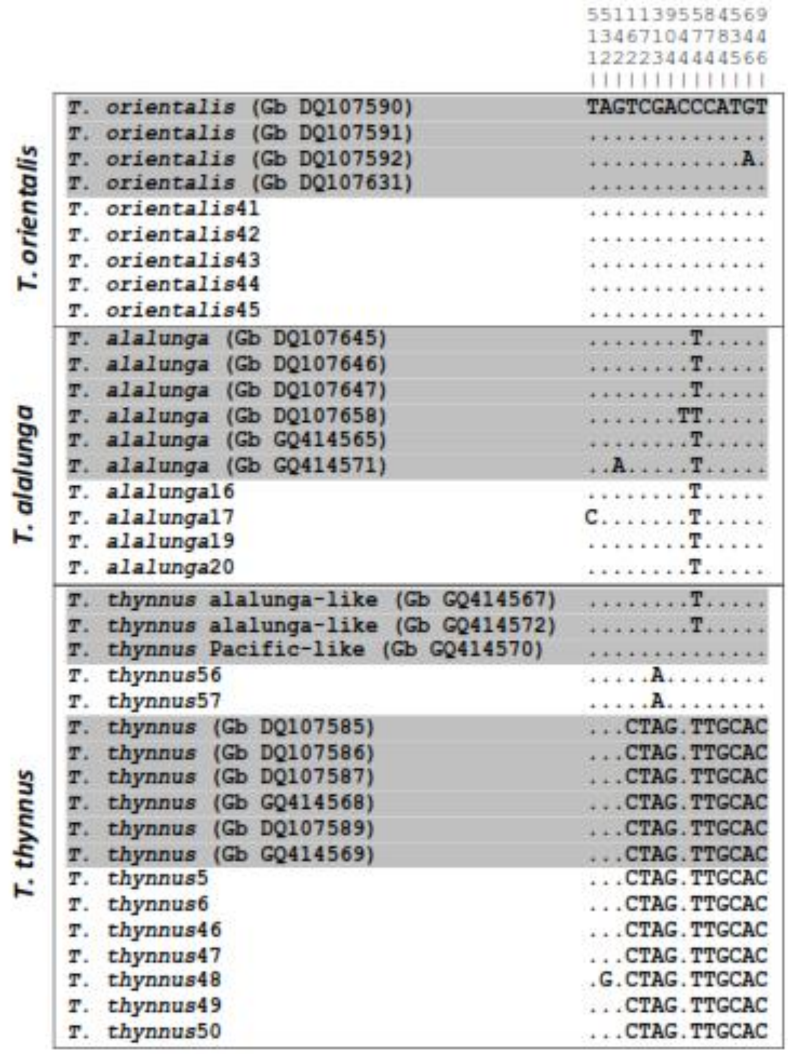
Figure S6. Average pairwise F_{ST} values for 2000 randomly selected SNPs from each catalog and population pairs for the three datasets: Northern/Southern green crab locations; Western/Eastern Atlantic Ocean, Adriatic Sea/Western Mediterranean Sea (intra-Mediterranean) and Western Atlantic/Adriatic Sea mackerel populations; Gulf of Maine/Magdalen Islands (northern/southern locations), Little Bay/Sunnyside (intra-North) and Gulf of Maine/ Browns Bank (intra-South) scallop locations. Color gradients represent F_{ST} values, from lowest (dark green) to highest (dark red). Minimum and maximum F_{ST} values for each pair are indicated in the corresponding cell.

Appendix B

RAD-seq derived genome-wide nuclear markers resolve the phylogeny of tunas

Díaz-Arce et al.

Supplementary Figures



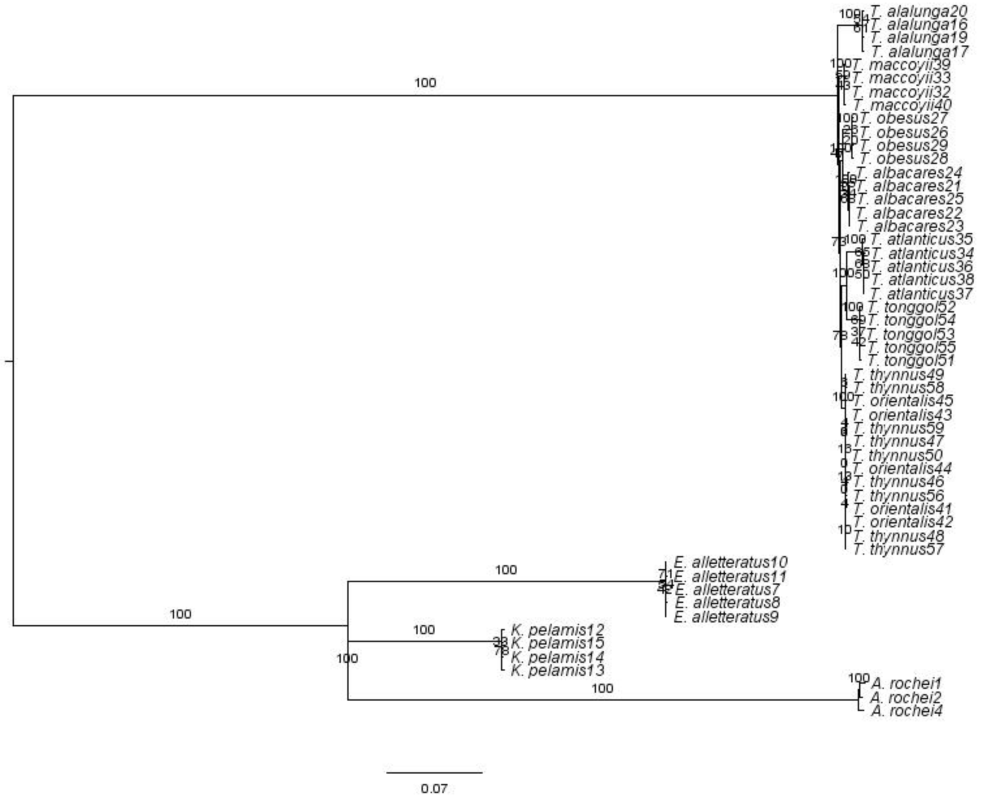
```
                                              55111395584569
                                              13467104778344
                                              12222344444566
                                              ||||||||||||||
T. orientalis (Gb DQ107590)                   TAGTCGACCCATGT
T. orientalis (Gb DQ107591)                   ..............
T. orientalis (Gb DQ107592)                   ............A.
T. orientalis (Gb DQ107631)                   ..............
T. orientalis41                               ..............
T. orientalis42                               ..............
T. orientalis43                               ..............
T. orientalis44                               ..............
T. orientalis45                               ..............
T. alalunga (Gb DQ107645)                     ........T.....
T. alalunga (Gb DQ107646)                     ........T.....
T. alalunga (Gb DQ107647)                     ........T.....
T. alalunga (Gb DQ107658)                     .......TT.....
T. alalunga (Gb GQ414565)                     ........T.....
T. alalunga (Gb GQ414571)                     ..A.....T.....
T. alalunga16                                 ........T.....
T. alalunga17                                 C.......T.....
T. alalunga19                                 ........T.....
T. alalunga20                                 ........T.....
T. thynnus alalunga-like (Gb GQ414567)        ........T.....
T. thynnus alalunga-like (Gb GQ414572)        ........T.....
T. thynnus Pacific-like (Gb GQ414570)         ..............
T. thynnus56                                  .....A........
T. thynnus57                                  .....A........
T. thynnus (Gb DQ107585)                      ...CTAG.TTGCAC
T. thynnus (Gb DQ107586)                      ...CTAG.TTGCAC
T. thynnus (Gb DQ107587)                      ...CTAG.TTGCAC
T. thynnus (Gb GQ414568)                      ...CTAG.TTGCAC
T. thynnus (Gb DQ107589)                      ...CTAG.TTGCAC
T. thynnus (Gb GQ414569)                      ...CTAG.TTGCAC
T. thynnus5                                   ...CTAG.TTGCAC
T. thynnus6                                   ...CTAG.TTGCAC
T. thynnus46                                  ...CTAG.TTGCAC
T. thynnus47                                  ...CTAG.TTGCAC
T. thynnus48                                  .G.CTAG.TTGCAC
T. thynnus49                                  ...CTAG.TTGCAC
T. thynnus50                                  ...CTAG.TTGCAC
```

Supplementary Figure 1 Alignment of the only 14 polymorphic nucleotide positions observed in the amplified region of the cytochrome oxidase subunit I (COI) gene for the *T. thynnus*, *T. orientalis* and *T. alalunga* individuals included in our study and those obtained from GenBank (in grey).

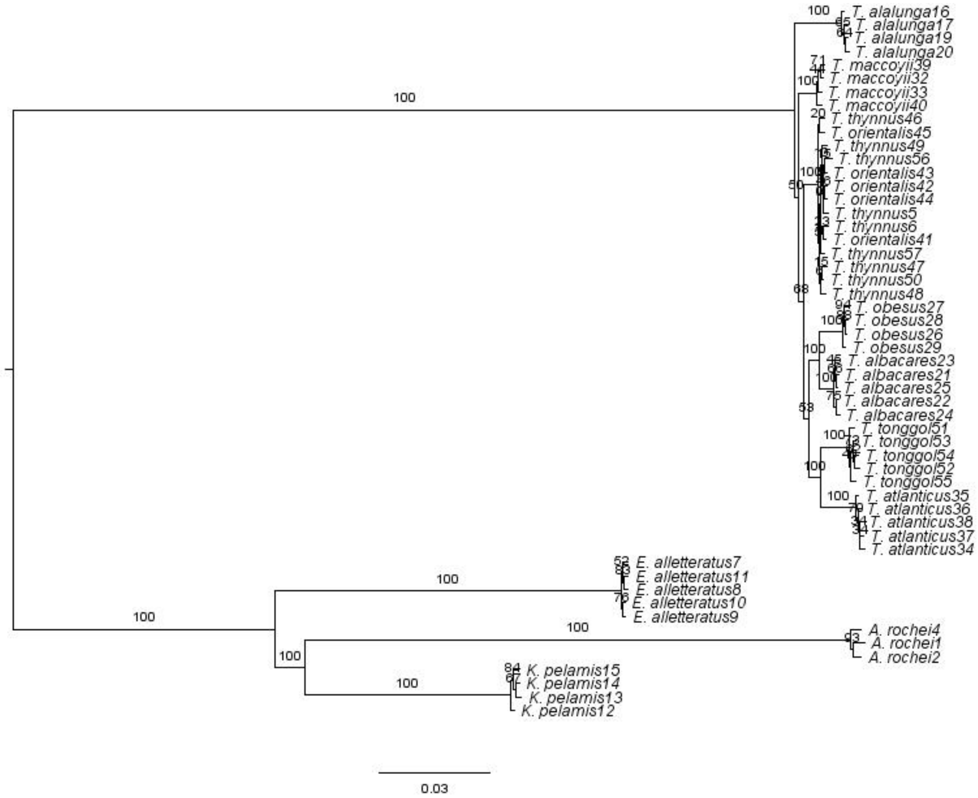
RAD-seq derived genome-wide nuclear markers resolve the phylogeny of tunas

Díaz-Arce et al.

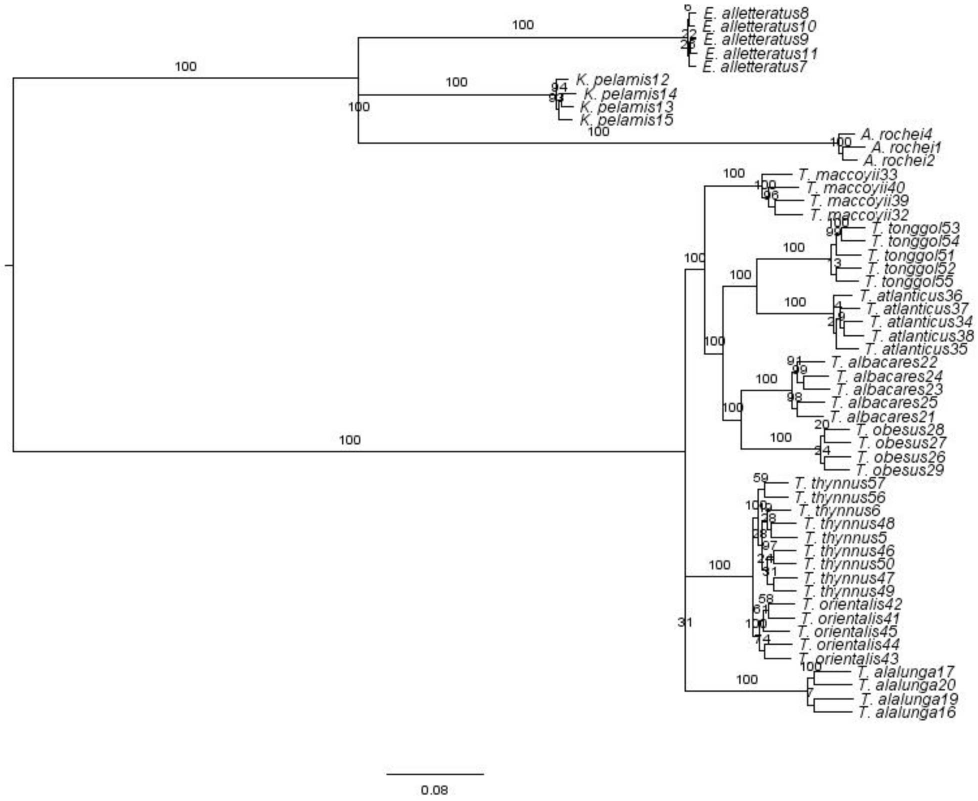
Appendix I: Trees obtained from each of the 128 matrices. Rooting is arbitrary, values above branches represent bootstrap values and scale bar represents estimated nucleotide substitutions per site.



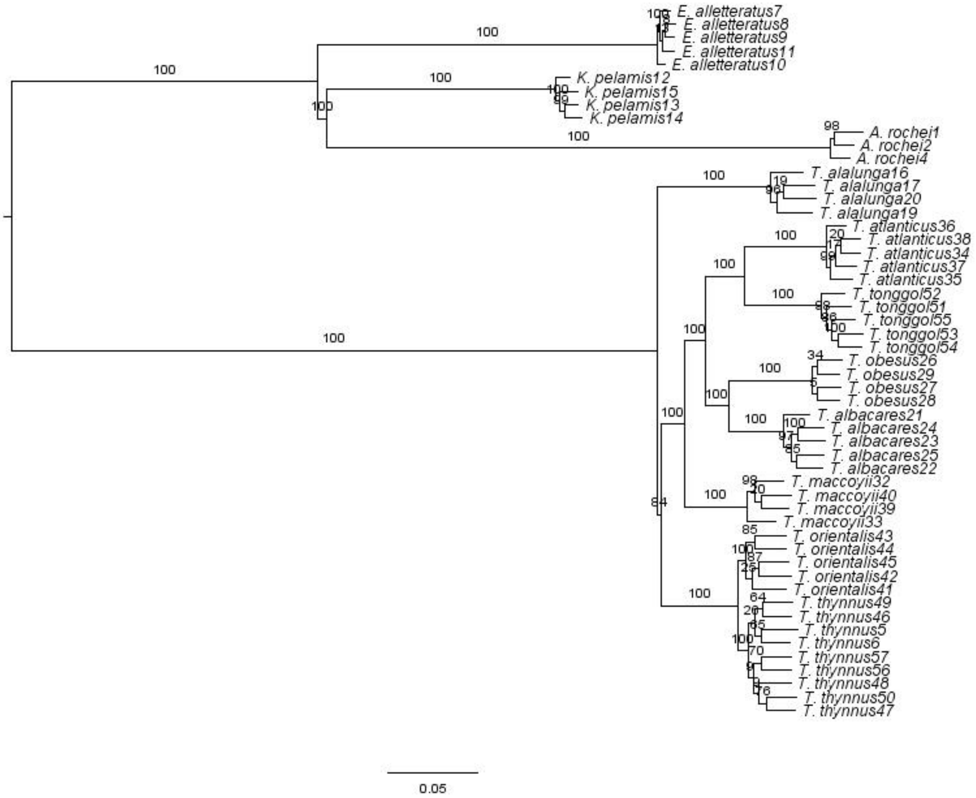
Tree 1: M=1, n=4, all species, per individuals, 0% missing, fixed positions.



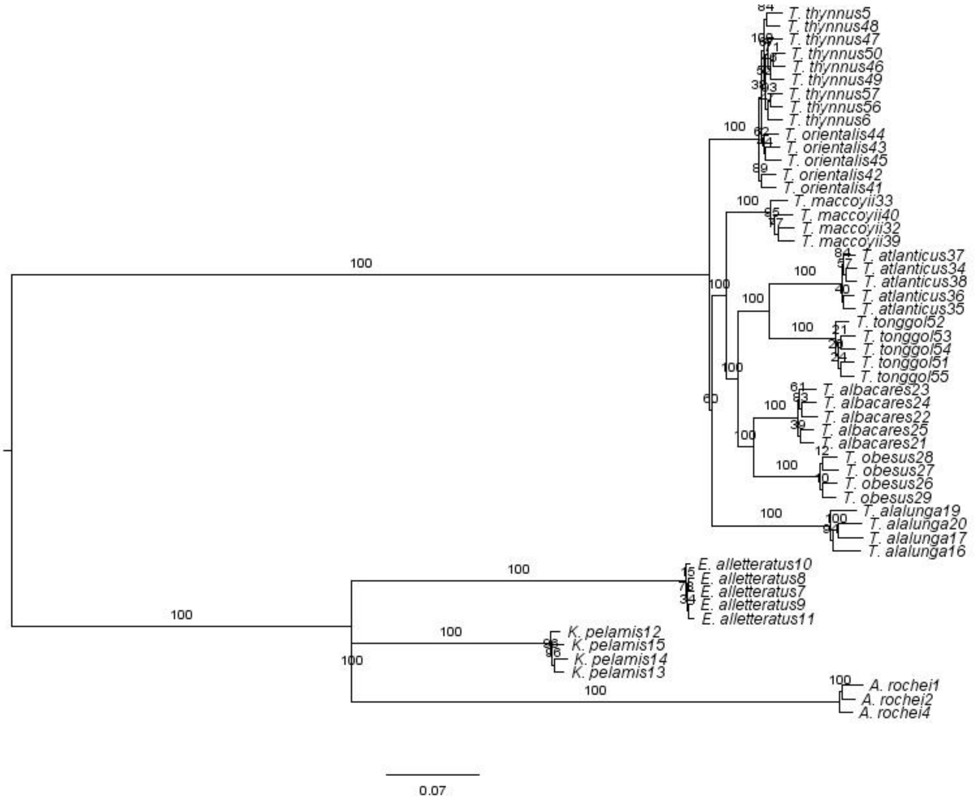
Tree 2: M=1, n=4, all species, per individuals, 0% missing, IUPAC encoded sites.



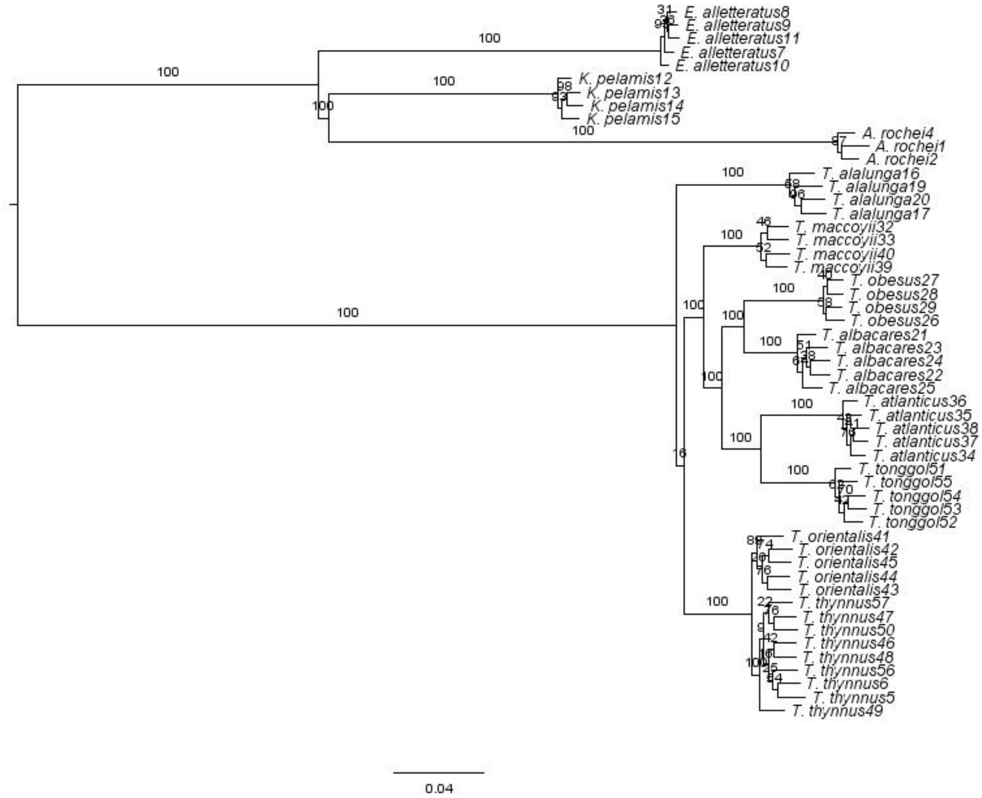
Tree 3: M=1, n=4, all species, per individuals, 75% missing, fixed positions.



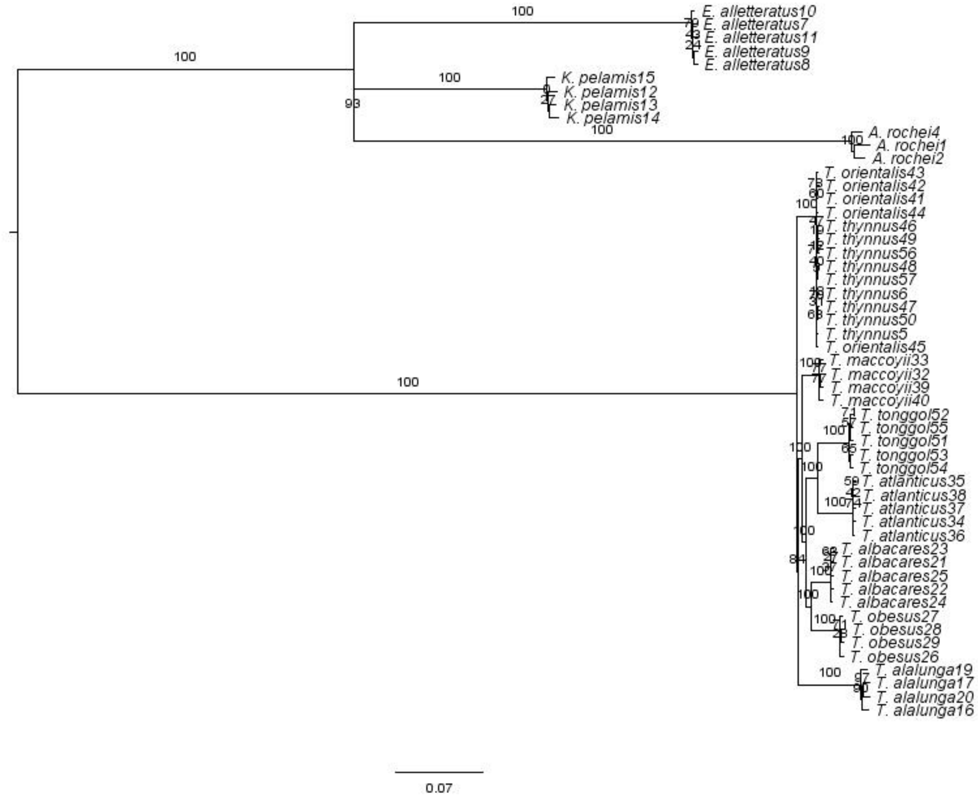
Tree 4: M=1, n=4, all species, per individuals, 75% missing, IUPAC encoded sites.



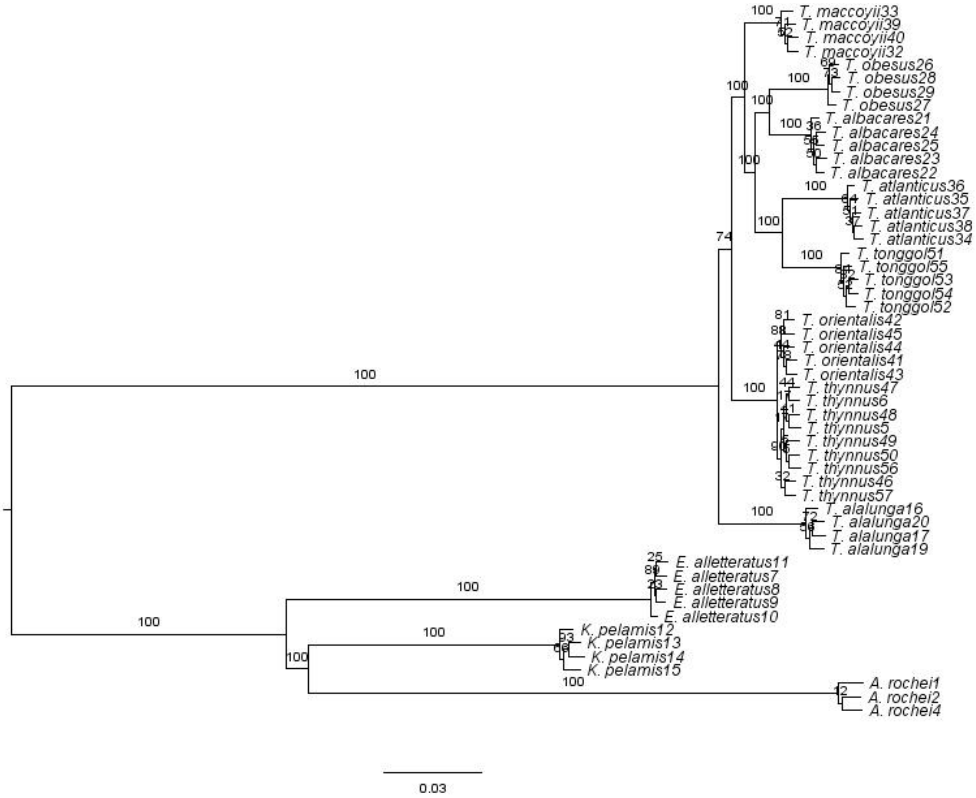
Tree 5: M=1, n=4, all species, per individuals, 50% missing, fixed positions.



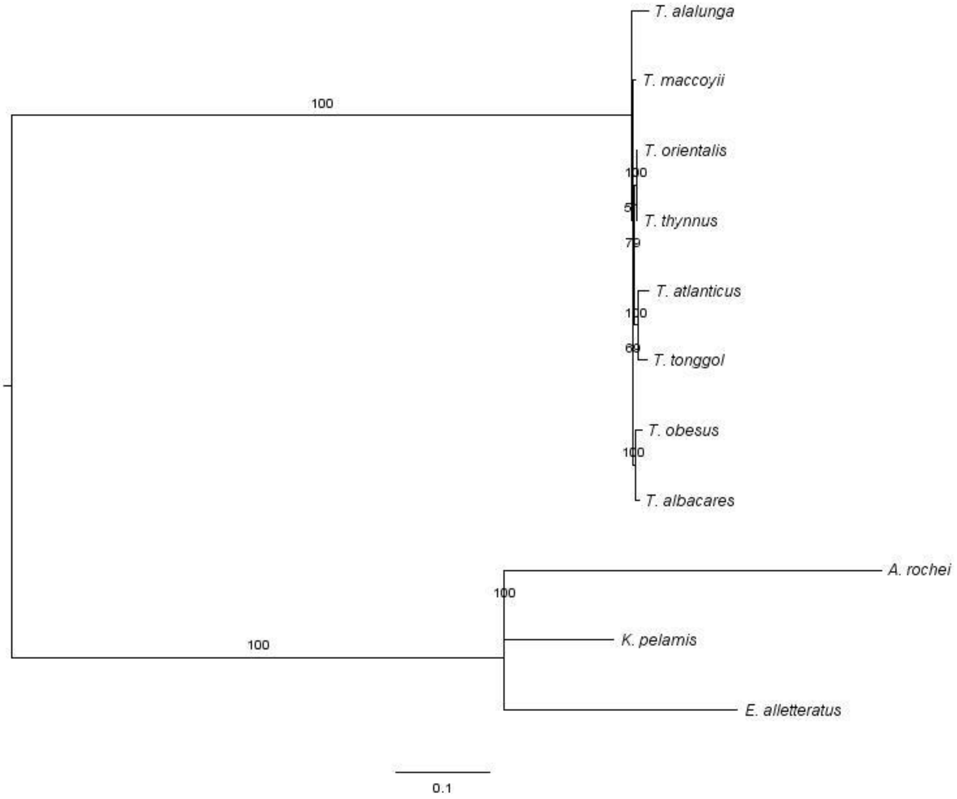
Tree 6: M=1, n=4, all species, per individuals, 50% missing, IUPAC encoded sites.



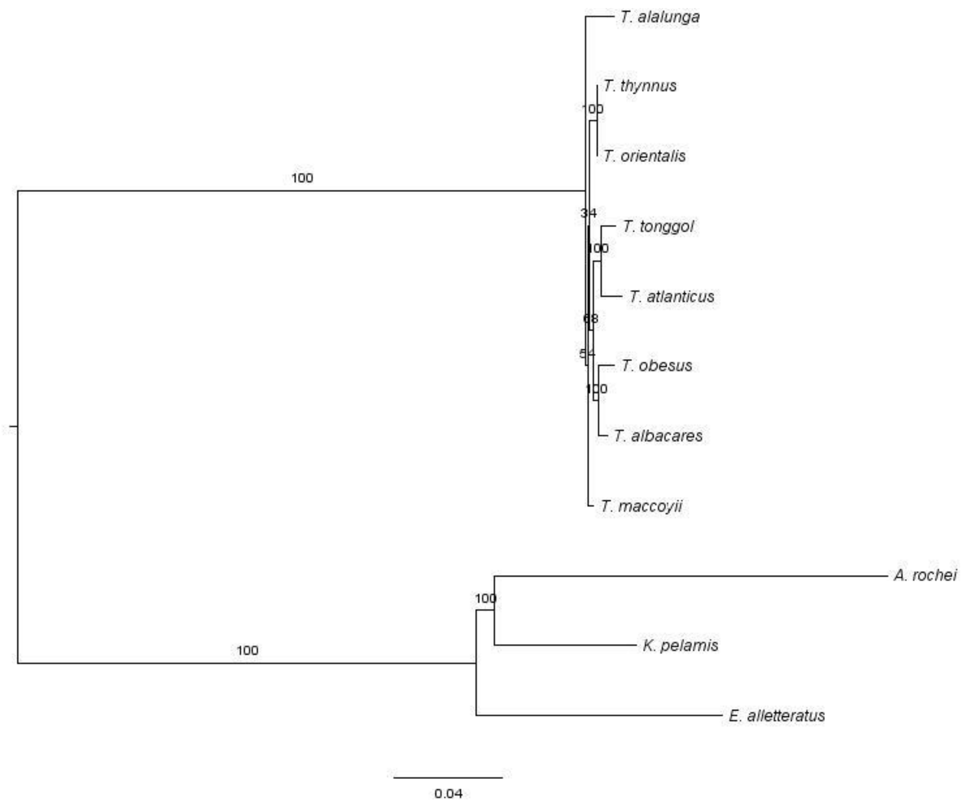
Tree 7: M=1, n=4, all species, per individuals, 25% missing, fixed positions.



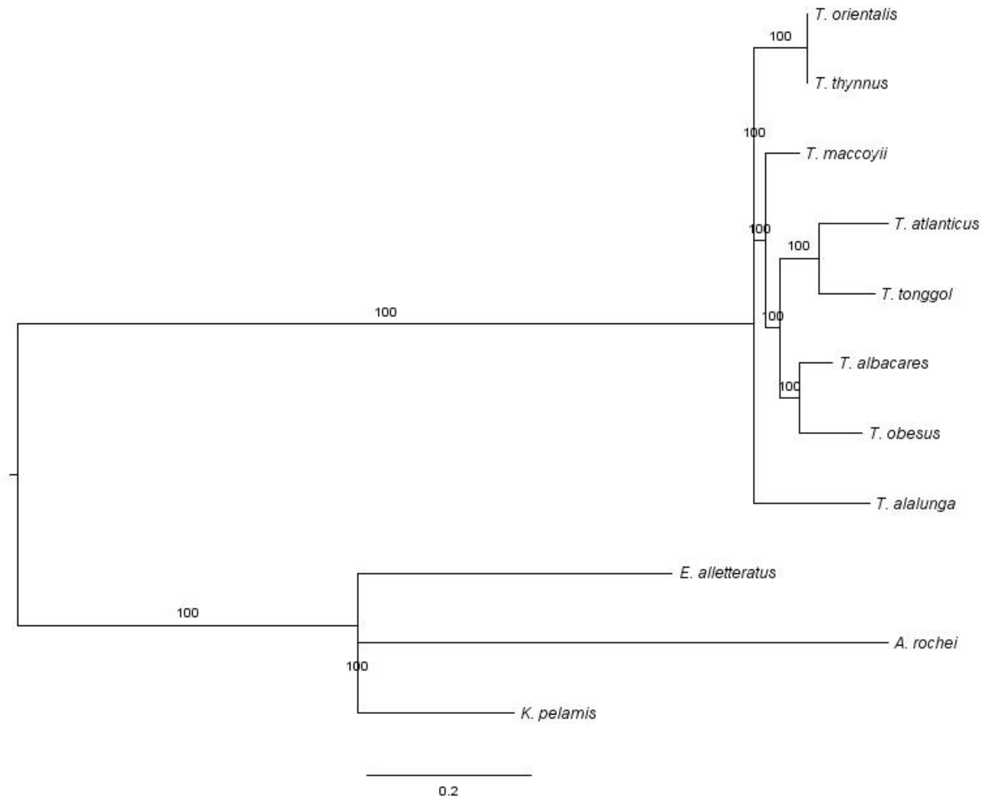
Tree 8: M=1, n=4, all species, per individuals, 25% missing, IUPAC encoded sites.



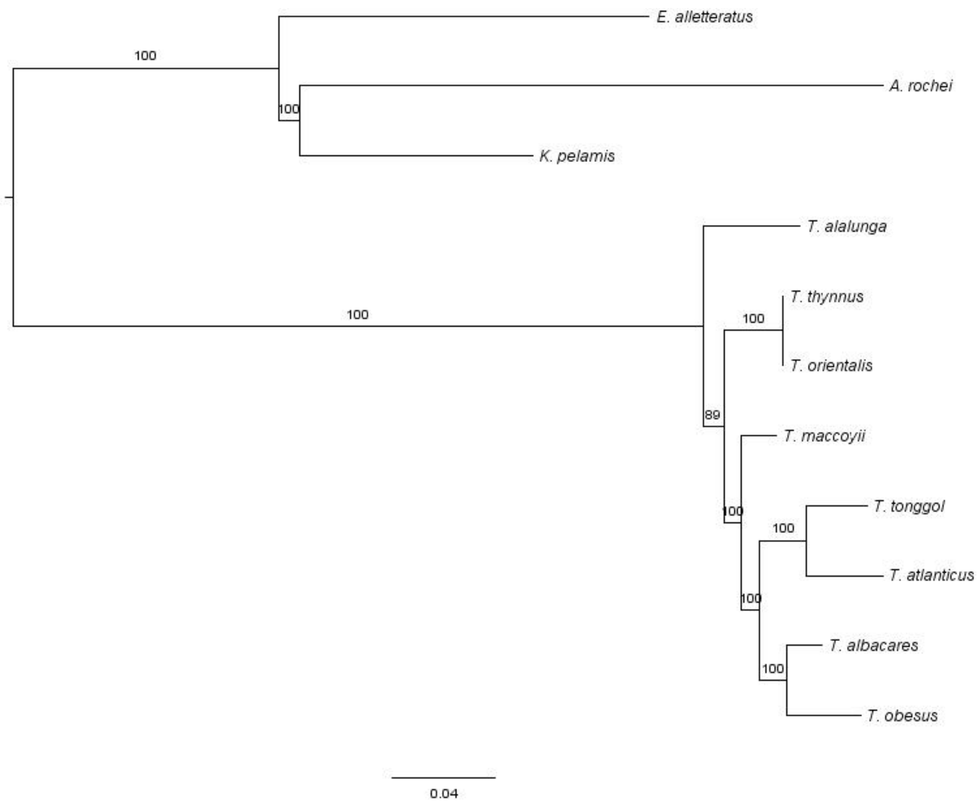
Tree 9: M=1, n=4, all species, per species, 0% missing, fixed positions.



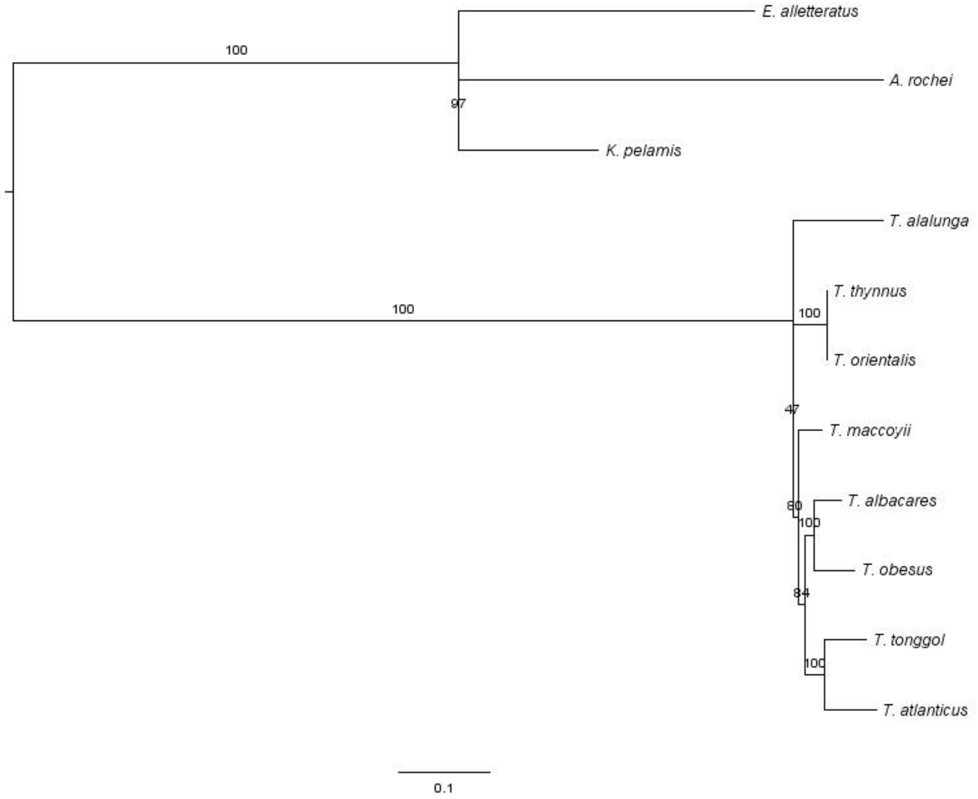
Tree 10: M=1, n=4, all species, per species, 0% missing, IUPAC encoded sites.



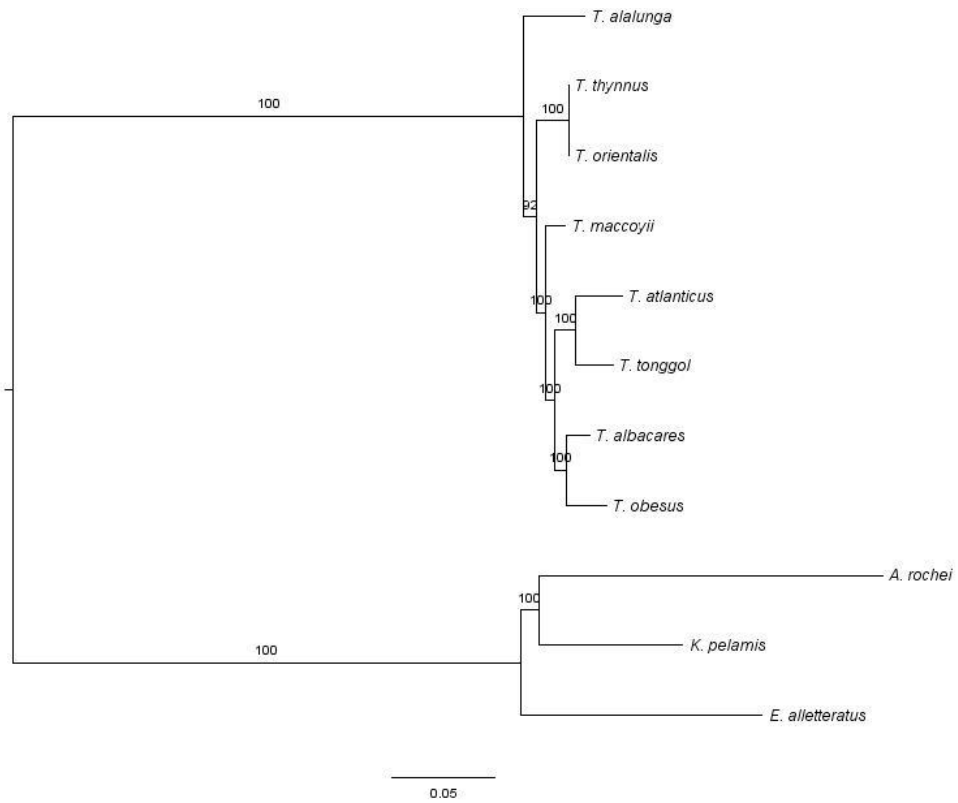
Tree 11: M=1, n=4, all species, per species, 75% missing, fixed positions.



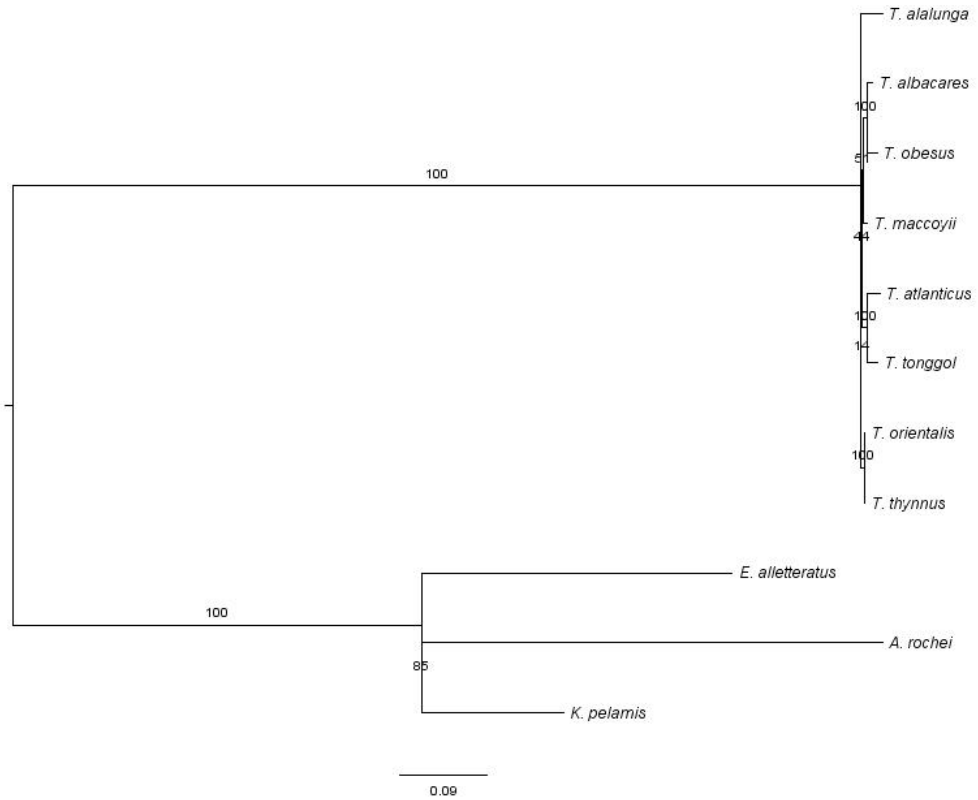
Tree 12: M=1, n=4, all species, per species, 75% missing, IUPAC encoded sites.



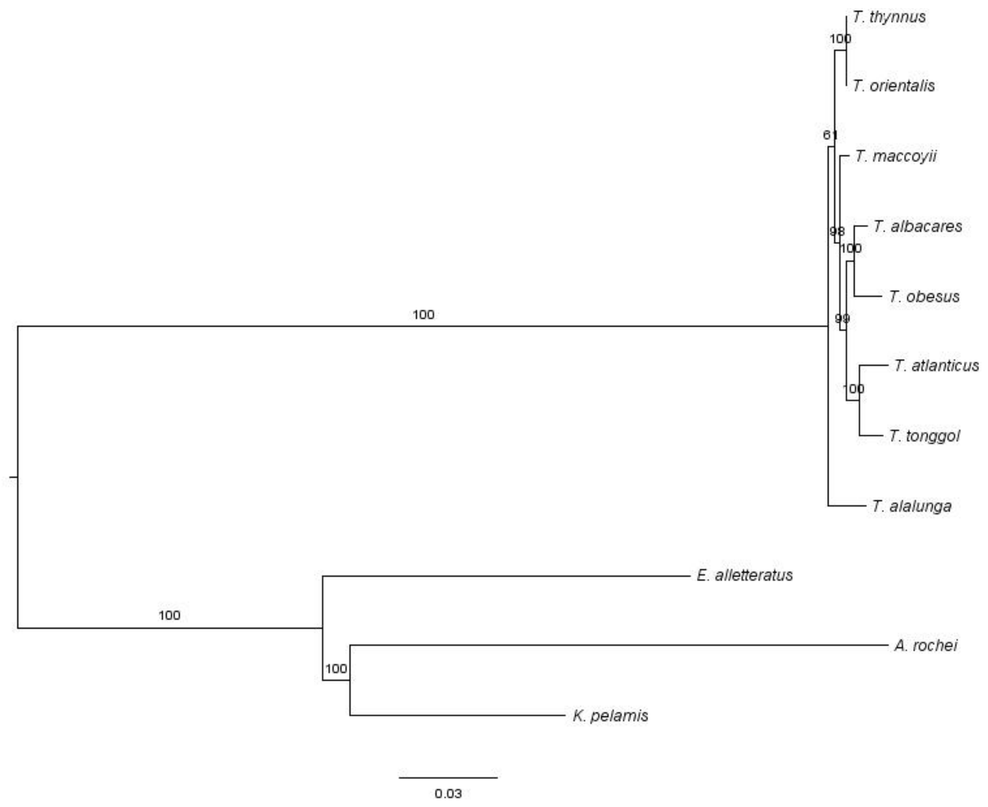
Tree 13: M=1, n=4, all species, per species, 50% missing, fixed positions.



Tree 14: M=1, n=4, all species, per species, 50% missing, IUPAC encoded sites.



Tree 15: M=1, n=4, all species, per species, 25% missing, fixed positions.



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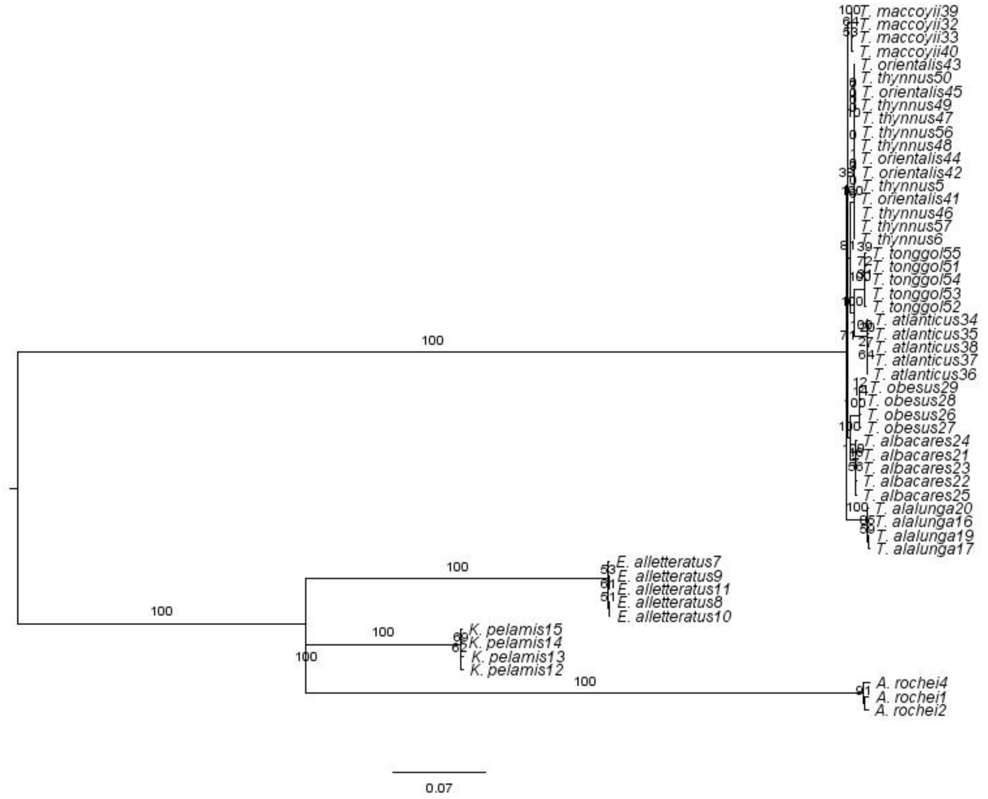
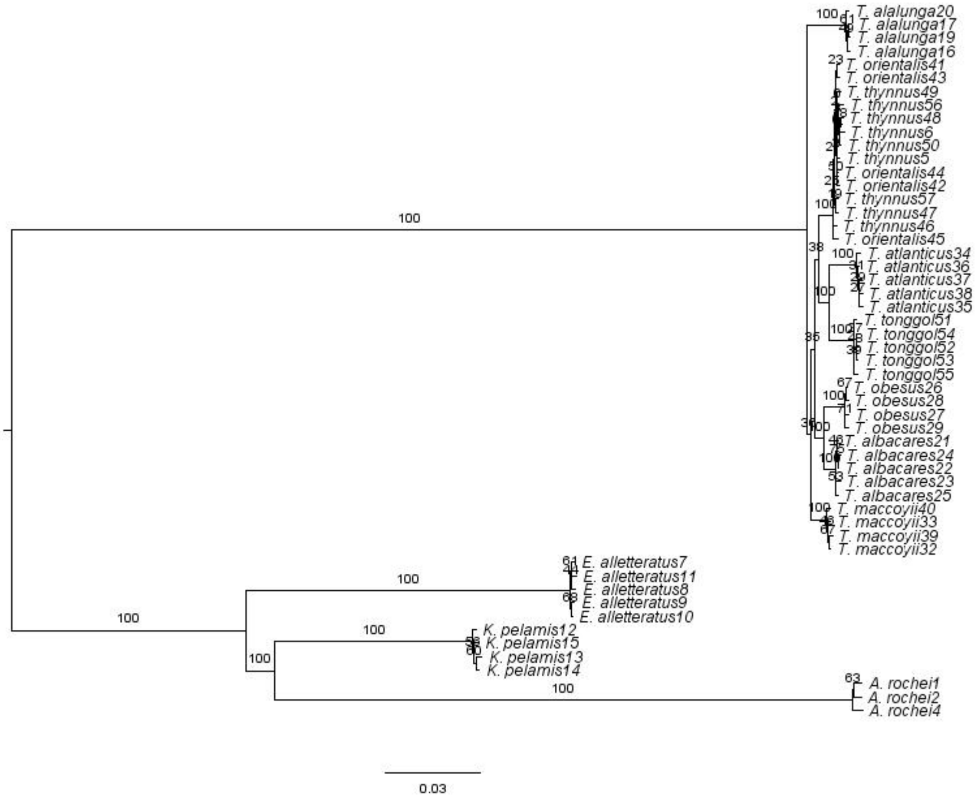


Tree 17: M=1, n=8, all species, per individuals, 0% missing, fixed positions.



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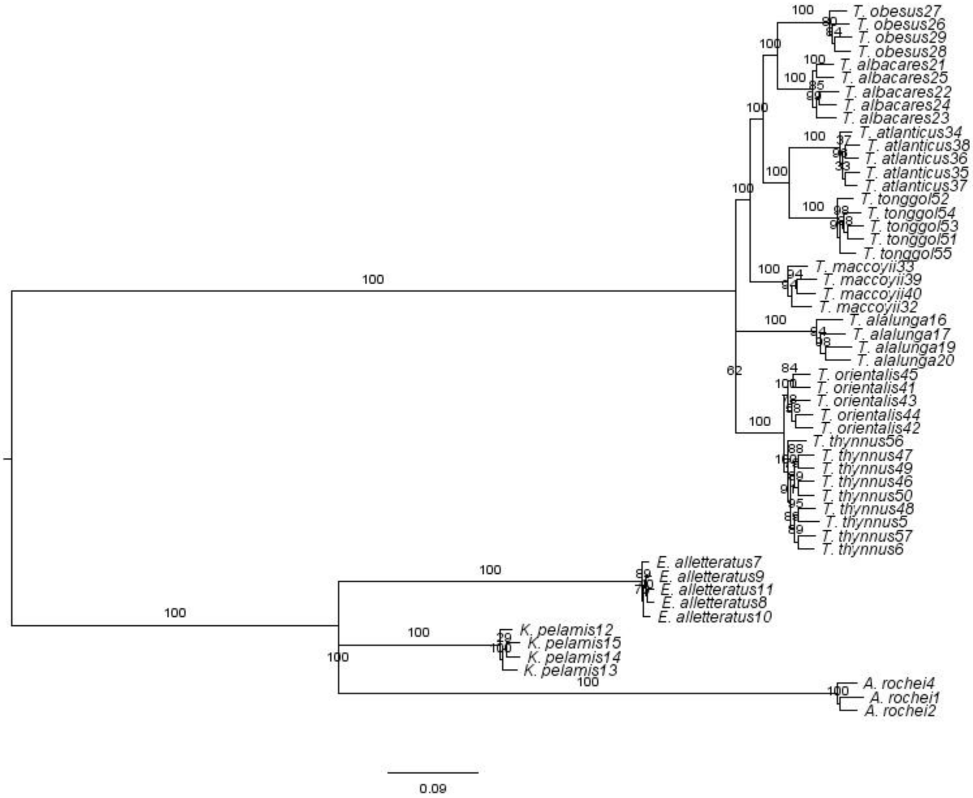
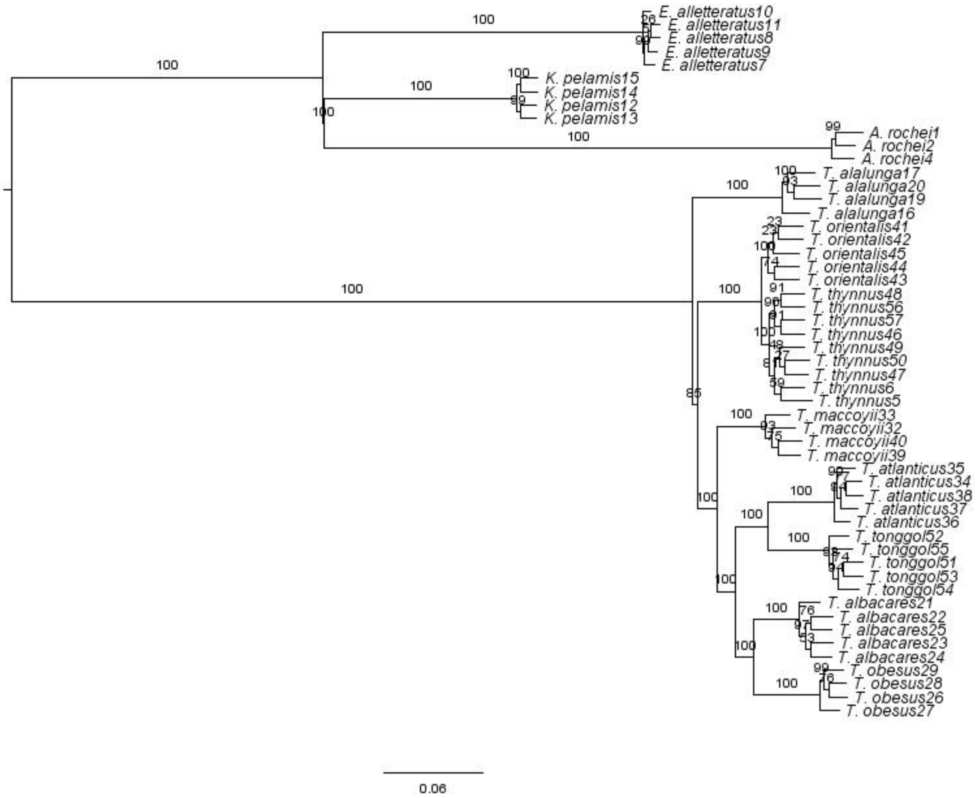


Tree 19: M=1, n=8, all species, per individuals, 75% missing, fixed positions.



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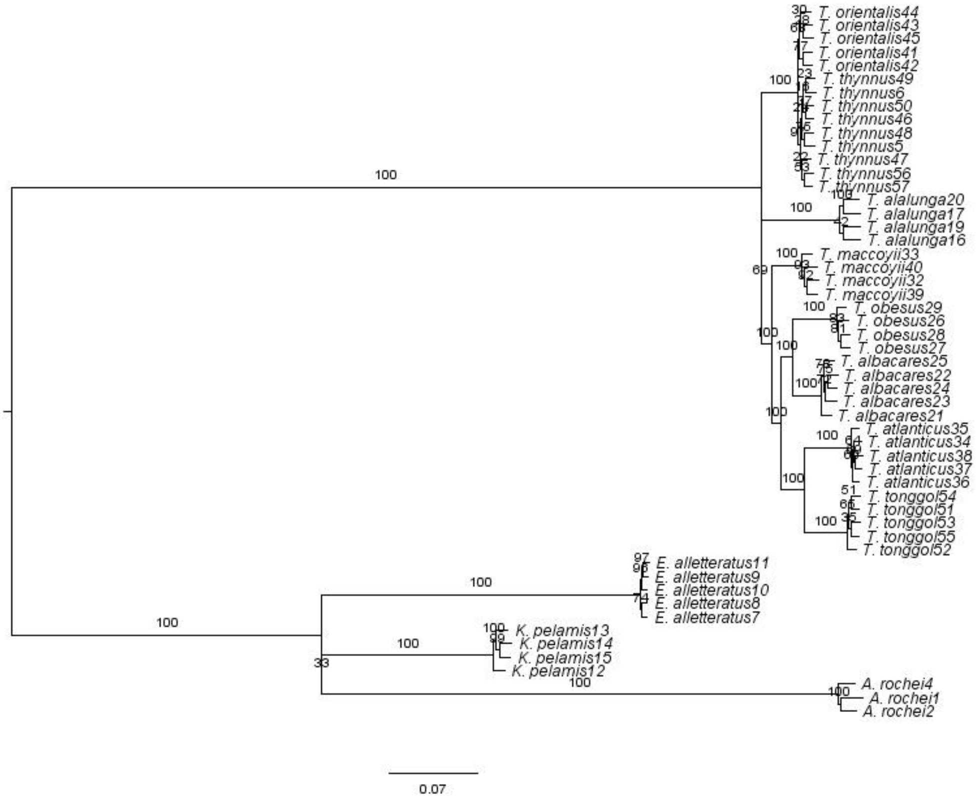
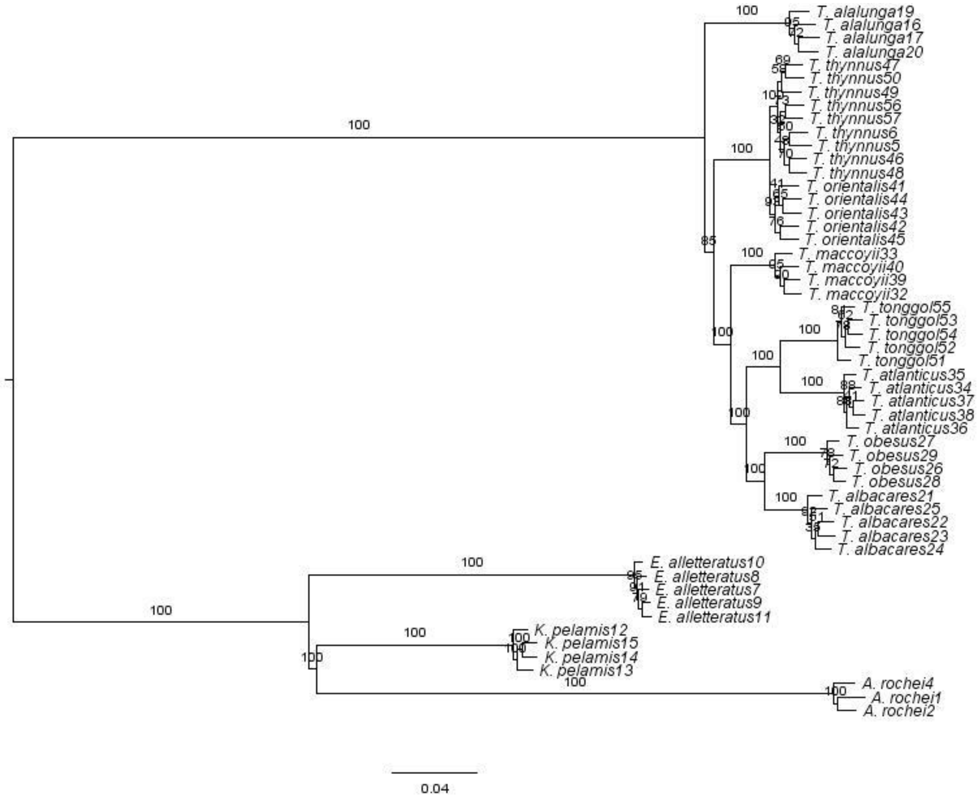


Tree 21: M=1, n=8, all species, per individuals, 50% missing, fixed positions.



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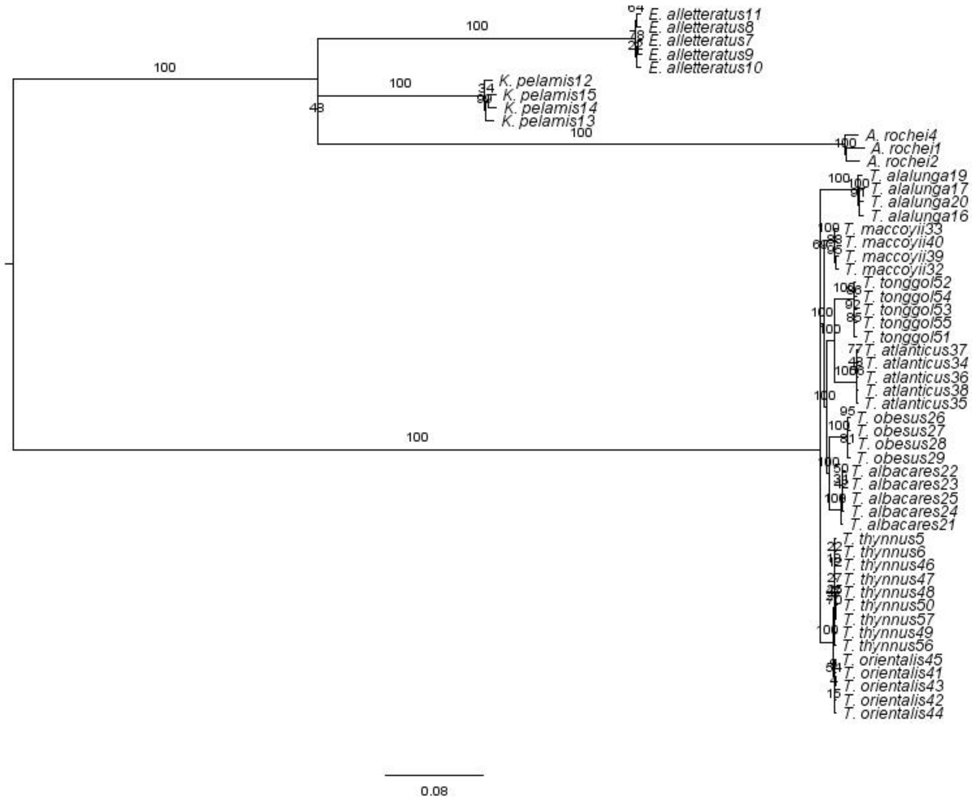
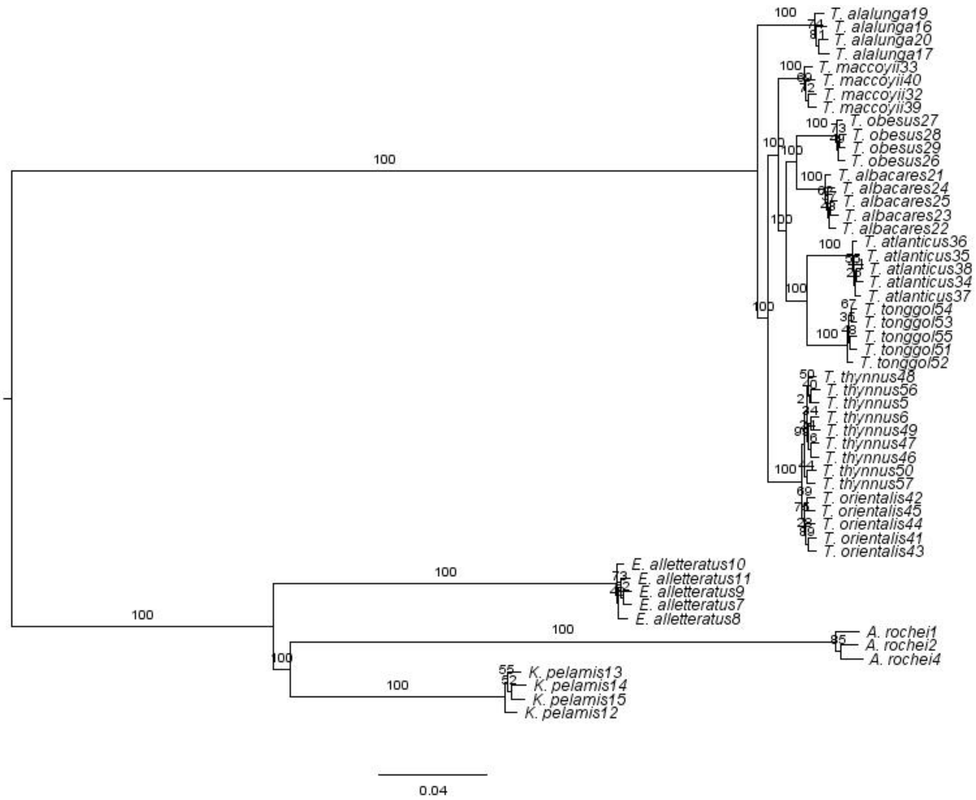


Tree 23: M=1, n=8, all species, per individuals, 25% missing, fixed positions.



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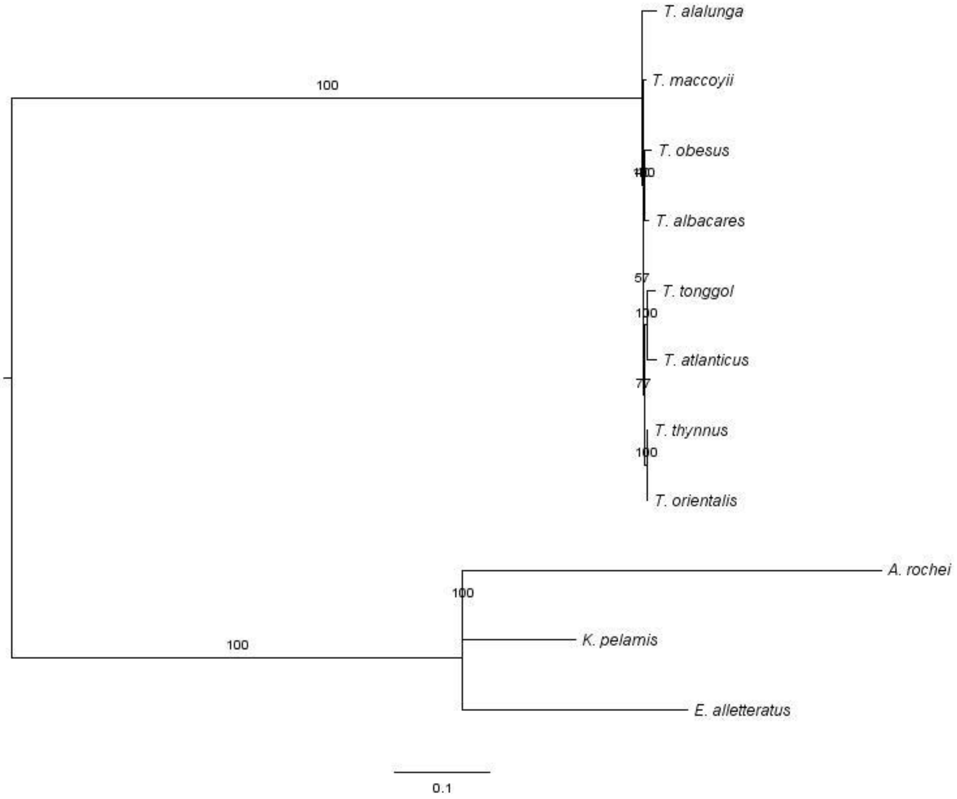

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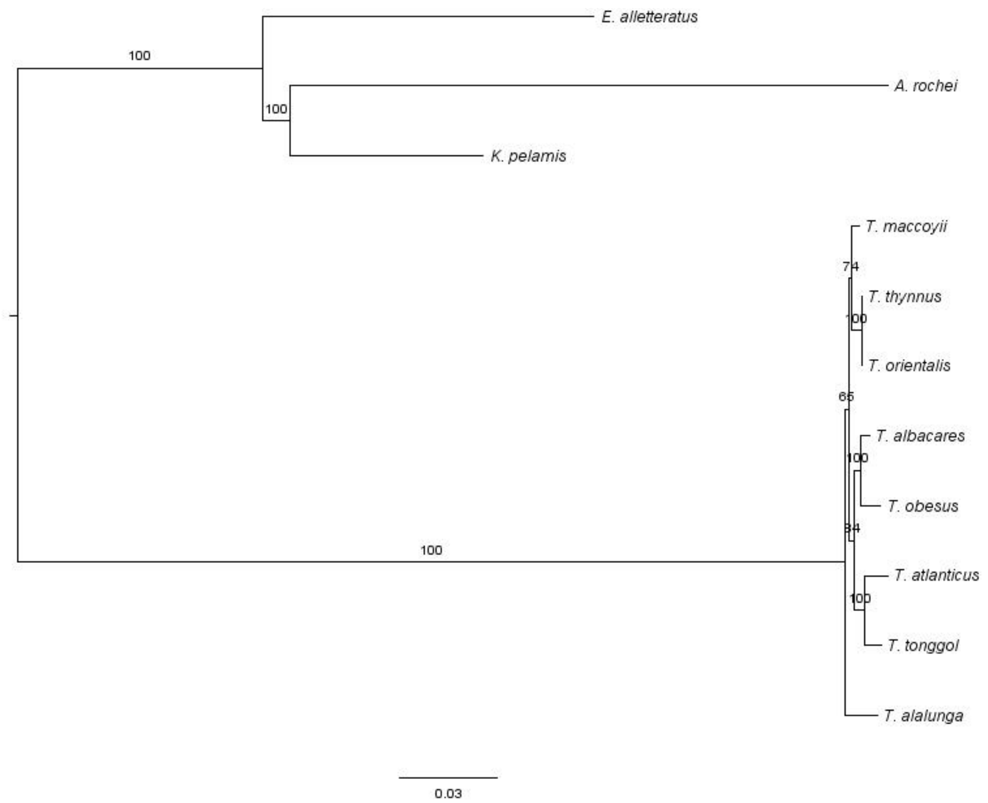

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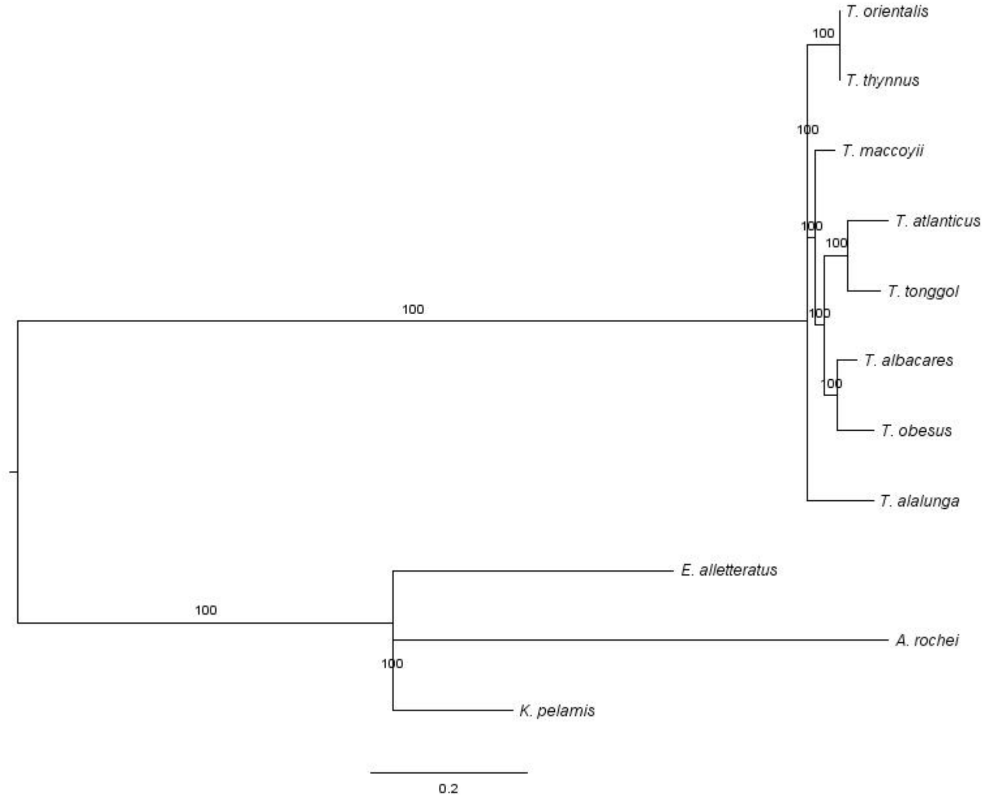
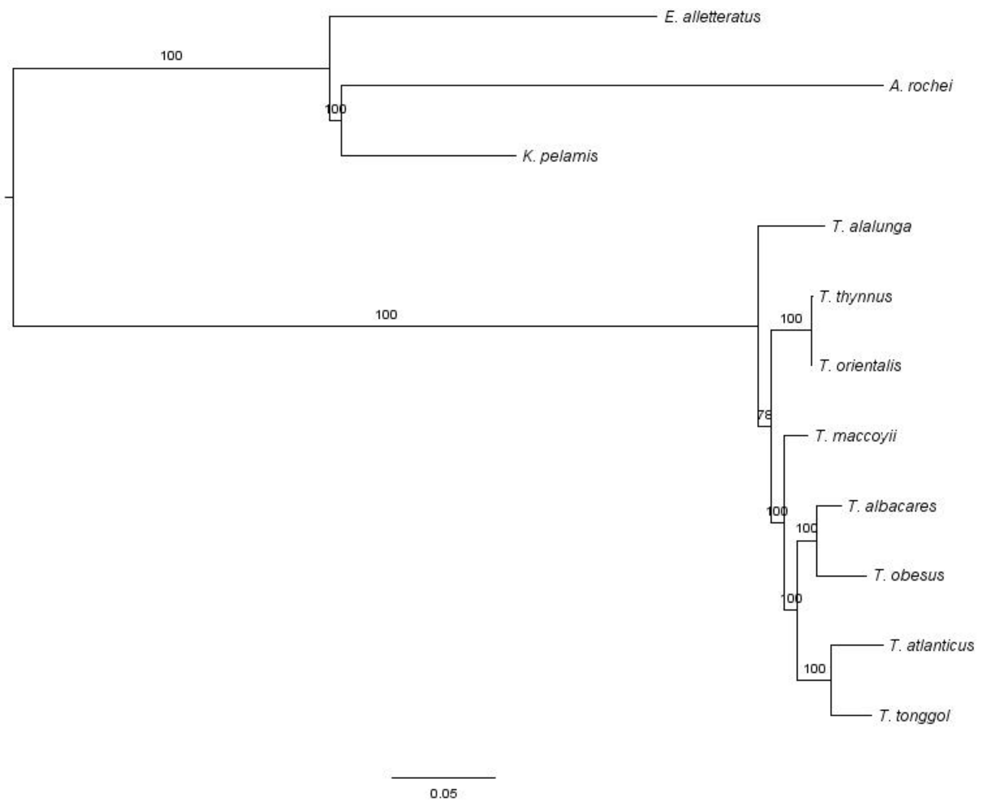


Tree 27: M=1, n=8, all species, per species, 75% missing, fixed positions.



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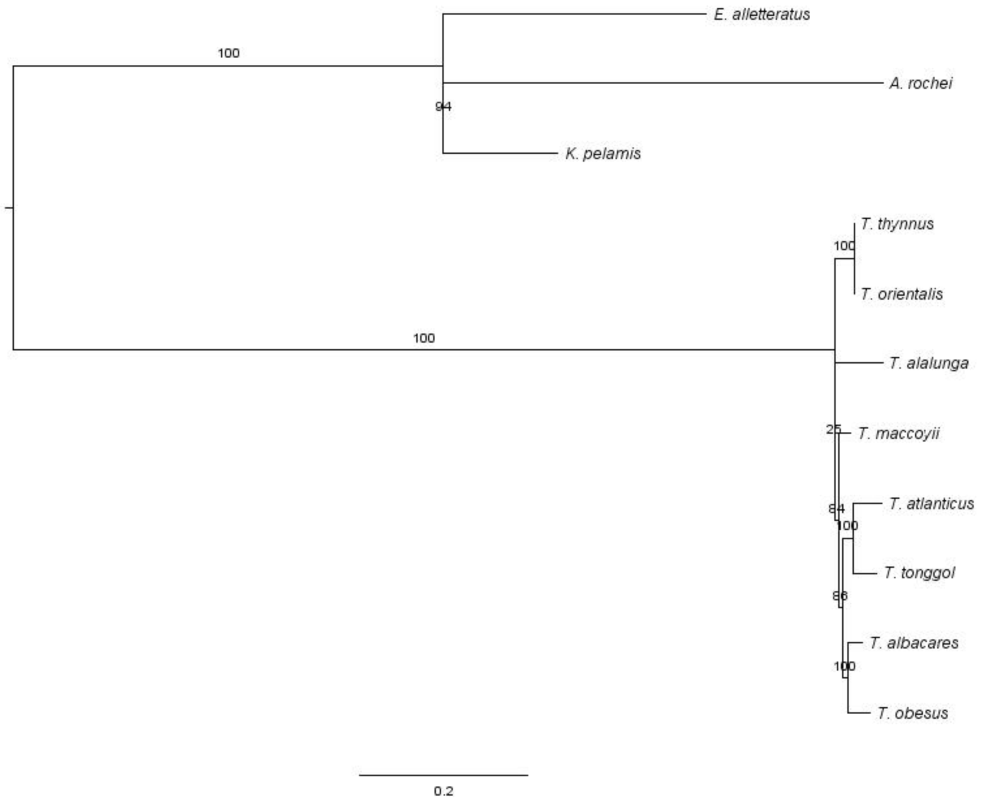
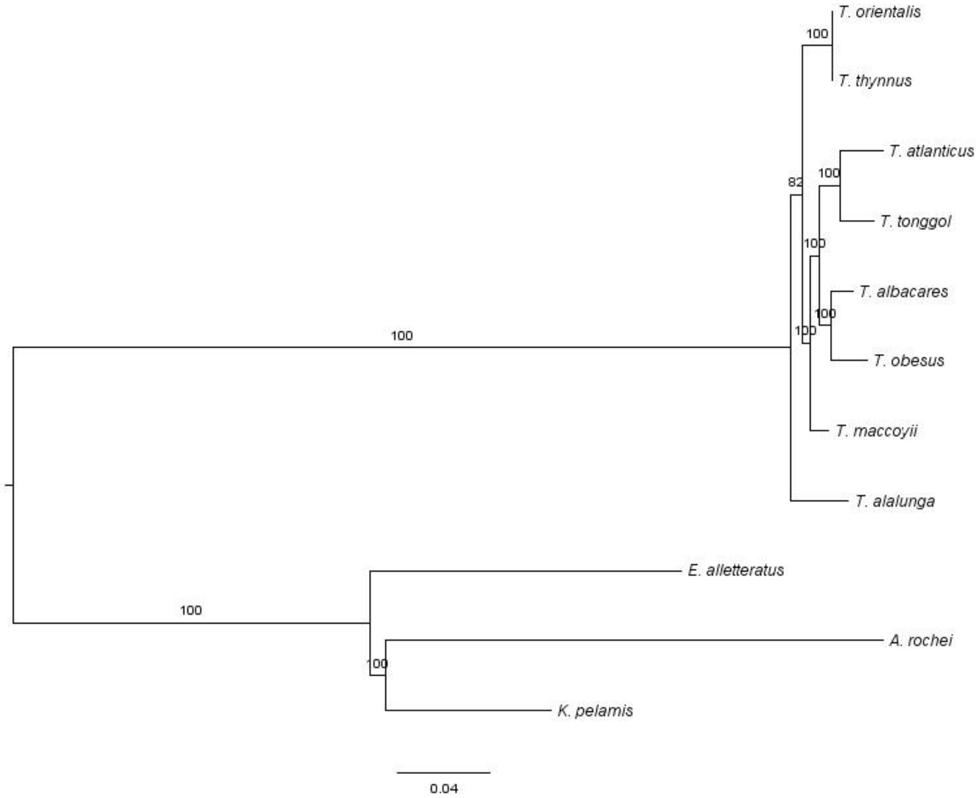


Tree 29: M=1, n=8, all species, per species, 50% missing, fixed positions.



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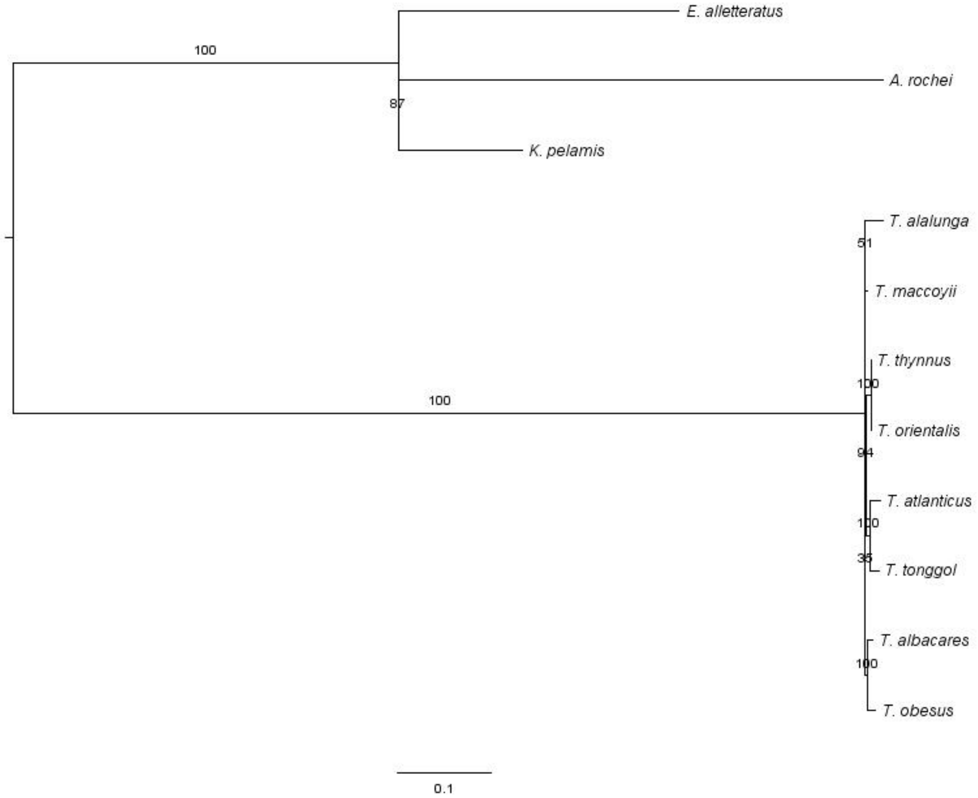
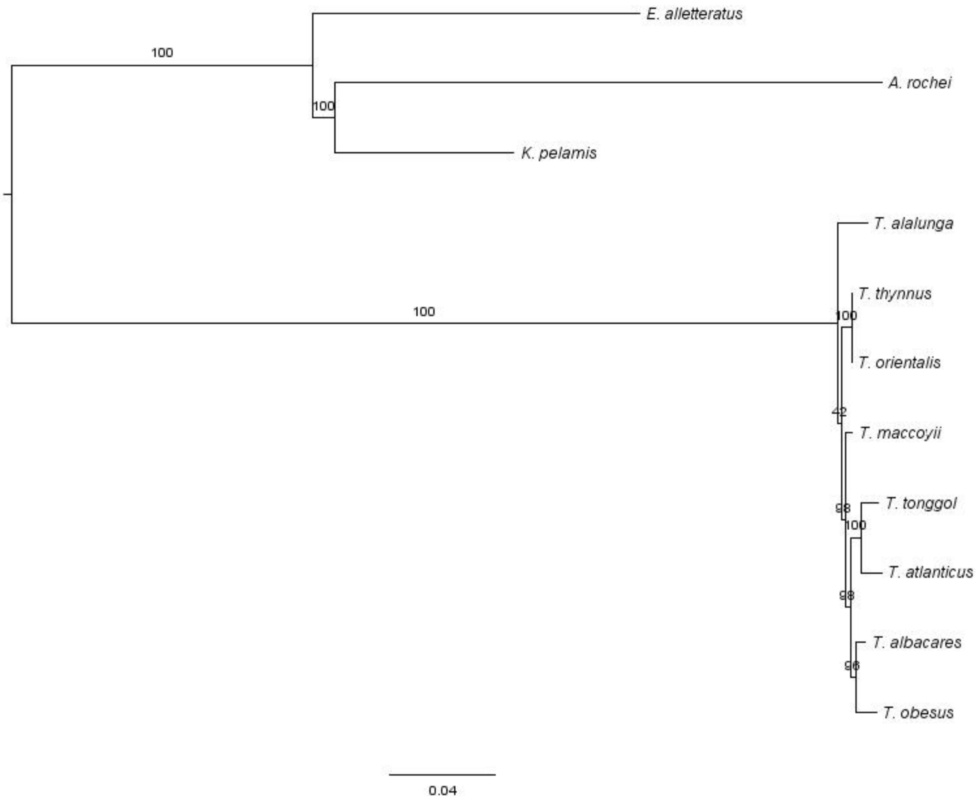


Tree 31: M=1, n=8, all species, per species, 25% missing, fixed positions.



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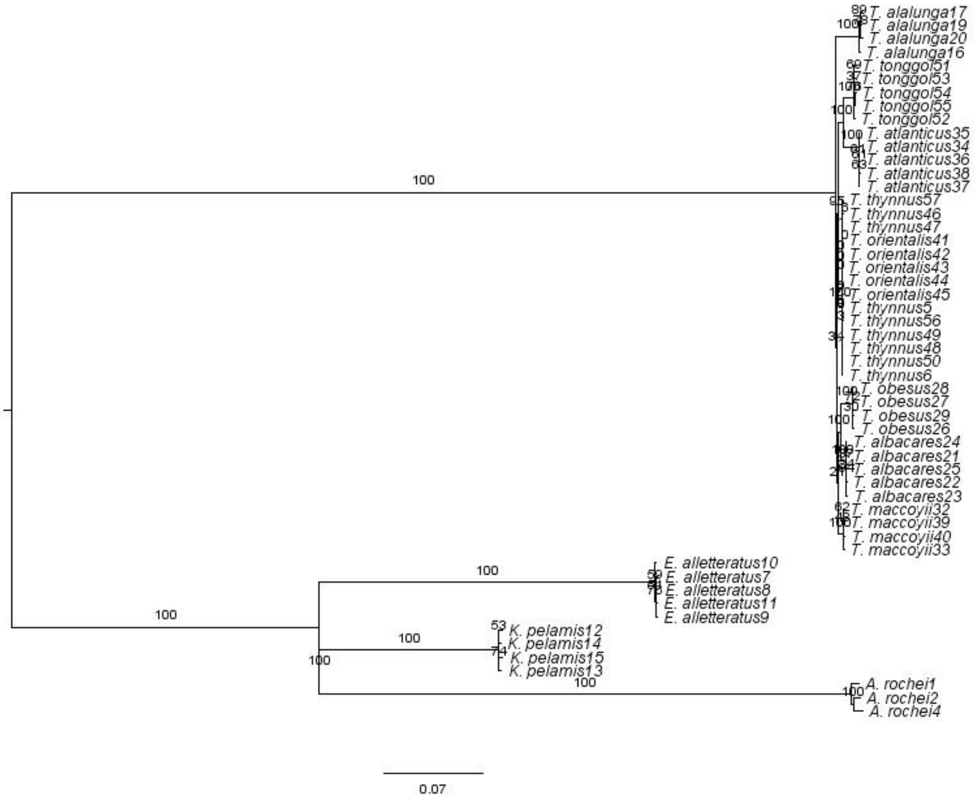
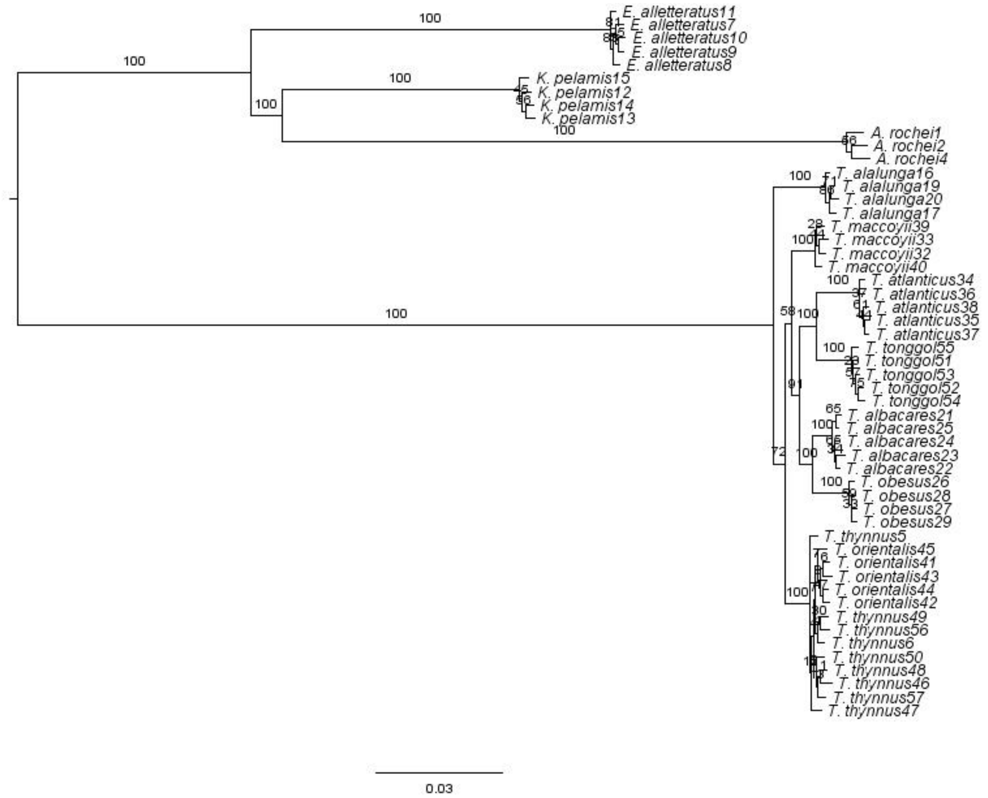


Tree 33: M=2, n=4, all species, per individuals, 0% missing, fixed positions.



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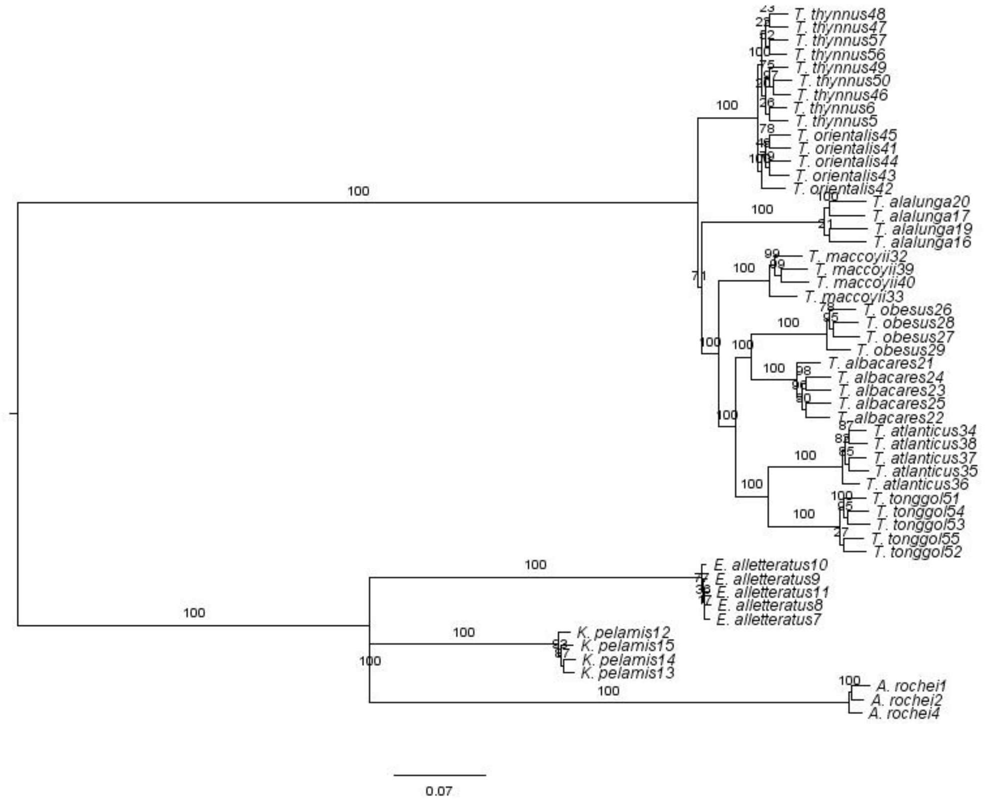
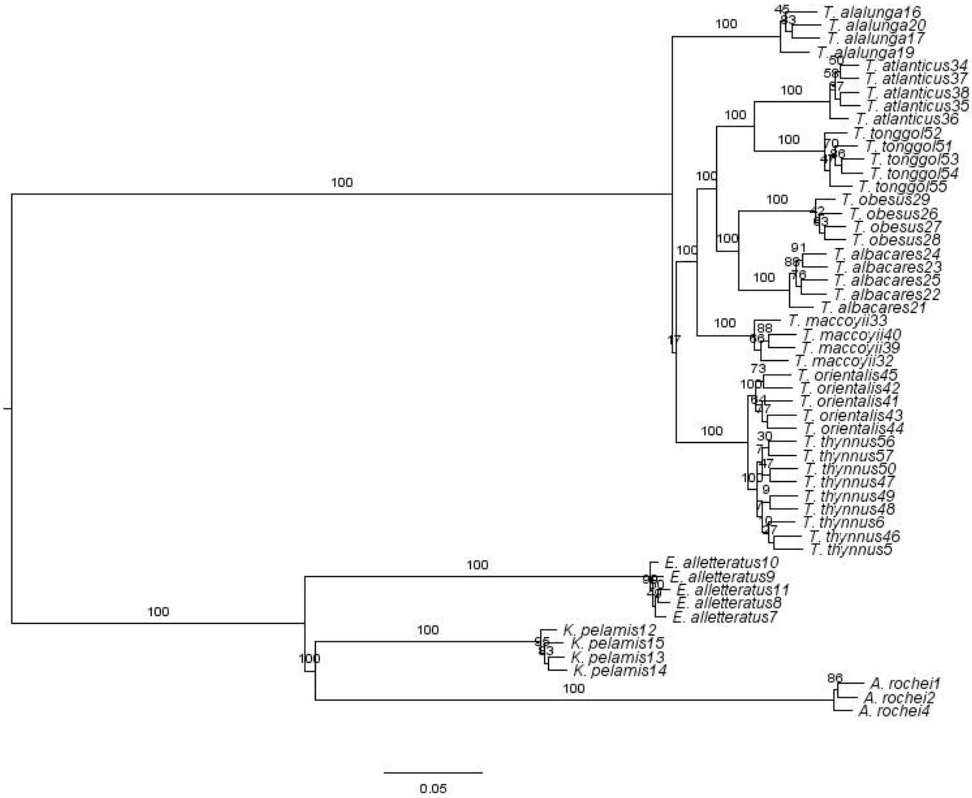


Tree 35: M=2, n=4, all species, per individuals, 75% missing, fixed positions.



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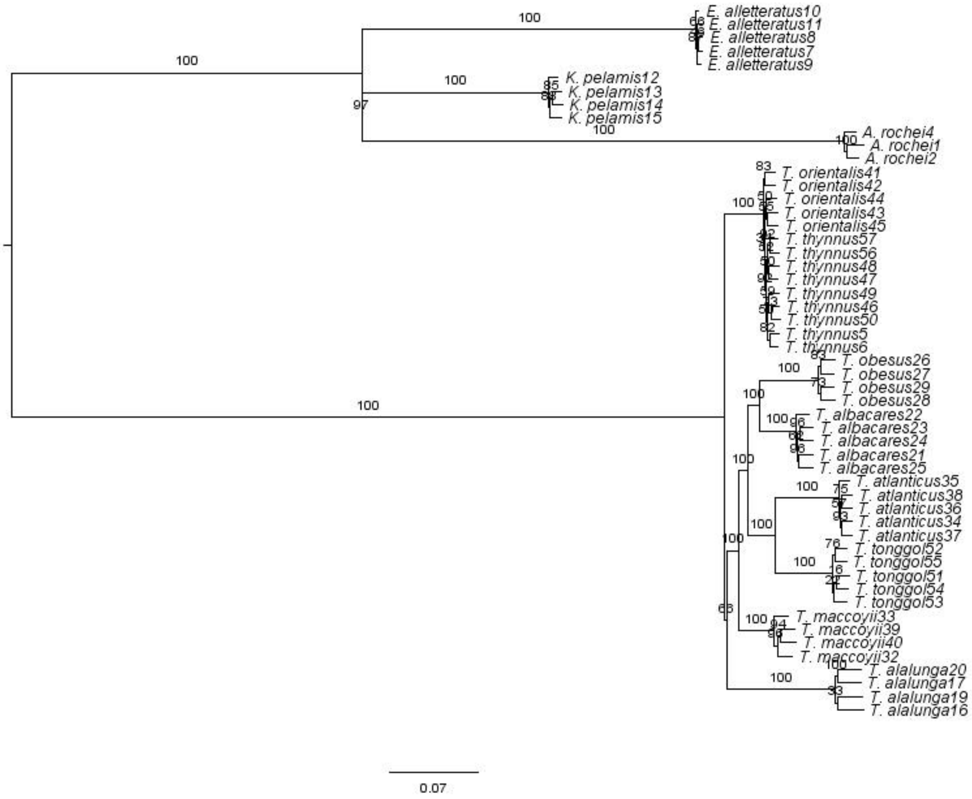
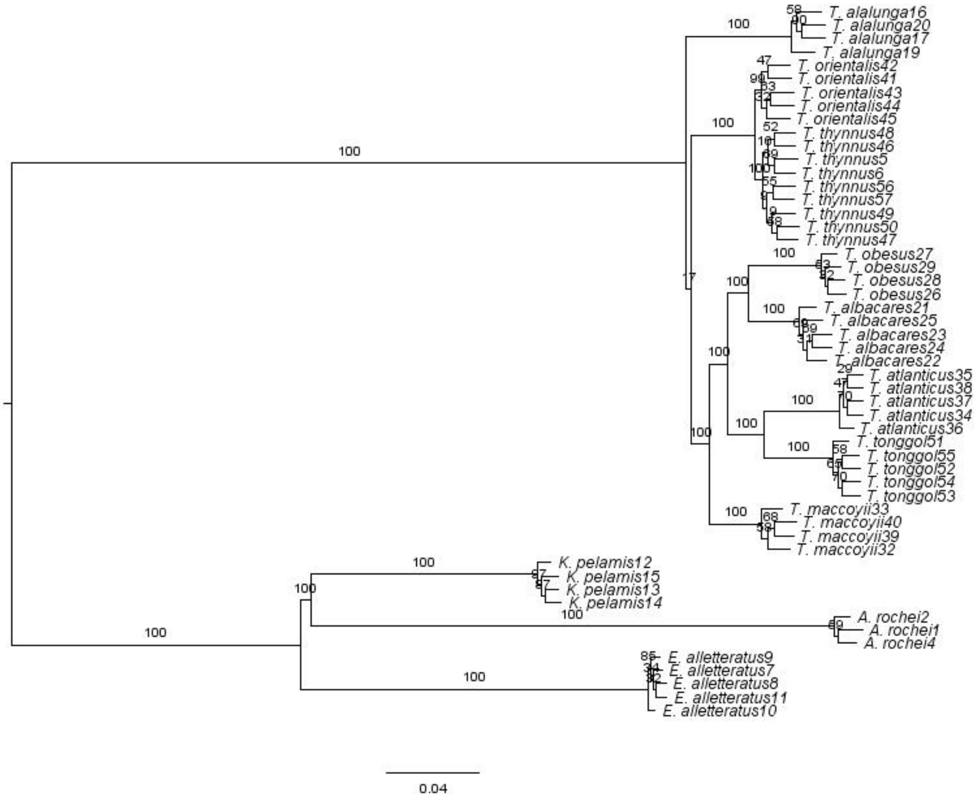
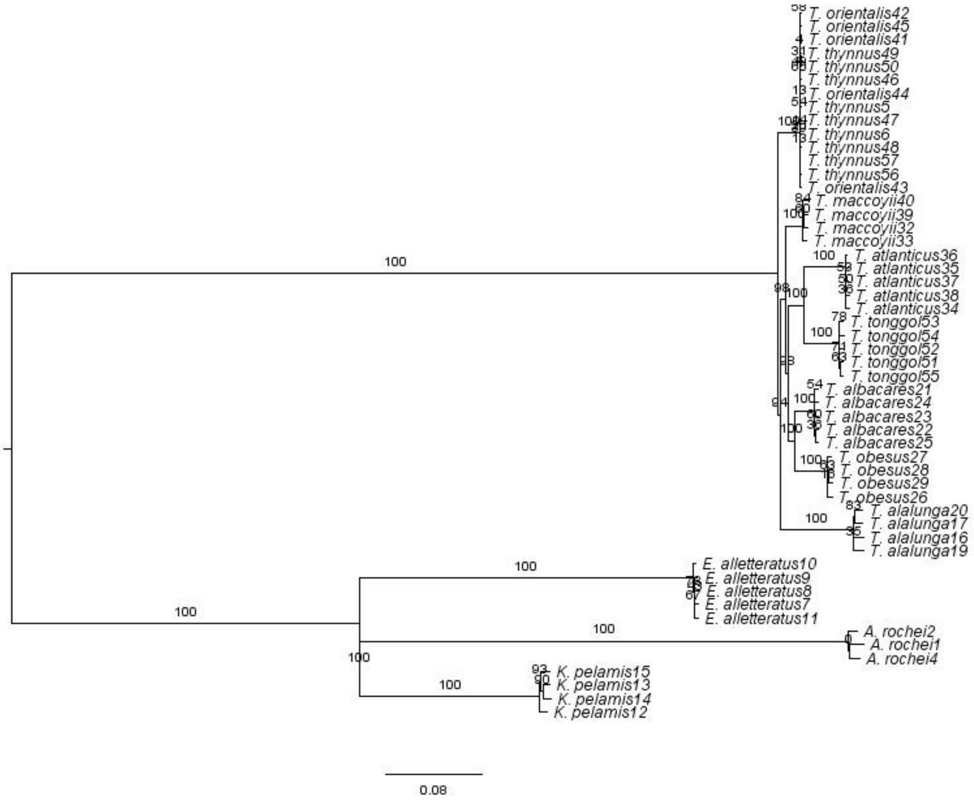


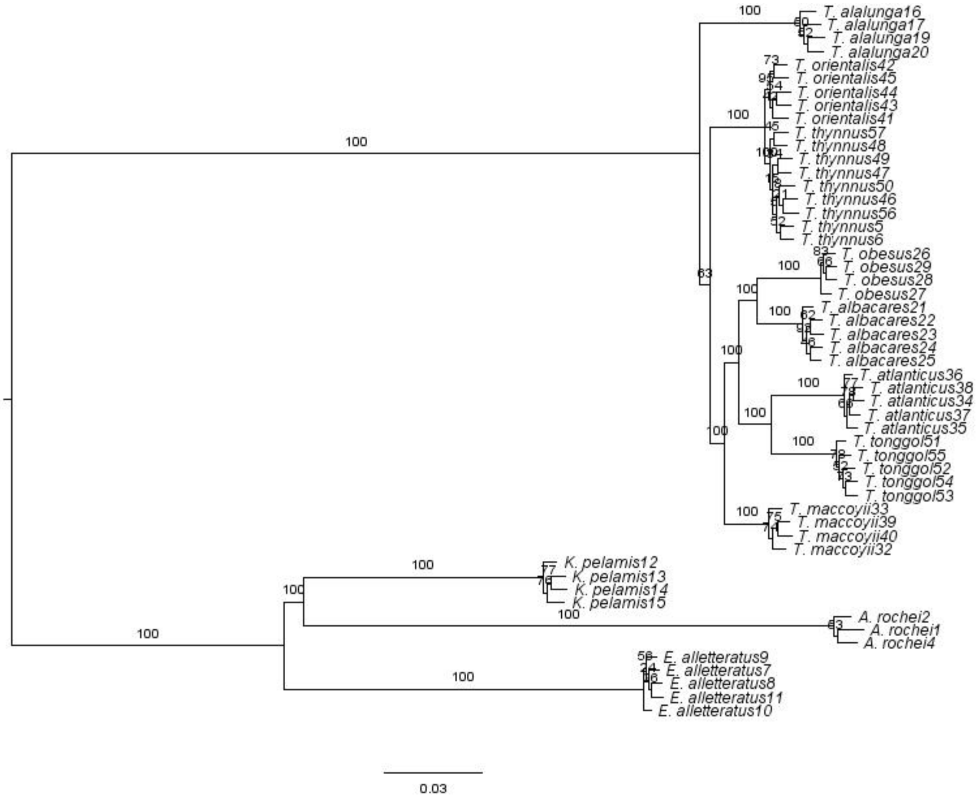
Tree 37: M=2, n=4, all species, per individuals, 50% missing, fixed positions.



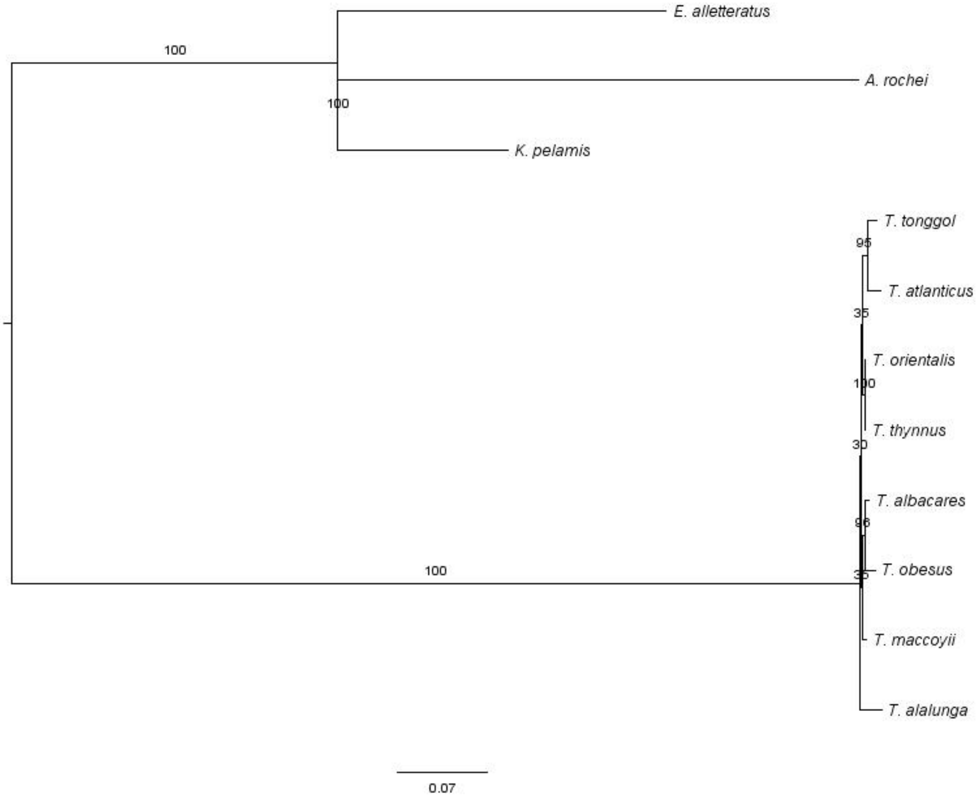
Tree 38: M=2, n=4, all species, per individuals, 50% missing, IUPAC encoded sites.



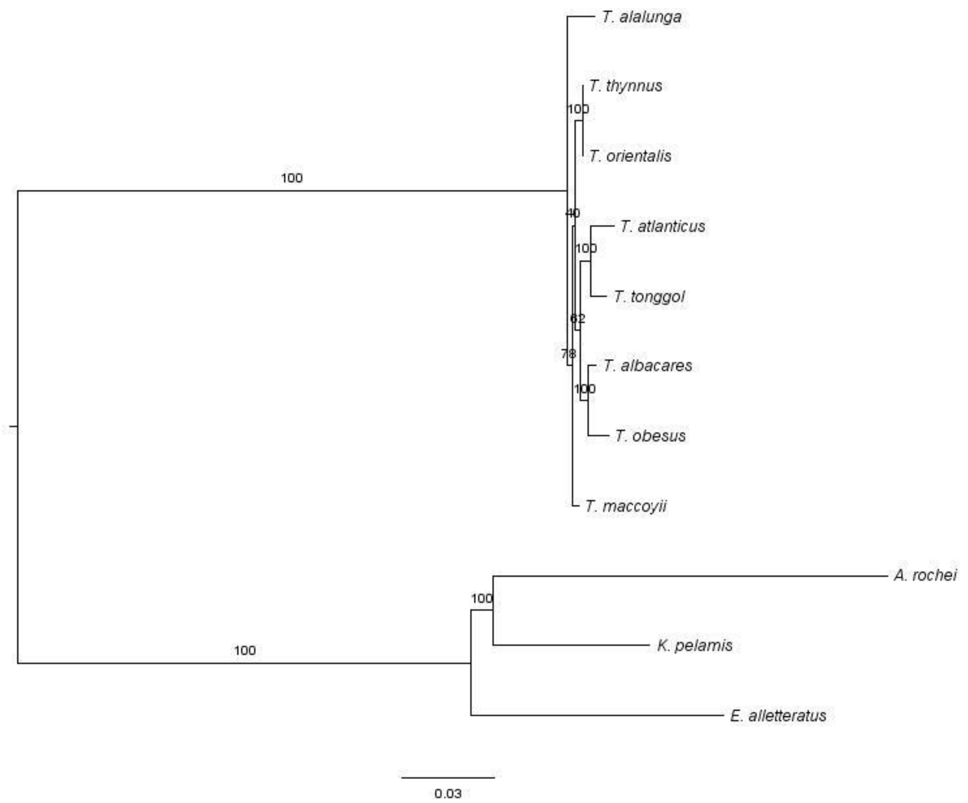
Tree 39: M=2, n=4, all species, per individuals, 25% missing, fixed positions.



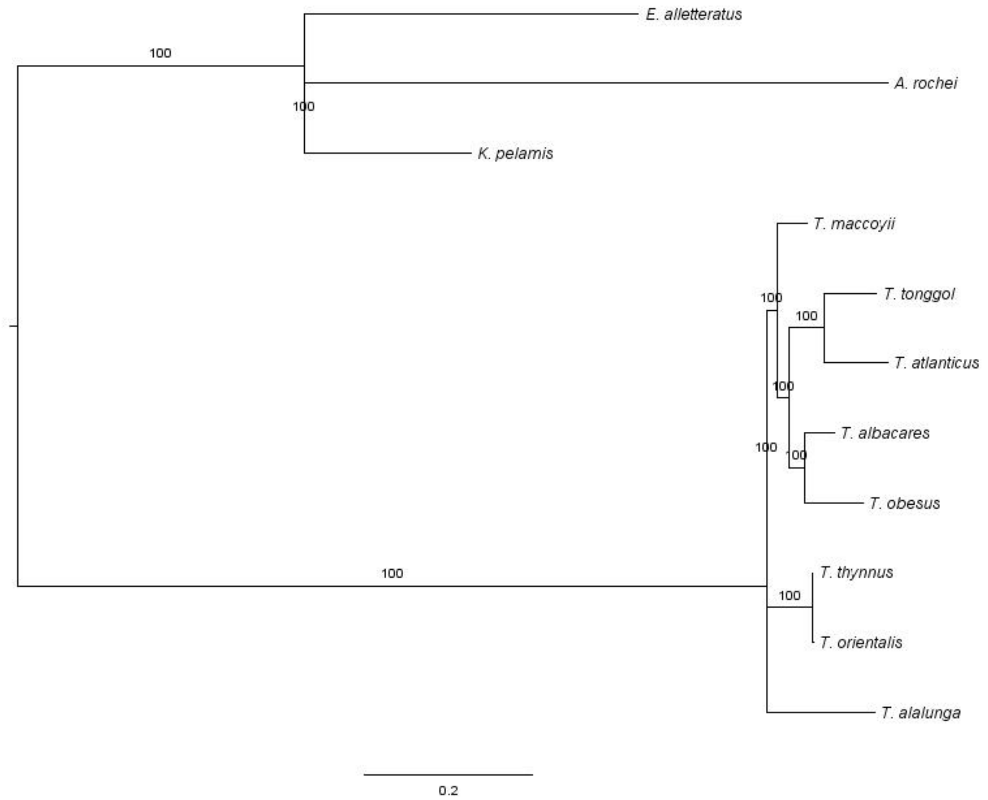
Tree 40: M=2, n=4, all species, per individuals, 25% missing, IUPAC encoded sites.



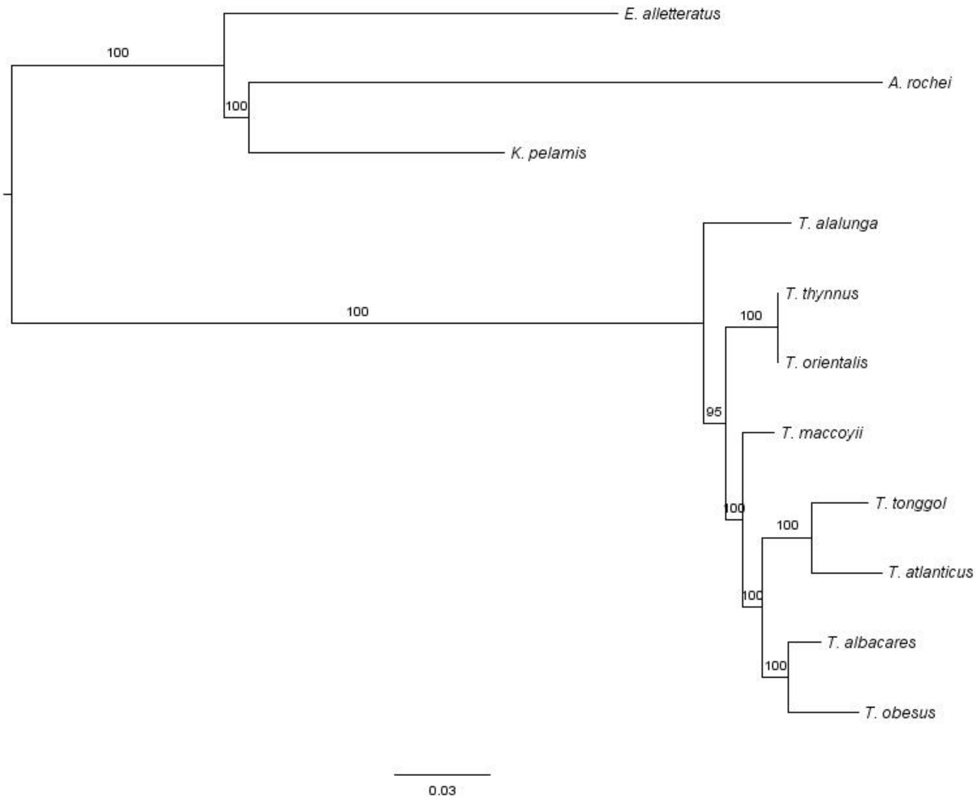
Tree 41: M=2, n=4, all species, per species, 0% missing, fixed positions.



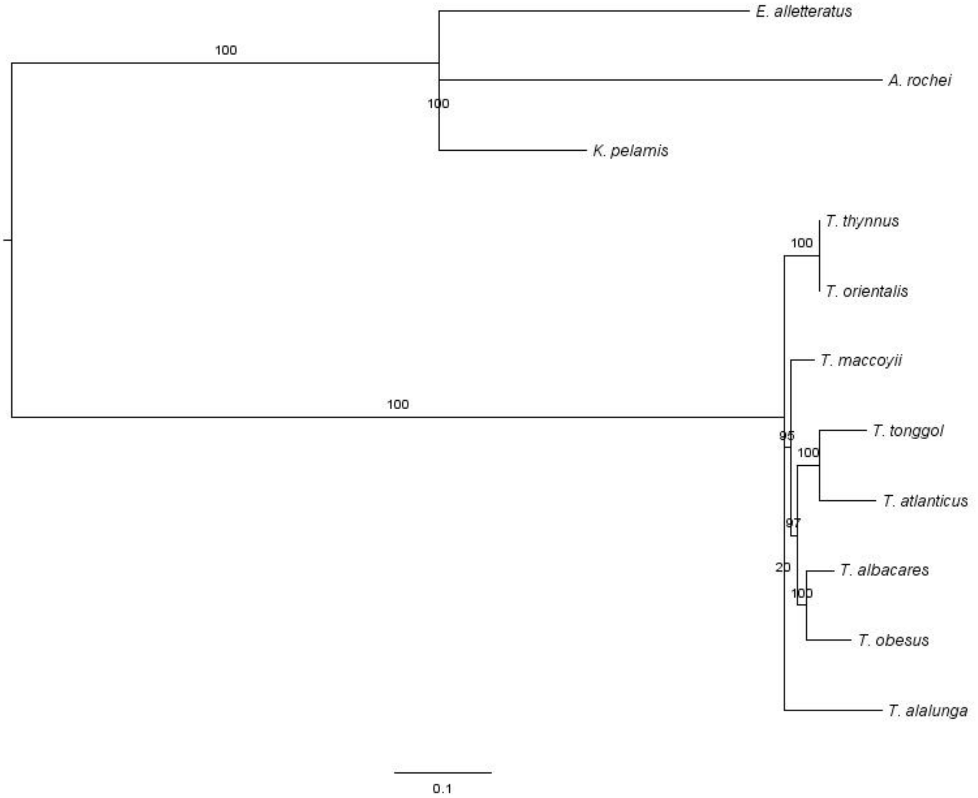
Tree 42: M=2, n=4, all species, per species, 0% missing, IUPAC encoded sites.



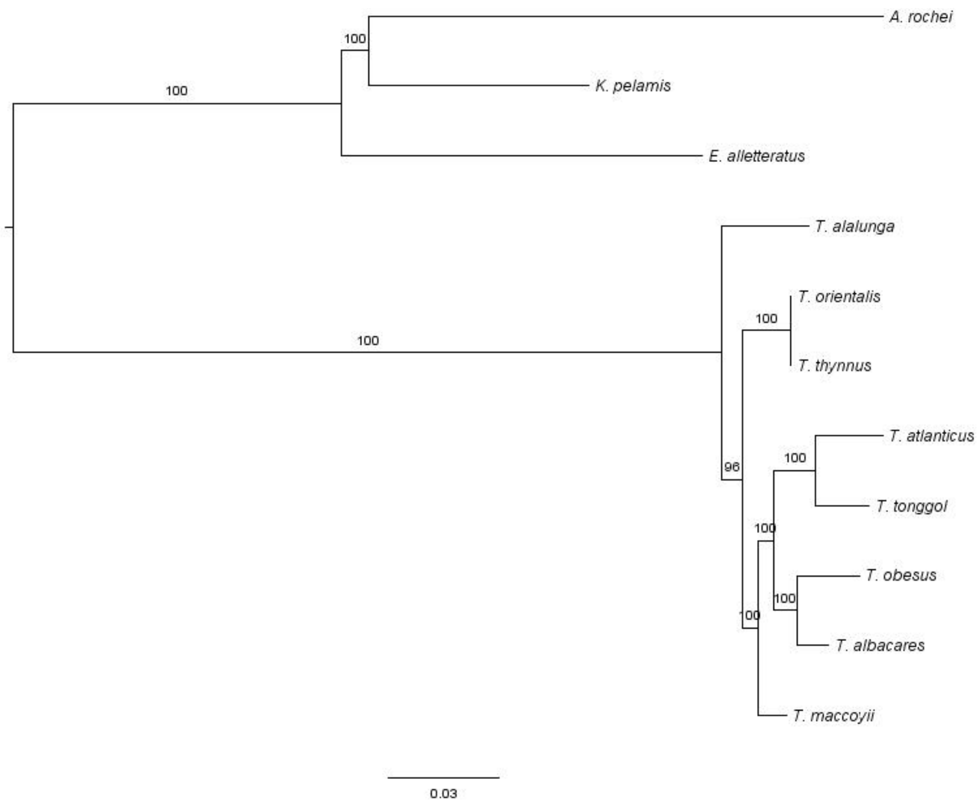
Tree 43: M=2, n=4, all species, per species, 75% missing, fixed positions.



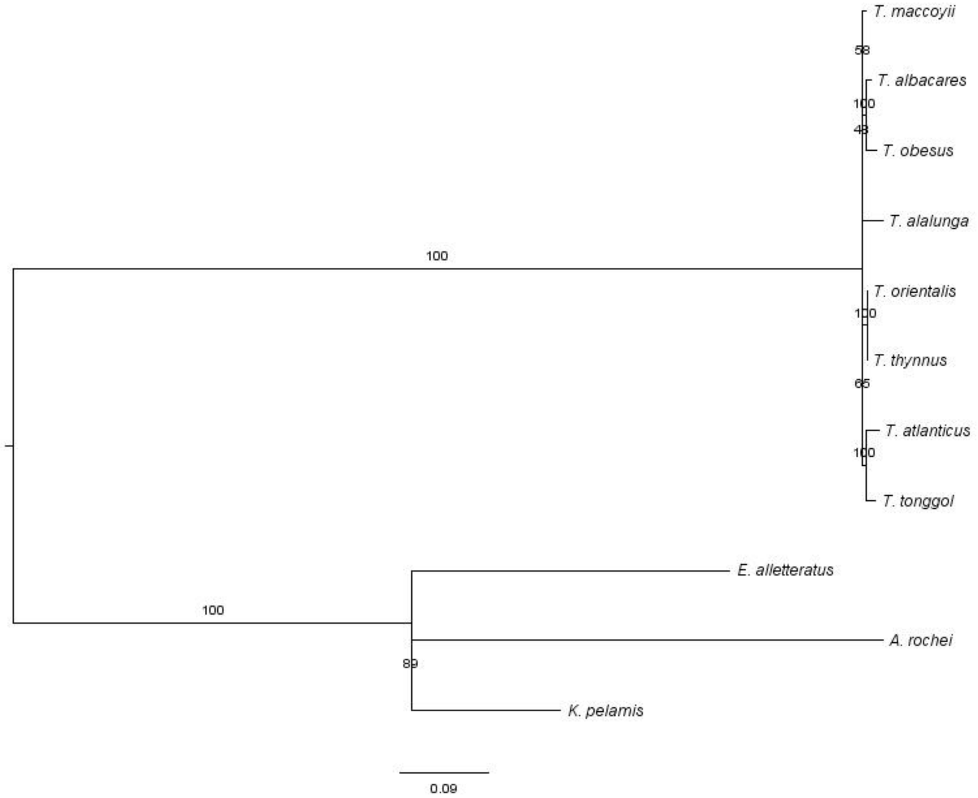
Tree 44: M=2, n=4, all species, per species, 75% missing, IUPAC encoded sites.



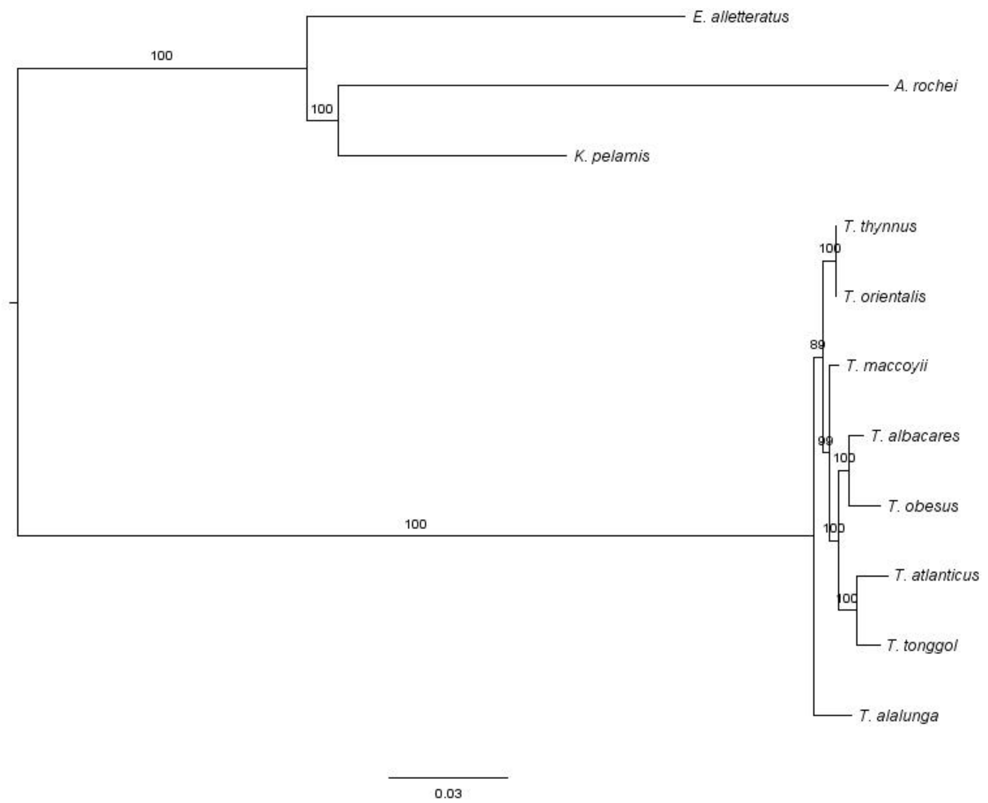
Tree 45: M=2, n=4, all species, per species, 50% missing, fixed positions.



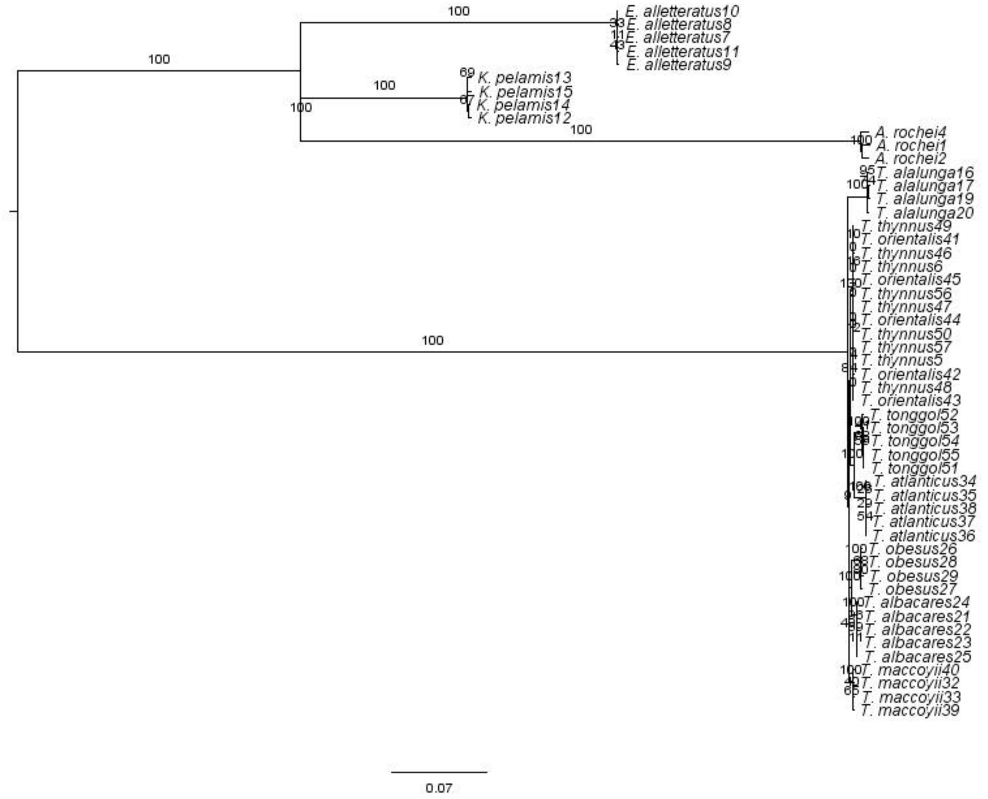
Tree 46: M=2, n=4, all species, per species, 50% missing, IUPAC encoded sites.



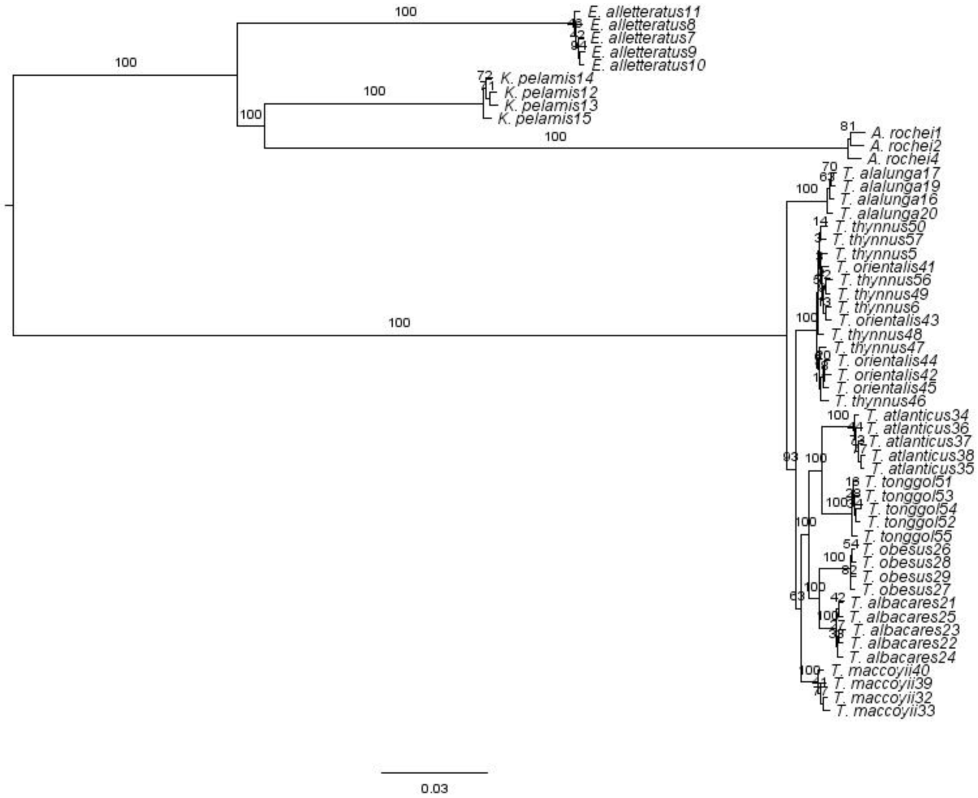
Tree 47: M=2, n=4, all species, per species, 25% missing, fixed positions.



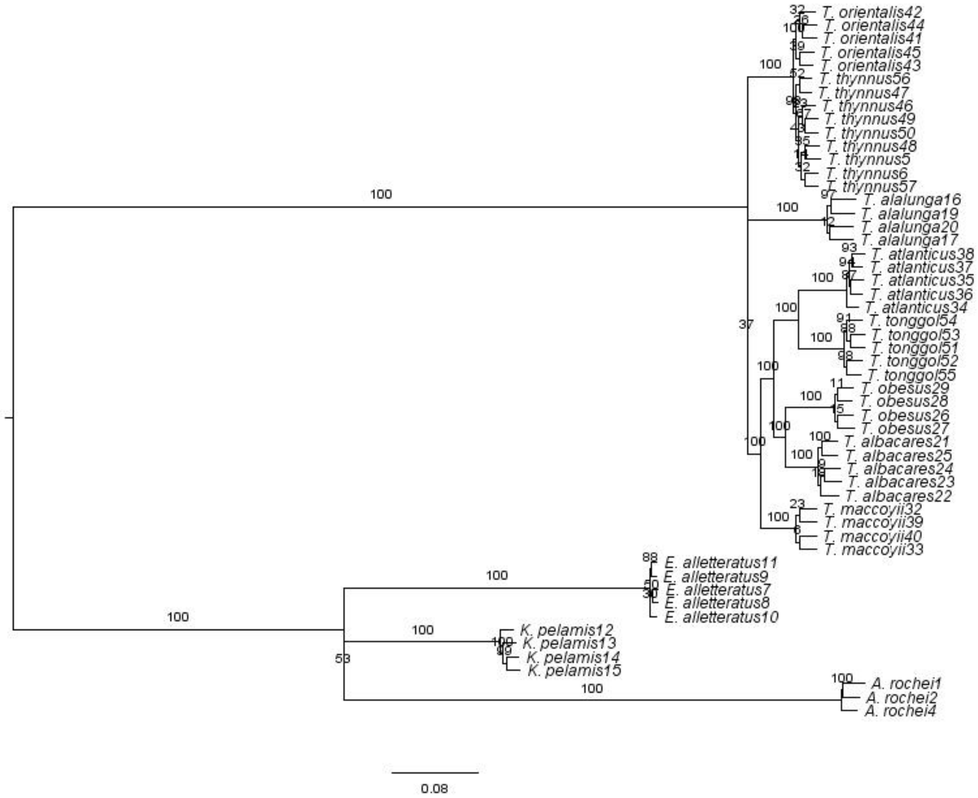
Tree 48: M=2, n=4, all species, per species, 25% missing, IUPAC encoded sites.



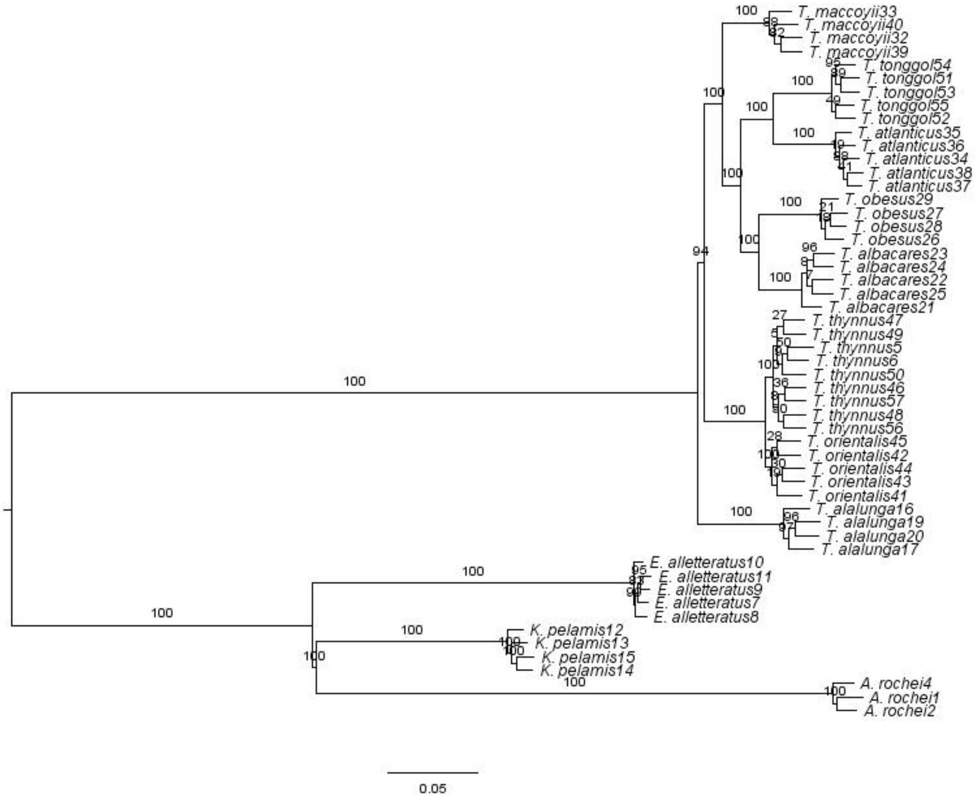
Tree 49: M=2, n=8, all species, per individuals, 0% missing, fixed positions.



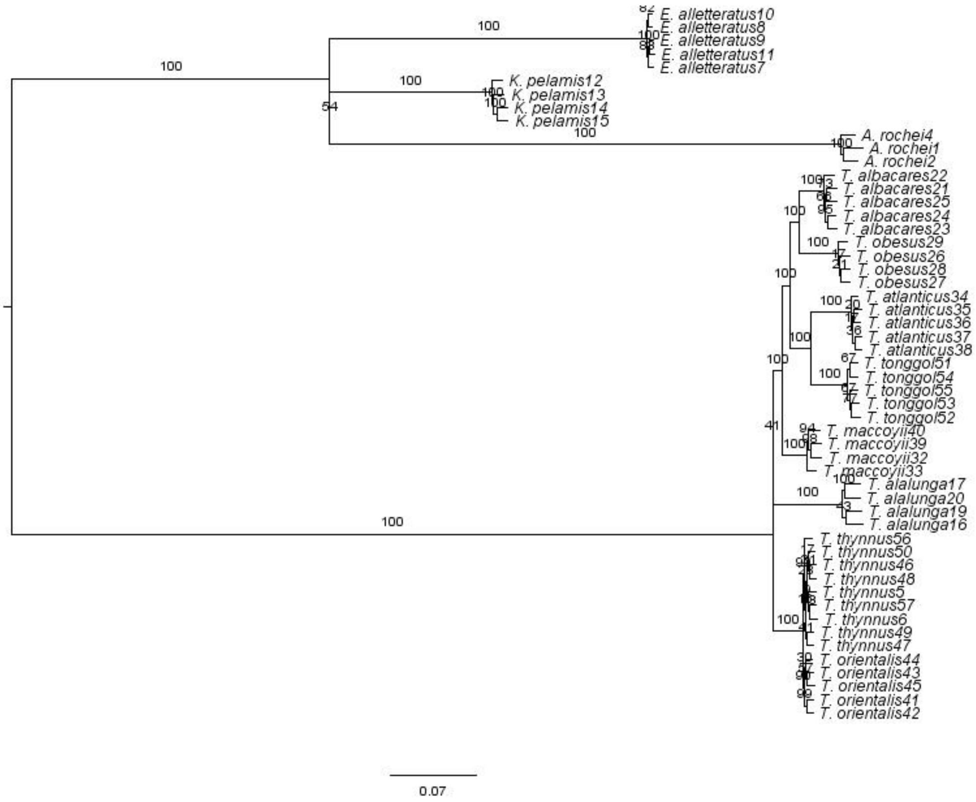
Tree 50: M=2, n=8, all species, per individuals, 0% missing, IUPAC encoded sites.



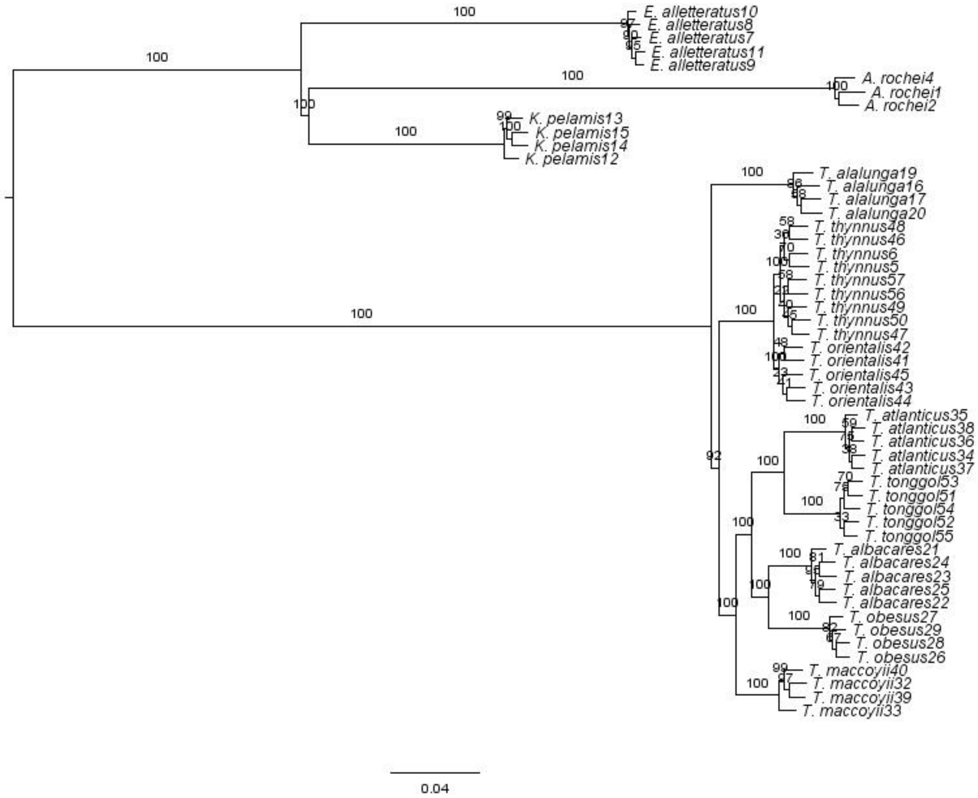
Tree 51: M=2, n=8, all species, per individuals, 75% missing, fixed positions.



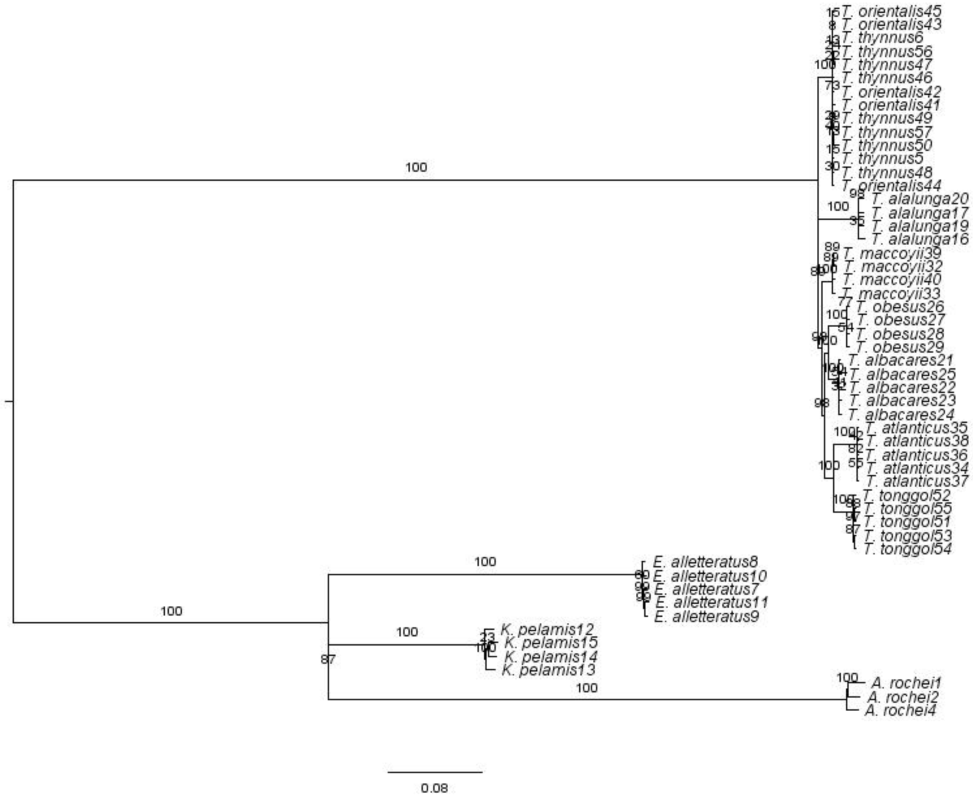
Tree 52: M=2, n=8, all species, per individuals, 75% missing, IUPAC encoded sites.



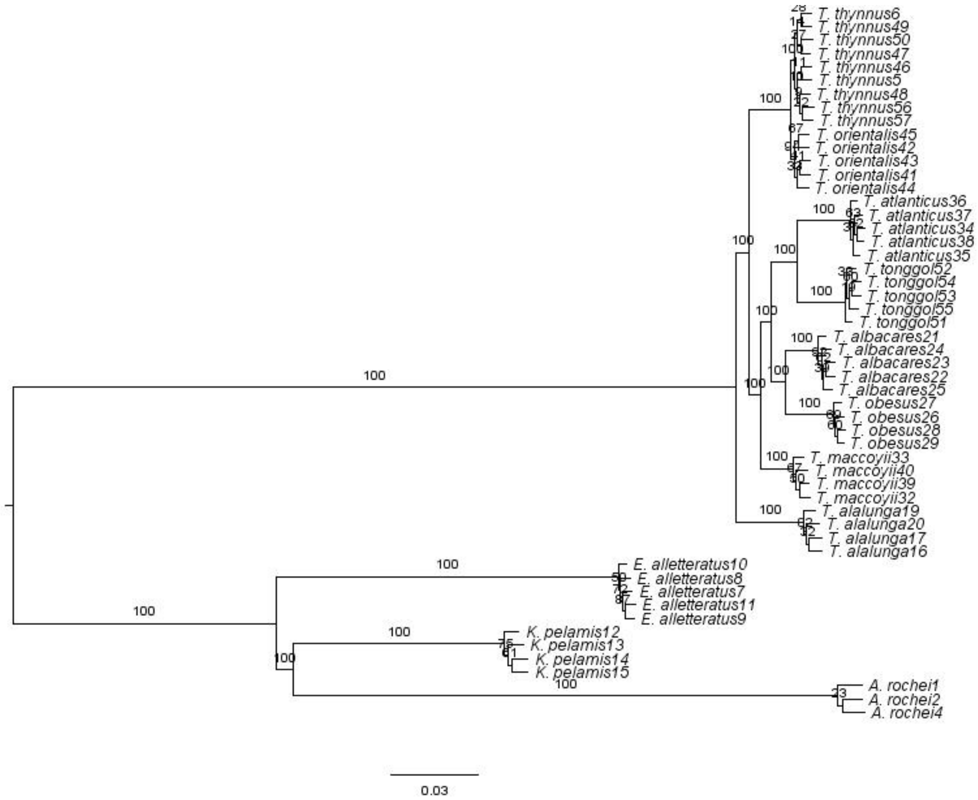
Tree 53: M=2, n=8, all species, per individuals, 50% missing, fixed positions.



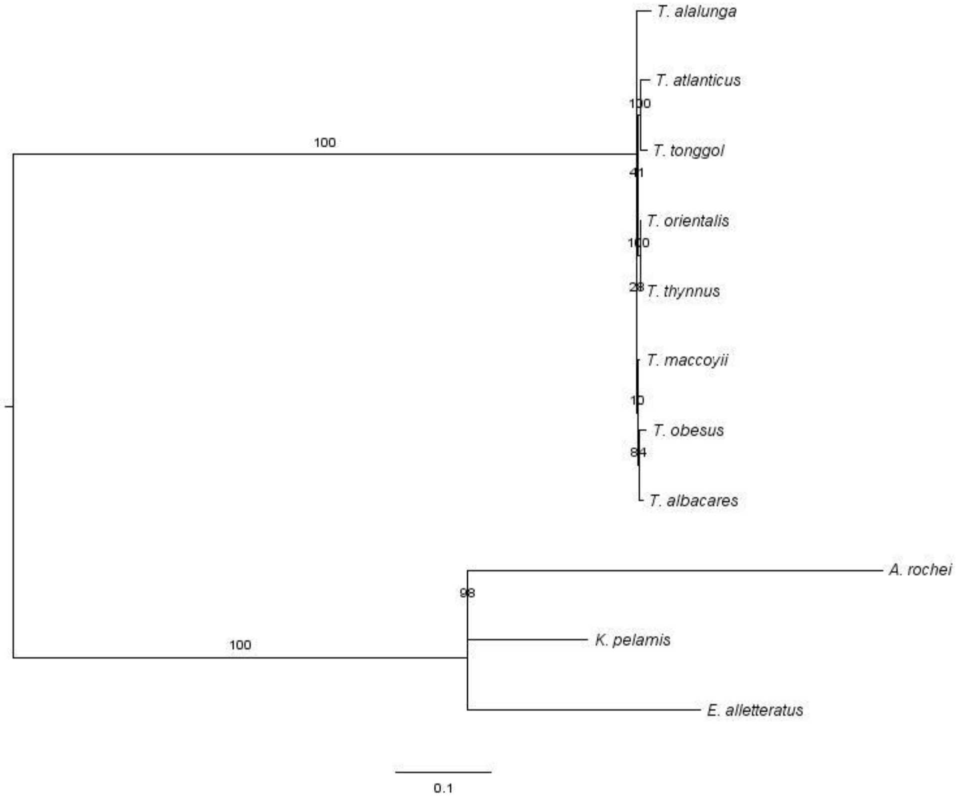
Tree 54: M=2, n=8, all species, per individuals, 50% missing, IUPAC encoded sites.



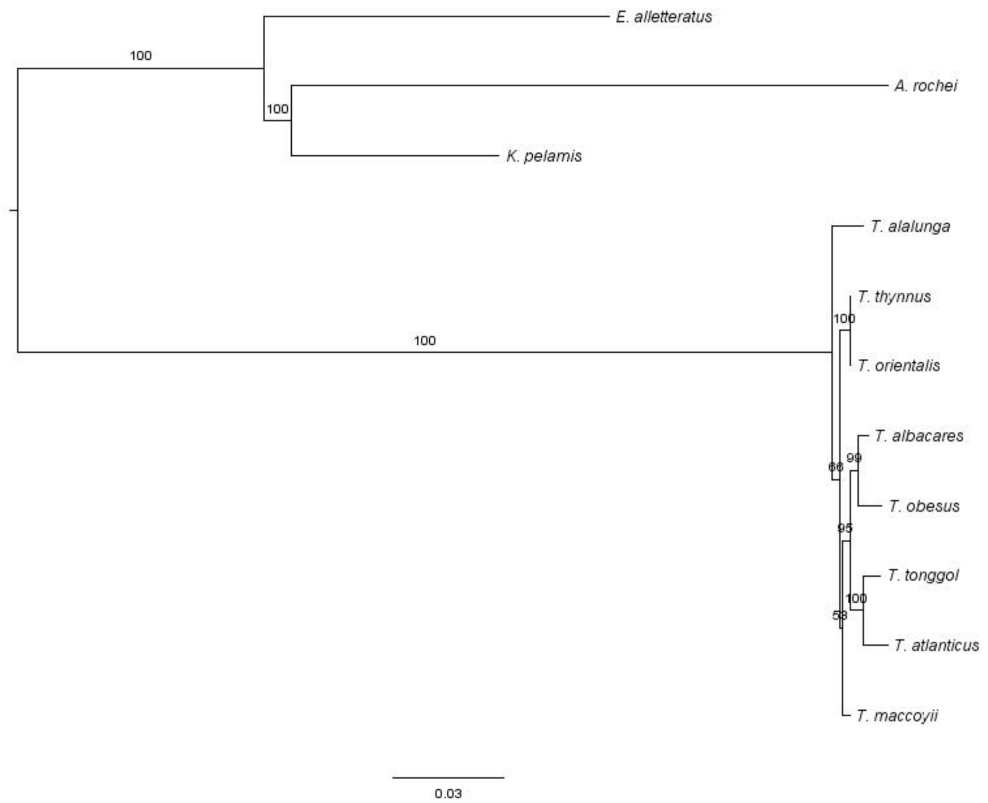
Tree 55: M=2, n=8, all species, per individuals, 25% missing, fixed positions.



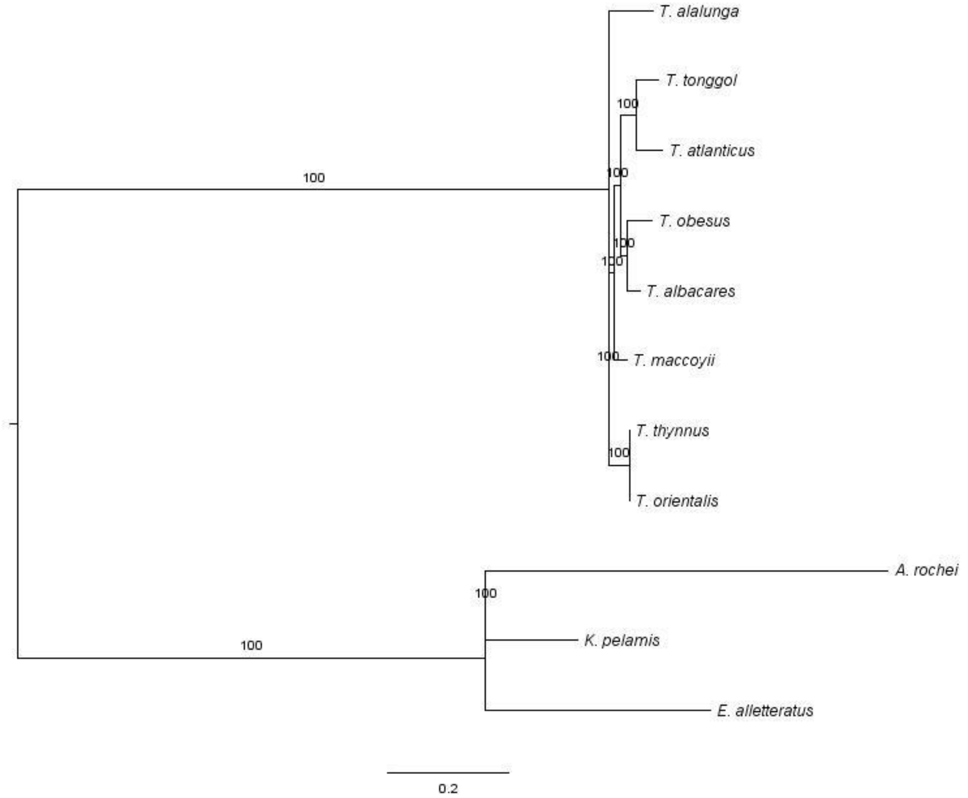
Tree 56: M=2, n=8, all species, per individuals, 25% missing, IUPAC encoded sites.



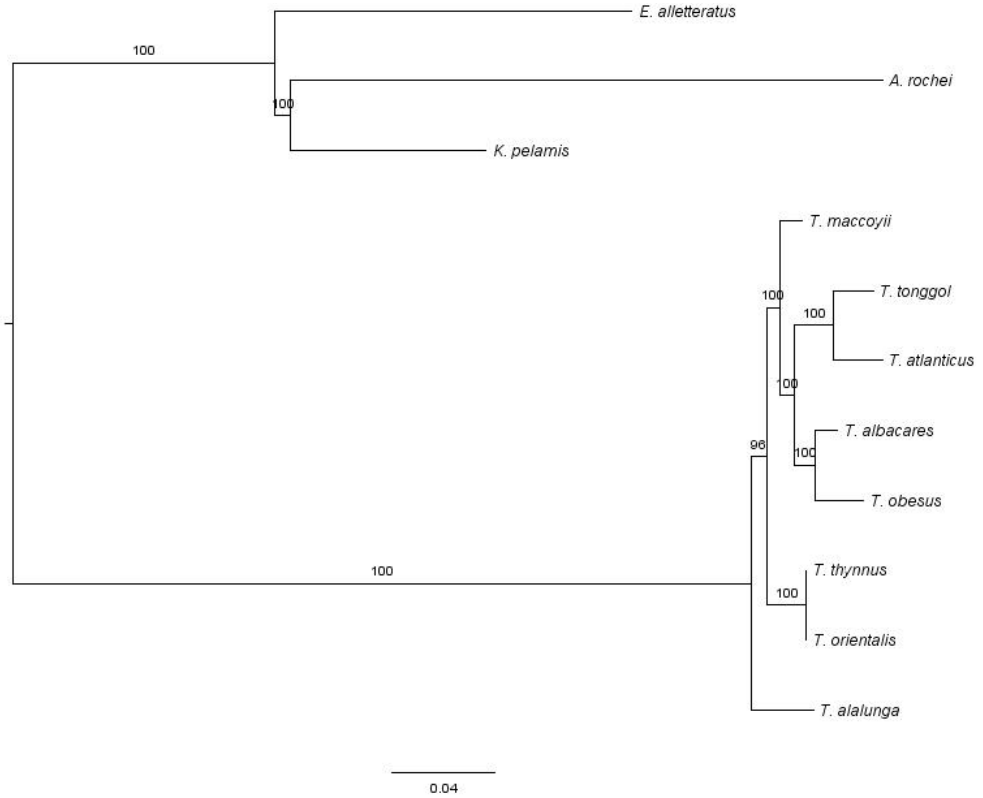
Tree 57: M=2, n=8, all species, per species, 0% missing, fixed positions.



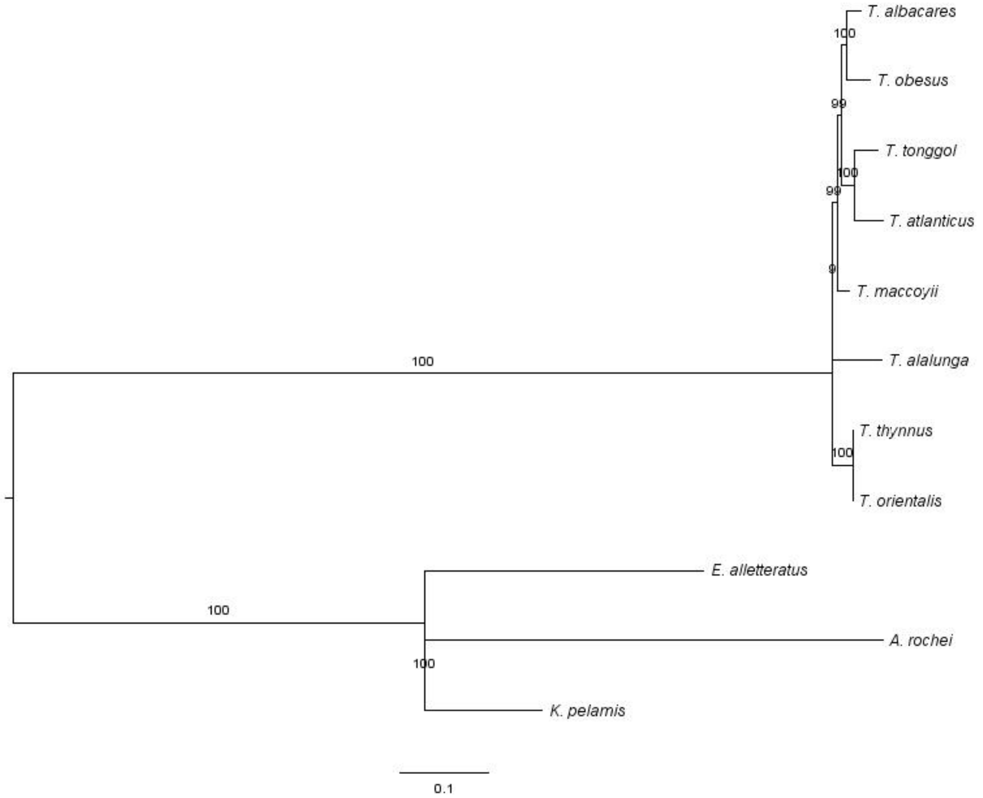
Tree 58: M=2, n=8, all species, per species, 0% missing, IUPAC encoded sites.



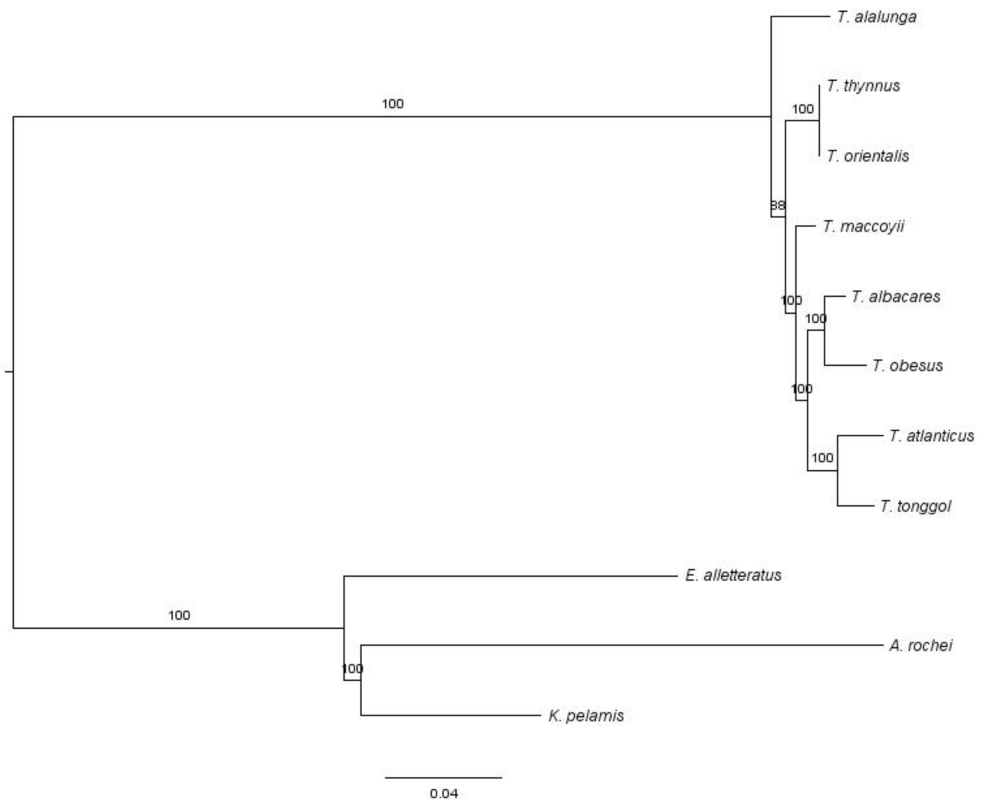
Tree 59: M=2, n=8, all species, per species, 75% missing, fixed positions.



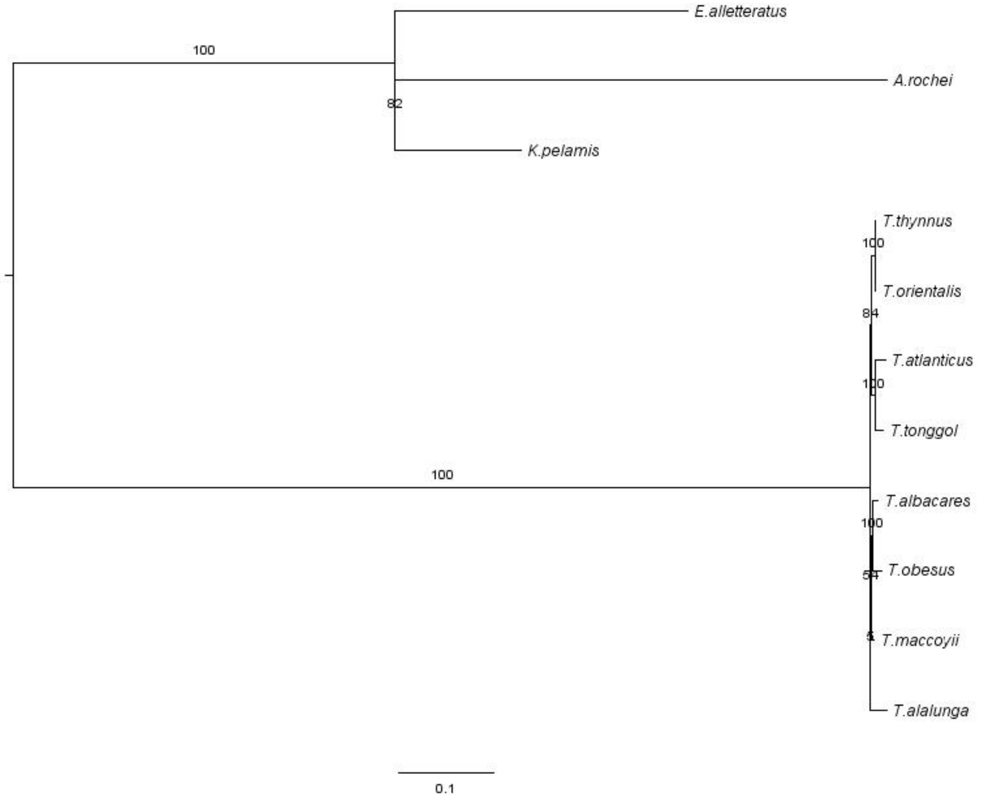
Tree 60: M=2, n=8, all species, per species, 75% missing, IUPAC encoded sites.



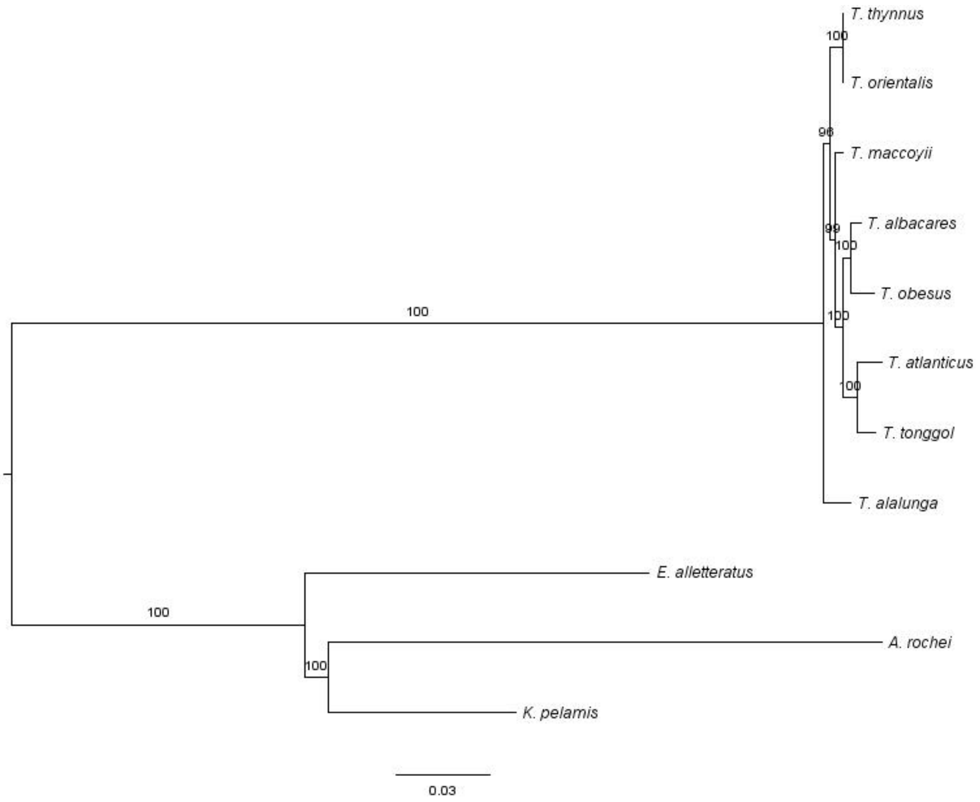
Tree 61: M=2, n=8, all species, per species, 50% missing, fixed positions.



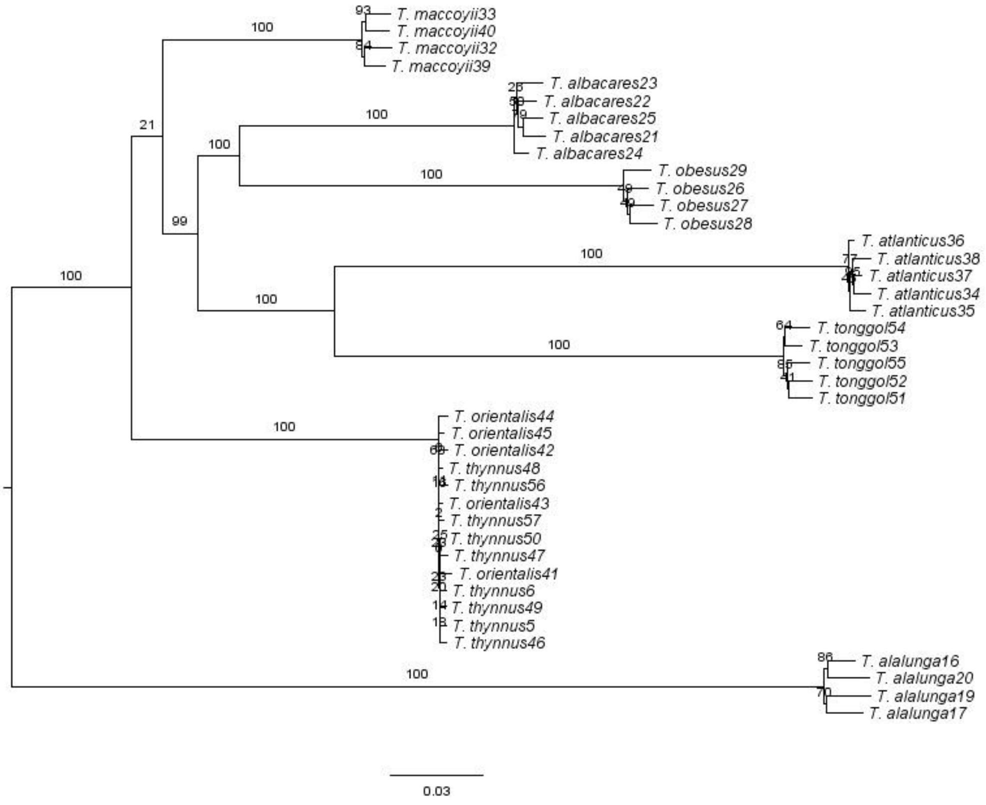
Tree 62: M=2, n=8, all species, per species, 50% missing, IUPAC encoded sites.



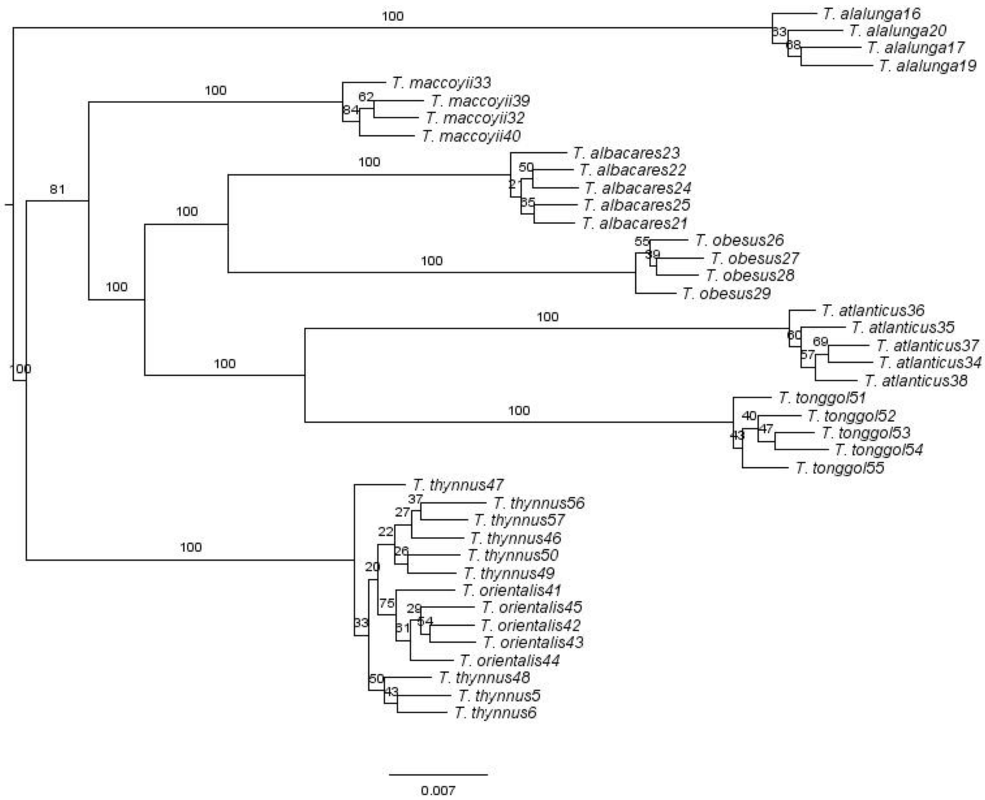
Tree 63: M=2, n=8, all species, per species, 25% missing, fixed positions.



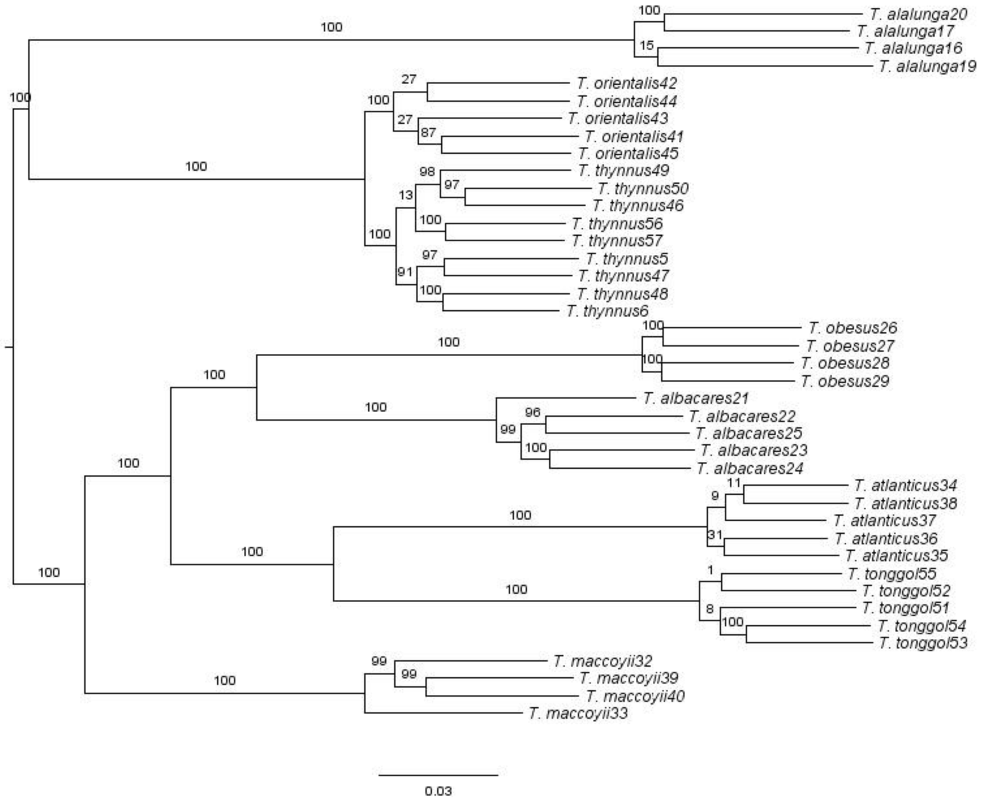
Tree 64: M=2, n=8, all species, per species, 25% missing, IUPAC encoded sites.



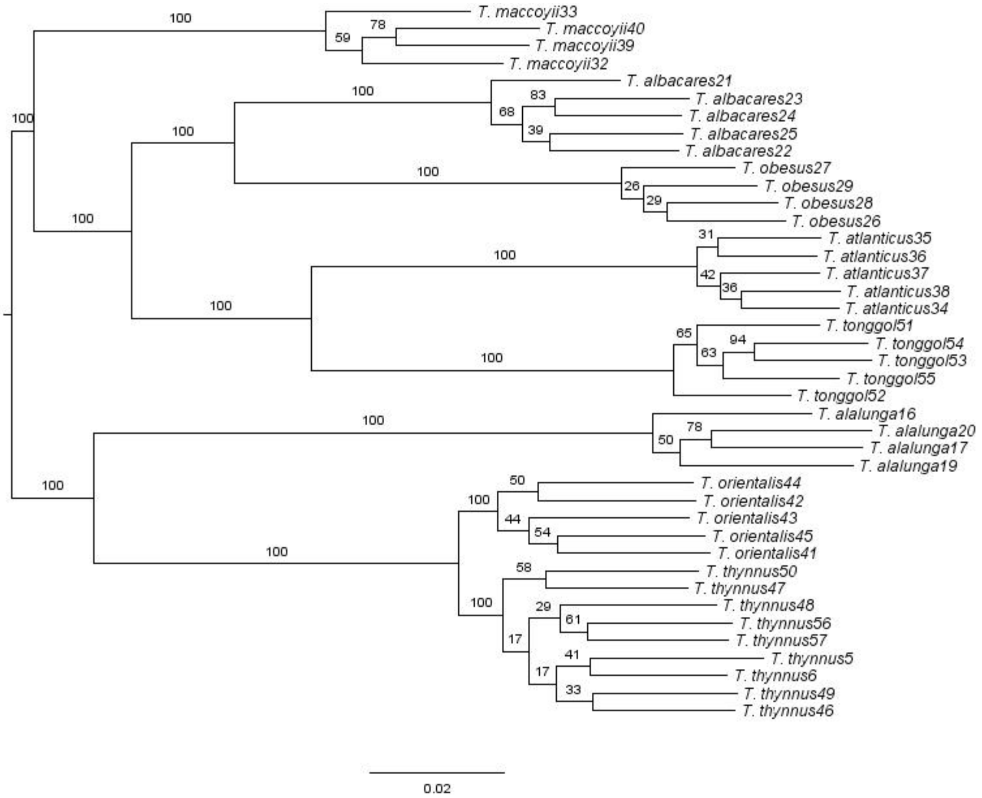
Tree 65: M=1, n=4, only *Thunnus*, per individuals, 0% missing, fixed positions.



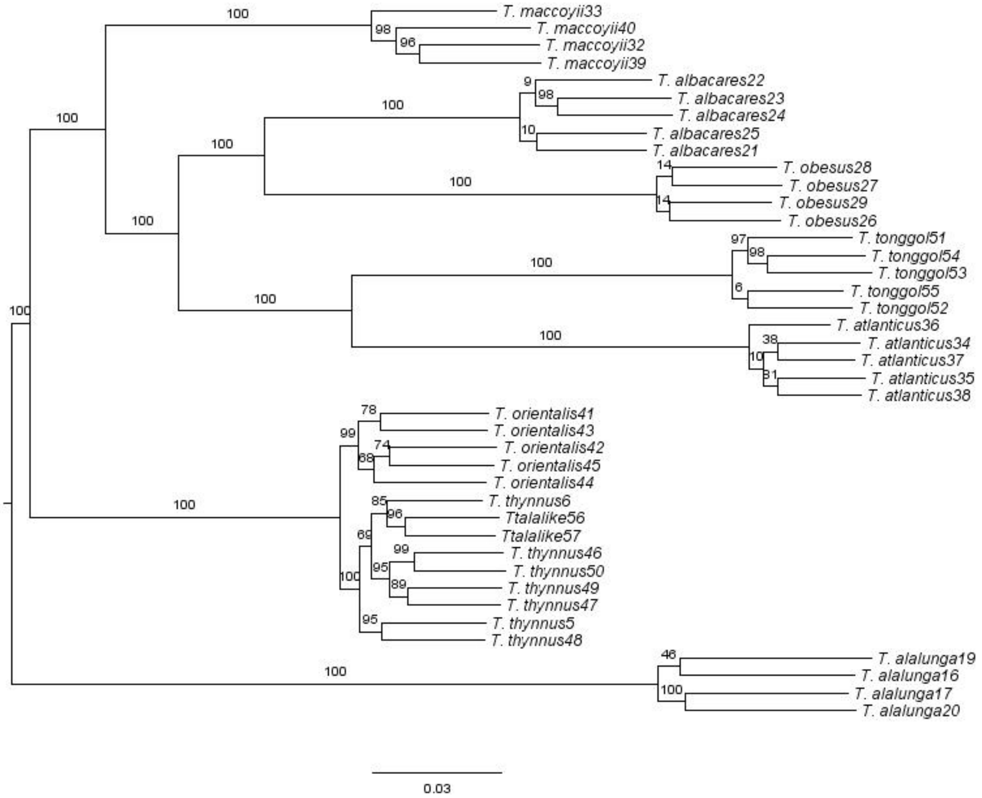
Tree 66: M=1, n=4, only *Thunnus*, per individuals, 0% missing, IUPAC encoded sites.



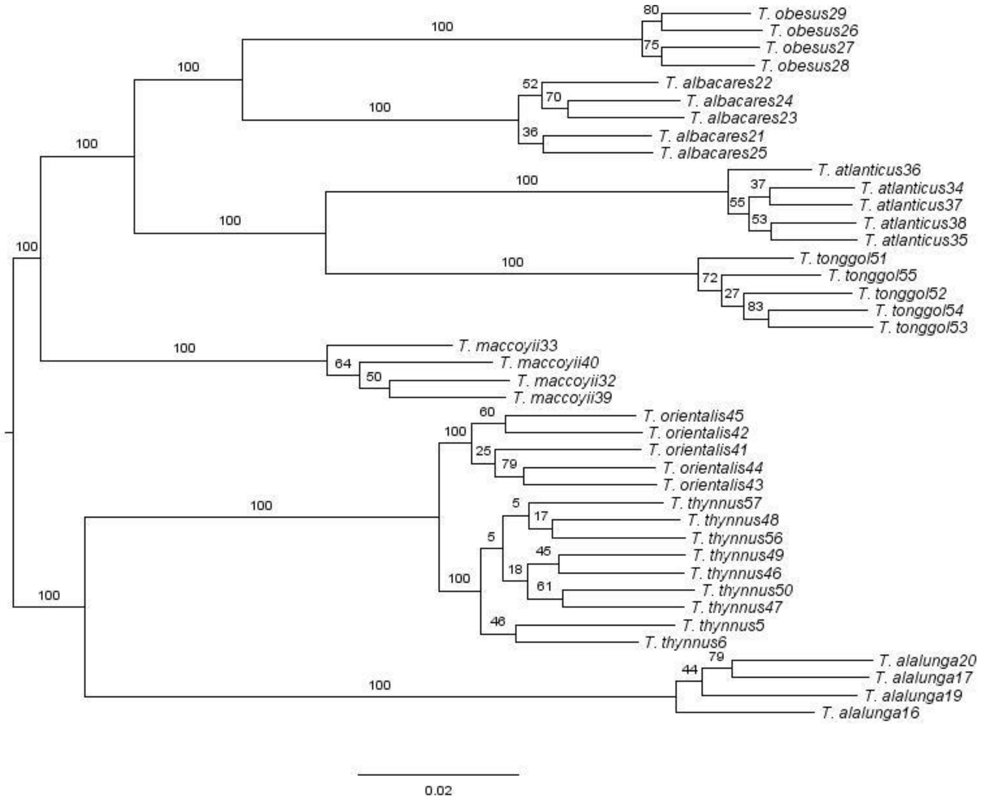
Tree 67: M=1, n=4, only *Thunnus*, per individuals, 75% missing, fixed positions.



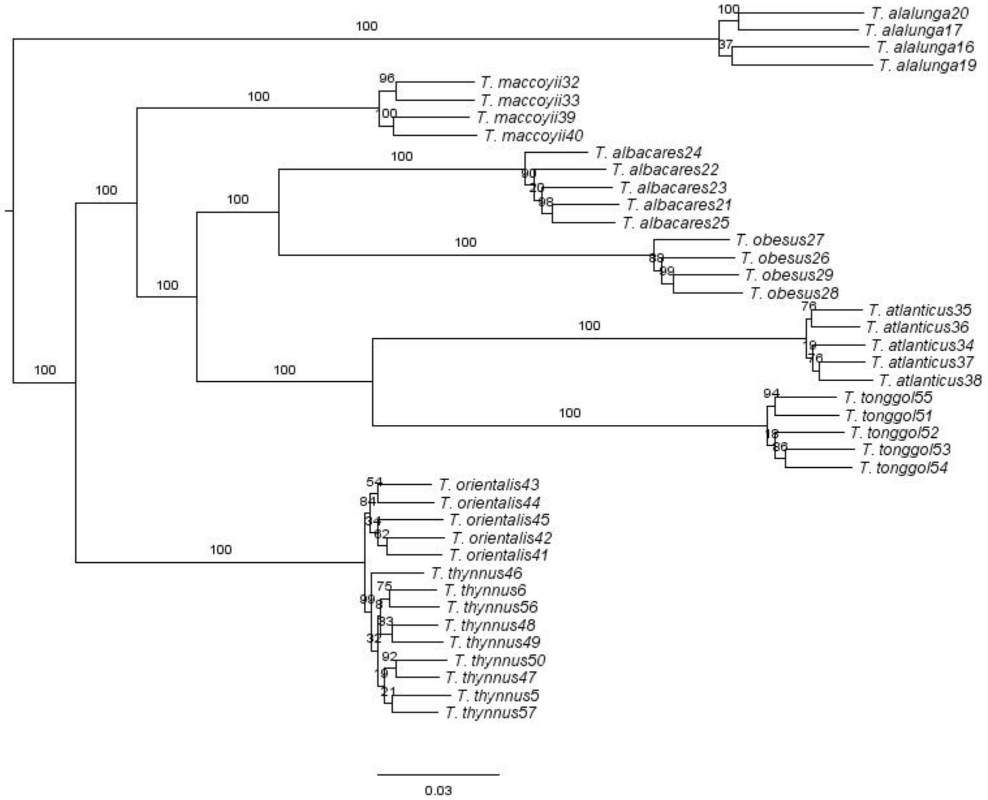
Tree 68: M=1, n=4, only *Thunnus*, per individuals, 75% missing, IUPAC encoded sites.



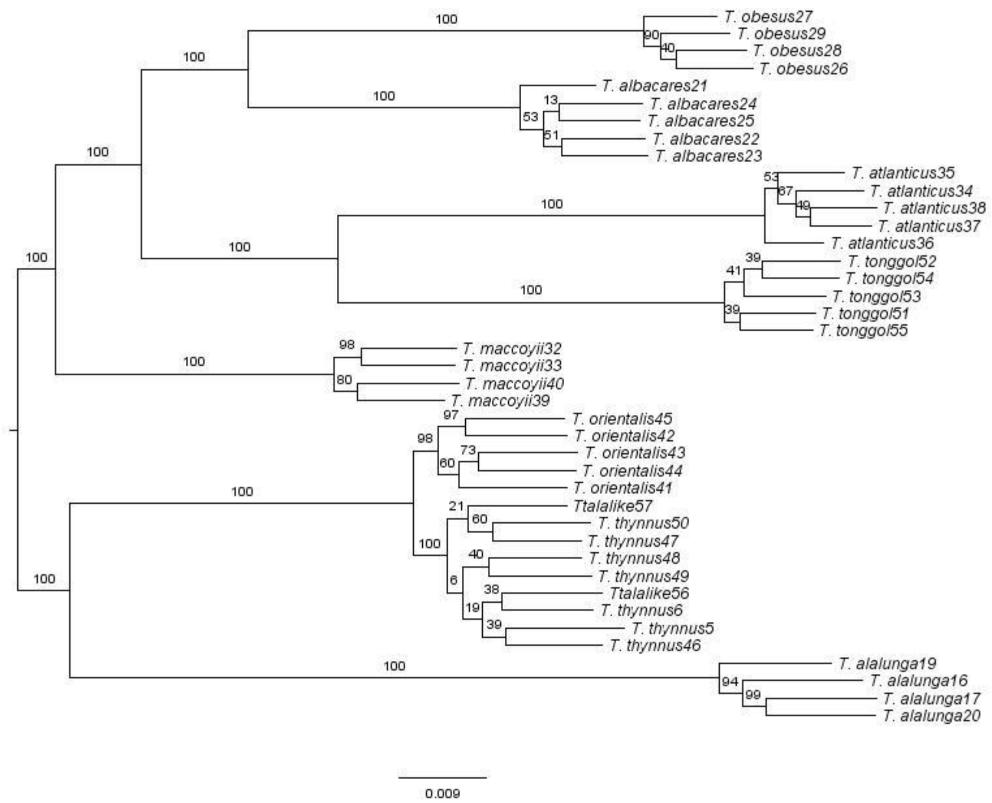
Tree 69: M=1, n=4, only *Thunnus*, per individuals, 50% missing, fixed positions.



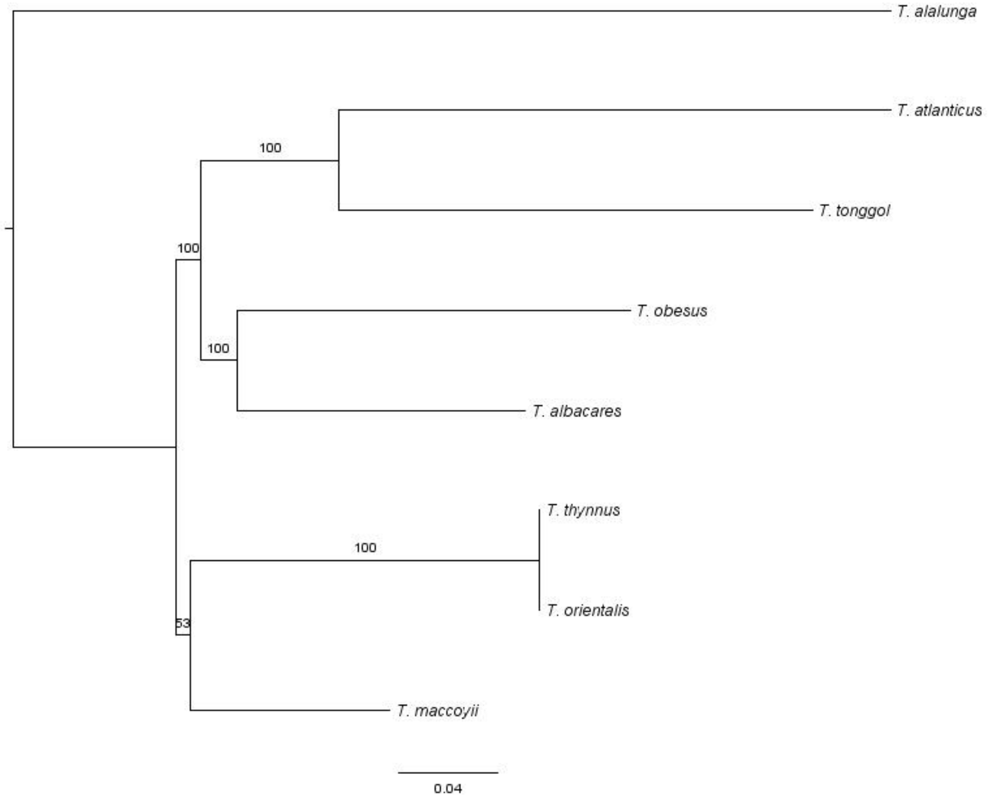
Tree 70: M=1, n=4, only *Thunnus*, per individuals, 50% missing, IUPAC encoded sites.



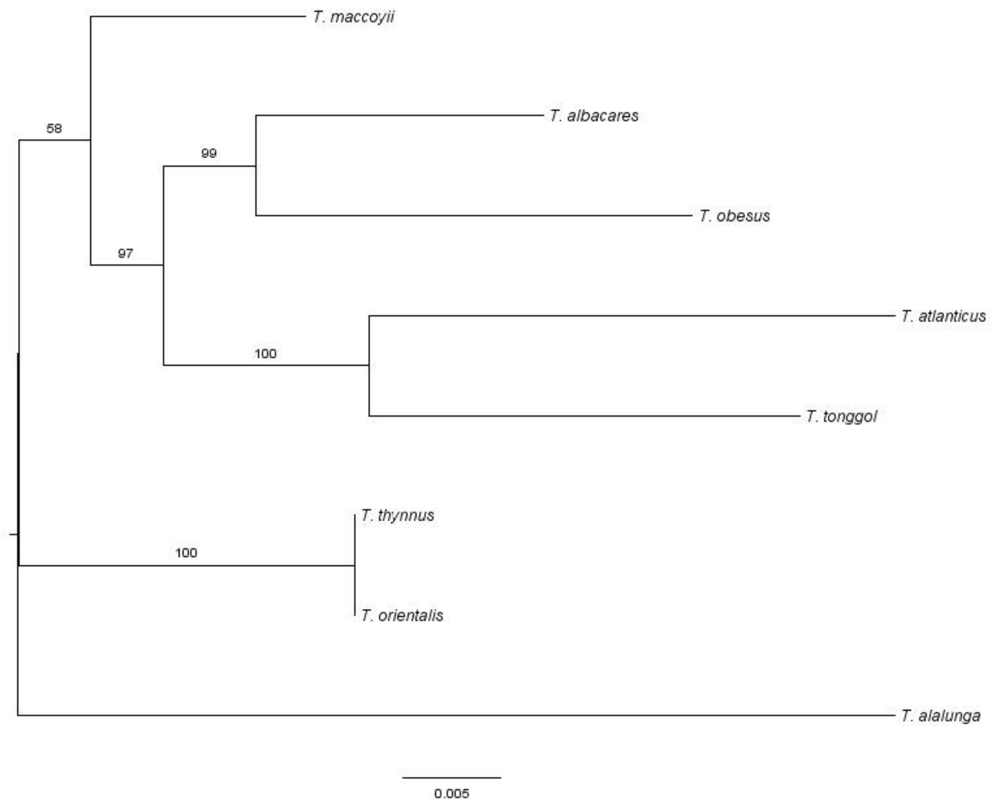
Tree 71: M=1, n=4, only *Thunnus*, per individuals, 25% missing, fixed positions.



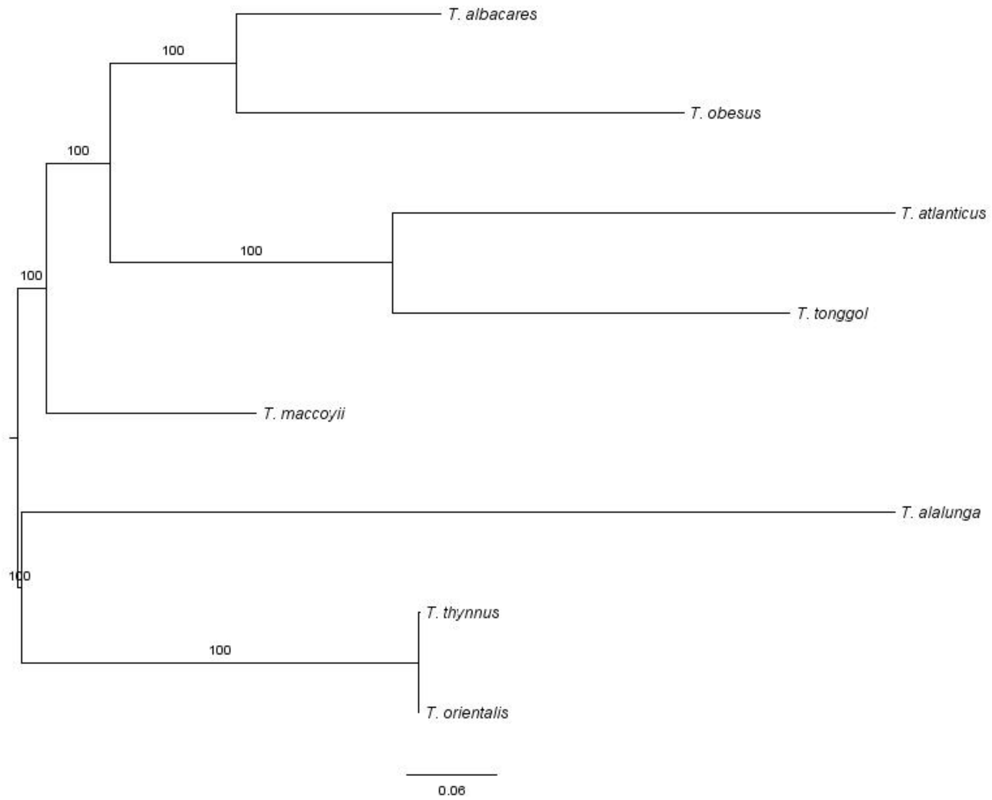
Tree 72: M=1, n=4, only *Thunnus*, per individuals, 25% missing, IUPAC encoded sites.



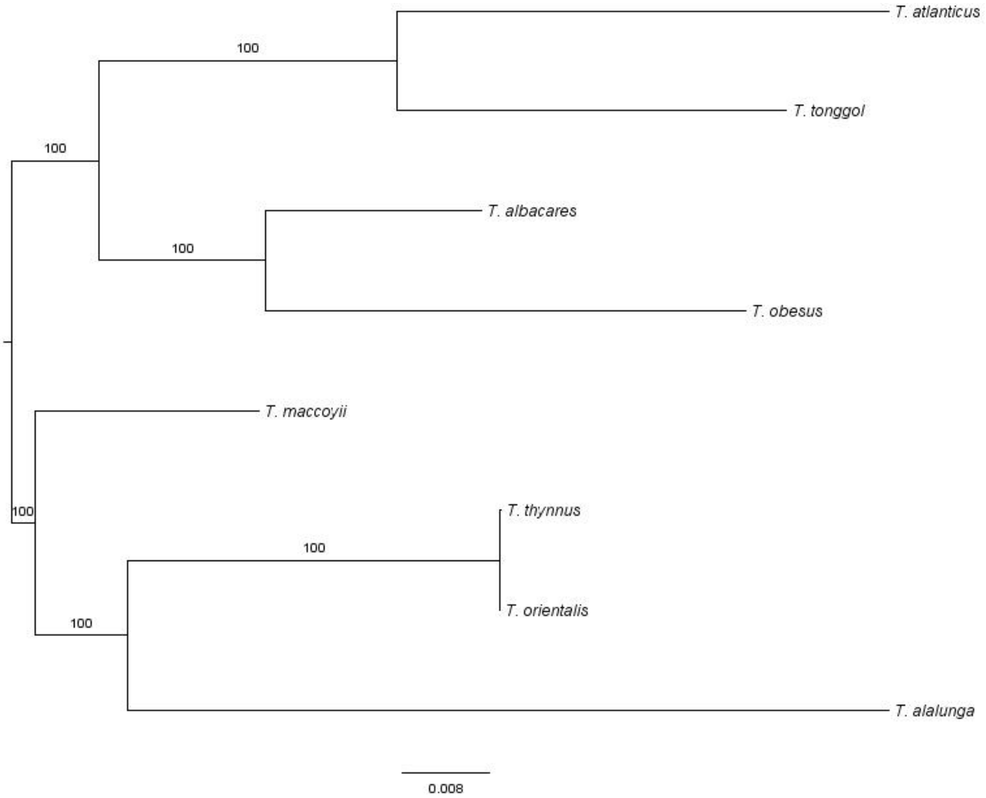
Tree 73: M=1, n=4, only *Thunnus*, per species, 0% missing, fixed positions.



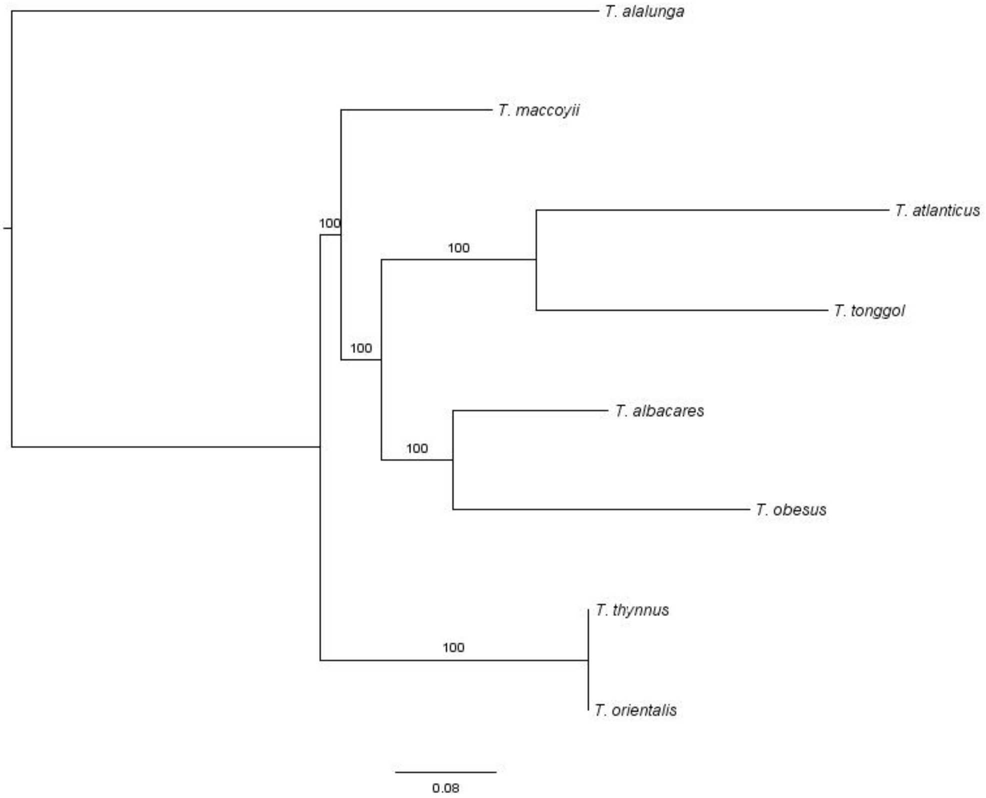
Tree 74: M=1, n=4, only *Thunnus*, per species, 0% missing, IUPAC encoded sites.



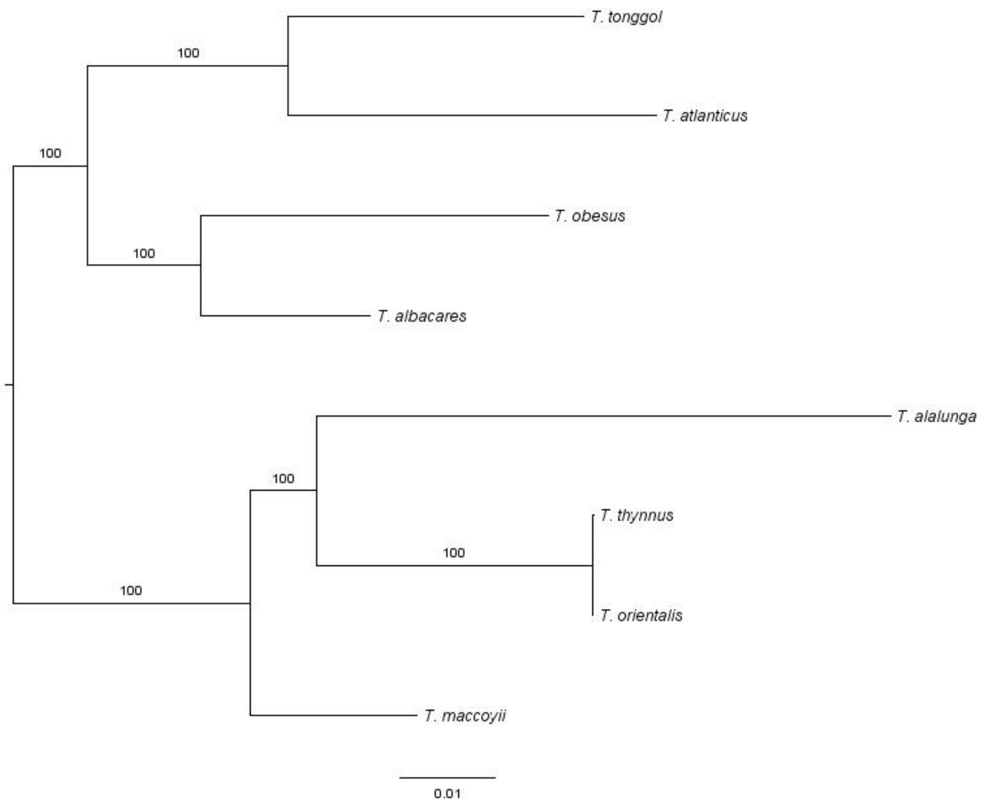
Tree 75: M=1, n=4, only *Thunnus*, per species, 75% missing, fixed positions.



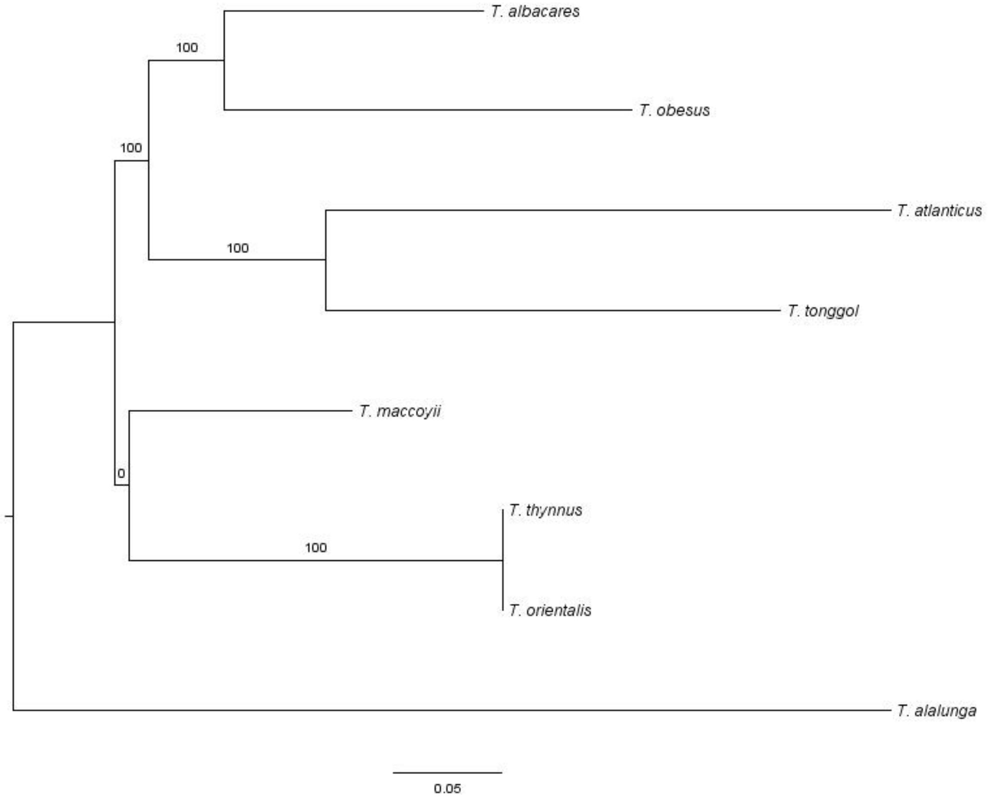
Tree 76: M=1, n=4, only *Thunnus*, per species, 75% missing, IUPAC encoded sites.



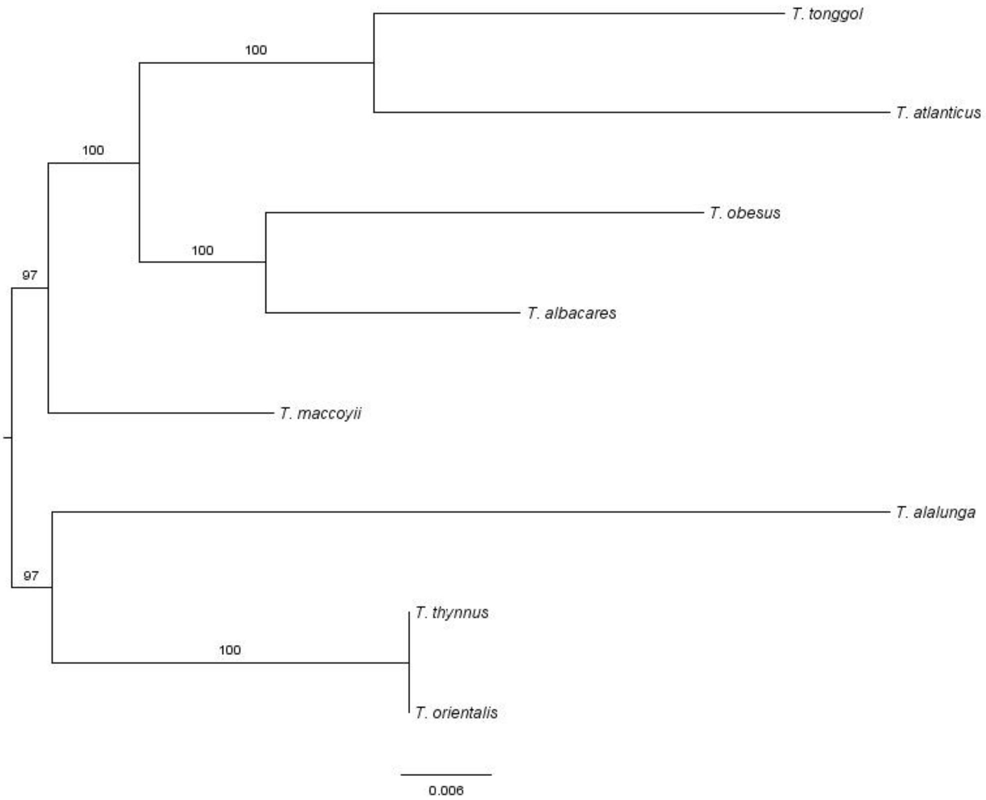
Tree 77: M=1, n=4, only *Thunnus*, per species, 50% missing, fixed positions.



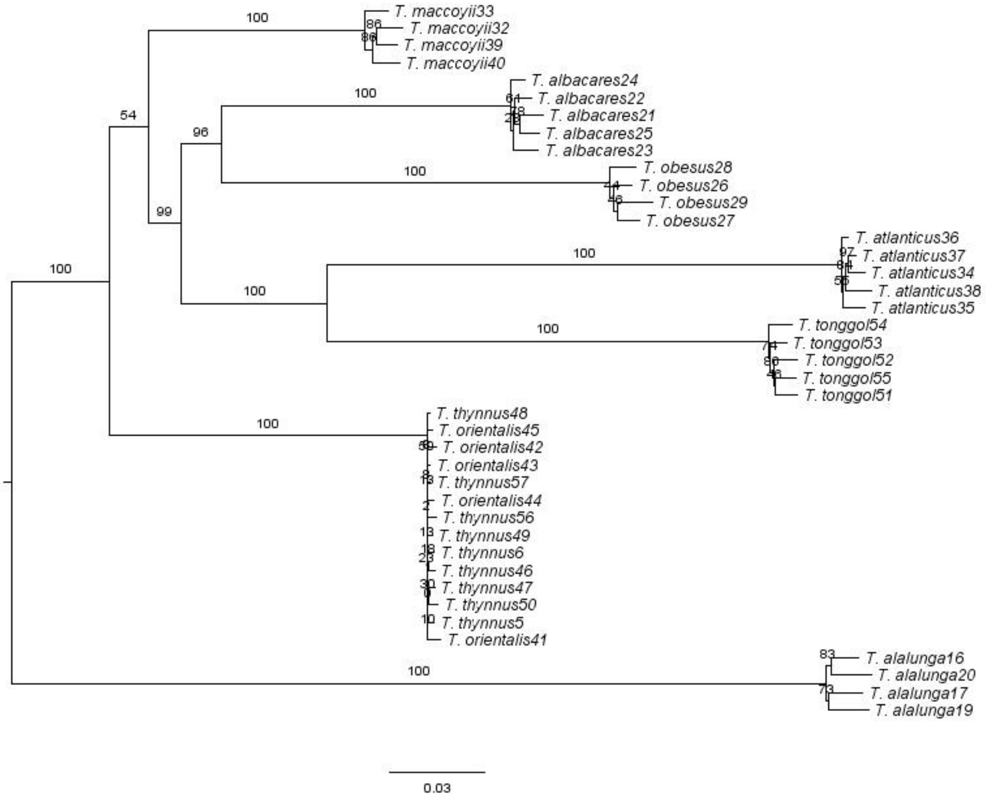
Tree 78: M=1, n=4, only *Thunnus*, per species, 50% missing, IUPAC encoded sites.



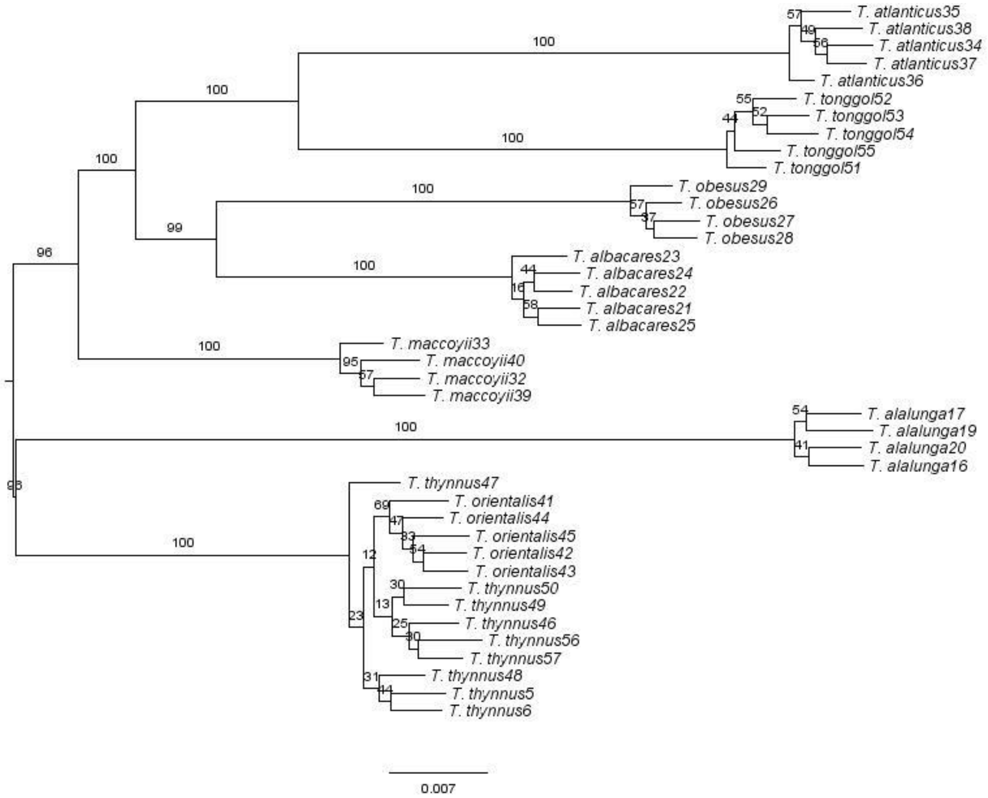
Tree 79: M=1, n=4, only *Thunnus*, per species, 25% missing, fixed positions.



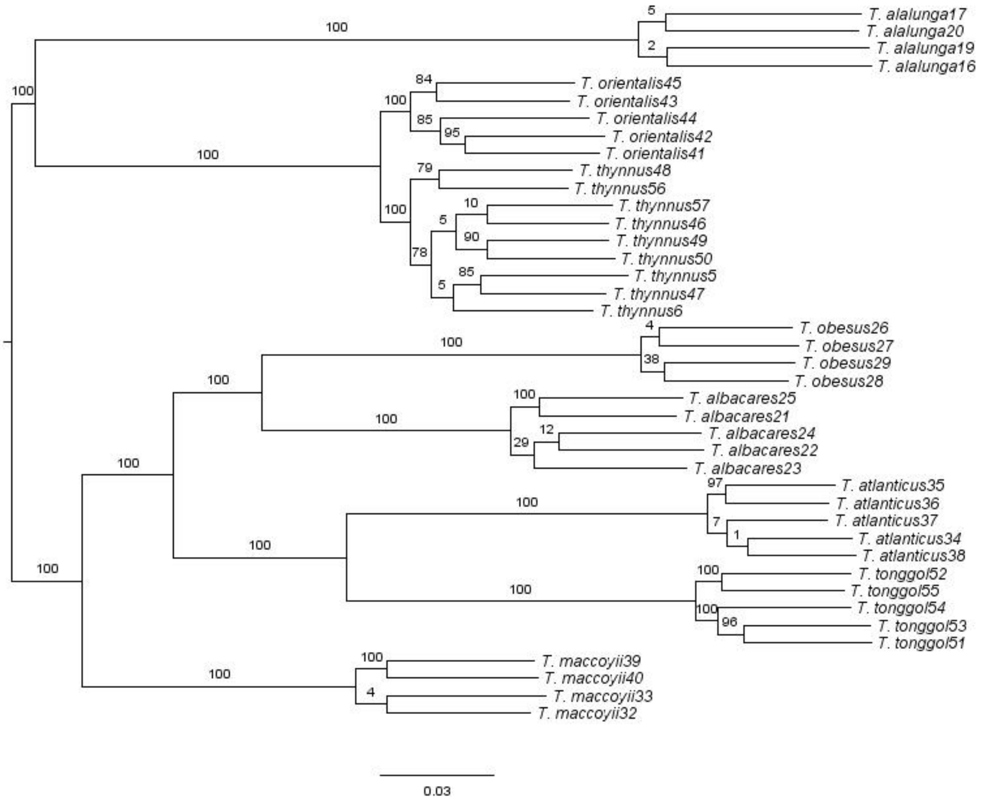
Tree 80: M=1, n=4, only *Thunnus*, per species, 25% missing, IUPAC encoded sites.



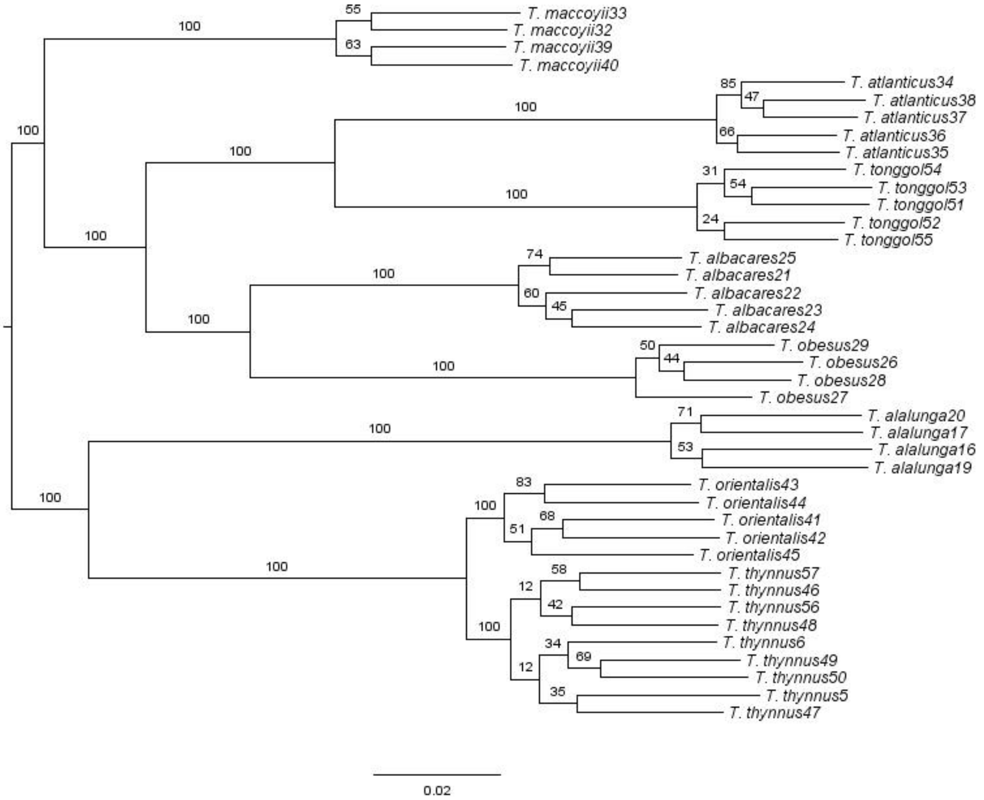
Tree 81: M=1, n=8, only *Thunnus*, per individuals, 0% missing, fixed positions.



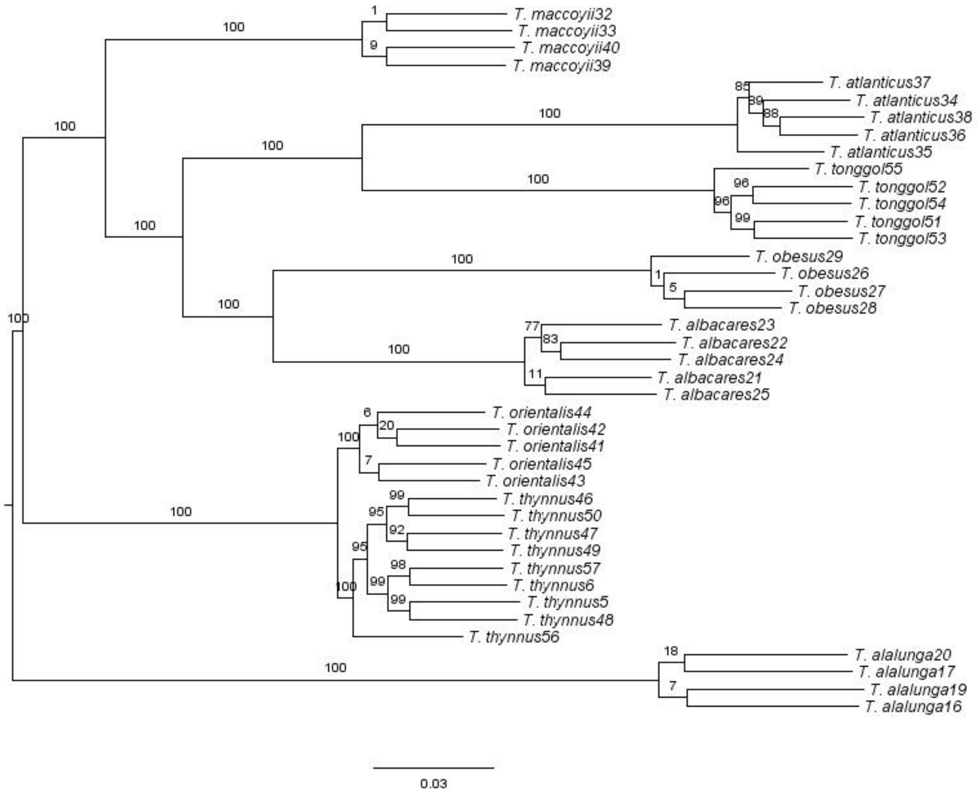
Tree 82: M=1, n=8, only *Thunnus*, per individuals, 0% missing, IUPAC encoded sites.



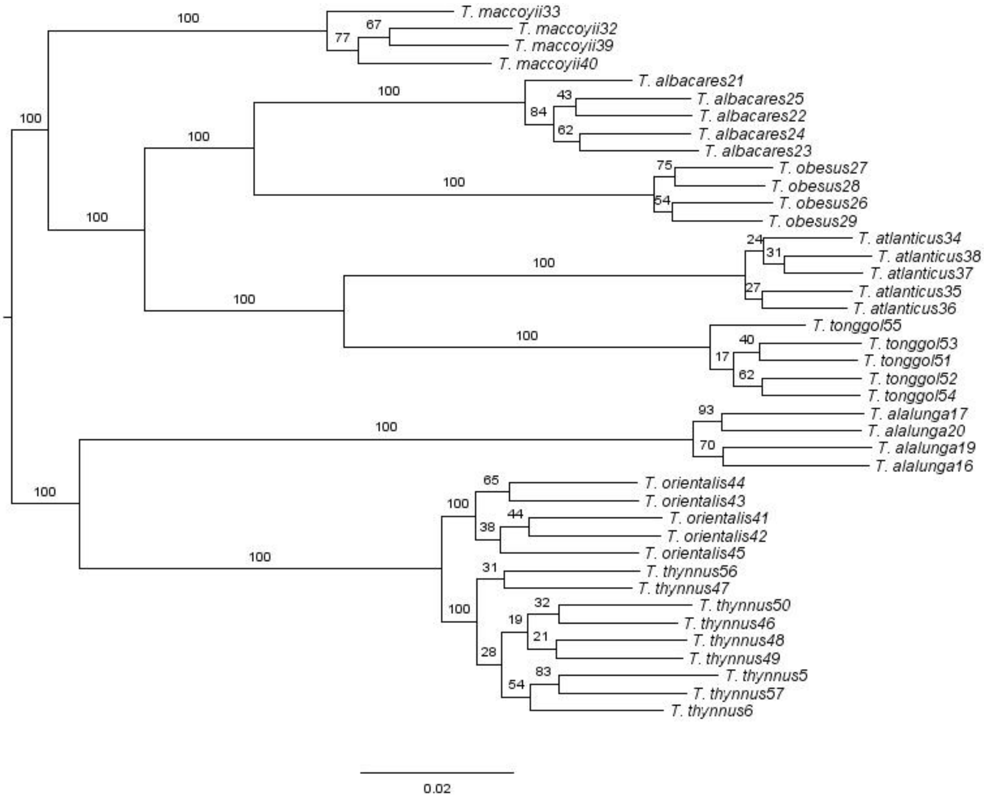
Tree 83: M=1, n=8, only *Thunnus*, per individuals, 75% missing, fixed positions.



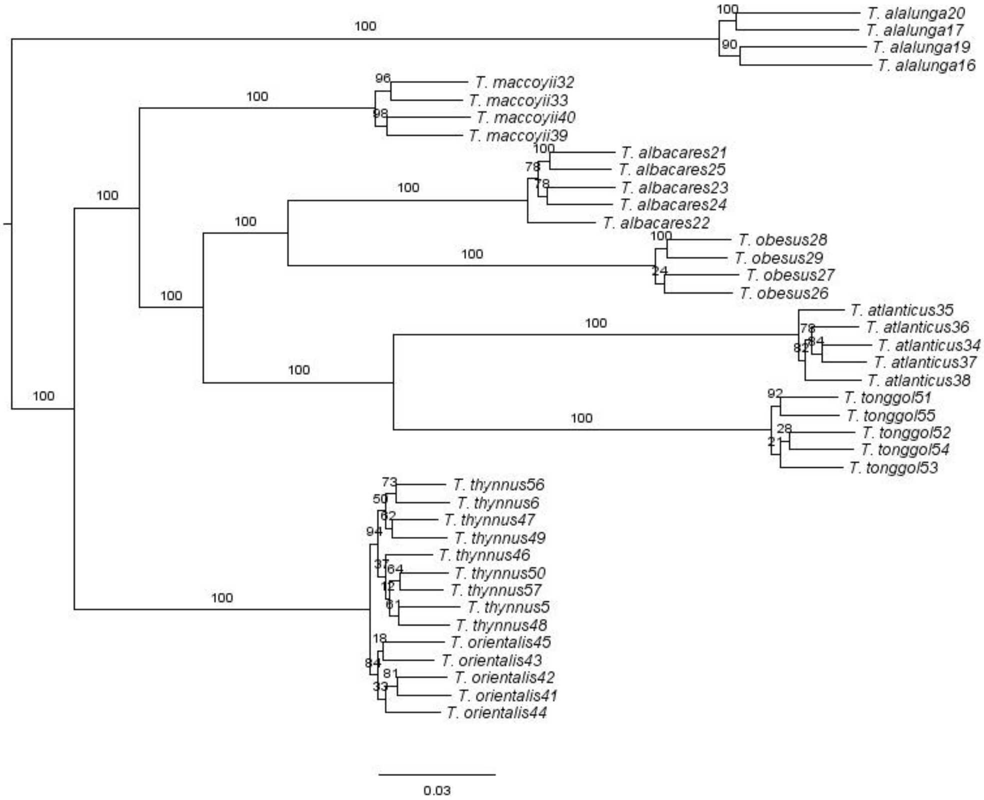
Tree 84: M=1, n=8, only *Thunnus*, per individuals, 75% missing, IUPAC encoded sites.



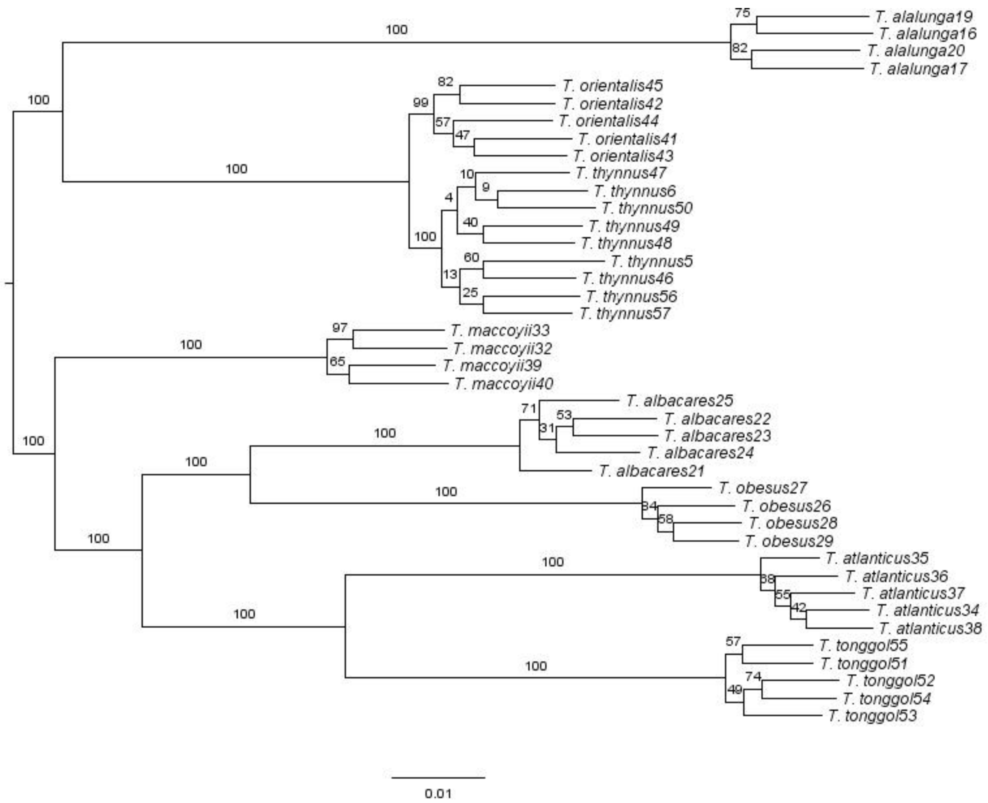
Tree 85: M=1, n=8, only *Thunnus*, per individuals, 50% missing, fixed positions.



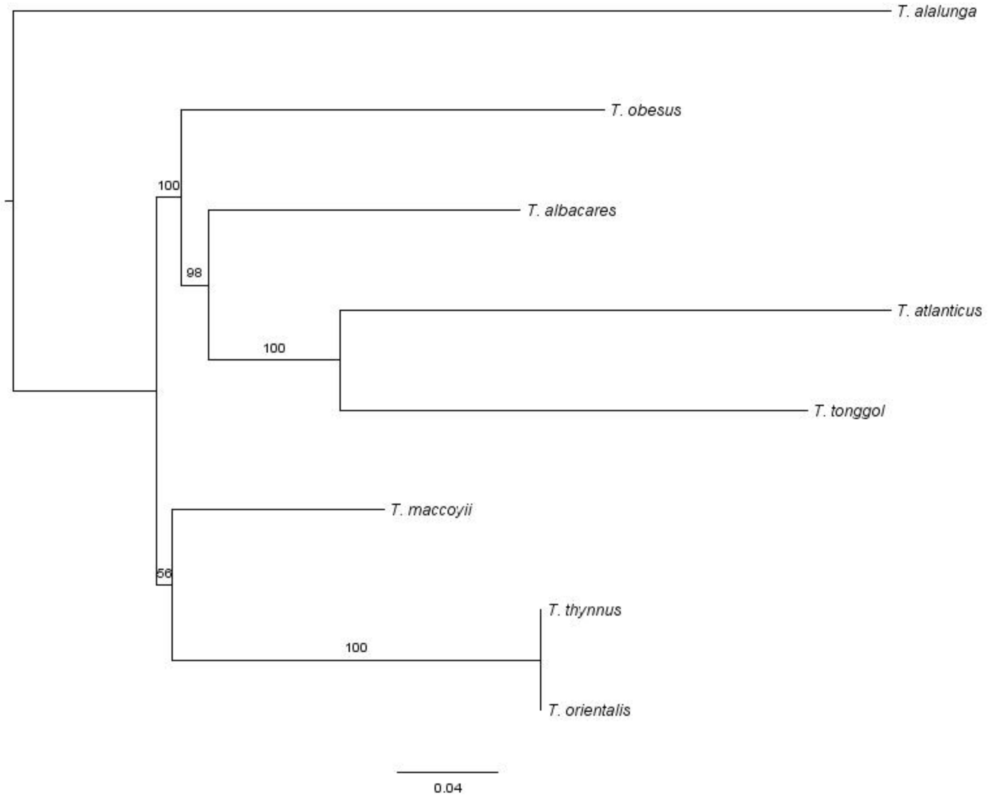
Tree 86: M=1, n=8, only *Thunnus*, per individuals, 50% missing, IUPAC encoded sites.



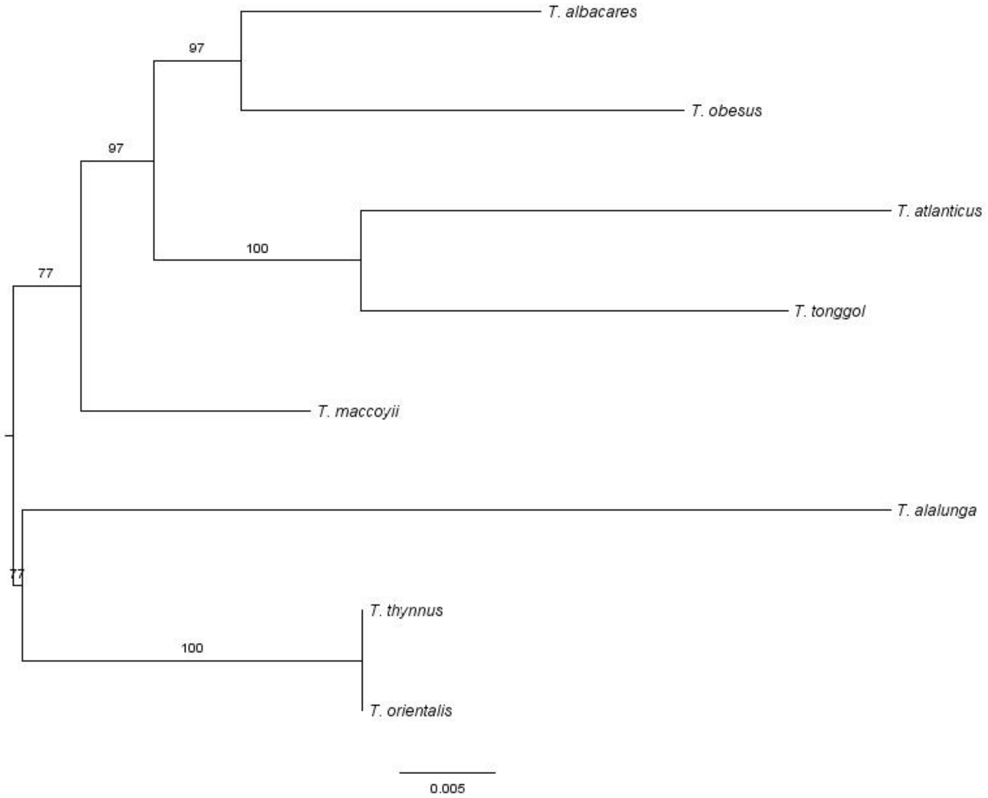
Tree 87: M=1, n=8, only *Thunnus*, per individuals, 25% missing, fixed positions.



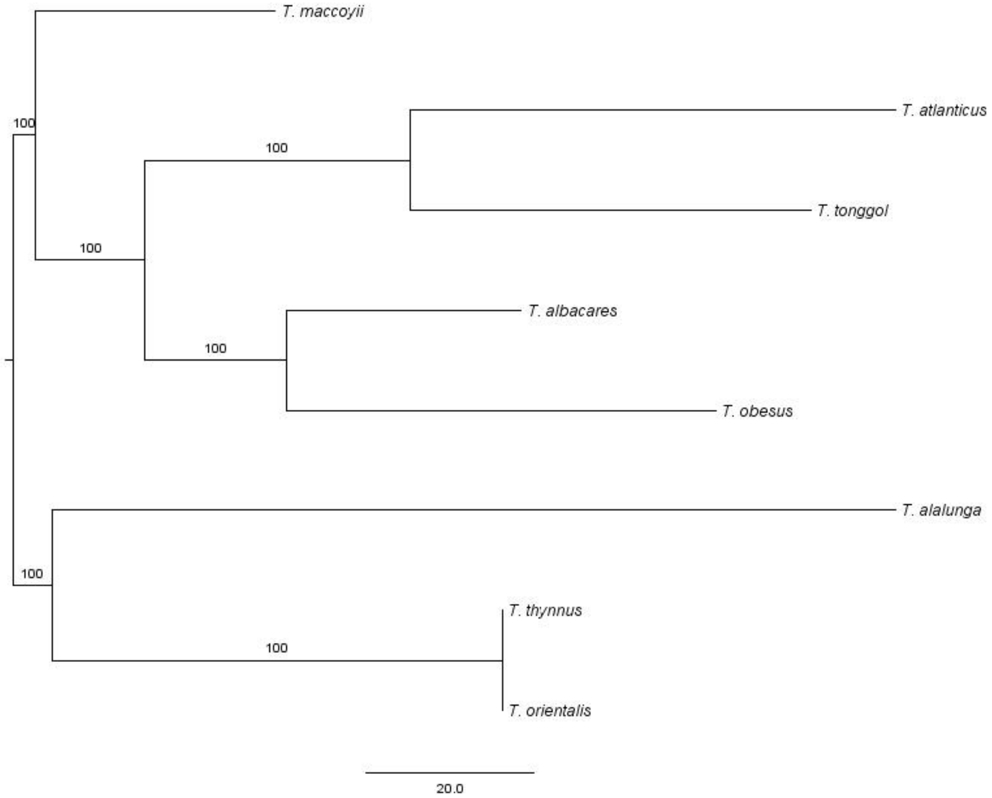
Tree 88: M=1, n=8, only *Thunnus*, per individuals, 25% missing, IUPAC encoded sites.



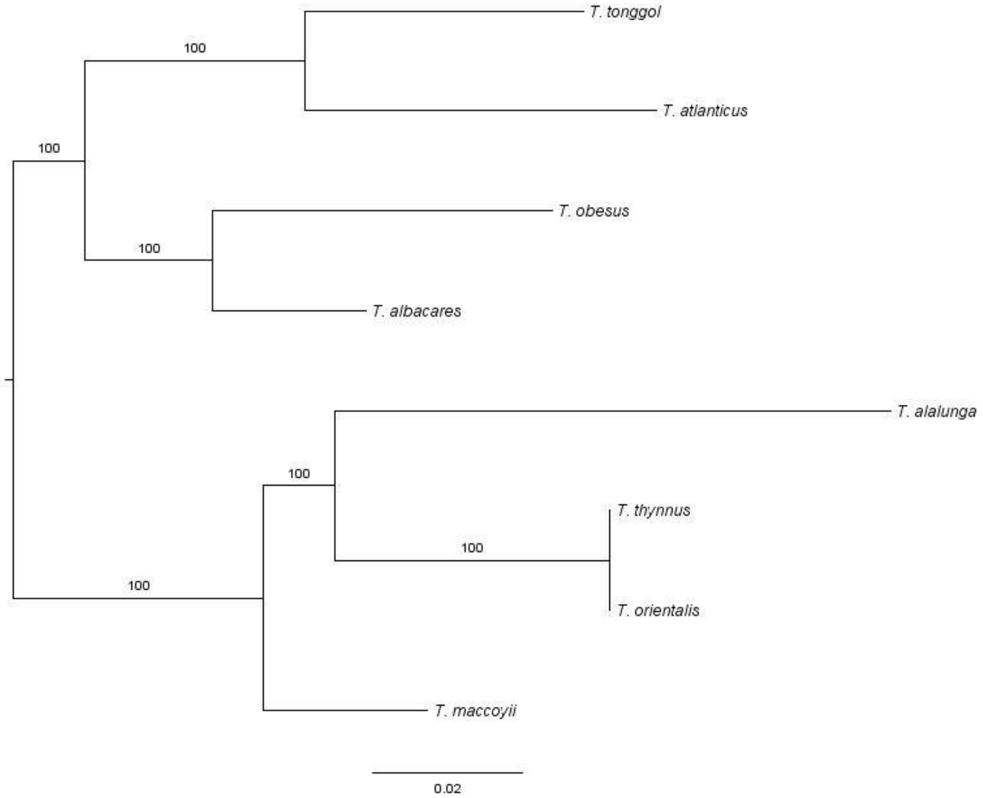
Tree 89: M=1, n=8, only *Thunnus*, per species, 0% missing, fixed positions.



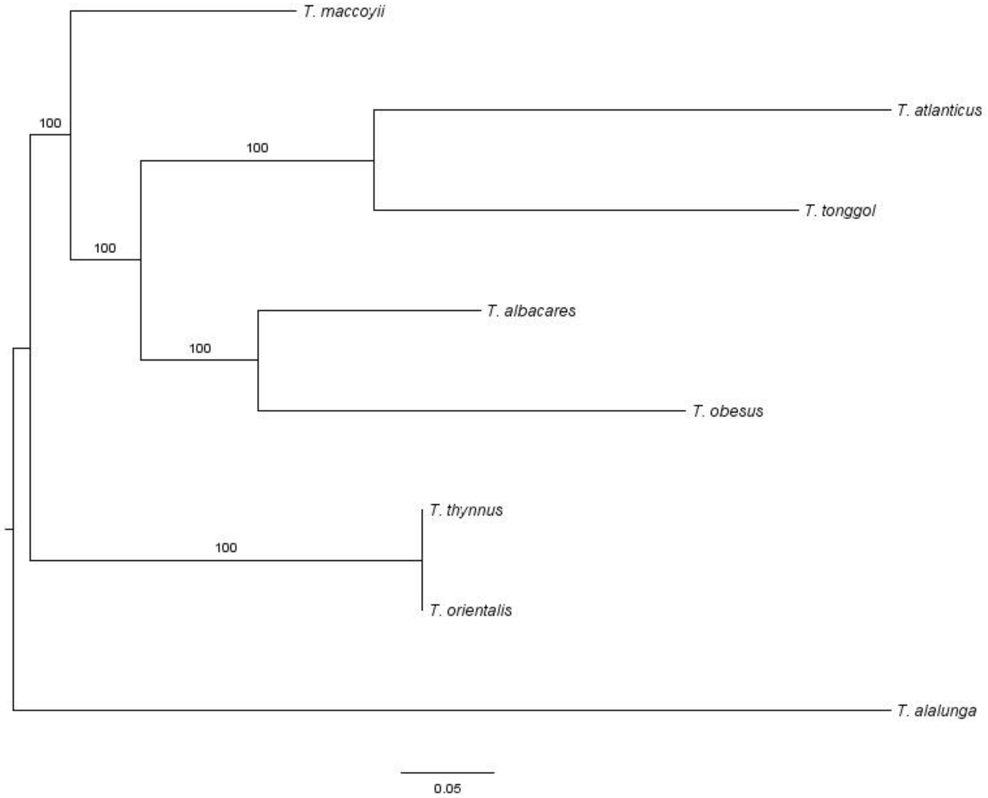
Tree 90: M=1, n=8, only *Thunnus*, per species, 0% missing, IUPAC encoded sites.



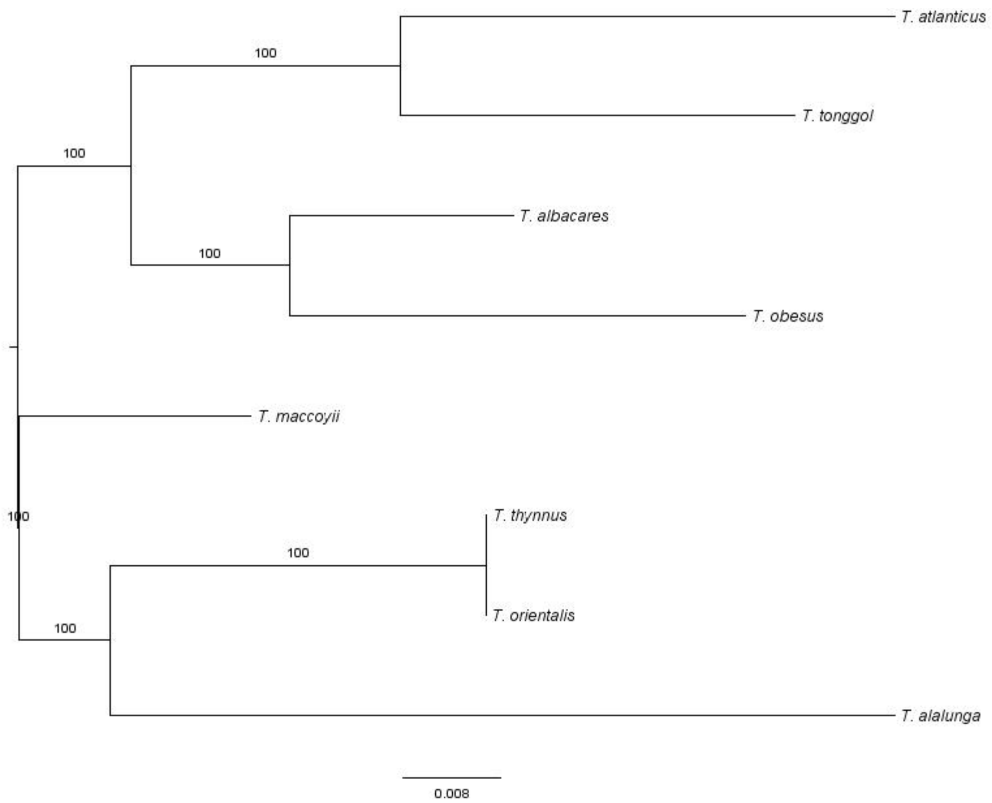
Tree 91: M=1, n=8, only *Thunnus*, per species, 75% missing, fixed positions.



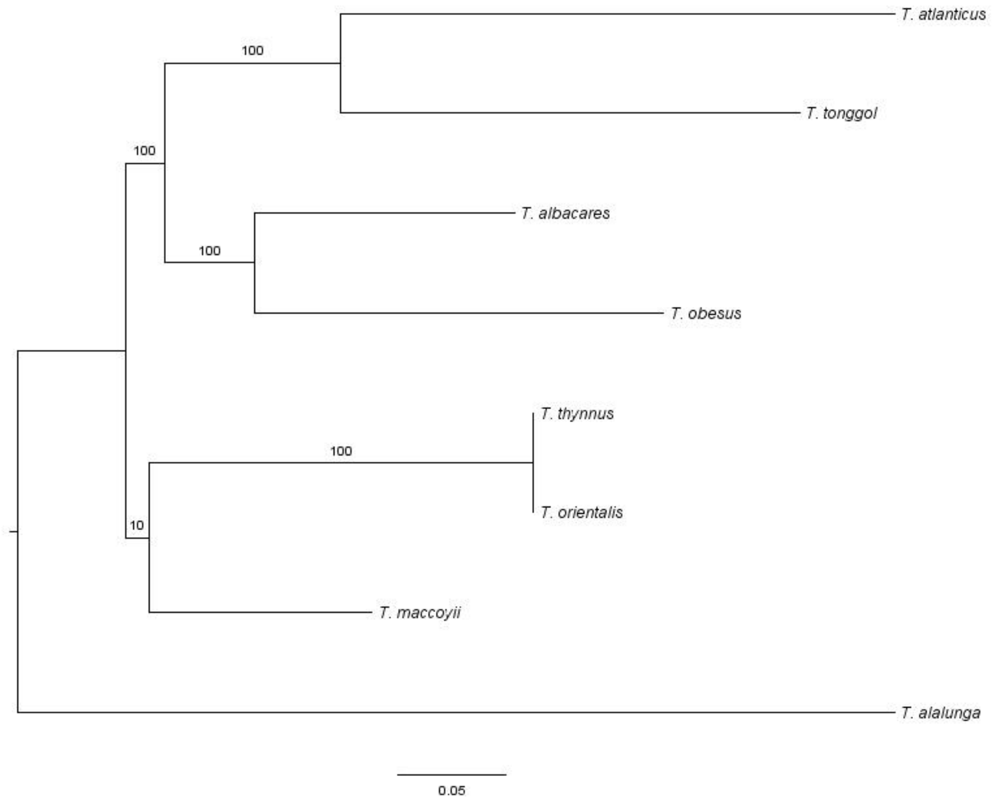
Tree 92: M=1, n=8, only *Thunnus*, per species, 75% missing, IUPAC encoded sites.



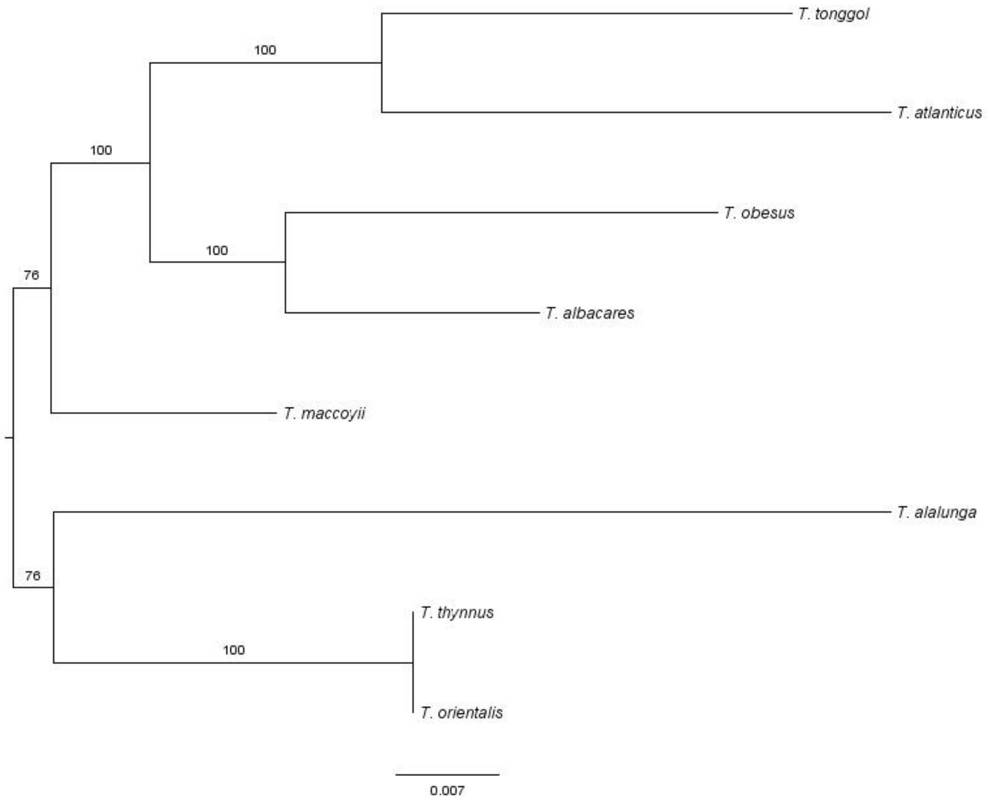
Tree 93: M=1, n=8, only *Thunnus*, per species, 50% missing, fixed positions.



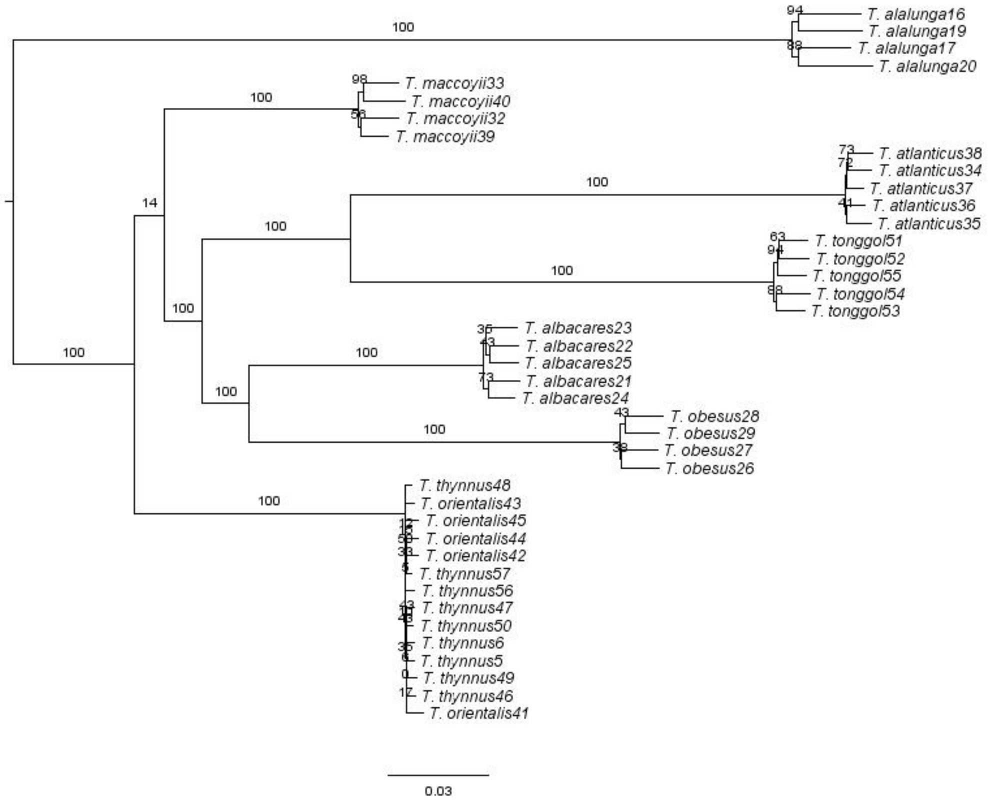
Tree 94: M=1, n=8, only *Thunnus*, per species, 50% missing, IUPAC encoded sites.



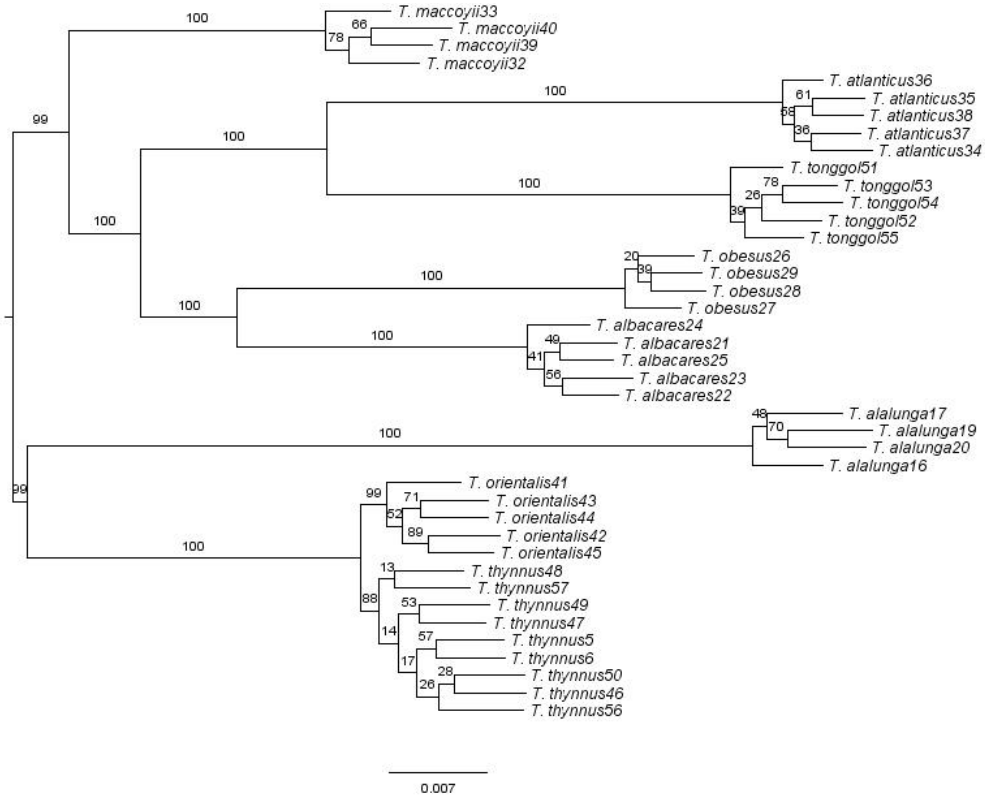
Tree 95: M=1, n=8, only *Thunnus*, per species, 25% missing, fixed positions.



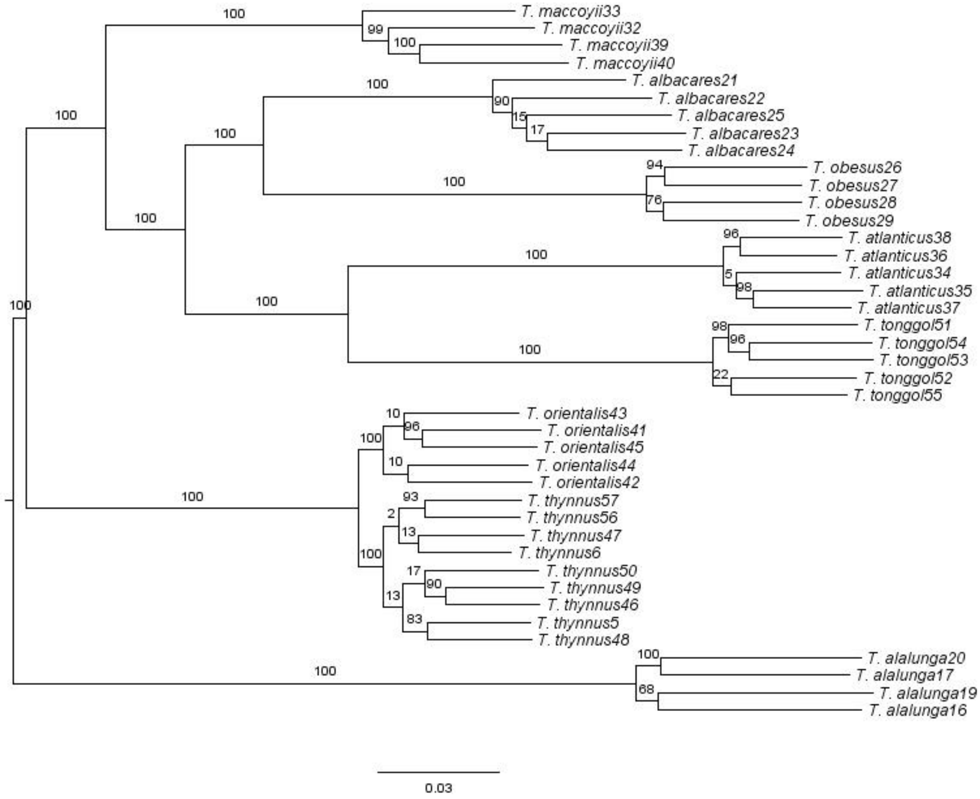
Tree 96: M=1, n=8, only *Thunnus*, per species, 25% missing, IUPAC encoded sites.



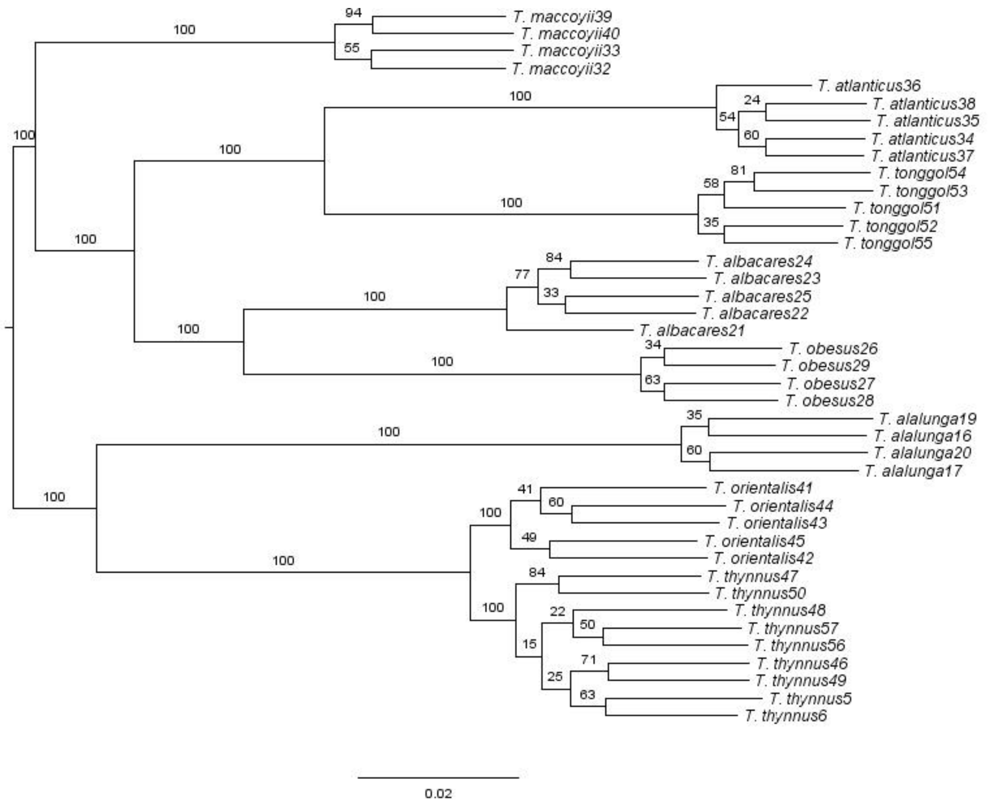
Tree 97: M=2, n=4, only *Thunnus*, per individuals, 0% missing, fixed positions.



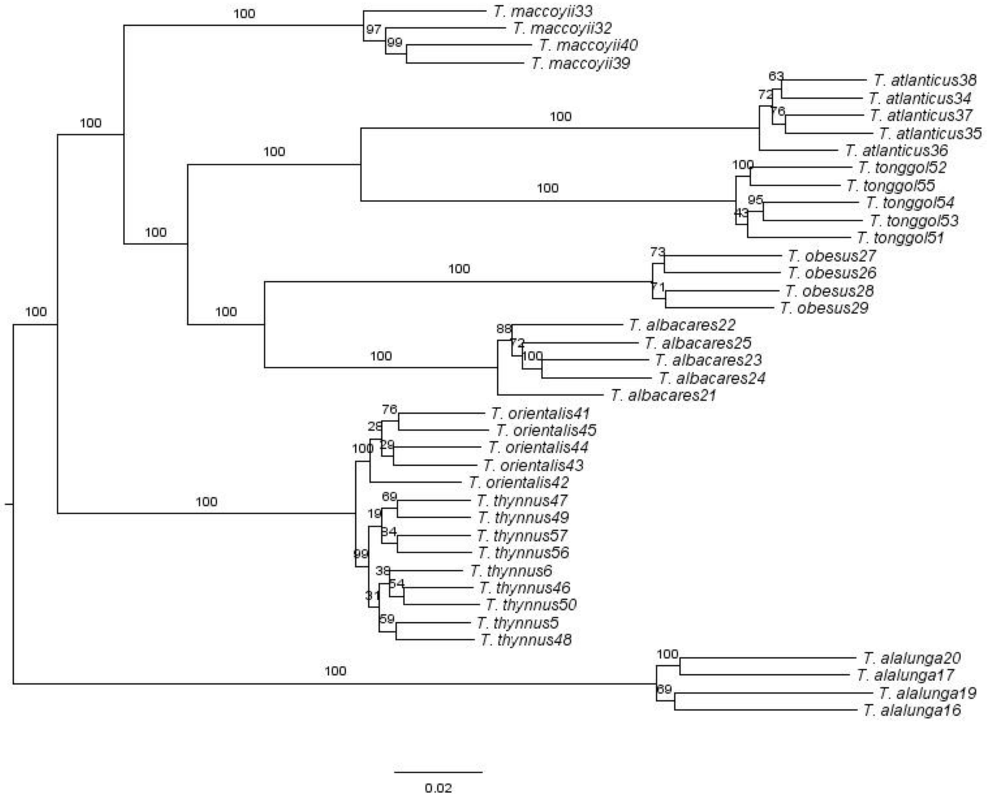
Tree 98: M=2, n=4, only *Thunnus*, per individuals, 0% missing, IUPAC encoded sites.



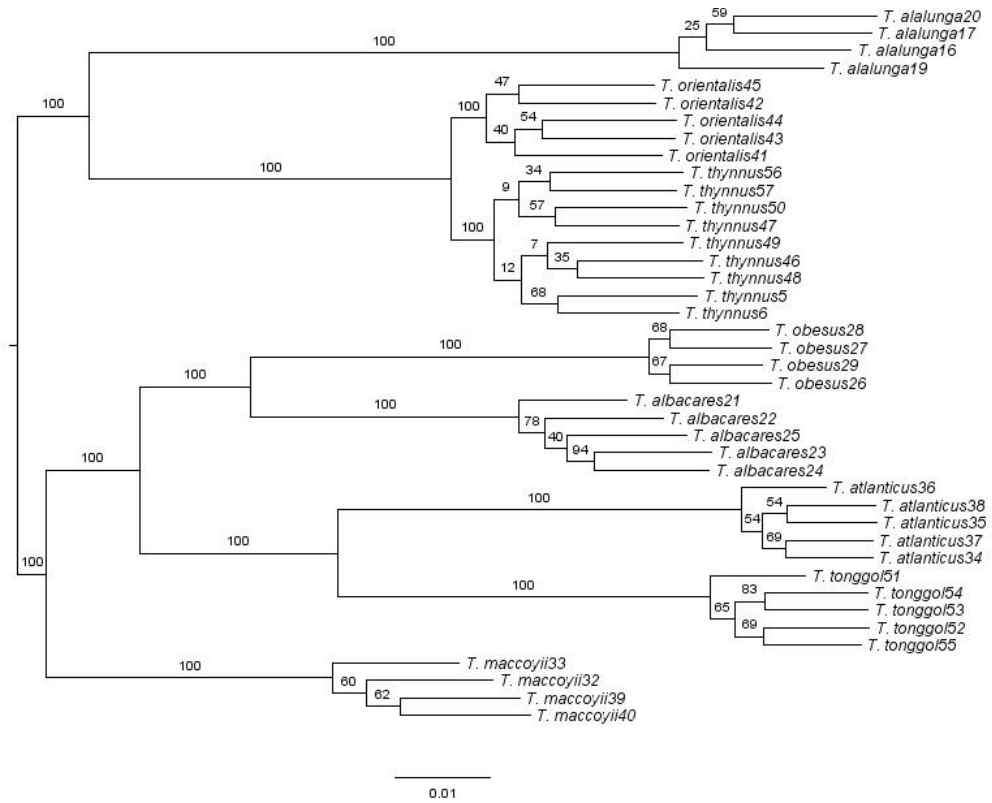
Tree 99: M=2, n=4, only *Thunnus*, per individuals, 75% missing, fixed positions.



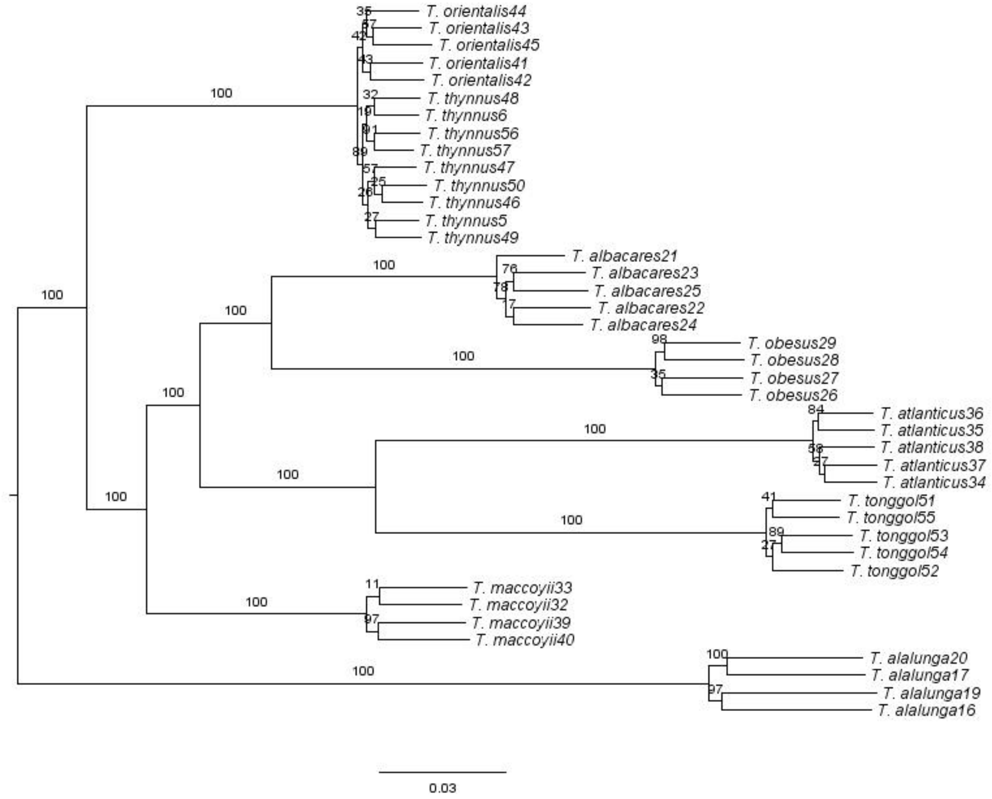
Tree 100: M=2, n=4, only *Thunnus*, per individuals, 75% missing, IUPAC encoded sites.



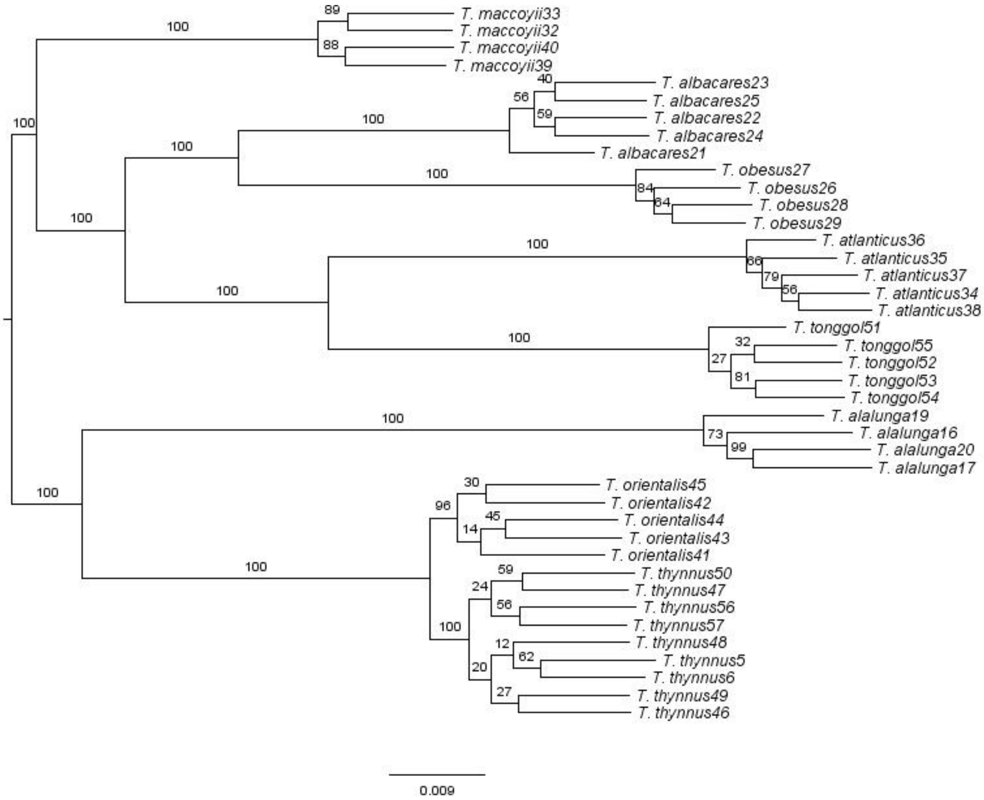
Tree 101: M=2, n=4, only *Thunnus*, per individuals, 50% missing, fixed positions.



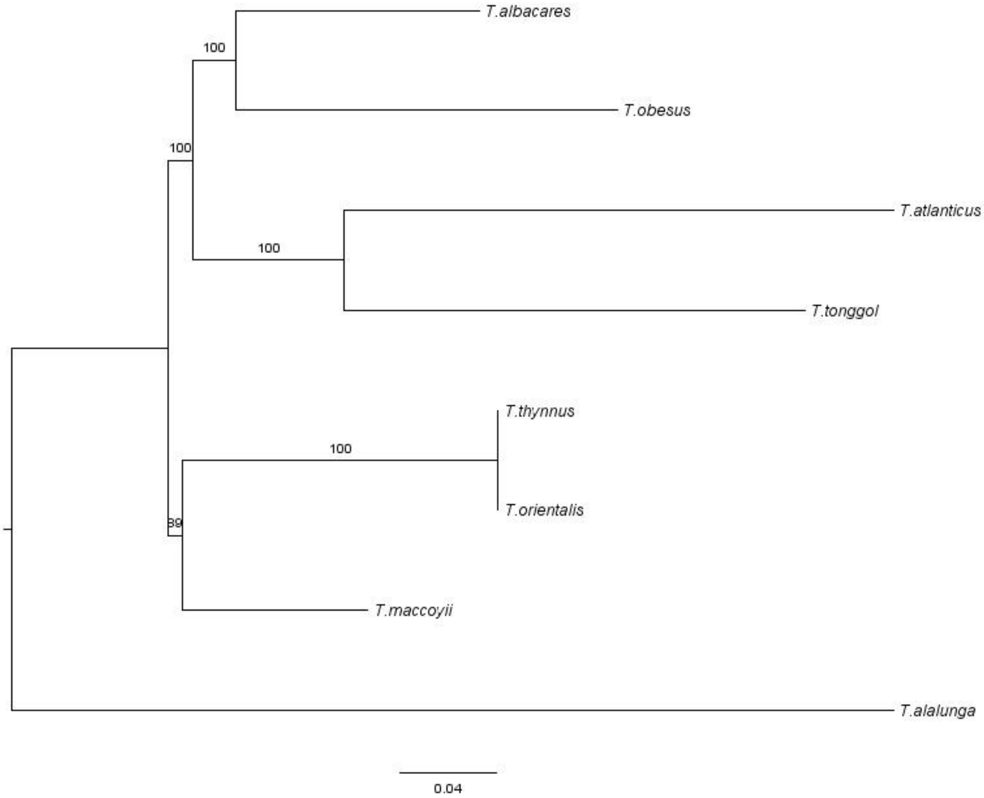
Tree 102: M=2, n=4, only *Thunnus*, per individuals, 50% missing, IUPAC encoded sites.



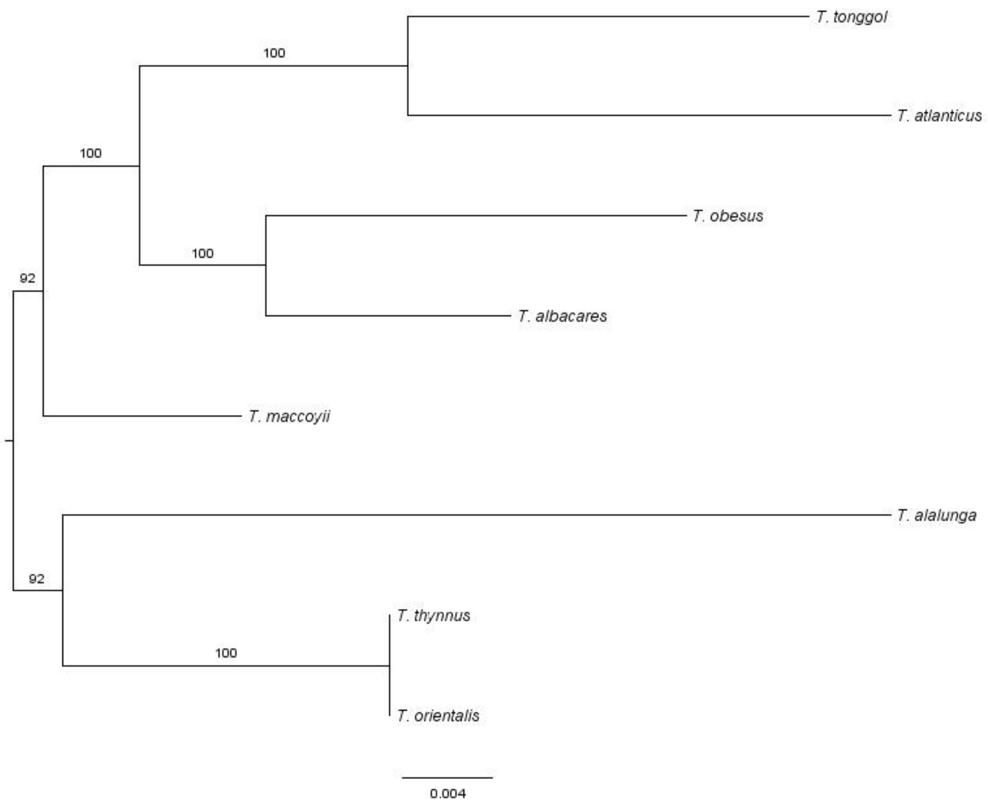
Tree 103: M=2, n=4, only *Thunnus*, per individuals, 25% missing, fixed positions.



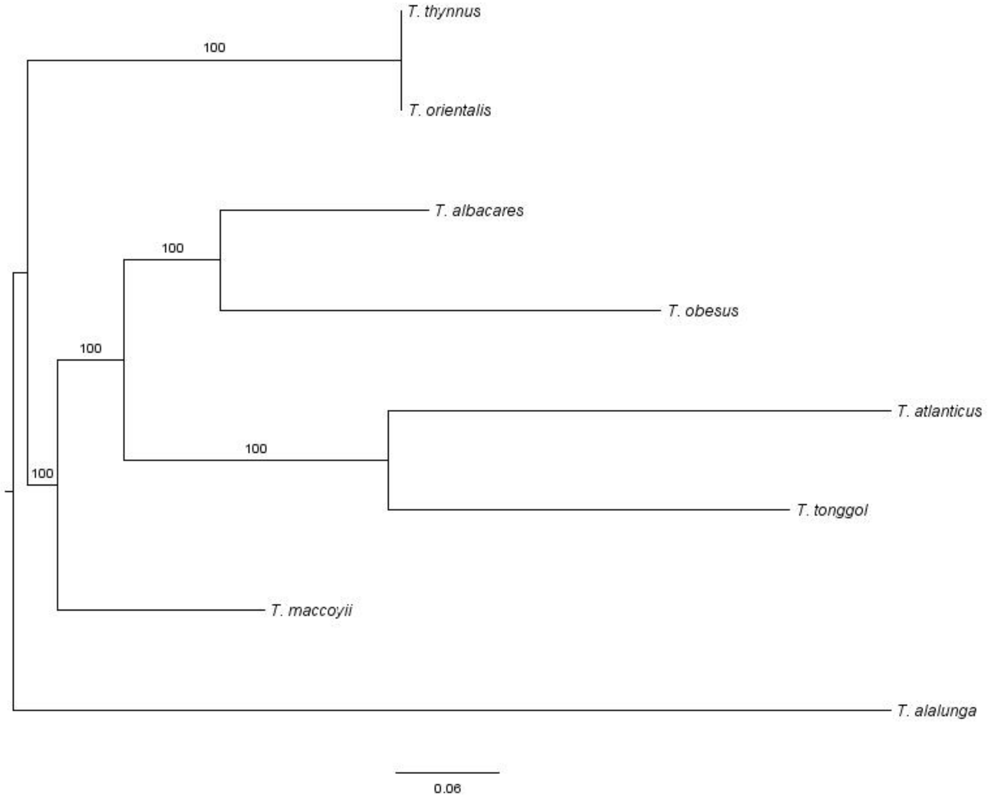
Tree 104: M=2, n=4, only *Thunnus*, per individuals, 25% missing, IUPAC encoded sites.



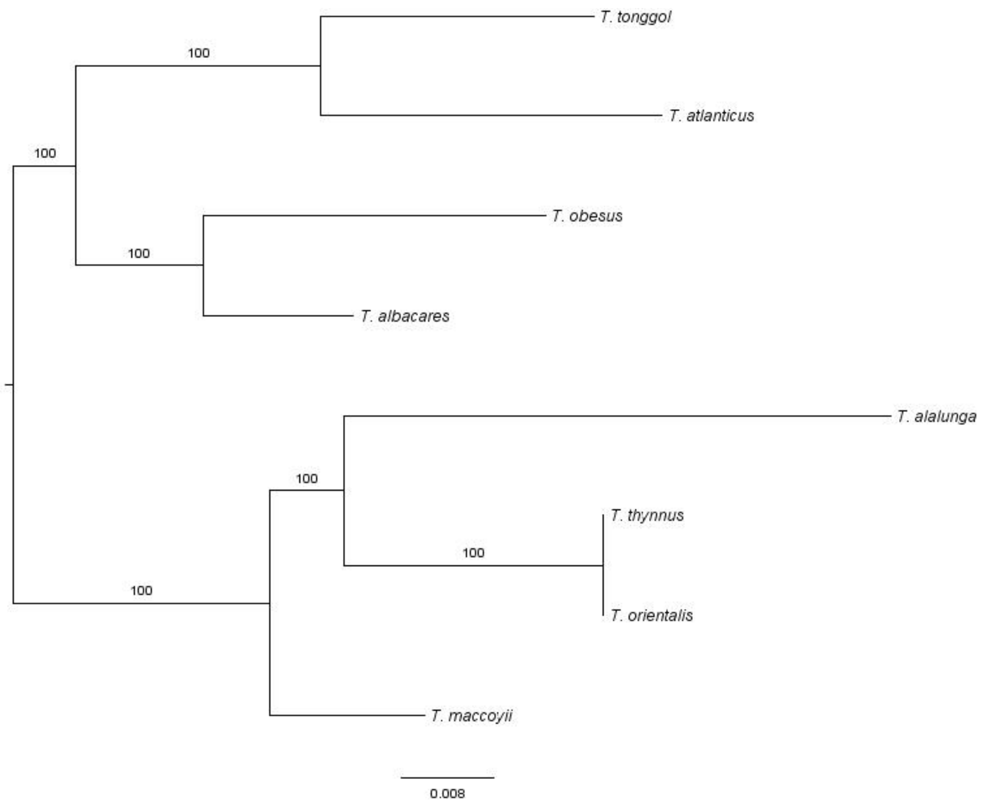
Tree 105: M=2, n=4, only *Thunnus*, per species, 0% missing, fixed positions.



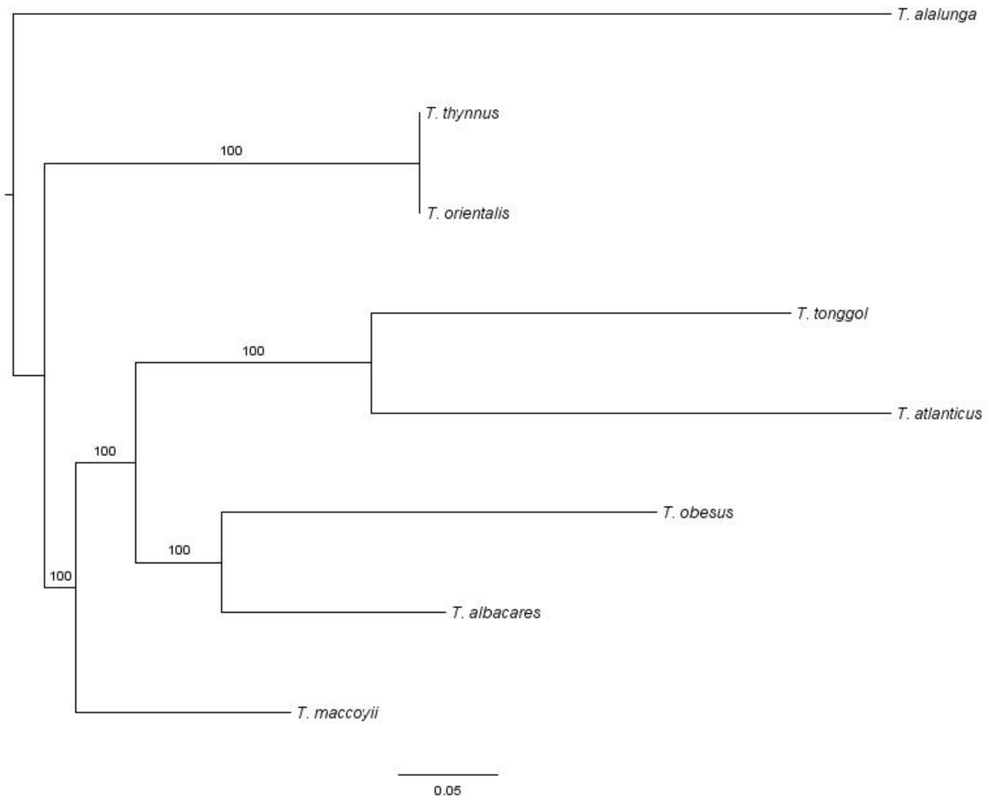
Tree 106: M=2, n=4, only *Thunnus*, per species, 0% missing, IUPAC encoded sites.



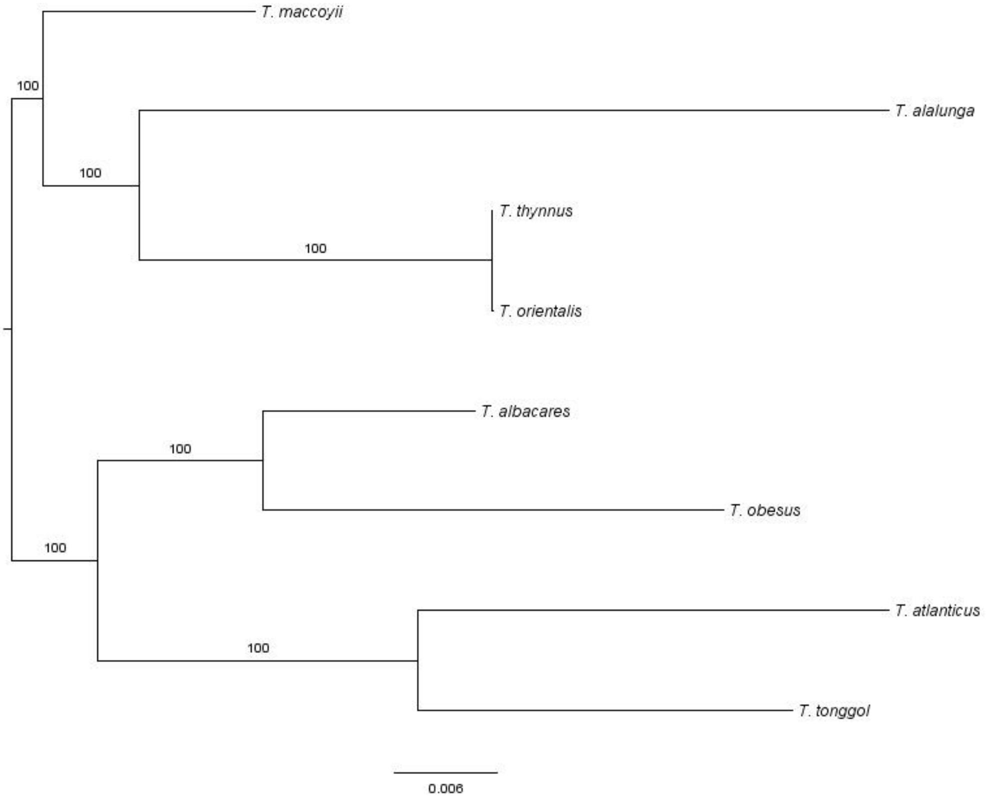
Tree 107: M=2, n=4, only *Thunnus*, per species, 75% missing, fixed positions.



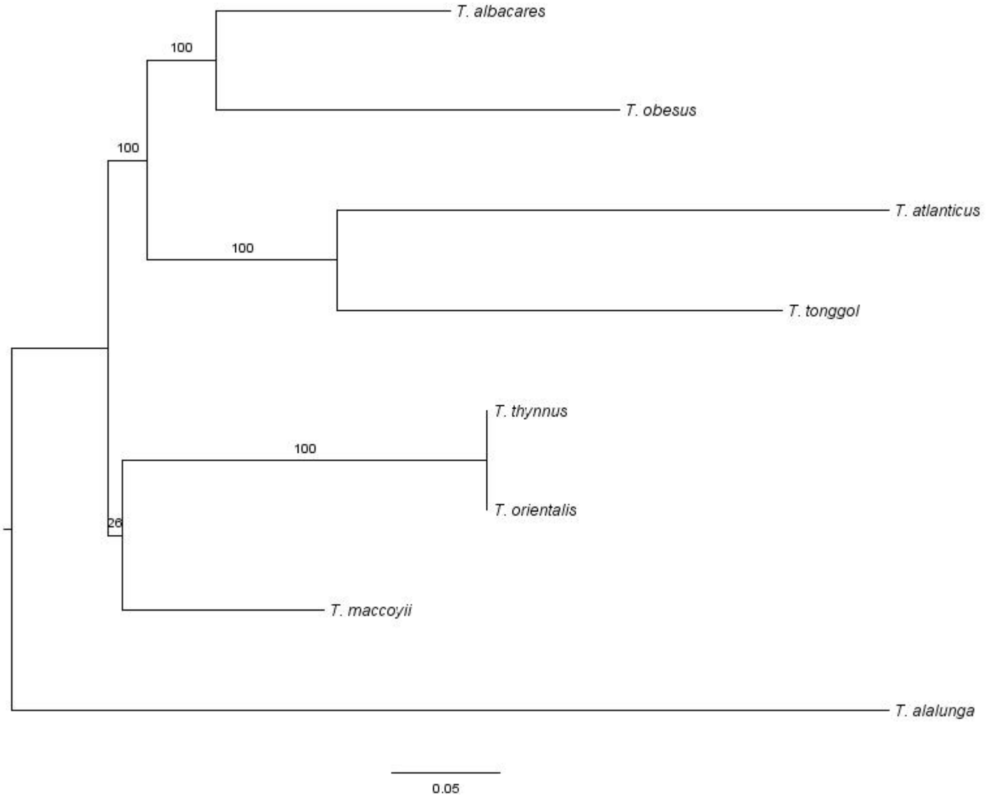
Tree 108: M=2, n=4, only *Thunnus*, per species, 75% missing, IUPAC encoded sites.



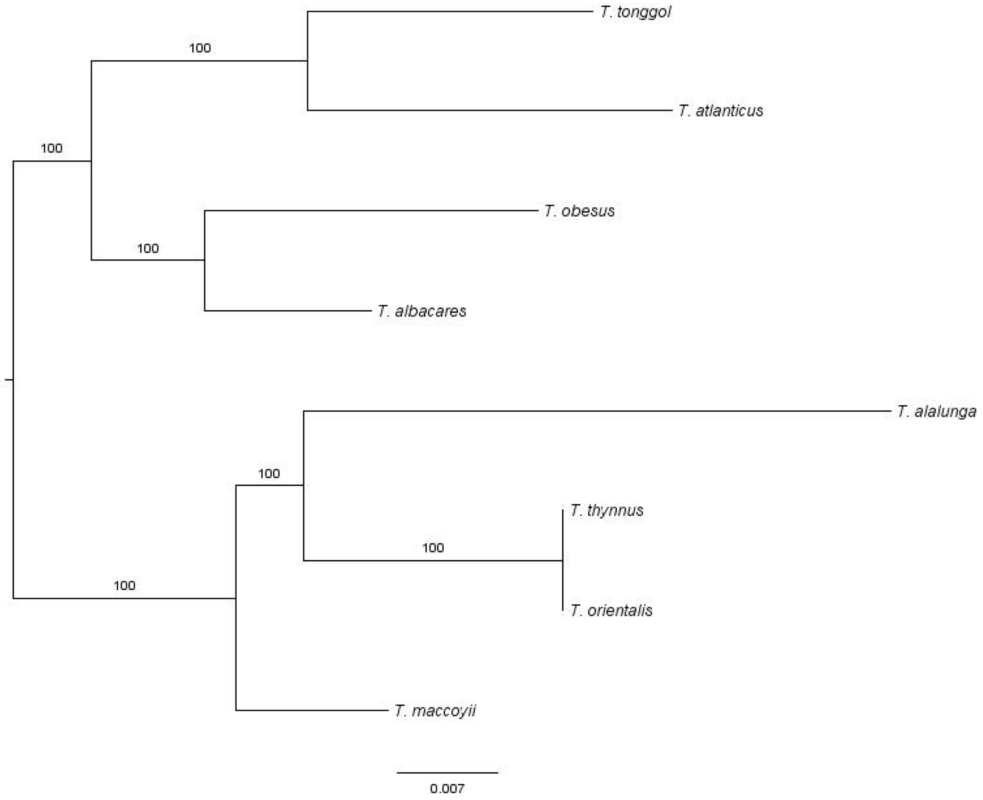
Tree 109: M=2, n=4, only *Thunnus*, per species, 50% missing, fixed positions.



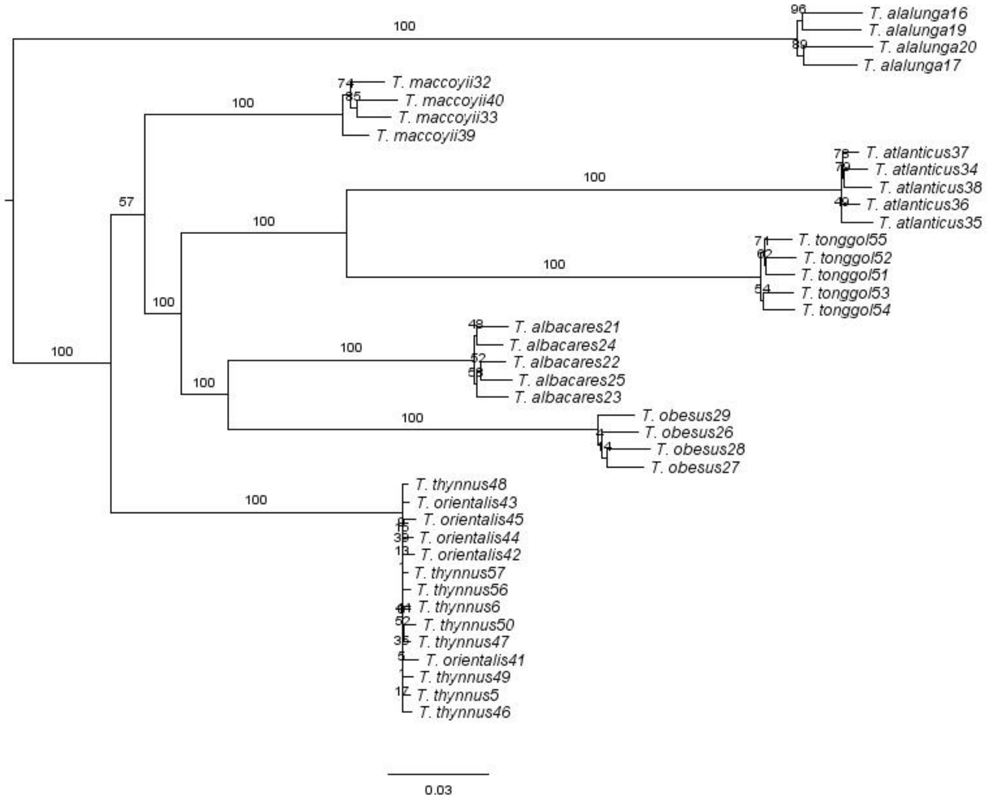
Tree 110: M=2, n=4, only *Thunnus*, per species, 50% missing, IUPAC encoded sites.



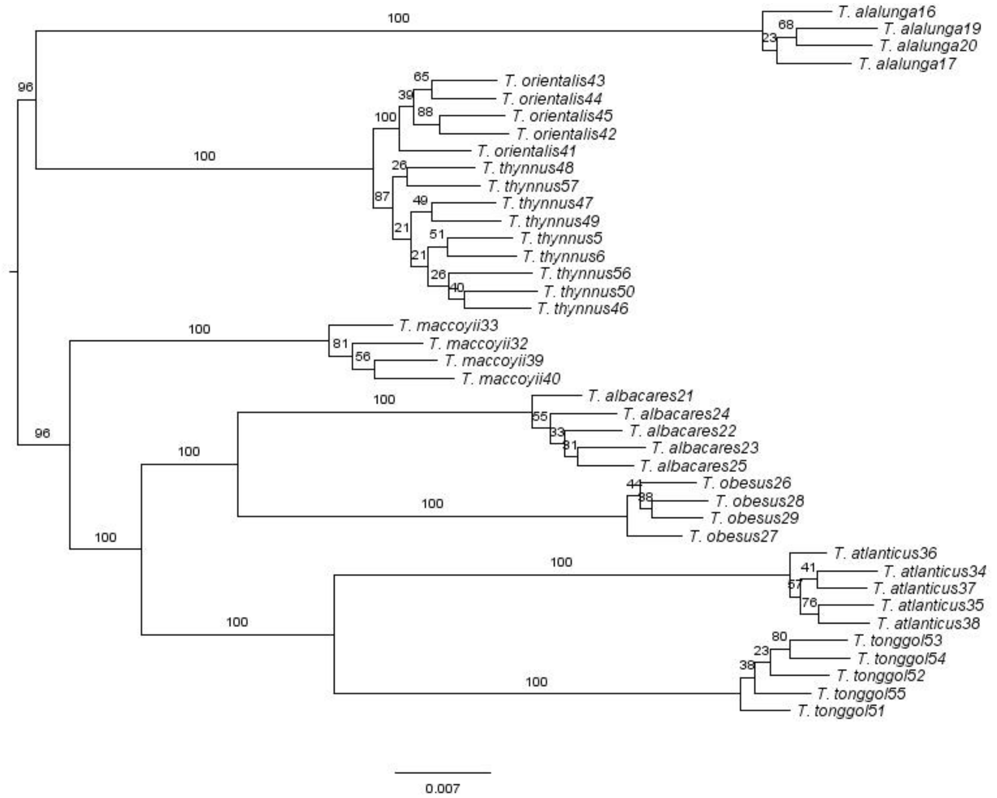
Tree 111: M=2, n=4, only *Thunnus*, per species, 25% missing, fixed positions.



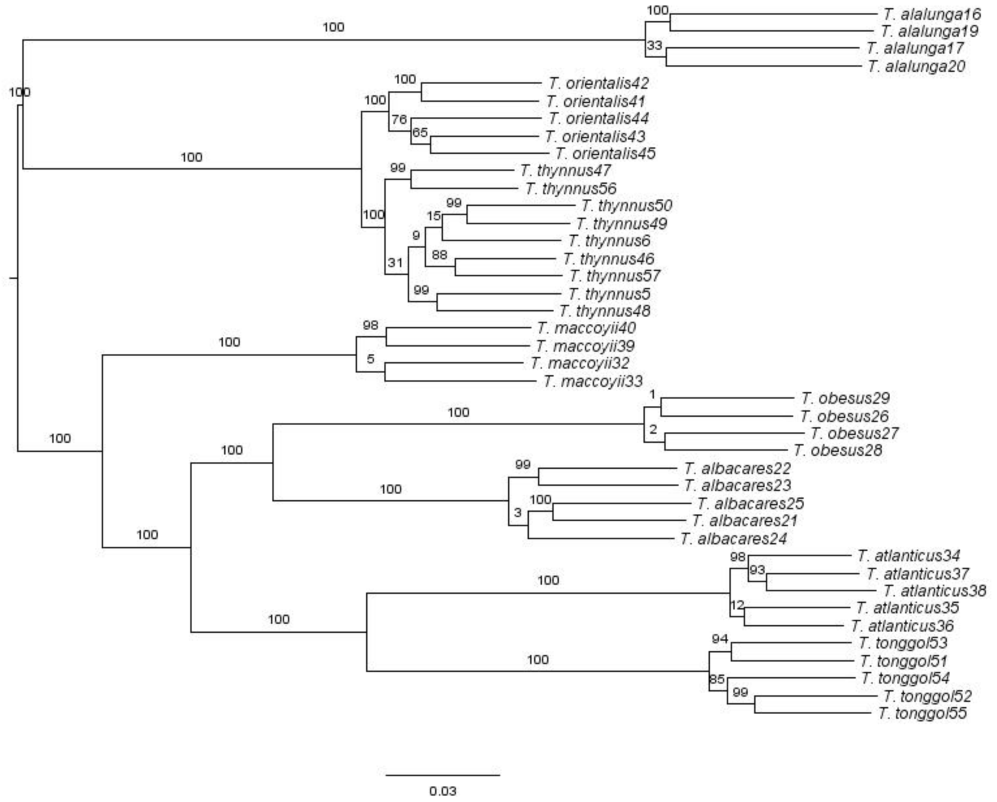
Tree 112: M=2, n=4, only *Thunnus*, per species, 25% missing, IUPAC encoded sites.



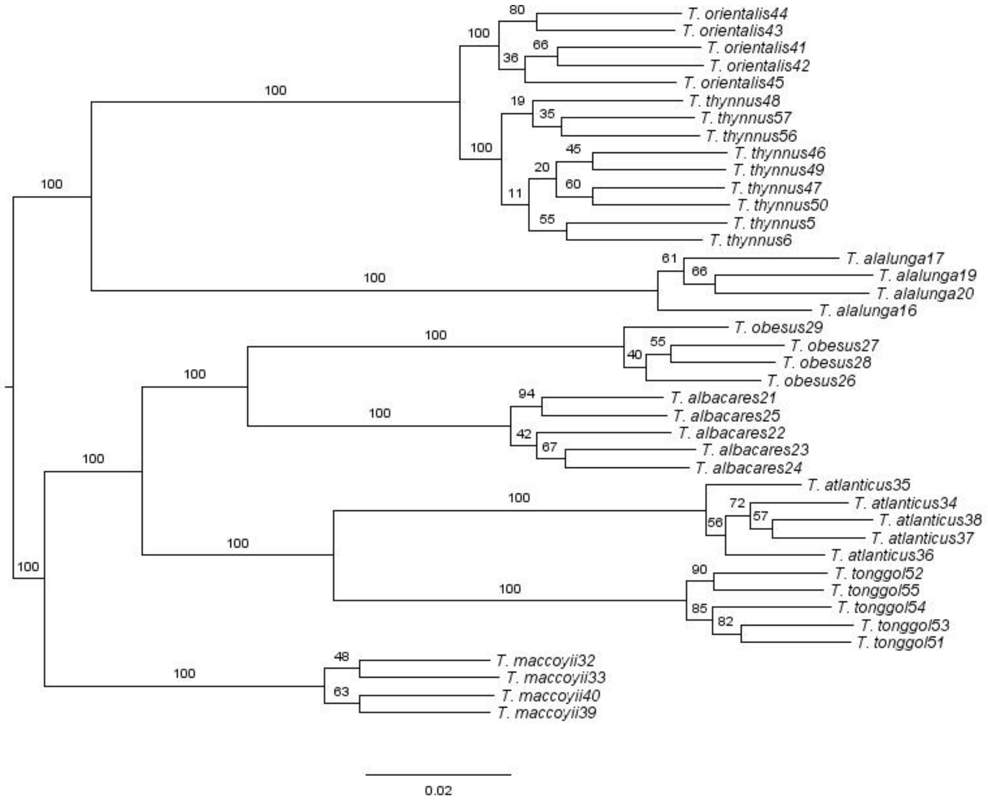
Tree 113: M=2, n=8, only *Thunnus*, per individuals, 0% missing, fixed positions.



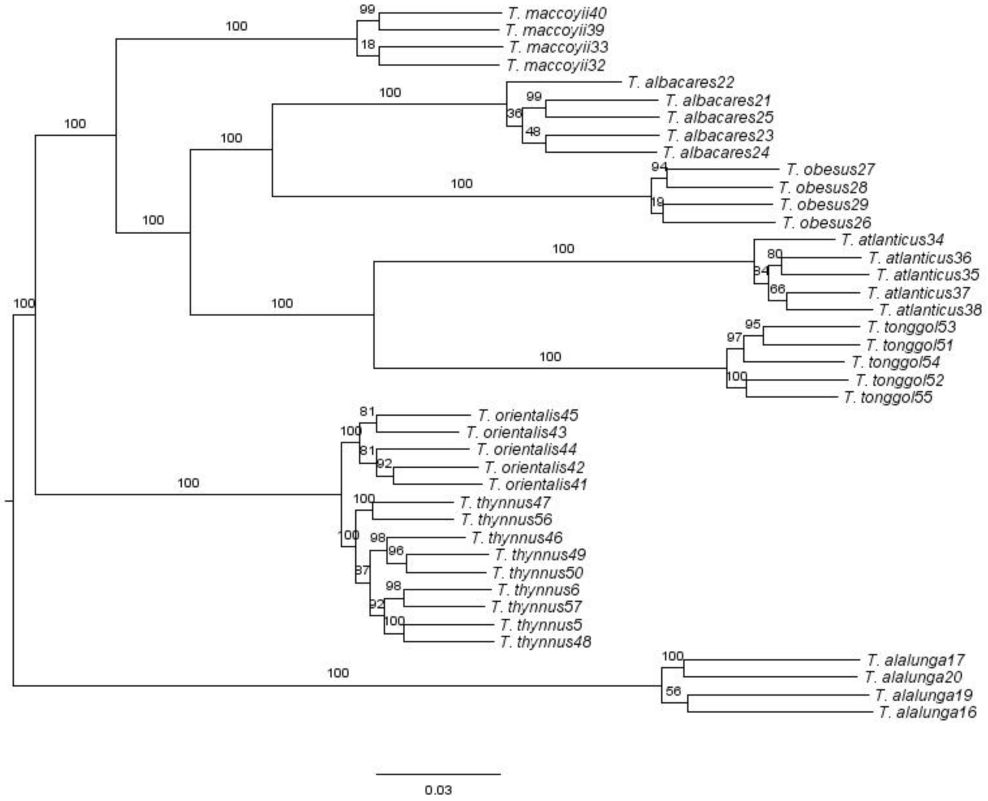
Tree 114: M=2, n=8, only *Thunnus*, per individuals, 0% missing, IUPAC encoded sites.



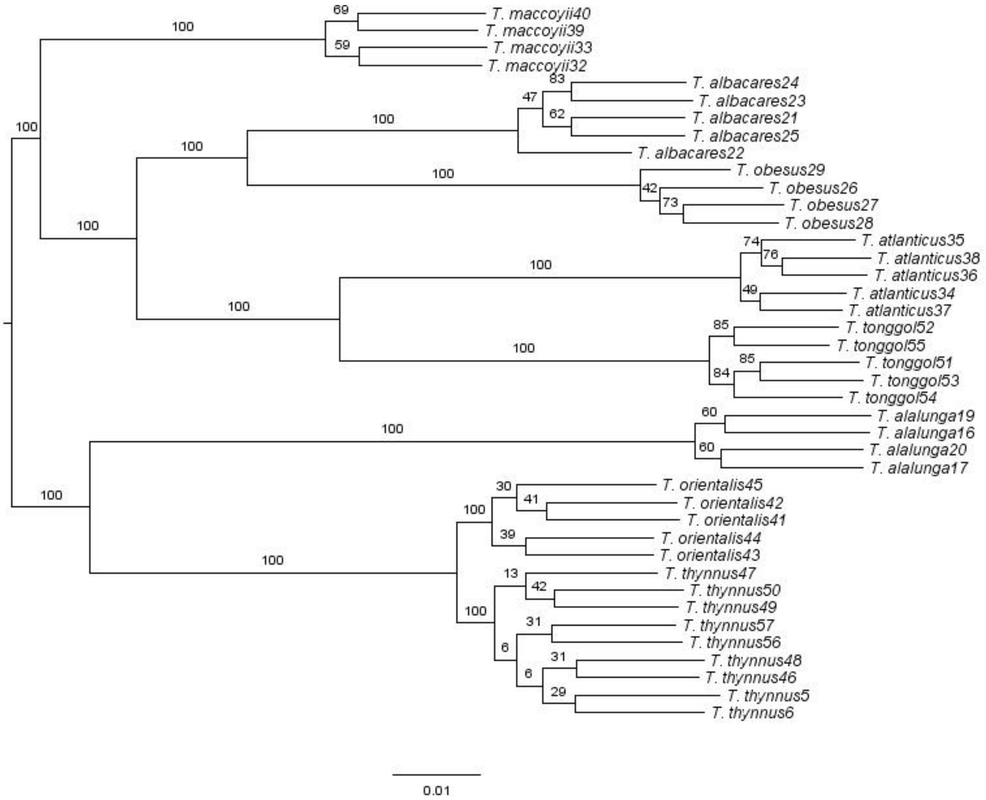
Tree 115: M=2, n=8, only *Thunnus*, per individuals, 75% missing, fixed positions.



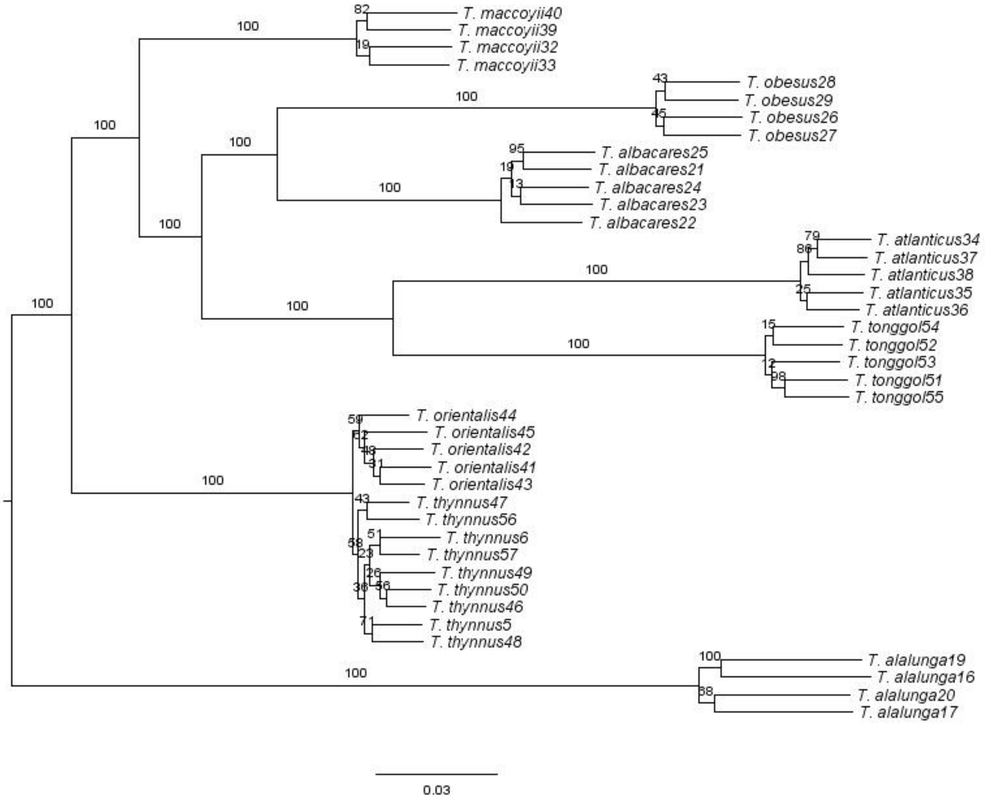
Tree 116: M=2, n=8, only *Thunnus*, per individuals, 75% missing, IUPAC encoded sites.



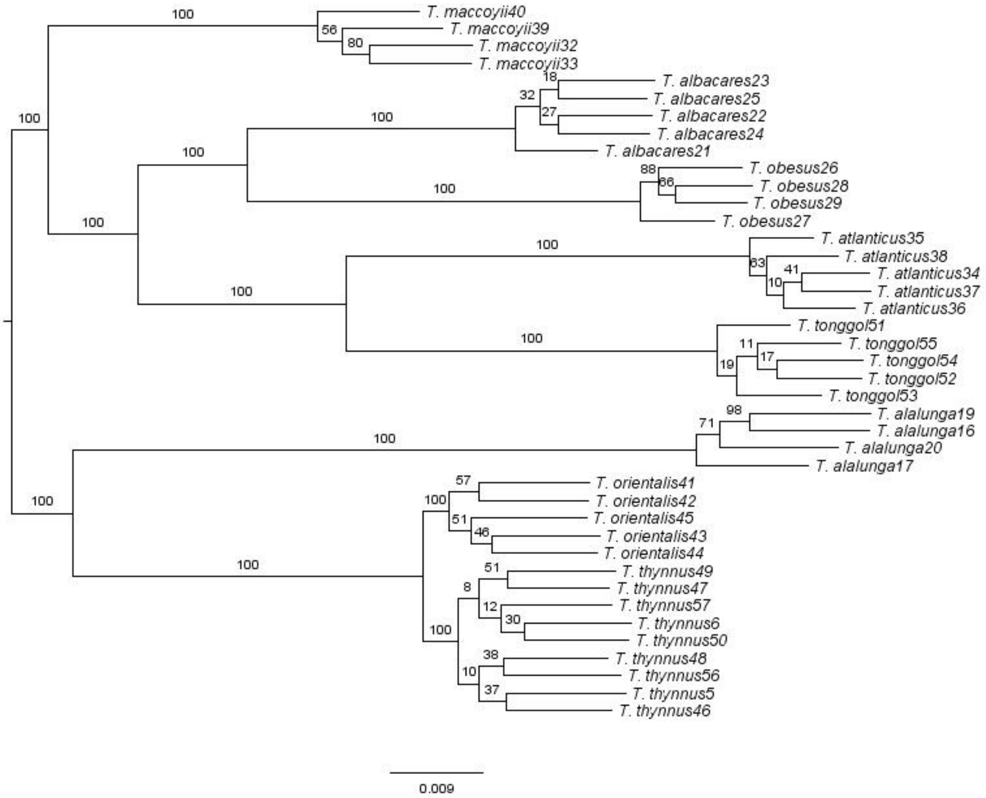
Tree 117: M=2, n=8, only *Thunnus*, per individuals, 50% missing, fixed positions.



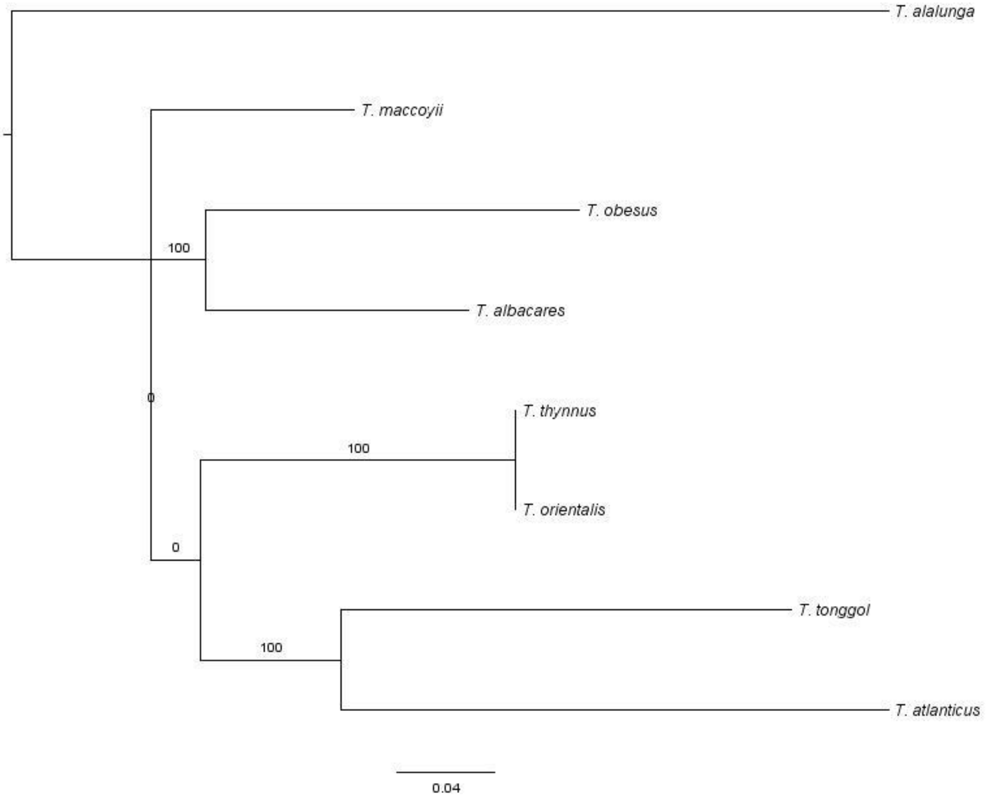
Tree 118: M=2, n=8, only *Thunnus*, per individuals, 50% missing, IUPAC encoded sites.



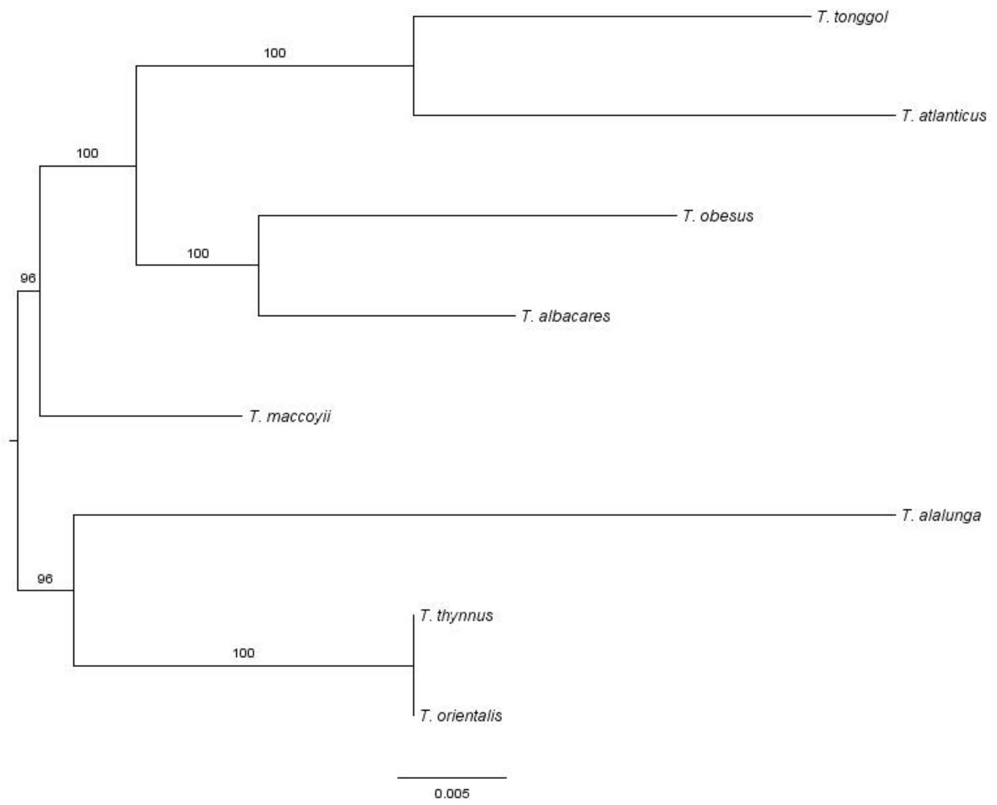
Tree 119: M=2, n=8, only *Thunnus*, per individuals, 25% missing, fixed positions.



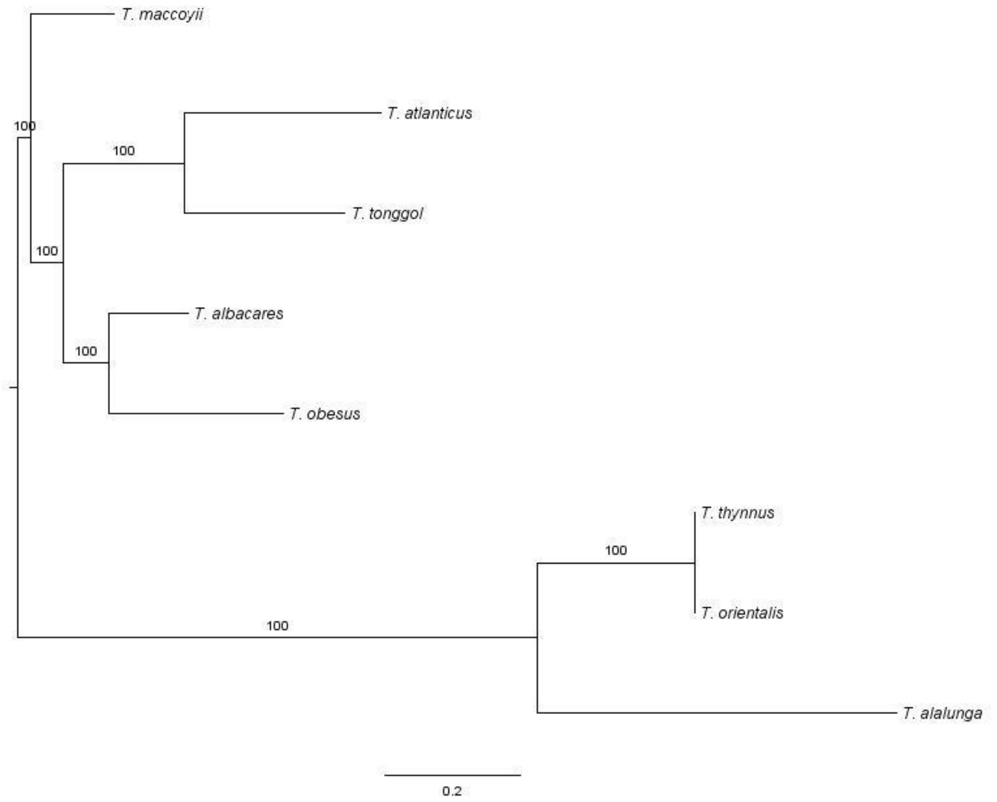
Tree 120: M=2, n=8, only *Thunnus*, per individuals, 25% missing, IUPAC encoded sites.



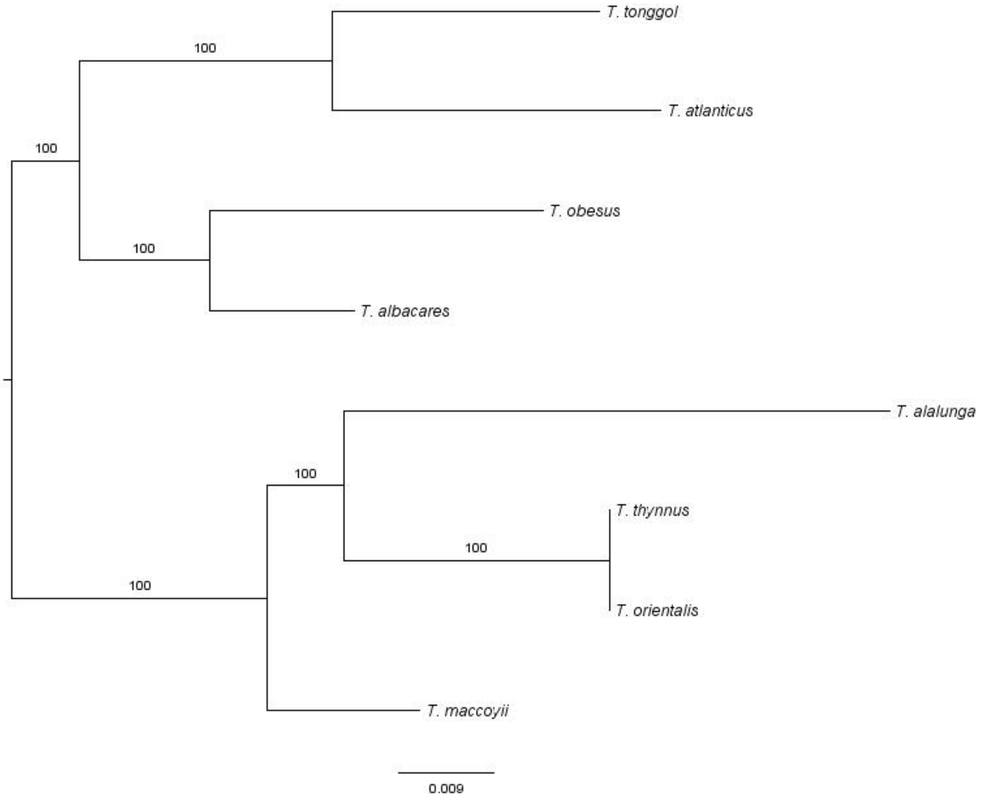
Tree 121: M=2, n=8, only *Thunnus*, per species, 0% missing, fixed positions.



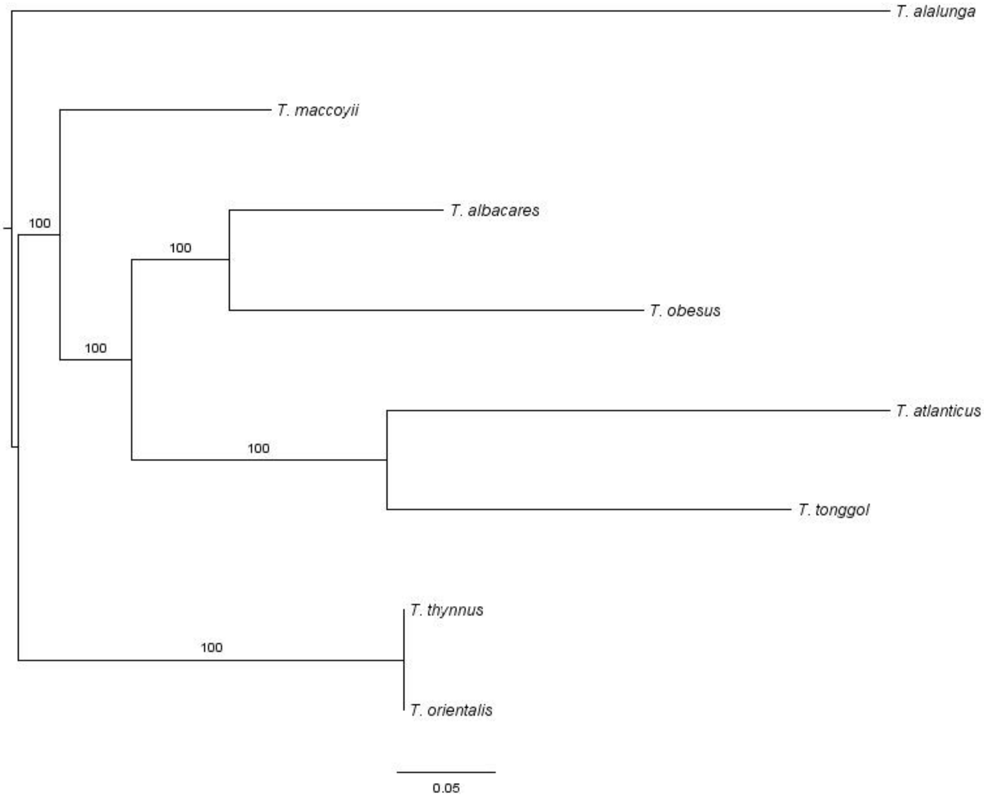
Tree 122: M=2, n=8, only *Thunnus*, per species, 0% missing, IUPAC encoded sites.



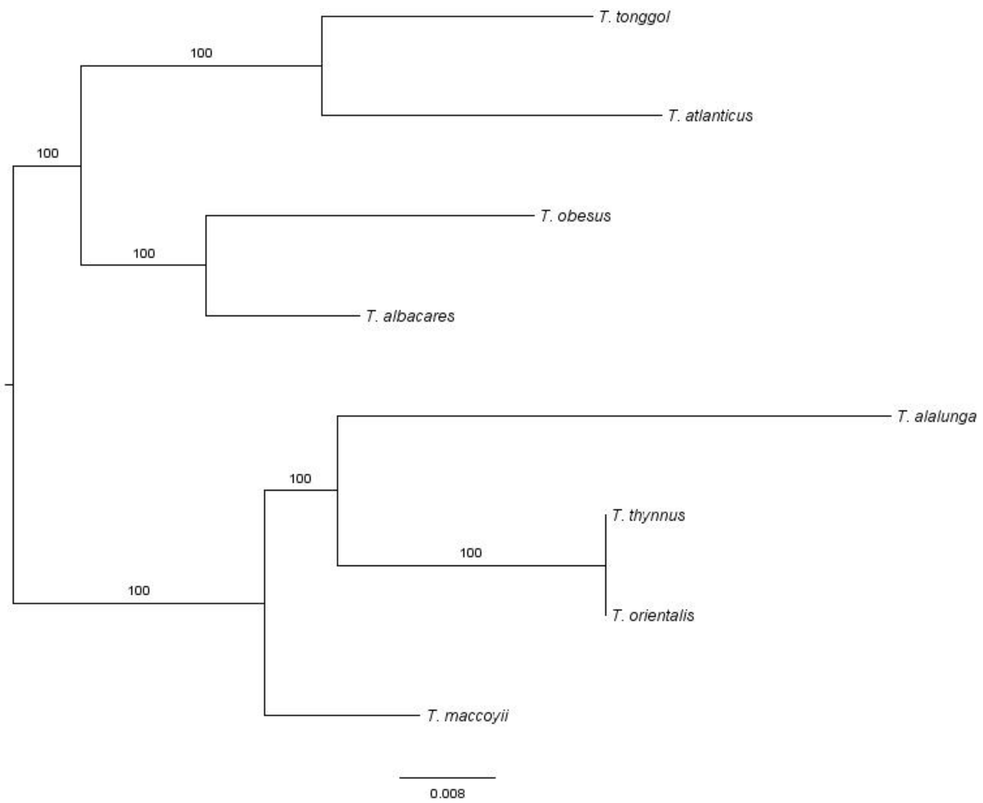
Tree 123: M=2, n=8, only *Thunnus*, per species, 75% missing, fixed positions.



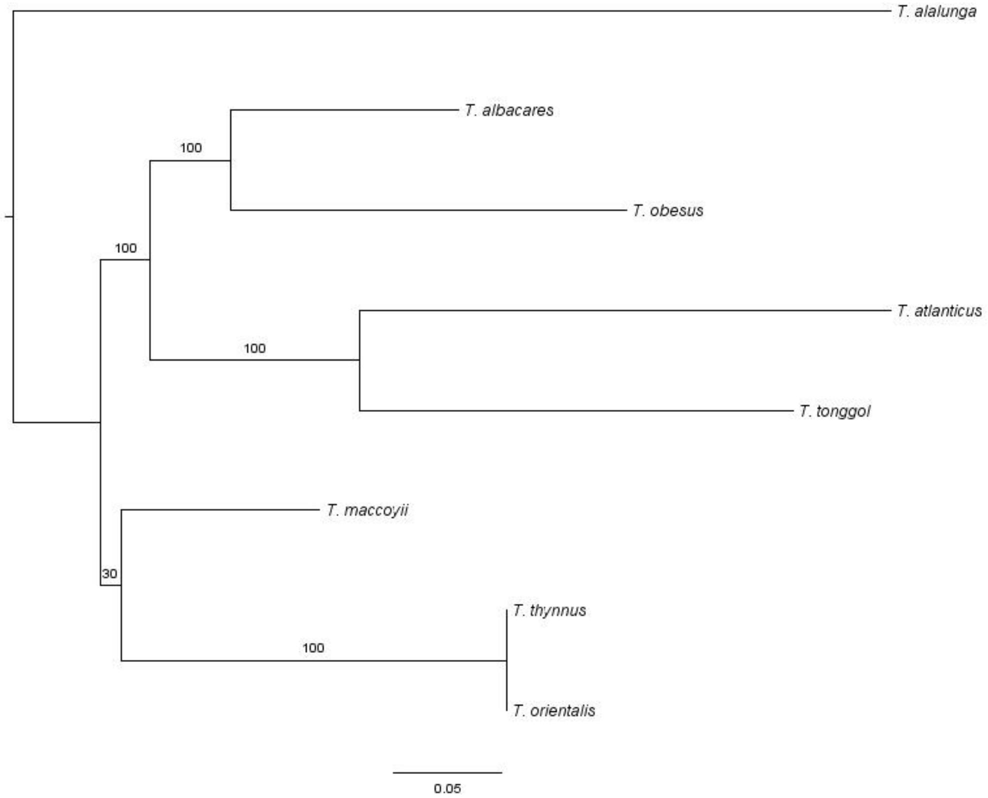
Tree 124: M=2, n=8, only *Thunnus*, per species, 75% missing, IUPAC encoded sites.



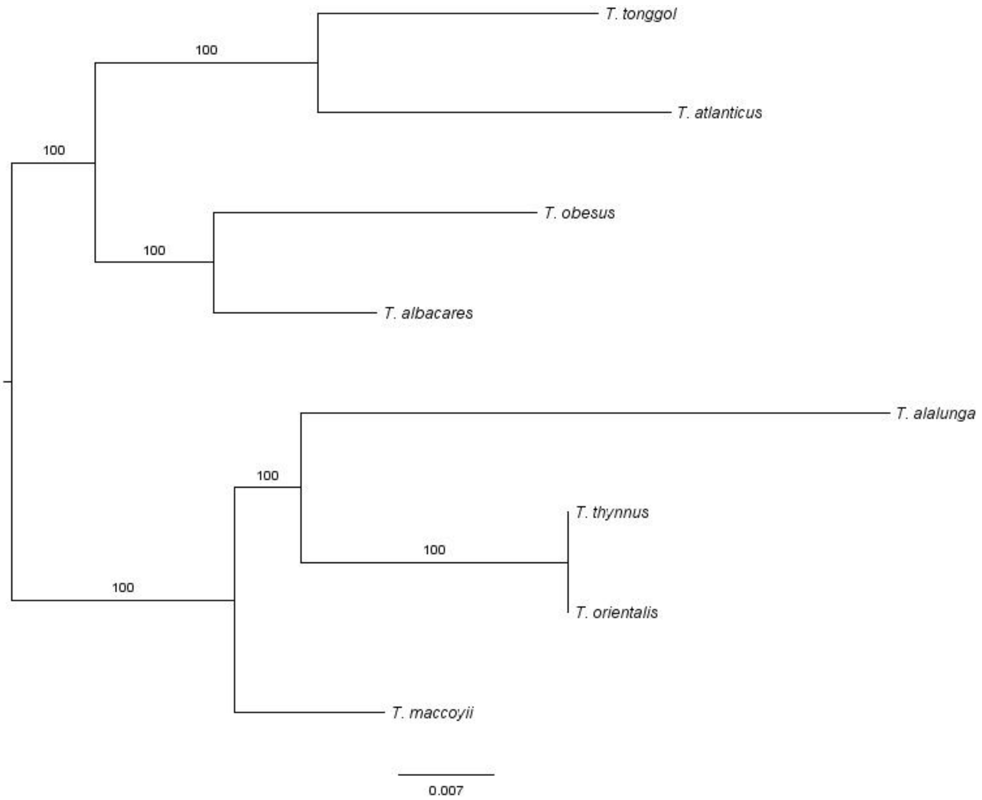
Tree 125: M=2, n=8, only *Thunnus*, per species, 50% missing, fixed positions.



Tree 126: M=2, n=8, only *Thunnus*, per species, 50% missing, IUPAC encoded sites.



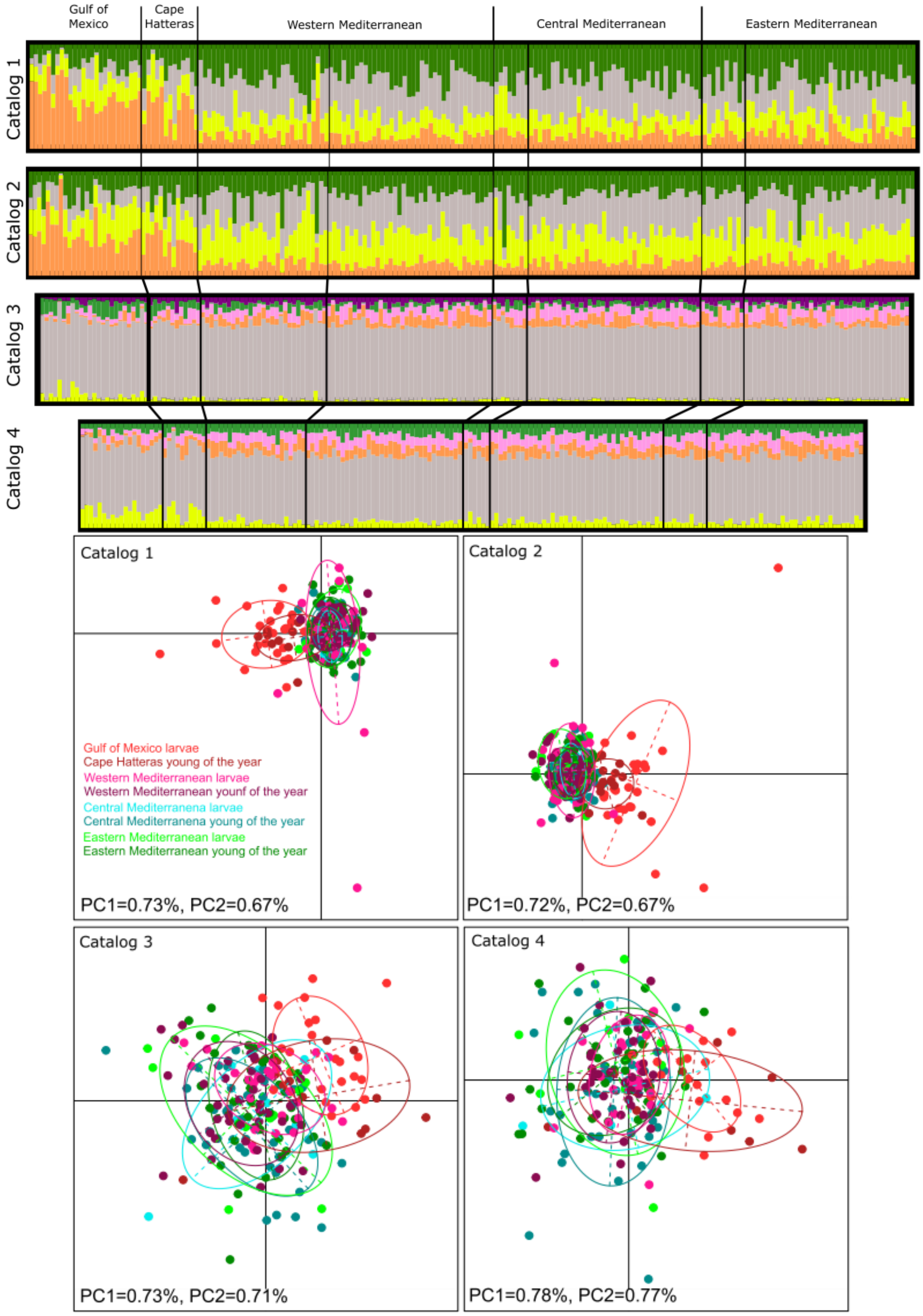
Tree 127: M=2, n=8, only *Thunnus*, per species, 25% missing, fixed positions.



Tree 128: M=2, n=8, only *Thunnus*, per species, 25% missing, IUPAC encoded sites.

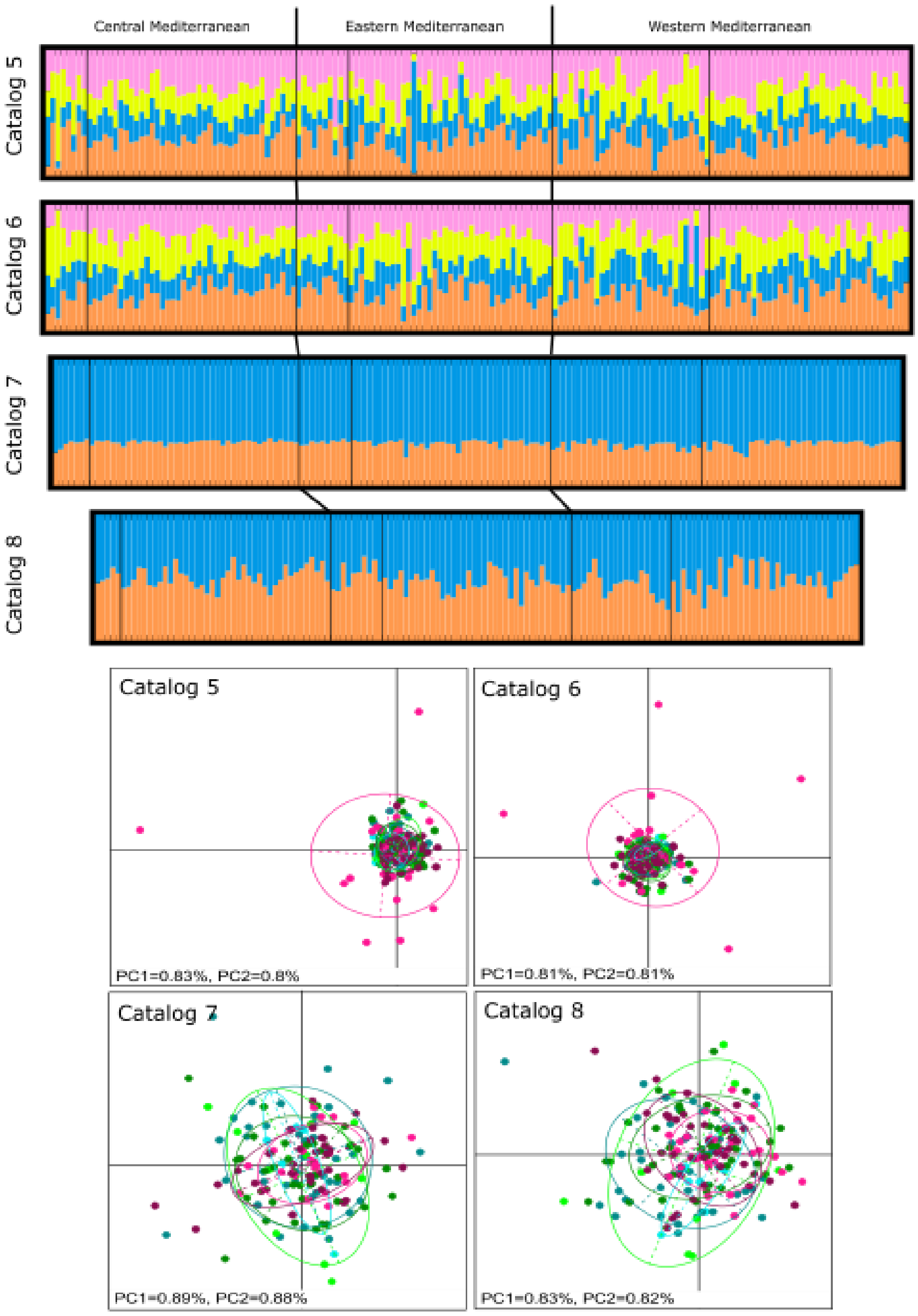
Appendix C

WebFigure I



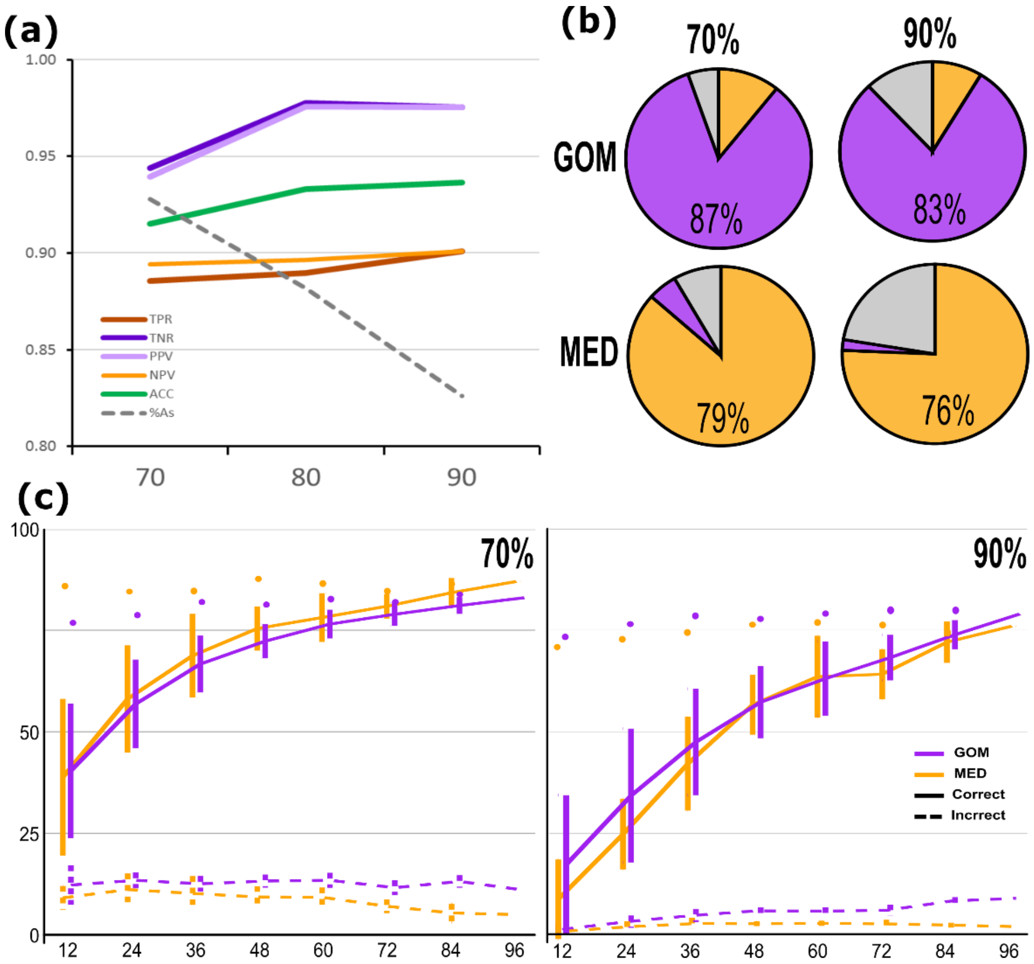
WebFigure 1. Graphical representation of the Bayesian clustering approach for the best supported K value (above) and Principal Component Analyses (below) for catalogs 1 to 4.

WebFigure 2



WebFigure 2. Graphical representation of the Bayesian clustering approach for the best supported K value (above) and Principal Component Analyses (below) for catalogs 5 to 8.

WebFigure 3



WebFigure 3. Origin assignment success rates. a) Sensitivity and specificity analyses of each threshold value tested where TPR is the true positive rate, TNR is the true negative rate, PPV is the positive predictive value, NPV is the negative predictive value and ACC is accuracy; %As stands for the percentage of samples assigned to one of the two main spawning locations at 70, 80 or 90% assignment score. b) For 70 and 90% assignment score thresholds, percentages of correct or incorrectly assigned samples for reference samples captured in the Gulf of Mexico (GOM) and the Mediterranean (MED); purple indicates Gulf of Mexico origin, orange, Mediterranean origin, and grey, unassigned samples. c) For 70 and 90% assignment score thresholds, evolution of the percentage of correctly or incorrectly assigned Gulf of Mexico (purple) and Mediterranean (orange) origin samples as number of SNPs used increases; vertical bars indicate standard deviation and dots, correct assignment rates for the most discriminant subsets of SNPs.

WebTable 1

Samples processed with RAD-seq. Only the 204 from the 240 original passing quality filters and used in subsequent analyses are shown. Dev. stage stands for Developmental Stage. Weight and Length are total.

Sample	Area	Dev. stage	Catch date	Lat.	Long.	Length (cm)	Weight (g)
AZTI-GM-V-51	Gulf of Mexico	Larvae	14/05/2010	28.08	-90.49	n/a	n/a
AZTI-GM-V-78	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	n/a	n/a
TAMU-GM-V-53	Gulf of Mexico	Larvae	15/06/2007	28	-89.8	n/a	n/a
TAMU-GM-V-54	Gulf of Mexico	Larvae	15/06/2007	28	-89.8	n/a	n/a
TAMU-GM-V-56	Gulf of Mexico	Larvae	15/06/2007	27	-90.47	n/a	n/a
TAMU-GM-V-58	Gulf of Mexico	Larvae	15/06/2007	27	-90.47	n/a	n/a
TAMU-GM-V-59	Gulf of Mexico	Larvae	15/06/2007	27	-90.47	n/a	n/a
TAMU-GM-V-60	Gulf of Mexico	Larvae	15/06/2007	27	-90.47	n/a	n/a
TAMU-GM-V-63	Gulf of Mexico	Larvae	15/06/2008	27	-87.5	n/a	n/a
TAMU-GM-V-64	Gulf of Mexico	Larvae	15/06/2008	28	-89.07	n/a	n/a
TAMU-GM-V-68	Gulf of Mexico	Larvae	15/06/2008	28	-89.07	n/a	n/a
TAMU-GM-V-72	Gulf of Mexico	Larvae	15/06/2008	28	-90.4	n/a	n/a
TAMU-GM-V-73	Gulf of Mexico	Larvae	15/06/2008	28	-91.53	n/a	n/a
TAMU-GM-V-74	Gulf of Mexico	Larvae	15/06/2008	28	-91.53	n/a	n/a
TAMU-GM-V-78	Gulf of Mexico	Larvae	15/06/2008	28	-89.07	n/a	n/a
TAMU-GM-V-80	Gulf of Mexico	Larvae	15/06/2009	26	-88.93	n/a	n/a
TAMU-GM-V-81	Gulf of Mexico	Larvae	15/06/2009	26	-88.93	n/a	n/a
TAMU-GM-V-82	Gulf of Mexico	Larvae	15/06/2009	26	-88.93	n/a	n/a
TAMU-GM-V-83	Gulf of Mexico	Larvae	15/06/2008	26	-88.93	n/a	n/a
TAMU-GM-V-84	Gulf of Mexico	Larvae	15/06/2009	26	-88.93	n/a	n/a
TAMU-GM-V-85	Gulf of Mexico	Larvae	15/06/2009	27.5	-91.07	n/a	n/a
TAMU-GM-V-86	Gulf of Mexico	Larvae	15/06/2009	27.5	-91.07	n/a	n/a
TAMU-GM-V-87	Gulf of Mexico	Larvae	15/06/2009	26	-91.07	n/a	n/a
AZTI-GM-V-77	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	n/a	n/a
AZTI-GM-V-80	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	n/a	n/a
AZTI-GM-V-81	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	n/a	n/a
AZTI-GM-0-29	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	28	0.34
AZTI-GM-0-30	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	32	0.51
AZTI-GM-0-32	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	28	0.4
AZTI-GM-0-33	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	31	0.5
AZTI-GM-0-41	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	35	0.76
AZTI-GM-0-42	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	28	NA
AZTI-GM-0-43	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	28	0.33
AZTI-GM-0-5	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	28	0.3
AZTI-GM-0-20	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	36	0.84

AZTI-GM-0-24	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	31	0.47
AZTI-GM-0-25	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	26	0.24
AZTI-GM-0-45	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	29	0.41
AZTI-GM-0-6	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	37	0.92
IEO-BA-V-1	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-11	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-14	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-2	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-23	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-24	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-25	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-26	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-27	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-28	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-3	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-31	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-32	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-4	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-43	Western Mediterranean	Larvae	01/07/2013	38.82	2.96	n/a	n/a
IEO-BA-V-46	Western Mediterranean	Larvae	01/07/2013	38.82	2.96	n/a	n/a
IEO-BA-V-58	Western Mediterranean	Larvae	13/07/2013	38.75	4.26	n/a	n/a
IEO-BA-V-62	Western Mediterranean	Larvae	13/07/2013	38.75	4.26	n/a	n/a
IEO-BA-V-7	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-73	Western Mediterranean	Larvae	13/07/2013	38.75	4.26	n/a	n/a
IEO-BA-V-74	Western Mediterranean	Larvae	07/07/2013	38.82	0.68	n/a	n/a

IEO-BA-V-75	Western Mediterranean	Larvae	07/07/2013	38.82	0.68	n/a	n/a
IEO-BA-V-76	Western Mediterranean	Larvae	07/07/2013	38.82	0.68	n/a	n/a
IEO-BA-V-77	Western Mediterranean	Larvae	07/07/2013	38.82	0.68	n/a	n/a
IEO-BA-V-9	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-10	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-22	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-29	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-30	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-5	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
AZTI-BA-0-52	Western Mediterranean	Young of the year	07/10/2012	40.9	1.07	36	0.76
AZTI-BA-0-54	Western Mediterranean	Young of the year	07/10/2012	40.9	1.07	35.6	0.85
AZTI-BA-0-56	Western Mediterranean	Young of the year	07/10/2012	40.9	1.07	39.7	1.2
AZTI-BA-0-68	Western Mediterranean	Young of the year	07/10/2012	40.85	1.03	37.8	1.04
AZTI-BA-0-69	Western Mediterranean	Young of the year	07/10/2012	40.85	1.05	34.6	0.78
AZTI-BA-0-70	Western Mediterranean	Young of the year	07/10/2012	40.83	1.05	38	1.11
AZTI-BA-0-71	Western Mediterranean	Young of the year	07/10/2012	40.83	1.05	37	1.05
AZTI-BA-0-72	Western Mediterranean	Young of the year	07/10/2012	40.85	1.03	37.5	1.02
IEO-BA-0-101	Western Mediterranean	Young of the year	21/09/2013	39.28	-0.04	25.5	0.32
IEO-BA-0-102	Western Mediterranean	Young of the year	21/09/2013	39.28	-0.04	28.5	0.49
IEO-BA-0-103	Western Mediterranean	Young of the year	22/09/2013	39.28	-0.04	27.6	0.4
IEO-BA-0-104	Western Mediterranean	Young of the year	22/09/2013	39.28	-0.04	29.6	0.48
IEO-BA-0-106	Western Mediterranean	Young of the year	12/10/2013	39.28	-0.04	32.8	0.71
IEO-BA-0-109	Western Mediterranean	Young of the year	13/10/2013	39.28	-0.04	32.7	0.76
IEO-BA-0-110	Western Mediterranean	Young of the year	17/10/2013	39.28	-0.04	29.3	0.42
IEO-BA-0-120	Western Mediterranean	Young of the year	28/10/2013	39.28	-0.04	30.2	0.53

IEO-BA-0-142	Western Mediterranean	Young of the year	15/09/2013	39.28	-0.04	27.5	0.41
IEO-BA-0-143	Western Mediterranean	Young of the year	15/09/2013	39.28	-0.04	28.7	0.48
IEO-BA-0-59	Western Mediterranean	Young of the year	05/05/2012	39.71	3.86	48	2.58
IEO-BA-0-60	Western Mediterranean	Young of the year	15/09/2012	39.28	-0.04	26	0.31
IEO-BA-0-61	Western Mediterranean	Young of the year	15/09/2012	39.28	-0.04	26.4	0.32
IEO-BA-0-63	Western Mediterranean	Young of the year	15/09/2012	39.28	-0.04	26	0.32
IEO-BA-0-64	Western Mediterranean	Young of the year	15/09/2012	39.28	-0.04	27.1	0.33
IEO-BA-0-65	Western Mediterranean	Young of the year	15/09/2012	39.28	-0.04	27.2	0.38
IEO-BA-0-66	Western Mediterranean	Young of the year	16/09/2012	39.28	-0.04	28.1	0.42
IEO-BA-0-67	Western Mediterranean	Young of the year	16/09/2012	39.28	-0.04	25.7	0.29
IEO-BA-0-69	Western Mediterranean	Young of the year	16/09/2012	39.28	-0.04	28.5	0.44
IEO-BA-0-71	Western Mediterranean	Young of the year	16/09/2012	39.28	-0.04	23.8	0.22
IEO-BA-0-75	Western Mediterranean	Young of the year	16/09/2012	39.28	-0.04	36.1	1
IEO-BA-0-76	Western Mediterranean	Young of the year	16/09/2012	39.28	-0.04	35.2	0.94
IEO-BA-0-77	Western Mediterranean	Young of the year	16/09/2012	39.28	-0.04	25.1	0.28
IEO-BA-0-79	Western Mediterranean	Young of the year	16/09/2012	39.28	-0.04	27.5	0.37
IEO-BA-0-91	Western Mediterranean	Young of the year	15/09/2013	39.28	-0.04	28	0.44
IEO-BA-0-99	Western Mediterranean	Young of the year	21/09/2013	39.28	-0.04	29.4	0.46
IEO-BA-0-100	Western Mediterranean	Young of the year	21/09/2013	39.28	-0.04	27.6	0.41
IEO-BA-0-107	Western Mediterranean	Young of the year	12/10/2013	39.28	-0.04	31.7	0.6
IEO-BA-0-92	Western Mediterranean	Young of the year	15/09/2013	39.28	-0.04	30	0.54
IEO-BA-0-93	Western Mediterranean	Young of the year	15/09/2013	39.28	-0.04	28.9	0.49
IEO-SI-V-42	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-47	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-54	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a

IEO-SI-V-61	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-71	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-70	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-76	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-78	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
FMAP-MA-0-10	Central Mediterranean	Young of the year	23/09/2013	35.5	14	26.4	0.34
FMAP-MA-0-11	Central Mediterranean	Young of the year	23/09/2013	35.5	14	26.6	0.33
FMAP-MA-0-13	Central Mediterranean	Young of the year	23/09/2013	35.5	14	27.2	0.35
FMAP-MA-0-15	Central Mediterranean	Young of the year	23/09/2013	35.5	14	23.3	0.21
FMAP-MA-0-17	Central Mediterranean	Young of the year	23/09/2013	35.5	14	23.9	0.22
FMAP-MA-0-23	Central Mediterranean	Young of the year	23/09/2013	35.5	14	21.6	0.18
FMAP-MA-0-29	Central Mediterranean	Young of the year	23/09/2013	35.5	14	22.5	0.2
FMAP-MA-0-31	Central Mediterranean	Young of the year	23/09/2013	35.5	14	26.5	0.35
FMAP-MA-0-33	Central Mediterranean	Young of the year	23/09/2013	35.5	14	22.8	0.19
FMAP-MA-0-34	Central Mediterranean	Young of the year	23/09/2013	35.5	14	20.9	0.14
FMAP-MA-0-35	Central Mediterranean	Young of the year	23/09/2013	35.5	14	23.5	0.22
FMAP-MA-0-36	Central Mediterranean	Young of the year	23/09/2013	35.5	14	25.8	0.32
FMAP-MA-0-37	Central Mediterranean	Young of the year	23/09/2013	35.5	14	26.1	0.32
FMAP-MA-0-38	Central Mediterranean	Young of the year	23/09/2013	35.5	14	26.7	0.38
FMAP-MA-0-8	Central Mediterranean	Young of the year	16/09/2013	35.5	14	22.1	0.2
FMAP-MA-0-9	Central Mediterranean	Young of the year	16/09/2013	35.5	14	23.1	0.24
UNIB-SI-0-1	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	29	0.46
UNIB-SI-0-10	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	30	0.5
UNIB-SI-0-11	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	30	0.47
UNIB-SI-0-12	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	28	0.37

UNIB-SI-0-13	Central Mediterranean	Young of the year	03/10/2012	37.85	15.33	31	0.34
UNIB-SI-0-15	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	40	1.48
UNIB-SI-0-26	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	39	1.27
UNIB-SI-0-27	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	38	1.24
UNIB-SI-0-29	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	37	1.14
UNIB-SI-0-3	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	34	0.65
UNIB-SI-0-30	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	36	1.16
UNIB-SI-0-31	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	38	1.25
UNIB-SI-0-33	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	36	1.14
UNIB-SI-0-35	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	37	1.16
UNIB-SI-0-36	Central Mediterranean	Young of the year	05/10/2012	37.63	15.22	38	1.25
UNIB-SI-0-4	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	31	0.49
UNIB-SI-0-5	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	31	0.52
UNIB-SI-0-6	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	32	0.59
UNIB-SI-0-8	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	28	0.36
UNIB-SI-0-9	Central Mediterranean	Young of the year	23/09/2012	37.7	15.27	31	0.5
FMAP-MA-0-1	Central Mediterranean	Young of the year	10/09/2013	35.5	14	25.2	0.3
FMAP-MA-0-3	Central Mediterranean	Young of the year	10/09/2013	35.5	14	19.4	0.12
FMAP-MA-0-4	Central Mediterranean	Young of the year	16/09/2013	35.5	14	23.1	0.22
FMAP-MA-0-5	Central Mediterranean	Young of the year	16/09/2013	35.5	14	21.8	0.2
CYPR-LS-V-1	Eastern Mediterranean	Larvae	22/06/2011	36.13	33.75	0.58	n/a
CYPR-LS-V-46	Eastern Mediterranean	Larvae	24/06/2011	36.08	33.69	1.2	n/a
CYPR-LS-V-49	Eastern Mediterranean	Larvae	24/06/2011	36.08	33.69	1.2	n/a
CYPR-LS-V-55	Eastern Mediterranean	Larvae	24/06/2011	36.08	33.69	1.25	n/a
CYPR-LS-V-62	Eastern Mediterranean	Larvae	24/06/2011	36.09	33.72	0.58	n/a

CYPR-LS-V-71	Eastern Mediterranean	Larvae	24/06/2011	36.09	33.74	1.18	n/a
CYPR-LS-V-19	Eastern Mediterranean	Larvae	23/06/2011	36.11	33.56	1.04	n/a
CYPR-LS-V-26	Eastern Mediterranean	Larvae	23/06/2011	36.11	33.57	0.95	n/a
CYPR-LS-V-45	Eastern Mediterranean	Larvae	24/06/2011	36.08	33.69	1.26	n/a
CYPR-LS-V-52	Eastern Mediterranean	Larvae	24/06/2011	36.08	33.69	1.03	n/a
CYPR-LS-0-110	Eastern Mediterranean	Young of the year	03/09/2012	35.34	33.32	28.7	0.44
CYPR-LS-0-111	Eastern Mediterranean	Young of the year	03/09/2012	35.34	33.32	30.4	0.54
CYPR-LS-0-112	Eastern Mediterranean	Young of the year	29/07/2012	35.34	33.32	23.8	0.28
CYPR-LS-0-113	Eastern Mediterranean	Young of the year	29/07/2012	35.34	33.32	26.1	0.38
CYPR-LS-0-114	Eastern Mediterranean	Young of the year	29/07/2012	35.34	33.32	23.1	0.24
CYPR-LS-0-321	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	24.3	0.27
CYPR-LS-0-322	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	24.8	0.27
CYPR-LS-0-323	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	24.4	0.29
CYPR-LS-0-325	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	24.6	0.28
CYPR-LS-0-327	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	23.9	0.25
CYPR-LS-0-334	Eastern Mediterranean	Young of the year	17/08/2013	36.17	33.85	23.4	0.24
CYPR-LS-0-336	Eastern Mediterranean	Young of the year	17/08/2013	36.17	33.85	24.5	0.28
CYPR-LS-0-337	Eastern Mediterranean	Young of the year	17/08/2013	36.17	33.85	24.7	0.29
CYPR-LS-0-369	Eastern Mediterranean	Young of the year	19/08/2013	36.17	33.85	22.9	0.23
CYPR-LS-0-37	Eastern Mediterranean	Young of the year	24/07/2012	36.14	33.87	22.1	0.2
CYPR-LS-0-371	Eastern Mediterranean	Young of the year	19/08/2013	36.17	33.85	22.9	0.22
CYPR-LS-0-372	Eastern Mediterranean	Young of the year	14/08/2013	36.17	33.85	22.7	0.2
CYPR-LS-0-373	Eastern Mediterranean	Young of the year	14/08/2013	36.17	33.85	21.4	0.18
CYPR-LS-0-374	Eastern Mediterranean	Young of the year	14/08/2013	36.17	33.85	20.4	0.17
CYPR-LS-0-375	Eastern Mediterranean	Young of the year	06/08/2013	36.17	33.85	22.8	0.21

CYPR-LS-0-376	Eastern Mediterranean	Young of the year	06/08/2013	36.17	33.85	21.5	0.17
CYPR-LS-0-377	Eastern Mediterranean	Young of the year	27/07/2013	36.17	33.85	18.2	0.1
CYPR-LS-0-379	Eastern Mediterranean	Young of the year	03/08/2013	36.17	33.85	20.4	0.16
CYPR-LS-0-39	Eastern Mediterranean	Young of the year	24/07/2012	36.14	33.87	24.9	0.3
CYPR-LS-0-393	Eastern Mediterranean	Young of the year	16/08/2013	35.34	33.32	26.7	0.4
CYPR-LS-0-394	Eastern Mediterranean	Young of the year	16/08/2013	35.34	33.32	28.5	0.39
CYPR-LS-0-395	Eastern Mediterranean	Young of the year	13/08/2013	35.34	33.32	26	0.37
CYPR-LS-0-396	Eastern Mediterranean	Young of the year	13/08/2013	35.34	33.32	27.1	0.39
CYPR-LS-0-397	Eastern Mediterranean	Young of the year	13/08/2013	35.34	33.32	26.2	0.36
CYPR-LS-0-398	Eastern Mediterranean	Young of the year	13/08/2013	35.34	33.32	27.1	0.4
CYPR-LS-0-43	Eastern Mediterranean	Young of the year	24/07/2012	36.14	33.87	24.5	0.29
CYPR-LS-0-52	Eastern Mediterranean	Young of the year	25/07/2012	36.14	33.87	21.7	0.19
CYPR-LS-0-56	Eastern Mediterranean	Young of the year	25/07/2012	36.14	33.87	24.5	0.3
CYPR-LS-0-60	Eastern Mediterranean	Young of the year	25/07/2012	36.14	33.87	23.2	0.24
CYPR-LS-0-68	Eastern Mediterranean	Young of the year	25/07/2012	36.14	33.87	24.2	0.29
CYPR-LS-0-315	Eastern Mediterranean	Young of the year	15/08/2013	36.17	33.85	21.6	0.19
CYPR-LS-0-317	Eastern Mediterranean	Young of the year	15/08/2013	36.17	33.85	21.1	0.18
CYPR-LS-0-318	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	23.3	0.25
CYPR-LS-0-320	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	22.4	0.21

WebTable 2

Samples genotyped with 230 selected SNPs on the Fluidigm platform. Those samples already used in the RAD-seq analysis are marked with an asterisk. Only those included in subsequent analyses are shown. Column descriptions as in WebTable 1.

Sample	Area	Dev. stage	Catch date	Latitude	Longitude	Length (cm)	Weight (g)
AZTI-GM-V-77*	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	n/a	n/a
AZTI-GM-V-80*	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	n/a	n/a
AZTI-GM-V-81*	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	n/a	n/a
AZTI-GM-V-101	Gulf of Mexico	Larvae	22/05/2008	26.5	-89.17	0.36	n/a
AZTI-GM-V-102	Gulf of Mexico	Larvae	22/05/2008	26.5	-89	0.44	n/a
AZTI-GM-V-103	Gulf of Mexico	Larvae	22/05/2008	26.5	-89	0.41	n/a
AZTI-GM-V-104	Gulf of Mexico	Larvae	22/05/2008	26.5	-89	0.41	n/a
AZTI-GM-V-105	Gulf of Mexico	Larvae	22/05/2008	26.5	-89	0.39	n/a
AZTI-GM-V-106	Gulf of Mexico	Larvae	22/05/2008	26.5	-89	0.48	n/a
AZTI-GM-V-107	Gulf of Mexico	Larvae	22/05/2008	26.5	-88.75	0.6	n/a
AZTI-GM-V-108	Gulf of Mexico	Larvae	28/05/2009	26.67	-88	0.39	n/a
AZTI-GM-V-109	Gulf of Mexico	Larvae	28/05/2009	26.67	-88	0.43	n/a
AZTI-GM-V-110	Gulf of Mexico	Larvae	28/05/2009	26.67	-88	0.38	n/a
AZTI-GM-V-111	Gulf of Mexico	Larvae	28/05/2009	26.67	-88	0.4	n/a
AZTI-GM-V-112	Gulf of Mexico	Larvae	28/05/2009	26.67	-88	0.41	n/a
AZTI-GM-V-113	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.04	0.4	n/a
AZTI-GM-V-114	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.04	0.41	n/a
AZTI-GM-V-115	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.04	0.43	n/a
AZTI-GM-V-117	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.08	0.44	n/a

AZTI-GM-V-118	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.08	0.38	n/a
AZTI-GM-V-119	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.08	0.44	n/a
AZTI-GM-V-120	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.08	0.46	n/a
AZTI-GM-V-121	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.13	0.41	n/a
AZTI-GM-V-122	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.13	0.45	n/a
AZTI-GM-V-123	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.13	0.41	n/a
AZTI-GM-V-124	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.13	0.43	n/a
AZTI-GM-V-125	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.13	0.43	n/a
AZTI-GM-V-126	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.38	0.39	n/a
AZTI-GM-V-127	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.38	0.42	n/a
AZTI-GM-V-128	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.38	0.54	n/a
AZTI-GM-V-79	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	0	n/a
AZTI-GM-V-82	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	0	n/a
AZTI-GM-V-84	Gulf of Mexico	Larvae	17/05/2010	26.76	-96.01	0	n/a
AZTI-GM-V-89	Gulf of Mexico	Larvae	20/05/2008	27.66	-87	0.37	n/a
AZTI-GM-V-90	Gulf of Mexico	Larvae	21/05/2008	26.5	-88.33	0.47	n/a
AZTI-GM-V-91	Gulf of Mexico	Larvae	21/05/2008	26.5	-88.33	0.5	n/a
AZTI-GM-V-92	Gulf of Mexico	Larvae	21/05/2008	26.5	-88.33	0.4	n/a
AZTI-GM-V-93	Gulf of Mexico	Larvae	21/05/2008	26.5	-88.33	0.73	n/a
AZTI-GM-V-94	Gulf of Mexico	Larvae	21/05/2008	26.5	-88.33	0.63	n/a
AZTI-GM-V-97	Gulf of Mexico	Larvae	22/05/2008	26.5	-89.17	0.4	n/a
AZTI-GM-V-98	Gulf of Mexico	Larvae	22/05/2008	26.5	-89.17	0.46	n/a
AZTI-GM-V-99	Gulf of Mexico	Larvae	22/05/2008	26.5	-89.17	0.38	n/a
AZTI-GM-0-20*	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	36	0.84
AZTI-GM-0-24*	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	31	0.47
AZTI-GM-0-25*	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	26	0.24
AZTI-GM-0-45*	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	29	0.41
AZTI-GM-0-6*	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	37	0.92

AZTI-GM-0-31	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	33	0.54
IEO-BA-V-10*	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-22*	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-29*	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-30*	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-5*	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-13	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-15	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-16	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-17	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-18	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-19	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-20	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-21	Western Mediterranean	Larvae	26/06/2012	38.67	1.21	n/a	n/a
IEO-BA-V-33	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-34	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-35	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-36	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-37	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-38	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-39	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-40	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a

IEO-BA-V-41	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-V-42	Western Mediterranean	Larvae	13/07/2012	38.83	2.63	n/a	n/a
IEO-BA-0-100*	Western Mediterranean	Young of the year	21/09/2013	39.28	-0.04	27.6	0.41
IEO-BA-0-107*	Western Mediterranean	Young of the year	12/10/2013	39.28	-0.04	31.7	0.6
IEO-BA-0-92*	Western Mediterranean	Young of the year	15/09/2013	39.28	-0.04	30	0.54
IEO-BA-0-93*	Western Mediterranean	Young of the year	15/09/2013	39.28	-0.04	28.9	0.49
AZTI-BA-0-220	Western Mediterranean	Young of the year	19/10/2013	40.94	1.03	32.5	0.67
AZTI-BA-0-249	Western Mediterranean	Young of the year	19/10/2013	40.94	1.03	30.5	0.59
AZTI-BA-0-257	Western Mediterranean	Young of the year	19/10/2013	40.94	1.03	33	0.75
AZTI-BA-0-259	Western Mediterranean	Young of the year	19/10/2013	40.94	1.03	31	0.57
IEO-BA-0-113	Western Mediterranean	Young of the year	25/10/2013	39.28	-0.04	46.1	0.51
IEO-BA-0-114	Western Mediterranean	Young of the year	25/10/2013	39.28	-0.04	30.2	0.31
IEO-BA-0-115	Western Mediterranean	Young of the year	25/10/2013	39.28	-0.04	32.5	0.68
IEO-BA-0-121	Western Mediterranean	Young of the year	01/11/2013	39.28	-0.04	31.4	0.65
IEO-BA-0-124	Western Mediterranean	Young of the year	02/11/2013	39.28	-0.04	31.8	0.65
IEO-BA-0-126	Western Mediterranean	Young of the year	02/11/2013	39.28	-0.04	34	0.78
IEO-BA-0-147	Western Mediterranean	Young of the year	21/09/2013	39.28	-0.04	30.9	0.53
IEO-BA-0-150	Western Mediterranean	Young of the year	22/09/2013	39.28	-0.04	25.3	0.3
IEO-BA-0-153	Western Mediterranean	Young of the year	12/10/2013	39.28	-0.04	31	0.58
IEO-BA-0-155	Western Mediterranean	Young of the year	13/10/2013	39.28	-0.04	31.5	0.61
IEO-BA-0-157	Western Mediterranean	Young of the year	19/10/2013	39.28	-0.04	30.2	0.54
IEO-BA-0-160	Western Mediterranean	Young of the year	25/10/2013	39.28	-0.04	32.8	0.79

IEO-BA-0-162	Western Mediterranean	Young of the year	26/10/2013	39.28	-0.04	34.4	0.76
IEO-BA-0-97	Western Mediterranean	Young of the year	21/09/2013	39.28	-0.04	28.8	0.47
IEO-BA-0-98	Western Mediterranean	Young of the year	21/09/2013	39.28	-0.04	28.9	0.45
IEO-SI-V-70*	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-76*	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-78*	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-22	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.05	n/a
IEO-SI-V-37	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-38	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-41	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-43	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-51	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-55	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-56	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.08	n/a
IEO-SI-V-57	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-62	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-63	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-64	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-67	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-69	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.08	n/a
IEO-SI-V-72	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-74	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a

IEO-SI-V-75	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.07	n/a
IEO-SI-V-77	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
IEO-SI-V-79	Central Mediterranean	Larvae	15/07/2008	36.71	15.29	0.06	n/a
FMAP-MA-0-1*	Central Mediterranean	Young of the year	10/09/2013	35.5	14	25.2	0.3
FMAP-MA-0-3*	Central Mediterranean	Young of the year	10/09/2013	35.5	14	19.4	0.12
FMAP-MA-0-4*	Central Mediterranean	Young of the year	16/09/2013	35.5	14	23.1	0.22
FMAP-MA-0-5*	Central Mediterranean	Young of the year	16/09/2013	35.5	14	21.8	0.2
UNIB-SI-0-51	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	41	1.29
UNIB-SI-0-52	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	39.5	1.12
UNIB-SI-0-53	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	32	0.57
UNIB-SI-0-54	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	41.5	1.37
UNIB-SI-0-55	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	37	1.09
UNIB-SI-0-56	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	30.5	0.51
UNIB-SI-0-57	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	38.2	1.07
UNIB-SI-0-61	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	42.3	1.41
UNIB-SI-0-62	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	41	1.3
UNIB-SI-0-63	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	39	1.08
UNIB-SI-0-64	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	42.5	1.51
UNIB-SI-0-65	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	41.3	1.31
UNIB-SI-0-66	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	40.5	1.26
UNIB-SI-0-67	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	41.2	1.39
UNIB-SI-0-68	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	40.3	1.27

UNIB-SI-0-69	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	39	0.99
UNIB-SI-0-70	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	38	1.01
UNIB-SI-0-71	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	40.7	1.31
UNIB-SI-0-72	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	34.5	0.56
UNIB-SI-0-73	Central Mediterranean	Young of the year	18/10/2013	37.58	15.67	33.5	0.77
CYPR-LS-V-19*	Eastern Mediterranean	Larvae	23/06/2011	36.11	33.56	1.04	n/a
CYPR-LS-V-26*	Eastern Mediterranean	Larvae	23/06/2011	36.11	33.57	0.95	n/a
CYPR-LS-V-45*	Eastern Mediterranean	Larvae	24/06/2011	36.08	33.69	1.26	n/a
CYPR-LS-V-52*	Eastern Mediterranean	Larvae	24/06/2011	36.08	33.69	1.03	n/a
CYPR-LS-0-315*	Eastern Mediterranean	Young of the year	15/08/2013	36.17	33.85	21.6	0.19
CYPR-LS-0-317*	Eastern Mediterranean	Young of the year	15/08/2013	36.17	33.85	21.1	0.18
CYPR-LS-0-318*	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	23.3	0.25
CYPR-LS-0-320*	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	22.4	0.21
CYPR-LS-0-1	Eastern Mediterranean	Young of the year	10/08/2011	36.25	35.8	35	0.75
CYPR-LS-0-10	Eastern Mediterranean	Young of the year	14/08/2011	36.25	35.8	31.6	0.56
CYPR-LS-0-11	Eastern Mediterranean	Young of the year	15/08/2011	36.25	35.8	34.3	0.78
CYPR-LS-0-116	Eastern Mediterranean	Young of the year	29/07/2012	35.34	33.32	25.7	0.34
CYPR-LS-0-117	Eastern Mediterranean	Young of the year	29/07/2012	35.34	33.32	24.7	0.29
CYPR-LS-0-118	Eastern Mediterranean	Young of the year	29/07/2012	35.34	33.32	22.3	0.23
CYPR-LS-0-12	Eastern Mediterranean	Young of the year	16/08/2011	36.25	35.8	26	0.3
CYPR-LS-0-126	Eastern Mediterranean	Young of the year	31/08/2012	35.34	33.32	29.9	0.58
CYPR-LS-0-128	Eastern Mediterranean	Young of the year	31/08/2012	35.34	33.32	25.5	0.31

CYPR-LS-0-129	Eastern Mediterranean	Young of the year	31/08/2012	35.34	33.32	28.3	0.45
CYPR-LS-0-13	Eastern Mediterranean	Young of the year	16/08/2011	36.25	35.8	32.5	0.66
CYPR-LS-0-14	Eastern Mediterranean	Young of the year	16/08/2011	36.25	35.8	32	0.61
CYPR-LS-0-15	Eastern Mediterranean	Young of the year	16/08/2011	36.25	35.8	29.5	0.43
CYPR-LS-0-16	Eastern Mediterranean	Young of the year	17/08/2011	36.25	35.8	35.3	0.81
CYPR-LS-0-17	Eastern Mediterranean	Young of the year	17/08/2011	36.25	35.8	34.3	0.74
CYPR-LS-0-18	Eastern Mediterranean	Young of the year	18/08/2011	36.03	35.95	26.6	0.38
CYPR-LS-0-19	Eastern Mediterranean	Young of the year	18/08/2011	36.03	35.95	33.5	0.62
CYPR-LS-0-2	Eastern Mediterranean	Young of the year	10/08/2011	36.25	35.8	31.5	0.54
CYPR-LS-0-20	Eastern Mediterranean	Young of the year	19/08/2011	36.03	35.95	29.3	0.44
CYPR-LS-0-3	Eastern Mediterranean	Young of the year	10/08/2011	36.25	35.8	30.3	0.52
CYPR-LS-0-314	Eastern Mediterranean	Young of the year	15/08/2013	36.17	33.85	22.2	0.21
CYPR-LS-0-316	Eastern Mediterranean	Young of the year	15/08/2013	36.17	33.85	21.4	0.18
CYPR-LS-0-324	Eastern Mediterranean	Young of the year	16/08/2013	36.17	33.85	24.9	0.28
CYPR-LS-0-33	Eastern Mediterranean	Young of the year	24/07/2012	36.14	33.87	23.6	0.27
CYPR-LS-0-366	Eastern Mediterranean	Young of the year	19/08/2013	36.17	33.85	24.3	0.27
CYPR-LS-0-378	Eastern Mediterranean	Young of the year	27/07/2013	36.17	33.85	12.2	0.03
CYPR-LS-0-382	Eastern Mediterranean	Young of the year	05/08/2013	36.17	33.85	20.9	0.17
CYPR-LS-0-4	Eastern Mediterranean	Young of the year	10/08/2011	36.25	35.8	31.8	0.55
CYPR-LS-0-48	Eastern Mediterranean	Young of the year	25/07/2012	36.14	33.87	23.4	0.26
CYPR-LS-0-5	Eastern Mediterranean	Young of the year	10/08/2011	36.25	35.8	33.2	0.79
CYPR-LS-0-6	Eastern Mediterranean	Young of the year	10/08/2011	36.25	35.8	30.3	0.5

CYPR-LS-0-64	Eastern Mediterranean	Young of the year	25/07/2012	36.14	33.87	22.8	0.23
CYPR-LS-0-7	Eastern Mediterranean	Young of the year	10/08/2011	36.25	35.8	30.3	0.53
CYPR-LS-0-8	Eastern Mediterranean	Young of the year	12/08/2011	36.25	35.8	34.7	0.79
CYPR-LS-0-9	Eastern Mediterranean	Young of the year	14/08/2011	36.25	35.8	29	0.42

WebTable 3

Spawning adult and larvae samples genotyped with the final selection of 96 SNPs on the Fluidigm platform for validation. Only those included in subsequent analyses are shown. Column descriptions as in WebTable 1.

Sample	Area	Dev. stage	Catch date	Latitude	Longitude	Length (cm)	Weight (g)
NOAA-GM-L-100	Gulf of Mexico	Adult	15/04/2010	25	-85	261	n/a
NOAA-GM-L-101	Gulf of Mexico	Adult	15/04/2010	25	-90	255	n/a
NOAA-GM-L-103	Gulf of Mexico	Adult	15/04/2010	25	-85	234	n/a
NOAA-GM-L-104	Gulf of Mexico	Adult	15/04/2010	25	-85	242	n/a
NOAA-GM-L-105	Gulf of Mexico	Adult	15/04/2010	25	-90	223	n/a
NOAA-GM-L-111	Gulf of Mexico	Adult	15/04/2010	25	-85	243	n/a
NOAA-GM-L-114	Gulf of Mexico	Adult	15/04/2010	25	-90	230	n/a
NOAA-GM-L-115	Gulf of Mexico	Adult	15/04/2010	25	-85	251	n/a
NOAA-GM-L-117	Gulf of Mexico	Adult	15/04/2010	25	-90	248	n/a
NOAA-GM-L-118	Gulf of Mexico	Adult	15/04/2010	25	-85	249	n/a
NOAA-GM-L-119	Gulf of Mexico	Adult	15/04/2010	25	-85	247	n/a
NOAA-GM-L-120	Gulf of Mexico	Adult	15/04/2010	25	-85	272	n/a
NOAA-GM-L-79	Gulf of Mexico	Adult	15/04/2010	25	-85	276	n/a
NOAA-GM-L-80	Gulf of Mexico	Adult	15/04/2010	25	-90	261	n/a
NOAA-GM-L-82	Gulf of Mexico	Adult	15/04/2010	25	-90	278	n/a
NOAA-GM-L-83	Gulf of Mexico	Adult	15/04/2010	25	-85	249	n/a
NOAA-GM-L-85	Gulf of Mexico	Adult	15/04/2010	25	-85	280	n/a
NOAA-GM-L-87	Gulf of Mexico	Adult	15/04/2010	25	-90	238	n/a
NOAA-GM-L-89	Gulf of Mexico	Adult	15/04/2010	25	-85	262	n/a
NOAA-GM-L-92	Gulf of Mexico	Adult	15/04/2010	25	-85	257	n/a
NOAA-GM-L-93	Gulf of Mexico	Adult	15/04/2010	25	-90	252	n/a
NOAA-GM-L-95	Gulf of Mexico	Adult	15/04/2010	25	-85	249	n/a
NOAA-GM-L-96	Gulf of Mexico	Adult	15/04/2010	25	-90	238	n/a
NOAA-GM-L-97	Gulf of Mexico	Adult	15/04/2010	25	-90	239	n/a

NOAA-GM-L-99	Gulf of Mexico	Adult	15/04/2010	25	-85	213	n/a
NOAA-GM-L-69	Gulf of Mexico	Adult	15/04/2011	20	-80	270	n/a
NOAA-GM-L-70	Gulf of Mexico	Adult	15/04/2011	20	-80	251	n/a
NOAA-GM-L-71	Gulf of Mexico	Adult	15/04/2011	20	-80	232	n/a
NOAA-GM-L-72	Gulf of Mexico	Adult	15/04/2011	25	-85	236	n/a
NOAA-GM-L-36	Gulf of Mexico	Adult	15/04/2012	25	-85	239	n/a
NOAA-GM-L-37	Gulf of Mexico	Adult	15/04/2012	25	-85	283	n/a
NOAA-GM-L-38	Gulf of Mexico	Adult	15/04/2012	25	-85	241	n/a
NOAA-GM-L-39	Gulf of Mexico	Adult	15/04/2012	25	-85	221	n/a
NOAA-GM-L-40	Gulf of Mexico	Adult	15/04/2012	25	-85	257	n/a
NOAA-GM-L-41	Gulf of Mexico	Adult	15/04/2012	25	-85	255	n/a
NOAA-GM-L-42	Gulf of Mexico	Adult	15/04/2012	25	-85	273	n/a
NOAA-GM-L-43	Gulf of Mexico	Adult	15/04/2012	25	-85	234	n/a
NOAA-GM-L-44	Gulf of Mexico	Adult	15/04/2012	25	-85	241	n/a
NOAA-GM-L-45	Gulf of Mexico	Adult	15/04/2012	25	-85	234	n/a
NOAA-GM-L-46	Gulf of Mexico	Adult	15/04/2012	25	-85	268	n/a
NOAA-GM-L-59	Gulf of Mexico	Adult	15/04/2012	25	-85	259	n/a
NOAA-GM-L-12	Gulf of Mexico	Adult	15/04/2013	25	-85	250	n/a
NOAA-GM-L-13	Gulf of Mexico	Adult	15/04/2013	25	-85	231	n/a
NOAA-GM-L-14	Gulf of Mexico	Adult	15/04/2013	25	-85	231	n/a
NOAA-GM-L-25	Gulf of Mexico	Adult	15/04/2013	25	-85	266	n/a
NOAA-GM-L-26	Gulf of Mexico	Adult	15/04/2013	25	-85	275	n/a
NOAA-GM-L-6	Gulf of Mexico	Adult	15/04/2013	25	-85	235	n/a
NOAA-GM-L-7	Gulf of Mexico	Adult	15/04/2013	25	-90	233	n/a
NOAA-GM-L-126	Gulf of Mexico	Adult	15/04/2014	25	-85	249	n/a
NOAA-GM-L-127	Gulf of Mexico	Adult	15/04/2014	25	-90	269	n/a
NOAA-GM-L-128	Gulf of Mexico	Adult	15/04/2014	25	-85	227	n/a
NOAA-GM-L-129	Gulf of Mexico	Adult	15/04/2014	25	-85	219	n/a
NOAA-GM-L-134	Gulf of Mexico	Adult	15/04/2014	25	-90	234	n/a
NOAA-GM-L-135	Gulf of Mexico	Adult	15/04/2014	25	-90	221	n/a
NOAA-GM-L-136	Gulf of Mexico	Adult	15/04/2014	25	-85	266	n/a
NOAA-GM-L-137	Gulf of Mexico	Adult	15/04/2014	25	-85	225	n/a
NOAA-GM-L-146	Gulf of Mexico	Adult	15/04/2014	25	-90	235	n/a
NOAA-GM-L-148	Gulf of Mexico	Adult	15/04/2014	25	-90	225	n/a

NOAA-GM-L-149	Gulf of Mexico	Adult	15/04/2014	25	-90	228	n/a
NOAA-GM-L-173	Gulf of Mexico	Adult	15/04/2014	20	-80	218	n/a
NOAA-GM-L-174	Gulf of Mexico	Adult	15/04/2014	20	-80	218	n/a
NOAA-GM-L-176	Gulf of Mexico	Adult	15/04/2014	25	-85	205	n/a
NOAA-GM-L-177	Gulf of Mexico	Adult	15/04/2014	25	-85	246	n/a
NOAA-GM-L-123	Gulf of Mexico	Adult	15/05/2010	25	-85	212	n/a
NOAA-GM-L-124	Gulf of Mexico	Adult	15/05/2010	25	-85	222	n/a
NOAA-GM-L-125	Gulf of Mexico	Adult	15/05/2010	25	-85	219	n/a
NOAA-GM-L-81	Gulf of Mexico	Adult	15/05/2010	25	-90	262	n/a
NOAA-GM-L-84	Gulf of Mexico	Adult	15/05/2010	25	-90	239	n/a
NOAA-GM-L-86	Gulf of Mexico	Adult	15/05/2010	25	-90	261	n/a
NOAA-GM-L-88	Gulf of Mexico	Adult	15/05/2010	25	-85	238	n/a
NOAA-GM-L-90	Gulf of Mexico	Adult	15/05/2010	25	-85	220	n/a
NOAA-GM-L-91	Gulf of Mexico	Adult	15/05/2010	25	-85	246	n/a
NOAA-GM-L-94	Gulf of Mexico	Adult	15/05/2010	25	-85	230	n/a
NOAA-GM-L-64	Gulf of Mexico	Adult	15/05/2011	25	-85	245	n/a
NOAA-GM-L-65	Gulf of Mexico	Adult	15/05/2011	25	-85	262	n/a
NOAA-GM-L-66	Gulf of Mexico	Adult	15/05/2011	25	-85	252	n/a
NOAA-GM-L-67	Gulf of Mexico	Adult	15/05/2011	25	-80	232	n/a
NOAA-GM-L-68	Gulf of Mexico	Adult	15/05/2011	25	-85	258	n/a
NOAA-GM-L-47	Gulf of Mexico	Adult	15/05/2012	25	-85	253	n/a
NOAA-GM-L-48	Gulf of Mexico	Adult	15/05/2012	25	-85	230	n/a
NOAA-GM-L-49	Gulf of Mexico	Adult	15/05/2012	25	-85	234	n/a
NOAA-GM-L-50	Gulf of Mexico	Adult	15/05/2012	25	-85	243	n/a
NOAA-GM-L-51	Gulf of Mexico	Adult	15/05/2012	25	-85	233	n/a
NOAA-GM-L-52	Gulf of Mexico	Adult	15/05/2012	25	-85	243	n/a
NOAA-GM-L-53	Gulf of Mexico	Adult	15/05/2012	25	-85	251	n/a
NOAA-GM-L-54	Gulf of Mexico	Adult	15/05/2012	25	-85	263	n/a
NOAA-GM-L-55	Gulf of Mexico	Adult	15/05/2012	25	-85	245	n/a
NOAA-GM-L-56	Gulf of Mexico	Adult	15/05/2012	25	-85	271	n/a
NOAA-GM-L-58	Gulf of Mexico	Adult	15/05/2012	25	-85	225	n/a
NOAA-GM-L-60	Gulf of Mexico	Adult	15/05/2012	25	-85	248	n/a
NOAA-GM-L-61	Gulf of Mexico	Adult	15/05/2012	25	-90	242	n/a
NOAA-GM-L-62	Gulf of Mexico	Adult	15/05/2012	25	-85	235	n/a
NOAA-GM-L-63	Gulf of Mexico	Adult	15/05/2012	25	-85	204	n/a
NOAA-GM-L-10	Gulf of Mexico	Adult	15/05/2013	25	-85	235	n/a

NOAA-GM-L-15	Gulf of Mexico	Adult	15/05/2013	25	-85	194	n/a
NOAA-GM-L-16	Gulf of Mexico	Adult	15/05/2013	25	-85	240	n/a
NOAA-GM-L-161	Gulf of Mexico	Adult	15/05/2013	25	-85	224	n/a
NOAA-GM-L-162	Gulf of Mexico	Adult	15/05/2013	25	-85	260	n/a
NOAA-GM-L-163	Gulf of Mexico	Adult	15/05/2013	25	-85	281	n/a
NOAA-GM-L-169	Gulf of Mexico	Adult	15/05/2013	25	-90	225	n/a
NOAA-GM-L-17	Gulf of Mexico	Adult	15/05/2013	25	-85	231	n/a
NOAA-GM-L-171	Gulf of Mexico	Adult	15/05/2013	25	-90	251	n/a
NOAA-GM-L-172	Gulf of Mexico	Adult	15/05/2013	25	-90	259	n/a
NOAA-GM-L-18	Gulf of Mexico	Adult	15/05/2013	25	-85	228	n/a
NOAA-GM-L-19	Gulf of Mexico	Adult	15/05/2013	25	-80	254	n/a
NOAA-GM-L-2	Gulf of Mexico	Adult	15/05/2013	25	-90	204	n/a
NOAA-GM-L-21	Gulf of Mexico	Adult	15/05/2013	25	-85	226	n/a
NOAA-GM-L-22	Gulf of Mexico	Adult	15/05/2013	25	-85	244	n/a
NOAA-GM-L-24	Gulf of Mexico	Adult	15/05/2013	25	-90	243	n/a
NOAA-GM-L-3	Gulf of Mexico	Adult	15/05/2013	25	-90	230	n/a
NOAA-GM-L-30	Gulf of Mexico	Adult	15/05/2013	25	-90	226	n/a
NOAA-GM-L-31	Gulf of Mexico	Adult	15/05/2013	25	-90	224	n/a
NOAA-GM-L-4	Gulf of Mexico	Adult	15/05/2013	25	-90	245	n/a
NOAA-GM-L-8	Gulf of Mexico	Adult	15/05/2013	25	-90	245	n/a
NOAA-GM-L-9	Gulf of Mexico	Adult	15/05/2013	25	-90	255	n/a
NOAA-GM-L-138	Gulf of Mexico	Adult	15/05/2014	25	-90	225	n/a
NOAA-GM-L-139	Gulf of Mexico	Adult	15/05/2014	25	-90	253	n/a
NOAA-GM-L-142	Gulf of Mexico	Adult	15/05/2014	25	-85	238	n/a
NOAA-GM-L-143	Gulf of Mexico	Adult	15/05/2014	25	-90	211	n/a
NOAA-GM-L-144	Gulf of Mexico	Adult	15/05/2014	25	-90	223	n/a
NOAA-GM-L-145	Gulf of Mexico	Adult	15/05/2014	25	-90	210	n/a
NOAA-GM-L-150	Gulf of Mexico	Adult	15/05/2014	25	-85	220	n/a
NOAA-GM-L-151	Gulf of Mexico	Adult	15/05/2014	25	-85	220	n/a

NOAA-GM-L-152	Gulf of Mexico	Adult	15/05/2014	25	-85	252	n/a
NOAA-GM-L-153	Gulf of Mexico	Adult	15/05/2014	25	-85	210	n/a
NOAA-GM-L-154	Gulf of Mexico	Adult	15/05/2014	25	-90	213	n/a
NOAA-GM-L-155	Gulf of Mexico	Adult	15/05/2014	25	-90	223	n/a
NOAA-GM-L-156	Gulf of Mexico	Adult	15/05/2014	25	-90	233	n/a
NOAA-GM-L-157	Gulf of Mexico	Adult	15/05/2014	25	-90	240	n/a
NOAA-GM-L-158	Gulf of Mexico	Adult	15/05/2014	25	-90	227	n/a
NOAA-GM-L-178	Gulf of Mexico	Adult	15/05/2014	25	-85	259	n/a
NOAA-GM-L-179	Gulf of Mexico	Adult	15/05/2014	25	-90	268	n/a
NOAA-GM-L-180	Gulf of Mexico	Adult	15/05/2014	25	-90	228	n/a
NOAA-GM-L-57	Gulf of Mexico	Adult	15/06/2012	25	-85	243	n/a
NOAA-GM-L-159	Gulf of Mexico	Adult	15/06/2013	25	-85	213	n/a
NOAA-GM-L-160	Gulf of Mexico	Adult	15/06/2013	25	-85	204	n/a
NOAA-GM-L-23	Gulf of Mexico	Adult	15/06/2013	25	-85	250	n/a
NOAA-GM-L-5	Gulf of Mexico	Adult	15/06/2013	25	-85	235	n/a
NOAA-GM-L-130	Gulf of Mexico	Adult	15/06/2014	25	-90	217	n/a
NOAA-GM-L-131	Gulf of Mexico	Adult	15/06/2014	25	-90	235	n/a
NOAA-GM-L-132	Gulf of Mexico	Adult	15/06/2014	25	-85	250	n/a
NOAA-GM-L-133	Gulf of Mexico	Adult	15/06/2014	25	-85	276	n/a
NOAA-GM-L-141	Gulf of Mexico	Adult	15/06/2014	25	-85	199	n/a
NOAA-GM-L-175	Gulf of Mexico	Adult	15/06/2014	25	-85	225	n/a
NOAA-GM-L-181	Gulf of Mexico	Adult	15/06/2014	25	-85	213	n/a
AZTI-GM-V-87	Gulf of Mexico	Larvae	20/05/2008	27.66	-87	0.32	n/a
AZTI-GM-V-129	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.38	0.44	n/a
AZTI-GM-V-130	Gulf of Mexico	Larvae	28/05/2009	26.67	-88.38	0.39	n/a

AZTI-GM-V-131	Gulf of Mexico	Larvae	30/05/2009	27.66	-86.3	0.48	n/a
UNIC-SA-L-4	Western Mediterranean	Adult	21/05/2011	39.18	8.3	183	n/a
UNIC-SA-L-6	Western Mediterranean	Adult	21/05/2011	39.18	8.3	193	n/a
UNIC-SA-L-140	Western Mediterranean	Adult	31/05/2015	39.18	8.3	184	n/a
UNIC-SA-L-10	Western Mediterranean	Adult	04/06/2011	39.18	8.3	252	n/a
UNIC-SA-L-12	Western Mediterranean	Adult	04/06/2011	39.18	8.3	230	n/a
UNIC-SA-L-13	Western Mediterranean	Adult	04/06/2011	39.18	8.3	180	n/a
UNIC-SA-L-16	Western Mediterranean	Adult	04/06/2011	39.18	8.3	208	n/a
UNIC-SA-L-21	Western Mediterranean	Adult	04/06/2011	39.18	8.3	256	n/a
UNIC-SA-L-23	Western Mediterranean	Adult	04/06/2011	39.18	8.3	240	n/a
UNIC-SA-L-24	Western Mediterranean	Adult	04/06/2011	39.18	8.3	201	n/a
UNIC-SA-L-27	Western Mediterranean	Adult	04/06/2011	39.18	8.3	190	n/a
UNIC-SA-L-8	Western Mediterranean	Adult	04/06/2011	39.18	8.3	226	n/a
UNIC-SA-L-30	Western Mediterranean	Adult	17/06/2011	39.23	8.37	260	n/a
UNIC-SA-L-31	Western Mediterranean	Adult	17/06/2011	39.23	8.37	243	n/a
UNIC-SA-L-32	Western Mediterranean	Adult	17/06/2011	39.23	8.37	180	n/a
UNIC-SA-L-34	Western Mediterranean	Adult	17/06/2011	39.23	8.37	220	n/a
UNIC-SA-L-35	Western Mediterranean	Adult	17/06/2011	39.23	8.37	226	n/a
UNIC-SA-L-36	Western Mediterranean	Adult	17/06/2011	39.23	8.37	200	n/a
UNIC-SA-L-37	Western Mediterranean	Adult	17/06/2011	39.23	8.37	252	n/a
UNIC-SA-L-38	Western Mediterranean	Adult	17/06/2011	39.23	8.37	192	n/a
UNIC-SA-L-44	Western Mediterranean	Adult	17/06/2011	39.23	8.37	213	n/a

UNIC-SA-L-48	Western Mediterranean	Adult	17/06/2011	39.23	8.37	240	n/a
UNIC-SA-L-50	Western Mediterranean	Adult	17/06/2011	39.23	8.37	190	n/a
UNIC-SA-L-51	Western Mediterranean	Adult	17/06/2011	39.23	8.37	184	n/a
UNIC-SA-L-52	Western Mediterranean	Adult	17/06/2011	39.23	8.37	229	n/a
UNIC-SA-L-53	Western Mediterranean	Adult	17/06/2011	39.23	8.37	197	n/a
UNIC-SA-L-54	Western Mediterranean	Adult	17/06/2011	39.23	8.37	189	n/a
UNIC-SA-L-55	Western Mediterranean	Adult	17/06/2011	39.23	8.37	215	n/a
UNIC-SA-L-56	Western Mediterranean	Adult	17/06/2011	39.23	8.37	204	n/a
UNIC-SA-L-57	Western Mediterranean	Adult	17/06/2011	39.23	8.37	215	n/a
UNIC-SA-L-58	Western Mediterranean	Adult	17/06/2011	39.23	8.37	196	n/a
UNIC-SA-L-59	Western Mediterranean	Adult	17/06/2011	39.23	8.37	240	n/a
UNIC-SA-L-60	Western Mediterranean	Adult	17/06/2011	39.23	8.37	218	n/a
UNIC-SA-L-67	Western Mediterranean	Adult	13/06/2012	39.18	8.3	252	n/a
UNIC-SA-L-101	Western Mediterranean	Adult	21/06/2012	39.18	8.3	213	n/a
UNIC-SA-L-69	Western Mediterranean	Adult	21/06/2012	39.18	8.3	207	137.8
UNIC-SA-L-70	Western Mediterranean	Adult	21/06/2012	39.18	8.3	210	n/a
UNIC-SA-L-71	Western Mediterranean	Adult	21/06/2012	39.18	8.3	219	n/a
UNIC-SA-L-72	Western Mediterranean	Adult	21/06/2012	39.18	8.3	207	n/a
UNIC-SA-L-73	Western Mediterranean	Adult	21/06/2012	39.18	8.3	226	n/a
UNIC-SA-L-76	Western Mediterranean	Adult	21/06/2012	39.18	8.3	211	n/a
UNIC-SA-L-77	Western Mediterranean	Adult	21/06/2012	39.18	8.3	200	n/a
UNIC-SA-L-79	Western Mediterranean	Adult	21/06/2012	39.18	8.3	206	n/a

UNIC-SA-L-80	Western Mediterranean	Adult	21/06/2012	39.18	8.3	206	n/a
UNIC-SA-L-81	Western Mediterranean	Adult	21/06/2012	39.18	8.3	241	n/a
UNIC-SA-L-82	Western Mediterranean	Adult	21/06/2012	39.18	8.3	238	n/a
UNIC-SA-L-83	Western Mediterranean	Adult	21/06/2012	39.18	8.3	207	n/a
UNIC-SA-L-84	Western Mediterranean	Adult	21/06/2012	39.18	8.3	210	n/a
UNIC-SA-L-85	Western Mediterranean	Adult	21/06/2012	39.18	8.3	204	n/a
UNIC-SA-L-86	Western Mediterranean	Adult	21/06/2012	39.18	8.3	220	n/a
UNIC-SA-L-87	Western Mediterranean	Adult	21/06/2012	39.18	8.3	206	n/a
UNIC-SA-L-88	Western Mediterranean	Adult	21/06/2012	39.18	8.3	207	n/a
UNIC-SA-L-89	Western Mediterranean	Adult	21/06/2012	39.18	8.3	204	n/a
UNIC-SA-L-91	Western Mediterranean	Adult	21/06/2012	39.18	8.3	213	n/a
UNIC-SA-L-92	Western Mediterranean	Adult	21/06/2012	39.18	8.3	226	n/a
UNIC-SA-L-93	Western Mediterranean	Adult	21/06/2012	39.18	8.3	217	n/a
UNIC-SA-L-94	Western Mediterranean	Adult	21/06/2012	39.18	8.3	214	n/a
UNIC-SA-L-95	Western Mediterranean	Adult	21/06/2012	39.18	8.3	196	n/a
UNIC-SA-L-97	Western Mediterranean	Adult	21/06/2012	39.18	8.3	210	n/a
UNIC-SA-L-98	Western Mediterranean	Adult	21/06/2012	39.18	8.3	208	n/a
UNIC-SA-L-99	Western Mediterranean	Adult	21/06/2012	39.18	8.3	197	n/a
UNIM-TY-L-2	Western Mediterranean	Adult	13/06/2013	39.2	15.65	215	175
FMAP-MA-L-2	Central Mediterranean	Adult	08/05/2011	35.5	14	246	209
FMAP-MA-L-3	Central Mediterranean	Adult	08/05/2011	35.5	14	244	217
FMAP-MA-L-5	Central Mediterranean	Adult	13/05/2011	35.5	14	235	237

FMAP-MA-L-100	Central Mediterranean	Adult	02/05/2012	35.5	14	207	145
FMAP-MA-L-101	Central Mediterranean	Adult	04/05/2012	35.5	14	239	194
FMAP-MA-L-102	Central Mediterranean	Adult	04/05/2012	35.5	14	248	216
FMAP-MA-L-103	Central Mediterranean	Adult	04/05/2012	35.5	14	222	188
FMAP-MA-L-104	Central Mediterranean	Adult	04/05/2012	35.5	14	252	240
FMAP-MA-L-105	Central Mediterranean	Adult	04/05/2012	35.5	14	247	179
FMAP-MA-L-106	Central Mediterranean	Adult	04/05/2012	35.5	14	254	204
FMAP-MA-L-109	Central Mediterranean	Adult	10/05/2012	35.5	14	224	177
FMAP-MA-L-110	Central Mediterranean	Adult	10/05/2012	35.5	14	256	210
FMAP-MA-L-111	Central Mediterranean	Adult	10/05/2012	35.5	14	184	89
FMAP-MA-L-113	Central Mediterranean	Adult	10/05/2012	35.5	14	254	212
FMAP-MA-L-114	Central Mediterranean	Adult	11/05/2012	35.5	14	250	221
FMAP-MA-L-115	Central Mediterranean	Adult	11/05/2012	35.5	14	244	216
FMAP-MA-L-116	Central Mediterranean	Adult	11/05/2012	35.5	14	250	219
FMAP-MA-L-117	Central Mediterranean	Adult	11/05/2012	35.5	14	266	249
FMAP-MA-L-119	Central Mediterranean	Adult	11/05/2012	35.5	14	240	181
FMAP-MA-L-120	Central Mediterranean	Adult	11/05/2012	35.5	14	230	170
FMAP-MA-L-121	Central Mediterranean	Adult	11/05/2012	35.5	14	270	308
FMAP-MA-L-122	Central Mediterranean	Adult	29/05/2012	35.5	14	216	130
FMAP-MA-L-123	Central Mediterranean	Adult	29/05/2012	35.5	14	210	123
FMAP-MA-L-124	Central Mediterranean	Adult	29/05/2012	35.5	14	209	130
FMAP-MA-L-125	Central Mediterranean	Adult	30/05/2012	35.5	14	216	128

FMAP-MA-L-127	Central Mediterranean	Adult	30/05/2012	35.5	14	225	172
FMAP-MA-L-128	Central Mediterranean	Adult	30/05/2012	35.5	14	223	184
FMAP-MA-L-129	Central Mediterranean	Adult	30/05/2012	35.5	14	230	185
FMAP-MA-L-130	Central Mediterranean	Adult	30/05/2012	35.5	14	218	177
FMAP-MA-L-131	Central Mediterranean	Adult	30/05/2012	35.5	14	252	201
FMAP-MA-L-132	Central Mediterranean	Adult	30/05/2012	35.5	14	210	132
FMAP-MA-L-133	Central Mediterranean	Adult	30/05/2012	35.5	14	223	184
FMAP-MA-L-134	Central Mediterranean	Adult	30/05/2012	35.5	14	215	150
FMAP-MA-L-135	Central Mediterranean	Adult	30/05/2012	35.5	14	232	168
FMAP-MA-L-136	Central Mediterranean	Adult	30/05/2012	35.5	14	203	144
FMAP-MA-L-137	Central Mediterranean	Adult	30/05/2012	35.5	14	202	111
FMAP-MA-L-138	Central Mediterranean	Adult	30/05/2012	35.5	14	220	146
FMAP-MA-L-140	Central Mediterranean	Adult	31/05/2012	35.5	14	198	112
FMAP-MA-L-141	Central Mediterranean	Adult	31/05/2012	35.5	14	235	189
FMAP-MA-L-142	Central Mediterranean	Adult	31/05/2012	35.5	14	217	150
FMAP-MA-L-143	Central Mediterranean	Adult	31/05/2012	35.5	14	216	124
FMAP-MA-L-144	Central Mediterranean	Adult	01/06/2012	35.5	14	214	143
FMAP-MA-L-146	Central Mediterranean	Adult	01/06/2012	35.5	14	210	123
FMAP-MA-L-149	Central Mediterranean	Adult	02/06/2012	35.5	14	214	140
FMAP-MA-L-150	Central Mediterranean	Adult	02/06/2012	35.5	14	207	137
FMAP-MA-L-151	Central Mediterranean	Adult	02/06/2012	35.5	14	251	228
FMAP-MA-L-152	Central Mediterranean	Adult	02/06/2012	35.5	14	233	179

FMAP-MA-L-153	Central Mediterranean	Adult	03/06/2012	35.5	14	255	228
FMAP-MA-L-154	Central Mediterranean	Adult	03/06/2012	35.5	14	202	119
FMAP-MA-L-155	Central Mediterranean	Adult	03/06/2012	35.5	14	230	174
FMAP-MA-L-156	Central Mediterranean	Adult	03/06/2012	35.5	14	198	109
FMAP-MA-L-158	Central Mediterranean	Adult	08/06/2012	35.5	14	214	126
FMAP-MA-L-159	Central Mediterranean	Adult	08/06/2012	35.5	14	238	186
FMAP-MA-L-160	Central Mediterranean	Adult	08/06/2012	35.5	14	208	138
FMAP-MA-L-161	Central Mediterranean	Adult	09/06/2012	35.5	14	228	147
FMAP-MA-L-162	Central Mediterranean	Adult	09/06/2012	35.5	14	234	157
FMAP-MA-L-163	Central Mediterranean	Adult	09/06/2012	35.5	14	207	121
FMAP-MA-L-164	Central Mediterranean	Adult	09/06/2012	35.5	14	207	122
FMAP-MA-L-165	Central Mediterranean	Adult	09/06/2012	35.5	14	211	133
FMAP-MA-L-166	Central Mediterranean	Adult	09/06/2012	35.5	14	207	121
FMAP-MA-L-167	Central Mediterranean	Adult	09/06/2012	35.5	14	214	134
FMAP-MA-L-168	Central Mediterranean	Adult	09/06/2012	35.5	14	250	209
FMAP-MA-L-169	Central Mediterranean	Adult	09/06/2012	35.5	14	210	116
FMAP-SY-L-148	Central Mediterranean	Adult	05/06/2015	33.51	13.47	211	190
FMAP-SY-L-150	Central Mediterranean	Adult	05/06/2015	33.51	13.47	205	190
FMAP-SY-L-153	Central Mediterranean	Adult	05/06/2015	33.51	13.47	237	240
FMAP-SY-L-156	Central Mediterranean	Adult	05/06/2015	33.51	13.47	196	140
FMAP-SY-L-158	Central Mediterranean	Adult	05/06/2015	33.51	13.47	172	100
FMAP-SY-L-159	Central Mediterranean	Adult	05/06/2015	33.51	13.47	196	140

FMAP-SY-L-160	Central Mediterranean	Adult	05/06/2015	33.51	13.47	170	100
FMAP-SY-L-161	Central Mediterranean	Adult	05/06/2015	33.51	13.47	171	100
FMAP-SY-L-162	Central Mediterranean	Adult	05/06/2015	33.51	13.47	185	110
FMAP-SY-L-163	Central Mediterranean	Adult	05/06/2015	33.51	13.47	199	140
FMAP-SY-L-164	Central Mediterranean	Adult	05/06/2015	33.51	13.47	205	160
ISTA-LS-L-183	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	272	472
ISTA-LS-L-185	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	240	324
ISTA-LS-L-188	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	242	379
ISTA-LS-L-189	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	210	226
ISTA-LS-L-191	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	227	282
ISTA-LS-L-192	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	231	284
ISTA-LS-L-194	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	229	255
ISTA-LS-L-196	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	243	289
ISTA-LS-L-197	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	229	258
ISTA-LS-L-202	Eastern Mediterranean	Adult	28/05/2015	36.26	31.53	233	294
ISTA-LS-L-158	Eastern Mediterranean	Adult	30/05/2015	36.43	31.51	250	n/a
ISTA-LS-L-159	Eastern Mediterranean	Adult	30/05/2015	36.43	31.51	242	250
ISTA-LS-L-161	Eastern Mediterranean	Adult	05/06/2015	35.56	35.16	231	203
ISTA-LS-L-163	Eastern Mediterranean	Adult	05/06/2015	35.56	35.16	234	220
ISTA-LS-L-168	Eastern Mediterranean	Adult	05/06/2015	35.56	35.16	230	185
ISTA-LS-L-173	Eastern Mediterranean	Adult	05/06/2015	35.56	35.16	222	172
ISTA-LS-L-176	Eastern Mediterranean	Adult	05/06/2015	35.56	35.16	227	213

ISTA-LS-L-177	Eastern Mediterranean	Adult	05/06/2015	35.56	35.16	223	200
ISTA-LS-L-179	Eastern Mediterranean	Adult	05/06/2015	35.56	35.16	214	172
ISTA-LS-L-181	Eastern Mediterranean	Adult	05/06/2015	35.56	35.16	232	222

WebTable 4

Canary island young of the year and Slope Sea young of the year and larvae genotyped with the final selection of 96 SNPs on the Fluidigm platform for origin assignment. Only those included in subsequent analyses are shown. Column descriptions as in Table S1.

Sample	Area	Dev. stage	Catch date	Latitude	Longitude	Length (cm)	Weight (g)
E12_GU1302_N141_Thun_02	Slope Sea	Larvae	23/06/2013	36.31	-74.29	n/a	n/a
F02_GU1302_N141_Thun_04	Slope Sea	Larvae	23/06/2013	36.31	-74.29	n/a	n/a
F04_GU1302_N141_Thun_06	Slope Sea	Larvae	23/06/2013	36.31	-74.29	n/a	n/a
F05_GU1302_N141_Thun_07	Slope Sea	Larvae	23/06/2013	36.31	-74.29	n/a	n/a
F06_GU1302_N141_Thun_08	Slope Sea	Larvae	23/06/2013	36.31	-74.29	n/a	n/a
F07_GU1302_N141_Thun_09	Slope Sea	Larvae	23/06/2013	36.31	-74.29	n/a	n/a
AZTI-GM-0-44	Slope Sea	Young of the year	13/09/2008	36.41	-74.83	12	0.48
IEO-CI-0-1	Canary Islands	Young of the year	19/05/2016	28.31	-17	42.7	16.25
IEO-CI-0-2	Canary Islands	Young of the year	19/05/2016	28.31	-17	44.8	19.98
IEO-CI-0-3	Canary Islands	Young of the year	19/05/2016	28.31	-17	45	19.12
IEO-CI-0-4	Canary Islands	Young of the year	19/05/2016	28.31	-17	44.1	18.67
IEO-CI-0-5	Canary Islands	Young of the year	19/05/2016	28.31	-17	47.2	23.8
IEO-CI-0-6	Canary Islands	Young of the year	19/05/2016	28.31	-17	42.5	17.82

WebTable 5

Feeding aggregate samples genotyped with the final selection of 96 SNPs on the Fluidigm platform for origin assignment. Only those included in subsequent analyses are shown. Column descriptions as in WebTable 1.

Sample	Area	Subarea	Size	Catch date	Latitude	Longitude
AZTI-BB-J-184	BB	BB	Juvenile	7/2012	43.6	-1.67
AZTI-BB-J-187	BB	BB	Juvenile	7/2012	43.6	-1.67
AZTI-BB-J-199	BB	BB	Juvenile	7/2012	43.6	-1.67
AZTI-BB-J-208	BB	BB	Juvenile	7/2012	43.6	-1.67
AZTI-BB-J-211	BB	BB	Juvenile	7/2012	43.6	-1.87
AZTI-BB-J-213	BB	BB	Juvenile	7/2012	43.6	-1.99
AZTI-BB-J-216	BB	BB	Juvenile	7/2012	43.6	-1.77
AZTI-BB-J-218	BB	BB	Juvenile	7/2012	43.6	-1.79
AZTI-BB-J-220	BB	BB	Juvenile	7/2012	43.6	-1.87
AZTI-BB-J-228	BB	BB	Juvenile	7/2012	43.6	-1.67
AZTI-BB-J-244	BB	BB	Juvenile	7/2012	43.6	-1.78
AZTI-BB-J-246	BB	BB	Juvenile	7/2012	43.6	-1.78
AZTI-BB-J-255	BB	BB	Juvenile	7/2012	43.63	-1.83
AZTI-BB-J-261	BB	BB	Juvenile	7/2012	43.63	-1.83
AZTI-BB-J-264	BB	BB	Juvenile	7/2012	43.63	-1.83
AZTI-BB-J-276	BB	BB	Juvenile	7/2012	43.62	-2.08
AZTI-BB-J-288	BB	BB	Juvenile	7/2012	43.71	-2.12
AZTI-BB-J-290	BB	BB	Juvenile	7/2012	43.71	-2.12
AZTI-BB-J-321	BB	BB	Juvenile	7/2012	43.75	-2.07
AZTI-BB-J-324	BB	BB	Juvenile	8/2012	43.68	-1.53
AZTI-BB-J-325	BB	BB	Juvenile	7/2012	43.75	-2.07
AZTI-BB-J-332	BB	BB	Juvenile	7/2012	43.63	-2.07
AZTI-BB-J-333	BB	BB	Juvenile	7/2012	43.59	-1.89
AZTI-BB-J-359	BB	BB	Juvenile	8/2012	43.53	-1.85
AZTI-BB-J-364	BB	BB	Juvenile	8/2012	43.47	-1.8
AZTI-BB-J-370	BB	BB	Juvenile	8/2012	43.47	-1.8
AZTI-BB-J-418	BB	BB	Juvenile	8/2012	43.68	-1.59
AZTI-BB-J-481	BB	BB	Juvenile	7/2012	43.68	-1.59
AZTI-BB-J-532	BB	BB	Juvenile	8/2012	43.48	-1.77
AZTI-BB-J-533	BB	BB	Juvenile	8/2012	43.48	-1.77
AZTI-BB-L-1	BB	BB	Large	7/2011	44	-3
AZTI-BB-L-10	BB	BB	Large	7/2011	44	-3
AZTI-BB-L-12	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-14	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-15	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-16	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-18	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-2	BB	BB	Large	7/2011	44	-3
AZTI-BB-L-20	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-21	BB	BB	Large	8/2011	44	-3

AZTI-BB-L-22	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-25	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-27	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-29	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-31	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-33	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-35	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-37	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-38	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-39	BB	BB	Large	8/2011	44	-3
AZTI-BB-L-4	BB	BB	Large	7/2011	44	-3
AZTI-BB-L-6	BB	BB	Large	7/2011	44	-3
AZTI-BB-L-61	BB	BB	Large	8/2011	43.59	-1.88
AZTI-BB-L-62	BB	BB	Large	8/2011	43.59	-1.88
AZTI-BB-L-63	BB	BB	Large	8/2011	43.59	-1.88
AZTI-BB-L-64	BB	BB	Large	8/2011	43.59	-1.88
AZTI-BB-L-7	BB	BB	Large	7/2011	44	-3
AZTI-BB-L-8	BB	BB	Large	7/2011	44	-3
AZTI-BB-M-100	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-102	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-103	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-104	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-105	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-106	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-107	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-109	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-110	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-111	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-112	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-113	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-115	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-116	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-117	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-118	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-126	BB	BB	Medium	8/2012	43.58	-1.71
AZTI-BB-M-128	BB	BB	Medium	8/2012	43.58	-1.71
AZTI-BB-M-134	BB	BB	Medium	8/2012	43.58	-1.71
AZTI-BB-M-158	BB	BB	Medium	8/2012	43.58	-1.71
AZTI-BB-M-161	BB	BB	Medium	8/2012	43.58	-1.71
AZTI-BB-M-164	BB	BB	Medium	9/2012	43.58	-1.71
AZTI-BB-M-166	BB	BB	Medium	9/2012	43.58	-1.71
AZTI-BB-M-168	BB	BB	Medium	9/2012	43.58	-1.71
AZTI-BB-M-171	BB	BB	Medium	9/2012	43.58	-1.71
AZTI-BB-M-173	BB	BB	Medium	9/2012	43.58	-1.71
AZTI-BB-M-88	BB	BB	Medium	7/2012	43.58	-1.71

AZTI-BB-M-97	BB	BB	Medium	7/2012	43.58	-1.71
AZTI-BB-M-99	BB	BB	Medium	7/2012	43.58	-1.71
NRIF-CA-L-1001	CAE	CAE	Large	10/2013	58	-19
NRIF-CA-L-1008	CAE	CAE	Large	10/2013	59	-19
NRIF-CA-L-1013	CAE	CAE	Large	10/2013	59	-20
NRIF-CA-L-1015	CAE	CAE	Large	10/2013	58	-20
NRIF-CA-L-1016	CAE	CAE	Large	10/2013	58	-20
NRIF-CA-L-1021	CAE	CAE	Large	11/2013	58	-21
NRIF-CA-L-1028	CAE	CAE	Large	11/2013	58	-20
NRIF-CA-L-1032	CAE	CAE	Large	11/2013	58	-20
NRIF-CA-L-1040	CAE	CAE	Large	10/2013	58	-21
NRIF-CA-L-1042	CAE	CAE	Large	10/2013	58	-21
NRIF-CA-L-1058	CAE	CAE	Large	10/2013	58	-22
NRIF-CA-L-1060	CAE	CAE	Large	10/2013	59	-21
NRIF-CA-L-1063	CAE	CAE	Large	10/2013	59	-21
NRIF-CA-L-1074	CAE	CAE	Large	10/2013	58	-20
NRIF-CA-L-1096	CAE	CAE	Large	11/2013	59	-21
NRIF-CA-L-1098	CAE	CAE	Large	11/2013	57	-26
NRIF-CA-L-1101	CAE	CAE	Large	11/2013	57	-26
NRIF-CA-L-1104	CAE	CAE	Large	11/2013	58	-26
NRIF-CA-L-1108	CAE	CAE	Large	11/2013	58	-26
NRIF-CA-L-1111	CAE	CAE	Large	11/2013	58	-26
NRIF-CA-L-1113	CAE	CAE	Large	11/2013	58	-26
NRIF-CA-L-1114	CAE	CAE	Large	11/2013	58	-26
NRIF-CA-L-1118	CAE	CAE	Large	11/2013	58	-26
NRIF-CA-L-1122	CAE	CAE	Large	11/2013	57	-26
NRIF-CA-L-1125	CAE	CAE	Large	11/2013	57	-26
NRIF-CA-L-1148	CAE	CAE	Large	10/2013	58	-21
NRIF-CA-L-1157	CAE	CAE	Large	10/2013	52	-22
NRIF-CA-L-1162	CAE	CAE	Large	10/2013	52	-22
NRIF-CA-L-1164	CAE	CAE	Large	10/2013	58	-22
NRIF-CA-L-1306	CAE	CAE	Large	10/2014	59	-18
NRIF-CA-L-1312	CAE	CAE	Large	10/2014	59	-18
NRIF-CA-L-1354	CAE	CAE	Large	10/2014	59	-18
NRIF-CA-L-1413	CAE	CAE	Large	10/2014	59	-18
NRIF-CA-L-1485	CAE	CAE	Large	10/2014	59	-18
NRIF-CA-L-150	CAE	CAE	Large	10/2011	59	-29
NRIF-CA-L-156	CAE	CAE	Large	10/2011	59	-29
NRIF-CA-L-1609	CAE	CAE	Large	10/2014	59	-23
NRIF-CA-L-1632	CAE	CAE	Large	10/2014	58	-21
NRIF-CA-L-164	CAE	CAE	Large	10/2011	59	-28
NRIF-CA-L-1683	CAE	CAE	Large	10/2014	59	-22
NRIF-CA-L-170	CAE	CAE	Large	10/2011	59	-28
NRIF-CA-L-1715	CAE	CAE	Large	10/2014	59	-23
NRIF-CA-L-1724	CAE	CAE	Large	10/2014	59	-22

NRIF-CA-L-1763	CAE	CAE	Large	10/2015	59	-17
NRIF-CA-L-1777	CAE	CAE	Large	10/2015	59	-17
NRIF-CA-L-1793	CAE	CAE	Large	10/2015	59	-18
NRIF-CA-L-180	CAE	CAE	Large	10/2011	60	-28
NRIF-CA-L-1811	CAE	CAE	Large	10/2015	59	-18
NRIF-CA-L-1827	CAE	CAE	Large	10/2015	59	-17
NRIF-CA-L-1836	CAE	CAE	Large	10/2015	59	-17
NRIF-CA-L-184	CAE	CAE	Large	10/2011	60	-28
NRIF-CA-L-1860	CAE	CAE	Large	10/2015	58	-25
NRIF-CA-L-1876	CAE	CAE	Large	10/2015	58	-21
NRIF-CA-L-1887	CAE	CAE	Large	10/2015	59	-19
NRIF-CA-L-1910	CAE	CAE	Large	10/2015	59	-24
NRIF-CA-L-1929	CAE	CAE	Large	10/2015	58	-25
NRIF-CA-L-1959	CAE	CAE	Large	10/2015	59	-22
NRIF-CA-L-199	CAE	CAE	Large	10/2011	59	-25
NRIF-CA-L-2004	CAE	CAE	Large	10/2015	58	-22
NRIF-CA-L-2061	CAE	CAE	Large	10/2015	58	-19
NRIF-CA-L-2107	CAE	CAE	Large	9/2015	59	-21
NRIF-CA-L-2120	CAE	CAE	Large	10/2015	59	-22
NRIF-CA-L-2130	CAE	CAE	Large	10/2015	59	-21
NRIF-CA-L-2138	CAE	CAE	Large	10/2015	59	-16
NRIF-CA-L-2158	CAE	CAE	Large	10/2015	59	-22
NRIF-CA-L-2167	CAE	CAE	Large	10/2015	59	-21
NRIF-CA-L-2175	CAE	CAE	Large	10/2015	59	-21
NRIF-CA-L-2184	CAE	CAE	Large	10/2015	58	-21
NRIF-CA-L-2199	CAE	CAE	Large	10/2015	59	-16
NRIF-CA-L-2207	CAE	CAE	Large	10/2015	59	-16
NRIF-CA-L-2219	CAE	CAE	Large	10/2015	59	-15
NRIF-CA-L-224	CAE	CAE	Large	10/2011	59	-24
NRIF-CA-L-2241	CAE	CAE	Large	11/2015	58	-19
NRIF-CA-L-2250	CAE	CAE	Large	11/2015	58	-19
NRIF-CA-L-230	CAE	CAE	Large	10/2011	59	-25
NRIF-CA-L-2308	CAE	CAE	Large	10/2015	58	-25
NRIF-CA-L-2342	CAE	CAE	Large	10/2015	59	-20
NRIF-CA-L-235	CAE	CAE	Large	10/2011	59	-25
NRIF-CA-L-2393	CAE	CAE	Large	10/2015	59	-19
NRIF-CA-L-242	CAE	CAE	Large	10/2011	59	-23
NRIF-CA-L-260	CAE	CAE	Large	10/2011	59	-22
NRIF-CA-L-267	CAE	CAE	Large	10/2011	58	-26
NRIF-CA-L-273	CAE	CAE	Large	10/2011	58	-26
NRIF-CA-L-278	CAE	CAE	Large	10/2011	58	-23
NRIF-CA-L-288	CAE	CAE	Large	10/2011	56	-25
NRIF-CA-L-299	CAE	CAE	Large	10/2011	56	-25
NRIF-CA-L-305	CAE	CAE	Large	10/2011	56	-26
NRIF-CA-L-317	CAE	CAE	Large	10/2011	52	-30

NRIF-CA-L-324	CAE	CAE	Large	11/2011	55	-26
NRIF-CA-L-331	CAE	CAE	Large	11/2011	55	-26
NRIF-CA-L-346	CAE	CAE	Large	11/2011	54	-27
NRIF-CA-L-347	CAE	CAE	Large	11/2011	54	-27
NRIF-CA-L-353	CAE	CAE	Large	11/2011	54	-27
NRIF-CA-L-363	CAE	CAE	Large	11/2011	55	-26
NRIF-CA-L-479	CAE	CAE	Large	9/2012	60	-26
NRIF-CA-L-485	CAE	CAE	Large	10/2012	60	-26
NRIF-CA-L-510	CAE	CAE	Large	10/2012	59	-26
NRIF-CA-L-517	CAE	CAE	Large	10/2012	57	-26
NRIF-CA-L-526	CAE	CAE	Large	10/2012	58	-24
NRIF-CA-L-529	CAE	CAE	Large	10/2012	58	-25
NRIF-CA-L-537	CAE	CAE	Large	10/2012	57	-24
NRIF-CA-L-544	CAE	CAE	Large	10/2012	57	-23
NRIF-CA-L-545	CAE	CAE	Large	10/2012	57	-23
NRIF-CA-L-553	CAE	CAE	Large	10/2012	57	-23
NRIF-CA-L-558	CAE	CAE	Large	10/2012	57	-23
NRIF-CA-L-566	CAE	CAE	Large	10/2012	58	-21
NRIF-CA-L-597	CAE	CAE	Large	11/2012	58	-21
NRIF-CA-L-634	CAE	CAE	Large	11/2012	58	-22
NRIF-CA-L-636	CAE	CAE	Large	11/2012	58	-22
NRIF-CA-L-663	CAE	CAE	Large	11/2012	57	-27
NRIF-CA-L-819	CAE	CAE	Large	10/2012	55	-25
NRIF-CA-L-820	CAE	CAE	Large	10/2012	55	-25
NRIF-CA-L-838	CAE	CAE	Large	10/2012	54	-25
NRIF-CA-L-839	CAE	CAE	Large	10/2012	54	-25
NRIF-CA-L-841	CAE	CAE	Large	10/2012	54	-25
NRIF-CA-L-843	CAE	CAE	Large	10/2012	54	-25
NRIF-CA-L-851	CAE	CAE	Large	11/2012	54	-25
NRIF-CA-L-856	CAE	CAE	Large	11/2012	52	-32
NRIF-CA-M-19	CAE	CAE	Medium	10/2011	59	-24
NRIF-CA-M-20	CAE	CAE	Medium	10/2011	59	-23
NRIF-CA-M-24	CAE	CAE	Medium	10/2011	56	-26
NRIF-CA-M-25	CAE	CAE	Medium	10/2011	56	-25
NRIF-CA-M-26	CAE	CAE	Medium	10/2011	56	-25
NRIF-CA-M-29	CAE	CAE	Medium	10/2011	56	-25
NRIF-CA-M-37	CAE	CAE	Medium	11/2011	55	-26
NRIF-CA-M-40	CAE	CAE	Medium	11/2011	52	-29
NRIF-CA-M-46	CAE	CAE	Medium	10/2011	59	-20
NRIF-CA-M-47	CAE	CAE	Medium	10/2011	59	-20
NRIF-CA-M-48	CAE	CAE	Medium	10/2011	59	-19
NRIF-CA-M-52	CAE	CAE	Medium	10/2011	59	-20
NRIF-CA-M-54	CAE	CAE	Medium	10/2011	59	-20
NRIF-CA-M-56	CAE	CAE	Medium	9/2012	60	-26
NRIF-CA-M-57	CAE	CAE	Medium	10/2012	60	-26

NRIF-CA-M-58	CAE	CAE	Medium	10/2012	59	-25
NRIF-CA-M-65	CAE	CAE	Medium	10/2012	59	-27
NRIF-CA-M-67	CAE	CAE	Medium	10/2012	57	-25
NRIF-CA-M-69	CAE	CAE	Medium	10/2012	58	-25
NRIF-CA-M-72	CAE	CAE	Medium	10/2012	57	-23
NRIF-CA-M-77	CAE	CAE	Medium	11/2012	58	-22
NRIF-CA-M-79	CAE	CAE	Medium	11/2012	58	-22
NRIF-CA-M-80	CAE	CAE	Medium	11/2012	58	-22
NRIF-CA-M-81	CAE	CAE	Medium	10/2012	60	-26
NRIF-CA-M-82	CAE	CAE	Medium	10/2012	59	-22
NRIF-CA-M-83	CAE	CAE	Medium	10/2012	59	-26
NRIF-CA-M-85	CAE	CAE	Medium	10/2012	58	-22
IMR-NW-L-28	CAE	CAE	Large	5/2016	55.75	-15.5
IMR-NW-L-29	CAE	CAE	Large	11/2016	51.75	-16.5
NRIF-CA-L-1238	CAW	CAW	Large	9/2014	45	-48
NRIF-CA-L-124	CAW	CAW	Large	9/2011	42	-50
NRIF-CA-L-1241	CAW	CAW	Large	9/2014	45	-48
NRIF-CA-L-1249	CAW	CAW	Large	9/2014	45	-48
NRIF-CA-L-1250	CAW	CAW	Large	9/2014	45	-48
NRIF-CA-L-1259	CAW	CAW	Large	9/2014	45	-48
NRIF-CA-L-1262	CAW	CAW	Large	9/2014	44	-48
NRIF-CA-L-1264	CAW	CAW	Large	9/2014	44	-48
NRIF-CA-L-1270	CAW	CAW	Large	9/2014	44	-48
NRIF-CA-L-1273	CAW	CAW	Large	9/2014	44	-48
NRIF-CA-L-1275	CAW	CAW	Large	9/2014	44	-48
NRIF-CA-L-130	CAW	CAW	Large	9/2011	42	-50
NRIF-CA-L-139	CAW	CAW	Large	9/2011	42	-49
NRIF-CA-L-141	CAW	CAW	Large	9/2011	42	-49
NRIF-CA-L-142	CAW	CAW	Large	9/2011	43	-49
NRIF-CA-L-143	CAW	CAW	Large	9/2011	43	-49
NRIF-CA-L-147	CAW	CAW	Large	9/2011	42	-49
NRIF-CA-L-1532	CAW	CAW	Large	9/2014	45	-48
NRIF-CA-L-1552	CAW	CAW	Large	10/2014	45	-48
NRIF-CA-L-1557	CAW	CAW	Large	10/2014	45	-47
NRIF-CA-L-158	CAW	CAW	Large	10/2011	42	-49
NRIF-CA-L-160	CAW	CAW	Large	10/2011	43	-49
NRIF-CA-L-162	CAW	CAW	Large	10/2011	43	-49
NRIF-CA-L-171	CAW	CAW	Large	10/2011	42	-49
NRIF-CA-L-179	CAW	CAW	Large	10/2011	42	-49
NRIF-CA-L-186	CAW	CAW	Large	10/2011	42	-49
NRIF-CA-L-187	CAW	CAW	Large	10/2011	42	-49
NRIF-CA-L-188	CAW	CAW	Large	10/2011	42	-49
NRIF-CA-L-195	CAW	CAW	Large	10/2011	42	-49
NRIF-CA-L-261	CAW	CAW	Large	10/2011	43	-49
NRIF-CA-L-373	CAW	CAW	Large	11/2011	41	-51

NRIF-CA-L-377	CAW	CAW	Large	11/2011	42	-50
NRIF-CA-L-381	CAW	CAW	Large	11/2011	42	-50
NRIF-CA-L-388	CAW	CAW	Large	11/2011	42	-50
NRIF-CA-L-396	CAW	CAW	Large	11/2011	42	-50
NRIF-CA-L-404	CAW	CAW	Large	12/2011	42	-50
NRIF-CA-L-409	CAW	CAW	Large	12/2011	42	-50
NRIF-CA-L-416	CAW	CAW	Large	12/2011	41	-50
NRIF-CA-L-423	CAW	CAW	Large	12/2011	41	-48
NRIF-CA-L-431	CAW	CAW	Large	12/2011	41	-48
NRIF-CA-L-438	CAW	CAW	Large	12/2011	41	-48
NRIF-CA-L-669	CAW	CAW	Large	8/2012	42	-49
NRIF-CA-L-677	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-684	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-691	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-696	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-702	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-707	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-712	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-720	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-725	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-733	CAW	CAW	Large	9/2012	45	-48
NRIF-CA-L-738	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-744	CAW	CAW	Large	9/2012	45	-48
NRIF-CA-L-795	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-796	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-797	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-798	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-799	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-800	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-801	CAW	CAW	Large	9/2012	44	-48
NRIF-CA-L-802	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-803	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-804	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-805	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-806	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-807	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-808	CAW	CAW	Large	9/2012	45	-48
NRIF-CA-L-809	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-810	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-811	CAW	CAW	Large	9/2012	45	-47
NRIF-CA-L-859	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-863	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-867	CAW	CAW	Large	9/2013	43	-48
NRIF-CA-L-871	CAW	CAW	Large	9/2013	43	-48
NRIF-CA-L-876	CAW	CAW	Large	9/2013	44	-48

NRIF-CA-L-878	CAW	CAW	Large	9/2013	43	-48
NRIF-CA-L-880	CAW	CAW	Large	9/2013	43	-48
NRIF-CA-L-884	CAW	CAW	Large	10/2013	44	-48
NRIF-CA-L-887	CAW	CAW	Large	10/2013	45	-48
NRIF-CA-L-890	CAW	CAW	Large	10/2013	45	-48
NRIF-CA-L-894	CAW	CAW	Large	10/2013	44	-48
NRIF-CA-L-897	CAW	CAW	Large	10/2013	44	-48
NRIF-CA-L-901	CAW	CAW	Large	10/2013	45	-48
NRIF-CA-L-904	CAW	CAW	Large	10/2013	44	-48
NRIF-CA-L-906	CAW	CAW	Large	10/2013	44	-48
NRIF-CA-L-908	CAW	CAW	Large	10/2013	44	-48
NRIF-CA-L-911	CAW	CAW	Large	10/2013	44	-48
NRIF-CA-L-917	CAW	CAW	Large	8/2013	44	-48
NRIF-CA-L-920	CAW	CAW	Large	8/2013	45	-48
NRIF-CA-L-930	CAW	CAW	Large	8/2013	44	-48
NRIF-CA-L-934	CAW	CAW	Large	8/2013	44	-48
NRIF-CA-L-944	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-950	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-956	CAW	CAW	Large	9/2013	45	-48
NRIF-CA-L-963	CAW	CAW	Large	9/2013	45	-48
NRIF-CA-L-974	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-975	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-978	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-980	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-993	CAW	CAW	Large	9/2013	44	-48
NRIF-CA-L-1558	CAW	CAW	Large	10/2014	46	-47
DFO-GSL-L-1	GSL	GSL	Large	10/2013	46.03	-62.29
DFO-GSL-L-10	GSL	GSL	Large	9/2013	47.07	-63.9
DFO-GSL-L-11	GSL	GSL	Large	9/2013	47.17	-63.96
DFO-GSL-L-12	GSL	GSL	Large	9/2013	47.15	-63.93
DFO-GSL-L-13	GSL	GSL	Large	9/2013	47.09	-64.11
DFO-GSL-L-14	GSL	GSL	Large	10/2013	47.16	-63.84
DFO-GSL-L-15	GSL	GSL	Large	9/2013	46.52	-62.39
DFO-GSL-L-16	GSL	GSL	Large	9/2013	46.53	-62.76
DFO-GSL-L-17	GSL	GSL	Large	9/2013	46.56	-62.73
DFO-GSL-L-18	GSL	GSL	Large	9/2013	46.03	-62.23
DFO-GSL-L-19	GSL	GSL	Large	9/2013	46.36	-62.21
DFO-GSL-L-2	GSL	GSL	Large	10/2013	46.03	-61.69
DFO-GSL-L-20	GSL	GSL	Large	9/2013	46.02	-62.33
DFO-GSL-L-21	GSL	GSL	Large	9/2013	46	-62.25
DFO-GSL-L-22	GSL	GSL	Large	9/2013	46.5	-62.03
DFO-GSL-L-23	GSL	GSL	Large	9/2013	46.52	-61.95
DFO-GSL-L-3	GSL	GSL	Large	9/2013	46.11	-61.51
DFO-GSL-L-4	GSL	GSL	Large	9/2013	46.11	-61.51
DFO-GSL-L-5	GSL	GSL	Large	10/2013	45.98	-61.6

DFO-GSL-L-6	GSL	GSL	Large	9/2013	46.42	-61.3
DFO-GSL-L-7	GSL	GSL	Large	9/2013	46.12	-61.56
DFO-GSL-L-8	GSL	GSL	Large	9/2013	46.01	-61.6
DFO-GSL-L-9	GSL	GSL	Large	9/2013	46.05	-63.78
UCA-GSL-L-1	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-11	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-13	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-14	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-16	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-18	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-20	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-21	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-22	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-24	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-25	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-28	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-30	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-32	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-34	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-35	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-37	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-38	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-39	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-41	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-42	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-44	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-45	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-47	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-48	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-5	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-50	GSL	GSL	Large	10/2016	46.17	-61.8
UCA-GSL-L-7	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-8	GSL	GSL	Large	9/2016	46.17	-61.8
UCA-GSL-L-9	GSL	GSL	Large	9/2016	46.17	-61.8
DFO-NL-L-1	ECA	NL	Large	9/2013	45.6	-55.75
DFO-NL-L-2	ECA	NL	Large	9/2013	45.58	-55.68
DFO-NL-L-3	ECA	NL	Large	9/2013	45.6	-55.67
DFO-NL-L-4	ECA	NL	Large	9/2013	47.47	-53.08
DFO-NL-L-5	ECA	NL	Large	9/2013	45.58	-55.7
DFO-NL-L-6	ECA	NL	Large	9/2013	45.58	-55.72
DFO-NL-L-7	ECA	NL	Large	9/2013	45.57	-55.7
DFO-NL-L-8	ECA	NL	Large	9/2013	45.6	-55.7
DFO-NL-L-9	ECA	NL	Large	9/2013	45.58	-55.68
DFO-NS-L-1	ECA	NS	Large	8/2013	44.07	-64.38
DFO-NS-L-10	ECA	NS	Large	10/2013	44.07	-64.38

DFO-NS-L-11	ECA	NS	Large	8/2013	44.68	-66.67
DFO-NS-L-12	ECA	NS	Large	10/2013	44.2	-64.22
DFO-NS-L-13	ECA	NS	Large	10/2013	45.34	-60.78
DFO-NS-L-14	ECA	NS	Large	10/2013	45.43	-60.77
DFO-NS-L-15	ECA	NS	Large	10/2013	45.43	-60.77
DFO-NS-L-16	ECA	NS	Large	10/2013	45.3	-60.25
DFO-NS-L-17	ECA	NS	Large	10/2013	45.35	-60.8
DFO-NS-L-2	ECA	NS	Large	8/2013	45.35	-60.8
DFO-NS-L-3	ECA	NS	Large	8/2013	45.35	-60.8
DFO-NS-L-4	ECA	NS	Large	8/2013	45.35	-60.8
DFO-NS-L-5	ECA	NS	Large	8/2013	42.07	-65.57
DFO-NS-L-6	ECA	NS	Large	10/2013	43.83	-64.65
DFO-NS-L-7	ECA	NS	Large	10/2013	43.9	-64.63
DFO-NS-L-8	ECA	NS	Large	8/2013	44.68	-66.67
DFO-NS-L-9	ECA	NS	Large	9/2013	43.87	-64.62
IEO-GI-M-50	GOC	GI	Medium	7/2012	35.92	-5.7
IEO-GI-M-51	GOC	GI	Medium	8/2012	35.92	-5.7
IEO-GI-M-52	GOC	GI	Medium	8/2012	35.95	-5.55
IEO-GI-M-53	GOC	GI	Medium	9/2012	36.12	-7.03
IEO-GI-M-23	GOC	GI	Medium	10/2012	35	-5
IEO-GI-M-24	GOC	GI	Medium	10/2012	35.97	-5.05
IEO-GI-M-25	GOC	GI	Medium	10/2012	35	-5
IEO-GI-M-26	GOC	GI	Medium	10/2012	35.97	-5.05
IEO-GI-M-27	GOC	GI	Medium	10/2012	35.92	-5.58
IEO-GI-M-28	GOC	GI	Medium	10/2012	35.92	-5.58
IEO-GI-M-29	GOC	GI	Medium	10/2012	35	-5
IEO-GI-M-32	GOC	GI	Medium	10/2012	35.95	-5.47
IEO-GI-M-33	GOC	GI	Medium	10/2012	35	-5
IEO-GI-M-35	GOC	GI	Medium	10/2012	35.98	-5.47
IEO-GI-M-36	GOC	GI	Medium	10/2012	35.93	-5.55
IEO-GI-M-37	GOC	GI	Medium	10/2012	35	-5
IEO-GI-M-38	GOC	GI	Medium	10/2012	35.93	-5.62
IEO-GI-M-34	GOC	GI	Medium	11/2012	35.93	-5.55
IEO-GI-M-39	GOC	GI	Medium	11/2012	35.93	-5.53
IEO-GI-M-40	GOC	GI	Medium	11/2012	35.97	-5.47
IEO-GI-M-41	GOC	GI	Medium	11/2012	35.97	-5.47
IEO-GI-M-42	GOC	GI	Medium	11/2012	35.97	-5.47
IEO-GI-M-43	GOC	GI	Medium	11/2012	35.97	-5.52
IEO-GI-M-44	GOC	GI	Medium	11/2012	35.93	-5.58
IEO-GI-M-45	GOC	GI	Medium	11/2012	35.95	-5.48
IEO-GI-M-46	GOC	GI	Medium	11/2012	35.95	-5.55
IEO-GI-M-47	GOC	GI	Medium	11/2012	35.93	-5.47
IEO-GI-M-48	GOC	GI	Medium	11/2012	35.93	-5.47
INRH-MO-L-103	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-104	MO	MO	Large	5/2012	35.12	-6.28

INRH-MO-L-105	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-107	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-112	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-115	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-117	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-126	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-138	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-141	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-146	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-147	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-148	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-152	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-153	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-154	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-155	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-156	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-159	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-160	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-161	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-162	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-164	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-165	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-166	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-167	MO	MO	Large	5/2013	35.35	-6.15
INRH-MO-L-168	MO	MO	Large	5/2013	35.35	-6.15
INRH-MO-L-169	MO	MO	Large	5/2013	35.35	-6.15
INRH-MO-L-173	MO	MO	Large	5/2013	35.35	-6.15
INRH-MO-L-174	MO	MO	Large	5/2013	35.35	-6.15
INRH-MO-L-175	MO	MO	Large	5/2013	35.35	-6.15
INRH-MO-L-177	MO	MO	Large	5/2013	35.35	-6.15
INRH-MO-L-182	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-184	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-185	MO	MO	Large	5/2013	35.52	-6.07
INRH-MO-L-189	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-195	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-196	MO	MO	Large	5/2013	35.12	-6.28
INRH-MO-L-199	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-201	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-207	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-210	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-211	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-212	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-213	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-215	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-222	MO	MO	Large	5/2014	35.12	-6.28

INRH-MO-L-223	MO	MO	Large	5/2014	35.12	-6.28
INRH-MO-L-225	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-226	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-227	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-228	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-229	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-230	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-231	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-232	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-233	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-235	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-236	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-237	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-239	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-240	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-241	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-242	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-243	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-244	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-245	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-246	MO	MO	Large	5/2014	35.52	-6.07
INRH-MO-L-247	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-249	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-250	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-251	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-252	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-253	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-255	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-258	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-260	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-261	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-262	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-263	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-264	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-267	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-269	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-270	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-271	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-272	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-275	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-276	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-277	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-278	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-279	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-282	MO	MO	Large	5/2015	35.12	-6.28

INRH-MO-L-284	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-287	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-289	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-292	MO	MO	Large	5/2015	35.12	-6.28
INRH-MO-L-299	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-302	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-304	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-306	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-318	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-319	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-320	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-322	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-323	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-324	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-325	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-326	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-327	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-328	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-329	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-330	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-331	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-332	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-333	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-334	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-335	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-337	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-338	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-340	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-341	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-342	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-343	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-344	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-345	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-346	MO	MO	Large	5/2016	35.12	-6.28
INRH-MO-L-37	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-38	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-39	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-40	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-41	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-43	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-45	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-46	MO	MO	Large	5/2011	35.52	-6.07
INRH-MO-L-48	MO	MO	Large	5/2011	35.52	-6.07
INRH-MO-L-50	MO	MO	Large	5/2011	35.52	-6.07
INRH-MO-L-52	MO	MO	Large	5/2011	35.52	-6.07

INRH-MO-L-54	MO	MO	Large	5/2011	35.52	-6.07
INRH-MO-L-56	MO	MO	Large	5/2011	35.52	-6.07
INRH-MO-L-58	MO	MO	Large	5/2011	35.52	-6.07
INRH-MO-L-60	MO	MO	Large	5/2011	35.52	-6.07
INRH-MO-L-63	MO	MO	Large	5/2011	35.35	-6.15
INRH-MO-L-65	MO	MO	Large	5/2011	35.35	-6.15
INRH-MO-L-67	MO	MO	Large	5/2011	35.35	-6.15
INRH-MO-L-69	MO	MO	Large	5/2011	35.35	-6.15
INRH-MO-L-71	MO	MO	Large	5/2011	35.35	-6.15
INRH-MO-L-73	MO	MO	Large	5/2011	35.35	-6.15
INRH-MO-L-75	MO	MO	Large	5/2011	35.35	-6.15
INRH-MO-L-76	MO	MO	Large	5/2011	35.35	-6.15
INRH-MO-L-77	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-79	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-81	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-82	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-83	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-85	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-86	MO	MO	Large	5/2011	35.12	-6.28
INRH-MO-L-88	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-91	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-95	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-96	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-97	MO	MO	Large	5/2012	35.12	-6.28
INRH-MO-L-98	MO	MO	Large	5/2012	35.12	-6.28
IPIM-PO-L-108	GOC	PO	Large	5/2012	36.87	-6.97
IPIM-PO-L-109	GOC	PO	Large	5/2012	36.87	-6.97
IPIM-PO-L-163	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-164	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-165	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-167	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-179	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-181	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-182	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-185	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-186	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-189	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-190	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-193	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-196	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-203	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-207	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-208	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-209	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-214	GOC	PO	Large	<10/2012	36.87	-6.97

IPIM-PO-L-216	GOC	PO	Large	<10/2012	36.87	-6.97
IPIM-PO-L-125	GOC	PO	Large	<8/2012	36.87	-6.97
IPIM-PO-L-140	GOC	PO	Large	<9/2012	36.87	-6.97
IPIM-PO-L-142	GOC	PO	Large	<9/2012	36.87	-6.97
IPIM-PO-L-149	GOC	PO	Large	<9/2012	36.87	-6.97
IEO-CI-L-100	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-101	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-102	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-103	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-104	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-105	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-106	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-107	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-108	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-109	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-11	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-110	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-111	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-112	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-113	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-114	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-115	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-116	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-117	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-118	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-119	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-12	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-120	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-121	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-122	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-123	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-124	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-125	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-126	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-127	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-128	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-129	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-130	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-131	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-132	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-133	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-134	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-135	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-136	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-137	MC	MC	Large	3/2016	27.83	-16.92

IEO-CI-L-138	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-141	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-142	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-143	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-144	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-145	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-146	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-147	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-148	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-149	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-15	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-150	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-151	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-152	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-153	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-154	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-155	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-156	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-157	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-158	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-159	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-16	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-160	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-161	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-162	MC	MC	Large	3/2016	27.83	-16.92
IEO-CI-L-17	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-19	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-2	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-21	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-22	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-23	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-24	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-26	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-27	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-29	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-3	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-30	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-31	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-33	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-34	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-4	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-40	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-41	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-43	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-44	MC	MC	Large	3/2013	28	-16.67

IEO-CI-L-45	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-48	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-49	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-5	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-6	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-9	MC	MC	Large	3/2013	28	-16.67
IEO-CI-L-90	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-91	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-92	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-93	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-94	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-95	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-96	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-97	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-98	MC	MC	Large	3/2015	28.27	-16.98
IEO-CI-L-99	MC	MC	Large	3/2015	28.27	-16.98
CROD-MS-L-1	MS	MS	Large	12/2013	18.48	-17
CROD-MS-L-10	MS	MS	Large	12/2013	18.47	-16.92
CROD-MS-L-11	MS	MS	Large	12/2013	18.32	-17.9
CROD-MS-L-12	MS	MS	Large	12/2013	18.32	-17.9
CROD-MS-L-13	MS	MS	Large	12/2013	18.32	-17.9
CROD-MS-L-14	MS	MS	Large	12/2013	18.32	-17.9
CROD-MS-L-15	MS	MS	Large	12/2013	18.3	-17.98
CROD-MS-L-16	MS	MS	Large	12/2013	18.3	-17.98
CROD-MS-L-17	MS	MS	Large	12/2013	18.3	-17.98
CROD-MS-L-18	MS	MS	Large	12/2013	18.5	-17.23
CROD-MS-L-19	MS	MS	Large	12/2013	18.5	-17.23
CROD-MS-L-2	MS	MS	Large	12/2013	18.48	-17
CROD-MS-L-20	MS	MS	Large	12/2013	18.5	-17.23
CROD-MS-L-21	MS	MS	Large	12/2013	18.72	-17.33
CROD-MS-L-22	MS	MS	Large	12/2013	18.72	-17.33
CROD-MS-L-23	MS	MS	Large	12/2013	18.72	-17.33
CROD-MS-L-3	MS	MS	Large	12/2013	18.48	-17
CROD-MS-L-4	MS	MS	Large	12/2013	18.45	-17.07
CROD-MS-L-5	MS	MS	Large	12/2013	18.45	-17.07
CROD-MS-L-6	MS	MS	Large	12/2013	18.45	-17.07
CROD-MS-L-7	MS	MS	Large	12/2013	18.47	-16.92
CROD-MS-L-8	MS	MS	Large	12/2013	18.47	-16.92
CROD-MS-L-9	MS	MS	Large	12/2013	18.47	-16.92
IMR-NW-L-1	NW	NW	Large	8/2013	61.66	4.5
IMR-NW-L-10	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-101	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-108	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-109	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-11	NW	NW	Large	9/2015	63.15	3.47

IMR-NW-L-110	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-111	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-112	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-113	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-114	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-115	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-116	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-117	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-118	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-119	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-12	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-120	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-122	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-123	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-124	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-125	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-126	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-127	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-128	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-129	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-13	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-130	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-131	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-132	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-133	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-134	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-135	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-136	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-137	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-138	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-139	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-14	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-140	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-141	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-142	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-143	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-144	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-145	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-146	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-147	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-148	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-149	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-15	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-150	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-151	NW	NW	Large	9/2016	62.9	6.3

IMR-NW-L-152	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-153	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-154	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-155	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-156	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-157	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-158	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-159	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-16	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-160	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-161	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-162	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-163	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-164	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-165	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-166	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-167	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-168	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-169	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-17	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-170	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-171	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-172	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-173	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-174	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-175	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-176	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-177	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-178	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-179	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-18	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-180	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-181	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-182	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-183	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-184	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-185	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-186	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-187	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-188	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-189	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-19	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-190	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-191	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-192	NW	NW	Large	9/2016	62.9	6.3

IMR-NW-L-193	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-194	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-195	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-196	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-197	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-198	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-199	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-2	NW	NW	Large	9/2015	62.15	5.32
IMR-NW-L-20	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-200	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-201	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-21	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-22	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-23	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-24	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-25	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-30	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-31	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-32	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-33	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-34	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-35	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-36	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-37	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-38	NW	NW	Large	9/2016	62.95	3.35
IMR-NW-L-39	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-40	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-41	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-42	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-43	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-44	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-45	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-46	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-47	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-48	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-49	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-5	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-50	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-51	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-52	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-53	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-55	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-56	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-57	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-58	NW	NW	Large	9/2016	62.9	6.3

IMR-NW-L-59	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-6	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-60	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-61	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-62	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-63	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-64	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-65	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-66	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-67	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-68	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-69	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-7	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-70	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-71	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-72	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-73	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-74	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-75	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-76	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-77	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-78	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-79	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-8	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-80	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-81	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-82	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-83	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-84	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-85	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-86	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-87	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-88	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-89	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-9	NW	NW	Large	9/2015	63.15	3.47
IMR-NW-L-90	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-91	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-92	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-93	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-94	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-95	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-96	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-97	NW	NW	Large	9/2016	62.9	6.3
IMR-NW-L-98	NW	NW	Large	9/2016	62.9	6.3

WebTable 6

Name	Sequence
GBYP-RAD_1	GTGTGTGTGTGTGTGTGTGTGTTTGGGGTGATTAACTCGCGGGTTGAGAAGCGTGTCGGGGAGAGAGCAGAGAGAGTCAGGAGGATGGAGGGAATATAAAGCGCTCCCCTCCTCCATCACAGTGTTTCAGTTCATCGGGAGGTTCTGACTCATAAACCTGCAGGAAGTKCGTCC[C/T]GTTCGCTCGGCTTCATGGGAAATCTGCKCTTCTTTACAAGAGAATAAACAAYGTCTTTCCGTCTMTACMWGWRTGAAAACTCCTGGACGTGTCAACTCAACCTTTTTATATTAAAGTCAGTGAAGTCAAATCTTTGATATGAAGCTTGTTCCACATGTGACCTCTGTGAAGTTAATAGTTAAATACTGTAAGTTTAAGAAGTTAAAGTATTACACGACTCTGCAAAAAAAGAAGAAAGCAGAGTTTCATCTAAAGTGAGAAGAGAGAAAAACGCTGTTTCAGTCTGGAGACGGAGAGAAGAAGAAGAAGAAGGTTAGTGTGTG
GBYP-RAD_2	GTATTAAATCTGAATAGTTCTCTGATACTTCAATTATCTTCTTTTGTCAAACAAAACATTCAGTTTATGAAACATTTCAGGAGCTGCAACCAGCAAACATTTGGACATTTTTGCTTAAAAAACAATGATTTGATTTGTTGATTAATTATCTGGTGATTGATTGTTTCAGTGATGATCAGCCTGCAGGTTGGTTC[A/G]CATCAACMTGTTGGAATAAGAACGTGACGTCAACMAGTCAGTGAYRTATCRCTAYGCTACGTTAATAAAATGTTTTATGATGTGACAGCGCCGTGGTGACGTCTGGTTCGGTTCAGACAACAACTCCTCCCAAGAAGTGAAAAATCATCTGAACTGCTTCACTTCCTCAGGTCATAAAGTCAAAGGTGACAGCTAACAGGCATAGCAGCTTCCCGCTAACA
GBYP-RAD_3	TGCAGGCGGTGAACGCASSAGCATATGCTCATGCACCTTAT[C/T]TCATCATCTATACAGATAGTAGCTATGCTTTTGSGATGGTCCAGGATT
GBYP-RAD_4	TCCAAGAGAGACCGCTGCTGCAACCAGCACCCTCAAATCCCCTGCAGGAATAAGAAACKAAGTTTCTTTAGGAAGACGTGGAACTTCTCTGTCCCGCTCTTCTTCACT[C/T]AGTTGACTCTGCTGTTTTCTCCT
GBYP-RAD_5	TGCAGGACTGCAGGATTTATTCTGCAGTGCTTGCCTCTA[C/T]GGGATTTTAGGTTCCTCCCAAGBGCTAAGCGCCCTCTAGCAACCTGTTTAAGC
GBYP-RAD_6	CCCTAACCCCTAACCCCCAACCCTAACCCTTTCTAAAATAATTTTGTTGCACAACAAACAGTCAAAGCAAAACTAAATCCGAGTATCCGATTAGCTTGAGATGACTGGTTTGACATGTCACGTTTGTTCGAGTCGGGGAAATCTTCTTCTTCTGTTTATGGGTCATTTCCTTCGTTTCAGTCTCAGTGCTGATGTTGGTGTCCTGCAGGTTTTTTGTT[C/T]CTCCCTGATAGATAWAGAACTACAMCTGGTGTCAGATTAGCTGCGGCTCATTAACCACGACGGAGGAAAAARVMACATCTGGTCAGACAGTAGAAGAGAGAAACAACAGGGTCAACATTCTGCACAGCACAAACAGAAAACAATACTGCAGACAATAATGTGACACCTGTGATGTGATGCAATGATAATCTGCAACACCCTCCCCAAAATGAGTAAATACACATTATTCTATAACTATGTTCATCCTCATTTCAAGTGGTGCCAGTTTTACAACTTTAAGATGACACATATGAGACAAAAGGACTCTGAGTGTCTTTAAATCAC
GB	CACAATTTGATGTAAGGTCATTAGACCCCCTACACTAATATAATAATAAATCAGCGGATCATGACATTGGCAACTAACCTAAATGGCGATAATACAGCACAGCAGGATGGTCTACATATTAGCTGAGCAAGTGAACATTTTACCTAATTAATTA

YP-RAD_7	TAGCAACAACAGACAACCGAAATCACAATTAACGTTGAACAATACTCTTAATAATGATGTTAACTTATTAGCAAGTTAGCTGCTGACATGTCAACCTGCAGGTGAACTG[C/G]CTGGCTKTTTTGGGCGATGTGGCTAACAASCCAACTAATATATATATCTAGCTGGTTAGCATCACCTAACCTCTAAATAAGCATAAAGACAGCGGCTCAGATAACACATTAAAATCGGATACACACAGCAACAGATGTTCCTTCGACCCTTTCAAACTCGGCTAGGCAGCTAAGGGTGGCCACACACACAGGCGAAAAGGCTAGCAGACGATAACGAGCAGCTAATCACAACTAAATGATGCGACGTACAAAGAGAGCTAACATGAACAGCAGCAAGCGTTTCAACAAAGCTAAATGTGTGACTGACATCACCTACCGGTAAATTAGATGGTATTCGGCTCGGTGCAGCGTTTCACGAAGGCTCAATTGTGGTGGCAAAATGAGAAAGGACTCAGCTAGCTACTTGTTAGCTCATGGCTAGCGCCCTAGCTTGGCTGGGTAGCTGTTAGCAGCAGACTGACTGCGCGTCCTGTGGGCTCGGCTCCGTCTGACAACGCCCGCCCGCC
GBYP-RAD_8	TGTGTGTGTGTGTGTGTGTGTGTGAAATAGGGCACATCAGTGGTGCTGCTGCTGCTCATCTTCTCTCCACAAGCAGCCTGGAGTTTTCACAGGCTTGACATGAAGCTGCCCTGACAGTCCTCCTGCCCTCGTTTGTCTAACATCGCTCAAGCCATTCTGGGTCAAACCTGCAGGGTCACAGATTAGGCCAYTTACTGTACAGTGACTR[C/G]AGCCCACAACACACACTGTCAATTAGCTTCTCTCACAAGTAGGTGGATMAAATTCCCAAACTTTTGACACCTGACTATACTTTCCTCTCTGCCAAAGACTTAAAGGCAGCTATCTGTAAGTGGTGTGTAATTTTTGTCTGGTGACAGTCCTCAGTCTGCAGTTTAGATTTCACAGCACTCTGTAAATTGTGTTAATGTCAACTGAAGGCTGCAGTGTTTGTGAGTGAAAGACACCTCTCATGTGCAGCTGGGGTTAGTATTTCTTGAAGTGCTCCTTTCATGTTAGATGAGTTTGACCCATTGCTCAGGGTCTGCTGCATCTGCATCTGTCTGAGAGCCTCCAATGTGTTGCGCATGGCTTTTGTTGCTCTCTAAACCGGCCAAATGTGTATCTTCTGTGACACCTGAGTGAATATTGAAATGAGCCTATGTTTAAGTTTCATTTTAAGCCCGAAGCACGTGTAGGCCTATATTTTATC
GBYP-RAD_9	CTGCAGACGTTTCACTTGCTCATCTTCACATTTTTAAATTAAAAAAAAGGGGAAAAAAAATCAGTAGTTTGAGTCAAAATTAATCCGAAATGGAGCCGTGAGAGCTTTGTGTTGAATTTCTTGATGGTTTCCGTTGAAGCTTCTGGTAATGTGTCTGGGAAAAAAAACAGAGGAAAACACACAATATGATGTTAAAGTGTGTTTAGTTTTGTTATGTGTGTGTTTAGTATTGTGTGTGTGTGTGTACCTGCAGGTTGTTGTAGTGTTTCTGGCTGCTDCAGTGGAKATCCTTGGCTGTGGTCTCATTCA[A/G]GTAGAAAACAKAGCAGAGATTRCARRAWTACCCCGATTTAGGGACGACAAACTCCTGACCTGAAGAGAGAGAGAGAGAGAAACACAGGTAAAAATAAATATAACAAAACATTTTAATCTAAAATAATTAAACAAAACTACTGTGTCCTTGTCTTACCGAGCGGGTTGTTCGGTTTGAATGGCGGCAGTTTGAAGTCTGCGGCAACGCAAGGAGACTGAGAACGAGATCGCTTGGCTTCAGGTCCGATGAGCTCGCTCTTCCGTTTACTCACGACTAGA
GBYP-RAD_10	CCTCCTTTGGCGATGATGATGGATAGAAGACTACCAGTGTAGTAAGCGCAGCATAGCACAGTATACGTCTAAATGGAGATGGAGGTAGCATATGAGGAGAGAGATGATTCATACAAATGGTGCCCGTGTGCGTAAAGGCCAGAATGACTCTTGCGGCAGATGCACAATGGCTCGCACGCCACTGGTGACCACATACACAATGCATGCGCAAGCTGCTGATGGCGTATTGAGAAGCTACAAATTAAACCCCTGCAGGATTCCTYAATCTATCCATAGAAAATGTCACATATCCATGACAATGCTC[C/G]TCRTAGGAARTGAGCAAGGGCCCCSTCTCTGTTGTCCTGATTTATAGGTAACTGTGTGTGTGTACAGTATTCATGTGTGTGTGTGTATCTGTGGATGAGAAAGAGAAGGTGGGTTAGAGAGTGGTCATCCATCAGCCCCAGGACAGGTCTGTGGATGGTGATTATAGCAGAGGGGATCAGTTCTTCTGATTGATCTACCTCTCTCCTTCCCGGGTCACAGTTCAACAACGACCATTTTACACTTTTCACCGGCAAAAATCCACACCCAGAGCCATAAATCTAT
GBYP-RAD_11	ACAAGCTAAAATGTAAATGAAAAGTTAAGGGATCACTGAAGTGATTACAATTCATCCTGAGGGGAACATGAATGTGTNNNNNNNNNNNNNNNNNNCAAAAAATACAAAAAACTGTGAACCTCTTGATGGAGCTAGAGAAAAGGTCAGTAGATCACCAAAGCCAGTAGGATTTATCATCTGGAAACTGTAAATTTTGTGCTAATTCATTAAGATGTTGAGATATTTTAGAGAACAAGTGAAAACTTTGACCTGCAGGTGGCACTAAAAAGGYCACAGGGTAAACAAAGTCACTAGGACTCATCCTTAAGGAACCATGAATATCTKTAMAAATTTCA[C/T]AGCAATCCATCAAAACTGTTGACATATTTCAGTCTGGACCAAACTGACTGATGGACATATTGACTGGCATTGCTGTCCCTAGAGCCACTCTGCTAGCATGGCTGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTACC
GBYP-RAD_12	AGTGGGCACAGTAAGCAGCAAACTATAAAACAGCCAACTAATATTCACAATGTGGAGAAGTTGATGCCTTTTACTGGTCTTTAATGTCCCTGAAATGTTTCCTAAATCACTTTGTACAATGTCCGTAGCTCTAATGACGAGTAAAACAGAGACAAAGATATAAGAACATTTTTAAAGTTGAGTTAATTGTGTTGAAATTATAAGCAGTGTTTGTTGAACTGCTTCATTTAAAACAAATAAATATTAAACCTGCAGGTTGGAACTTTCAC[A/C]TATAAATGAACGTCTGTAACGAGTTCACACRGMGCTCATTAAGCTTTTCACCGCCAGATAAATCTCTCTGTTTCAGAGTTTTTAATCTGTGTCGGGTTTGACAGATGAATCATACTGAGCATGCTCTGTGGGCGGAGCATGTGCAGTAGAGACTTCCTGTTAACGGCTAACTTCTGGTTAGCTCTCTGCTAACTTGAATGGGAATAAAATAATTTAGTCGTTTGTCTTTTCTAGACTTTCCAAATGTTACTGGAACAAACGGATTGAACGGATTGAATTCTGATAATGAAACGTGTCATTTCATGGAGGACGTATGACGC
GBYP-	GGAAAATTCACTGCTCTGATGGCAGCGATGAGCCCATAACCTGCGGTAAGTTTGAGACAGATTCAGTGAATTACAATGATGGAAAATTTGGGCACAAACCGATACATCACCACAGAAACATAAATCAGGTTTTACATACATATTTCATACATATTTCTTCTAAGTTCATGTTTTTCAATCTCAGTTAAAAGCTTCTTGTGCATGAATTTCTGTAACGCTGAGGTGTGTGGATGCTTCATATGGCTCCTCCTGCAGGTCGTATCTGCTCTATGGATAACGGYGGCTGTAGCCACGTGTGTGTTGATGAA

RAD_13	CCCTGGGG[A/G]GCTCTGTGTGACTGTCCTGTTGGATATAAGCTCTCTCAAAACGGAGCAGTCTGTGAAGGTGTGTGGAGCAAGCATAATGACACTTTATTCACTTTCACTTTTACTGAGGGGTGATTGATTTTACAGCAAGAGTTACATCACAAACATGCTGACAGTTGATGCCAGTATGACTGTAGACAGTGGATCATTTTTGCAGCCGTATGATTGTCTATTTCCAAATTTTGGGCAATCTGTTTTTGATGTGCTGCTCATGCTTTTGAAGCTAAAACTCTCTCTCTCTCTCTCCTCAGATTTGGATGAATGTGCCCTTCCTTTTGCTCCATGTATGCATCACTGCACTAATACTGTTGGATCCTACTATTGTCACTGCAGAGACGGCTTCAAACTGAATGGAAGGTCCACATGTTTAGCTACAGGTAATGATACAGGGATTTCCCAACAGGTATATCATCA
GBYP-RAD_14	GTTTTCAAATGACTAAAGATATTGAAGTTACAATGATATAAAACGTGTTTTCTGCAGTGGGAGAGGGGTTACGTCACCTTTCTCCATCCACTTGAGTTTGCAGCAGTGAAGGATTCTGGGAGCTCACCTGGTATTTAGTGTAATGCGAGCGGCTGCTGCAGTGCTGCAGTTTGGCTTCGTCCTCATCGGCGTAGATCACCTGACACAAGTTACAGAAGTAACCGACGACCGGACGAACAAACTCTGTTCCTGCAGGAGAAACAGACACAACGAGGTGTCAGTGAACGCACYGCTGCTG[C/T]TCCTCCAATCAGACACAAAATGATGTCAGCAGCTYGTACAGGTGTTTACATTCAGTTTAAAGTGAGTGAAACATGTGAAGCAGCAGAATGATGTGGAGACAGGAAGTGTCTCTTCTTACCAACAGGTTTGAGTGGAGCTGCGGCGCCCTCTGCAGGTCCAGTAGCAGCTTTCTACAAACATCACAGATAAACAGCAGTCAGTTTTTTCTTAGAACAAACAAATCTAAAACTCATCACTCCTTCAACTTTAATAACTCCAACAACATTACACATTATTATAACAACATAAAGTACAAAAACAGCCACTGAGGCGTGTAGAGAGATGATTTTACTCTTTAGGTTTGGTGATTTAGGTGCAAACATGCTGGTACAGTCTTTAAAAACTCACTGAAGAGAGCTCAGGTAACGTCAGAGTCAGTTAAATGTGTTTTATTGACTTATTTTGAGTCAATAAAACACGTTTCTATGGAT
GBYP-RAD_15	AGGAGGAGGAGGAGGAGGAGGAGGAGGATGTAGTGGTTCTGCTGACAGACACGATGATCCCAGAGGCAGGAACATCAGCTGTGACGTAAGTTCTCCTTCCCCATGGTCTTTTTAGATACACAAATTAACACTTTTTTTTTAAGGATGAGAGTATCTATGACAACAGGACCACTGATACCTGCAGGGATTGTGCGTGTTTTGTGTGYGTGCGTGTTTATGTGCATACMTGTATGTG[C/T]ATTGCTAGGTGTGAGCTTGCCTGTCTGTGGGTGTTTTTGCTTCTGTAATAGAAGCCCTCCCTTCTGTCCTTCCACCTCCTCTGTGTGACGCACAAAGCAGTGTTTTCTTTTTTTATGAATGAACAGCCGAGGAGGGTGAGAAAGGAGAAACCGAAGCTTTATCTGCCGCTGCTGCTGTTGATGATGATGACGCTGAAAATGTGAGAGCGCCTAAAGGAACAAAACACCAAACAGCTTTATATTCCAACCAGAATGATTTTTTTTCAATTATATATATTTTTTT
GBYP-RAD_16	TCTCAGTGGTTTTGATTTTCCTCAATCTGCCCTTACTACTCTCCCCCCGGCCCATTCATGTATTCTGTCGATTGCCCACCAAATGCTGTCTTGACTCCCACATACACCTACTCACCTGTTCTCACTCTGCCTGTCAAATGCTATTTGCCTAACAACCTATGTGGAGTCCTTCTATACGTGCCCCTGTCTTAAATACCATGTTTGTTTTTTTTCTGTTTCCTTGTTCTGCTTGTTTTTCAGCCTGCCTGCCTGCAGGCACCCGTCYTTGAATAGTTGTTGTAGTTATTACGCTTCTGCCTTTAAAAGAGCCT[C/T]GAGCTCAGAAGCCAAACACRTACACAMMTCAGACATTCAAAGTATCACATGTTCAGATAACAAAAACCTAACCGCATGGTGGCACTCTGAACAGCCAGTTTTACATTTTGATCAAAATTAAGATAGAAGCCAAACTCTTGGATGAATACACCTCTTGTTGCAGGCCACAGCCATTTCTGAACACAGCTTCCCTCCAGTTTGACTAAAGTCTATTAGGATCAGTCTATTTGGATCAGGTCAGGTCTCCTTTTACTGCCACGGGTCTAACGTCTGAATATCAATATGTTCAATACCCAAGTGGATCCGATTGCACCTGACTGTATGTGGTATCAACTGTGATCATGTGGTACGTCACAATCACCATGGGGGAAAACGGTGTGTTTTGAGGAAGTGGAGAATGTAAACTGTGTATCACTGCGAAGAACAAGTTGAAGAAAAAGGAGAACAAAGAGGTAAAA
GBYP-RAD_17	GTTTAAAGGAAAAGTTCAGCATAAACTTCAATCCACGGAAACAAAACACTAAAGTTTGTTAAAGGTTTTTTTTTCTTTAAATCTGCATAAAAAGTTTCATATTTCTGTCTTCTGAGTGCAGCAGTTGATGCATTTTATAATCCAGCAGAACCTAACCTGCAGCCTTTCACGCAGACTTGACATCATTAGTGAAGTGTAATGTATATCAGGCTGTTTTTTCTACTGACTTCCTGTCTCTACTGGTTTCTCCTGCAGGTGTRAGCAGTGAGTCTCTGTACCG[A/G]GCACCTGCAGCCTCCGGTGGACCTGCAGAGCTGCGGCAGGCTCTGGACTCAGGTAAACACACCGTGATCAATGAACTGTTCGTCCAAAATGCCAAATATCTGCTGGTTCCTGCTTCTCAAACGTGTGGAATGTCTTCTTTTCTCTGCTTTAAAACATGATGACACTTTGAAGATGCATTTGTGTCTGAAAAGGAGAATAATGATATCCTGAGGCCAGAATGAGGCAAAGAAATTCAAGAACATGATGCTCATCAGACACAACAAATGGATCGCAAACAATATATGATAATATACTGTGCACACACACACACAGCGGGAGGAAAGAGAGAAGCGGAGAGAGCAGAAGACACTTTAATAAATTCACCTCGTTACATAACAGTGATCAATTTATGCAAAGTCGATCCTCATGTCTGCAAAAGTGTCTGACAGTCAGACCTGGTATTTTCACTATAACAACACCAATAAGGCACAAGTGAGATAAATGCATCA
GBYP-RAD_18	CATCTTTTGGTTTTGTTCTTGGTCAAACAGAAAACCTTTTGCAGACCAAGCCAGTGGTCCTCTGAGGGAATCAGCAGAGCACAAAGAAAGAATTTATGTTTTTCTGACAAATTTTAACCACTTGGCTGATGCTTTTATTCAAAACATGTTTCAAAGCCATTAAATCACATTAGGTTTGCATTGCCCCAAGTGTGGCTCTTTACAACAGCAACTGTCTGCTTGCTGCAAGATGCAGGTATTTTAGGCTGCCTGCAGGTAAGTTAGTCAATGATTCAAGCTCAGCTAAAAGTTAAAAGTCACATTTTGTGCTTGTATATGGAAATGAAGTWTCT[A/G]TTTGTCTGCACAGTTCTCTCCTTGGCACCACAACCTTATTTGCATAGATTTTTATTAAACAAAAACCTTGGGATATTTATAATCACCCTGTGTTTAGTAAGGTCTGTCAGTCATCTAAACTTAGACTGAACCTCACAAGCCTCAACAAACCCAACCAGTTTTAAACAGTCATAGGATTCATAATGACTAACAATGACACACACAGCAGTTAACACAAGAGTTGAGTACTTAACTTACGTGTCAGGCATCCAAAACCA

GBYP-RAD_19	GTCAAAGCCTGTAGATGATGTCTGAGGCTGGAAGGAGCTGTATGTTAATATGGAACCTGAACCAGCTGAAGCTGTTGCTGGTAAAGGCTGTGTAGGAGGCTGTGGCTGCAGGTACTTGCCAGAAGCTGCAGGCAGACACACTTTTCAGGTGACTGCTGTAGGCGAGGGCTAATGCAGCTGCCTGTCACCGAGGCAGTAGGCAGACATAGAGAGAACAGCTATGGAAGTGGCTTTTTGAATCTTGGGAGCCTGCAGGTGGGTGCATTCATGAAATGGCTGAGACTGCAGCTGGATGAACAAAGCTG[C/T]AGACAAAGACTGACACTGGGACTGAGTGGTTWWSTGTGTGCAGTAAAGGCTGCAGGTGGAGTATTGTGCTGGAGAGGGAGAAGCCTGACGCTGGATGCTGCTGGTTGTCAGAGGCTCTAAATGGAGGATGACGCTACAACTTGCTGCCAGAAGCTGCAGTCAGCTGGCTGCTGTTAAGATGGAGGCCACGGCTACTTTGCAGTATTAGGTGGACTTTGACTGGGCTTGGCTTTCCATGAAAAATCAGAATACTGATAAATTATGGTCTTTTTTTTTTTTTTAAT
GBYP-RAD_20	TTATATATGAGTTTAAAAGATTACTCGATTAACCATGTGATTATTGATTTGCACAAATCTATGCAGCATCTGCTGCATATTACAAGTATCAGTGTTACAGGAAGTATTGCACAACAAGTTTAATCTTAGTATTTCATTCCCTGTCTGTCTCCAGGTTTCATCCCAGTGTGCAGTCTAGGTGTGTGTCAGGTGGGGAGGATGAACTTTGGTAAAGACGTCAGCACTCTGAAATACTTCACCATCTGCGGCCTGCAGGAAGGCTATGAACCRTTCGCYGTCAACATGAACCGGGATGTCAMAATGTGGCTCAGCAAGAGGCTGCCTCAGTTTGTACC[C/T]GWMSCCCCCAACCACCAACACATAGAGGTGAGAGTCACCTGGAAGATGCTCTGCATGGTTTGGAACATGTAGCTATCAGCTGGTAGAGAAAAACCACAGATACTGTAAATTACTGGTAGCAGTCAGTGGTAGTGGGCTGAGAGCTTGACTGAAATTAAAGATCCCCTTCATACTCATTTCAAGACATTTATTAATCATTTATTTAATATGTTTTTTTCCCACAAAAAATTCCCGTAAACTACAGAAAAAGTAAG
GBYP-RAD_21	TCCTCTTATTGTAGAAGCTGGTAACTGATTGTTGGGGTAGACAGTTTAAAGAATCAATGTTCATTTACAAGTCTGTGAACACCCATCACATTAACACATACACACACATACACACACAAACCACCGCCCAGGCTGACATAGATCTAGATGTGATTCAGACAGAAAGGATTGCTATTCCTGTAAGGGCTATCGACTGCGCTCTATTTTCCCGTTGTTGAGATAAGACCCGCCCACCCAGAATAGTTTGCCCTGCAGGAYGAAATCAGCTGATAG[C/T]ACCAACGACCTGTCCATCAAACTGTAATGWACCAGTCGGGCCTCTATTAAACCAAAACCATMAGWHAGACAGATGGAAACCCAGCGAAGCATGAGTAGAGGGACTGAGTCACTCTTCGGTGATATCTTTCCATCTTCTCCTCTCCTCCTCTTCTTGTTTGTATTCTTTCACTCTTCATTATTTCATCAGGTGGTTTCATTCGTATTGAGATCAATGTCTCATGACAGATATGGGCATAAGAGAATGCATAAAAAACGATCATCCAAATAAACAAAACAAAGCAGCAATCAAACAGCCAGACACCCATGCACTTAAAGAAAAACAAAATCAAACCTCAGAGAAAATATGCGACCTGAGTTAATTTAAAGTGGTTTTGCTCCGTCTCTCGATGCATACTACGAGAGACCTGGGATACCATGTTCAGAATTTGGTATTTGAATCTGACTCACACCATAAATAATACATTTTAGAGCAAGAGTATCTTAAAAATCCAGCC
GBYP-RAD_22	CCAGCTCTCTCTGCAGGTCTTGCACACACATACACACAGAGACTGTAATACACATCTGCATTTTTTTTAACTCTGTATAGTATGTATGTATATACATATATGTCTGTGTTTTGTGTCCTGATGCCAGAACAACAAAATCGAGGAGGTAACAGTGGGGCACATTTCTCATCTGCATCAGCTTGAGACTCTCAACCTTCAGAACAACTGGCTCACCACAGCTGGTAAACACAGCAACACAATAGAAATCTCCTGCAGGAACCTGGMGCACAGCGGGAGAGCATATTACAGACCTGTTGTATACAAAGTTGTTCTKT[G/T]TGGGTCTGTTGAATTTCTGTTTGTT
GBYP-RAD_23	TTTGTCAGCAGCAAAAATGGACAAATATATACAGTATATGCTGATTAATAACATAGATATAAGATATAACTTAGATATAAATAGCTTCATTTGATCCATTTTAGATTTTTTCTTCGTCTTTAAAAAGATTATAAGGAACACAGACAAAATCAGGGCTCATAATTCTGGTTTTATTTCTGTAGGATTGTACTTTTCATAAAACCTAAGTTAAATGTTGGTAATATGTTAAATGCTAAGTGTGTTTTTGGCCTGCAGGATCAGTAATATTTTAACCCGCTMTCCATCWTGTTATTTAGTCACCAATATTTCAAGTGTTTGTTTGTTGTTTTGGCCA[A/G]CDTTATGACTTTCGTAATGATGCCATTTTTCACATGATGCAGCATTTTTAAGTTTTGTTATTCTGTATTTTCTCATGTGATACTGTTTAAAGGAATCGTACAAATGGAGCCCGTGGACAACAAGAAATGGGACAGTGAAGACACTCGTGAGACTGGGAATGCAGGCACATTTAACCCAAAACTCATTCCTATCCAGAGAGACAGCTACCTGGGTGAGTTTCTACTCTGGTCGGAGTCGGTTTGTGGTAGTCAAGTTACATCTTGCTTCATACATCTGTTAAGGTTGTGGTTTNNNNNNNNNNNNNNNTTTTTTAAGAATTAAGAGGTACCCAACAAGTCTGATTTTATTCTGTTATAAGGTATAAATTTTCTGTCCTCCAGGATTTTCCATTGACTCAGGAATGGCCCTCATAAGGAAGGGTGAGCTGACGATA
GBYP-RAD	CTGACTGCCAGCTCCTGCAGGAAGTGGCCAAACAACCACTG[A/C]AGGCAGAAAAGTAACACCCCCYTCCATAAGAACGGKGTTCTGCTGAGAASCTAGTATWAMMMWATTGTTATTAACACCGACGTTTTAATTTAAGCAGGATTGTGGTCAGTGAGGACAATCAGTGAAGATACCCCAGAGCCAACAGACATTGAAATGCTGCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAGAAACTCACAGGGCAGTCTACCCCCTCTGCATTATCCTGCAACAGCACCAGCACCCACATAGCTGGCATCTATGTG

_24	
GBYP-RAD_25	GTTATCCTGATGTGTTGAGGCTGCAGCAGCGACGACACACAGCAGGAGGTCTGAGTGTGTCAAATCGACATCAACTCAAAAAAGTTGCTGATCACATGTCGATCCGCTGCTGTGCTTCTCTGTCGCTGCAGTAAAAGTTGTTTGTTACACACAGTTCCTCATAAGAACAGGAATACTGAAGTGTATGAGAAGCAGATAAAAATAAACCCTCCGTAAGGATAAAACCAGATCTCTCAGGCACCGTCACACCTGCAGGCAGTGAGTTTCTGACTAACGAGACAATAGTGCTGCTCCCTTTGAAMGAGGAGTTTTCTGTATTTTTAGCTTTTCTT[C/T]TGCCTTCTGCACTACCTCTCTTTTATGAAAACTTTTTTACAGAGCTTAAAAATTGTATTAACTGTGTTTTTAAACTTTCTTTTTTGGATATATAATATAAGTGTATGATTTAGGTTGATTTTAGTGGGTTGAATCTTTTATTTTATTTAAGGCTTATTGAGATTTATATCTTTTCTCATGTGTGGGAGGAACAGATAACTGAAGATATCACAAAATCAGCTTTAATCAAAAAATGCAATTAAATAAAATTATAAAAT
GBYP-RAD_26	TGTACNNNNNNNNNACTTTAACATGTGAGTTAACACGTCTGTTAATGTGTATTAACTTGTGTGTTACCCTGTGTGTTCAGGTGATCCTGATGGGTTTGGACTCGGCTGGAAAGTCAACTCTGCTGGCCAAACTGCTGACAGGACAGGTGAGACTTCTCTCCACAGGTAGTGACTGTAATGTTGGATATAAGCTCAGTGGCAGAGAGTGAATATATGAGAGTTTGTCCAGGTGTGACTGACTGTCTGAACCTGCAGGTGATGGACACGTMACCTACTGTCGGATTCAATGTGGG[C/G]ACTTTGGACCTGGACAAGAACACGTCTCTGACTGTCTGGGAWGWYSGAGGACAAAAGAGCATGAGACCCAACTGGAGGTAAACATGAACCCAAACAAACAAATCTGCTTCTTCTGGTACCCTAACCCTATGTGAATGACTGTAAGGCTCTGGTTTCATGTCGTTACTGATGAATCTTCTTCTTCAGGTACTACCTGGACGACTGTAAGGCCCTGGTCTTTGTGGTGGACAGTAGTGATCCAGGCCGGCTCCCAGAGGCCCAGAAGGCCCTGAAGAAGGTCCTGAGTGATGAGAAGTTACGACAAGTTCCTCTGATGGTTCTGGCCAACAAGAAGGACCTGCCCAATTCCATGACCATACGAGAGGTAGGAAACACATCCCACAATGCACTGTGACATCAGCAAAGAAGAACCCAGTTACCTCAGTTGTTGATAAACATAATAATGTCAAAACGTTTGAGAGGAAGGTTGGTCCAGA
GBYP-RAD_27	AGAAACCTTAGATTCAGATGTAATTCACCTGATAGTTCTTGATCCCAAACATCCCACAACCTGCCTCCTGATTAAACATTATGATGAACAACTCCTTCATCCTGGACCAGAAAGGGTCTTTGCAGTCATCCACTGTACTTACTAGATTCTCTGTGGTAGGTAAGCTGTGAAGAAACATCTGTAGTCATATTATAAATGTAGGAAATGGCGTACAAAACCTGCCTATCCTAAGGTGGTGGACTTACCTCCCTGCAGGCTGTGACTATGRAAGC[C/T]TCCCTTTTGGTCAACAGGTGTTGAGTGCTTTGGTCCACTCAACATCAAGTTACRGAGAAGACAAGAGAAAAGGTGGGGAATTTTGTTTAAATGCATAACCACTCACTGCACTCATATAGAGGTACTCACCAGTCTTGATACTGACAGTTTTCTCATGTCCCTTTGCTGTTTCATTGCCTGTAGAGGGTAACCCTATGAGTTATAATCTGACTGTGGTACCAACTTTAAGGGAGGAGAAAGGGAGTTCAAAAAGGTATTCTCCACCCTCAATCCAAATCTAAAGGAACATTTAGAAAAACAACAAATAAATTTCTGCTTCAATCCACCAAATGCCCCTCATTTTAGTAGTATATGGGAGAGAGGTAAGATCAAACAAGTCTGCCTTAAGGGTCATATTAGGGACTCAAATTCTAACTGAAGAAGTCTTAAACTCCAAACCATTGGATATGTATTTGTGGATGTAGCTGGTCCTGATCCTATAACCCTAAATCTCCTCC
GBYP-RAD_28	AGTAAAGGTAGAAAGTTAGAAAAGAAACAGAGTTGTTGATTTTAATATTATTTGTGTAAACTTTTTATAAAACATGTAGACTGTATCTCTCAAAGAGGTGAATAATATGTTTTTGGATGAAATGTGAATACCCTGCCTCCACCCAGGCTTTCATTCTGCGGAGTCACAGAGAAAGGCTGCACTTATTTGGCTTCAGCCTTGAACTCCAACCCTTCCCACCTGAGGCAGCTGGAACTCAGCTACAACTACCTGCAGGACTCTGGAGTGAAGCTGATCTCTGTTCATYRGGACAATCCTCTCTGTAAACTAGAAGAACTCAGGTAAAACAATTTATCATA[C/T]AGATTTTGAAATCTTTCTGGGATGTTGTTGTGGCCCCACCCCCACCACCATCCACCACTGTATGTTTCCTAGGTTTGAATCTCTTATGGTACCATCAGTTCTTTAATATCAACAATACAAAGAGCAAAAATGCCATGAAAATAGATTCAAGAATATTTTTGAAAAAGAAAAAAGTTAAAAACATCATTATACCACATGGCTTGTTAAGATGGGTATTTCTTAGAACATGCAACATGTCTTGTGGTTCAAAA
GBYP-RAD_29	TAATCATTCAAGTGTGTAGGCACACTTTTCTCAAATATACAGTACCATGACAAGCACATTATACTGTATATAGATTTTAAGAATATACACATTTGAACCAGTTCATCCTTAGCAAAAAGTTACAGCAGTATTCATATAGTACAGGGCGACTCTGCATGTTATACTGTCCTGGTAATGCTCATTGCTGGTAGGTGAAGAAAAGCAGCTGGTGACTACGTGTGTATCTGGGGGTAAGCAGTCCACACCCTCCTGCAGGCCAAGGCARTTAGTAGCAACGAGGGCTGCAGTRCAGGGAAAATTGCCCCTTTCCCACTTG[A/G]GAGAAAATTTTAAAAAGGKRRCACACACAATTCTCCAAATATTGCAAAAAAAAAAAGGCAGTGTTGTACTATATACTGTTACTACTACTAGTGTGTGTGTGTGTGTGTG
GBYP-RA	ATTGTGTTTGAGGGTTTGGTGAGTGAAGCTGGGTGGAGTTTGAGCCGGGGCATTCCACATCGCCAAGGCCTGATGAGACATTTGCTAGACTCAACATATTTTCAAAGTGACATCATTCTAACAGTTTCATATTAATGCTCATTTTGACTCACAATTTTAAAAAAGAATTGCCCTGTTGACCCAAGTTAGTCATGATATCTGTCATGGAAATTCTTCTTGGTCTGTCTCTTTAATTAAGTCATCACAAACCTGCAGGTTTGGTAAAAATGAGTGTGCT[G/T]TTTGCAGACTATACACATTACCTAATAGGAWTTCAGGGTAAAGAAGTTTAATAAACTTTTTGCTGCAATTTTTAAGGCACCAACCAATGTGCGGTGTTTAGATATTTTGCTGATCTCATTGACTGCTCACATCCTCTGTTTGTATTATATTTATTGTACTACTTTTTCTTCATTTAAAGCAAGA

D_30	CCATAACTGTAACTGTAACTTTTGCTGTCATTGTGGCCACAAGTAGAAAATTACAGATACTGAATAAGCCAAGTATAAATAAGAAAATGAATGATGGCTAAATTCCATGTAGCTGCTTCAGTTTCATGGTAATGACTTGTGTATGCTGGCTCACTGTTACATTGGCTGTGTCTGAAATCACTCCATCGTTCACTCATTCACTCCTCCCTATAAAATGGACATTCAATAGTGACCAATAAACTGAGATTTCAGAGACTTATAAATCATAATTATTTCCCTTCATCACTGAAAGATTAGTGTCTCTAGAC
GBYP-RAD_31	ATGAGAGGTTCCAACTCAGATGCCACTGATGATGAAAGTGCAGGCAGGGAGAGACTGACTGAGCCAGTGAAGAAAAAGTACTACTTTCAACCACAATGGCTAATGCAGTACCCACTGTTGTAGTATGAGGGGAAAGCTATGCTGTGTGTGTATTGTAGGCCCGTCCACTGCAGGCAAATTGTTACCAGGTCAACACAGTTTAAGCTTTAAACTTTGAAGTTGCACAACAACAGTAAGAAACACAAAACCTGCAGGGACCGATGCATGA[C/G]CCGAAACACTGAGCCCCTCCTGATGTCTTTTCAGTGGTTAGATGAGAGAAATTGCTCAACGGAGGAGAATGAAATGGTCATCAAGTTCAACACTGCCTATAACCTAGCGAAAGAGGAACTCTCGTTCACAAAATCACAGATCACACTGATAAAGAAGAATGGATTGAATGTGGATCCAACCTATGCCAACGACATGGCCTCTGCCCAGTTTATAGGAATGATATCAGACAAACTCTGGGAAAAGATTGGTGACAAAATTGCCTTCACCCCTTACCTGTCATTTATGATAGATGGTGCCACCAAAGAATGGGAGATTGTCTATGCCCATGTCATTGATAATGGAAGACTGTTCAGTATCCTAATTGACCATATTGAGGTTGAACACGCCCATGCAGAAGGTAAGGGGTATGTGTTTGTATGTACTTCTGTTTCCATAAAATTATAAATAATGATAATGATAATGATAATGAAAAATGCTCTATAAGTTAATTATAATAGCC
GBYP-RAD_32	CCTCCTAACAATGTAAACAAATAACTGTACGAAAAAAGTCTAATGATCATTTTAATGATGCTTTCTTAAGTGGAAACACTTTTTGGGCCCTGACTGTATACATTTGGCCCAAGTCTTTGGTTTGGCTCCCTGTACGAAATAATCACATTTCATTCGACCTTAGATAAATGCTGTTAACCTGTCTGATTTACTAACGCTAGTATTACATCATTGTAATAATGAAGAATTGCAAATGCACCTGCTGCCAGCCTGCAGGCTAACTGAGCAGGCCCCTCACCAGGATAGCCAGCTAACAGTAAACAGATGWCAACATTAACTACTGCTCCACTGGTTTTC[C/T]ACACAGTGAGCTAACGTTACACGACAGAAACCCCCACAATCTTCTAAAATAAAAATTATAACAATTACAGGACAGGAAAGCCAACGAGTCCGATCCGTTCAACAGAAAACTGATCAGTAATATCAGCTGCTCTAACGTTACGCCATTTCAGGGGAATATTGAAGGCTTTAGCTCGACGTTTTGGCCTTCTCTGACAAGAAGAAACTAAGTTAATGTAAACTATGTTACTTGATTATGCATCCACAACAAAAGG
GBYP-RAD_33	ATCTATCTCTCTATCTATCTATCATCTATCTGTCTTTTATAAACACATAAGCTATAAATGTACTTCTTCCATCTTGTTTCGTAGCAACATTCAGCAGAACATGTGCTCAATAAAAGTATCATAGATCTCACAGGAAACATCATGAAGTTTATTTTCTGTTGAAACAGGAACATGTGACATCATCATAGCAGATAAATCCTGCTGCTCACTAACACACAGCCTGCAGGAAGATCGAT[A/C]ACAACAGTTATCAAGAAGCTCAAAACTAGAATAAAAGAAGAYWCAGATTGTCCATCATGAGACTGATGAARWKATAAATGAAGTTCTCTTCATGGTTGTCACTTCTGTAAACGTCCAAAACAAGTTAGAGATAAAAAGACTGAACATCCAGACGTGGTCAGGCTGCTCTGAACTGATCTTTCAAAGATGTACCAACTATAAACCTGTAGTCCTCATCCATCTAACAGGTTCACACACCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTGCACAGAGGAACAGACATCACATGTTTACTGCGTGTTGATTGGTTTAAATGAGTCTGTCAGACCGGCCTGGAGGCACATCTGATAGAAGTGGCCCTGCTGCTGGAAGAGCTGGGAGGGGGAGTCCATCTCTGCGATGGAGCCTCGGTCCATCACGACGACCCTGAGACACAGAAACAAGACGAATCAGACCGACGTCCGCAGGTTTTAACAAACAGAATCTGTATTAAAGGGTC
GBYP-RAD_34	ATGCTGAAGCTTAATATCCTTCCCCAAGTAATATTTAATTTCTTTCCACAGTCTTGATGACATAAAATAAAAACAGCCAAGAGGAACTCTCTGTTGGAAACAGTCTAGATGTAAAGCTGGAAGAGCCTGGATAGAGTAAATAACTGCCTAATGCAATATTATCCAGTGCCTCTCCTACAAACCACAGATTCCTCTTCTCCTACAGATTCTTAAAAAAAGGGAAATCATATCATCATAGAAGCATAAACCCTGCAGGRCAGTGTTGTCTTTGGGTGCT[C/T]ATAAGTCCCCTTTATAAAAAATATATAAKTCATACTYTCAGATTGAATTSAGCTACTGGAAATAAGGATCCTCACTTGTGATGCAGGAACTGTTTCATACTGTGTATGCTGTTGATCTCCTACACTACATCTGCAGTGCACATACTGTGTCAAGTAAGAGAGGGATATTATCTACTTTGGTATGGTTCAGTCAAAAAATTCCACATAGGGTAAATATCATCCCCTCAAAACTTAAAATAGATCAAAACCCCTCAGATGCTGGCATCTGTGTGAAAGTTGGTACTCTATTGCACATGCTGTGGCAACACCTGG
GBYP-RAD_35	CTGACTGATTGCTATGAATGATTGATTACTGTTAATGATTGATCTGATGTGACTTTCGATCGTTTACAAAGATCAATAACAGAGAGATCGATCAGAGTAAACGTGGGTCCTCACCTGCATGTTGACTCCGAAGGTCCAGATGTAGAGCGAGTAGATGGGTTTTCTGAGCCATGTGGGGAGTTCCACCCCGTTCAGACGCCCCCAGGCCCGAGACAGGAGGCGGGTTGGGAAGGAGCGATACAACGCCACCTGCAGGGCAAACACMCACACAGCARCTGTAGTGATTCTCTCGGTTCAACACGATCACTTTTATATTTTACTATTGGAYA[C/T]ATTTACAGTTTATAGACTGAGGAATAAGAAGAGAGGAGTTCTCACAGATGATGGAGAGGAAAGACAAAAACAGAGGAGGTACAAGAAAAAGGTAAGGCAGAAGAAAGAAGAGGAAAGGAAGAACGAAAAGAGGAGGAAGTTAATGAGCATGACGAAGAAGAGTTTATCCATTCATTCCCTCCCTCCCTGTTTCCCTTCGTCCAATCAGAAGCCAGTCGGCAGCCGCTCTTACCCGATTGGCCAGCGGCCGCAGAGCACTG
GBYP-R	TGCAGGTGCATGCTGCAGTAGTTGTCAGTGTTGTTGTGTCATC[A/C]ATGTGTAGCCCGTGGAATTAGATGCCACACYRGACACARWKMYWYMTTGTTGTGTCATCCATGTGTAGCCCGTGGAATTAGATGCCACA

AD_36	
GBYP-RAD_37	GGTCACCACTACGATGATCATCATCTTCACCACCTGCAGGAGAAAAAAKRAAAATGCAAAAAAGAATCATCAGCAGGACAAAAACACAAATAG[A/G]GAGACATTTTAACATGTCACAGTAGGAAATGCACAGCTAAAATTAATGATTTAGCCATTTAGCTGCTTCAGTTTCAGGGTCCTG
GBYP-RAD_38	AGTCAAGTAGTCCGGTAGCCAAGCTTGTTTGTATGAAAACTACTGAGGAGAGCTCCAGGAGTCTGAGATGATTTTAATGTGTTTGGCGTCTCAGCCAGATTAACTTGATTTTGGGGGGTTTTAAGGTTTTTAATCTTAGTTTAATCTTAGTCGAACACTTTGCTTGTTGGGTGGTCACATTAATTTGAAATTTGAACTGTTGTTCACAAAAATTCTGTGTGTACGTGCAAGACGACATGCTTTATACTCCTGCAGGGAGCACTGGCAAAATTMAGTCTAAACTATTGCATGCCMTGYTGCCCTTT[A/G]TTAACGCCAAATGGAGGGAAATRKWGATMRMYWKATAATCACAACACCAAACCATCTGCGAAGTAACAACTTTTTGATTTGATACCATAGATCATGAGTGAAAGTGAGGCTGCTTGCTGACTTTGTGAAATGCAACTGCCGTACTGAAACGTCACAATGACAGCAGATCTGAAGTCATCTGAAGTCAACAACGCCAATTCTGCAATGTAGTCTATGGTTGAATTACATGAAAATGTTACAGATGTTAAATGGTGTGATTTATTTCAATCCCTCTTGTGTCACTA
GBYP-RAD_39	AGAGTGTATCTTAGCAACCACACAGTACAAGTCTCTGCCTTCTCTGCCAGAAGCAGAGGATGGACCTGAAGAAGAAGAAGAAGAAGAGTTTTAACAGACCCTGCAGTTAATAAATGATCTGCAGATGTGATCATTAAACACTGTTTAACAACACGCTGTTTTTATTTCCCTCAATCACTTCAGCCAGCTGCTGTCAGAAATTTCACGTTAAAGGTAATTAATCCCTCTCAGGTTTTTATTGTGAAAAACCTGCAGGAGTTAAACCTTG[A/C]AACGCATCACTTCCTGYMTGTTTTTAGAAATAAAAGGGAGAAATTAGAAAGAAATAATCAGAGACCTGGTGGGTGACCACCACCTGGTGAGTAACCACCGCC
GBYP-RAD_40	AAACACACACACAAACACATACACACAGAGTGTGTTGTCTTGTTTACCAGCCAGTCTTTTCATCCAGGCCCCCTCATCTATACCCAGGTTATTGTAGATGATCTTTAGGATGTTTCCCAGCAGAGTGTTCATATGTTCAGAGGTCACAGAGGTGCAGCAGCTGTCTGCTCTGTCTGGGTTGCTCTCTGGTCCATGTTCCCACCAGTGAGACATGTAGCTGCACAACATTGGCAACACCACCTGCAGGAAAAGCAAAAATACATACTAAAGAGTTTGACAG[C/T]ACACMCATACACATGCAAGTGTCAGMTAGACACTATTTGGGAARAWMRRWGGATATATAGAGAAAGAAAGAAAGACTCAAGTTTACGCAGCAAGGATTATATGTGTTTTTAAACGTTTTTTGGTTTGTCATATATCCTACCTCCATGACATGGGGCATCTGAGTGTATCTCATGCCAGACTCCGCCAGCTCCATGATCTCCTCCAGAGACTTCTCTAAGTTTGGGATCAGAGGACAAACCTCCCCAACCTGCCCTGGAAGCCCTAGAGCTGGAAGGCAGACAGAGAAATGCACTTTAACACCAAAGATGAATTAAAACATGGCTATAAAGTTCAATAATTAATACATTAATTATTATTATCAATATGTCTTTGTGAACAACTTTGTAGCAAATTAGTGCTGTATAAAAAACCTTGATGAATACTGACATGAGAGGGGTAGACAGAAAGAAGGACAGAGATTCATGATTTCAAAGAATGAA
GBYP-RAD_41	AAGAATTAATATAAGTTGCAATACCTGTGTAAAAGTGTTTTAGAATTAGTTCTGCCTCAGTCCCCTGTTGTGTTTAGTCTAACATTTGAACTGTCAGGTTCAACATTGATAACAAGCCACACTTTAGCCAGCTGGACTATCATAACAGCAGCCCTTTCAGCCATTGATAAGGTGCCAAATGGCCCTGTAGGCGATATCGAGGCACCAGGCTTTTGACCTTCCTGATCTACTAAACAAAATCACTGGACCCTGCAGGAGCTCTCTGGTTCAGCAAATTGCTGTTTTGAAATGACCAGTAAAATTCCACACAGATTAAATATC[A/C]TGGTGAGATTTKGKKGRWTTAAACAAGAGGTTTTGGGCTGGGATGTTTTGGCTACCGGTAAGATTACCTGCTATGTGGTCTCCCTCTTGCTCAGAGTCTATAGCAGCCACACACTCTCTCTACCTGACAGCTCCATGGTGGCAGGACAAAATAAAATCTTCTTTAAATTTTATCTTAAAACTAAAATAGATTAGAGCTTATGCTCAAACAATATATACTATTATTCTCAACATTTTCCATGTGTACAGGCCAAAACAAGATCCTAATCCAGGGTAAAGAGTCGGTAATAGCCAGACACATAAAAGGGCACCCAATAATTGAAGCATAAATGTCTCTGCAGCTAATGTTAGGAATGGCGTCAGCATGCTTTCCAGCTTTACAAAATGTACCAAGTGACTCTACGTATTGCCAAATGTGTTAAAGCTGGCAGAGCAAAGCAAGCATGTGC
GBYP-R	TAGTTTACTCTCATAATTTGAAAGTTCTTATGTGCTCTGAAAATAACTTCCCACTCAGAACATTGTCTAACTCAACTGGAAAAGAACAGTTCAAAGCAGAGAGCCATGTCTGATGTTTAATTCAAACTGTCTTTTAACTCTGAGCCACAGGAAAACATCTGGGAAAGTAATCTTCAAAATTAGAGGCTTTCTTAAGGTAGTGGGCAGAGCAGCTCATGTAGTGTGCCTCAAAAGAGCCGATGCAGTGTCCTGCAGGATGTAGTCAAAGATCTTTGCCTGGTGTCTGATTTKTCTGATTGCTCTCTCAGTGTCACCTGGAATCAGATGGYCWMSWTCRRA[A/G]GAATAGTTTGATCTTTCTGTGAGATATGCTTATGTGCTTT

AD_42	CTTGCCAAAAGTTAGATGGAAACATATGTACCACTCTCATGTCTGTGTGTTGACTATGGAACTATGGAGTCTAGAAGTGATTAGCCTAGTTTAGCATAAAGCAAGGCTGGACTGGGACAAAAATTCAGGCCGGAATTCTTACACTTACTCAGGCTACCTCATACATCAAGGGTACTCAATAGGCAGACTCTGGTCC
GBYP-RAD_43	GGTATCGCTGGAGGAGCTGGTGCTGCGGCGGATGGGCGGCTCAGTGTTGGCGGTGGACCTCAGCATGACGCCATGGATGGGGCTGAGGGACTCGCTGGAGCTGGCCGGCGTGGGACCCCCGCCGCTGCTGCCGGAGGTCTGCCGCTGCTCCAGGGTGTCCAACACCACGTCGGGGGCGTGCTTGGCTGAGCTCTGCCGCTCCAGCTCGCGCAGCTCGTTAAGAGCCGTGTTCATTGTTTCCTCTATGTCCTGCAGGAGACAAAGAGAGTGTGTGTAAGAGAGGAGG[A/G]GGGSGGGRKGKGGAADGATGATAATGACATAGGKGAGAAAAATKAGTTGGACACAGGAAGGTTGGTGTTAAAAATGAGAAAAAAACCAAAAAAGACAGGGTGGGGGAAGAAGAAAAAGAAAAGCAGAGATGATATGAACAGCAAAGACGTGAGAGAAGGGATAAGGTAGAGTTAGGCTCGGTACGAAACATAAAAAGCAATGTTAACAGAGGACCACAGTGACAGATTCTCAAGAAAACACATAGCATGCATTATACATGCAGAGAGTTAGTAGAGAGTATTACTTTGCACCGACACCCTCCC
GBYP-RAD_44	TGCAGCCTTCAGTTGACATTAACACAATTTACAGAGTGCTGTGAAATCTAAACTGCAGACTGAGGACTGTCACCAGACAAAAATTACACACCACTTACAGATAGCTGCCTTTAAGTCTTTGGCAGAGAGGAAAGTATAGTCAGGTGTCAAAAGTTTGGGAATTTGATCCACCTACTTGTGAGAGAAGCTAATTGACAGTGTGTGTTGTGGGCTCTAGTCACTGTACAGTAAGTGGCCTAATCTGTGACCCTGCAGGTTTGACCCAGAATGGCTTGAGC[A/G]ATGTTAGACAAACGAGGGCAGGAGGACTGTCAGGGCAGCTTSATGTCAAGCCKKKRAAAMSTCCAGGCTGCTTGTGGAGAGAAGATGAGCAGCAGCAGCACCACTGATGTGCCCTATTTCACACACACACACACACACACA
GBYP-RAD_45	ACAGTTTAATACCTGCAAATTACTCAGAAAACTTCCGGTATAAAATGAAGCGGTCTGTAAAATAAAGCTTTACCTTAAGTTTCACCTTGGTTCGATGATGTAATGGTGAAACTAAGCATTTCTCTGTGCCGTGCCTGCTATGTTGCCTTACATTATCTGTCCTGCAGGGGACAGT[A/G]TAGTAACGTKYGAATGATRTCAATGCCAACAGCCTKAAGGATCCTHCTATGAGCATTTTAATAACCMTGCACTCTCATCCTAGGATAAATTAAAAAGAGAGCGACAAGCTCAGCTCAGCCTGAGAGAATGAGTGTGTGATGCATGTTCATACGTTCAAGAGTTCCTCAACAATGTGAGTTACTATTGATCAGCCAGTATCAGTTATTGTAAGCCCAACTTTGTGAACACAGAAATGAAATGGGAGGGACCCACAGTGTGAATTTTGTTGATCATTAATTAATGATTTCGGAATTAAAATATGGTGGAAAATATTTGTCTGTTCTTG
GBYP-RAD_46	AAAGCAGATTATGGGCTGCTACGCTAGATGACCGTTTCAATGCTCCGCTCTCTGTGTTTTCTGCGGCTTGTGGCTTGAAGTCTATCTATACACTGGGCAGCCTGAATTGAACCAGAGAGGCTTAAAAGAAAGCTGTAGACTTATTGACAAATGAGCTCTGTTATGAGCTCACCATGTGACAAACAAGAAAAGTCTGTTTCAGAGACTCTCAGAAGATTAAAAAAAGAAGTTTAAACCATTTTTCTGTTCCTGCAGGACTKAGTAAAGACTCSCTGYCCTCRTTTTTTGTGGTTTAAGTTTTTATTTCTTCAGGAGTACAATGTTTAA[C/T]ATCTGGASATATTAAAGTGTCAGAATCAGAAGGGCAGCTGTAACAAGCTCCCATCTCTTTCTATTACTCAACAGGAAATTGATTGATTGATTGATTGAGTTTATTTGCCCCAAAGGTTAGATGTCACTGCTGTTTTAATGCTCCTGCAGCACTGGAACAAACCTGCTCTTATGTAAACATTCAAATCAACCTCATGTTAATACTCATTCATGACCTAACACAGTGCATCTTTCCAAATAAAGCTGGGATATATTGATTTAAT
GBYP-RAD_47	TGTCTGATTCTCAGCTGCAGATCGGTCTATGTGAAGCTGAAGGGAGGCAGCAGTCGGGAGCATCTTGCCTAAATTAACTCAGTGCAGGACTACAGTCAGTGGTACTGAGGGGACACTGGCATCTGTGTGTAAGTGGCAGTGAAGGGCTTGCTGTGCTGCCTTGCCCTCTACTGTGAGCAGCCAGTTGATGGGGTCGTGCCAGGATCGGGATGGTCAATGAATGCAAAGATCATTGCTCACAAAGAGGTCCTGCAGGATGAKGAT[A/G]AACTCCTATTGAGGGTGGAGTCGCATTATAAAAGGCCTGTTTTCACTTCAATGGAKAGATACAGGAGRAGMWSKSCTTATCAGTCCTTCACAGATTTACAGTATGCATCTACCTGTGGCTGTGACTTAGCTTTTAACATAACAAAGAAGATAAACAGGAAAAAGTTACCCACAGTGAAAGCAGTCTTTCAACCTCGGCAGCTTGGCCGACACGCATTTCATTGAGTGATACTAGAGTTGATACTGACCACTTAGACAGTCTCACTTCACTATAACTTACTTTGACTGTCTGGATGCAAACCAGAGACTGCAGTGCAGCATTCCTCCACTATCAAGTAGCTATCACTGTCATGTTAGCAAGCTAAAAAACAAAATGCATTTCAATAACTTAGCTCATTTAACACCGCAGCAGACATAACAACATTTCTATAGCTTGTGCAGAAAGTCCTCAACTTCAGACAGCCCCCCAGCTTTTTCTTTCAAGCTAACAGTTAGCCTAACTTCCA
GBYP-RA	TCTCATATTCTAACAAAATATGCATTACTACAGTGGATGAAATTGTCGATATGAAACCTAAACGCTGTTGTTTGCCTTTGGAGAGCAGTACAGTTATTCTCAAATGCTTAACAGTGATATTAATTTGCTACTTTCGTTTCCTGGATCTTTATAAATATTCATGTTTGATCATCCTAAACTGCAAAAGTGTGCAATTTTTCATTTTAAGCTGCTAGAATAACTTACAGGTTTTATTTTTATTCTACAGCCCTGCAGGTAATCACCTGGTATAT[A/G]GTATGAATCTCACACACAAAGCAAACACTCATTGATCAGTAACGTTTGCATGTCACAGATMARMYSSCAGCGTCTAGATAATAAATGCATGACTGTAGAACAAAAACTAAACATAAAAAGTGTCAAGATCTGCATGCAAATGATTGTAAACTCCAGTGTAAAACCAGAGAGACATGCAAACCCTGATTG

D_48	TACAGAGACAACAATTCCAACGTTAAACCGACTTCCTCAAAATGTCAAAATAGTGCACACTCTACTAGTGGCGATTTTTACCTCTGGCGAGCCAGCCCTCTCCAACAAAGGTTACAAGGCTGTGAATG
GBYP-RAD_49	CTACTGAAGCTGCAGTTTTATATTTTTTTTTATAGATTTTTAATCCTTTAACATAAACTAGTACGCTCACTAATCTGAACCTGTTGATGCTCTGAACATCTGATCTGATTCAGAAATAAAAACACTGGTGATTTTATGATTTAACCAGTAAACATCTGAATGTTTTCATGTTTTACATTTTACTGAATAAAACTAAACCTGTAAGAATAAATGAGAAGTGAAGGAGTTTCTTTCATACTGAACATCTCCCTGCAGGACCTTTTTATTTGATAGTTGATA[A/G]CAGCAGATGCTRASTGTTTCACAGTTTATTGGCTGATCTTAATGATGGGCATGACMMRAYTGATTAATTTTTCACGCGGCGCATTTACTTCCCAGATAGCACACGGTCGTGGGCCACTTCAGGCAATGATGCAGCACTGCTGGCCTCCTTCTGGCCCGGACAAAATGGATGTGAGCC
GBYP-RAD_50	GAAAACACTCAGTGGCAGTAAGCAGTGATCTATATTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAAAAATGATTCACAAGATAATGAAGAGAAAGTTTTTAGATGTGTTTTTTAAAAGTAGACTTCTTGATTAATCTCAGTTCATTCTAGAGCAGCGGGATCCAAATTAAAGTTTAAAAAAAAAAAAAAAAAAAACCTCCATCAGCCTTCGTTTTCAGTTCAAACTGTGGAAAAAAAAACCTGCAGGATCTGCAGGATCTYRAGGATTAACGGCTMAGTGAGAGATGCAGAGATGMT[A/G]CTTCAGGCATTTTATGGAGGGYTAAGAGCWGCAGYCCCMMMAAAAAACAAGTGAAAAAATCAGAGATAATTTGTTTTCAGTGTAGAGGATCAGAGCTTCTGACAGTGAGTTGCGTCTTATAACACTGACAATAGAAAACGCTCCTGGTAATGGAAAAATTGTGAGAAAACAAGACGGAGCTGCTGTTTAAACGCCAGGAAAGAACAAGAAATGATCAAACTACACTGTTCATTTGGGGGCTGTTTAAAATCTGATTTTACCCTAATTTTTGTATATTTTTTTACTGATTTTT
GBYP-RAD_51	GCTTCACCTGAAGCAGCCATAAGCAGAATTATACTTTCAACTACGTCATTAGGACTTTACAAAATATGCAACTGTTCAGATATTTTAATATTTTATATGTGACTTAGGTAAAATTACTTAACTAAAGTAAAAAAAAAAAAAAGTTTAATGGAGGTATTATTACATTTTGGCATCAATAATTTTATTCAATTACATGAGAGACACTTAATGAGGACCAAACCCTGAAACAGAGCAGAGACAGAAGAAAACCTGCAGGAGGCGCTACAGGAAAACACA[C/G]YGAACACTGAGTCTGAGCTCCTCCTGCATCCTGCATGAAACWATGTAATGAAYTGTATRWWRWTACATGATATTCTCCTAAAAAAAAGATAAATGTCAAATATCAGACAATAAAGGACTAAAGACACAAATACGACGTTGTGATAAAGATAAAAGAATATGATTTTAAGAGTGCAGTGTCAGTGTGTTACAGTAATAATACATTTTTTTTGTTATACTATCATGCATGACAGCCAGTTTCCTCATGATATGTTATTTGCTAGATTGATATAAATCTACAAGGAAACTGCATAATTTATTTATTCATTTATCTAAAGAAACTCTTCACTCTCAAGTTTTAAATATGAAATTATTACAAATATGGAAGTAAAACAGCACAAAGAACAATAAATGTTCCAAACACAATGAAACTTGTGACATTTCATGCTTTCAGGTGTAAAATGATGTAAAAAGGAATTCAAATTATTATGTCATGATAGTTTTGGGAAGGTTAG
GBYP-RAD_52	TAAGAGTAACTACAACTCTGTTATGTTGATTGTCAACATTTTTTGTCCCTGTTAAGTTTTTTTTTTTAACTTGCAAACAGGCAAGTTCATCTGGGTAAGGACCCCATGTCGGAGCACACCAGGAGGCAGGTACTGGAGGAAAGAGAGATTGCACTACATGAATACATGGTAAGATTTTTCCCTCAGTTTGAACATGTGGTTATTGAGGGTCTGTTTTCATTAACAAATACAGTAGAAAGGAGCAAAACCCTGCAGGAYRCTGACCTTCAAGAACCACAGTTGAGTAK[A/T]TTTATGGCCTTTGAGTTGTTCTTTCCATTTAATTCAACATGACATGTACTGGATGTGTTGATAACTAATAACTTGTGCGGGATGTTTTTCTCTGAAGGCACCATATGCATGCTGATGTCATAACCCGATTCTGTTGTAACAGTATTGAATCACACGGCAATTTTCATCCTTTAAAAAAACAAAACATTCTGCCTCTGTGATTGATTTTATTGAGGAAACTCAATAACTCAGACTCAGCCAAAGTAAAATCAGTTTTGAATTATGAGTCTGTGTACGTGTATGAGTTTCCTTTGAGAAGTTATTTGAATAGTCGACAGAACTCTCACAGACACTTAACAGTACTTCCTCCCTCGTCTCATCTTCACCTGCACTGTTTATAATGCGCGCACACACATGCATGTTTACAGCCTCATATCTTTCACCATACTTTGATATTTTATGGAAACTCTGTTGTTTTTATTATAGGAAGAGCTATCATCTTC
GBYP-RAD_53	AAAGCTACTCACTGTGTCTGTCTAAAGAGCTTTCCATCTCAAAAAGCCACTCCAATGTTAATCCTCTTTTTAATGCTTTCTTTCATCTCTTTTTCTCTTTTAAAAACTAATTTCTGACTCTTCTGTCGAGTCTGCCAGTAAGATATAACGATGATCTTCCATACTTGACTTGTTAGCCAGGTAACACTGCACTTAGATGAGAAGATCAATACAACTCTTAAATCTGTAAGTTAAATATGAAGCTGCAGCCTGCAGGCAGTTAGCTTAGG[C/T]TAGYACACAGACTAAAGGCCCTTTTYTTGTGRAGGCGCAACAACMAGCACTCCGACTATTTGGTATTTTMCTGACCTTGAAACTTGCTTTGCCTGTCTGTGTGGTATTTTGGTGACCCGTGCAGAGCAAAAGGTGGGAGGAGAGGCACAAAGGTGGGAGGATCATTCAAATGAAGCAGCACAAAGCGAGTTGTTGTATTTTGGTTGAAATTTGGTCC
GBYP-RA	AGTCATTTTTCTAAGCAATGAAAATGATTTATTAATAACTAATGTTTTTGAGACAGTTTTGTTTTTTGTAGTTTATTTATGTACAGTATAATTACAAGGCTAATTAGATGCTAATATATATCAGGGATTTATGTTTTTTAGATTAGTAGGTTTATTGAGGTAACATGGATTCACCATTTAGAGTTTTATAGGCTTTATAGTTATGGTGCGGGGAGAAAGCCTCTACAGCTGTACAGAGGTGATGTGACCCTGCAGGATYCAATGCTGAACATCTTATTTACTATTATTAGCTG[C/T]CACAGMTTAGTTCCAAAACAGTGWKCAGGAAGGACATTTTBGGATTTGTAGGTACTGCTGGGTGGTACAACAAAATCAGAGAGTGTGTCTTTAGGCTGGCCTTCACTCTGAATCTTGCAGATACAGAGCTGCACTCTATTGTTACTGTGCAGGATATGGAAAATG

D_54	TCAATTTCCATAATAATGCAAGTGCTCATCTGCAATATGAAGCCAGATAAAGTATGCAGATGCTGGGAACTTCACCTACTTTCTCTTGCTTTTGATGCACTGTATGTGTACACAAGTCTACAGAGAACATG
GBYP-RAD_55	ATTGACAGCAGGTGTAACACAGACGGCAGATTGTAAATACACTGATGACATGAAACTGTCCCCTCAGGTGGGTCTGGGTCAGGTGCTGGAGCTGCTGGGCGACCTGTTGCAGTACCTGCAGAGCCTGCTGGTGGCGCTGGTGTACCGGACAGAGAGCCTCAGGGAGCTGACCCTGGACAGGGTCAAAGGTCAnGTCCAGTCCGACAGGTCCGAGAGCTGCCGATCCAGATCCAGCAGCTCCTCAGAGACCTGCAGGAACTCTCCAAGCTCCTCCTGCAGCTGGTCATCAAYGCCACACCGCTCTACAACATGGTGAGCYCACCKGAGAMAYMYSKGARR[C/T]ACACTTGAGATACACCTGAGACACAACTTAAACATACCTGAGACACACCTGAATCTTCCCCTGGTTCCAGTCTTTGTGCTAAGCTAG
GBYP-RAD_56	CCCTACTGCAAGATCCAGAGCACGCACGCTTTCATATGAAAGCTCCTTCACTACAACAACAATCTGTTTGGTGTACTCTACAGTACTCTACAGTACAGTATGGTTTTGCATACTTAATACCCAATGGTTTTGTATACCCAAGTGAATACTGCATTACACTCTCCTTGTTAGGCACATTTTTTGCTTTATTTTATTCTTCTTACAGCAGAAATAAGTTTTGCATGAGTGGTTCGCTCTCCAAATTAGCTCCTGCAGGAGCCATTAATGTAGACAGTAGCACAYG[A/G]GAGTGTCAACAGTCCTGTATATCAACTYGRGTAAGACGGTGATCTCGTGACMHVWHTTATTGACTTTTCTTGATAAGTACATCTATGGGATTCACATGGAGAGGGGTGAGCAGCCTCCCGACTGACACATAATTTTCCATAGCAGCTATCATCAGATGTTTATTTTGTCTTTAATTTAGTGTTATCTAATATGTGTTTGACTTAAACTGAGTAACCAGCAAAAGAGAAAACCCTATAATGTACATTGTGAGAAAAAAAAAAAAAAAGTACTATAATATACTCGATATGTGGTCATTCTTCAGTCTG
GBYP-RAD_57	ACATCCTCAGTGCTGGTAAATAAACATGCGTTAACTTTTATTTACAATAATTTAATGATATTAATCAGGTTTTATTTGTAATTATTTTCTTTTGTTTACTTTGTTTCACGTTAATTTAATTATGAGAGGAAACGTAACGATGATTTTTAGGATTATTTAAATGTTAAGTGTGTCTCGCTGCCGCCTGCAGGTCAGGAYGGRACGCTGCAGTCCTTCTCCACC[A/G]TCCAYKAGCGATTCAACAAGAACCTCGGACACGGYCRRTKCAGCCTCCAACATAACGACACCTCACACACTCGAACCAGGTCTCCGTCTGACTGGCCATGTTTGGTATCCATGGCAACAACCAATCAGTAGTTGTTTTGTGAAAGTGGATATATTTTAAATAACGGGTGTATGTTTCTGCAAATCTCCGGTCTCATCATGAACAAGAAGAGGTCCTGATAAACATTCT
GBYP-RAD_58	AAAGAAACAGGTTTAGATGCAGAGGTGGTGAAGGAACAGGTTTGTAGAAGGAGCAGAACAAGGCATGCAATGAGGTTTTTCATTAGGACTCATTTACATGAACAAGTGAAAAATGGGAAAGAGAAGATTAAAGATGCAGCCATTGCAAAAGTTCATGCATACATGGCTTTGTTCCATCCTGGAAGAGGAATTCTTCATTAAATCCTAATTTTGTTCTCTATTCTGCTGTCAGAAAGCACAGGTCAACACCTGCAGGGAGCTGTGCAGG[A/G]AAAGCTGCAWTSAGATGAAACAAATGTTTTGTTYATAGGCAACATTCAGTTTGTCCTTTATGTARCAGMYWGTCAGGCTGTTAGATGGGCTTGTAGTGTGTCTTGCCACAGACTTGCAGTTAATGTTAGCCTTTCTTTTAACTATCACCATCATCTTTCCCTAGCCTTAATGATTTATTTCCCACATTCACAACCTTTCGCTGTCCTCAACCAAACCATCATTGTCATGAACGGATATTGTAGAAAGAAAACATCTGCACTGAATGTTACAAAAACTTTGTCAACAAACGTAATCTAAGGCTTTGCAGAATCATCCAATATCAACATTCTTGTCTGGTGATGGGGTTTGGGCGAGGAAGAGATAAGGTGAACGAGCAGGACACAGCTTTTTCTCTGAATGTCTCTTCTTTTTCGCTGCTGATGTTGACACTTACATTAAATATTTCAACTTATAAATAATGTCTATATTGACATCAACAGATATCTGAATATACAGTGAGT
GBYP-RAD_59	TCAAAGTGTCCTTGACCAAGACATTGGCCAAGGCTAAATCCCTGCCCTAAACTCTAAAAACTGAAATATCACAGATTTTGAAAGATCAGAAAGAGAATTTCCCCTTTAGAGAAAAGGAGGCAGATGGATAAAAAGATATGAAGTATATCTACACAAATTTTAGCAACTAAAAAATCAAAACATGGTAGTATTCAACAGTCCAAGCAAGGTGAGAAGAGTCTTTCACACCAGACATAAGACATAAAATGCCTGCAGGGAATMAAAATGCAGTTTTCATGTHAGTGCAAGCTTTATATGTGCTTTAAT[C/G]AGATTTCTCCYTGTAGATAGARATARATTAACATGACCATGTAAAGGTACGTCACTGTAATTATAATAATGGGCATATCCTGTATTATTGTACAGACCACCCATCACGGTATACAGTTTCTCCCCTTCCCCACCTCATTTATGATGTGAGGCCAAATTTATAGTGGTTGCACACAAAATTCTCTGAAGTTCATTGTCTGGTTCCTCTAATGACGGCGCCCTGACTGACCTTGCTGAGCTTATACAAGCAGATTAATCTGCAGAGGGACAGAGGTGACACAGTG
GBYP-RAD	GTGGGCAGGTCAGGGAAAACAAAAGTTTATTGTGTCCAAAGTGCAAAGTTTGGAGGTAAAAAAAGAGGGCAAGGCAAGCGAGATAAAATGGCACAGAAACAGGCAGAGAAAAGGATGACGGGAGGCACAAAAGCGAACTGAGGCAAAGTGGCCAGTACATATATATACATATATATAGAGAGAGAGTGCTGATTAGGGGAATGAGAGGCAGGTGAGAATCAGGTGACTGGGAAGAGGTGAGGACCACTCCTGCAGGTTAGGYAAATAGGGGACAGGCGAAAGA[C/T]GAAAYTAATATTAAGGAATGGCACTGTAGAAGTCATGACATGCTMWGAKCKGRAGWCAGGTTTGGTTTTCAAATATAATTTATTGGGAAATTTCTCTCTTTCTCTTGATGATATGCAATGCCCAGTAGGAAGAGGGAAAGAGTGTAGCCAAAGTGTTGCT

_60	TGAACCTGGTGAGCTGATGGTCACAAAAATATAGCCTCAGGTCATTTTTTAAAAACTTCTCAGGGATGGTCTGTTTTCCACAACAAGCAAAATGAGGCCTCTTTAATTTTATGGACACATAAGGAGACAAACAGGTTGACAAGTGG
GBYP-RAD_61	GCAGTGTGCTGCAAGAGATGGACACCAGCAGGGAGTCTAATGGTTTCAGCTGTAGATACTACACATACACCAGAGAACAACCTGAACAACACATATTCATAATAAAGCATCTAACTGTTAGTATTTAAACAGAACTGTGATTTTCTGCAGTAAAGCACCAAATAAACACCTCCCTCTTGAGCTCCCAGAAATATTAAGCACCGAGTCAGATATCTGCACACAGAGGCTCCGATACTGATCTCTGTCAACCTGCAGGTGAAGTTTGAMGAYAACAACCCGTTCAGCGAAGGTTTCCAGGA[A/G]AGAGAGAGGAGAGAGAGGCTGAGAGAGCAGCAGGARRRKBAGAGAGTTCAGCTCATGCAGGAGGTAAAACAGCTCACACACAACAGGAAGTAGAAACACACACACAGTGCTTTTAATGTGAAGACAACAGGAAGTAGAAACACACCTGTTCCTGTCCTCGCAGGTGGAGCGCCATCGAGTCCTGCAGCAGAGGCTGGAGCTGGAACAGCAGGGCCTCCTGGGAGCCCCCCCGGGTCCTGGTGCTCGAGTGGGGCCCCCTCCGGGTCCCGGGGCCCCCCCTGGGGAAAGTC
GBYP-RAD_62	AGTTCTTTGAGAGTAAAGGCATAAATGGCCAGTGGATGGGAGTTAGAGTGACAAGCCAAGGTCCTGGTAAAAATGTAATGGTAAGGAAAACACTCCACATTCAAAGACAAAAAAACAGTTAACAGCATTTGTAATCATATTACTCTTCCCTTGCAGACCTGTGCTCATCGATACGGGCAGTGGAGCCCAGTCCCAATCAGTGATGGCCCTCACATGGTGACGGGTCAGTGCTACCTGTTAGGAAATGACCTGCAGGTTCAGGTTGGGCATGAAGGCAGGACATGGAGGAGGGTAGTTTGTGATGAAG[A/G]ACACCAABAWAATCATCAAAAGACMMRMKMGKGGTTTGCATACTGCCAGCAGGGTCATGGAGCAACTTTTGCAAAGGACAACAGATCTGTGTTATTTGGAGCACCAGGCGCTTACCTGTGGAAAGGTAAAACATATCAGCCAAAATGTGCAAATATATACAGTATATGTCTTTTAACATTCACATATTTTCATTGTCTTTTAAAGCATTTTAAGGAAAATAGACAAAATTATGGTTCAAAATTTTATTTTTGTAGAAATGTACTTTTCATAAAACCTTAAATGTTGGCAATATGTTTAATGCAAAGTGTGCTTTTTGCCTGCAGCATGAGAAATATTTTAATTTATTTTATTTTCCTGTTTAAAGGTAAAATAAAACTTTCAGCAGCAGCTCAGGTGTTTTGTTTGTCAGCAGCAAAAATGGACAAATATATACAGTATATGCTGATTAATAACATAGATAT
GBYP-RAD_63	CTTTTAAGGTCAGGGTTGATAACATTGTAACACACACATGAACAGACAAGTTTATTGTTCCTCTCAGTACTTGTCATCTGCTGTAAGGCCACTACTATTGAGAGTTTTATTTTATCTTTTTTTTGTTGTTGTTGTTGTCTCAGTCTGTGTATGGGCTGCAGAATGATATCCGTACCCATAGCCCAACCCACACCCCTGCCCCAGAGGCCAAGCAACCTACAGAAGAAGAACTGCAAGAACAGGTCAGACCTGCAGGTGGCGC[A/G]CTACCACWAAAGATCAATRCHAGCACTMAAATTGTAGTTGYAVTTTATATTTTTCATCTGTTTTTCAATTATTCAATTATGATTCATACATTCGTAAGTGCAATGTAGTGCAGAGTTTAAAGTGCACATTTAAAGTCAAAAAAGGAAAATATCATGCAGTTGGTATGTAAATAGGCATGCAAACCAACATTTTCTGTGAATTCATGGTGACAGATGTGTGCTTATTGTTCCCTGCTATGGTTTCAGATCACCTTTTGGCAATTGCAATTAGACAGGCATCGACTGAAAATGTCCAAAGTGGCAGAGAGGTGAGCAATGCTCTTTGCA
GBYP-RAD_64	AGGAAGAAAAGGTCGAAAGAGGGAGGGATGAGAGGATGAAATTGTAAATTTGTAAAGCTGTTTTTTAAGCTTCTAAAGAAATTCGCAGACAAACCAAGACAGACGAGTAAGAGTTACCCTGTTCATTTTCAGGAGAATGCACGGTTTTCCCTCAGAGTATCCGAAGTTGATGTCAGAAAGACCGGAGCAGAAACTCAGGACGCTCCTCTTGAAGCGACAAGTCTTCTTATTCATGTTGTCACTGTCGTCCTGCAGGAAATAGACTCCTGAAAGGCATTCCTCGTTCTTCTCMTGCTCTGTATCRTTATAACCTAGGAAAAGAAAGAGAGAGATATATTC[A/G]GGTGTCAATGAGTGGAGAAAAGATCCAGGAGGAGGAGAGTGGAATTCAATTTATTACATCTTGCTTTCGATCCCTTTTTAATACAAATTCATCAGGGCGAAGTGCACTTACTTTGCAGGAAGGACTCCAGGTGTTGGACATACTGTGAGTACTTGAGTGGGTCAGATTTGTTGAATGAGATGTCCAGTGAATTTGGACGGATCACCAACCCTGCAGCACAAAGTAAACATAGAGTGAAGTAGTAAAAGCA
GBYP-RAD_65	GCTGCTTTCTGTGTGTGACGACCATGAAGTTCAATTGAAATCTAAAACTTAAATCCATGTAGAATAAGAGAAGAATCAGGAGTGAGATGGTGCTGCTGGTTGTTTTCTTATATTTATTTATTTGTGCTGGAACTGATTCTCCAGACGTCAGCTGATCAGCTCCCGACCACACAAAATATAAAAACACAAAAGTAATATTTACTCAGAGAAACAACCTAAATAAAAATAAACAAACTACCAACATAGAGCCTGCAGGTGTGTGACTATCGTAGCACTAAACTCTG[C/T]CTTAACGCAGGTTTATTTGTTTARTATYAACTCAAGTTCACAGCAACRARRWCKGAAAGGTCTGAACAGACCGCAGCTTCCGGCTGATAAAATCTGCTAAATGAGGTTTGCAGCNNNNNNNNNNNNNNNNNNNNNNNAACTGAGACGCAGTTTCTCTCTTCTCTTCCAGTAAAAGGGCGTCGTCACCCAGCTGTTACTGGTCAGGATCCACCTGCACAACAGGTGATCTGAACAACCGTCCAATCAACAACATTCAACTACAACACCTTCAGAGGAGGGAAATGGCAGCAAGTCCCAACAATAGGTGACTGCCACATATTAATGATATAATATAATAATAACAGGAGCTGAACAAGGTGTTGCAGCCACATTTAGACGACATGTTCTATTAACTCTGAGACTAAATCCTGCTGAAACGTCCCGACAGCAGCAAACACAACCAACCGTTTCCCGCCGTCGATCAGAGACTATCTGTGTTTTCAACAC
GBYP-RA	TTTGATATAGCTACTATTAAAACAAGCATGAATTGCCTTATTGAATTACTTTAAACCAAACTAGTCACAGTCATGTTGTCACCACTATGTACGGCTCCTCAAAACAACCATGGGCATGTCTCGCATCTTCTTCTATGGTTTTTAATGCAGTGCAGAAAAAAACACAAAAAAAACATGTGATTTCCTGGCCTGACAGTGGAGCTGCCCCAAGTGTGCAGCCTGCACCGGAAGTGTCCCCATAGAGGAGACCTGCAGGCAGAYCCYTMTCACAAGTTCTGTKAGGTCCATTCTCTCATTGAATGTAATCTGGGGTTTTGTGT[A/T]GAATCCAGTGTTGTRGGCAGAAATTGTATTTTGGGTGGGCCAATACAAAAGTAAGTGGGC

D_66	CATCTTCTCCCAGAAAAACACAATTTATGAAAGTTAGAAAAAGGAAAAAAATGAACAAACATAGATGAACTGACAAACAAGCGACCAGTTTACTTTGCAATGTTCTGCAT
GBYP-RAD_67	GCAAAACCCTGAGTAACATCACAAAACACAAAGTTTAAATGAAAAGTTGTGTGTGTTTGTGTGTGTTAGAACCTGTACTTGAACTTCGGGGAGATCGGCACCAACATTAAGAACCTGATGGAGGATTTCCAGAAGAAGAAGCCTAAAGGACAACAGAAGCTGGAGTCCATCACAGACATGAAGGTGACTGACGGACTGACGGTCAGTGTTCAGTCAGTGTTGGTCTGTGTGTTTCATGTGTGTTTCCTCCTGCAGGCGTTTGTGGATAACTACCMTCAGTTTAAGAAGATGTCGGGCACCGTGTCCAAACATGTGACGGTGGT[C/T]GGGGAGCTGWMMSRKYTGGTGTCGGAGCGTCAGCTGATGGAGCTGTCGGAGGCGGAGCAGGAGCTGGCCTGTCAGAACGACCACTCCAACGCTCAGCAGGTAACACTGGTTGATCTGGTCTCCTTTACAGCAGAGAGTCAACATCAGAAATCAGAGTAGAGAAGCTTCTCCTGTTTATCTGCTTTGAGCTTCGCCATGTTGGGCGGCAGCTAGTATCACTGATGAACCTTCACTCTCTGAGAAACTTAATGACAAAATGAAACTCATCTGTTGTCGGTTTGTGTGTCTGCACTCGACCAAAGATCATCTGTTAGAGAAGAAGCTCCACTCTGTAACACAGCTGTACAACCAGAGTGTTTCTGTAGTTCCAACAACTCCAACAGAGTGAGACGTCTTCTCTCCAGAGGATCAGGAGTCTCACTCAGTTATGAACCTGCATCTTCAGT
GBYP-RAD_68	ACCCTGCTTCATGTTGAAACATAATCAGTTAAATGTTGAAACTGTGGTTATGTATAACTAACCCCAGTTTAATCAAGATGTCTTGATCTTATTTCATCTTCAGTGAGAAAAAACTGTTTACTGAGCATGTGTGCAACATTTATTTACTTATTGCAAGTCAGTGTGAACCAAAAATGCACCAGAACTAAAAGTCAACTGTAGATAAATAGAAGATTATTTGTTTCTTTGATTCATGCAAAGTAAACTGACCTGCAGGTGAGATRAAATAYATTTTTGATTGGATCAGGACAAAGAACCATAATACTGAC[A/T]GGAAGCATCACAGCAKSCTGTATAACAGGRATAATAACAAGTATTACAGCATGGATCGAGTCAGGAGCGTGGGTCATGTTTAGTGTTTAACAGAACAAAAGCCTTTTCAAACATCTTCTCACCCAAACCACACCTCAGTCTCCTTGATATCACAACGAGAAAACACAAACAAGCAGAAATCGCTCTCAGGACTTCTGTTCCTAGCAAAATTCCTCACAAACAAGTTCAAGGTCTGTGGAGCACTTCTTCCATTAAGCGAGAAATGTTTAATCGTCTCTGCA
GBYP-RAD_69	AAGAGGAGAAGAAAGAGGGGAGCGATGGAGTGAGATAAGAGCCGAGCAGGGAGTTTATCTGCATTGCTGTACCACACAGTCAGTGGAGCATTGTAAAGCCGTCAGCATAAATTCTCCCGCACTATGCAGATCTTAAAACGCATCTGCATTCCAGCAACCGCACATCAGCCACTGCAGGATTAATCTCATCCACGTAATTTAATCTCATTCACAATAATTTAGGCGTCAACAGACCATCGGCGGCATAACCTGCAGGCGTGTGCAGATCTTTATCYGMTGCAGAATGGCCGGCTTCACGGTGTTCAT[A/G]TGAAACAGGTCGRGACTGCTARAGAGMWSRYMDCTTCAGCTAAGCTCTTCTACCCCCCAGATAAATAAAGGTTAAGTGAATCTATCATCTGCAGGAATTGAGGAAAAACACCCCCAGTTCTTTATTTTGACCCCCGAATGTGAGTAAAACCTTGAGGTCAGCTGCAGAATCCGACGTTAATGTGTTTTTGTATGTCTTACGGTAACAGGAAACACGTGTTTCTCTGCAGCAGACTCAGCAGGTCTCGCAGAGCGTTTTCTAAATGCTGCACATGTTGTAAAAT
GBYP-RAD_70	GCAACAACCATCAGGACAGGGACCACAGTGAAGTTGTGTTCAGACCTTGAAGCTTCTCTTCCTCTTCTGGACATTCTGCTCAGGGTGGAAAATGATGACATAAACCTTCGGCATGTAGAGCATCCCGAGAGAGACGGACGCACTGAGAGACATGGACACAGTCAGAGTGGCTGTCTGGATAAACAGCTGTAGAGACAGAGAGACAGACAAACAAACAGAGATATGGACACAGTCAGTGAGTCTAACCACCTGCAGGAACTGCAGAACCCTYTTAATGATCATGAGAASCATCTACATACATCC[C/G]AAACCTCCTCTGTGACTAATATAACCTCCTWARRKMAAGGTTGAACCACCTAAAGAACCCCTTGAATTTTCACAAAGGCCACAAGAAAGGACCACTGAAGCACACGAGGAACCATGAGAACCCCCTCATTGATTACAAGAACCTCCTAAAGGACCTTTACAGTCTCCTCAATGACTTCAAGAGCCACTACAACCTCATAAATCACCACAGACATCTCCTAGAAGACTTCTAGAACCACCTAGAGAGCCTCAAAAATCTCTTCAATGACCACTAGACCCACATAATTTATTATTGTTTATTTACCTTCCACAAAAAGAGTGTAAAGTACCAAAAAAAGGTACTGTTGGCTACCGAATTCCAGGTAACAATACTGGTATCGGTTCAATTGTTAACGGTAACCCTAGACGACATATAAAAAAATACTACAACCACTTACAGGGCCCAACAAACTTCCAAAGTGACCTCA
GBYP-RAD_71	CAAGCACGTCTTGTTATGCAATTTAATCATGGCGGGAGAAAAGGTAAATAAAATGAGTTTATGGGTCAGACCTGGATAAAAGTCTTGTTGGGTCGCTAAACCAGGTCAGACTCACACCAGCAGGGAACAAGTTTTTTTCAAAGTCATCTCATGTGTATGAAAAGAGTTCGAAGGAGGACATGGTTGTGGAACTTTTTACCTAGTAAGTGTGAGATCATGGCGATGGTACTCCAAGGCCTTGTTATACTCCTGCAGGTGAAAGTAGGC[A/G]TTGCCCAGCTGGCTGTAGATGGCACTGAGGATCTGGAGGTCCTCTGTTCCAACCTGGATGGCAGAVWHVVDVAAAGACACACCGGCACGGTAGTCACCAGCCTTACAGAGCCGCTCACCTTCCAGAGCCAGGTCCAGACACGATGACTCCATCCTGCGGGGGAAGTGGGATCTAAGTGAGACGTGAAAGTGAAGTCTACTCTATGTCTAGAGTCATGAAATNNNTGAAATAGGAGGGTTTCAAATTTTCCTCACTGCAGATTAGTTTAACAAATGCTATAAAACATACAGACAACCTCAGTGAAAGAAGGCAAGTATAAAGT
GBYP-R	GCCATTGGCCTTTTTTCAAGGAGGGTCATGGACACTCACAGTTATTTCCACATACAGAGAGACTCAAGGTGTTAAAGCTATTCACACTTTCATTTGGAAGTTTTACTCTGGGACCAAGTTATTGTGAATATTCTCTCAGCTGTAAGAAAACCCCAGCCAAGTAGAATGAGGGGAGGTGATTTCATTCAAATACAATTACAGTTGGATCAGATCACACAATTACACACCCTGCACACAAATTCACATGACCTGCAGGCAGGAGCCWTATTCATAAWGTGATACTGATTTAGTAAAAGATGGAAATTGATTTCTTAACTTTTT[A/G]CACAAAGWTTGTGATTCTCAAAAGCTTTATGAATCCTGCATGTCTCACTTTTTGTCTGTT

AD_72	GGTGGGTGTGTCAGTGGAGTATAAGAAAACAATGCACATATGTTTTAATGTTTTCCTTCTGATAATAGGTGAAATGCGTCATTAAAATGATGTGAATGGAATAGGGGAGGATAATTTGTGCCATATTACCTGCTGATTTTAGTTGAAGATGACAGGTAAAATGGCACATGGCATGGTGATAATCATATGCTATCTCACTGGATTAATAGTCCTTGACTGATGTGTGTGTGTGCATGTGCGTGTGTGTGAAAATGAATTAAAAATGAATAAAATGTCTGGAGGTTGAATTGGATAATGGTTTGCAATGCTATTACAGGGCCTAAAAAGGTGGTGTTTGGAACAAGATTCATACTTAGAAGACAATTCTATGTGTATGTGCATGAATTTG
GBYP-RAD_73	GTCAAGATGAGAAGACCAAGAAAACTCTGGGAGAGACAAACCCCCCCAATTGACTGCAAAAAACCTGCAGGAAGATTTATCAGACTCAGGAGTRGTKGTGCAGCGATGCACTAACAAGACCTTCATGGAAKAATCAGAAGAAGAAAACC[C/T]GCATCACTCTGGGAGAGACAAACCCCCCCAATTGACTGCAAAAAACCTGCAGGAACATTTAACAGACTGAAGAGTGGTGGTGCAGCGATGCACTAACAAGACCTTCATGGAAGA
GBYP-RAD_74	TAGCTCCTGTCTCTTTAAGCCCCGCCTCCCTTTGACCTGCAGGCAGCATTTCTAC[A/T]AATGTTCTACAAAAGTTTTGGAGCTTTGGTCGTGTTTAACATCCAACATCAGAACAGGACATAAATAACAGAAAA
GBYP-RAD_75	CCTGGTGACGACATTGTTAGTGCCAGTAGTGACTGCAGCACCTGTTTTACCTCCCGAAGTGGAACCTCCCAGGCAGCTGCACACGCTGCTGGTATACACACACACACACACCTAAAACATCTAAAAACAACACAAGTAACCAAAAACAAAGCATGCACCTGTGGCTGCAGAATAAATGGTTTATATTCATGTGTAGGTATAGCAGCAGTGATCCTGTCGTCCAATCAGAACGCGTCACCGGTGCAGGTCCTGCAGGTGATGCTGCAYTATTCCATCAGCAACARAATCAACCTTC[A/T]CCCTCTGTCTGAAACACATCATCTCACTACTCCAAACCTGCTGGCAGCTATGCCTCCTGCCAACAACACAACAAGTTAGTGACTCACACTTTGTGATCTTACACACATGAACAGCATCTGTGTGTAGTTTACACTGTGTGCTCACTTGGGTGTGTAGGTGGGGAGCTTCTGTGTCGGTCAGTGTGGTCAGAGAGGTCAGGGGTCACGAACACGGACAAGACTATCAGTCGCTGTCGTCAGGGGGAGGAGATGATGGGCTGCAGCAGCTACGCTCCTGACGGTGTACGCGTGGGA
GBYP-RAD_76	CAAACGACAAATCGATTAATGGAGAAAATAATCGTTAGTTTCAGCCCTCATTAAATCAAGAATAAAATTGAAAGTATGTGGTTTAAAGAACATGATGCAGCCAGTCACATGATGTGGACCACCTGCAGGTAGTGATCACAGCTGGTTAGTGRGGCTGTGGAAACA[G/T]ATAACGTGTTTGACACGCCACATYGTGCAGACTGAAACTTMATTYTGGTTTTCCTGTGTGAACATTCAAAGTTGAATTTAGGTTGGTGTAAGCCATCAGACAAGTCCCCGCTGCTTTACTGTGGCCTGATTGGTCGACAGCTGGAGAATCTGGACAAGTTTTAGTACTATTTATTTATGGCGTTTTTTTTCAGCATTTGATATTCATTCATTCATATTTCCATGCTGTGGTTTCCTCTTATATGTACTTTTAATTGCTAGTGGCTAGGAAGGTCAGTGATTAATTGATTATCAAGTA
GBYP-RAD_77	GGAAGAATATAGTATAGAGTATGAGCTCATTTACTGTGTTCAGTATTAGTTAGTTGTGTGAATAGTTGTATGTATGTATTTGTCTCTGTTTCCGTGTCGGTGCATGTGAGTACATTCATAATAACTCTTTATATTGTCAGGAGGTAATGATGTAAATTGCTGCATTGGAAGCCTGAATGCAAAGCCAGGCTTTTTTCTCCCTGATGCCTGTATTAATGCGGTGTCCCTCTGGACTGAAATCAGCTTTTCCTGCAGGTTTTTCACTGTCAGGCCAT[C/T]TTACCTGCTGCACAAATGCTGGTAAACCTCTTAAGCYCATTCTGCCCCATTTCTTTCTMTCYYYCCCCCCTCCCAAGTAGTCTCAGAGGATTCACCAAAGACAAAGACACAGCCTTTCCGGCTATTAGGGCCATTTAAAGGTATCCCCATGTTGAACATGCTTGAAATATATTGCTGTCAAATGTACTGTGATGCCTGTGATCAGTGTTTTTATATTTTATTGCCCTTGTTAGCTGCAGTGCTGCTCAGGGGTTTTGCTGATTTTAAAACAGATCTTTGACAGTCCCCCATGTCAGGAGGATCAGATATCACATACTAATTTGCACACCAATGGCCTCAGGCCTAGACCAATTTCACATTGTCTTAAAGTTTCATAAAGACCTTGAAAGACCTTTTTAAAGCCAATTAAAATGAAACATCAGACAACTCACCACTTAATGTAAAAAAATGAAGATGAATAAGAGCGCTGGGTTGCCTGACAGGGTTGATTTCAA
GBYP-R	GGTGTGCTGTTAAATCACCTAAGATGGAGCGTTCTCTTGTCTCCTGCAGGTTGGCTATGGCCTCCRGCACGGTTTGTTTTGTCTG[A/G]TAGGTGTTAAGCTCCCACTCCATCCCTGAGATGTACTGAACCATATCTGCAGGAAACACACAGAAATGTGTGAAACTGACACA

AD_78	
GBYP-RAD_79	GGTCTTTTCTTTCTGTTGTAGATCAATCCTGCAGGCTGAATAAATGAAACATGCATGTCCAGTCTGCCTCT[C/T]TTGGAAACACACATACATHRGCGGCWCACARAAGCACACRCATWGAAACTAAACATGTATAGCAACACCTAGTGGACTTAATTTGCTGTTACATTATCAGTATATGGAAACTGCCCTTTGAAACAGTCATGTCACTGTGTGTGTGTGTG
GBYP-RAD_80	GCTCTGAGGTCTTTAAGGGACACTTATTTCTGTATCACACAGAGACACACACATCTTTAACTAAATATGACTTTGCAGTTGGAATTAGCCCACTGTTTTAAATGTGCAGGTACATATTTGCACCCAGTTAAAAAAAAACATCAAGTGACAGTCAGTGATGTTAAAAATACATAAAACATACAGATAGTGTATTTTCAGAGAGATACTGGTGTGTTCAGTGGGTAGGTCTTTAGGATGGTACTGGTGCTCCTGCAGGAAAAGGGCTGAAATCTT[A/C]AAATACCTCATACTCATRTGYATATGAGCAGGAGAAAACRGGAATTTATCATAGAMAAGCCTTCRTTAGTGCCATGGCTTGACCATTAGACAATTTAAAAACTACATTTTTTTTAATTTGCAGATCTTCATCAGTTTATTAGGTTCATTGTGGGTTGAAAATTAACCAGAACCCAATAGCATACTCACAGATTATATCAAAATTAAAATTTAAGTGCACTAAATTCTAACAAATTCTTGCTAAAACTCAATTAAAATATTCTAAAGGTTCAGCATATGAAGTCATTTAAAGCTATAAAAAGCTTCATCTCTGATAC
GBYP-RAD_81	TTAGTCCTTTCCATTCAAGAGGCAAATGCAGATGCAAATGCACCTCAGTGACATCTTGAAGGAGATCTTGCAGGCTATCCTCGAGTCTTAGTGACCCATCTGCTACCGTAGAGGAGACAGCTGTTGTTGCTGCCTCTCACCAGGACCCAGAGGAGGCAACACCAGCTGCACGGGCATGAACAAACCTCTTTGTCATAATTATCTACAACATGGACCCTCTGATCTGTGCCAAGGTGAGACAGTGAAAACCTGCAGGTGAAGAGGAGAGCCCAAGTCGAGCYCCRAAGCATCCGTCCAACAAAATGAGGAGCAATGASC[A/G]CACTGCAGGCAGGACTGGACATCAGGCCACTTCTCTTGGATCATTTCTTTCTCAGTCCACATAGAACATGCTCCTAACTGGGGAAAGCAGAAAATTTGGTTCAAACTTTCCCCACTGACTCTCCTCATCTGAAGGAGGATGGTATGACTGAGAATCCTCAGAAGGATTCTAGATGTGAAGAGACAACAGCCTCATCATCTTACTGGTCACAGGCTTTAACGGAAATTGATCACTGAATGCAGACTGCAGGTTGCTTTTGGTTGGCTGCACCGGAGGCTTGAAAGTCCAGAGCTGGTGAAGGATGGAGGCGTCTTTATCCGGAGCTACAAGGAATCATGAAGAGGTTGTGGATGAGACGAAAAAAGGATAGAGGCAGTGTGGACCAGATGACAGAGAAGAAGCAAAAAAGTTCAACTGTTTCTCTGTTCTGTGGATGGTGGAAGAAATAACA
GBYP-RAD_82	ACTTCCACCCTAACATTCAATCACACCCTCCTGCTTTTGTTTCTTATTCCTCTTTATTCCCTCCATCATGTTTTCTGCATCCATCTACTTCTCTTCCTCCTTCTTTTCCATCACACTTCTCGCCTCCTCTTATCCCCTCCGCAGTTTGTCCCTCTGATCGTGGAGATGTGCTGCGGTGTGGTGGAAGACACAGGTCTGGAGTACACCGGCATCTACCGGGTGCCAGGGAACAACGCTATGGTGTCCAACCTGCAGGAGCATCTCAA[C/T]AAGGGCATGGACATCAACACTGCTGAGGAGGTGTGGAGGGMATGTCTGTTAWACTGTAGTTTTACTTTACWTTTACCAGGAATTGTTTTGTAATATTAGGGGTGTTGCTTTTATAATTCTACACCAGAAACACTAAATCTTTCCCCCTCCTGTCTCCACAGAGATGGCAGGACCTGAACGTAATCAGCAGCCTGCTCAAATCGTTCTTCCGAAAACTGCCTGAACCACTGTTTACTGATGGTGCGTCCAGTTATTTGTGTATCATGAATCATAATGAACATGTACAATGTATAAGTAAAATTAGATTGCTAATTGATTGTTTTCTTAGTTTGTAGAAAGTTTGTAGAAAATTTTTCTTTTACTTCAAAAATCTGCTTGTTAGCTAAAGATGTCATCTGCATGTGGAAATGACCATTATATTTTTGATTTTCAGACTTTTGTAATATTCCTGGTTTTTCATTTTTCATACACCTTCTCTGTCAGACAAATACAATGATTTCATT
GBYP-RAD_83	TCCTTCCCAGTCCGGCGTCATAGCACGGGGCTGTGTGGGGGAGCAGTAAAAAGGTGGGAGTCTGCTGAAGGAGAAGTTGCTCCGTTTCAACATGGAGAGTGAGGAGCGGACTGGACTGGATCCTCCTGCTGCGGTTCATGTGGCTGCAGTCTGCTGCCACACAGGGAGCTCTGGCGACACCTGCGGCCACAGTAGCGCACCACACCTGCTGCATGGCTCCGAGCTGCGGATCAACTTGATTAATGTGACCTGCAGGCAGCGGCGGAATGTRGCTAAGTACATTTACCCAGGTTGGACAATTTTTAGATGTCTGT[A/G]CTTTATGCKTTATTGAAAGTACTGCTCCACCACAGTCCAGAAGGAAATGTTGTATTTTCTATTTAACAACATTTAATCCGGAATCAGAATCTGTTCATTAGCCAAGTATG
GBYP-R	TCTCCACAGGAGAGGAACCAAGCGGCAGACCTGCAGGAGGAAGGTDGTTGAGGAAACAGTTCCAWAAGTTATGTGGAGGCAACAGAGTTCAAGCTGGTCCAAACA[C/T]MATCTCTGTAACTGATGGACACCTCTCACCTGGCGATAAGGAACCCCAAAATGGTCAGTTAATGGAGCTAACATCAGA

AD_84	
GBYP-RAD_85	TTTTAAAACCAGAAAAGGTTCTGGATACATTTTGCAAAAAAAGAAAGGAAAAAACAAGATGAATAGAACAAGTTTTGTGAAGAAAGACCTTTTTTCAGGTATTTATTATTTCTAATATTATATTTAAATGTGTCCTTCAAATATGAAATGTAGACAGTACAGTAGAGAGGTTTTAAGGTTGTAGATACAGTTTGTATATGAGGGTTTTCAATAGCTTTTGGCAATGTTGACTGACCACTTCAAGTGTGCCTGCAGGTT[A/T]ATTAAAGAAYATTAATTATTTTTAACARTGTGTGGTGAACATYAGCATCCATGTTAAGAAGWRTAACATGTCTCATCCTGAACAGTATCTTCCCTTTGCATGTGTGTACAAATACACAAAGATATACACATGTATTATGGTGTCTTTTCAGAGTCATGCATGTATTACCTGCCATTTTAAGGAAGTGCTTGTGCTGACAGTGTGGTGTGTTATCTTACTATCTTGAATCGCTGCCCACATCTCTAATTTTTCAAGTGATTTAAATGAGTCTGTTGTGCTTTTATAGTCTGCGGCTGATGAAACAACCAAAGCTAATGAGAGCTTTGCAGAAGTGAGAGTCTCAGTCTGGTTATCAGCCTGGTGTCTACACCACAATCTGAACAATCTGTCAGATCATTTGAGGATAAATAAACTGTCATGCAGCTTCAGGATAGATCAAACTTAGATTACAGCGTATGAAGCATCTGCAGCTTTTGAATATACACAAATGAGTGGAAGGAAGTGATTTAGA
GBYP-RAD_86	GAAGACGTTGGGTTTGTGGCAGATGGTAACTGGCTAGAGGAAGTGGCAAAGACACTAGAGCAAGAAAGGGAAGAGATTCTCGGTTGCGCAGTGTCAGCCGCCCCTGCTGACGAGGTGGTGGCTTTCTCTGCCATGTTAGATGCTCCGGAGTACCCTTCTGGAAAAGATTGAGAAAGGAAAAGTTAAACCTTCTGTTGCCTACTAAAACAATTAAAGCACAGGGTTTCCATACACGGTACCTTGCATCCCCTGCAGGATCTCAATCCGYTTGGCTCTCAGACTGTTGAC[C/T]TCAGCAGTAAACTARAACAGCAGGAAGAACAATTCAATRTAAACCTATGGATAGCCCGCTGAAAATAATCATTTCATGTTTTCTTCATTAGAGGTGTTTCTATACCTGCTGTCTCAGTAACAGGAGTCTTTGGACTTCTGTGTAGGCAGCTTGCAAGGCATTGCGGGCTTGAATCAAAGACTTGTCCAAATCCTGCAGCGAATGGCTCAACTCCTCCTCCCTCAGAGACACCGCCAATAGCTGGTCCATTTGGCCCTGGTCTAAAGGGGAGAAGACCAAGAAAAAAAATCACAATGGTTAT
GBYP-RAD_87	AAAACTGACTGCTGTTTATCTGTGATGTTTGTAGAAAGCTGCTACTGGACCTGCAGAGGGCGCCGCAGCTCCACTCAAACCTGTTGGTAAGAAGAGACACTTCCTGTCTCCACATCATTCTGCTGCTTCACATGTTTCACTCACTTTAAACTGAATGTAAACACCTGTACGAGCTGCTGACATCATTTTGTGTCTGATTGGAGGAGCAGCAGCGGTGCGTTCACTGACACCTCGTTGTGTCTGTTTCTCCTGCAGGAACAGAGTTTGTTCGTCCGGTYGTCGGTTACTTCTGTAACTTGTGTMAGGTGATCTACGCCGATGAGGR[C/T]GAAGCCAAACTGCAGCACTGCAGCAGCCGCTCGCATTACACTAAATACCAGGTGAGCTCCCAGAATCCTTCACTGCTGCAAACTCAAGTGGATGGAGAAAGGTGACGTAACCCCTCTCCCACTGCAGAAAACACGTTTTATATCATTGTAACTTCAATATCTTTAGTCATTTGAAAACGTCACCTTATGAAAAGTGTTTTTCACTGTTTTCTGATATTTATTGACTGGACAGTTGATCAAAACAACAATTGATGTGAGAAAGCT
GBYP-RAD_88	CATATTCTCACAAGTCCAGCTCTCGTGCAAGGAAACATTAGTGCTACACTGAGCACCATGCCATCATTGAATCTGACATCTTATTGTAACCCCACTGTGTTTGGCAATAACCTGTCAAGGAGCAGAGTGTGATATTAGGTCATTATTCTATAACTGTGAATGTTCACACAGTGCCCCTCCTCCAAACCCCCCAAAAGTAGCTAGTGCTCTCACTTTGCAGACGGTTTGCGTGTACTTGCGGCAGTGTTCCTGCAGGTCCCACAGGAGCTTATTAGAGGGAATGGTAGGGCTTCWCACAACCTCAGCACACGC[A/T]TGCTGGCTYCCATCACAACAGCCAGCGGAGAAAGGGGAGAGAGGTTCACAATTACCAGGCTCACGTCACCCGGACTTCAGACACATTCTCACTGCAGTGGCTCTGCAGCATTAAGCAGAAAGGTCACTGGCTTGTTTGAAATTCTGTTTTCAAAGATTCTAATCATAAAGTAGATAATGTTATCCACATTCATGGCCATTATTCGCTTACTGTGCAAGGATACATAAAGAGAGCCACCAGTCAGCGTCTTGTTGGCCTTAACTAATGGCAAAATGTG
GBYP-RAD_89	GAATGTGGATAACATTATCTACTTTATGATTAGAATCTTTGAAAACAGAATTTCAAACAAGCCAGTGACCTTTCTGCTTAATGCTGCAGAGCCACTGCAGTGAGAATGTGTCTGAAGTCCGGGTGACGTGAGCCTGGTAATTGTGAACCTCTCTCCCCTTTCTCCGCTGGCTGTTGTGATGGGAGCCAGCAAGCGTGTGCTGAGGTTGTGAGAAGCCCTACCATTCCCTCTAATAAGCTCCTGTGGGACCTGCAGGAACACTGCCGCAAGTACA[C/T]GYAAACCGTCTGCAAAGTGAGAGCRCTAGCTACTTTTGGGGGGTTTGGAGGAGGGGCACTGTGTG
GBYP-RA	AAACACAAAAAAAAATTCTGGTTGCAGCTTCCTGAATTTGAGGATTTGACACTTTTCTGTGTCATAAATGATGATAAAGTGAATATTTTAGAGTTTAGACTGTTGATTGAATAAAATAAGACAAGATGTCACTATGAGCTCTGATGAAATTATAGACAGAATGATTTATTGAAAAAATAATCAGCAGATTAATTGATAATgaAAGCTCTMCTATAGATTAAACTCTTCCTGACGTCGTCTCGACTTCGTCCTGCAGGTTTAYGAGTTCAGGGTCAAGGAGTCGAGCATCATCGCTCGCGCTCCCRCTGAAGACGAGGACACGCCACC[A/G]AGRAAGAAGAAGAGGAAACACAGACTCTGGGCCACTCACTGCAGGAAGATCC

D_90	AGCTGAAGAAAGGTCAGAGGTCATATCAACCTGAACATGAAAGGAAACAGACGTGTAGACGTGCTAATGGAACTGGAAAAAAACCCACTAAATACACTTAAATTCATACTCAGTTACAGTTTGTTTTGTTGTTGTTTGGACTCAACT
GBYP-RAD_91	TTGATAGCTAATCAGTGCCTTCCTAATGTGTCCTCTGCTTCCAGCTGTAAGGAGGACATCTGTCGTGGGGTTGGCAGCCTTCTGGTCTATGTGAAGAGCCTGAAGGGATTGGCGGCCATTAGGGACGCTGTGTGGGACCTCCTGTCCACnGACTCCATCAGTCAGCACTGGAACACTGTGTGCCAGCGGCTGCTGGAGCGCCCCCTGGCTGTCTGGGATGACTTCCTGCAGCAGCTCTTCCTTCAGCGCCTGCAGGTTAGTGTGCTCCAATTTTCATGATCTTGGTGTAACAGAAAATKAAGTCTGCATCTTTAAGCATCTGATCAG[A/G]TCATTCCATTGKCATATTTGTACGTGTTCATGCCTCCTTGAAATTCTGGGTCATGTTCACTCTCACCGTACTCACAGGCCTGCCTTCTTATGCAGTAAAAATTGTGCATATTGTTATATTTCAATGATTCCTTCCTTCCATTCCAAAAGGCCATCACCAAAGATGAAACTGAAGCCATCTCGACGAGCTCCGTCCAGCTCCTCACCTCGGCTGTGAGGGATCTGGAGGGCCAGACCATCCATACTTCTTCAAGTATCAACCCTGGCTCTGGCCGTGGCGCCCAGTACGAAGTAGATGTGGCCTCCTTCTTGTGGTCGGAGTCTTCAGGGGACCTGCTGAGCGATGCAGGGTGGGTCAGTGTTACCCAACGGGGGCAGCAGCAGCAGAGGAGTGGTCTGGCCATGAAGACCCAGGCCCTGACACCCTGCGTTCAGAACTTCTG
GBYP-RAD_92	CGCGCTCCGTACGTACATCAAGCCCCTGACCGACGGCTCTACGTGACGTCAGCGCGCTTCGTTCCCAAACAATGCTCAGGAAAAAGCCACGTTGACGATCTAGACTGAAGTGTAGTCCACAATTTGAGCCAGAATAAAGCAGCATTTTTTGTGTGGAAGCTCTTATTCCTTCTCGCCGCAGACTCCAGATCAGAGAGGACATGTCGTCGCCGCCGAAGGAGAAAGTCGAAACCAAAGGGGGACACCTCCCTGCAGGTAAACCCCCTGTCCTGTGATGTTGTTTTTGAAAGCTTCCCACAAACCTGGAGGCCTTTGTTTTTGTG[C/T]AGTGTCTCTCAAACCAGAAAAAAATCACAAGATGAATCACATACTGCTGCAATCATTAAAGTGTCAGATTCCAGCGATGACAACGTGTCTTAACGGTCGAGATTGCTTGTACTGTAGTCAGCTTTATTTCTCAATTTCGCACCTTTCCTTACTTCCTGATTGACGTGAGATGTTGCAACATCAACACATCTGGTGATAATGTAGCGATTTGGTAAATGATCGCAGTCTAATTTAGAGGTTTTGGTGACAATGTTGCAATTAATGGT
GBYP-RAD_93	AAAAAAAAAAGAAAAAAAGAAAAAAAAAAATCGAGGCATTGGTTTAAATTAAGTGTTCCTTCCTTCTCCTTTCCTCCCGGGTGTCGCTGCACCATTGTGCTTGTTTATACTGCACAATATTTCTGTTGGCCATCCCTCACTTCATCCCAGTAAAAATACACAGAGTAGGTCAGAAGTTCAGGCCCTAGATCAACACTGGCATTGTGTCCTGCAGGTGCTGTCAGCTGCTCCRGGGACAGCCAGGGATGGAAAATATACACATGCAAGCAGCAGCTCTGTGGATACACACTGTCTCTA[C/T]ATTGAGATGGTACTTGGGACAAAGTTACAGTGGCACAACTACAGCTTCGAGGAGTTACTAAAGCTGTTATAGCACAAAATGAAAATGAGGCATTTTGTGAAACAGCAAAGTAAATAACAGCTAAAGTTGTATGTAAAAATAATAATTGGGTGTAAGTCCCTCAAACTAATTCGCCCAAGTCATGATTTTnTTCATTTTCAGCTTTCCATCAAGGCCAATAGGTCGTGTATACAGAAATAAAACCTTCTTTC
GBYP-RAD_94	GTATGTATGTATATGTCAGACACAGATTAAGAGAGGCAGGTAGAGAAAGCAACTGAGTTTGTATTTTTTGCAAATAAGTAAAAGTGCCTGCAGGTAAAYATTTTTTGTGTACTTGTAGAAGTTGAGCTATTTTCTGAGCACAAGAACATGC[C/T]AGCTAAAGAKAGAGAACCAKATTTTYGGTCAGATTTTGAGCTAGAGTAAATACCTGTGCTTGGTATCATTTAAGGCCAGTGAAATCATATCNNNNNNNNNNNNNNAGCATCCAGTTCCTTATGCAGAGTTGTAAAACAGAGAACTTAGGATGTAAATGCATGGACTGTGCTGTCTAATTTGTATTGGGCTGAATGATTATCTGTGATTCTGAAATTACTTCCCAGGAATATATCACTCCTTTCCTGGGATTCCTGGGATTTTTTTTGTTTGGTGAG
GBYP-RAD_95	AAAAATTATGTGTGATGCAACCTCATTTTCTTTTCATCTTTTCTGAGTTTATAATAATTTATCCTTGATTGCTCTCTCCATGCTCAAAAAGATGAGATTGCTGTTGGGAAAATTATATTTATACTCATTACTTGATAAAATTCCCTTTTATTTAACATGTCCTTATTAGTAACAGCAGTGGACAATCTAATCTGGCTCAAGGTCTGGATCAAAAGCAATTAACAAACACAACCTCTGTGCTATTTCTCCTGCAGGGAGAAGARGATTGACCAGGAAGCSAGGACGAAGACTGGSTTCAGTATGCAAAAGGTCTGGATAGA[A/G]ATCTTTAACCMCACAGAGAATGACCAAGGCCAATACACCCTGGAGATGTTTGATGGCAAAGAGACACACAAACGTGTTCTTAACTTAACTGGACAAGGTGAGAACAAATGGCATTTTGGTTTACAAGTTTGATTTATTTGAAGGATTATGTGTGATGCAACCTCATTTAACAACACAATATAAGATTTGTGAGATGTTTTGAGCTGTCAAAACACAAAACTGATGAGATTATCTTTCTTATTATCTCATATGGACTCAATCTTGAGTGGCACTTTTCTGTTAAGAACTTAATTTGTAGTCGATTAGTAATTTACAAAACCAAATCAAACTAAAATCAAACTAAAGGTAAAGAAAAACTAATGAAACATGAATTAAATGTAAATAATGATTAATATTATTATTTATTTACAGCCTTTGCTGATGCTTTGCTGGAGTACCAGAGGTTGAA
GBYP-R	GGAAGTTACAACTACAACTTGTCCTGCTAAAGTGATTTTCTGTTTGACTGGCGCTGCACATAACTTTCATTATCTAAGTATTTCCCGGTTAAGTTATTTCTCCAGTTTTATTGACGCAATCTGATATAATATAGATCACTTGAAACCAGCTACTAGTTTACGCACTAGGACTTTCCACACAGATGTAATGCTACAGTAGTAATGATTTTACAAATAGCTGGTGCAGCCCAATCCAGGGTATTCTTGTTCCTGCAGGAGTGCCACCAYAAGAAATTATTATCCCGTCTATTTCACTTGGTAACTTAAATDACTCA[A/G]ATTCTAATTTGGTCTAAGTGCATTATTTTCATGCAAGAGAGTCATTTGGCTTTGTGCACAAAAGTGTTAAT

AD_96	GTTTATTTGCCAACCAACCAGGGAAGTTGTTTCTTCTATATGAGGCTGAAAATAGATTTGATACGCTTGAAATAACATTCAATGAATGAACCATAATTGTGCATTACCAAAACAGCCAACTATAATCACTCAATAATAACTGTATTACATGGCCGCCTTCAAAATTGGTGCAGCCAGACATTGAAGCGTCTACATCAGTTATTCTGCCCGCAGGAGTCGCCACGCAAATGCTGCTCTCTTGGAAGAAAGGCATTATGGAAACCTCCCTATCAAAGCTCGGGATCAGAGTTTTTAAAGTGTTTTGCCCCTAAAATGAGCAAGCGAGCCGAGGCTCTGAGGTCGTGTTTACACTCCTCCTCCATGGAAAAGTGGACCCTGCATGTA
GBYP-RAD_97	CAGGAGCACCTAGTGGAGCGGAGGGGTCGTCACATGCTTAAGACATCAAGGGTTTTCCTGGTATTTCATTTTCATTTCATTTTGCCCATCCACCACTGGGAGSAGAACATGCAGTGTCTGACTCCTTGTTCAAGATTTCCAGAACATGCTTGCGCTCATGCTCCTGCAGGTCTTTAGCAMCAGGGCAGCAGRGTTTCATRYRAGAAATGTGGAYAACTWTCAAG[C/T]TGAGAGCAAACCAGAACTCTGGYTGGTCTAGGGATGATAGGCAGATGTTAATTTGTGTCCCACGTTGTGGGGGCCAGATGCATAAACAATGCATACATACAACTTCGCTCCTTTTTTCTTTAAGGCATTGAGTGGCTCAGTAATCTGTGAGGTTGTAACAAACTGATGATACTGCCTTGCCATGCCCAGGACCTTCTGGATCAACATGAACTCCAGCTGTAGACCCAACACTTACGTTACTGACACTATGTTAATAATTTGGTTCATCATAGCAAAATC
GBYP-RAD_98	GTCAGTAAAAAAATGTTGTCCCTCTTAAAGTCTACTCAAAGTGAGAAGCTGACAGCCTACGCCAAGTACAGCTATGATGCACTGGGAAAGCGCTTCCGCATCAGAGAGTTTGGATCTTATAAAAATCAGACCTTCCGTTTTGATGCACTGCTACTCTTCAATCTGGTAATGAAAACAAAGCAATGATATCTGCATTAAGAAATGTCATATACAACATAAATTAATTGAATTGTATAATGCCATTGTGTCCTGCAGGGTGTTATGTATAAGATCAACTACAGGAGAC[A/G]CACGTGTCACAAGAAGCCACTGAGTGTAGACTTCCACCCACTGGCGATACCACAGGATGCTTCCCTGCTTGGCCAGGTTGTATTGGGCAGCTCCTCTGGCCCAGGGCAGGGTATCCTGGTCAACACCTGGGCGGGGGATCTCCAGATGAAGAATGGAACAGGTAAGAGGAAACTAGACTAGGAGATATTAAGACAGAAAAACTGCACAAAGTCATGTGGTGTATGGTAGCACATGACTTTCCCTGATTCATCAATCTAATCGCTGCCCTTGTTTTTATGCTCATGAACCTGCTTGTCTGGTTGTGCTGCTTCAACTTCCTCGTGATCCACTTCTGTTTTCAGCAGCCAAGTACATGAGCACTGTCACTGAGTTTGGATGTATTCCTGTCAGCACTCTGTTTCATACCAACAAAAGTGGATGGGTGGTGACCAGGTTAGTGCATACACAACAAAAAATCTATCTAATCCATCTAGTGTTCACAG
GBYP-RAD_99	TTTATGACCTAAATACTAATAAATCGTCTTCAATGACATTTTAAGACACAACTGGTGTCATACCCATAATACCCGGCCAGGCTAGATCTTCATTATCGTCCCTCTCATGTCCAGGAGCCAGGTGATTAAATCGGTCAAGATGCTCCAGGAGACCAGCCAGGAGAGGGATAGAACCCGTCTCCTGCATCAGACCAGCGTCAATGGTGAGGAGGAGGACGATAGACACCACCAACTCAGGCAGGAGCACTCCTGCAGGAGA[A/G]AAGACCGCAAGTCATYCACAATTTATGYTGCATATACACACTCAGCAAYTTTTRAGAGAGGRAATTACCRGTTAGATCTCCTTCAATAACACGAGATACTTCAGCAAAGTGGCGGCGACCGGTAGAAGCAATACTTGTTGCCACTGGGAGGATGTCTCCAATGTGAGTGCACAGCAGGGCAATGTACTTTTTCAACAGGGAACCAACACCCAGAAGCTCAGGATCTACAAAACAGCAGACAAAACTGTCCATTTAGAAGTAATTTTCAAACTTCATCTCTAGTTACTCCAATCTGGAAGACTAGAAAGGTCATTTCAAAGTTGAAATACA
GBYP-RAD_100	GGGTTTAACAAAACATGCAGTACAAGGTCCTATCTTGGACTCCCAGATGGCCTTCCTCCAACTTCAAAGCTTGGTTTCCACATAAGCCCTCTCACTATTTTTGTATCATTAAGTCACAGCCTGTCTGGTGAGGTAATATCATCTCTGTCTGTGGGCATTATTGTAAATGGTGCTGGAAAAATTGTTAATGAACCATTACAAGATACAAAAGAATGAATGTTGGCACCGTGTTGGCACAGGAAGCCTCTCCTGCAGGCATTAAGGTCCTTGTGCTR[C/G]TCTGCTCTTTTGTTTGTGTTATTAGGCTACACCTCCATCAAAGCATGACAGTCTTTATGATAAT
GBYP-RAD_101	CTGGCATCTACATCTACATAGATATTTTTTCAATTAAATGAATGCATACTGTAGATGATGGTCTGAAATCATCTCTTATATTATGTTGCTCTTTCTCATAGCTACCCTGGGGGGCCTAATGCAGGACCTGGTGGAATGGGGATCCCTCCACACTCTCGTCCTCCTTCAGACTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAGCTGCCCTGCAGGAAACTCAGAACAAGGACATGAACCAATACGGACCGGTAGGACAAGACACACACCTGATTGTACCTGTGTGATACCATCTGTGT[C/T]CATAAACATTTTGTGATCTATAATAGACTCTTTCCAGTAGCAAATTTGCAATATTTACAATCAACTCTGAGATGGTTGATCGAACCCATTTTGTCTTCCAGATGAGTTCCTCTTTCCAGATGGGACCAAACCAGGCGTACAACAGCCAGTTCATGAACCAGCCAGGACCCCGCGGCCCTCCATCCCTCCCTGGGAACATGGGCACAGGCATGAATGCATCCAACATGAGCGGGCCCCCCATGGGGATGAACCAGCCTAGAGGCCAAGGCATGGGGCCTTTTGCAGCCCACGGCCAAAGGATGCCTCAGCAAGGCTACGCAGGGCCCCGGCCTCAGGGCATGGGAATGCAAGGCATGAAAAGACCGTACCCAGGGGAGGTGAGTGCATGTGAATTATACACTTTCTCCTTCACATTTTAGCTCCTTTGCTG
GB	CGGCTGGCATATTACTGCCAGGAAATGGGATCTGCAGGTGTGAATTAGAAACCAGCAGTTTACTTTGTCCGCTGTTTCATCCCATATGAACATCCCATAGTTTAGCACTAGTGACTATTCTTAGTGACATTCACTAGTTTCTGGGACGTTCTGA

YP-RAD_102	ATCAGAATAAGTGTTAACGCAGGTCCATCTTCTTCAGTATTCAACAGTAGTCGAGGTCTCACATGTTATATGAAGTAATGTGTCCATGAAGGGACCTGCAGGA[A/C]TGACAGAGTTATGRSGCCTYGCAGCTTCTTGCTGTTMACAMTGATTAGGAAACAYGTCTGTCACATACRGTTATGACTGCAGGTGAAACGCAGCCAGAGAGTCAGAATGACCTTTCAGACAAACGACTTTATAATCAAAGTTCAGGAATGGATGCAGAGTCACATACAGCAAGCTGGATAATGTCATGTCTTGACGTAAAGCATTACCGTAGTGTTCATCTTCAAGTATAAAGTGTTGATGGAAAGTGGTGCATGTTTTTAAAATCTATATTTAACACAGACATCATGAATCATGTAAAATAAACGGTTAATGGCCAGAATAAAAGACAGAG
GBYP-RAD_103	AGGAAGCAGGAAGAGAAACGTCCAGTAGGAAAAGAGAGCCAGGACCCAAGAAGGAGCACCACATGCCTCGATCCCCAGAGTCAGACGGAGAGCGAGAGAGGAAGTGTGCAATTCTTCTTTTCCTCTCTCTACCCCCCTCTTCCTCTCCCTCTGTCTCTCTCTTGGTCTTACCACGCAGTGGGGTCTTTTCTCTCTTTGCGGGGAGCCTCCTCATTCCCTTCATGCCTCTGTCTCCTCCGCTTGCACCTCCTGCAGGACACRATGATGACGAGGAGGATGAYCACGGCAGCGATACCRCCTCC[A/G]ATGGCCAACACCAGAAGGAGAAGCTYGGAGAAAGAGGCTGCAGAAGGAAAGACAGGAATGGAGGCTGAGTGTGCTTGCTTGACATTTTCAGAGCCATTTAATTGTGTATTCATATCTGTGTTTGCTTTATCGACACATTTCCATTGTTAGACATGCTAGCAGCATGGTCCACCAGTTTGTTCCAGACTGAAATATCACAACAATTATTGGATGGATCGTCATGAAATTTTGTTTAGAGATTTGTGGTCCTTAGAGGATAAAATACAGACTCTGGTGATCCAGTGATTGTACGTCTAGCACCACCAGCAGGACATTTTCAGGCTCTTAACGAAATGAGGCACCACTTTAGTCTTCTTGACATGTTGTTTCCTGTTTAAGAAGATAACATGTCTCCTTATAAAAGAAGCCAGAATAAAATATCTAATTAATATTTGTCATAATAGGTCATTTAAACATTAATGTGACAA
GBYP-RAD_104	TACATCTTATTTCATTTAAAAGTGGAACAAATGAGATACAAAGCAAGATCGCTACTTCTTACAGTAAGTTCTTTTTGCACACGCAGTCTTTTGTACGTTTTTCTTTTTACAACTTACCATTCGTACCCTCACCTCGGTGCATCCACACTGTCATTGCTAACGGATGAAAATAACTGTAATTTGTATCATTAGATGTCCTTTCCCACAAGCAGCCTGATGCCTCTCTGAATCCCTGACTGTCAGAAATACCTGCAGGCTCAGCATGAGTCTATGAGTCACTGCTATCTT[C/T]TCAGAGAACAAAGACAAGTACRGAAAAGACTATCTCAAGCTYTCCAAAATGATCGGACACTGTCAGAACATTTAGAGACTGTTAAATGAAATGACACAAATTGTGGTCAAACATATAGAACAAATGATTGAAAACTTGAAAAATGCTTTAAAAATACAGTATATGGCAGCAACACCGTGTGTTGCTATATGTCAGACTTTACACACTCTCTGCCTTAGTGGGAAAGAATGAATCAAGGCGATCCTTAGTTCATAGGGGGAGATAGACAGACAGAGGAACAAAACGAAACGGTGCGAGGAGCTTACTGGCAGTGATGGCAGTGCCAGATGGGAGAGGGAAGAGCTGCCCATGAGAGGCGCCAGTAAGCAGAGACAAGTGGTGCCAGCCCAACTGTGTCTAAAAGGAGGTCCAGCTATTTAATCAAACCCAACACTGAAACCGCACCAGTGCCAGATGCAATTCAAATCCTTATATAACCCAA
GBYP-RAD_105	TATGGCTCGACCGGGACAGACCGTGATGTAATGTAATGTGATGTTTAAATCTGTGATACTGAGCTATTTAAACAAAACTGATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATGAAAACAGAATTAATATGTGTGTGTGAGAAGATAATGAAAGCAAAGTTTTGCGATGAATATTTACTAGATTTTCCAGCTGTTCTTGGTTGTGCAGCACGTTCAGAATCTGCAGCAGGTCGTGGTCCTGCAGGAGGTTCAGGMTCYGCAGAWGATGCAGGTTCTA[A/C]CCGTGATCCAGGTGTTGGTGYTGGAGGTTTTGGGTCCATGGAAGGCTCCTTCCTGTGGGCTGAACGGCTCCTAGAGGCTGGTAATGAAGAGGAGAAGGAGGAAGACATCTAAAGCATTAACATACCAACATGCTAAAATAACTTTTTTGCAATTTTAACATCATTGATGTTATGCATTAACACACTAACATTAGACATGCTATATTTATTGTAACATACTGATAAAATATTAGTAGCTACAACCGTAAGTATGTTAACATTACATACTGTATTAAAAGCTTGCATACTGACACGCTGACTG
GBYP-RAD_106	CTTGCAGGGATAAACAGCCACAATTCACTCGGGGGTTAGTTTCTTGTGTGAAAATGGCAACCTTTCCCCATAACACCTGTATGAATAATTCAGCACTCTGGGCTCTATCAGAGGCTGTCAGAAATGTCAGACGGTTGGAAGTACCCTTGGCCTCCCCCAGAGGATGTTGTCTTAGGGGCTTGCACACACACTCACAACATACACACTTGACCAAATGCCACAGCTTTTTCATTGCCAGAGCTCTACTGCCTGCAGGACACTGAAAGCYGAGCACACCTGCAGTGAGCAAACTGTTGCAGTTTTCCCCYTTTTTTATGGGCTGTTATTG[G/T]TAAATGTGACTTTTTCCACTAAAAGGTGCTACTTCAGTCAGCACTTTAAAACTGAGATAAACAGGCAAGGCTGCACTGGTTAGTGACCATAATTACAGATCATAAGCTGGACATGTTACTTTTGACTGAAACTTGGCTGGACTATAGTGGTAGCTTTACACTAATAGAGGCATCACCGCCAAATTTTAACTTTTTAAATGTTTTTAGGTTTGATAGAAGAGGTAGATGTGTATCTTCTCTGATATATTTTTATGCAGGTAA
GBYP-RAD_107	GAAGTTGGTGATCCACCTGCAGGTACAGTCAGAAAYGTGCAGTTGGTAGAGCTTGTCCTGCAGCAGAGCTGGGATGAT[G/T]GTGTWAAAGGCGGAGCTGAAATCTACAAACAGGATCCTGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGTGAACTGCAGGGGGTCCAGGAGTGGGTCTGTGATGGATCTGAGGTGGTGAGGAGGGGGAACTGGAGATGATTGCTGGAGTCAGGAGGGATGTGTTAGGACTGTCCTTTTGTCTTTCAAATTGAGAGTAGAACTGATTCAGGTTGTTGGACAGGTGTGAGTTGTTAGGAGAG

GBYP-RAD_108	TGCAGGAAGATTCAGCAGACTCAGGAGTGGTGGTGCATCGTTCCACTGTG[C/T]ACAATGCTTGCACAAACAAGACCTTCAAATGAAAGAGTCAGTAGAAGAAAACCTTACCTGC
GBYP-RAD_109	TGCAGGAAATAAAACTGTKCAACTGTTCTGTGAAGCCACAGAAATGTGCTCATYTTAKAYCATTTCATAAACATCCTCTTTGAAT[A/T]ATATTTCAACCATCTCATCAACTTCCAGCCATAATACC
GBYP-RAD_110	AGAGACGGGGCCTCCAAAGAGCGAGGAGAGAGCATGTGTGAACGTTGCTCCAAGCTGCGCACCGAGCGCAAGGAAGCCATCCTGGAGTTTCTGAACACAGAGTCGAGCTACGGGGAAGACCTGCGGATCATCAAGGAGGAGTTTTACTGCCCCATGCAGAGCGCCGGGCTGCTGACAGCTGAGCAGCTCACTGTGGTGTTTGGTAACGTTCAGGAGCTGATAGACGTCAACGACCGCTTCACTGAACACCTGCAGGACAGCATTGACCA[A/G]GCCTTTKACCAGGTGACTCYCTCATACACATACTGTACATATACACACACCYACACATCRGRGCTTAAATACAGTGGTCCTCTTTTGCTGATTTTTAATGCTCTATGCTTAGAGCGCCTGCTAGTATTACATAAGTCACCTTCAGATTAACATTTAGAAAAACCTTAAATGTCATGCTTCCTTTTGAGTGCAGTTGCCTACAATACATTGGCACTGCTAAAATCTCCATCTTAAACATTTTAGACTGTTATTGAGTGCAAAAAGGCACACACACACACACACACACA
GBYP-RAD_111	TGTCACTGGGGATTTAAGCTTCATTTTCTCACTGGAGCATGAAACCACTGTTGACCAAAAGAAAATACATACAAGCTACACACCTTTAACCATTTAACATCCAGTTTCAGTTCTGCCATGCATTGTACCAGGACCACAATGATTGAAAAGATGGGAGTCTAATCTATAAATACATTTATTACATGTTCATATTCATTTAACTTTTCATAATACAATCAGTCCATGAAAATCCAACATAGTGTTACTATCCTGCAGGCAGAACAATGGGTGGCAAAGAGATAATATGTTCC[C/T]TCGCCTTGTGGTTTTTGGTATTGTGCTGAGATTGTTGAGCAGTGGAGCATCACAGGAGGAGGATGATCAGCTGCGTCCTGCCCAGCAGGAGCTGATGACCCCTGAGTCAACCTCATCTGTTTTCCCCTGCAGACGAACACTCCTGGAGCTCAGAGTGGGCTGCTGCTGAGCCGCTGTTCATGTATCACCAACAAAATCTGCTTACAGCAGCCCACTGTGCTACACACATCTCACTGTAAAGAAGGCTGGGAAAACAGCTCCTATGTCTTGTACACCTGTAAGATAGGTTAAAAAAACCT
GBYP-RAD_112	GCCTGCAGGARRAGAAATATGGATGTCAAAAAATGGTGAAATTGAA[C/T]GGTCTTCTTTCMCAAGGAAYGAACCAGCCTGCATSGCTGCCAATGTGATAAGGGTGCAACCAGGGCCGACACAGATGCCGGTTACCCATGTTCAGGACATAAAGTCTTCTTTTGAACTTTTCATCCC
GBYP-RAD_113	GTTATATCCTGCAGGGAAAATTATGAAACAATGAGGT[A/G]AAAATAAAGGAGCTGTTCTTAACATCTCTCCTTTTAAGGCAGAAATTGAATCAAACCATTAAAATTGTAGCTGAACAT
GBYP	TGCAGGTCTGCTGCAACTCTCAGTCCTTTTACATCAAGGCTGAAGACTTTTCTGTTTGCCACTGCCTTTTTTAAATCA[C/G]ATTTGAGGCTTTACATCAAGGCTGAAGACTTTTCTGTTTGCCAC

-RAD_114	
GBYP-RAD_115	TTCCAATGCAACAACGTCTTCTGCTCAACTGTCATTCTTGGCAAGCATCCAGACAAACTCAGAGTGTTTATGTTAGAAAACTGGAAAAGCACCACTCTAAACATTTTGGAGGAAATCAACCACCATGTTTTGAATATTCCAAACATGTATTTCTCTTCAGTCATTCCATTTCATACACATATACAAATGTTCTCACTACTTCTTCATGTGCTCTCTTTAATCTCCATGGTAAGAAACAGATTTTTTCTCCTGCAGGCAATAGTGAGAGGTACACTCCCAAACCCACATTGCCACTTTCAACATTTTAG[C/T]ATCAACAAAACATCAGTCAGTCCACCACWTTGCTCCAAACTAAAGTGTCTCACCAACTA
GBYP-RAD_116	CGCCTGATTTGGTCTGAATATGGCCTAATCCGGCCATGATTCTGAATAGCTACTTGATCCATTGTTGATATAAAATTTTTATTACATTTCAAAATACAAACAGTGAGCTTGGAGACAATTTAGATACGTAGGGTAGTGCATTTTTAAGTGGCCATATAACTGTGCCACTTTTTAGTATGGCTGTCCTCAAGAGTCTATAGGCCTACTGTAGACTATAGGCTAGAACAACCACCTTCAGCTGTGACACCTGCAGGCTGTAGGTGTTGGTGGGATCYCTGTGTTGACTCTGATCTCCCTGCCTCTGT[A/T]ATMAYAGTCCAATCAGAAACAACACAGGCTGTATTTCATGTGTTCTTGCTTCTGAAAGGTCCTAAAATAACCCAGAGTTCTCCTTTAAAGAAGCAGCCAATTGGCCTCTGAAAATAAGGGCTGATTGAAATGTGTCTGTTGGGTGGAGCTGGGATGAAGATTGAGTGAACGGTCTATGTGTGTGTGTGTGTGTGTGTG
GBYP-RAD_117	CACACACACACACACACACACACCACTACAAAGAGGGTTAATAGAGTGCTGCAGTTGTCCTGCAGGACAGTC[A/G]GAGGAAGGTAAATAAATCAATGTGACACTGAAATGAGGAAGTGAGTGAAAGAGAGAGAGAGGGKGTGTTAGAGTGDKGATGTGTGTGTGTGTGTCTCTGTCTGCACAGAGATCCGTGTGTTTGTGTGTGTGTGTGTGCGTGTG
GBYP-RAD_118	AATGGCCATGTCTTCCCTACTGAGTAAGAGACTCATATTCCACTGACTCACTCCTCTCAGAGCTGGTCGAAACACTAATCAAATCTTCCGCTGGTCTTTTTTCACAGACAGACAGCAAGATAACAGAGAAACGAGAAGATCTGTGATAAAAATGCCAGTTAAACAGCCAACAACAACAGGCAGACTTCCTAATTGCTCACACCGTACATAAACAGTCCCTCTTGAGCAGGTTTCATTCAGTTCACTGTCCTGCAGGCTTGGTGAAAATGAAGCCACYTCWTAATGAACTCTGCAGTATTTGGACA[C/T]AGAAGACAACCTTCCACTCAAATCTTGGATAAACAGACTTTGAAATACTGTATTGATTATCCAGCAGATCTGAGAGCCATGGAGAAAAGTTTTGATATGCTCATGGAAATCAACAATGTGCACACTCTAATGATTCATTGAAAATAATTTGGCAACAAGTGCGCCACATAGCAGTCGAGTGTTAAGATACTGACGCTTTACCTCGGTACACCAGTTTTAAAATGTTTTGTGTGCGTTTGTTTTTGAGGGCAGGCGGTCAAATAAACGGGTGATTGCTTTTCAAACAGGCTGGTGGAAACCACCCCTCACACCACAACAAAGTGCAGTCTGAGTGCCAACCACACTGACAAGCTGTGGACAGCAAGTTTACTCTCAAAGAAGGAATGAATCAGCCAAAATCAGACATGTCCCTGCTCTATAATCTGACCTGTATTTGCTGGATAAGTATTTTACTTTTTCACCAC
GBYP-RAD_119	GTTACAGAGCAGCACATTACCTGCAGGTTTATAGATCAGTTATAA[A/G]CCATTACAAAAAACAACTTTTGGTTGCCATGTTGCCCAAAAAATCACTTTGGCTGGTGTTTATCCTGCTCCATCATGTCACTCCTCCCATGGACCGTTCGACCTCTTACCCTCTGGAAATGGGCTGCAGAGCATCTGGACCAGAATCCAATTATTACCATCATTTCTTTTTTTCTCCCCCTCTTTATTTGGTCAACAGAGACAGAAAATATAAGACAAGACACACTACAAATAAAACAGACACCATACAGAACATATAGGGGAGTGTGAGTAATAGAAATACACAGAGAGCAGCATGGCTGCCAGGAACAGCTGA
GBYP-	GGGTGTGCTTACACATGTAAGTATGTGTATGTCTCCTTTGTACCTGAATGCTTTGTGGCAAACTCTATCCACCCAGCCAGCAAGTGAAGAAAACATCTTTTGTTAACATACTGTAACATTTAATACTAGAACCCTCTAACTCTCGTACTATAATGGACACACACAAGCATTTACATGAAAATACACCCTGACAGATGCACACACACTCTCTCACACACACAAGTAGCAGTACCTCTTGCCACCTGGTTCCTGCAGGCACGYAGAGACTGAAAGAGGCTGAAGCCATC[A/G]ATGGTGACCAGCGCAGC

RAD_120	AGGATACAGGATACTCAACTCCTCATGCTGWAATCAAACAAATCAGTTATCATACATGTGCTGAAGAAGACCGTAGGATAAACTTGATAGCTCAGGACAAAGCTTGTGAGATTTAACTACAGATATGTGTTCCCAATAAAAGAACTTGAACAGAATTTCCACAGGTGTGACAGCAATGGCCAGAGTATGTATTACCTGCTCGGTTACTCCAGGATGACGAGGGATCTCATATGTGCGACACTTGAGTCTCAACACAGGGTCCTCATGCAGCAGCTGGGCCAGGAG
GBYP-RAD_121	CTGTTAAAATGCACACACAGCTGCAACCTGAAAACCCTCCAACCCTCCACCTCTGCAATCTTCTTTCTATGCACCACCGGCTTTTTCTTGTCTGACAACTCATCTCGCACCTGACGCCTTTTACATCAACTTCTACACATTTATGTCAGGTCGAGTTGTTCCTTCGTTCCAGAAACTGTGTCTCCGTGCAGAAGAAACACTCCCGTGTGACACAAAGACGTCAAAATAAAACATTTCTTTACTTCCTGCCTGCAGGA[C/T]TGTACTGAACACCYGTCAGTTCTGGATGTTTGCTGCAMCCDTRACRGTTTCATTTCRCACYTGATTTTCACAMCTTTTCMCTGTGAGGGAACTGAAGTGTTTCTGTCTCAAGCGGCAGGTCTTAACTGTCTGTCAGCGCTCTGAGATGACCCAAAGTCCCTCTAAGACTTTTCCCAGCAGCTCCTGAGCTCGTCATGGTTTCATAAGCTGCTGGAAGAAATGCATGTTGGGAGGATTTTCACTGTCTCAGCGTCTTGTGTGAAGCGTGAGGAATGACAATTATCACCGACGCTGTGGGACGTCTGAAGGCGACAGGACGGAGATACAGACGTAGAATGCTTTGTTACTGCTGCTTCATTAAATTTCACTGTTTTCTATTTATTTTCTTCTTTCTGCAGTTTCCACAGAACAACTTCGCTGGTTCCAGCTTCTCCACTGTGATGATTTACTGCTTTTCTGTTCTGTTTTGTCTGTTTTACAGCGTTGTAAATTTTTGGGGTTTTGGACTGTTG
GBYP-RAD_122	CCCTGCCCAGACCTTGCAGACCCCAAACATGTCGTCTTAAAACCTGATGTTAGTCTATCTGAGCTTAAAAAACATCTCTCCCTCTCCCTCTCCCTCCTGCCTTCTGCTAAGCAGCCTTTAGTTCTGATCCTTGATGGCTTGGATCAGATCGGAAATAACTTTGCAGCGCAAATCATTGACAGCCTACCCTCCCCCCTTCCTCCCGCAGTCAAACTCATCCTGACAGTCTCCTCCAACCGAACTCCTGTCCTGCAGGCCATCGAAGCACATTAYCCACAGTGCAGTCCA[C/T]CTCCCTGTGTTTCAGAGGGCAGTGAGAAGAAGTCAGGATATGTGTGTGTCYGGCTGGGGTTGGCCGACAGGAAACAGTGTGTGAAGATGTTGGAATCGCTGCTGAGCAGTTCAGGGAGGAAGGTGACATCAGGACAGCAGGCGCTGGTGAACCAGGCGCTTGCTTCCTGTTGTCTGACTCTCTATGCTCGCCTCCTGCACATGCACACATCTCTCTGGCTCTCTGGTATAACTGATTAGAGTTAAATAACACTTTTTAGAGATATAATCACCTTGCTTTTCTCTTATTCTGCTTCTTTTCTTTTTCCATCCATCAGATTCAGAGCTGACTGAGTCGTCTCTCCACGATGGCGTCCATTCATCCATTTCTGCACTGCTGGATCACCTCGAGCAGAAACATAGTCCTGGTCTCGTGGCTCGTGCCGTCTCTTACCTCACCCTCTCCAGGGCTGGACTCACAGAGGCCGAGCTCACCGATCTCT
GBYP-RAD_123	GAGAAAGGATGCAGCCTTGAGGGGAACCGGCTCTGATGGTCTGGGAGTCAGAGATGTGCTTCCCCGGCTTCACATGCTGCTTCCTGTCAGACAGAAAGTCTGTGATCCACCTGCAGGTGGAGTCGGGTACATTCAGCGGGGAGAGCTGGTCCTGCAGGAAAACCAGGAGGATGAATGTTTTAATGGTGAAGCTGAAGTCCACA[A/G]ACAGGATCCTGGCRTAGGTTYCTGAAGAGTCCAGGTGCTGGAGGATGAAGTGGAGGGCCATGTTGACTGTGTCTTCTACCCACTCGTTGGCTCTGGATGTGAGGTGGGACAGCGCAAGAACTTCATGACCACAGAGGTCAGGGCGATGGGTCTGTAGTCATTGGTCATTTCTGGTATACAGACAGTAAGCACTGGTGCTCCCCATGGATGTGCCCTCTCTGCACTGCTCTTCTCCCTCTACACCAACAACT
GBYP-RAD_124	CTGCTCTCTGTTTCAGATCATCTTTTACGAGGAGAGGAACTTCCAGGGCCGCTCCTATGAGTGCATGAGCGACTGYKCTGASMTGWCCTCCTACCTGAGCMGSTGCMASTCCTGCAGGGTGGAGAGCGGCTGCTTCATGGTCTACGAGCGTCCCAACTACATGGGCCTGCAGTTCTTCATGAGGAGGGGCGAGTACTCTGACATGCAGCGCATGATGAGCATGGGAATGATGTTTGACTCCATCAGATCCTGCAGGCTGATCCCCTATGTAAGAKAMCTCATCKAACKCTGACAGCATCCCTTTGATTGATATTAATTTAAAGTTGCTTG[C/G]ATTTTTTTWAACGTGTGGTAATATTTACATTTGCCATCTTCTGAATTACAGCACAGAGGCCCATTCAGGATGAGGATCCATGAGAGGGAGAACTTCAGTGGTCAGATGAATGAGCTGATGGACGACTGTGACTCCATCATGGACCGCTTCCGCATGACTGACTGCCAGTCCTGCCAGGTGATGGACGGCCACTGGCTGATGTACGAGCAGCCCCACTACAGAGGCAAGATGATGTACGTGAAGCCCGGCGAGTACAGGA
GBYP-RAD_125	CACCCACATCATACTGTAGGTATCTGATTATGCTGTCAGATTACTAAAAGTTAATCCACACCTTCCAGCCAGTCAGAATGAAGAATTCTCAGTGGTCAGGGTGTAAACAAATTTAAGAGGTTCTTATCTTATTTGTTTATGTTTCATGTTAAATAACAAATATCAGTAGGTGGCGTAGGCCTAGTGTACCTGCAGAGTCAGAATACACTTGTACATCTGTTGAACATCACCCCCCAGCAGGTCACAAGCCTGCAGGTTTGTGTAGATTAATCCCATTCATTCTG[A/G]TAGAAMAACATCAAACTGCACTCACATTCCCTTRTGCATCTACAGCGTGTAAAGATGCACTTTTGAGAAAATTGTTGTCCAATATTCTCCAGTGAGGTTAACTTAATTGTAACATCTACTCTGATGATGTAGTGGCCACATTTTTCAAGAGAAGCATCTCATTTTGTTGCACAAGACTTTTTGCAGTTCCAAAACAACTCATATTTTTAGTTGAACAGCTGAAGCCAATTTGCTATTTTGCTCTTTTAAGTGAGGGACAGTAATGGAATAGAAAAGCAAGTCTCCAGGTAACATTCATTTATTTT
GBYP-	GTTTCCTTCCTCAGTATTTTTCCCTCAGTTTCCCCAAAGAAAACAGGGTCATGTGGGAGTGAGGAGTCATGCTGTGCTCTGTTGTAGTGTCCTAAGATCCCACGTCTAACTATATACTTAACAGAACAACATAAGAAAGTCATTTCCTCTTCCATTAATTAGTTTGCCTGGTATTTAAAGCAAACTCTGATCACATATTGAGAGTCTGTGTTCATCCAGGGGCTGACTTGACCTAGTGGTCAAGGTGACCTGCAGGA[A/C]TGAAATGACATTATGCTCTATTTTCAGCATATACAYAATGTCAGGAAG

RAD_126	CCTTTTCAGTGCCGCCAAAGTGTCCTGTCTTGTATTTTTGTCTTCGATCGAATGTCAGTTCATTAACTGCTTTTGCATTTAGTGCTGCACAAAATGTTATAGTCATTATTTTTTTCAAACCAAGGACTTAAAAACCTTCTGTCATTTAGATGTAGTACTTGTTCTATTCATTTAAACTACCGCATTCATGTTTTAAAAATGAAAAAATAATTTGAAACTTCACTTTTTCTTAAGAACTTGTGCAGAACATGTGCTCTGGTGGAGTTTTGAAAGCCTGATCCCCCCTGTCCCCCTACTTTCATCCTTACAGCGTGGATATTTGTCTTTGCAGACAGCCAGCCCAAATCCCTTTGGTGAGTTACACTCAATGACATTTCGGACAGTTATGAGAACAGCTGCAGTGAAATTGTACTTTTTTCTTGGATCAAACATTAGGAAACAAACCCTTCCTCTCCTCCTGGGAG
GBYP-RAD_127	AGGAAGACTATTTCTACCGGAGTGGGAAGCATGAAAGGTGGAGGCATTTGATCCTAGATATCTTAAAGGCTCCAGTGGTGTTCTGTAGCTTTCTAATAAGCTCTTTGAAGACCACCTTCACAGTGTGTCCTTTTACCACAGGGGTCTTAATGCAGCTTTGCCACAAAGAGCGAAATAGGCCTGGGAGGTTTTATCCCTGGTCAAAGCATGACTAAATGGTTCAGATGTTAATGTGTTCGCTCTTCCTACCTGCAGGCTCCATTASCTGAGTTTTTTTTAAACCACCATCCTTTAAGTGATGGAAAAATCTGTTTTGCTGCAGGGAAACAGACAGTC[A/G]CATCCCTCAACCCCCTTGCnCATATCATTTCTAGAATATTTACCTCCTCGATTTGAACTTCTACTGTATATATTTATTCTGCTAAATTGCTGTTGCCACAATAATGGGTTGGACAGAATAATAGAGCAACCGCCTACAATTTGGTGGCTGGACCACTGGAAGACTGCAGGATTTAACGTGAATGAAAACCTGCCTTTTTCCATATAGTTTTAATCAATCACTGAGTGGAGTAACAGAGCATCAGGTGTGCAAG
GBYP-RAD_128	CAGGCAAACTTGACATTGTCATTGCTGCTATTAGCTACATTAAATTTCCAGTCTTTTAATACTTTCAAGATAAGTGTCTAAACCGAGTGTTAAAGAGATGTAACATGCAAATTGCATTAGCGGCATCAATTTATGAATGAGGTGCCGTAATTGTACATTTGCATGCAGGGAAGCGGTGATCGAGTCGAGAGCACATCTATGCCTGGCAAGATGAAGTCATAGCCCTGAGAATGAAAAATCAATAGAGTCCTGCAGGCTGTAYDGAGTGGGAGTTGATCCAATATTGATGGATGGATGGCAGGAGTGTGTGAG[A/T]GTGAGATGGTGCTMMAAYCCTACAGTAAGTAAAAGTCTGTCCACACTCCTACAATAGACACGAGTTCAAGTGATGCAGAGTGCATCTAAATATAGGTAGAAAGACACATGTGCACCCACACATGCAGGGAATGTGACCGGCTGAACCATATCAAGACTGTATCAAAAAGCGACACCCTGTAAACCTAATCCAGTCATTTCAACATCTTGAAAATGAACTGCTCTGCTGTTTCAGTATTTAAGCCAACTGTCTTGGTATAAAGGCTCTCCAGATTGCGCAAAGAGAGACTGTTTGTCTATGACTTAAATCTAACACATAGTGAGATGTCAGATGAGCTTACATGCAAGTTAATCAACTGTACAGATCAGTCTTGTGAGAGAGAGACTGTGGTGAGTGCACACCAGTCTAAACAGCATTGTGGAAATAGCAGTGACAGTAGGTACATATACGCAGTAGC
GBYP-RAD_129	TGTTGTTGTTGTTGTTGTTGTTGTTGTTCAGACTTTTGCAGGTGACGTGGGACATTTGTGGAAAACGTCAGAGTCTCTGCTGGTTTATCAGGAACTGGTGCGAAAAGGAGTTCGTGGTTTAATGTGAGTTGACATCAGACGCTCTGAGTGTTTGTTAACGAGGTGAAAAGTGAATAAAAAACGATCCTGCAGGCAGAAGCTCGAATGACTCAGAGAGCAGATCTGTTCRGATGTGGTTCACTTCCTGTTTGTCTCCAGTTATATAAACAT[C/T]GTTTYYTTTTCACTGACTGGAAGGAAAAATCCTGAAGCCAAACAAAATGATGAATTATTTAGGATAAAGTATCCTGCTTGTCCTCTTTTGCACTTTAACTTCATCATGTTTTCAGTAACTAAACATTTTAACTTTTCACACAAGCATTTGTACATCTTCAGTCCTAGTTAGTGTATATAATTAACCTTTAATTGAATTTGTTTCTTTGACCTTTTTTACCTCTTTGTTTTTGAATTTTGATTAATTTAACTCTGTA
GBYP-RAD_130	AGGCATTATTTAATCCAAATAAATATGTGAAGAGACTTGTATCGCTTAGCTGTGGCCTGTAAGTTAATAACCAACCAGAGTTTGATGTGAAAAATTGGTGGAATTCCCCTTTAAACCACTCATCAAACTAAAAAAATCATCAACTGCCAAATCATCAAGCTCTTCTCTGCGATGTGTTTCTCTTCACAGGAATCAATGCTGGTAGAAGTTCCACGTTTCGAGGAGATCCCCACAGACATACCGCCCAACCTGCAGGAGCGGKTAAATGGYGTCACAGATRTCCTGTCCCGAGTCTCCAAGATGGTGTCTGAGGAC[C/T]TGGAGAAAGCTGTGAGCACCGCTGTGGGTCAGGACAAAGAAGGTAACCGGCCTCCGGGAATGATGTTCACTGTGTAGCGAGTTGCTTCGCTGCAGGTCGTTCCTCACTTTGCTGTGTGTTCTCATGTCGGTCTCCAGGTTCTCCTCAGGACAAGAGGCCGATCCTCGCTGTGGTTCCCAGTCCGGCTGCTCCGTGCCACCCTGGAGGGAAGGAAGGCCTCAGTGCTTGTAAGTCCTGCATTTTTTTCACTAATGTGTTTACCTGATTCTGTGCTTCTTGTGATTATAAGTCAGAGGACAGCAGAGGTCACACAGTGCTTTAGTGTTATTCCTGTGATCATAAAAAATAAGAGAAAAAAAAAGACCTGCATTAACAGTGTCTGCTTCCTCTCTTCCTCATTACAGACCGATGCTCTCTGACCTTCGACCCTCGCACGGCCAACGGGCACCTGTTT
GBYP-RAD_131	TTTTGTGGCACCCGATAAGAGAGCCCTGAATAAATGTGCCTGCATGCATGAAAGACTTGAGAGGGAGAAGTGTTTGCAGGGTAAATATTGCAGTTGGCCTTCGTGCATGTGTACAGAACAATTACATGCTTCATTGTTGTGACAAAAACGGGCCGAGACAGCAGATATTTGCTGCTAATTTAGCTTGAGAAGTCCCCAACGGTGGGGGATAAATCTCATTGGATACTGTATGTCAGCAGTTACACTCTCCTGCAGGCTGCTGGCTGTAAAAGGCACAAGAAGCTCAAATGTAACTCTGCAAGCTGACRGATAAAAATAACTCAGCCRTACTGGACACA[A/T]GGTTTGGTCTAAGTACTGTAATGTGGATCCATTGTGGATGATCAGATCTTTAGGTTAATTTAATAATGGATGTGAGTTTGACTTCTAATGTATTTCTCTACATTGTATTGGCTTCAGCCAATTCAGGAACAGCAGCACAAGGTATTCTAACTACTCATAAGTTATCTCTGCTGTAATTGACGATGACATGAGACTGTCTGTAAATCAAGCTGTCGCTTTGTCTTGCCAAGATATAATTTTTCTCACACTCA
GB	GTAGTCGAGATGCTGTGATAAGCTTTAATTTCATTGTTTTACAGTTTTAAATGAAGCTTTGTTCAATAAATGCTAATCTTCTCCATCACTCCTGTTATCCAACACTGTCAAAGTCCTTACATTCTCAATTCTCAAGCCAATCAGTCCTTGGATGCCA

YP-RAD_132	GAGATGTTTAATGATAATGATTTAATTACAATTATATTTAATTACTGTCATTCTGTCCTTCCACCTCCCCACAACCACCGCAACACAACGACCTGCAGGATGTCCAGAGAGATTCAACRGAGAMTTTCCATCGACTAGYTGCTGGCTTTACTGCACCAGC[A/G]TCTAGMCTCCAGGGGATCMTGTCCTACCTCCTATCTTCACATAGATCTAAGCTTAATGAGCATTTTTCACATCATTAGAATCTTATCACCAAGTCTTTTTTCTGTTGCTAACCTAAATATTGTCATACACTTTCTATTGATCTCGATTGACCTTACTGAAGTGTTGGCAGAGACAGAACAGCACATTTCCAATTATATTCAGCCATGTGTTTAATAGTGCTGATTTTTTACAATGCTGTGGGACACGTGGTATTTTGTTTACTTGCAACACAAGCCATTGATTCAAGTCTGCGTAAGGAGCTTGTGCTGTTTTGTGTGCCTATTTGAAATGAAGTGGAAAGCGTGCCCACCCGAATCAAACTGGCACTGTGCCAGTTGGGTTTTAGAGCGCTGCTGTCAATTAGACCTCTGCTCTTGTTGTGCTCAAGTTGTGAACACATTGACATATCATC
GBYP-RAD_133	ATGTCATAATAACACATAACATAAAAATATATAAAACAAATAAAGCTAAATAATGAAATACAATACAAAAAAACTCTGACTCTGGAGAGACTTCGGTCCGCACCACATCTCAAAGTTCAAACTCGGGAGTTTTGTGTATAAGTAGATGTATAAGTGTGTGTGTTGTGTGTGTGTGTGTTGTTTAAGTGTGTGTGTGTTGTATTTGTGTGTGTGTTGCTGGTGAAATCATCCTGTGTGTCACCTGTCGTCCTGCAGGTGTGAAGGAGATCGACATYGCTGCRACGTTGGAGCACGTTCGGGACCAGAGACCTGGGATGGTYCG[C/T]ACCAAGGTGAGTCTCACTGACACATGAATGGTTTGTGTTTTTCTTGTGGAGGAATATGATTTTATTTGTATATTTTGATAGTTTGTCGTCATGTTTAATACAGTCTATGTTGAATATGTGTTGCATTTCAAATAAAATTTCCTGAACGTTTTCATACCCTGAAAATGTTTCTCATCACAAATATAATGTTGAAAACTGAGCAGCTCAGAGGAGGAAGAGCTGGTTTAATCCCTGACAGAGGAGACATATTCTTGTTAGTGTAGTGTGTCAGACTGGGCCCACATTTAGGTTTATCAAATTACACTGGACTGAAAACTACTTCTAAATTTAAAAGCTTTCAGTTTAATTAAAAGCTGTTTTTCTGTCTCTTTATTGTCTGCAGAAGACGTCAGATTCTTTTGTTTTTTTTGTTTCCATGTCATCAGATCTCCTGATGTTTCATTCCTT
GBYP-RAD_134	ACAAATGCAGGGCTGTTCAGAGACCTTCAGAGGGGCAGGTGTTCAAAGTTACAAAGAGGCACATGGAACAAGACTTTAAAACACCACACACCAACATAATTCATAGCATAACCTGTTGAATAATAACCATATTCAAACAGAATTTAACATGGACTATTACAACAAACCGCATCATATTATCTCATTGTCCCCCATCCAATGAAATCAGACGGGGGGACTGTGATTCGCTCTCTGTTGTGTGTGTATGTCCTGCAGGCAGGRTGAAGCAC[A/G]CTGAGAGCTGAGAACCATAATGGTCACRGTATAGATCATAAATTGATCATAAACTGTGAGGACKGAGGTT
GBYP-RAD_135	TTCCACTCATGTGTCTCTCCCACCACGTCTTCTTCTCTTTGCTCACACTCCACCCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGAGCTGGAGAGGAGGCTGATGCAGCTGCAGGATGAAGCTCACATGGCCAATGAGGCCTTGGTAAGATTCGATTGGTTAGCTGAAACCAAAATTTCTTGGTTAAGTCACATATCCTGCAGGTTTCATAACAAAGTATTTTTT[G/T]TCTAATTCAGTRCTTTTCAMRCCRTCCTCMTGCCTCTTCATTTCATCTCCCCCCGGTCTTTCTTTTTTTGTCATTTACTTCTTCTTCCCCTCTCACTGTCGCCTCTCTTCCCTCTATTAATTGCACCGTCTGTATTCTCGCACATCCCTCCCTCTACACCCATATTCCCTCTTTTCTCCTCTCGCTCTGCACATATTCTCATCTGTCCTTTCATCTCTTTCTCTGCTCCATTTCCCTATCCCCCTTTTCCCGTCTTCAACTTTTCTTGTCACTTTTTCCCCTTCTTATGTTCTCCTACCCTTCCTCCCTCCT
GBYP-RAD_136	TGCCCTTTTTTGCAAATTCTCCAATTATGTTTGTTTGACTGGAAGAGCTGAGGGCGAAGTTTGACTCAGAGGAAACTCAGCACACTATTTAAAAAGTTTCAGCAGTTAGAGAAGACACCGACTGACAAGCAGCAGCAGATGACACGGGTGCCGGTGAGAACTTTTTTTTTTTTGATGGAACTTTTTTTTTTTTTTTTTTGCTGCACAACCTGTCCTCCTCCCTCTGCTGCCGCTGCTGTGATTCACTGCCTGCAGGTTCTGCTGGTAKACAGAGACCA[A/G]GTTCTGGTTTTGTCTCAGCCAGCAGCTCAGYTTACAABAATGTGCYAAATTTKAAGATACGTGACAAACTCAGCTAAACAGTTCGACTACATACAGACAGCTTTTGTTTTAGTTTGTTTGTAAGAA
GBYP-RAD_137	TTTAAGTTTCTCAGCTCTCGACTTCTCCATGTTCTCCAAATCTTGAGGCCATGGCTCCTCCTCCTCTGGCTCCGCCTCCAGCCCAACGTCCTCATCAGATGATAGGTCAATGGTGCTGAGCCCGCCCTCCTGGGCCCGGTTACCGTCAATGACACCTGGCGCTGACTCATCGCCTTCCTCCAAAATCTCGTCACGAGGGTACGGAGGAGGATCCTTCACGAAGACGCTGGATGGAATCTCGTTCTCCTCCTGCAGGAGAACATCAGGGGAATGTCA[A/C]GAGAACGTYAGGAGTAAACACAGGAGAAYGTCAGTGGAACATAAGGAMGCTGGTGGAATTTCCTTAACTGAACCTTAGTGGAACCTCAGGGGAACTTGAGGGGAACCTTAAAGTATGTGGACAGCCAGACTTTGTGTCATGCTGAAACAGGATCAAGCTGCACACACAAAGTTGGAAGACTTTTATCATCAGTCTTTCCTTCATCAAATCTCTGGACACATACTTCTGTCCATATGGTGGTGTGCAGGATATAGTATAGACACAAGTATGTGAACATCCTGTCCTCATACTTGTGTCCCTGTGAAGGTGTAAACTGAGGTTAGTGTGATAAAAAGTGTCTGTAAGAAGATAAAGTTCAGAGAGAAACAAAAAACATGCAGGAAGATGAAGACCAGGAAGCAGAGCTGAGAGCTTCCACAGAGAAAGGCTACGCTGCAAGGGAGGAGCTGCAGCTATGAGGAGAGATCTCACTGCTATGAGAGAGGGACTGATA

GBYP-RAD_138	TTGTTTCAAACAGTAAAACACAAAGAAAAGCTGCATACAAACCTCTTTAAGGTTGAATGGATTGAAGAAGCAGTCCATCAGTTTGAGCAGACTACAGGTAAGGTTGCTGTCAAGTGATGTAATGACCTCCTTTACTGATGTGCGCACAAATGTGATGGAGTCCTGTGTACAAATACAGAAAAATAAAAACAAAGGCAGCAAACATGATTCCCTGCTGGTCTCTCTCAGTCATGTTGTGTTTCCTCTCACCTGCAGGAAYY[G/T]GGTAAACAGGGAGTTGAGCTGCTGTGTGTATGGCTTCATAGGTTSAGGGACCTGCTTCAGCCAGCACTCTGTGAAGGGGGCAAGGCCCAGAATACTGGGCTCCAGGTAGACCATACCACAGCGAGACACTGTGGCCGGGGAGGCCACCGCCAAGTCCTGCACCTCAAACATCATGGTCATCACCTGCAGCAGGAAGACACAATGCACCTGAATGCACATGGGACAGGAGACAACTCACAGACTGAAAATCCAAGCCTGTGTGTGAAAACGTAACCTTACGTCAGTGAGCTTGATGATTTCTCCTGAGCTGAGACACAATTTTTTGTTGTCATCCAGCACAGTGTTCATGTTCTCAATCCACACAGCATCTACTGGTCCATCAAACATGTACCACTTTTTCTCTTGATCCATAACGGTTGTCCCTCCACGGATAAGAGATGAGAGGATACCATCTGTCCTGCATGGATGGATAAAAAGTAAAATGTGTGTGTGTGTGTACAGTATACATC
GBYP-RAD_139	TGCAAAGAAAAGTATAGATGCATTTTCAGTTCCGTCTTCCTGTACCCACATTTGACATCTTCCGTGTTGCCCTGCTTTCGTCAGGTGTTGGAGTGTGGAGAGGAGAAAGTGCTGACTCTGACAGAAGTGGAGCGTATCAAGGCTCTGGCAGCTCAGCTGGTCAAGCTGCTGCGAGCTCAGAAAAACTCCAGCCTTCCTGTCAACCAGCTGCTCACAGAGTACAGCAAGACCTTTGGTTATGGTCTCCGCCTGCAGGACTATGATGCTA[C/G]CTCCCTGCCTGCTCTGCTGGCCAAACTCTGCCATGTTGTCAAGGTAAAGAACACCTMCAMCMGGATTAATGTTTTTTTCAGTTTGTTTGTGTTAAAAGCATTTGTAGAGCTTCAAGTCATTGGAAATGAAGTTAAATTAAGTTTGCCACAAACAAACTACATGTAATCCTAAATTGATCTTGTTTAGTCAATTTAGCACTGTGGTTATGCATCCCTCACATAGAGTTCATGTCCGTTTTGTTGTCACAAGAGTCTGTTCAGTGCTCCGCTTTACACTATTGCTCCTTCGGCAAGTCTGACTAACTACCAACATAAAAGCTGCCACTTTCTTTCCATTTCAAGGTGGTGGATGGCTCAGAAGGTCGGGAAGTGCTATTGATCAACAGGAAGTCTCTGCGTTCGCTGACCTCACAGCTACTTGCACTACTCATGTCCCAAGAGGAGCAGGTCACTAGGGGTCTTAAGGTGGAGGAGCTGAGTCAGCATTACCTGGCTGTCCAC
GBYP-RAD_140	ACACACACACACACACACACGCATGCAGAAACCTGCTCACACAAGTGCACACTCTAGCCTGAATCAAATCCCCTTCTCCAGAGAGGGTGGTTCACTTGTAATTTAATGGAAAGGTCCTGCAGGCAGGGAGCTAAATGAGAAGATGATCATCTCCATCAGTAGCAGCCCACMTGTCAGAGTAAAGGGTTTGAAAGGTTTCAACA[C/T]TCGAGGCGCTAGCAACTTGTTCTGTTTGGTACTATTATGCCCACAAGGAGGATTAATTATTTCCAGAAAACAAGCTTTTTTTTCTGCCTATAGTCCTATGACAAGGGAAAGCAGAGCAGATAATTTAGTTGCACGCCCACTCATAATAAGCAGTAAGGATCTAATAGCCTTTTAAGGAGTGTCCTGCTGGCCACCTCTTCACACACACATCTTGGGGTCAGCCCTTTAGGACCATTGAGGCAGAGCAGCCCGTCGCGCTACACAGTTAATCCTGCGGTGGAAAATGTCGGTGGGATCCGTCTCACATGGGCGCACAGCAAGAGATGAGGGGGCAGACCAATATTTGAGACGAATTAAAGATATATGAGTGTGTGTGGAGGGTTGGGGGTGTTGGGGGTGTTGAGGGTGCGGCCTTGCCTGTGTGTGTGTGT
GBYP-RAD_141	GCATTATGTCAGTATCCTATCTTTTGTGGATAAGGATCTGCTGGAGCCGGGCTGCTCGGTCCTGCTCAACCACAAGGTACCCCGCGTGATAAAAAGACTGATTCAAGACATTAAAACAGAAATAATTTGTGTTATGTAACTTCTTGACAGTGTGTCTTAACTATGCCTTTGCACAAGTTTTGAAAACTTCTCCCAGTTGTTGTAAAAATTCTCTGTAGTTGCCTATCACTAACTGTATTTGTGTATAACCTGCAGGTTCATGCTGTGATTGGGGTGCTGATGGATGACACTGATCCCYTGGTRACAGTGATGAAGGTGGAGAAGGCCCC[A/G]CAAGAAACCTATGCCGACATCGGAGGACTGGACAATCAGATCCAGGAGATCAAGGTATATCACGCACGCACAACAGTTTTCTTAAAGGTTGTGGGAAAACAACTCAAAACAACATTAAGCTGAACACAGCCTTCATATATTCTACAGAGGGTTGAATCCTTATCAAATCAGAGCTACACACATTAATGACCAACCTCCAGTGGATGTACAGAAACTTAAAAATAAAGGTCCACAACAAAATTAAACAAACAGCAAAAAAAGCATCTCATAGTCAAAAAATACCATCACAAACATAAGGATAGAATTTTAAACTTGGATCAGTATTTAAAACTGCTAAAGCAGTTCATTTATTATTTGAGCACCAAGTGAATGCATATAACCCCTACAAGTCATCAAAGCCTAGTGTCTTAATTTTATGATGATACGAAATGAAGAGACAC
GBYP-RAD_142	AGAGTCCAAGCCAGCTAATAAAGATATCTAGGTGACACCGCACTCTTTTTGCTTACAAACATTCGCCTCAGACTCTTAAGATCCCGATAAGCACTCTGCAGTGCCTGAGGGGGGAACTGCAGCCAAAAGCTGTTGGAAAAATCTGGAGTTTAGGAAAGCACCTGGAACCATTCCACTCTCTTGCTAGGGGTCACTGAGTTTTGTCTGGAGGCCTTCCCTACTGTAGCTGTTAACAATGCTGCTGCTTTCCTGCAGGCTATGRCTGCACACACACTCAGAGCTCCCAATAGCGTCAGGGAC[A/G]AATTTGGAAACCATGCTTAGTGTAAAGTGGCACAAAATGGCTGCTGTTATACCTCAGGTGGGTGCAGGGTTACTTGATGCAAGAGGGGAAGTGTTTGTTTTTTGTTTGTTTTTTCTATATTTTGGCAGGAGGGTGAGGGTTGTGTGTGGTGGTTAATATCAGTTGAAGTCAACCCGTTATCACTTCACACATGGAAGACATCTGCCTGGTTCAGTCCGGTGAAATATTTTTAACCATTGTTAAGGGTACCGCTGCATGAACGCACATTTACATGCATATACTGTATTATGTGTCCCTGGTGGATTGCCGTGGAAAGATTGTGTGATGTGGGTACACCAAAACGGGAGCAGGGAGACATGTCCTGCCAGATATGATTTCATGTCTTACGTAAGCCTAAGATGGGGGCAGAGAAGTATTAACCCTGTGTGTGTGAGAGTGTGTGTGAGAGAGTTAGCACCCCTTGAATGAT
GBYP-	GGGGTCATTTCAGCTTAAGAGTGGGTTAACAATAAAATAAACAAAACTGAACTGAATTATTCAACTTCAAAATAAAGATAAAAAATACAAATCTCTTACCTAAAATTTAGAAACATGAGACAAGAGATTAAACAAAAATTCAACCCAGCCCTACAAGATCCTTGGGCTGCTACTTGAAACAAGCTATTTACGATATTTTACAAATGTGTAGTTCATGGCTGGCTGGCTGGCTGAAGTGGTGAGAGGAGCCTGCAGGAAAAGTGCATTTGTAGTGAACTGATATGACTGAATTGGCTGAGGTGTTG

RAD_143	TGAARGTATTTCTGAACTCCTGTGGTGTA[C/T]GTTGGTAACACATCTGTCCTGTTCGATGGAAGTACCAGGTTCGAATCCTGGCAGGAGCATCTGGTTTTACAATATTTTCTTGGCCAATGATGCTGTAACATTAGTCAGTGGCAGAGCAATAGCCATGCTACTGCCATTTCAATAGACATAATCACAATCACAGCCCCAGCCATAGCTGTGGTGGTGGTTTCAGGGCACAATCCACAGCCAGGTATAGCCAGCCAGTGGCTGTACTGAGGCAGGTGACTGGAGAACAGATGAGCAGGTGGGTGTGGAAATTCAGGGGCAGGGACTGAATGAGCAGAATGAACAGGACTGAGGCAGTTGTTGAGACAGTGATTGCAAATTGAAATTCAAAAAATACTTTACACTAGCACAGACTAGTTGTGATGATAACTGTGGTGTTAGGACTGGAACACTACTGAACTGTCTGTC
GBYP-RAD_144	ACCAACCATTAGATCCTGATGATTATGACAAGTAAGACTTGATCAAATCTTACTGCTTCTCTTTATGGATGTTATAGAAAAAAAGTCATTATTACCTTAATTTATTACTGGATCACTCCATTACTTGTAAACCAAGCAGTTATTGTCACATAATGTTCTTCTGGGGAATTACAGCTTGCAATTCAGAAAATAAACACTAGATGGTGACAGTAAGCAACCATTTAAGTCACCGACATGATTCATTGGCACCTGCAGGGAYCTGTCTTTYATCAAGGTGATGAATGTGGGCCGGCGTTTTYGGTGAAYCGGKTGCAGGACTACATCCAGAGCAAGATTGW[C/T]TACTACCTCATGAACATCCATGTGCACTCTCACTCCATCTACCTGTGTCGGCACGGAGAGAGCAACCACAACGTCGAAGGCCGCATCGGAGGAGACTCAGAACTTTCTCCTCGCGGCAAACAGGTACGATTTTAATAGTCTTCATTTTATGAACTGCAAAGCCAGTGTCTTCTCAAAACCCAATTACAAACCTCTCTCAGGGAGATGTAACTGAAATATTATGAACACCTGAGTCCTGACCTTTATCACA
GBYP-RAD_145	CAAAACACGTAACCTGCAGGTAAGACGAGAC[A/G]AAGCTGTGTTAAAATATCACCGATRATGATGATGATGATGATGATGCCTGTYGTATGACATCAGCGGCTKMWAAGACGAGACGAAGCTGTGTTAAAATATCACCGATGATGATGATGATGATGATGATGCCTGT
GBYP-RAD_146	AGCGCCGTCAAAAGGCCAAATAGAAAAAAGGCCAAACAGCAGCCCTGATCCTCTGTATCGACTGCTTGGATTATAGAGGATCACCCTCTGGGCTCTCTACGTGATTTGGCCATAACTCCAATACTATTTTATGATGATAACTGCTAACTTCAGGAATCAAGCAGTGTACACCTGTCCTCCTGCTTGTCTGCCAATCTGTAAAATGATCGATCTGTGTGAATAAAATGATGCATCTGTTCTGCATTATACCTGCAGGAAATATGTTG[A/G]TGAAAGTTATATTRTACAGCATAATCAATGTATTCCAACATGAAATGCMATATATATTCCAAGAATTTACTCTGGCAAGCAGAAACATAGCAGGGGTACTTAAGCATGCATTCAATAATGGCCAATCTGTAACAGCTACATTTTGAAATTAAATAGTGTGCATCTGTCTTCTGATCTGACCCCCCCACCCCACTACCGATCTGACCAACCCTGCTATCTTTGTGGGTTTGACAGCAACAAGTCAATGGTTGCTTCAGGTGCGGAGATCTGTGCATTGTGCATTTACAATAAAATGGCATTTGAATTACACTCCCAACAGTCAT
GBYP-RAD_147	ACACACACACACACACCAAGTACAGCACTTCGGACAGACAGACAAAGGCAGGTCAAGGTACACTTTCCCATCTGGATATGCCTTTGTCTATAAGAACAGTTAAACATCTAAACCACCAATAAAATGTGGCGATGAGAGAGACTCTTTGACTCCAAGTGGCCGGACGATTGTGGACATGAATACAGAGAGCAGTACACCTGTCCGAGTCTTAGATGCTGCTAATGCCCCAATCCAGAAGTGGCCTTTTGCCTGCAGGGTTTAAGCTGACAATTTCTATGCATGTATGCATGAGTGTGTATGTGTGAAAGAGGDAGASTGAGCACTCAGTGTTC[A/G]GGAACAGAAGCTCTTTGGCAATAATCTGTCACAAAAGCGCACGGGCCGTACGTGATGTGTGGATGATATATTATGACCAAATGCAGATAAATCAGCAACTTTTACAGTTACACTTTTGAAACAGTGACGTGTAGCATCAATTCAAATAGATCTAGGGAGGAAAACGTCTGCGCTTCTCTTTTTGTCTTGGGCTCACTGAAATGATTTAATAACCCTTTCCTTTTCTGCTTATGTCATGTCTGGGGGAAAGCAGCAAGGCAAGGGACGAGATATAAAGTGAAGACAAAACAAGTCAAAAAGTAAAGAGTAGACTGAGGAAGTTTGGAAGGATGGAAAGCTTTCTCCCATAATTGACACTGATATGAAGAGACAGAAATGTGAAAGAGGAATGAGAAAACACACACAATCTGCAGGATACAGTAGCCTGCAGTGGAATC
GBYP-RAD_148	TACACAATAAAACCCTCATATACCATGTTACATTAGTCGCTATTATCTTTGTTTCTCTCTTTAAGGCACTAACATTTTCTTTCAATTTTTCTTATCAGAATGCTGTGGAACACTTGAAGAATGATGAGCTCCAAAGAGGAGGAAACTCTCCGTTTTTTCCAGTATGTCGAGGAGAACGGGCTGAGAGCCTACAATGGCCTGGTAGCTCAAAACTTGGACCACGCCAGGAATGAGAGAAATAGGGCATTCCTGCAGGAGAAAAACGACAAGAAGAGAAAACAGGAGGAAGCCATAAGGAGGTAGGCSGAAATAAAA[C/G]TAACAATTAGACAAAGTAAAGACAACAGATTACTTGACACAGGTTTATGAGCATAGACATATCCTATAAAGACATTTCCATTTCTGTTGGACATGCCAGCCTTTTATGAATTAGACACAGCACACCAAGGAGACTCTGTTCTGTACATACAAGGATGTCACTGGGTTCACTTCAGGAAGAGGTTGTAAGGAATTAGGACAAGTGGCCAGAGGGTCCCTTTGGCAATGGCAGGTTGCCGTATTTTGGGGATTGCCAGTGTGGACTGGTACACCCCATGATCTATAGAGGATAATTAATTTTTCACGTTTAGACTTATTTGGGACTTGTCCTTGGATGGAGGTCATTACTGCTCCATTTTTGAGATGGCGAGCTCTTTAGAATTAAAAAGGAAAGGGGTGGGCTGTCACAGAAAGCGTGTTAGGATGTGAGGGTGTGAATGAGACATGGTCAGAAG

GBYP-RAD_149	GACCCCGATGACGAAGTGCAGGTAGAGGCCGACGGCCACAACATACCCCACCGCGCCCACTGCCTGAAACGCCAGCGCTCCGAACAGAAGCTTCCGGGACATCCGGTGGGGGGGTTTGTTCCCGGCGACCACGAACAGCAGCGAGACGACCCCGAAGGTCAGGCTGAAGGGGATGCCGCCGTACATGCCCGGCGCTCTCATCTGGCTGTACTGCATGTCCAGGTCTCnCACCTGCTGCAGCTCGGTGCCCTGCAGGTTAAAGTT[G/T]GAGTTGATRTTGAAGCCGCCYAACCCSGCCATGGAYGACATGCCTKATGTCAMCATCTGAGCTGCGACCAWRSAKATCAGGACCAAACCGTTGGTCAGTACGGAGCAGATCAGAACGATGCCTAATCAACACATGACACAAGTTAGGAAGAAAATAACAATTAATCAGCCGAACCATCCAATTAATCAATAGAAAGATAAATATAAGAACAAATAATAAAACAAAATTGAAATGTTCTGTACTGGTCAGACACACACAGAGAGCTGTGAGACTTAACTAGAGCTGAAAGCATCAGTCGATCAACCGATTGACAGAAAATTGATCA
GBYP-RAD_150	GACTAATTAATGACCAACAACACAGCCTTTATTGACAGTCTTGAGATAAGACACAATGCTGTCAGCAAAATGTGCAGCTGGTTAAATCCATATATAGGAAAGGCTACCACCCTATTGAAAACATGCACAATTAATCACCATATTTCATCAGACCTTCTTTTATTTTCTCAACCTACTGACCCAGAATACAACTGATCAATATGTTACAACACTGCTCTTTGTTGGTGATATGTAATATGGGAAAGGAACCTGCAGGGKTACTGTAAAACTAATMAATGCTTGGCACCACAACCTYTTATTGATGAYATTTTATATAGCAAAGGATTGCCWGTGATACAG[A/C]CTCACCGGCAAACTGAACAACTAATCAATAGATAATGCCAAAGCCTCTAAGCAGTGCTATACTTGGGAAATTGATCCAGTCTGACATTCTATATGCAACTAATCAATACCTGGCACCGCAACCTCTTATTGATGATATTTAGTTTGGGAAATGTAGTAACTGGCTACACAATAATATGTGGTGTATTATTGTTTATTATCCAGCGAAACATCAAGAAGAACTGAGGTCAAAGAAGAGTTAATGATCTCGC
GBYP-RAD_151	TTAAGACAGAGTTTGTACTTGTAGAGGACAGAGGATAAAGTGGCGAAGCTGTGAGTCTATAGTGACCTTTTGGCACTTTGGGTTTTGTCTCCCATGGAATGACATTCCTACACAGATCTGAAATGCTGGGGTGTCATTTCTGCAGATTCCTAGCCTCATCATCAGGAAGGACAACTCCTTTAAATTCTTATTCTTGTACATAAATATTCAAGTTCCAGCTACAGTACAACTAACTTGAGTTTCCCCCCCCTGCAGGATTGCTGTACTGCTGMAGCAGCTCTATGATMAAACATCATGTATTTTTCACAGACAAA[A/G]ATCTTTACATGTGCATGCCTTAGCACAGCAGCTCATGAGGCACAAAGAGCACTGCAATATTGTTACATTGTTTCCCTGCACAGATAATGAACTTGGCTCCACATGCAGCATTCTGTTTGCTTATTTTATTTGTGACTTATCCATGTGGCACTTTTATTCACAGACATTCCCTGTTGATGTTTCTGAAGGTAGAGAGGATTAGTGGAGTTCAAACTGAGATATTTGAAGTCCAGTTAACACGTTCACTGCATTTTTTCTGACTTGCTCCCTTGTGTTCATGTCAGTACACCATCAGTCTCATCTCTGGCAATTTATTATTGTCTCAGGCGACAGGTGCTATTTTCAGTGTGGCTGCTTGTCATCATTACTCTGCATTAAGTCTCTAATAGGGCTTTTGTTATTAGTTAAGTGCCTAAAGCTTTATAGCTGCCTGTGAGAATGAAGATGAAAAGACG
GBYP-RAD_152	TAAAATGTGTGTCACAATATGAGATGTTATATGAGCTGACGAGGATCCCCTTTTTTATTGAATACATTCGGTTTTTAAAGATAGTATAGCATACTGCCGCATGTGGTCATAGGTATAATAAACACACATTTAAAATATATATATATATGTTTAAAAACTCACAGAAACAAACTTTTCCTTTAAATGAAGTCTTGTGATAAGTGACATCACCTACCGGCTTGTGGCCAGTCATCTCTATCAGCTGATGTCCTGCAGGAATTTCACTTTCAAGTCAAGTTAAACCCAAATTGACGGAAGTTGTAMGRTTTTGCTATCAAACTAAAGTAGTCAG[A/C]GTGTGCTATTAAGGAAAACGCCTGTTTATTAGTATTACAGTGGTACTTATGTTATTTATTGAGTTTTATAGTATTTATTAAGTTTACCAAATAAATTCAATGATCAATACTAATCTCAGCTCTCACAGGCGGTTGCATCTGTAGCTAAATCAGCTCAAGATGCTGTTGTGAGTTGTGGAATAAGTGCCATCATATTGCGGCTTCTTTTCTATCATTGGCATATGCCTGCTCTTGCATATTCAGTAGGCTAACTTTATTTTTAAGTTGCCTGTTTGCTTTTTGTTTCTTTGTTGATTTCATTCTATTTATCATCATTGAATTTCTCATTTTTATTGTTTGACCTGACAGACAATGACAATATTAACTTCATTAAAAAAAAAAAAGTGTGTCCCTTTTGAACCCAGGCAGCAGCCTGCAAATACTGATTGTCCAAAAAAT
GBYP-RAD_153	TTTATGCAGTTAAGAGCAGCTTCATAATTATCAAAGAGATGCTGTATTACCGGCTAGGCCTGCAGGCATCAGCAACTA[A/G]TACTAATAAMAAACCCATATAAATAAAGACTATTAGTGCATACTGAGTAAAATAAAGCAACTACGAGACAGGTTTTTTTATTTAATAACCATGTGTGCATAGTTAAAATGTTCAAAAATACCCCATCACTCAATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATTTCATATAAATCTCTTATCAGGTTTCAAATATAAATAAATGAACAACAAAACAATTCAGTCAATCTGAAACTGAAAATGTAAAGTCTTGGTAAGTATGAGTAAGAACTGTATAATTAACTTGTAATAAAACTGAGAACCACAACATCCGTTCTGGGT
GBYP-RAD_154	TTGACAAGTTCTTCCAAAGTGTCCTGGAAAGAAAACAAACAACCACAAAACATTAATTAACACCAGCATGACATATGCATTAGTCATCTACTGCTATCATTGCCTATTTACAATTACAGTGATAATTTACAAAGCTAAGCTGGGACATACCTTTGCTATCTGCCAGCCTTTAACAGCCTCCTCTCCATCATTTTTTCCTTCTGCTTGGGCCAACCGTACACGCCAGTCGTGCAGCTGACGATTGAAGTCCTGCAGGTCATGYTCTAACTGTGSTGACTGGCTGCTGAACTCCTGYTCAGAGGTGGCTATCTGMGAGAGGGCAGTYTMCAGACT[A/T]GCCCGTGTCTGTAGCGCCCCACGTTCCCACTGTTCCCATGATGACAATAGGGCTGCTTCCTCTCGCTCCATAGCCTCATAGCCCCCAGAGCCAGTGTGATCTCTTGCCACTGCCCCGCATCTTTGGACGCGGTTCAGCCTCTCTCTGCCTCGCTGCTTGGAGTCAAGCAACTCCTGGAAAGGGCAAATTATCATATCAGATCAGCTAGTTTCCCCCCTCTGGACTCAGCCACTTGGAATTCCCTTCTTAAGAAAGT

GBYP-RAD_155	GCAAATCCCAACCTTTCCGAGTGAATGTGCAAGACTGTCCTAAGAAGAATAACAGCATCAGTTGTCTCAGCAAATGCCACAAAACAAATGTTTACATTCAAGTGACAAAGAGGAAGGAAGCTGCCACAGCATCTCCTCTGAAAGCAGTGCTAAGTCCTAACACACACTCATACACCATTGGGAACTATCTGCCACGATGCACCTCACTTCATCAGGTCAACGGGTCAGCTTGTCGATTTTTTACCTAACCTGCAGGCCTCTTGTTCTTAATCCTCTCTGGAAATAATTAACAACAGTGAAATTTATTCATCCCCACGATGCAGCATCA[C/T]CTCTCACCATCACAGATCCTAATAACAAAGTTCTGCATGAACGCATCGAGTGTCAGCTGATAAGACTTGGCACAATGCGGCTCAATGCACCCAGACAAAGAATTTATTTTCCATCTGCCAAATGAATGGACAACATTAATAAAGATGAGATCAGTTCAAATGAATTTAATGAGTGAATGTTATGAAGATATCTCCATTCCAAAACATGGTCATGTGGGACTAATATTAAACATATTATATCCTCCTTCCTCCTCTCTCTTCATCCACTCTTTCTTTTTCTCCTTATTTCTTGACTGCTTTCACTCTTCTCTTAACCCGAACCCTAATTCCAACCCCCTTCTTTTTCTTCCCCCTCCTCACTTCTTTGACTTCTTTTCCTGTGCTTCCACTCTCCTCTTTTCCCACCTTTCCTTTGTTGCTTACTCCTCCATACCTTGTTGC
GBYP-RAD_156	TTACTTCATATGTGAATATAAGCACAGAGCAAGCCTAACACAGCATATGGGGAGGGGGGGAGATAATGTTATCATCCATCAGCTGTATTTATGTTGATCATCTGGAGTGTTTGCTAAACATCATCAATTAATGTGTTTAGAAACGCCAAAGCAAAAGAACCAACAGCTCATATTCCAGTTTTGGCCGGTTTTTAAAGAAAAAAATGAAGTACTGTGTTGTTTCTGGTTTAGGTTTGTTGTTTATTTTGCCTGCAGGGAAGTA[C/T]GTTTTTACATAATTCTTACATGCTCAATGGACATKCTAAAGAKACACAAGGACAAGATGAGATACCTATAAATAAGAGTAACAAATTACACCATATCAAACTGAATTATCCAATAATTCACCTACCAACTTTGTTCTATATAAAATACTGCAAACTAAAAATGCCACAACATGGCCATTTGAGTATGGGGGAAACAGATATAGGTTAATAATGTTTCGTTAAATGGAAAATTGAGTCAATCTCTACATTTTACCTGCTGTAACTCAAATCGGGGGAAATAAGTAGAGTGCACTTGTTTTGTCACTTGTTATGTGTTAATCTAATGTCGACTTTGGCCTAGTTTGAGGCTGAACCACTGCCAACAGTTGATGTTAAATGTATTTGTTTACACCCTACCATGGGATTTCTGCAGTGGCAGGAACGTTAACTGGCTACATATTTTGCCTGAGATCATCCTGACTATTTTAAAGACACCAAAGAGCTTATGAGAGCCATCAAAACAATATC
GBYP-RAD_157	TGCAGGCAGTGAATCACATCAGCA[A/G]YAGAGGGAGGAGTGCAGAAGAGGAATGACTGATGCYGACTGATGTCTGTGTTCTTCATTMWKYMWGAATCACATCAGCAGCAGAGGGAGGAGTGCAGAAGAGGAATGACTGATGCCGACTGATGTCTGTGTTCTTCATTCTT
GBYP-RAD_158	AAAGCATCACAACACACGAGCAGAGCGTCAGAGAAAAGACAAAATAACATATACTTTAGGGTAAATATGGTAATGGTAGATTAATAAGCTAAATGCATTTGTGAGATGTTTATCCGGTTATTGTACTGAAAGAAAGAATCTATGCTTTTCAATGGTTGTGTGTTGCATTTGAAGTTCTTTTCTAAGAAAGAAGCGGACAGTCTCACCACGGGGGGGAGAATAATAACTTTCAGAGCTAAACACTGAAACCTGCAGGAAGCATAGAGGACTGACTTCTGA[A/G]AGAAACTGCCTGCTCATCATCCCTTGCAGATGAATGGCTCAATAGTGAAMMSAKCDRRAKCTGTCATGTTTTGATAGTCCACCATCATCCCTCAAATAGCATGAGAACATCTCCTAAAGCTCACCAGAGGATTTATTTCCAGAAGGCCCGCAGGTAGGCTCAGAGCTTCACAACCAATTCTTAGGTTTAGTAATCAAAAGCATCTTCACATCCTCCATTCCAGTCTGGCTCTGCTCTAAGCACCGCTGTATTGCTGCTCAGTAGGCAGCCCGCAGAAGGACAGGACAAGAGAGATTGTCATGAAGTCTCC
GBYP-RAD_159	TTTTTTTTTGCAGCTATGGCATAGTGGCCACCCACTGTCTTGGGTCGTTGTTTGTATTGACAAATGAAGGCAGTGAATTAATGTGAAAAGACATGTTAATCATCATCCACTTACCCTCCAATTACACCCCGAGGCTGTCGGGCATCAATCACGCCTTCTATTTTCTGCTCCAACAGCTGGCCTCCCTGCAGGAGCAGCTGGACTCACTGATCGAGAAGTGACCACCAGGGGGCAGCCTCA[C/T]GTCATCTTMAGCCACACACACCTGMARRRRWSRRRGAGAGGAACCTTCATCCAGGCTTTATTAGATGACTTGCACTGTCATTCCTTTCAGTTTATGAGTTCTTTTATGAATTACACATAGAGCAAACAGCTTTCTGTGTAAAAAAAGTTTTTTATTAAGTTGACAGAATGTGCTGTTAGTTAATGTATGATTAAAGTTTTTGGTTGCCTTCAAGGAAGAATATTGTGTCTGTTTTGCTTGTCATCCTAAAGCTAATTGTACTACTAGTTAACGCTTTTACCTCAGCTCACCCTGTTTGTACTGCGTTACCTGTATGAAGAATAAATTGTGTTGATACACAAGTGTCAAACAAATGTCAATTTTATTGCATGGATAAACCACCTTCAGTGTTTTTAACTAGGTTAATATATAGCTGACTGGCATCTTTGCAAATTCTCACTGGCTTATTTAGTGCACTGTCCACTG
GBYP-RAD	TTAAAATGATTAATCAATAGCAAAAATGTTGGCGATTCATTTTCTGTCAACCGAATTATGTGTTGCAGCTCTAATATATAACAATATAAAACACCAGTAATATGATAATTGATATCTAGTTCATGAAAGCTTTTTACAATCACTTCTCTTCATCCTCAGTGTCTGGTAGCTCCGTCCTGAGAAGAAATCTGTGGTGCACCTGTGATGAAGTGAAGCATTTCATATTTTAAATCAATAAACAGAACAAGCCTGCAGGTAACGTGAG[A/C]AGYGAGCGACAGMGTGGMTGAGCAGAGCAGAAGAAGAAGAAGGAAACTTAAATCTCTTCAGTAGGAWRAKMMKWAGATTTGAAAACATAACAGCAAAGAAACGTGAGAAGAAAAAAAACTGTGCTCTGCTCTGCTTCATTTTACATTTAAACAAGTAAATTTAGGCGATGATGCTCTCTGGTGGTCGATGTCTGCTGCATGTGAACTGGTCTCAGGAGAAAAAGAGTGAAATTGACAGGATGCACGAATATAAAGTTTCATTATCTTGGATTTTTACACATCCTGAAGATATAGAACAGCTGATACTAGTACAACTATGTGATATTTCTTGGGTGTAAAGGA

_160	CTATAGGGGAAGGAAACATAGCGAGGGATCAGTAGACTGTGTAAGAAACTACACATGTGGGGAATTAGATATGCAGACTTCTGCTCACTTTATTTCAGAAAATAGGGTGTGAGGAGATTTTCTGCATATCAATGGCCGAAGTGCAAAACCTCCTATCTGAAA
GBYP-RAD_161	ATAGGGGAAATTTGTGAAATTGTGCCTGTGAAGTGAATTAGGAGAGGAAGACTTGGGTGAACAAAGGCACACATTAACACCCCACAACCCCACCTCACCCTGAGTCAACCTGTCTGTCTCTTACCATTACTGCAGCATACTCACTGAAAGAATCCTGCACAGTGGTTAATAGATTTCTTGTCACAACACTCTTCTGTTTGGATTTTGGACAACAATAAAAAGTAGGTGTAAGAGTAAACACATGACAGCCTGCAGGACTAGAG[C/T]ATGCATACTGGASAYGAAGGATGATTAGTCRGGAGCTGAATGATGTTGCTCATTTTCTGTTGCAAATTGTDGTTYANNNNNNNNNAGTTTATATTCAAGTGTACTCCGTGGCTCCGGGGCCAATCCGAAGTAGTAGAGTCACTTTTTACATCAGAAAAAATACTATATTTTAGAGAAAAAACAAGCAAAAAAAACCCCAAAACTGACACATCTTTAGCTTTTGTTCTCAGTGGTTACAGCCATGTGCTCCGGTCAGTAACTGGAAGGTGTTGTTGTAGTAACCTGAAGCAGCAGCTAACGCCCTATGCACCAGACACATTTAATCAACCCTCATTTTCAGGCACGACACGCTCACACAGTATACCTACAGAGAAAAGAGATCGTAAAGGAATGCTTTGGAAGAGTGGACTTTTGATGCATCAAATTCTGTGAACATAGACACCAAAAGTCACACATGTGTTCTTGGTTATAGAAAGAAGTCAAGCAGCGTTGTTTGGAAATG
GBYP-RAD_162	CTGGATGGCGCTCTTCACCACATTTATAGATTTGTCCATCAGTCGTCCCACAGTGAGCCCCATCACCTCACTGTACCTACACAGGGGCAAAGCCTAAACACAAACACAGTTTTAATGAGCAGGAGGGACTTAAAACATGCTTTTAGATATACACTACAAGTCGAGAAGACATACTTTGCTGTTGACGATACGTGCATAGACCTGCAACACACGTGCCCTGACGTGGGAGTGTGTGTCATGCAGATGTTCCTGCAGGGTATCAAAGAAGCGGTCGCGGTC[A/C]GCTTTACCAGACTCGTCGAGCCCGTCACCACAMAGGACCCGCACRAGGATCTCTCCCAGCACCTCACACACAGCAACACGCATTGCGTGGCTCTGGAAAACAGAGAGAAACAGGGTATAAATCTGCATCYAAATGTGTCATCAAGATTCTGGTTCTACTACGATCATGAAGTACTAAATGGGGATTAGTGTTTGGTGATATAAACATCACTTTGCTTCCATATGAGTTTCTGAACTTGGCCCTCAGATTACCAAAGACACAACTCATTGCTGACTGAAGAGCAAAGAGAGCTGGGTGAACTCCTTGCCT
GBYP-RAD_163	ATAAGATATATCAGACTTTGATACACACAGAATACATAGCGTACATTTATTGTTGGTTTGACTCTGCACATGGGATTTGCTTTGGTTTGGAAAAATATAGAATATCATAAGACTTATCCTTTAAGGTTTTCTACAGAGCCCTGCAGGTGTCAGGGRTAAATATTTGATAGTTCATGCACAAGTATGAGCAA[G/T]AATTAGTATTTGGTGCTCTCAAATGAAAGAGCWRKAYMSTCAAATTAATTAACCTTTGTGCATGATGTAACAGAACAATCTTACAGTTCACCTCTACAACATATTTAAGAGACATCAAAGATATCATAATTTAGTGTTTAAAAGGCCAAATCTGAAGTATATTTAAGTACCTCCATCCACAGCTTTGGCTCAGTGAGCTGGACAAAAAGGGCGATCACACATGATTTAAAGTATTTCAACGAATATTTTATTAACAACAAAAAAATGACAACAATCAATGAATCTGTAG
GBYP-RAD_164	TTTTAATACGTATATGTTTATGTAATGTGAATGTAAAATATTTGTGGAGGATGCAGGCGAAAAGTGATCATGTGATCTAAAATAATAATAAAGTTGAAACTATGATTTTATGTTTATGGCATCATGTCATGGACTCAAAAAAAAAAAAAAACAGCTTTACCACATATTGAATTACACATAACAGATCTGCACATAACAGATCAAAGTAATTGATTACACACTTGTAATGTACCCAATCTACCAAGAAACCTGCAGGACAGTCTGATGTAAC[A/T]GATCATRAGAGTTGATCTCTGATGTAATGRTGCATGATRGRATCAAGAGTTTGAATAAAAATGARTCTTTTTGAGCTACTGGTGTCACTCCGACTGTCTCGTACTCATGACCTGAATTCTGTCAGGGGTCAAAAAAGTTTTGGACGTGAATACAACAGGGGGAAATAGTAGTTACCTGGATTTAACTCCAGTTCTTTCGTTCCTTGCCTTTGTAACATTAAATACATCATTTGAGCTTTAAATG
GBYP-RAD_165	TGTTCATTCATCTTTAACAAAGTCCTGACCGCTGCCAAAAAAAATTATGATAGTACCAGAGTGGAGTAAAAATGTTATAACTTTTAATGAAACCTCTGGACCATCTGGATATTACATTGAGGTGGACAGTTTGTAATGACTGTATCCAAAACACATACACACTTTTTGCATGAATTAAATATAAAATCTAGTTTTATTCCTTCATTTAAGGTTTAGTTAATTTCTCCGATTGTCTGCTTGCTGGCTGACCTGCAGGTGGTGGTAGTC[A/G]CSRTAGGTGTAGACCTCRTCACCRGTGTCCACGTTGAACAAYGAGTGCAKACACTTGGAGGGGCTGKRRWMMTGTTTAAACTGCTCCACCTGGTAGAAGGACAGACAGGGACACAGAGATTCAGTAAAAGATGAAAGAGAGATGTCGAGGGTTAGAGAGGAGTGGAGAAAAAGATACAGAAGGAAAGAAGGCCATTGGCTCTAGAAAATGATTTCATCATAAAAGATAGATTTTTACCGCAGTAGCAGCCTTGAAAACATTCAAAACATCAAACTCATAATTGGAAACTCTGTGTAATGAGTAAATGTATGGTAATGAACTTTCTTAATCTCTGCTAATGTCTCCATTAAATGCATTGTTATGTTGGATATTAAAGCTACCCCATCCCATCCTTTTGTTTACACCTCACCCATCAACATCTCAACTGACACTTCAACTCCATTAAACACTGGCATTTCAATGGACTCAATCAACTGCAACAGTGCTTAAAAATATCTGCCAC
GBYP-R	GACTATTGATTCTCCATTTTCTCTCATACTGCCCAACTCACCTTTATTAAAGTGTCCAATAACACCTACAATAGGAGGTAGAGTGGCATACAGCTCCTCTGCCTTCTCAGCCTTTTGTGTCCTCGCCTCCTGGATGTCCAAGTCTTCATGCTGGTTGGAGCGAGTGCTGTTGGGCGTTCTCCTCTTAGACGCACCTTTACCTCGCCGACGCTCTGATCCAGGCAAAGTATACAGAGGGTCCTGAGGGTCCTGCAGGTCMTCTGACTCTGTGTTGAGCTCATTAGCAGGGCTGAT[A/T]GGRTTAGTCTTCAAGTCTGAGCMKGAAATGTCCTGGTCCAGRWSMTTCCCCAAGAAGCTGGACTGAGATCTGGAGTTGTCACGGGT

AD_166	CCAAAGCGCGGGCGGTGGGCTGACAGAGGAGGGGCCTTGCTGCTGCTGCTCTGAGGTCTNNNNNNNNNNNNNNNCCCCACTGGTAAAGCTACAGGTCTCAGACAAACTGAGGCAGCGGTCGCTGTCTTCATCTTTCACGCTGATGTCCAAAGAGGATTTGATGAAGTTCTTGCAGTAGTTGATGACATTGTTCATCTGCAAGTAACTGGCTGCAGACATCACTTCAATCACATTGTGACTGGAGAGGTCCAGCTGGCCGGAGTAGATGAAATCCAGGATGACGGTGAAGGTCTCAGGGCTGAAGACATCAAAGGTGGCGTTGACAGAGTCGGACAGCCCGTCGGGCCCCTGGGACAGCAGCATGCGGAAGTAGCCGCTGCTGGCGAACA
GBYP-RAD_167	TTGGTGCCACAGTAGTACAGAAGCCCACTAGTTCAGAGCAACCTGCAGGTC[C/T]ATGGTWCAACACTCTGCACCCACCACTGATGAAATGATGCCCATACCTCATTTTCTATTTTAWTAGKATATTAGTTGTTTATTTAGTTATTT
GBYP-RAD_168	CGCACTTGCTAATTGGCATTCATTTACTTGTGTACTTAATTTACTTTCTGCATAATCACCTGTGTTAAATCAGTTACATTTTCATGTATGTCTCCCAGTTCACTTTGGTGATGGACTTACTCTTTAATAGTGCAGGAATCAGGACAGGTGGGGCATTTTTCACAGGTGGCTCCGTAGGCACCAGGCTGAGTGCACTGACACACTCCACACTCACAGTTACCACGGCCGCTGCACACGCCCATGCTGGTCCTGCAGGTGTCTTTGCG[C/T]GTGGTGCAGTTACAGTTTTCTCCTTCCCAWCCAGAATCACACTGGCAAAACCCACAGTTACACTTCCCATGATCTGTAAGAATCAAAAAAAAAAAAAAAGATAATCCTGTTAAAATCCTTCAAAATATTCTTTCAATTCTAATTTAAACATATAATACAGATCAAATATTCCATCTTAAAACATTTGAATTGAAATATGTTTCTCAGTGTCCGTAATCTCATGGGTGGAGTCCGGAAGCCAGACCACAAGATACAAATTACACAATTGCACAATGATTCACTGAGTGTGTGTGTGTGTTTGTGTCTGTGAGTTTCTCCTCTTAACCTCTGTGTTTTTAAAGCCAAAGCATGCTTGGGCAAGTGTACCTGTGAGCGAGTTTGTGGAATCTGCACCTATGTAACTAGCGTTAGGTATAATGTGTTACTAAGGTGTTTTTTTACTTATTTGTAATGAAAATGTTGCTCATTTGTCATTATTTGGTTAACTTAACTGATTAACAGGTT
GBYP-RAD_169	CCATAAGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTGTTGACACATGAACTGATGTAATATTCATGTATAAATTTAATGACAAAGTATATCAAGCATGTCTGCCACATGCATAAATGCCAGAACATTAGTCCAACCCTTCGCACAGAGCGCGCCCTGCAATTTGTCTTCTTCAGAAAGATGGTAATAGAGGGGTCCTGCAGGCTCTGTGCTTGTGATTCAAAGAGGCT[A/G]GGACTGGTRAYGGTGARAGAAATGACTGATACTCTGGTATGTTATGATTTGGTCTCTTGGAATATGTTGTCCTTACAGTATCGCCCAGTAACTCAGTGCATTAACTTGTGAATGTGACGCATGTGTTTCCTTCCTTTCCTGAACACAGTTAACCTGATTTCCGGCAGTTCAACTTTTTATTACTCGGTGACTCTGACACTGAAATAATGACACACTGTCTGTATTACAAAGGATGTGACAATTTG
GBYP-RAD_170	GAAGTCAGGGATGGGGATCCACAATAGAGCCAGAAAGAATTGTGAGTTGCTTTTCCTTTTTCTCTTTTCTCTCTCTTTTGGAAAATGTTCACAGGTCACTGTTCATGGGGTCAGTAAAAGGAGCTTTAAAATGTTTCTATTGGCATGGACTCGCATGTCAACAGGAGTTTGGCAGAACAAGAAGACGCTACACATTTCAGACCCAACCTATGAATCTACTCATACCCCAGGCTCCACAGTGCACCTGACCTGCAGGAGTTGGAGACGGAGGAGGAGAAGGAGTTCTTGATTTAACTACGYTTCCT[C/T]TCTCTTTTTGACATCCAGCCATCMCCTTCGTTCCCTGAAGGGAGCAGAAAGGTCACAGCGAAGCCTTTATTCTGGCTCGGGTTTAGCAACACGCAGCTCTGGCCTCCAGAAGAACTCCTATTCTCTCTGGCACATGTTAAGACGCTCTATCATCTCTCTCCCTCTTATACTCTCCCATGCTCTCTCTTCCCCATTCTTTCCTGTCAGATCTGTCTTCACAGGGGCTTGTAAAATTACCTGGCAAGAACAGCTTAAAGCACTGGACAGGACCAATGTCCCCAGTG
GBYP-RAD_171	TCCACAGGCTGTGTCAGGGAGGGGCATGAGCCCGGGATCCAGCCTCCTCAAGGGGGGAACTTTGTCCCTCACTTCTGTAAGGGACAGCTCAGACGCAGACAGAGGCACTGAGGGACAAGAGAGGAGAACAGTAAGTAAACGAACCTCTGAATGAATGCATCCTGCAGGTTGTAGATGTTATGA[A/C]AGMRAAACAAMCTGTACAYAACAATCCTCATGARATTGSTTTCAYTWCTGAGCTCCTYACAACMACAAAGAATGAAACTTGGCAGCTAATTCTCTGAACTCAGCAGTGTTGGCAGAGAACATTCAACACTGTCCACCTGCCTGAAAACACAAAACGACAGCGGCGCAGTTTAAACTCACCCTTCTTGCTCTGCATGTGGTTGGAGGAGACGGCGTGTCTGCGTGTGGGCAGCGTACAGGTGAAAAGCACATCCATGGGGGTGGTCTGGTTCTCAGAGTTGGCAAAGCTGGCATCCTTGCGCCCGCTGCACAGAGACTCATCTGAGAAAGTGCGCTGCAAGGTGCGTCTGGGAGACTAAAGTAAGAGAGACAAAAGAGATCAGAGCTGTGTGTGCGAGTTCATCATCGCGAGACTGTTAACTGAAGCGTAACGTGACCGTCTTCAAGTGTGCGTTCCTCACCGGATCTCTTTGTGGCGCCTCTCCCGGGTTGTCCATGA
GBYP-	GCTGCCCACACGCAGACACGCCGTCTCCTCCAACCACATGCAGAGCAAGAAGGGTGAGTTTAAACTGCGCCGCTGTCGTTTTGTGTTTTCAGGCAGGTGGACAGTGTTGAATGTTCTCTGCCAACACTGCTGAGTTCAGAGAATTAGCTGCCAAGTTTCATTCTTTGTGGTTGTAAGGAGCTCAGTAGTGAAAGCAATCTCATGAGGATTGTTATGTACAGGTTGTTTTGCTTTCATAACATCTACAACCTGCAGGATGCATTYATTMAGAGGTTYGTTTACTTACTSTTCTYCTCTCTTGYCYYTCAG

RAD_172	TGCCTCTGTCTGC[A/G]TCTGAGCTGTCCCTTACAGAAGTGAGGGACAAAGTTCCCCCCTTGAGGAGGCTGGATCCCGGGCTCATGCCCCTCCCTGACACAGCCTGTGGA
GBYP-RAD_173	GATTCACACTTGGTGAACTATAATCGCAGCATGCTGTTTCTATTTGTTGTGGTAGCCACATGTTGCACCTCGGCCGTCACCTTGTGCTGTATGAGATGTAGCAATTTTCACTTCTAATGCTAATGGTAGTTTATATTATAGTTAGTTATGTTAAGAGCTGGTGACCACACAGAAACAAGTTTATGTTGTTGTTATGTTTTCCTGCACATCTCGAGTGATTCTCAGTCCTGGTCATCAGGACCCAGAGCCCTGCAGGTAGTCCTTGTAGTCATCTGA[A/C]CHRTGACTGAACTACASTATACCTGAGATACAGGGTAMAARCAAGCTRTTAATCTAGAAAAMCAACAGTAATCTGCGTCTTGAGGGCCAGGATTACAGACCACTGAGGTATTATAATAACACCTGTCGCTAATTCCATTCATAGACTGCTGTAGGTTACGCTTAGATGCTAATGCTTAGTTAAAAAATATTCAGCTTGAGCCACAGGTTCACTTGTATCCATGACATTATTATTTATTATTTTCCATAATAACAACTGAATCTCCCCATATCCTACAGAGTGGACCCCTGTTTTATGTGAGTAGTATGTAGTTTCTCACCTATTTCACCTCACTTACAATATAAAAGGGGTGCTTTACCCACTCTGTTGCCATCTATTCTTTTTCCACATAAGTGATTTATTAACTCTTTAATGTTGGCTGAAGTTGGGCGGTAGATGGTTTCCATCCACCTTAATCCACCTGCTGTAGTTTTGCTTTAACTTTTGTATTGCA
GBYP-RAD_174	GAGCCCTGTGTGAGGTTGTTAGATCACTGAGGCCCAAGACAGCACCATTCTTTGCAGACCCTTGACAGCAAATATGTGGTAATGATATTGTCTCCTGCTGGGTAATAACACACAATTCAGACTGCCACATACTGCAGTCGCCGGGGAAAAAATGGAGGGGAGAGAAAAAAAGAATTACACTGAAGTACTGGAGGAAAATGACAGGAGAAATGTCTTCAACCTGAAGTGCTATATTGAAAAAATTCACTCCTGCAGGACA[C/G]TGCAGTGGGAACAACTGTTTTATTMRCCTCTTCTCAGAGTGATGGTGYACAGAATATAASGRCCACTGTTGTCTGTAATAGGAACGGGGTGGTTTCCTCATGCAAATATCCATTTGCAGTTTTCCCTGCCAGTTTTGTTGTCTTTTGTTCTGAGACTTTTTAATGATCATTATGTTTTCACTCAGGGATTTTAGTAGCCCTGTGCCTAAATGCTAAATGCTGTGGTTAACAAAAACCATGGCTTCAAATGACTAAAGCCCTTTGTACCCATATAACACGCTGCATAGTTAGTGTTTAGTATAAACAGCATTTTCCTACCATGGAGACCTT
GBYP-RAD_175	TGTGTGTGTTTCAGAGCGCATGTGCTGTGTGCATGAACAAACAAGCAGCAGCAACCTTTGCCTCAACACTCATGAGAACTTTAATTTGCCGCTTGACCTCTGGGATGAAGTTATTGCCATCCTTTAGTGATACTGACCCACCTGCAGGRGTCMAATAATTCT[A/T]AAGTCACTCACATCCAAATGGACAGTTTCTACATGTTGCATCAATACCTCAAAACTGACTTCTAYATGCGAGGATACCATCATTACACACATACAGATTTGATGGTGATTAGCAAGATGTTTCACACTGTATATCAGCAGCAATGCAGTACAATTCATTAACACTCCACTACTGAATTTTGATTTTAGGCAGAGATCCTTATTAATATTGAACTGTGTTACTATTAACAGAAATGTTAATTATGATGTCAAGACAGAGAGAGTCAAGGTGAAAGCTGTACAGCAATAGCTAAAAATAATCCATGCCAGCTAGAGTACAG
GBYP-RAD_176	AAGAGACTCTGATAAACAGCCACAAAGTATTTGGAAGATCAAATTTAAAGGTATTTATGAACTGGATGTATTGTATGTTAAATCCCTTTTGTGATGTACTGATCCCCAACTGGACATTGATATTAAAATATCGGCTTATTATTGGATGAATCTTTCTATGTCGAGGAAACCTTTAACTGTATCATGCTTTTGTTGTTTGCTAGGTGGGCTGGCAGCTGAAGAACCTGGTGAACTTGTTGCGTGGGGACCCTGCAGGTGTCACC[C/T]TGACGCTGAAGAAACGCCCACAGAGCACRCTCACCTCAACTCCYGCTCTGCTCAAGAACATGAGATGGAAACCGTTGGCTCTGCAAGTATGACTGCTGCTTTCATCCTCCACAGATAATATTGATGCATACCTGTTTCTGTATGTGAATATGGATGTGCATCATGAGTGTTATGTTTGTATATGTGTATATTTCTGTGCTTCTGTCCCTTTTCATGTTAAAAATAAGACTGGACAGACTTCTGACACAAGACACCAAAGTCTCGCATGAGCCAGTAAATGGCCAAGTTATAAAATAAACAGAAAAGTACAAAGTAAAGATGGGGTGGGCTCAATTAAAGTAGTAGCTTTGGAATACAATGCAATCTAATACAAGAGCCCTGAAACAAACATCATCCATGTAAAGCTCATAATGTTCAGTTTCTTTTCAGAGATAGCTATGGGTGTTGCACTGTATTGTACTGATATTGCTTTTATTGCGTCCACCCCGTTTATGTAGCACAACTTG
GBYP-RAD_177	TTAAGACAGAGTTTGTACTTGTAGAGGACAGAGGATAAAGTGGCGAAGCTGTGAGTCTATAGTGACCTTTTGGCACTTTGGGTTTTGTCTCCCATGGAATGACATTCCTACACAGATCTGAAATGCTGGGGTGTCATTTCTGCAGATTCCTAGCCTCATCATCAGGAAGGACAACTCCTTTAAATTCTTATTCTTGTACATAAATATTCAAGTTCCAGCTACAGTACAACTAACTTGAGTTTCCCCCCCCTGCAGGATTGCTGTACTGCTGCAGCAGCTCTATGATMAAACATCATGTATTTTTCACAGACAAA[A/G]ATCTTTACATGTGCATGCCTTAGCACAGCAGCTCATGAGGCACAAAGAGCACTGCAATATTGTTACATTGTTTCCCTGCACAGATAATGAACTTGGCTCCACATGCAGCATTCTGTTTGCTTATTTTATTTGTGACTTATCCATGTGGCACTTTTATTCACAGACATTCCCTGTTGATGTTTCTGAAGGTAGAGAGGATTAGTGGAGTTCAAACTGAGATATTTGAAGTCCAGTTAACACGTTCACTGCATTTTTTCTGACTTGCTCCCTTGTGTTCATGTCAGTACACCATCAGTCTCATCTCTGGCAATTTATTATTGTCTCAGGCGACAGGTGCTATTTTCAGTGTGGCTGCTTGTCATCATTACTCTGCATTAAGTCTCTAATAGGGCTTTTGTTATTAGTTAAGTGCCTAAAGCTTTATAGCTGCCTGTGAGAATGAAGATGAAAAGACG
GBYP	CATCTACAAAAAAACTGTAGTTACAACATCACATAGTCAATAACGGCTTAGAAAAAAAAAAGTATCCCATCTTGCTTAGACATGTGCAGACAACTGGTCTCTCTCGTTCTCACCGCTGCTGTACAGGGTGCAGCTGTGCCTGTTGAACATCACATTTCCTGAGGACAGGGATAGGCAACAATCTGACATGGAGCTCCAAGAGTCCGCTCTCTTCACCACCAACCGGGTTT

-RAD_178	CCAGTTTCACTCGTCCCTCCTGCAGGGTGCAA[A/G]YGACAGCCTCCWTWTYCAYAGCCACATTKTTCATTATGAGRCTKGATTTTTGAACAGGYRAGGTYRCACTKCTATWCAGAAGCAGATCAACCCTGGTGTTAGCACAGGAGGCGGCTGTATTCGGAGAGGGCCGAGGACTTTTTAACCCCATCCCAGATACGAGCTGCATAGTGAAACCTGTAAAACACAGTAAATGTATAACACAACTGTTCACCTTGATGAAACCACTGTGTTTTTAAGCTGCAGCTAACAATTATTTCATTATGTCCTACCCTCAAGTACTGCAACATATCCTTAAATCCTTAAAAACAACAGCTCCACAATCAACTACACTCATAAACTGAAACAAAGAATATTGTTTGCACTTCATATTCTCATAATAAGATAAGTAAAAACATATAACCTTTGTTGTAGCCGTAAAGGCTTTGACCACGTGTCTTGAATTATTGTTTGTGTTCAATAAGGACAATTACAAAAAGAGTTTCATATCTGAAACAAGCTAACGT
GBYP-RAD_179	TTACAAGCTGCTAACTATGCTACACAACGTGTTAATGAAGTCCCAGTTTGAGTAAAAACCTCATAGAACAAGTGCAAAACCTATAGTGCAGCCTTATGCTTCTTTGTGTTGAGACAGCAGTATACTATGTGCCCTGGGCGATATTGAGAAACTCCATTTCCACAAGCAAGCAAGCAAGCAAGCAAGCCACTAGCAATTATACACCTGAAGCATCCAGACCTGTTGCACTATCATCAAACAAATATCTGCCTGCAGGCGAAGTAGGGTCYATAAATTAGGAAAYGYAGCAGGCGGWAGACAAGAC[C/T]GAGATGGAAAGAGGCATCTCGTAGCACAAAAACACTCTTGTAGGAGGAATTTTTTGATCAAATTGTACAAACCCGCCTTTCAGAATTCACCTGTCTGATGTTTATGAGTCACCTTAGACCCGGCATAAAAACTGGGAAATTGCGGACTTCGACACAACTGTGAAAAGCAACTGTGTCACCCAACATATGGAACAGCGAGAGGAAACGTATACTTTCAGAAGCCCTGGAATCTCCGTTCACGCCAAGATCCCATTTCCCCAGCTGTATGGTGTGGTAATTGCACAGTAATGGCTTTTTATGTGGCTGTTCTCAGGTGGCTAATTATATACACATTACATACCCCAAAGTCCTTGTTATTCTAACTTTGGCAAATTAATGACATCTAGCAAACATGATGGGAAATTGTGGCCACAGTAGAACAAAAACTTAAACTCATAGAGGAAAACAAACAACTTTTGGCGAAAC
GBYP-RAD_180	AGTTAACTGCTGTATCTATTTCCCCCCTAAAATAAAAAACTCTCATTGGAAAGCCTGTACATGATGATCCACTGAAACTTACCAGCAAAGTTCCTATAGTGCAAGACCACGTAACTTACTGTATCAGATGTGGGAGTTGCAGTTTTATGACTCTGTGTTCGTGTATGCAGTGGCACAGGGAACATAGATGTAATCTGTGTGTGTGTGTGTCGACTCAAGACAGAGAGGTGGTTGTAAAGTGCTGAAAGCCTGCAGGAAACCTCTGAGGCAACCACTTTGCAAAACTGAGACCAGACCTTGATACCATTTCGCTCACTCATC[C/T]GTTGGACTACRTGTGTGTGTGTCACACAGAGAAAGAGAGAGAGACACACACTGAATGTGCATACGCGCTGATGAACAGTGAGTGATCTGATCAATAGTTTGCAATTTCGGATTTGTTAACTACAGCCATTCACAGTGAGCTTTGTTTCACATGTTTGTTACAGTACTTCACAGGACTAATATAACCAAGAGTGTTCAAGCTTGTATTTAGATTACAGACCAGTGTGTGTGCTCCACAGTGTTCATTTTTCACTGATTAAGCTTTTTATTTCTTTTTCTTCTCCCAACTAACTCAGGTGGTTCAGGCAAAGACAAATAAAAGACATGATAAATTGGAAGGGGGGAAAAAAATGAGAAAAAAAAGAGTGTGGGAGGGAATATGATGGACCCACAGCAAGAAATAGAGGACGGTTATGAAAGAGATGAAAGATAATATATGAGAGAGAAGG
GBYP-RAD_181	GAAAAAAAAACACACACACATACATAGTTGTTTATTTGACTGAAAGAGACAAGATCCATTTGTCATCTTCAAAGCATTGCATAAGCCCAGCTGCAGGCTCAAATAAGTCCTGAACAAACCAAACGATTCAATTCAACTACAACAAGCAAATACATACACACACCACAAACATTCATTCACAAACACTCTCTTTATACCGTAGGACTCATATCCATCCAGCGATTTCACAGTTAGCAGCAGATGTTGGTCCTGCAGGTACTCGATCTCAGAGAGRAGAGGTTTGAG[C/T]GTTGTTAGCTGCTTGTTGGACCAGCCCACACGSAGGAAGTTCACGTTGTCACTGCTCTGACTGTCGTTCTCGTAACTCTTCTTAAACTCTACAGATGAGAGACAGAGAGAGAGA
GBYP-RAD_182	AGGATGGTTTCTCATCCCTCAAACAAAACCCAAAGTGATCAAACACAAGCTAACGACAGAAATATCAAGTGAGAATGTTTGTGCATTTTTTAAACAAATATGAAACTGTAGCATGTTGGCATTGAATACACAACACTGAAATGAGAGCCGGGGCAAAGAGCCAAGCCCATATTTGAACATGTCAACCCAGCAGGCAGATCAACCATGCTGTGTTGGGATTAGATCCAACACTAATATGAGGGACGACACCTGCAGGAATGAGCTACAGGAGACA[A/T]GATGMCATTTAATWAATCCACATCACTACAGGACAAATGACAKARAGACAGACAGAAGAATCRCACAACACAGGTGAGAGCAACTGAGCAAACGAACACACAGCCTAGTGAGAACCAAAGAGGAAAGGCAAAAAGACTGTGTGCCCTTGATTGTAAAGGTGACCGCAGACTACCTTCACACAGAACTTGTTGCTCTTCATCCATCTCTTCTTCCTCCTGCTGCTCTGTACTTCCATGACTGGCAAGACATACATATTCCTCTTCTTCTTCCTCCTCCTGCTCTGTGCTTCCTTGACTTGGCAGACAAACATATTC
GBYP-RAD_183	AAAAATTGAGAAAAATATTATCACTGCTGTCTGGAAAAACAATATTCATTATATTTTCTTAAATGTGTGTTTTTGTTGAGTGTTTTTGCAGATTTTGAGGCTGTAAAGTATCCAGTCAGAAAAAGAAAAAAGGAACTTATCAAATTAAATTGAATCTAATCCATAAAACTGTGCACATATAACTAATCTAAATCTAAATATCTCTGCTGTGTCTGGACTAACAAGACCGTCTCGGCCTCAGATGCGGACCTGCAGGAGTCCTGGGATGATGTCAGGCAGCAGCTGCARCAGAGAGTCCTTGGCGATGCGTTCAATGACTTTGGTTTGCATCTT[G/T]ATGGCGGCCAGGTTGATGGGGTAATCGGCCGTCTGCACGATAGGGCACAGCACCTTGATGCACTGCTCTGGATGGATAGAACCGGCCAGAGTGGACGCCGCCTCCTCAGCCGCACGCACCACCTAAAAGCACATCAACATGTGATAATACGGAGATATAATGAGGGAAGAAGAAGAAAGTATATGACATGTACAATAAATGGAGTGTTTTGCCCCTCCATATTTATTTCTGAGGCTTGAAAAAGTTATAAAGTTCA

GBYP-RAD_184	CTGTGACTATTGGAGCACAGTTCCATTCGAATCAAGGCAGATATTAGGTGTTGCCAATTTGTCTGGTATGTGTTTTGTTTTTTTTAATTCTTTTGTCTTTCAACTATCTCTCCATAGCAGAGGTGATCGCGTCCCATTTTTATCCAACATCACATTCTAAATGTGACATTGTTTTTCAACCATCTGTAGAGTATAGTGCAATTGCATCAGTTCAGGTAAGAAGGTACCCTTTATGTAAGTGTCTGTGTCCTGCAGGTGGTTGGCTCTGACTAGCTGCCACCAGGGAGGCCTTTAGTAATAAGACAC[C/T]CACTGTTCTTAGTGAGRCATGGYTGYCCGTGRGTTAACAGATTTATATTGTGCATGTCCAAAATAATGAAAGGAAAAAAATAGCACAGCTGTACAAAAATAGTGATTTGCTTAAAACAAAAACTGAGGTCAAAAGCAGAATATGAGCTACAGCTGCAAATGCTGACCAAACTGACACACCACTACACCTGCTGGACCAGACAATGAACACAACAGTTCAGTTTATTCTATAATATTCATTTACTAGAGTTAAGGTTAAGTCAGGATTTACCTGAATTTGATTT
GBYP-RAD_185	AGTGTATTTCTAGAGTTTCATTTTTTATATATTTTGATCATTTTGTGAGTATATAATATCCTGTATTAGTTCATACTAAGCTACAGCTATATTTCTCTAGTTTATAGACGTATTTACAGTAGTTATATACTATCAGTACTAAAAGATAATTTAGTTTAGAAGATCAATTAATAAGCTAAGCATATAATAGCTTGTTGTCTGATTCAATGCAGTTGAAGTGATCACACCTTCTGTATCCAGCCAATAAACCTGCAGGCWARATATCATCTYGTCTGTGGAGTCTTGGTGACAGTGAGGAGTTTATCTGACCAGCACACATRCRA[C/T]GCTGCATTTTCCTAACAAACAATTTATAGATTGAAGAATAATCCCTCAATCATCACGTATGAGCCGCCAGCAGAGTGAGTCTGTATCTGCAGAGACTTCTGGGTCGGTCGGTGTGTAGCTGTCAGCCAATAACAGTGCAGGTTGTGAATGTGGGACTGTATGAAACCATAGCAACATGGACGAGAGGAAACTACAAAAATGGCGGACAGAGCGCCGATGTTCTGCTTGTTCAACAGTTGTGTGATAAATTGCTGGTATGTTCTCTGTTACAGCAGCGAGCAGTCAGAGTCTGTTTTCTGCAGCACAAACCCAAAATATTCACTTAACAACGATATGAAACAGAGAAGAACAGGATGGACGAGAAACTGACACCAAAATAATGAACTGATCATCCAAACAGTTGTGTCTATCTGCTCACAGCCTTTCATCACATATAAAATATATTA
GBYP-RAD_186	CTCTTCATCCTCCATCTCCATTGCCTCGGCTTCTTCCTGCGCCAGACGCTCCTTGGCCTTTTCTGCTTCTTTTTCTGGACACAGGGAGGACGAAAacACACACACACACACACAAACATACAGAGTGAGCAAACTAAACGTGATGTGGTGGTGGCAGCATACAGCATGTCAACTATTCCACCAATTATTCCATTACCATAAATTCTTTACAAACACTAGCTTAAACCTATTATTTATCAGGTGTCATACCTGCAGGTGACACTGGTAAATTTTAGGACACCTAATGTGGGATC[A/G]GGGTTCTTGTGTGTTTGGCTGCGCATCTCATCTGACAAATAAGWGTGTTGTTGGTGAGCGGAAAGTGAAACAGGGTGAAGCTTATGATATTAGTGATTCAGCTTTTAGCTTAGCACTCATACCAGTCATGATGACAGTTTTGAAAGCTTCTGAGTGTTTCAAAATCTTCTGTGTGTGTGTGTGTATGTACGCATGTGTGTGTGTATACTGGTCAGCTGTGCATACCTTTCTCCACCAGGGCCTGTGGTTTCTCCCAGGTGGATTCCAGTGTTCGGTTATTGTAGTAGTATGTTTTC
GBYP-RAD_187	TAGTCTCAGCAGCATTCCATCTGAGCTAGAGAGCCTCTCAATGGTGGTGCAGAGAGACAGAAGTCTACTTTCACAGTAACACTGCAGGAGTCATTGATGGATTGTTACAACGTGGCCCTTGACTTGTGACGTAAATCAGGCCAATCTTTACAGAGACAGATCCCATAAAGCCGTTGTAATGGTCAACAGGCAGCTGCAGCACAGAGTAAAAGAAGAGGTGTCTGGCCCATGTGGACTGCTCAAGTCGACCTGCAGGCATG[C/T]TGTTTCTCAGGTATGTGTACTGCTCATATTTCCCTCAATSTTGCYTAARGATGTGGTGAGAGCAKATGACACTTAGTAGTGTTGCACACTTACACGCTGGTCAGACTAGATTAGATCCAATTCACACAGTCCTCTGTTCCCACCTCATTCTCAAGTGGGAGAGGGGAAAGTGCCAGAGAGATTTCATGCCTGAGACAGAAGAGTTACAGTTGCATGTTCCCTATAGACAATCCTAACCAGCACTCAGTGCTCTATCCCACCGACGCATGGTGACAGCATAAAAATGTGAATCTGCCAGCAAAGCAGGGAGCTAACTGTGACCCAAAATC
GBYP-RAD_188	GGGCGAATGGGAGACAGGAGGAGAGTAAACTTCCCTGAGGCCAGTGACACGAAGCAGAACAGCCATTTTACTTGATTCAGTCAAGATAATGAAAACAAGAATGGAGCACTGTGAATAAGCTGGGCCAGCACAGTGTGTAGTACCATTACTGAAACCAAGGGTACATCACTTATTGTACTGCAAAGAAATGATCAAGGTCAGCATAGTTTTATAAGTAGTAATAATGTGGTTGAAATCTATATTTTTATCCTGCAGGATCAGAAAGGTGTGGCAGAAGAGGAAATGTGGAGTCAAATTTGGCTGCCTGACTATCTCCCACAGTAYGGTRAGGACTAWTWM[C/T]CGACACTGTCCTCTCAAGACGATACATAAGATCAAAGTGCATTTGTCAATTGAATTTTGCCAAAATTCTTCAATACATACTGACATGATCGTGTGTGTTTGTCTTCAGATCAATCGACCGCCAGCCAAATTGAACCTCCTGACCTGTCAGGTGCGGCCAGACCCAGAGGACAGGAGGACCTTTGACCTGGTCACTCGTAGGTTCATTCCTAACTTTTGACCCTTACACTTTACCCTCAACTTATCATCAT
GBYP-RAD_189	CTTTAATGTTGCACTTTGACAGTTTGAAAGTCTTTACATCATTTGTTCATTGTCTCTGTGTGTCTACAGTCACTTTGTTATATTTTGCTTCAGGCCCTTACAGTGATAGTTTAGATCAGTTTAGATGTCGCTCTGTGTCTTCATGTTCCAAACGTCACGTCCAGGAAGTCTGTGCAGAAACTGGAGGACGACGTGAAGCAGCTGAAGGCTAAACAAGCTTCATCTGATCAGAGAGCGACAGACCGACACCTGCAGGATCAGGTCAGACAGGAAGA[C/T]GCGTCGCTGAGGGACAGTAGAGCKGATTGATAYGKTGTTATTATTTCCTGCTGYGCTCAARATGAAATGTCTGGTTTATATGTCAGTTTGCTGAACAGTAAGCACGTCAGTCAGCTGATCATCAGGTGCCTAAAAAGAATGAACGACGAACAGGAAATACATTTTAATAAGTCACATTTTCTTTACACAACACACACTATAAACATTTTTGATAAGGTTCCATTAAATCATTTTGTTTAATAATTGTGACCCAGAGATGTGCTGGACAGGATGTTTTATATCTGATATATTGACTTTTACCACCAGATATCAGT

GBYP-RAD_190	TTAAAATTAAAATTAAAGCTCACCAACACAGATTTATCTGCCTCTGAATTACTCAAATTTTAACTCTCTGCACTCTTACCACTCTGGTTTGATGTCTGTGCAAGTGCGTATGTAGTTCTTGGTGGTGAGGACAAATTCATTGTAGAGCACCCATTCGGGCTTGTGGTCCAGGACTGTAGACGGGTGCAGTTGGACCACTTGGTTGTCTTTGACTGTGAGGTAATGACCTGTGCGCTCCAAGTGAGCCACCTGCAGGATGGAAAACAAGAAAAACAGATGAACTTCAACGAGGCACAGATGGAAGTGGGTCCR[A/C]AGATATCTCTGGTGCAAACTTAAGATMCTTCCTGACATGATGGAGGAATGAAGAACTGAGTGTGTGTTTACCTGCATGAAGAAGCCGGTGCAGAGCGCTCTGCGGATGTTGATGTAGTAATCTCTGCTGGTAAACTCTGTGCTTCGGCGGGGCAGGTTGAAGCGGTCCATGATCCTGGACAGCTGCTGCCGCACGTTGTCAGCAGACATCAGTGAACGGTAGTTGACAAAGTTGTCATAGCACCACTGGTTAGACTCGTGGTCTGGAACGGGGACAAGAAGGATTAATTTGGTTAATTATCATGTCTCTACACTCTTATCTGGCATGAGTAAACACTAATTTCATAACAGATTTAAAGCTGCACTAATCAATAACAATGGATCAAGTTGCTATGTGTAATGTGTATGGGGACGCATGTAAAAATGAACGCCTTAGCACTAAAGAGCTTTTTAGTTTA
GBYP-RAD_191	GACTTGAAAAATTGTGAGCCCATCCTTTAAGTTGATCACTTTCACCTCTGATATCAACTCACCATTGCCATTTATAAACTATCCTTCCATTTTCAAGTATAGCTGGAGTCTATCCCAGCATGCTTTGGGTGAGAAATGGGATAAGCCCTGGACTGATCACTAGTCTAGTCTGACACAAACAGACAAAACACACCTGCAAGACCTGCAGGTCTTTGCTCTGTGGGAGGAAACTGCTCATGMTGAGCCACCATGCTGCCATGAATAAACTAGAAAACAGTA[A/T]AATAKTTAYTTTTAATAAAGACAGAAAATATATATACAGTATATGTTAGCTGGAGTAGTAGTAGAGTAATTTTTTATTGTTGAAATCAACATCTACCTATCATGCTGTGGTAGTGTGTACAGATGGTCACAATCTACTGTATAATTAAAGTAGAGTAAGAGGTTTACCTGCCACAGTAAAGACATTTTAAAAAGGTTTTTCTTATnACTTTCAAATGAAGTTATGACACTCACATACATTATGTTAAGTAACCAGGTTCCTTA
GBYP-RAD_192	GTTCTCCGTCTTCCCGCTCCTGTGTCGAGCCATCTCTTCTTTCTATTAAATGCTTCAGTGGGAGTTACAAGCCACTCCATCATTTCCTTCCCCTTTGATCGAAGCTGATGAGAAAAAAAGTCTCATTGTGCAGGGACTCAAGGGTGAAGAGGCTGGACCCCCGGGGTCAGCTCCAAACTCACGCAAGTATTACATCATGTTTATCTAGGACGGGGTACAGACTCATCCCTAGCCATATGTGCCAGTGTCCTGCAGGA[C/T]GACTTTGATCTTGACTACCTACTGCCCTGCTGCYTCCCCAGGGTCAGATACAAGTGAAGGCCATAACTTCTCTTAGATTAAAGCTGCTAAACCCCCTTCACCAGGGGCTACAGATGCTATTGGCTGCCCCCTGACCTTTGACCTGTCCCATGCGGGCTGAAAAGAAAAATATAACCCCCCCCTGTTATCTACTCTTGTGAAGGGACAAACAGCAGCATTACTTCGAGTCAAAGGGTGATGTGAAAGCAAGTGAATGTGAGATCTGTTTCTGTTTTAATCCGTCTCTTTCCGTCTCACTCTGACCATTTTTTTGCCGTCAAGGTGATGTTGC
GBYP-RAD_193	GTGATACTGATTGAGCCGCGAGCCTTCCTCTGCCACCACCACTGACTTGGCCGCTCCCTGAGTCCATGTGTAGACCACCTCCGAGACTGGATACGCATCTAAGAACACAAGACAGGAAGACATACAAACTTTATTTTTGCATCATCAAGAAATTCAATTTTTACAATAAGCACTCTGTTACAAATATGACTTTGTTTAAATTTTAAATTCAACTGTTTTGCTTGTGATATCAGGAGGTACCCCACAGACCTGCAGGTCAATA[C/T]RGCTGCATTAATCTCTATGGACTCAACWKATTTWWAGCCRAACAAAGAGAAAACATAACAAAGRAGTTYATATCATACTTTATACACTAGTGTGTTACAGACGCTAGTGTAAAAATATAATTGGAGATTCACAAACATCAACATTCTCAGCATTCTAAACACAAGGTCCTCTTACTTACTAGCTGTTCCCAGAGCTTTTGACAATATTCCACTGTCAAAATAGTAAGTGGACCTTGTTTTTACATTCTTCTAGAGGGTTGCACTACACTATGTTGCACGTCTTACCGATAGTACTTGATCTGTTTCATCAGGTCATTCAGATACTGA
GBYP-RAD_194	TCACGCCTGCACAATAGAGTTGCATTGATTTTGTATCTTCTCCTGTCCTGCAGGGAAAACACATTTTTACTGTGTAGTATTCATWAAGRGA[G/T]GCATAACTGTTGCTAATAACGTATTGAAATTATRTTCMAGCTCCTAATGATGATGCAAGCTTACAACTCCTCCATTACCTCCTAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGCTCGTTCAGGTGAAGTCGGCAGGTTGCAGGTGTGTGGTGTCAGAGAGCACCAGGAGGAGCGCTGACTGAGTACTCAGCCCGGCTGCGTCAGAGTTTGGCCTGCAGTTCTGGCTAAATCTCAGGACCAGCAGTTTATTTTTTGAGCGCCCGCTCCCAACCGCAGCAAAGTTAAAACTGACTGCTCCTGCAAGATTTGCGTTGGGTCCCGCGGGACCCTCGGGATCCCAATCCCAATGCAGTCCTCTAATACATTGGACTCTTGGCTCCAGACACACCTCCCCCACCTGTTATTAGATCATGAGGAAGATGAAGGA
GBYP-RAD_195	ACTTATTTATTCACTATATGCCTGTTTTGTGCCCTGAAATGCAGAGTACTGTGGAACATTCTGCTACCCAAGTGTCTCTCAGTCCCCCTACCTCCACACAGTAGGAGAGAAGCTACTGCCTGGCATTGACATACTATGGACAGGTGAGTCTGACACTACTTCTGTTTTTATGCGTACAGTAGTGAAGTAGCTTTAACAAGTAACCACTCAAAGTCAAGAGAAAGATTCACTGGGATGTGTTTTTTCTTCCTGCAGGTCCCAARGTGGTGTCCRAAGACATCACAGTAGAATCTATTGAGGAGGTATCYAAAATCCTAAGAAGAGCCCC[A/G]GTGATCTGGGACAACATTCATGCCAATGATTATGACCAGAAGAGGCTTTTCTTGGGTCCGTACAAGGGCCGCTCTACCGAGCTCATCCCCAGGCTAAAGGGAGTCCTCACCAACCCTAACTGCGAGTTTGAGTCCAACTTTGTAGCAATCCATACTCTGGCCACATGGTACAAGTCTAACATGAATGGGGTGCGAAAGGATGTGGTCATGAGTAAGTATGGTCAAAATGTTAACTAATTTGTAAACTGTTCTTTAAAAAAA

GBYP-RAD_196	GTTCCTCCTCTTTTGCTCTCCACACAAGACTGTTGACCTGCATGCAACCAAAGCCTGCTCAAACGCGATTGGTCAATATTACACGGACTACAAATGAACTTTAAAAAGAAACCAGAATGCTTGCAATACCAAAATCTTATCCTGTTGCCTACAGATTCTGCATTCATATGCAGATATCCATTCATAGAGATTAAAATGTGGCTAACATACTATAGGTGCTAACAGTAGCTGGCTAGTAAGCAAATGTTCCTGCAGGACACTCYGCATGAAGCCTTTATTCTGTCTTGAGC[C/T]TTCAGTCCTSCAGCTCGGCTTAAAACCCTGTGGAACTGCTAATATTCACTGCCTAAGTGTAGACACTGAGACAAAATCCTTACTATGAACAGAGAGGGAACAAAGTTCAGACCCAAAAAGCTACAGAACACGAGTCAGTAGCTCTATAGTTATCCAGAGAGAGACAGAGATGACACAAGCTAAAAAAAAAAAGAAAGAAAGAAAAAAGCACCATTTCATGGATCAGCTGTAAGGCTGGGCGATTAATTGAATTTAATTTTCAATTATGATTTTGGATTCCAATGATTATGAAAACAAGA
GBYP-RAD_197	AAGCCATGTGCCTTACAGGGAGAGAAGAGTCATGTTCTTGTTCAAGGATTGTTTTCCTAGTCTCATTCAAAAATAAAAGGCAAAGATCGTGTTCCCACTGCGCTTTTAGTATATGTATTGAAGGTTTAACTATGATCTATCTCTTCATCTCAGGCCAGTAATAGTGCCAGTAATTCATCAGGGACCTAAATTCAGGCTGACAATAATGAGCGTTGCTGAGGAATCTGGGTTACATTCGTGTGATGAGGCCTGCAGGTAATCTGGCAGACTGSGACAGGATCCTTGTGCACACTGATTAAAAGAAAGAACTCTGTSYAACCACAARGTTTTGGYTGT[A/G]TTCAATACTCTTTGTGGCCAACTCACCAGTAATGAGAAAAACTAGCACACTGCTGCTGCCTGTGTTTATATCATATCCTTTCTATGCCACTGGTCATCACGCTCTATTTCTACCTATCTCAGCTGAACTTTTAAATGTAAGGATTCCCATGCCGCCAAAAGAACCGCAAATGTTTTCCACACTAAAGTGTAATGGCTATTTTTACTCATGCAACAGAGAGCTGGATGTGCAATTGTGTCAATTGGGTCAGAGG
GBYP-RAD_198	TTAGCTGATTTAAATGGTGATCTTTTTTGGATCTAATATTCTTTAATGATACCAAATTAACGCATGATGACTCTACATAGCTGGAAGATCTTTGAAATGATAAAGGCACGGTGCGTCTAGATATTATTAGTTGCTGTAGTTGGAGAGCTGCAGTTATTTCTGTTTATTGCAGAAATGAATGAATGTTGTTGACGCATCTCCTTAGGCGGAAGTGATCCACTGTGCGACACGTGCTGTCTCCATAGAAACCTGCAGGTTGTCTGTGCTTCAACACTTTGCTATATAAATTCCTC[C/T]GAGACCTGATCTGTAGCCCAGATGAGAAGAGATGAGAAAAMASAKCGGCTGAAACTCAAGGAGGAGTCTGCATCCTCAAGTTGTCAAATCAATCAGGCATCTGTATGTCGGGTGAACTCAGTGAGAAAGCTGCTGCATATAAGTCCCCTGCATCTTATATATATGTGTGTTTGTGTGT
GBYP-RAD_199	ACTGGGCTGTTCAGCCACAGCAGGCGCTGCAACTCAACCACAGACTAATCCTTGGTGCATACTCCATTGTCTTGTGAGACAGAAGGAAGCCAGTGATGCATTTTTTTTAGTGGACTCAGTACATAATCATTAAAGTATCATGGGCCAATCAATGCATTTATGAACAGTTGTTTGATATTTGATATGAAATATGAATCTTTACTGTCATAAATTTTTAAAAGGAGAATCCTTACCATCTATTTTAGATTCCTGCAGGGGTTAWTAGGG[G/T]CATTTACCTTACTGAAGTAAAAAACCTGAGCRGTATAGTGGTGTCCGATAATTCATTGCCAACAGAATCATGTACTCAAAGTATGTTGCACAAGTGCTGTGGATAAGAAAATACAGGATCATCACTTGCCTCACCAGCTTGTTGAAGTTCTGCATTCAAAACGTATGTAACAGTTAACATTTTATTGGTTAAATGTAGTTTAAATATCATCAGATAAAGTCTTCAACTGTTTCCTACTGTTGGAGGAAAACCTCTGTTAACATATCGTTAAATTTAACAGAGCTGAGCTTACTGTTAAACATCTACTCCTTTCTTGCCTCAG
GBYP-RAD_200	GCTTTCGTAATGAAGTTGTCGAATGACATATTCTTTCAGGACCGCGAGAGGCAACAGGCCCAGATCGGGATCATGGTGGAGTTTGCTATCGCTTTGATTGGCAAGTTGGATGGCATCAACAGACATTCCTTCAATAGCTTCAGGCTTCGTGTGGGTGAGTGCGCTCAGCCGCTTGGCAGCTTCAGCATCGAACTTTCATTGACTGAATACTGCACTGTATCCAGCTCTGTTAGTGCTGACACAATAACCCTGCAGGTTTCCCTGGTTACACTGTGCATGACTGGCACTTATTTACTGTTCTTGYAATGAGAGCAGAAGCATTTACTGA[A/C]AGTCGATWVWHTAGCTGTCATGTCACACTCAGGATCTTCTTAACTGAGTGAAGCCATCTTTTATACGCTAATTTAATCTTTGACAGAAATTTGCTGTATACAGTATTATTAGTAGAGTGGCAACACAGTATCCACCTAACGTGAATGGTCGGTATAAGCCTGCCCCATATACTnATGTTATACTCAAACAATGAGACAGACAGAAAAAATTCACCTCTGTCTATTGTGTCTGCGGTCTTGACACAGTCATCCTCAGCCAGA
GBYP-RAD_201	CTCGTTAGAGCGGAGATCCTGCAGAAGCATCTAGTTAGAGTAAGCATGTCAACTACTGAGATAGAGGCTGTTTGCTCTTTTGCTTTTTTGGCAGGAGAAAAGAGCTTTTAACCTTTTTTTTTTTTTTAAAGCCAGAAGCTGCTGGCAAGATTATTGCTGACTCATAAGTATTGATTAGCAAACTGTGCTGCGGATACTTTAGTTTCCCTCCGAGGGATTCAGACTCCTATTACATGGTGGGAAGTTTTCCTGCAGGS[G/T]AGATTGAGGAAGAGCATATTAACCTAACAATAAATATTGTGACAAAGTTCATTCCTACAGYTGRAGATSTKAGCTGAYTGATATCATCACCTTATTTGGATGTTTCTTCCTTCCCTGGTTTAAACAGAAAGATACGCTGTGACCAAACCCTGGAACAAAGCGTTCTTCTAATAGTTTCTCTGAGCATCCTGAACGTCTAAACAGGTACTTAAAGTACACGACGGCTTCAGCTGTTACCAGTAACAGTGTAAAGATAATAAACACAGTAGTGCTTTCTCTGCACTAATGTAACTTGAAGACTCTTCCTGATTCCCTCCGCCGACAGCGACAAGACATTATAACCTATTACACCACATTAAAGGTAATTAAAGTGTCAGTTAAAGCAGAACAAAGTTTGTCAAAATAAAAGCATCACCTCTGACTTTTCAATTCAGTGCATTAAAAATCTGGAAAAAAAAAAGTATTTAGATTTCCTCGGGGGGTGAAAAAAAAAAGCATTGTCACACAGTTAT

GBYP-RAD_202	CAAAAGTTGGTCTAATTGTATTGTACGGTATGTGGAGCTGTGTACTGTATTTTGCACCTATGTCCTTTGTTTGTATGCGGTGTATAGTTACAACCATTCCATCTGTACTGAGATTCATCCCACCAGCCTAGCAATGTGGTAATAAAAGGAACTTGAAACTTGAAAATGTGGTCTAACAGCGTCTTGCTCACAGGAAAATGAACTGGAACCGTCCTGCAGGGAGATYGCTCTGCCAAAAGTCTGTTC[A/G]GAGCAGCTGARATCCAGAGAGCAGTTAGCTCACTGTGCATTAGTCTGTTTAATGTWAGTGCAAACAACTTCCTCAACAGATGAATCCTTGGTTATTTTAGGGATGATCATTCAGTGATACTGTTTATTAACTTTCTCAAGCTGCCACATCTATACAGAGACATTTGATGTCACCGAAGTCGCACATCATTTAGCATCTGCTATAGTGTGCTCACATTCAGGTTGTGCTCTATCATACGGTTCAGGACACATATTGAATGTGATAAAAATGTGTCGTATCGTGATATAAATGATATCCTGATGTAAAA
GBYP-RAD_203	AGCCTCTGACCAGGCGTTAACAAAACGCTGCAGGCCGCTGACATGTTGTAGCACTTCCTCCAGTTTGCGCTCATCCCCCTCTTCCTCCTCCACGTCCTCTTCTCTCTCAGTGTGAGGGACGTTGTCATAAAAACTGAGCCGGCTGTCCACAGAGCCTGAAGAGCCACGACGCTGACGTCTGCTTTGCCGTCCTCTGAGGATCACTGAGTTCCCATTATCATTTACATTGTTGTTGCGTGAACTCCCGTCCTGCAGGGCTTTGGGGAAAGTTCCGGGCTTGTGACCYTCTGGTAAATAAAAGAARATCATRCTGTCCTCTTCCTCCTCTTCCTSYWCYYC[C/T]GCTTGTCTGCTATTGTCTCGAACACTGCGGTTGTTCCTACGGTTCTGCTCATGAACTGTCATCCCATTACTAGCTTGGCATGGGATGGCCGGGGCAGATTTGGGTGGGGGTGTTGGCTGTCGGTCTGAAGCTTGCTGGGGAACGCTGAAAGGATCAAAACCCTCTAAATACATTCCTCCTCTCTTACTAGAGCCTGCTGCTGTGCTGTGGCTGCGAGCGCGAGTCACTGGGCTTGGTGTGCTCACTGCACTTCCACTGCTGGCTTCAGATTGGCTGCTCCCAGTACTTCCAGTGCTGCCATTACTGGTCTGAGTGGAGTAGGATACGGAGCGATTCCGGTTAAGTGTCATAGTCTGAGTAGGATTGCGGTGGTGATTGAGGTTCTGGTTGAGGTTGATACTGGAGATGTCCACACAGTTGAGCCTCCG
GBYP-RAD_204	TTTTAACTAAAGATTCATGAATCATTGATAAAAGATGTGAAATATGTGAATAAGTAACATTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATATGTTTTATTCTTGTTATGGAAGGAATACTTAAACTAACCACAAGCTTTGTTTCATATATTCTTGTCCGTTAGAGTACCTTGCAGAGGGTGCAGAGCACATCTATCGCACCAACACCTGTCCCAAGTGTCGGCGTTGCTTCAAGATGCGCTCCCACCTGCAGGAGCAYCTCCA[C/T]TTACATTTCCCTGATCCCAGTCTCCAGTGTCCCACCTGTAAGCGTTAYTTCACMAGYAAGAGTAAGCTACGCATACACAGACTCCGTGAGGCGGGTGAAAAGGTTCATCGCTGCCACTTGTGTGAATATTCTGCTGTGGAGCGGAACGCAATCCGCCGCCACCTTGTCACCGTGCACGCCGACGAGGCAGAAGATGACATCAGCTATCCTTGCCCCACCTGTGGTGAAAGTTTTCGCCAGAGCAGGTTGCTTAAGGCTCACATGAAGACGCACAACATCGCGCCAGATAGCGAGCCGGTGGCCTGCTTCCACGAGGGTTGTTCTTTCCAGAGTTCTTTGCGCAAGGAGCTTCTTAGACACGCCGCCGAAGCGCATGGAGTCAAGGCCGTAGAATGCCGACATCACGCCTGCGGTGCCGTCTTTCAAAACGAGAAGGACATGGAGGCTCATTATCGGACGCACCTCGCCTACCACTGCTCGCTGTGTGATTTCTCTTGCTCCAA
GBYP-RAD_205	ACCCGTCCAGTTCTTTAAATAACATGGTGACATCAGGAAACGGAGCACATGACCTGACCTCAACTCATGACTTGGAGCTCCACACCAGCAGGAAGTGGAAGGATATGACTGAAGCTGCTTTGCGATTTGCTGTCATGGATCTGTTTGGTCATAAACTTGCAGGTATGTGGCGCTTAGGCAGTGCCTGTGTTTTACAAATGTCATCATTTGTATGCTGCAGAAAAAGTTAAACACCTTGCAAAGAAACACCTGCAGGCCAATCAGGKG[C/G]TGTTCTCACTGGGGAATTGAAACAGTGAAGGGAGCTATGTCTCAGGTTTTACCACACYGAGGYAGCTGCAGATTATATTTGAGATTAAATAAAATGATGTTGCCCTTATTATGCCCTGCTATAATAAGTTACAGTTGCACACTCACCTTTAGCTCCCTCTCATGGTCTCCGCTGCAGAGCGTGTTCAAGGAAACTTTGAAGGACTTCCAAACTGGGCTCAGGTTGTTCATGACTGTCTGCGCGTGCACAATACACAAACATCACAGTTATTATTAATCACACACCTCAAATAGTCAATTACATCTATATGTGTTTGCATGTG
GBYP-RAD_206	GCCTTTAACTGATTATCTATTTGTCAACATTTCTCACCATTTCCCCTTTTCAAAGCCCAAGGGAGGTCTGAGAATATTGACTTCCACTCCTACTGAATGTAAAGTCAGATCCCAAATTGAGTGCAGAGCCTCCTCTCCTGCCAGGCCTGATTCTAGACCTTCAAGAGAGGCTCTAAATCAGCTGAGTATTTAAAGATCGACCCTATACACTACAATAGTGTGTCAATTACTGGCCATCTCATGTATAACCTGCAGGAACAGG[A/C]TGKGAWTGAGGAGAAACRCTGGCAGCAGTTGACTGGAGGAGGCTATAAGCTCAGGCAGCACCATCTCACGGWWGAWYTTCCCTTCATTGGTTATTAGGCAAAGTGTCATTCCTCTGTCCTTCCCGTGACCATGTTTCTGGCCGATTTGAAACAAACAATTGAAAGAGTTGAAAGGCTTAATATGATTAAAAAATGATCAGCTACGTCTGTGGCAGGAGCCAGTGTGCATAATTGGATTACTAATGAGGAACGCAAATGAATAGTGGTGGGGCAAACAGAGCTCTGGACAGACCTGGATGAAATGTGATTTCTATTCTGATGCAGTGG
GBYP-RAD	CAGTAAATACACAGTTCCATTATGCAAAAAGTGTGGTAACAGCATCTGTGACTTTTGACCTTTGTGTAATATAAAGGCCTATTTTTATACAGTCTTAACCAGTGGAAGCAAACCATCATCACCTGTCTAAAAGTTTGACAGAACTCAATGAAATGTTTTATAAAATAGAAAGTTACTTAATTTACTAGTTTAGCAGAGAGTACTGTATAGTTGCGTAGTTGCAGCTTTTTCTTGTCTATTGCTCCAGTCCTGCAGGTGGCGGTGATGCSCTTWTAAGCTGCTTTGCTAACCGCCAATA[A/T]AACCGAGGCAGAAKAAGATATGATTCATTTCCGGCATAAACAAATAACTGCCCTTGTGAATGTTAGTTTCTGTCGATAACTTTAACTGCCATAATGTGTGTCAGAGTCTTTTAAATCACAGGACAGTTTAACTTAAACGTCTGCTGTTAGAAACGGACTTAGAGAATGGCGGCCCCGGCCCATGTTTCCAGAGTCCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCCTGCC

_207	GATAGATTTAAGAGCCCTCGGTGACCAGTATGTGAAAGACGAATTCAGAAGACATAAAAATGCATCAGCCGCAGAGGTGACGAACTTCATGACAGAGTGGGAGGTAACATAACATAG
GBYP-RAD_208	TTAATGTTTAATATGGCTTTTCTGTATATGACAGTGAAATACCTGTATGATCTGGGCGGCGCTCTCAGGTGTACCATGTCTCAGGTCATGTCCGTTGATGGCCAACACCTTATCATTATTCCTCAGTTTTCCATCTTTGGCTGCCAAACCACCGGCCAGCAGGTCCAGGATGAAAACCCCACTCTCATCTGATTTGCGGATGAGTTTGATGCCGAGCGGTTCGGTGCGCAGACTCTTCATTAGCATCACCTGCAGGACYGTGCCAGGGTTGTGATTGGAGGTAGCGTTGCCATGGTTACTGTGGGAAGGCTGGG[A/G]GGCAGTGGRAGTGTTGGAYRARGAAGGGTGATGATCAGAGCGTGGATCTCTTGATTTGAAACCTTTCTCCTGCATTACAGTGAGCCTGAGAGGGCCAGGCTGCCTCAGCACTGCGATGGCCCGAGCGTGAGGGACAGAAGCCAGACTGACGTCATTCACCTGGAAACACGACACCACAGATGGAAAAACAAGAGAGTCAACAGTCTACCACCAACAAGTCAGTACATACTGAACATGAGTGCCACTATGGCAAGTTATGAGAAGTATTACATTAA
GBYP-RAD_209	ACGGCAGTTACGTTCTAAAGCACAAATAAAGACGCCGACACCTCCGCACAACCCTGCAGGAAAGTGCAGCATTGCCAGATTTTGTGTGATTGCAGAGCTTCATCCTGTCTGCTGTGGCCTCTCTGCTCT[G/T]TGTGTGTATGTWGCACGCCGACACCTCCGCACAACCCTGCAGGAAAGTGCAGCATTGCCAGATTTTGTGTGATTGCAGAGCTTCATCCTGTCTGCT
GBYP-RAD_210	TCGGTAAGGCTTCGGGGGAATCTCCTTGGGTACGGCCCGGCTCAGGGTCGCAGTGGAGGTGTATCCCAGCTGGCTCATGGACTGGCCCATGTTCTGGTAGTGGGACAAGGAGCCCAAGGAGCCGGGAGTAGCGGGGCCCAGCTGGGTTAGAGGGCCCGAGCTGAGGGACGAGGCCACNNCCGGGCCCGGAGCCCATGGAGGCCAGCGGGGAACTGCTGAGGCTGGAGGTGGAGTACGCCATGTTCATACCTGCAGGGGAGGCRGTGGCYGGGTTCAGGTTGATGTA[A/G]CTGGTGCCCATGGAGGCCATGGARCCCAGACCAGAGTTCATGGTGCTGGGAGAGGAATACATCTGGAGACAAAGAGGAAAATCTGGTTATTCACAACAAAACACAGAGGAAATAATAAGTTTTAAATGTTGTGCAACAAAAGTTACAAGCAGTGAAAATAATTTTAATCTTGAATTTACTTTTGAACATTTAGAGAACAAATAACATGAACTCCTCAGTAGTTGATATAAATTTAAATTTCTTCTGTGAAATGAATGTTTGAATGTGGGAAGAAGACTGGTTAGACTCTCCATTTTAAAAGTGACTCCTTATCAATGCACAATGAAGCTCTCAGTGCGCGGAGAGAGGACATGGATTTCACACAGCGATGTTAACCTGAAAATGCGTAAAAAGCGCGTCATGGTGCCTCTCGGTTCAGACGGCCTCCTCCTCTGCTTCCATGGAAAAAACAAGTTGTTCAGTATTTAAGCTAAAGTGCAGAAT
GBYP-RAD_211	TTAGAACARCTGTTTGTCAATCACATTTCTATCAAACCATGGAGTGCTATACCACGTTTTGTTCAGAAGAATGAGGCCTTTCTGGTCAAATCAATCTCACAAGTAATCGGAAATATCTGAAAGCATGACTGCTGAAATAAAAAATACCTGAATTTTGACGAATTGGGAGTTTTCCTGAGTAAACAAACGTCATATTAATTGATTTTTGTTTAGGTGTTATTTTTATATGCCCAGACATGTCTGCCTTGCCTGCAGGTCRYAAGAGGTAATGAATATCTAATCACAGTGGCCCTYGGTGTGTAGGTGCACRTCTKTTATTCTCTGACAT[A/G]TAAGCTCTGGTGGCTCTGTCGTCGTTTTTATTTTTTTCTGCTGTTTGAACTCTCTCGCTTCCTCTTAGTTGTTGGATAACTGACAACACGCACGCAGGTGTTTGTCACATAGAATTATACAAGTTCACTTCTTGGAAACGCCACAATATCTAACCTCATTGTTTTTATACAGATCAAAATGTAATGCCTCCCCTCCCCCTACTAAAATGAGGCATTTTAAGACCTTGAATTACCAAAAACTATGGTAAGACTCTGTAAAGATTCACAGGGACTCTGAATGACAGCTGAAGAATGAAGATTTTACTACGAAATATTTCCTGCATTCACTCATGGAAACCTGTGACTTATGTTGTTTAAATTCATTTTGGACCATCAGCCTTTTAAAATATGCACAAAATGATTACAAATTCCTTTAAGGTGCTGTAGACTATATCTTTTTTT
GBYP-RAD_212	GATGGAGAACATGTAAATAATGAAGATGCTCCCACATCCTCTCTGCCACCCTGTGGTGTAGGATTCACAAAACTCTTCCTGGCTCCGTATGTCATCTGTTCACACAAATGTTAAGCAAATACAACACAGACATGAACACACATTAGATATTTACACGAGTAATACAACTCTAAGTCAAGTCTAGTTCATGTAGAGACCACTACACACACTGTGACAAAGCAACATTAAGTGTGTATACTACTTCTCGTCCTGCAGGAACTTGAGCAGATGAAGTCTCGTATTGCCAGGGACGAGGTGAATGTGGAGGTGGACTCGGCCCGCGG[C/G]CCAGAGCTRGGATCCATTCTGTCTGACCTGCGTACCCAGTATGAAGCCATTGTCAAGAACAACAAGGAGCATGCAGAGCAGTGGTATCACAAGAAGGTCAGTGGCCATTTCTTTCTCATGATGAGATAATTTTCTTTAATCAGTGCATTCACTGAAATATTTTGGGTGTCATGTCCAGCTGGAGACGGTCCAGAATGAGGTGAAGGAGAGCAACGAGGCTCTGCGAGGAGCCCAGAGTGAGTTGACTGAGAGGCAGCGCTTCCTGC
GBYP-RAD	ACGGCTAGTGGCCCTGGTCTAGAGCGGGGCAAGGTCAATGAGGCCGGGTCCTTCACGGTGGACTGCACTAAAGCTGGGGAGGCCGAGCTTACCATCGAGATCCTTTCTGAGTCCGGATCCAAAGCCGAAGTCCACATCCAGAACAACAGTGACGGGACTTATTCCATCACCTACATCCCATCGCTGCACGGCATGTACACCATCACCATCAATTACGGAGGCCACGCGGTGCCCAAGTTCCCTGTCCACCTGCAGGTGGAGCC[A/G]GCTGTCRACACCAGYGGGGTCAAAGTCTAYGGACCAGGAGTGGAACCCAGRGGTGAGGGTCTRWAGATAKCTYYKTATGCAGTTACAGGGTTTTCTTAGGGTTAAATACTCCTTAAAATTTACAAAATAGCATCACAAGAACTTCATTGTTCAACTAGAATATTTTCATTGTCTACCAAATGTTTCATCTTCGCCTCACCGTTTATAAGTTATTGGCTAAAACACAAAGATTTTTATAATTGGCCACAAGGTGGGGCTGTTGGTGCCAT

_213	GCTTCAATATGTTGTGCACATGCTCAGGGAGAAACTGTGTACCAAGTTTCATTTTATTAAATTAAGGTTCAAATTCAGGGGTTCACCCACAAATTTGGGGTCAATATGATTATATTAATGGGTTGTAAGTTTTTACAGGCTGCAAATTGAGGGATATATGTTCATTTTTTAAGGGGTTTTTAATCTCTGACAAAGCTGTTGAGTTATTTGGTAAATTAAATTCCATTTATATCAGTT
GBYP-RAD_214	TGAGTGTTTCTGTTTGAAAGCACTGGCAAGATATTTGTGCGTCTCTTTGCCAGNNNNNNAGCAGATATCAAAAATAAAATCGAAATATTGTGGCACTCTTGTGAATTCCTGGCAGAGTTCAGGACGTTCCTCGCCAAACTATCTACTTGCTTTTCATGTTTGGTAAAACTAAAATAAAATGAAAATGCTTGTGTTATTTTTCTACCGGTGCTTCTGGAGTTCTTGTCTTACCGAGTTGGTTCCCAGGACCTGCAGGTCTGGTTCTCTGGACTCCAGCAGCTTGGCCACCATGTGCA[A/G]GAAACTCTCCACGAAGGGTTTGATGCTCTGAGAGTGACAAGMYATCAGCAGCTGGTCCAGAGCCTCCATGGCTATCACCACGTACCTGAGGACAAGTCACGTACACTCAATCACCGGTTTCTATCAGGCATGTCAATGATTATCAATTCATTACTGAACTTGAATCTTCAACCGAAGCAACAAGCAGCTGCTCGGTTAACGCAGGCTGAGAGCAGCGCTGAAGCTGCTAATCCTGCTAATCCTGCTAATGTTGCTAACGCTGCTAATGTTGCAAATGCTGCTAATGTTGCTAA
GBYP-RAD_215	ACAGCAACTACAGAAAATAAACCTCTGACGCTTTCTAGTGACATGTTTCAACATGAACATGACTTTCATGTCTCTTGTCTGTTCGGGCTGACCAAAAGAAGTCAACATATCAAGGCCTTAAAATAGTAAATCAGAGCTATTCAAACTGCATGCTGGGATATGAACCTGTAACACGGAGGAATAACAGTACATGCTGGACTTTTCTACAAGTGTGACAGAAACTGTTTTCATCACCTGCAGCTAAAAACCCTGCAGGTGACCAGAACCAGGAA[G/T]GCCAAATCAACTTTCATATTATATTGTCAACMGTTTTKTTTRGCATTTTCAASCCCATAAGTCTAYTCTGTGTCAAATAAATTACATCATGTTAAAGATCAGCTGGTGCTATTTTGTATTTTTGTACTCATTGGGGATCATTGCCTGTGTTTCTCACTGATTCCAGTGTTTTTAGACTCAATATATTTACATTTGACTAGCCCTCAAACCACTAAAATTAGTAAATGAAAGATTTTTCCCACAGGATTTGCAGCCTCGGCAGTTTAAAGAAGGTTTTGGAATAGCATTAAGACCTCTATATTGGAAAATAAAAGTGAGTGAAAATGTGATTGCACAGTTTAATAAATAAAATCTATATAATTCCAAATATTTTAGAGACTTATTTAGGAGTCTGCTCGGGAATTTCTGAGCAGATGTGCATGAGCTCAGTATCTGGCTGAACATCTGCCATGACGATGAAAGACAACTAAAACAATTGTAGTCTGAAGGATATGTAT
GBYP-RAD_216	ACACACACACACACACACACACTCTCTGGTCTGAGCAGTACCTGCAGGCTGTGTYTGTGGTTGCGGTTGAGCTCCAGCAGACTCTCTCTGGAGGCTCGKGTRGACGGGGACAGMGAGAARGCTCT[C/T]TTCATGTTGACCGCTCCCTGACACAACTTCCACTGGATACAATATGTCTCATACAGCTCCTCCACCTGCAGAGACAACAGACAGACAAAGACGTTGTGTGTTCAGACTGAGAACAATACAGTCAAACAATAATCTATTTCTTTACAGCTGCATTAAGACAG
GBYP-RAD_217	TGAGCAGGGCACCGTATACTTCTGCTACATTCTCCGAGCACAGAGCAGAGTCTGTAGAGCCACTGGCGCAAGCACCCGCCTTCATACACACCCTAATAAAGAATGAAAAAGAAATACGTTCACATAATAAAGAAAGACTCAAAGGGCTGCTAAAGGAACTAAGAGATGTACTGGGGAAATTTGATAAATTTTGAGAAATGATACACAAAGGCAGCAGGGAAACAAATGGACAGACATGTCATTCAGGTCCTGCAGGTATAGTCAGTRAACTGTTTATTTTAGCCTTAGAAGCCTGTTAAAGCTAGCAGRCAAGCAAGACAAAGWGAAGYGAGC[C/T]TGAACAATAAGACAATATGGAAAGAAGATGATGGAAGAAATACAAATGAAAAGTCAATAAAAACTGATATGGATACTCACTGAGCAATTGCTCTGACTGCATCTCTCCTTGCCTCTGTAAAATTCCCTTCTTTCTGACTGACAATGCACATCTGCTGAAGGCCATCTAGGATCTAACACAGACAAAAACACACACACACACACACACCAATTTATACCTATATACTGAAGCAGTAAGATGTCAAACAGCTAGAAAATGTTCACAATACTTCAAACACACCTGTTTCAGTTTGCTATGGATCATAAATCTTGGCAGACAGCCAAGGGCAAGGGCAGATCCACAACGGGTGAGAATCTGTGGACTCTTCAGCCCTTCAGTGTACTGAGATACCAGGACAGCTACACATGTGCACACAAACACGCCATGCAGAGATTAT
GBYP-RAD_218	CCTCCTGCACACTGGATTCCCACACTGTTATCTGGATGAATATACCTTTTAAATAAAATCTGAAATCAAACCAAAACAATACTGTGATAAAACATACTGACAGCACTGCATATGGAAGAACAAGTATTAGTTGTCACTCCTTACAATAACATGCTGTCATATACACCCTGAGGCAGCTTCACAAGAACAAAGAAAGGTTCACTTCGTTTTTTAAAGGCATATCACAGTCACTGTCACAGTCCATGGATCCTGCAGGGCAACATTAGTTCACTCCCCTG[C/T]CATGTGCCTGGAAATCTAACCCTTTGGCTCTTGTMCCATAACGCATTAWGMTYKSARRMWSAAACCTAATCTTTGATATATGACTGAATCATTAGCATGCACAAGTTAATACAGTGTCACTGTAATGTATTAAAACTTGAAGAAATGAGGTGTCAGCTAAAATTCTAGTTTTTAGGTTTGACATTGAAGATTGAAGACGTGGTATATGGCCGATTTTTTATATTTTTCTTAGCAAATCTTATGTGCAGAGCCAAACCAAC
GBYP-	ACTTTCACACAACCCTACAATCATTACTGTCTTTATGAAACTTATAATATTCACAACACTATTAGAGAGAAGTTGATGCAACCCTATAGTCATGTCTGAGGTTATAGTTAGTAGTGGTGTTGTATTACAGCGCAGTATATTGAAGATGTGGCTTATCAAGCCTCATCCACCTCTATAAAAGGGGGACATTAGAAACCTACACTGGCTTCTTTTGTCAAAAATAAACCTGACATGTGATGTTAATTTCACCTGCAGGTTATCRAAAGCARCCCRCAGACAGAAACTACAGCTTCAACCTCC[A/C]CCCTGC

RAD_219	CYKGTGCTKCTGGGATTRACATCTCTCTCCRTGATGAAACCTCTGTGTGTCTGAGCAAGCCAGGCCAACTCGTCAGCATCCAACCACAAAATCACAGCAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCGAATCTGCGCCGGACACTGTCATCTCTGCCCACGTTCCCGCATGCTCAGCCGTCATCTCCAACACCGTCAACTCAGCCTCCGCTCTGCCATGCGAGGAGAACGGCATCGCTCTCGACTACAACGAACCAGAGGAGAACCACTACGAGTCTCCCTGTCTGAGCTTGGACGTGCATGACGTGCAGGTGAATGTGGTGCACGTGGCCGAGGAGCCGTCTATCCTTAACCTAGACGGCCAAATCTCAGCACCGCAAGTCAACGGTGAAGCAGCCAGAGAGATCACTTCTGCACC
GBYP-RAD_220	TGCATTTCAGAGAGAGAGTGTGACAGAGAAAGCACTTCACCGTCATCTCTCTCTCTGCCTCTGAAATAGGAGTATGCTCTTTCTTTTTATTATTTCGGGTGGGGTTAACGGAGGGCGCGGGAGGGCTCAATGGTCAGTCGGCGCACACTTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGCCTGCAGGTAGAGACGAAACTCCTTCCAGCTGTACTGCAGATGCAGGCCGAACGCCGTCTT[A/C]ACCTGGAGGAACATGGASGAAAGCTCCTGGATGTGGAAGATGTCTGTAAGAGATGGAGGAGGAAGACATTTCACAGAAGTGCATGTGCATATGATACAAACAAAATGAGGACTCCTTCATAAAAACATTGCTGCTAGTGGTCAAAAACCTTCAACAGGAAGTGAACACTGTGCTGGATATTTGATGGATGATGATTCCTTGGGTAGCTGGATTCACACGGTCATAACATCACGTGAGAATCCATCTCAGGCTTCAAGTTATGAGCTTGTGTCTGACCAAG
GBYP-RAD_221	CCATGAACACTTTCTGCATTATCCATTATAGTATATATTACACATCGACCCAGATTCCAGGTTTATTTACACCACATTTGATGTTGAAACACGCCCTCTGCTGTTCAAAAAGGCAGACGACAACTGGTTTAAACAAAAAATTTAACTATCAAACATATATTGTGCTACATACTCTATATCTATGATAGCAGAAGAAGTTTGGTTGGTTTGAAACAACGTTCTATGAGTATTTCGTTATGCAACCAAGTCCTGCAGGCTGAATAAGA[G/T]ATGACCTGAACTCATTCGCTAAGATGGACGTTTTTCCACTGAGAGATGTTTTCGTTGAGAGAACCTTGAGTTGTGTAGTTGCAGGACAGATTTAGAAAGCTGTCTCTAAAGAGACAGGTTATGATGTGATGTTGTGAAGGTCTTTCCTCCTAAAAATATAACGTTAGTTCAATGTCCTGGGTCTTTCTGACATGACAGAAAAAGTGGGATCTGTGCATTCACCACAAGGTCATTTATTATTGAGATGCTCATCAGGATGGACGCATTAGTCCCACTCAGCAACCAAACCACGTGTTTCCTTATGCAATCTCTCTGTCCCAGTC
GBYP-RAD_222	GGGGGGTTCCTACAACCCTTATAGAGATGTTAGTATGCACAACATCATTTGGAAATTCCCATTTACACAAATATGTGGTTTCTTTCTTTGTTGAGTCCCTTATTAGCTGTATAGTCTGTATCTGCACAGTACAGGTTGAACAACTACTGTGGCCAGAAAATTTTGAGATCATAACTTTTTTTTTCTCTCTCTCTCTTTATAAATGAATAGTTCACATTACATTATGCACAAAACATTAGATGTCAGCTCCTGCAGGAGAGAGGACTTATGATGAAATG[A/G]TTTATCTTYAAGTGATGCTWATCYGTCATCCTGCCCTGATGCAGTCTGACACTGAGYGGTTTGACCGGTTTGTGCAGTTTGGTGTAAACAGTCTTCATAACAGTCAAAACCTCAAAACCACTGAACTCTTCTAAATGACCTCTAAACACTGACGCTGTCGATGCAGCCGCAAGYTAAAGCTCTGTTGTCATGTCACTTAAGATCGTTTAAAGTTATTTGTTAAGTTATAATAACTCATTARAATMATTTATtaTATATATATGTGCTGTTGGAGYTTTGGGAAACACCATCATCAAGAAACAAGAATCTTCAAAACAACAGTCTGATGATAAGAAACAAAATCTCTCACCAGAAGTTTATTATTTAAAACCTTTTTGACTCGACTGACTCAATCATCTTGTTTCTATTTTTTCACTTCACTTCACTTCACTTGCTTGTGTATAATATGTCGTATGTTTATGTATCTCAGTTCAGCTTCGTCGTCCCTGTTT
GBYP-RAD_223	TATACAAAACATCACTATAATAATAGAAGAAATGAACTTTAGCTCCATGATTGGTAAACTGGAGGTAAATTAGTTGCACTCAAAATAAAAAATATTACTGTTTGTTTTTCAAACAGTTCGGTCACTTAGAAAAACTCGACTTGTGGCTGAAGTTAAATAACTCACCGTGATGGGGGCGTAGCGGGCGTAGCCGTCGTGGCGTCTGATGGCTTTTACGGAGAAAACACAGACGGGGACGACGACACAAACCTGCAGGACGAGCAGARCCAGGASGAGACCACGAAGTCCGAACAGAACCACCTGAAACATCCAGAGAAACGACTCA[A/G]CTGTGATCCATCGATCACCGATCGATCGATCGATCGTCTGTCACATCAGnCAGCGTTCAGCAGAGCAGTGATTTAACAAATAAAAACCATCTGCTGGACTGTAGCTGAACACTGGAAGATGTGACGAGAAACAACTGAATAATAACTAATAATAATAATAATATTAATAACTGAATAATAAAATGTTTTACTCACAGCCTGTATTTATCAAACTGATAAAAGTAAAAATTATTCAAACCATCAAACTTGTTTTGAGTGTTAAAA
GBYP-RAD_224	CTGGCAACCTAAGACTCACCTTGTGGACCTGGGAAGCCGTTGGAGGGCCAGCCGAAGGGATGTCCGTCTGTGCCCAGGATAGTGTACTCCTGCTCCATACCGAACCACGGGTGACTATTTTCCACCATGCTCATGATCTGTTTACAGGTTTGGCGCAGATTGGTCTCTGTTGGAACAGCAGGCAGAGATTAGCTGAAATACAAGACAGCTCTAACCCCAGAAATGTTCAGTTTTTAACTGCATTCATACCTGCAGGCTTGCGGTTGTACTTGAGCACTTCACAGAGCACCAGCTTGTTGGGGTCTTTCCTGAACGGGTC[C/T]CTGAACATGGCTGCAGGKATTAGGAACATGTCGCTATTGGAGCCCTCTGACTGGTAGGTGCTGGAGCCGTCGAAGTTCCACTCAGGAAGATCTGACAGAGAAAGACAGCAGAAATCAATGATTAACTTTAAAATCTTACAAAACAATGTTATGGTTGTTGTTACTGATCAGATTGGAGCCAGATCTTACCCTCGATTGTCTTGGGTTCAGAATCCAGCGTCCTGGTCTTGCAGCGCAGTCCTTCTCCAGATCCATCGATCCAGATGTACATGGCTTGGACTTTGTCTCCTTGAGGGAGATCCATGTACTGCTGCTTAACAGCTTTGTTCAGTTTTGAACTTGCTGAGGTGGCCATTTTTTTGACCCAGACACCTACAGAGTAAAGAGATCAGATGATGAGCTTCACTACTGATCACAGTGGAGCCACTATATTTGATTGCGCATGTAAGA
GB	AGTGACAAAATGTTATGGAACATATGTGCACCAAGCTTTCGACCTGCTCTGAGCAGGTGAGTGGCAAACGGCGTGAGGCACACTCATTCTTGACACCAAGATTGCAGTAAAGTGTGCTGCTGGATTGAGATCGTCACACTCTAAACAGAGC

YP-RAD_225	CTCTGTTTAAAGTCACACATGTGATCTGGATGACGCAAGGAACCTGATAAAGGGGCCTGGTACCCAGCAGTCGTCTCCTTTCATCTTCTCGCCTAAACCTGCAGGTCTTGTATGTTGTTAGCATTAGCTAGCAC[A/C]AGCRCTGTACAGCTTATGCCAGTTGCCTTGTAACCTATCGATTGGAGCTACGATTCCATCCTCCAGAGGCTGCATAGCCAGTGCTTATCTCCGCCAGGAATTTTACCGAAACTCTTCCAGGTAAGTAGCCAACTTTATTTCCCCGGCAGACATACCTTGCTAGCTTACCTGCTTAGTGCCTCCATTGCTATCATGTGCTGTATTAGCTTGTAGGTTTTATACTTTACCGACCAGTCTCGCTGTTCATCTCATTATGATGGTTGGGTCGATGGATAGGGAATCAGAGCAGAGGAAGTTTTGTTTCACTCCTTGGCTACTGATTTAACGCAGTGACAGTAATTACATGCAATTACACCTACCAGGATGACCAGTGTGAATTATCAGCGACTCTAGCAGAGACTGGATTTGTAGCTGAGTGTTTCTCGCTCTACTGATACATCACTAGCATCACAGCGATTATGCTCTCTGTTTGAACCTCCTCCTG
GBYP-RAD_226	GACGACTCCAGAGTTCTTGTAGCCCTTCTTCTTCTTCTGTTTCTCGGGGTGGACGCAGTCAAACTCCACCTGGAGGACAAGAGATCCTACAGTTTAATGACCTCCGACCAGCCAATAGAAAGACGTCAAACGTTTTATTATCAATGAGCTCACCGCTGAACTAGCAGCTTTCTGCAGCTCAGAGACTTTAGTGGTGAAGGAACCGATCAGATCATGAGATCCATCGCTGTCATGATCAGAACAATCCACCTGCAGGAGGRGRAGACTTAATGTGAGTGT[C/T]GGAGCTTTGGTTGATTGTTATGACKRAAGGTAAATTCTGATTGGTWGTTTTGAACAGAGGTAAAATCAGATTGGTGGAACCTTAATAGTTTTGTCGAGGTCACTGCCGCAGAACGTCTGCAGAGGAACAGTGAACTTCTTCCAGGAGGGACTCAGATTGTTCTTCACCACCTACACAGACAAACACACACCTTCATCACAATGACATCATCCCTTGCATGAGCTGCACTGATTGGTGCACAGAAGTATGTGACATAATCTTTTCCCAGCTGAGCCCCTCTCACTTTAAAAAGATACAAAAACACAAAATC
GBYP-RAD_227	GAAAAGCCAACAAGAGTAATTTATCACAACACCTTTTTCAACAAGCATAAACATGTAGAAAAGCGATATTTCCACCTGCTTTACTGGCAGTGTCCCATCCACTGCCAGTATGTTTTATACAACCACAGCGCTGGTTAGGCTAATAAAACACAAGCTGTCTGTATGTAGCCTGATTAGCATATATTAAAACTTATCAAATTCTTGTGAACTTGGATACTGGCTGAGACAGCAGTCCTCCTCCCAAACCACCTGCAGGCAGTGAATCACCCCTCCACCCCTCCACCCCACCCAC[A/G]CAACCAGCACTAAGCCCTCCAGAAACCCAGTGAAAAYCMTGGTCTCAACTGTTAATTTTCACTGCCTTACTTCGTCTTATGTGATTGTAAACTAAGTATCTTTGAGTTTTGGACTGTTGRTCAGACAAACCAAGCAATTTCAAGATGTTACTTTTGGCTTTTGGTAACTGCAATGGGTATTTTTCATAATTTTGGATGTTTAAAACAGTAACAACAGTTCTTTGGCATTTTATAGACCAAACAATGTTTCTATTAATCAAGAAAATAATACTTAGTCACAGCCATAATCTTCTTTGGTGAAATAGATCATTTCCTACTTCTCACAATGAGAATGTCACCAGTAGATCGGAGAATAGAAAGTAGATAAAGAAAAACATGACTTAAAATTCACTTCCTGATTTTGTTACAGTGTCAAATAAGTGGAAGGAAAATTGAAAACTGAAACCTTTTCCAACTCAGAGCAGGTCTTGATACCCG
GBYP-RAD_228	AGTTCTAGGACTACTGAAATGGGACTTTCTGACAGTTATTCCTATCCTTGCAGATATATTAGATTATAGTCTAGATATTGTTAAAAGCTAGATTTGTTATGGAGATTTGAGTATGGAGGTGTCAGATAAAGAAGACAGATTTTGGAAGGCAACATAAGGTGAATTAGATTCTTATTTAGATGTAATGGAATAGGGAGATGGAATAACTTTTATAACAGAAAGGAGGTTTGTTTTGTTTTTTTTCCCATCCTGCAGGTTGCAGGCTGGAGAAATGTTCCTGTARGAGAAAATSAGGTYGKGAGATGTTCATATGGAAATG[C/T]ATAGAGGGGTGACTTTTGGCAGAGATTGAGAGAAGCAGATTTCAGCCACTGGTAGGGTTCCAGGTGGCGTGGCTAGCTCGCCTCATTAGAGAATATTATCCAGCATGCCTCACAGCAACCGCCTATGTCCCCCCTTCCAACCCCTCCCACCCATCCACCGCTGACTGCTGGAAGGGACGTTTACCCTGGAAATCAGAGAGGAGAAAGACAGGGAGGGGAAAGGAGGATGACATTAATAGCTAGGAGCTTGACACAATCAAATGTCAGTTT
GBYP-RAD_229	TATATATGCGGACAGTTATGCTGCCATTATCCAGCAGATGTAGCACCTTAATACCTCCTACATTACTTTTCTATGTATGAAAGTAATCAAGGCATCTAATGAACCACTGATGACCAAGGATCGAATAAACTGCCAATGAATGAATTATTAGCAGCGTAGGTCATGTATTTCACATTAAATCATGGTCTTAAACCTGAAGACACTCTTTAATAGAATTTACGATGCATACAATTGTTCCCTGAGCTGCTCCTGCAGGTCAAATGTCTTCAATCCATAACTGGACCTTTTGTTTATAGCTA[C/T]MCYKTGTCTAAAAAAATCTCTTRAGATACAAGTYGCMACTATCTGTGTTTCAATAGTCTTTTCTTCCGTCCAGGCAAAGGACTTCATCCATTCAGAGCTGCTGGCCTACCTCTACTCCTCTGGGGACCAGAACAGTCTAATGGAGGAGTCAGCTGACCAGGCCCAGCGCAGAGACGAAATGTTGCGCATGTATCACGCACTCAAGGAGGCACnCACATTATCGGCGACATCAGCGCCAACACCATCACTACCCCAGTACCCCCGCCCGTAAATGACAGCTGGATGCAAGAAGCCAGGTGAGAGATAACTAGCATTTAATTGAGCTTTGAGCGTAACAGCTGGACCGTTCAGTATCTGATGACACACCAATGACATTACATATATATGAGATTAGAAACAAAGAGGAAAAAGATAAATCTTTCGCCTTAAGTATTCTGCCTGCATTTCAAGAAAAGCTGAAATTAAAAACA
GBYP-RAD_230	TGATTGTGACAAGCTCAGGCAAACAGTGTTTCAGCTCGCTACCGAGACCGAGGATAACGACAGCAACCTGGGTAAGAAATCCTGTCATGATGTGTTCTCATTATTCTGATAGAAACCCATCACTGTCTGAAAGTTTCTAAAATTTAACAAACACTGCGGGGGGGGAAAAAAACTGTTATTATTATTTAGTTGCTGTTTATTTTATAAAGCTCATCTATCCTTTATAAACTGCACTTATCAGGAGACATCCTGCAGGCCAGTGATGACCTCTC[A/C]CATGTCATTAATTCTTATAAGAAGATTGTGRAAGGACAKAYCATCAACGGAGAGRCTGAAGAAGMWCAACGAACACGATCGGCAGTTCAAAAGGGTAAATTTGAACTGATCGGTCTGCACAGTTACAATCAGAGAATTTCATGTCTCTATAATTATGTCTTGTGTTTTGTTTTTTTGTGTTTGGTTGAACTGATCCTTTAAACTTTGCTTGACAGATGGATGGAGGCAGACAGTATCACGTTTTTGAAACTGAATACATCTTTGTTTTCTCTGTACGTCTTAACAGGCACCGGCCGCACAACTCAGTCAGAGGTTCT

WebTable 7

Name	Sequence
GBYP-RAD_1	GTGTGTGTGTGTGTGTGTGTGTTTGGGGTGATTAACTCGCGGGTTGAGAAGCGTGTCGGGGAGAGAGCAGAGAGAGTCAGGAGGATGGAGGGAATATAAAGCGCTCCCCTCCTCCATCACAGTGTTTCAGTTCATCGGGAGGTTCTGACTCATAAACCTGCAGGAAGTKCGTCC[C/T]GTTCGCTCGGCTTCATGGGAAATCTGCKCTTCTTTACAAGAGAATAAACAAYGTCTTTCCGTCTMTACMWGWRTGAAAACTCCTGGACGTGTCAACTCAACCTTTTTATATTAAAGTCAGTGAAGTCAAATCTTTGATATGAAGCTTGTTCCACATGTGACCTCTGTGAAGTTAATAGTTAAATACTGTAAGTTTAAGAAGTTAAAGTATTACACGACTCTGCAAAAAAAGAAGAAAGCAGAGTTTCATCTAAAGTGAGAAGAGAGAAAAACGCTGTTTCAGTCTGGAGACGGAGAGAAGAAGAAGAAGAAGGTTAGTGTGTG
GBYP-RAD_2	GTATTAAATCTGAATAGTTCTCTGATACTTCAATTATCTTCTTTTGTCAAACAAAACATTCAGTTTATGAAACATTTCAGGAGCTGCAACCAGCAAACATTTGGACATTTTTGCTTAAAAAACAATGATTTGATTTGTTGATTAATTATCTGGTGATTGATTGTTTCAGTGATGATCAGCCTGCAGGTTGGTTC[A/G]CATCAACMTGTTGGAATAAGAACGTGACGTCAACMAGTCAGTGAYRTATCRCTAYGCTACGTTAATAAAATGTTTTATGATGTGACAGCGCCGTGGTGACGTCTGGTTCGGTTCAGACAACAACTCCTCCCAAGAAGTGAAAAATCATCTGAACTGCTTCACTTCCTCAGGTCATAAAGTCAAAGGTGACAGCTAACAGGCATAGCAGCTTCCCGCTAACA
GBYP-RAD_3	TGCAGGCGGTGAACGCASSAGCATATGCTCATGCACCTTAT[C/T]TCATCATCTATACAGATAGTAGCTATGCTTTTGSGATGGTCCAGGATT
GBYP-RAD_4	TCCAAGAGAGACCGCTGCTGCAACCAGCACCCTCAAATCCCCTGCAGGAATAAGAAACKAAGTTTCTTTAGGAAGACGTGGAACTTCTCTGTCCCGCTCTTCTTCACT[C/T]AGTTGACTCTGCTGTTTTCTCCT
GBYP-RAD_6	CCCTAACCCCTAACCCCCAACCCTAACCCTTTCTAAAATAATTTTGTTGCACAACAAACAGTCAAAGCAAAACTAAATCCGAGTATCCGATTAGCTTGAGATGACTGGTTTGACATGTCACGTTTGTTCGAGTCGGGGAAATCTTCTTCTTCTGTTTATGGGTCATTTCCTTCGTTTCAGTCTCAGTGCTGATGTTGGTGTCCTGCAGGTTTTTTGTT[C/T]CTCCCTGATAGATAWAGAACTACAMCTGGTGTCAGATTAGCTGCGGCTCATTAACCACGACGGAGGAAAAARVMACATCTGGTCAGACAGTAGAAGAGAGAAACAACAGGGTCAACATTCTGCACAGCACAAACAGAAAACAATACTGCAGACAATAATGTGACACCTGTGATGTGATGCAATGATAATCTGCAACACCCTCCCCAAAATGAGTAAATACACATTATTCTATAACTATGTTCATCCTCATTTCAAGTGGTGCCAGTTTTACAACTTTAAGATGACACATATGAGACAAAAGGACTCTGAGTGTCTTTAAATCAC
GBYP-RA	TGTGTGTGTGTGTGTGTGTGTGTGAAATAGGGCACATCAGTGGTGCTGCTGCTGCTCATCTTCTCTCCACAAGCAGCCTGGAGTTTTCACAGGCTTGACATGAAGCTGCCCTGACAGTCCTCCTGCCCTCGTTTGTCTAACATCGCTCAAGCCATTCTGGGTCAAACCTGCAGGGTCACAGATTAGGCCAYTTACTGTACAGTGACTR[C/G]AGCCCACAACACACACTGTCAATTAGCTTCTCTCACAAGTAGGTGGATMAAATTCCCAAACTTTTGACACCTGACTATACTTTCCTCTCTGCCAAAGACTTAAAGGCAGCTATCTGTAAGTGGTGTGTAATTTTTGTCTGGTGACAGTCCTCAGTCTGCAGTTTAGATTTCACAGCACTCTGTAAATTGTGTTAATGTCAACTGAAGGCTGCAGTGTTTGTGAGTGAAAGACACCTCTCATGTGCAGCTGG

D_8	GGTTAGTATTTCTTGAAGTGCTCCTTTCATGTTAGATGAGTTTGACCCATTGCTCAGGGTCTGCTGCATCTGCATCTGTCTGAGAGCCTCCAATGTGTTGCGCATGGCTTTTGTTGCTCTCTAAACCGGCCAAATGTGTATCTTCTGTGACACCTGAGTGAATATTGAAATGAGCCTATGTTTAAGTTTCATTTTAAGCCCGAAGCACGTGTAGGCCTATATTTTATC
GBYP-RAD_9	CTGCAGACGTTTCACTTGCTCATCTTCACATTTTTAAATTAAAAAAAAGGGGAAAAAAAATCAGTAGTTTGAGTCAAAATTAATCCGAAATGGAGCCGTGAGAGCTTTGTGTTGAATTTCTTGATGGTTTCCGTTGAAGCTTCTGGTAATGTGTCTGGGAAAAAAAACAGAGGAAAACACACAATATGATGTTAAAGTGTGTTTAGTTTTGTTATGTGTGTGTTTAGTATTGTGTGTGTGTGTGTACCTGCAGGTTGTTGTAGTGTTTCTGGCTGCTDCAGTGGAKATCCTTGGCTGTGGTCTCATTCA[A/G]GTAGAAAACAKAGCAGAGATTRCARRAWTACCCCGATTTAGGGACGACAAACTCCTGACCTGAAGAGAGAGAGAGAGAGAAACACAGGTAAAAATAAATATAACAAAACATTTTAATCTAAAATAATTAAACAAAACTACTGTGTCCTTGTCTTACCGAGCGGGTTGTTCGGTTTGAATGGCGGCAGTTTGAAGTCTGCGGCAACGCAAGGAGACTGAGAACGAGATCGCTTGGCTTCAGGTCCGATGAGCTCGCTCTTCCGTTTACTCACGACTAGA
GBYP-RAD_10	CCTCCTTTGGCGATGATGATGGATAGAAGACTACCAGTGTAGTAAGCGCAGCATAGCACAGTATACGTCTAAATGGAGATGGAGGTAGCATATGAGGAGAGAGATGATTCATACAAATGGTGCCCGTGTGCGTAAAGGCCAGAATGACTCTTGCGGCAGATGCACAATGGCTCGCACGCCACTGGTGACCACATACACAATGCATGCGCAAGCTGCTGATGGCGTATTGAGAAGCTACAAATTAAACCCCTGCAGGATTCCTYAATCTATCCATAGAAAATGTCACATATCCATGACAATGCTC[C/G]TCRTAGGAARTGAGCAAGGGCCCCSTCTCTGTTGTCCTGATTTATAGGTAACTGTGTGTGTGTACAGTATTCATGTGTGTGTGTGTGTATCTGTGGATGAGAAAGAGAAGGTGGGTTAGAGAGTGGTCATCCATCAGCCCCAGGACAGGTCTGTGGATGGTGATTATAGCAGAGGGGATCAGTTCTTCTGATTGATCTACCTCTCTCCTTCCCGGGTCACAGTTCAACAACGACCATTTTACACTTTTCACCGGCAAAAATCCACACCCAGAGCCATAAATCTAT
GBYP-RAD_11	ACAAGCTAAAATGTAAATGAAAAGTTAAGGGATCACTGAAGTGATTACAATTCATCCTGAGGGGAACATGAATGTGTNNNNNNNNNNNNNNNNNNNCAAAAAATACAAAAAACTGTGAACCTCTTGATGGAGCTAGAGAAAAGGTCAGTAGATCACCAAAGCCAGTAGGATTTATCATCTGGAAACTGTAAATTTTGTGCTAATTCATTAAGATGTTGAGATATTTTAGAGAACAAGTGAAAACTTTGACCTGCAGGTGGCACTAAAAAGGYCACAGGGTAAACAAAGTCACTAGGACTCATCCTTAAGGAACCATGAATATCTKTAMAAATTTCA[C/T]AGCAATCCATCAAAACTGTTGACATATTTCAGTCTGGACCAAACTGACTGATGGACATATTGACTGGCATTGCTGTCCCTAGAGCCACTCTGCTAGCATGGCTGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTACC
GBYP-RAD_13	GGAAAATTCACTGCTCTGATGGCAGCGATGAGCCCATAACCTGCGGTAAGTTTGAGACAGATTCAGTGAATTACAATGATGGAAAATTTGGGCACAAACCGATACATCACCACAGAAACATAAATCAGGTTTTACATACATATTTCATACATATTTCTTCTAAGTTCATGTTTTTCAATCTCAGTTAAAAGCTTCTTGTGCATGAATTTCTGTAACGCTGAGGTGTGTGGATGCTTCATATGGCTCCTCCTGCAGGTCGTATCTGCTCTATGGATAACGGYGGCTGTAGCCACGTGTGTGTTGATGAACCCTGGGG[A/G]GCTCTGTGTGACTGTCCTGTTGGATATAAGCTCTCTCAAAACGGAGCAGTCTGTGAAGGTGTGTGGAGCAAGCATAATGACACTTTATTCACTTTCACTTTTACTGAGGGGTGATTGATTTTACAGCAAGAGTTACATCACAAACATGCTGACAGTTGATGCCAGTATGACTGTAGACAGTGGATCATTTTTGCAGCCGTATGATTGTCTATTTCCAAATTTTGGGCAATCTGTTTTTGATGTGCTGCTCATGCTTTTGAAGCTAAAACTCTCTCTCTCTCTCTCCTCAGATTTGGATGAATGTGCCCTTCCTTTTGCTCCATGTATGCATCACTGCACTAATACTGTTGGATCCTACTATTGTCACTGCAGAGACGGCTTCAAACTGAATGGAAGGTCCACATGTTTAGCTACAGGTAATGATACAGGGATTTCCCAACAGGTATATCATCA
GBYP-RAD_14	GTTTTCAAATGACTAAAGATATTGAAGTTACAATGATATAAAACGTGTTTTCTGCAGTGGGAGAGGGGTTACGTCACCTTTCTCCATCCACTTGAGTTTGCAGCAGTGAAGGATTCTGGGAGCTCACCTGGTATTTAGTGTAATGCGAGCGGCTGCTGCAGTGCTGCAGTTTGGCTTCGTCCTCATCGGCGTAGATCACCTGACACAAGTTACAGAAGTAACCGACGACCGGACGAACAAACTCTGTTCCTGCAGGAGAAACAGACACAACGAGGTGTCAGTGAACGCACYGCTGCTG[C/T]TCCTCCAATCAGACACAAAATGATGTCAGCAGCTYGTACAGGTGTTTACATTCAGTTTAAAGTGAGTGAAACATGTGAAGCAGCAGAATGATGTGGAGACAGGAAGTGTCTCTTCTTACCAACAGGTTTGAGTGGAGCTGCGGCGCCCTCTGCAGGTCCAGTAGCAGCTTTCTACAAACATCACAGATAAACAGCAGTCAGTTTTTTCTTAGAACAAACAAATCTAAAACTCATCACTCCTTCAACTTTAATAACTCCAACAACATTACACATTATTATAACAACATAAAGTACAAAAACAGCCACTGAGGCGTGTAGAGAGATGATTTTACTCTTTAGGTTTGGTGATTTAGGTGCAAACATGCTGGTACAGTCTTTAAAAACTCACTGAAGAGAGCTCAGGTAACGTCAGAGTCAGTTAAATGTGTTTTATTGACTTATTTTGAGTCAATAAAACACGTTTCTATGGAT
GBYP-RA	AGGAGGAGGAGGAGGAGGAGGAGGAGGATGTAGTGGTTCTGCTGACAGACACGATGATCCCAGAGGCAGGAACATCAGCTGTGACGTAAGTTCTCCTTCCCCATGGTCTTTTTAGATACACAAATTAACACTTTTTTTTTAAGGATGAGAGTATCTATGACAACAGGACCACTGATACCTGCAGGGATTGTGCGTGTTTTGTGTGYGTGCGTGTTTATGTGCATACMTGTATGTG[C/T]ATTGCTAGGTGTGAGCTTGCCTGTCTGTGGGTGTTTTTGCTTCTGTAATAGAAGCCCTCCCTTCTGTCCTTCCACCTCCTCTGTGTGACGCACAAAGCAGTGTTTTCTTTTTTTATGAATGAACAGCCGAGGAGGGTGAGAAA

D_15	GGAGAAACCGAAGCTTTATCTGCCGCTGCTGCTGTTGATGATGATGACGCTGAAAATGTGAGAGCGCCTAAAGGAACAAAACACCAAACAGCTTTATATTCCAACCAGAATGATTTTTTTTCAATTATATATATTTTTTT
GBYP-RAD_18	CATCTTTTGGTTTTGTTCTTGGTCAAACAGAAAACCTTTTGCAGACCAAGCCAGTGGTCCTCTGAGGGAATCAGCAGAGCACAAAGAAAGAATTTATGTTTTTCTGACAAATTTTAACCACTTGGCTGATGCTTTTATTCAAAACATGTTTCAAAGCCATTAAATCACATTAGGTTTGCATTGCCCCAAGTGTGGCTCTTTACAACAGCAACTGTCTGCTTGCTGCAAGATGCAGGTATTTTAGGCTGCCTGCAGGTAAGTTAGTCAATGATTCAAGCTCAGCTAAAAGTTAAAAGTCACATTTTGTGCTTGTATATGGAAATGAAGTWTCT[A/G]TTTGTCTGCACAGTTCTCTCCTTGGCACCACAACCTTATTTGCATAGATTTTTATTAAACAAAAACCTTGGGATATTTATAATCACCCTGTGTTTAGTAAGGTCTGTCAGTCATCTAAACTTAGACTGAACCTCACAAGCCTCAACAAACCCAACCAGTTTTAAACAGTCATAGGATTCATAATGACTAACAATGACACACACAGCAGTTAACACAAGAGTTGAGTACTTAACTTACGTGTCAGGCATCCAAAACCA
GBYP-RAD_19	GTCAAAGCCTGTAGATGATGTCTGAGGCTGGAAGGAGCTGTATGTTAATATGGAACCTGAACCAGCTGAAGCTGTTGCTGGTAAAGGCTGTGTAGGAGGCTGTGGCTGCAGGTACTTGCCAGAAGCTGCAGGCAGACACACTTTTCAGGTGACTGCTGTAGGCGAGGGCTAATGCAGCTGCCTGTCACCGAGGCAGTAGGCAGACATAGAGAGAACAGCTATGGAAGTGGCTTTTTGAATCTTGGGAGCCTGCAGGTGGGTGCATTCATGAAATGGCTGAGACTGCAGCTGGATGAACAAAGCTG[C/T]AGACAAAGACTGACACTGGGACTGAGTGGTTWWSTGTGTGCAGTAAAGGCTGCAGGTGGAGTATTGTGCTGGAGAGGGAGAAGCCTGACGCTGGATGCTGCTGGTTGTCAGAGGCTCTAAATGGAGGATGACGCTACAACTTGCTGCCAGAAGCTGCAGTCAGCTGGCTGCTGTTAAGATGGAGGCCACGGCTACTTTGCAGTATTAGGTGGACTTTGACTGGGCTTGGCTTTCCATGAAAAATCAGAATACTGATAAATTATGGTCTTTTTTTTTTTTTAAT
GBYP-RAD_21	TCCTCTTATTGTAGAAGCTGGTAACTGATTGTTGGGGTAGACAGTTTAAAGAATCAATGTTCATTTACAAGTCTGTGAACACCCATCACATTAACACATACACACACATACACACACAAACCACCGCCCAGGCTGACATAGATCTAGATGTGATTCAGACAGAAAGGATTGCTATTCCTGTAAGGGCTATCGACTGCGCTCTATTTTCCCGTTGTTGAGATAAGACCCGCCCACCCAGAATAGTTTGCCCTGCAGGAYGAAATCAGCTGATAG[C/T]ACCAACGACCTGTCCATCAAACTGTAATGWACCAGTCGGGCCTCTATTAAACCAAAACCATMAGWHAGACAGATGGAAACCCAGCGAAGCATGAGTAGAGGGACTGAGTCACTCTTCGGTGATATCTTTCCATCTTCTCCTCTCCTCCTCTTCTTGTTTGTATTCTTTCACTCTTCATTATTTCATCAGGTGGTTTCATTCGTATTGAGATCAATGTCTCATGACAGATATGGGCATAAGAGAATGCATAAAAAACGATCATCCAAATAAACAAAACAAAGCAGCAATCAAACAGCCAGACACCCATGCACTTAAAGAAAAACAAAATCAAACCTCAGAGAAAATATGCGACCTGAGTTAATTTAAAGTGGTTTTGCTCCGTCTCTCGATGCATACTACGAGAGACCTGGGATACCATGTTCAGAATTTGGTATTTGAATCTGACTCACACCATAAATAATACATTTTAGAGCAAGAGTATCTTAAAAATCCAGCC
GBYP-RAD_24	CTGACTGCCAGCTCCTGCAGGAAGTGGCCAAACAACCACTG[A/C]AGGCAGAAAAGTAACACCCCCYTCCATAAGAACGGKGTTCTGCTGAGAASCTAGTATWAMMMWATTGTTATTAACACCGACGTTTTAATTTAAGCAGGATTGTGGTCAGTGAGGACAATCAGTGAAGATACCCCAGAGCCAACAGACATTGAAATGCTGCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAGAAACTCACAGGGCAGTCTACCCCCTCTGCATTATCCTGCAACAGCACCAGCACCCACATAGCTGGCATCTATGTG
GBYP-RAD_25	GTTATCCTGATGTGTTGAGGCTGCAGCAGCGACGACACACAGCAGGAGGTCTGAGTGTGTCAAATCGACATCAACTCAAAAAAGTTGCTGATCACATGTCGATCCGCTGCTGTGCTTCTCTGTCGCTGCAGTAAAAGTTGTTTGTTACACACAGTTCCTCATAAGAACAGGAATACTGAAGTGTATGAGAAGCAGATAAAAATAAACCCTCCGTAAGGATAAAACCAGATCTCTCAGGCACCGTCACACCTGCAGGCAGTGAGTTTCTGACTAACGAGACAATAGTGCTGCTCCCTTTGAAMGAGGAGTTTTCTGTATTTTTAGCTTTTCTT[C/T]TGCCTTCTGCACTACCTCTCTTTTATGAAAACTTTTTTACAGAGCTTAAAAATTGTATTAACTGTGTTTTTAAACTTTCTTTTTTGGATATATAATATAAGTGTATGATTTAGGTTGATTTTAGTGGGTTGAATCTTTTATTTTATTTAAGGCTTATTGAGATTTATATCTTTTCTCATGTGTGGGAGGAACAGATAACTGAAGATATCACAAAATCAGCTTTAATCAAAAAATGCAATTAAATAAAATTATAAAAT
GBYP-RAD	TGTACNNNNNNNNNACTTTAACATGTGAGTTAACACGTCTGTTAATGTGTATTAACTTGTGTGTTACCCTGTGTGTTCAGGTGATCCTGATGGGTTTGGACTCGGCTGGAAAGTCAACTCTGCTGGCCAAACTGCTGACAGGACAGGTGAGACTTCTCTCCACAGGTAGTGACTGTAATGTTGGATATAAGCTCAGTGGCAGAGAGTGAATATATGAGAGTTTGTCCAGGTGTGACTGACTGTCTGAACCTGCAGGTGATGGACACGTMACCTACTGTCGGATTCAATGTGGG[C/G]ACTTTGGACCTGGACAAGAACACGTCTCTGACTGTCTGGGAWGWYSGAGGACAAAAGAGCATGAGACCCAACTGGAGGTAAACATGAACCCAAACAAACAAATCTGCTTCTTCTGGTACCCTAACCCTATGTGAATGACTGTAAGGCTCTGGTTTCATGTCGTTACTGATGAATCTTCTTCTTCAGGTACTACCTGGACGACTGTAAGGCCCTGGTCTTTGTGGTGGACAGTAGT

_26	GATCCAGGCCGGCTCCCAGAGGCCCAGAAGGCCCTGAAGAAGGTCCTGAGTGATGAGAAGTTACGACAAGTTCCTCTGATGGTTCTGGCCAACAAGAAGGACCTGCCCAATTCCATGACCATACGAGAGGTAGGAAACACATCCCACAATGCACTGTGACATCAGCAAAGAAGAACCCAGTTACCTCAGTTGTTGATAAACATAATAATGTCAAAACGTTTGAGAGGAAGGTTGGTCCAGA
GBYP-RAD_27	AGAAACCTTAGATTCAGATGTAATTCACCTGATAGTTCTTGATCCCAAACATCCCACAACCTGCCTCCTGATTAAACATTATGATGAACAACTCCTTCATCCTGGACCAGAAAGGGTCTTTGCAGTCATCCACTGTACTTACTAGATTCTCTGTGGTAGGTAAGCTGTGAAGAAACATCTGTAGTCATATTATAAATGTAGGAAATGGCGTACAAAACCTGCCTATCCTAAGGTGGTGGACTTACCTCCCTGCAGGCTGTGACTATGRAAGC[C/T]TCCCTTTTGGTCAACAGGTGTTGAGTGCTTTGGTCCACTCAACATCAAGTTACRGAGAAGACAAGAGAAAAGGTGGGGAATTTTGTTTAAATGCATAACCACTCACTGCACTCATATAGAGGTACTCACCAGTCTTGATACTGACAGTTTTCTCATGTCCCTTTGCTGTTTCATTGCCTGTAGAGGGTAACCCTATGAGTTATAATCTGACTGTGGTACCAACTTTAAGGGAGGAGAAAGGGAGTTCAAAAAGGTATTCTCCACCCTCAATCCAAATCTAAAGGAACATTTAGAAAAACAACAAATAAATTTCTGCTTCAATCCACCAAATGCCCCTCATTTTAGTAGTATATGGGAGAGAGGTAAGATCAAACAAGTCTGCCTTAAGGGTCATATTAGGGACTCAAATTCTAACTGAAGAAGTCTTAAACTCCAAACCATTGGATATGTATTTGTGGATGTAGCTGGTCCTGATCCTATAACCCTAAATCTCCTCC
GBYP-RAD_31	ATGAGAGGTTCCAACTCAGATGCCACTGATGATGAAAGTGCAGGCAGGGAGAGACTGACTGAGCCAGTGAAGAAAAAAGTACTACTTTCAACCACAATGGCTAATGCAGTACCCACTGTTGTAGTATGAGGGGAAAGCTATGCTGTGTGTGTATTGTAGGCCCGTCCACTGCAGGCAAATTGTTACCAGGTCAACACAGTTTAAGCTTTAAACTTTGAAGTTGCACAACAACAGTAAGAAACACAAAACCTGCAGGGACCGATGCATGA[C/G]CCGAAACACTGAGCCCCTCCTGATGTCTTTTCAGTGGTTAGATGAGAGAAATTGCTCAACGGAGGAGAATGAAATGGTCATCAAGTTCAACACTGCCTATAACCTAGCGAAAGAGGAACTCTCGTTCACAAAATCACAGATCACACTGATAAAGAAGAATGGATTGAATGTGGATCCAACCTATGCCAACGACATGGCCTCTGCCCAGTTTATAGGAATGATATCAGACAAACTCTGGGAAAAGATTGGTGACAAAATTGCCTTCACCCCTTACCTGTCATTTATGATAGATGGTGCCACCAAAGAATGGGAGATTGTCTATGCCCATGTCATTGATAATGGAAGACTGTTCAGTATCCTAATTGACCATATTGAGGTTGAACACGCCCATGCAGAAGGTAAGGGGTATGTGTTTGTATGTACTTCTGTTTCCATAAAATTATAAATAATGATAATGATAATGATAATGAAAAATGCTCTATAAGTTAATTATAATAGCC
GBYP-RAD_35	CTGACTGATTGCTATGAATGATTGATTACTGTTAATGATTGATCTGATGTGACTTTCGATCGTTTACAAAGATCAATAACAGAGAGATCGATCAGAGTAAACGTGGGTCCTCACCTGCATGTTGACTCCGAAGGTCCAGATGTAGAGCGAGTAGATGGGTTTTCTGAGCCATGTGGGGAGTTCCACCCCGTTCAGACGCCCCCAGGCCCGAGACAGGAGGCGGGTTGGGAAGGAGCGATACAACGCCACCTGCAGGGCAAACACMCACACAGCARCTGTAGTGATTCTCTCGGTTCAACACGATCACTTTTATATTTTACTATTGGAYA[C/T]ATTTACAGTTTATAGACTGAGGAATAAGAAGAGAGGAGTTCTCACAGATGATGGAGAGGAAAGACAAAAACAGAGGAGGTACAAGAAAAAGGTAAGGCAGAAGAAAGAAGAGGAAAGGAAGAACGAAAAGAGGAGGAAGTTAATGAGCATGACGAAGAAGAGTTTATCCATTCATTCCCTCCCTCCCTGTTTCCCTTCGTCCAATCAGAAGCCAGTCGGCAGCCGCTCTTACCCGATTGGCCAGCGGCCGCAGAGCACTG
GBYP-RAD_37	GGTCACCACTACGATGATCATCATCTTCACCACCTGCAGGAGAAAAAAKRAAAATGCAAAAAAGAATCATCAGCAGGACAAAAACACAAATAG[A/G]GAGACATTTTAACATGTCACAGTAGGAAATGCACAGCTAAAATTAATGATTTAGCCATTTAGCTGCTTCAGTTTCAGGGTCCTG
GBYP-RAD_39	AGAGTGTATCTTAGCAACCACACAGTACAAGTCTCTGCCTTCTCTGCCAGAAGCAGAGGATGGACCTGAAGAAGAAGAAGAAGAAGAGTTTTAACAGACCCTGCAGTTAATAAATGATCTGCAGATGTGATCATTAAACACTGTTTAACAACACGCTGTTTTTATTTCCCTCAATCACTTCAGCCAGCTGCTGTCAGAAATTTCACGTTAAAGGTAATTAATCCCTCTCAGGTTTTTATTGTGAAAAACCTGCAGGAGTTAAACCTTG[A/C]AACGCATCACTTCCTGYMTGTTTTTAGAAATAAAAGGGAGAAATTAGAAAGAAATAATCAGAGACCTGGTGGGTGACCACCACCTGGTGAGTAACCACCGCC
GBYP-	AAGAATTAATATAAGTTGCAATACCTGTGTAAAAGTGTTTTAGAATTAGTTCTGCCTCAGTCCCCTGTTGTGTTTAGTCTAACATTTGAACTGTCAGGTTCAACATTGATAACAAGCCACACTTTAGCCAGCTGGACTATCATAACAGCAGCCCTTTCAGCCATTGATAAGGTGCCAAATGGCCCTGTAGGCGATATCGAGGCACCAGGCTTTTGACCTTCCTGATCTACTAAACAAAATCACTGGACCCTGCAGGAGCTCTCTGGTTCAGCAAATTGCTGTTTTGAAATGACCAGTAAAATTCCACAC

RAD_41	AGATTAAATATC[A/C]TGGTGAGATTTKGKKGRWTTAAACAAGAGGTTTTGGGCTGGGATGTTTTGGCTACCGGTAAGATTACCTGCTATGTGGTCTCCCTCTTGCTCAGAGTCTATAGCAGCCACACACTCTCTCTACCTGACAGCTCCATGGTGGCAGGACAAAATAAAATCTTCTTTAAATTTTATCTTAAAACTAAAATAGATTAGAGCTTATGCTCAAACAATATATACTATTATTCTCAACATTTTCCATGTGTACAGGCCAAAACAAGATCCTAATCCAGGGTAAAGAGTCGGTAATAGCCAGACACATAAAAGGGCACCCAATAATTGAAGCATAAATGTCTCTGCAGCTAATGTTAGGAATGGCGTCAGCATGCTTTCCAGCTTTACAAAATGTACCAAGTGACTCTACGTATTGCCAAATGTGTTAAAGCTGGCAGAGCAAAGCAAGCATGTGC
GBYP-RAD_42	TAGTTTACTCTCATAATTTGAAAGTTCTTATGTGCTCTGAAAATAACTTCCCACTCAGAACATTGTCTAACTCAACTGGAAAAGAACAGTTCAAAGCAGAGAGCCATGTCTGATGTTTAATTCAAACTGTCTTTTAACTCTGAGCCACAGGAAAACATCTGGGAAAGTAATCTTCAAAATTAGAGGCTTTCTTAAGGTAGTGGGCAGAGCAGCTCATGTAGTGTGCCTCAAAAGAGCCGATGCAGTGTCCTGCAGGATGTAGTCAAAGATCTTTGCCTGGTGTCTGATTTKTCTGATTGCTCTCTCAGTGTCACCTGGAATCAGATGGYCWMSWTCRRA[A/G]GAATAGTTTGATCTTTCTGTGAGATATGCTTATGTGCTTTCTTGCCAAAAGTTAGATGGAAACATATGTACCACTCTCATGTCTGTGTGTTGACTATGGAACTATGGAGTCTAGAAGTGATTAGCCTAGTTTAGCATAAAGCAAGGCTGGACTGGGACAAAAATTCAGGCCGGAATTCTTACACTTACTCAGGCTACCTCATACATCAAGGGTACTCAATAGGCAGACTCTGGTCC
GBYP-RAD_43	GGTATCGCTGGAGGAGCTGGTGCTGCGGCGGATGGGCGGCTCAGTGTTGGCGGTGGACCTCAGCATGACGCCATGGATGGGGCTGAGGGACTCGCTGGAGCTGGCCGGCGTGGGACCCCCGCCGCTGCTGCCGGAGGTCTGCCGCTGCTCCAGGGTGTCCAACACCACGTCGGGGGCGTGCTTGGCTGAGCTCTGCCGCTCCAGCTCGCGCAGCTCGTTAAGAGCCGTGTTCATTGTTTCCTCTATGTCCTGCAGGAGACAAAGAGAGTGTGTGTAAGAGAGGAGG[A/G]GGGSGGGRKGKGGAADGATGATAATGACATAGGKGAGAAAAATKAGTTGGACACAGGAAGGTTGGTGTTAAAAATGAGAAAAAAACCAAAAAAGACAGGGTGGGGGAAGAAGAAAAAGAAAAGCAGAGATGATATGAACAGCAAAGACGTGAGAGAAGGGATAAGGTAGAGTTAGGCTCGGTACGAAACATAAAAAGCAATGTTAACAGAGGACCACAGTGACAGATTCTCAAGAAAACACATAGCATGCATTATACATGCAGAGAGTTAGTAGAGAGTATTACTTTGCACCGACACCCTCCC
GBYP-RAD_46	AAAGCAGATTATGGGCTGCTACGCTAGATGACCGTTTCAATGCTCCGCTCTCTGTGTTTTCTGCGGCTTGTGGCTTGAAGTCTATCTATACACTGGGCAGCCTGAATTGAACCAGAGAGGCTTAAAAGAAAGCTGTAGACTTATTGACAAATGAGCTCTGTTATGAGCTCACCATGTGACAAACAAGAAAAGTCTGTTTCAGAGACTCTCAGAAGATTAAAAAAAGAAGTTTAAACCATTTTTCTGTTCCTGCAGGACTKAGTAAAGACTCSCTGYCCTCRTTTTTTGTGGTTTAAGTTTTTATTTCTTCAGGAGTACAATGTTTAA[C/T]ATCTGGASATATTAAAGTGTCAGAATCAGAAGGGCAGCTGTAACAAGCTCCCATCTCTTTCTATTACTCAACAGGAAATTGATTGATTGATTGATTGAGTTTATTTGCCCCAAAGGTTAGATGTCACTGCTGTTTTAATGCTCCTGCAGCACTGGAACAAACCTGCTCTTATGTAAACATTCAAATCAACCTCATGTTAATACTCATTCATGACCTAACACAGTGCATCTTTCCAAATAAAGCTGGGATATATTGATTTAAT
GBYP-RAD_47	TGTCTGATTCTCAGCTGCAGATCGGTCTATGTGAAGCTGAAGGGAGGCAGCAGTCGGGAGCATCTTGCCTAAATTAACTCAGTGCAGGACTACAGTCAGTGGTACTGAGGGGACACTGGCATCTGTGTGTAAGTGGCAGTGAAGGGCTTGCTGTGCTGCCTTGCCCTCTACTGTGAGCAGCCAGTTGATGGGGTCGTGCCAGGATCGGGATGGTCAATGAATGCAAAGATCATTGCTCACAAAGAGGTCCTGCAGGATGAKGAT[A/G]AACTCCTATTGAGGGTGGAGTCGCATTATAAAAGGCCTGTTTTCACTTCAATGGAKAGATACAGGAGRAGMWSKSCTTATCAGTCCTTCACAGATTTACAGTATGCATCTACCTGTGGCTGTGACTTAGCTTTTAACATAACAAAGAAGATAAACAGGAAAAAGTTACCCACAGTGAAAGCAGTCTTTCAACCTCGGCAGCTTGGCCGACACGCATTTCATTGAGTGATACTAGAGTTGATACTGACCACTTAGACAGTCTCACTTCACTATAACTTACTTTGACTGTCTGGATGCAAACCAGAGACTGCAGTGCAGCATTCCTCCACTATCAAGTAGCTATCACTGTCATGTTAGCAAGCTAAAAAACAAAATGCATTTCAATAACTTAGCTCATTTAACACCGCAGCAGACATAACAACATTTCTATAGCTTGTGCAGAAAGTCCTCAACTTCAGACAGCCCCCCAGCTTTTTCTTTCAAGCTAACAGTTAGCCTAACTTCCA
GBYP-RAD_48	TCTCATATTCTAACAAAATATGCATTACTACAGTGGATGAAATTGTCGATATGAAACCTAAACGCTGTTGTTTGCCTTTGGAGAGCAGTACAGTTATTCTCAAATGCTTAACAGTGATATTAATTTGCTACTTTCGTTTCCTGGATCTTTATAAATATTCATGTTTGATCATCCTAAACTGCAAAAGTGTGCAATTTTTCATTTTAAGCTGCTAGAATAACTTACAGGTTTTATTTTTATTCTACAGCCCTGCAGGTAATCACCTGGTATAT[A/G]GTATGAATCTCACACACAAAGCAAACACTCATTGATCAGTAACGTTTGCATGTCACAGATMARMYSSCAGCGTCTAGATAATAAATGCATGACTGTAGAACAAAAACTAAACATAAAAAGTGTCAAGATCTGCATGCAAATGATTGTAAACTCCAGTGTAAAACCAGAGAGACATGCAAACCCTGATTGTACAGAGACAACAATTCCAACGTTAAACCGACTTCCTCAAAATGTCAAAATAGTGCACACTCTACTAGTGGCGATTTTTACCTCTGGCGAGCCAGCCCTCTCCAACAAAGGTTACAAGGCTGTGAATG
GBYP	TAAGAGTAACTACAACTCTGTTATGTTGATTGTCAACATTTTTTGTCCCTGTTAAGTTTTTTTTTTTAACTTGCAAACAGGCAAGTTCATCTGGGTAAGGACCCCATGTCGGAGCACACCAGGAGGCAGGTACTGGAGGAAAGAGAGATTGCACTACATGAATACATGGTAAGATTTTTCCCTCAGTTTGAACATGTGGTTATTGAGGGTCTGTTTTCATTAACAAATACA

-RAD_52	GTAGAAAGGAGCAAAACCCTGCAGGAYRCTGACCTTCAAGAACCACAGTTGAGTAK[A/T]TTTATGGCCTTTGAGTTGTTCTTTCCATTTAATTCAACATGACATGTACTGGATGTGTTGATAACTAATAACTTGTGCGGGATGTTTTTCTCTGAAGGCACCATATGCATGCTGATGTCATAACCCGATTCTGTTGTAACAGTATTGAATCACACGGCAATTTTCATCCTTTAAAAAAACAAAACATTCTGCCTCTGTGATTGATTTTATTGAGGAAACTCAATAACTCAGACTCAGCCAAAGTAAAATCAGTTTTGAATTATGAGTCTGTGTACGTGTATGAGTTTCCTTTGAGAAGTTATTTGAATAGTCGACAGAACTCTCACAGACACTTAACAGTACTTCCTCCCTCGTCTCATCTTCACCTGCACTGTTTATAATGCGCGCACACACATGCATGTTTACAGCCTCATATCTTTCACCATACTTTGATATTTTATGGAAACTCTGTTGTTTTTATTATAGGAAGAGCTATCATCTTC
GBYP-RAD_53	AAAGCTACTCACTGTGTCTGTCTAAAGAGCTTTCCATCTCAAAAAGCCACTCCAATGTTAATCCTCTTTTTAATGCTTTCTTTCATCTCTTTTTCTCTTTTAAAAACTAATTTCTGACTCTTCTGTCGAGTCTGCCAGTAAGATATAACGATGATCTTCCATACTTGACTTGTTAGCCAGGTAACACTGCACTTAGATGAGAAGATCAATACAACTCTTAAATCTGTAAGTTAAATATGAAGCTGCAGCCTGCAGGCAGTTAGCTTAGG[C/T]TAGYACACAGACTAAAGGCCCTTTTYTTGTGRAGGCGCAACAACMAGCACTCCGACTATTTGGTATTTTMCTGACCTTGAAACTTGCTTTGCCTGTCTGTGTGGTATTTTGGTGACCCGTGCAGAGCAAAAGGTGGGAGGAGAGGCACAAAGGTGGGAGGATCATTCAAATGAAGCAGCACAAAGCGAGTTGTTGTATTTTGGTTGAAATTTGGTCC
GBYP-RAD_54	AGTCATTTTTCTAAGCAATGAAAATGATTTATTAATAACTAATGTTTTTGAGACAGTTTTGTTTTTTGTAGTTTATTTATGTACAGTATAATTACAAGGCTAATTAGATGCTAATATATATCAGGGATTTATGTTTTTTAGATTAGTAGGTTTATTGAGGTAACATGGATTCACCATTTAGAGTTTTATAGGCTTTATAGTTATGGTGCGGGGAGAAAGCCTCTACAGCTGTACAGAGGTGATGTGACCCTGCAGGATYCAATGCTGAACATCTTATTTACTATTATTAGCTG[C/T]CACAGMTTAGTTCCAAAACAGTGWKCAGGAAGGACATTTTBGGATTTGTAGGTACTGCTGGGTGGTACAACAAAATCAGAGAGTGTGTCTTTAGGCTGGCCTTCACTCTGAATCTTGCAGATACAGAGCTGCACTCTATTGTTACTGTGCAGGATATGGAAAATGTCAATTTCCATAATAATGCAAGTGCTCATCTGCAATATGAAGCCAGATAAAGTATGCAGATGCTGGGAACTTCACCTACTTTCTCTTGCTTTTGATGCACTGTATGTGTACACAAGTCTACAGAGAACATG
GBYP-RAD_58	AAAGAAACAGGTTTAGATGCAGAGGTGGTGAAGGAACAGGTTTGTAGAAGGAGCAGAACAAGGCATGCAATGAGGTTTTTCATTAGGACTCATTTACATGAACAAGTGAAAAATGGGAAAGAGAAGATTAAAGATGCAGCCATTGCAAAAGTTCATGCATACATGGCTTTGTTCCATCCTGGAAGAGGAATTCTTCATTAAATCCTAATTTTGTTCTCTATTCTGCTGTCAGAAAGCACAGGTCAACACCTGCAGGGAGCTGTGCAGG[A/G]AAAGCTGCAWTSAGATGAAACAAATGTTTTGTTYATAGGCAACATTCAGTTTGTCCTTTATGTARCAGMYWGTCAGGCTGTTAGATGGGCTTGTAGTGTGTCTTGCCACAGACTTGCAGTTAATGTTAGCCTTTCTTTTAACTATCACCATCATCTTTCCCTAGCCTTAATGATTTATTTCCCACATTCACAACCTTTCGCTGTCCTCAACCAAACCATCATTGTCATGAACGGATATTGTAGAAAGAAAACATCTGCACTGAATGTTACAAAAACTTTGTCAACAAACGTAATCTAAGGCTTTGCAGAATCATCCAATATCAACATTCTTGTCTGGTGATGGGGTTTGGGCGAGGAAGAGATAAGGTGAACGAGCAGGACACAGCTTTTTCTCTGAATGTCTCTTCTTTTTCGCTGCTGATGTTGACACTTACATTAAATATTTCAACTTATAAATAATGTCTATATTGACATCAACAGATATCTGAATATACAGTGAGT
GBYP-RAD_60	GTGGGCAGGTCAGGGAAAACAAAAGTTTATTGTGTCCAAAGTGCAAAGTTTGGAGGTAAAAAAAGAGGGCAAGGCAAGCGAGATAAAATGGCACAGAAACAGGCAGAGAAAAGGATGACGGGAGGCACAAAAGCGAACTGAGGCAAAGTGGCCAGTACATATATATACATATATATAGAGAGAGAGTGCTGATTAGGGGAATGAGAGGCAGGTGAGAATCAGGTGACTGGGAAGAGGTGAGGACCACTCCTGCAGGTTAGGYAAATAGGGGACAGGCGAAAGA[C/T]GAAAYTAATATTAAGGAATGGCACTGTAGAAGTCATGACATGCTMWGAKCKGRAGWCAGGTTTGGTTTTCAAATATAATTTATTGGGAAATTTCTCTCTTTCTCTTGATGATATGCAATGCCCAGTAGGAAGAGGGAAAGAGTGTAGCCAAAGTGTTGCTTGAACCTGGTGAGCTGATGGTCACAAAAATATAGCCTCAGGTCATTTTTTAAAAACTTCTCAGGGATGGTCTGTTTTCCACAACAAGCAAAATGAGGCCTCTTTAATTTTATGGACACATAAGGAGACAAACAGGTTGACAAGTGG
GBYP-RAD_61	GCAGTGTGCTGCAAGAGATGGACACCAGCAGGGAGTCTAATGGTTTCAGCTGTAGATACTACACATACACCAGAGAACAACCTGAACAACACATATTCATAATAAAGCATCTAACTGTTAGTATTTAAACAGAACTGTGATTTTCTGCAGTAAAGCACCAAATAAACACCTCCCTCTTGAGCTCCCAGAAATATTAAGCACCGAGTCAGATATCTGCACACAGAGGCTCCGATACTGATCTCTGTCAACCTGCAGGTGAAGTTTGAMGAYAACAACCCGTTCAGCGAAGGTTTCCAGGA[A/G]AGAGAGAGGAGAGAGAGGCTGAGAGAGCAGCAGGARRRKBAGAGAGTTCAGCTCATGCAGGAGGTAAAACAGCTCACACACAACAGGAAGTAGAAACACACACACAGTGCTTTTAATGTGAAGACAACAGGAAGTAGAAACACACCTGTTCCTGTCCTCGCAGGTGGAGCGCCATCGAGTCCTGCAGCAGAGGCTGGAGCTGGAACAGCAGGGCCTCCTGGGAGCCCCCCCGGGTCCTGGTGCTCGAGTGGGGCCCCCTCCGGGTCCCGGGGCCCCCCCTGGGGAAAGTC
GBYP	CTTTTAAGGTCAGGGTTGATAACATTGTAACACACACATGAACAGACAAGTTTATTGTTCCTCTCAGTACTTGTCATCTGCTGTAAGGCCACTACTATTGAGAGTTTTATTTTATCTTTTTTTTGTTGTTGTTGTTGTCTCAGTCTGTGTATGGGCTGCAGAATGATATCCGTACCCATAGCCCAACCCACACCCCTGCCCCAGAGGCCAAGCAACCTACAGAAGAAGAACTG

-RAD_63	CAAGAACAGGTCAGACCTGCAGGTGGCGC[A/G]CTACCACWAAAGATCAATRCHAGCACTMAAATTGTAGTTGYAVTTTATATTTTTCATCTGTTTTTCAATTATTCAATTATGATTCATACATTCGTAAGTGCAATGTAGTGCAGAGTTTAAAGTGCACATTTAAAGTCAAAAAAGGAAAATATCATGCAGTTGGTATGTAAATAGGCATGCAAACCAACATTTTCTGTGAATTCATGGTGACAGATGTGTGCTTATTGTTCCCTGCTATGGTTTCAGATCACCTTTTGGCAATTGCAATTAGACAGGCATCGACTGAAAATGTCCAAAGTGGCAGAGAGGTGAGCAATGCTCTTTGCA
GBYP-RAD_64	AGGAAGAAAAGGTCGAAAGAGGGAGGGATGAGAGGATGAAATTGTAAATTTGTAAAGCTGTTTTTTAAGCTTCTAAAGAAATTCGCAGACAAACCAAGACAGACGAGTAAGAGTTACCCTGTTCATTTTCAGGAGAATGCACGGTTTTCCCTCAGAGTATCCGAAGTTGATGTCAGAAAGACCGGAGCAGAAACTCAGGACGCTCCTCTTGAAGCGACAAGTCTTCTTATTCATGTTGTCACTGTCGTCCTGCAGGAAATAGACTCCTGAAAGGCATTCCTCGTTCTTCTCMTGCTCTGTATCRTTATAACCTAGGAAAAGAAAGAGAGAGATATATTC[A/G]GGTGTCAATGAGTGGAGAAAAGATCCAGGAGGAGGAGAGTGGAATTCAATTTATTACATCTTGCTTTCGATCCCTTTTTAATACAAATTCATCAGGGCGAAGTGCACTTACTTTGCAGGAAGGACTCCAGGTGTTGGACATACTGTGAGTACTTGAGTGGGTCAGATTTGTTGAATGAGATGTCCAGTGAATTTGGACGGATCACCAACCCTGCAGCACAAAGTAAACATAGAGTGAAGTAGTAAAAGCA
GBYP-RAD_65	GCTGCTTTCTGTGTGTGACGACCATGAAGTTCAATTGAAATCTAAAACTTAAATCCATGTAGAATAAGAGAAGAATCAGGAGTGAGATGGTGCTGCTGGTTGTTTTCTTATATTTATTTATTTGTGCTGGAACTGATTCTCCAGACGTCAGCTGATCAGCTCCCGACCACACAAAATATAAAAACACAAAAGTAATATTTACTCAGAGAAACAACCTAAATAAAAATAAACAAACTACCAACATAGAGCCTGCAGGTGTGTGACTATCGTAGCACTAAACTCTG[C/T]CTTAACGCAGGTTTATTTGTTTARTATYAACTCAAGTTCACAGCAACRARRWCKGAAAGGTCTGAACAGACCGCAGCTTCCGGCTGATAAAATCTGCTAAATGAGGTTTGCAGCNNNNNNNNNNNNNNNNNNNNNNNAACTGAGACGCAGTTTCTCTCTTCTCTTCCAGTAAAAGGGCGTCGTCACCCAGCTGTTACTGGTCAGGATCCACCTGCACAACAGGTGATCTGAACAACCGTCCAATCAACAACATTCAACTACAACACCTTCAGAGGAGGGAAATGGCAGCAAGTCCCAACAATAGGTGACTGCCACATATTAATGATATAATATAATAATAACAGGAGCTGAACAAGGTGTTGCAGCCACATTTAGACGACATGTTCTATTAACTCTGAGACTAAATCCTGCTGAAACGTCCCGACAGCAGCAAACACAACCAACCGTTTCCCGCCGTCGATCAGAGACTATCTGTGTTTTCAACAC
GBYP-RAD_68	ACCCTGCTTCATGTTGAAACATAATCAGTTAAATGTTGAAACTGTGGTTATGTATAACTAACCCCAGTTTAATCAAGATGTCTTGATCTTATTTCATCTTCAGTGAGAAAAAACTGTTTACTGAGCATGTGTGCAACATTTATTTACTTATTGCAAGTCAGTGTGAACCAAAAATGCACCAGAACTAAAAGTCAACTGTAGATAAATAGAAGATTATTTGTTTCTTTGATTCATGCAAAGTAAACTGACCTGCAGGTGAGATRAAATAYATTTTTGATTGGATCAGGACAAAGAACCATAATACTGAC[A/T]GGAAGCATCACAGCAKSCTGTATAACAGGRATAATAACAAGTATTACAGCATGGATCGAGTCAGGAGCGTGGGTCATGTTTAGTGTTTAACAGAACAAAAGCCTTTTCAAACATCTTCTCACCCAAACCACACCTCAGTCTCCTTGATATCACAACGAGAAAACACAAACAAGCAGAAATCGCTCTCAGGACTTCTGTTCCTAGCAAAATTCCTCACAAACAAGTTCAAGGTCTGTGGAGCACTTCTTCCATTAAGCGAGAAATGTTTAATCGTCTCTGCA
GBYP-RAD_70	GCAACAACCATCAGGACAGGGACCACAGTGAAGTTGTGTTCAGACCTTGAAGCTTCTCTTCCTCTTCTGGACATTCTGCTCAGGGTGGAAAATGATGACATAAACCTTCGGCATGTAGAGCATCCCGAGAGAGACGGACGCACTGAGAGACATGGACACAGTCAGAGTGGCTGTCTGGATAAACAGCTGTAGAGACAGAGAGACAGACAAACAAACAGAGATATGGACACAGTCAGTGAGTCTAACCACCTGCAGGAACTGCAGAACCCTYTTAATGATCATGAGAASCATCTACATACATCC[C/G]AAACCTCCTCTGTGACTAATATAACCTCCTWARRKMAAGGTTGAACCACCTAAAGAACCCCTTGAATTTTCACAAAGGCCACAAGAAAGGACCACTGAAGCACACGAGGAACCATGAGAACCCCCTCATTGATTACAAGAACCTCCTAAAGGACCTTTACAGTCTCCTCAATGACTTCAAGAGCCACTACAACCTCATAAATCACCACAGACATCTCCTAGAAGACTTCTAGAACCACCTAGAGAGCCTCAAAAATCTCTTCAATGACCACTAGACCCACATAATTTATTATTGTTTATTTACCTTCCACAAAAAGAGTGTAAAGTACCAAAAAAAGGTACTGTTGGCTACCGAATTCCAGGTAACAATACTGGTATCGGTTCAATTGTTAACGGTAACCCTAGACGACATATAAAAAAATACTACAACCACTTACAGGGCCCAACAAACTTCCAAAGTGACCTCA
GBYP-RAD_72	GCCATTGGCCTTTTTTCAAGGAGGGTCATGGACACTCACAGTTATTTCCACATACAGAGAGACTCAAGGTGTTAAAGCTATTCACACTTTCATTTGGAAGTTTTACTCTGGGACCAAGTTATTGTGAATATTCTCTCAGCTGTAAGAAAACCCCAGCCAAGTAGAATGAGGGGAGGTGATTTCATTCAAATACAATTACAGTTGGATCAGATCACACAATTACACACCCTGCACACAAATTCACATGACCTGCAGGCAGGAGCCWTATTCATAAWGTGATACTGATTTAGTAAAAGATGGAAATTGATTTCTTAACTTTTT[A/G]CACAAAGWTTGTGATTCTCAAAAGCTTTATGAATCCTGCATGTCTCACTTTTTGTCTGTTGGTGGGTGTGTCAGTGGAGTATAAGAAAACAATGCACATATGTTTTAATGTTTTCCTTCTGATAATAGGTGAAATGCGTCATTAAAATGATGTGAATGGAATAGGGGAGGATAATTTGTGCCATATTACCTGCTGATTTTAGTTGAAGATGACAGGTAAAATGGCACATGGCATGGTGATAATCATATGCTATCTCACTGGATTAATAGTCCTTGACTGATGTGTGTGTGTGCATGTGCGTGTGTGTGAAAATGAATTAAAAATGAATAAAATGTCTGGAGGTTGAATTGGATAATGGTTTGCAATGCTATTACAGGGCCTAAAAAGGTGGTGTTTGGAACAAGATTCATACTTAGAAGACAATTCTATGTGTATGTGCATGAATTTG

GBYP-RAD_74	TAGCTCCTGTCTCTTTAAGCCCCGCCTCCCTTTGACCTGCAGGCAGCATTTCTAC[A/T]AATGTTCTACAAAAGTTTTGGAGCTTTGGTCGTGTTTAACATCCAACATCAGAACAGGACATAAATAACAGAAAA
GBYP-RAD_75	CCTGGTGACGACATTGTTAGTGCCAGTAGTGACTGCAGCACCTGTTTTACCTCCCGAAGTGGAACCTCCCAGGCAGCTGCACACGCTGCTGGTATACACACACACACACACCTAAAACATCTAAAAACAACACAAGTAACCAAAAACAAAGCATGCACCTGTGGCTGCAGAATAAATGGTTTATATTCATGTGTAGGTATAGCAGCAGTGATCCTGTCGTCCAATCAGAACGCGTCACCGGTGCAGGTCCTGCAGGTGATGCTGCAYTATTCCATCAGCAACARAATCAACCTTC[A/T]CCCTCTGTCTGAAACACATCATCTCACTACTCCAAACCTGCTGGCAGCTATGCCTCCTGCCAACAACACAACAAGTTAGTGACTCACACTTTGTGATCTTACACACATGAACAGCATCTGTGTGTAGTTTACACTGTGTGCTCACTTGGGTGTGTAGGTGGGGAGCTTCTGTGTCGGTCAGTGTGGTCAGAGAGGTCAGGGGTCACGAACACGGACAAGACTATCAGTCGCTGTCGTCAGGGGGAGGAGATGATGGGCTGCAGCAGCTACGCTCCTGACGGTGTACGCGTGGGA
GBYP-RAD_77	GGAAGAATATAGTATAGAGTATGAGCTCATTTACTGTGTTCAGTATTAGTTAGTTGTGTGAATAGTTGTATGTATGTATTTGTCTCTGTTTCCGTGTCGGTGCATGTGAGTACATTCATAATAACTCTTTATATTGTCAGGAGGTAATGATGTAAATTGCTGCATTGGAAGCCTGAATGCAAAGCCAGGCTTTTTTCTCCCTGATGCCTGTATTAATGCGGTGTCCCTCTGGACTGAAATCAGCTTTTCCTGCAGGTTTTTCACTGTCAGGCCAT[C/T]TTACCTGCTGCACAAATGCTGGTAAACCTCTTAAGCYCATTCTGCCCCATTTCTTTCTMTCYYYCCCCCCTCCCAAGTAGTCTCAGAGGATTCACCAAAGACAAAGACACAGCCTTTCCGGCTATTAGGGCCATTTAAAGGTATCCCCATGTTGAACATGCTTGAAATATATTGCTGTCAAATGTACTGTGATGCCTGTGATCAGTGTTTTTATATTTTATTGCCCTTGTTAGCTGCAGTGCTGCTCAGGGGTTTTGCTGATTTTAAAACAGATCTTTGACAGTCCCCCATGTCAGGAGGATCAGATATCACATACTAATTTGCACACCAATGGCCTCAGGCCTAGACCAATTTCACATTGTCTTAAAGTTTCATAAAGACCTTGAAAGACCTTTTTAAAGCCAATTAAAATGAAACATCAGACAACTCACCACTTAATGTAAAAAAATGAAGATGAATAAGAGCGCTGGGTTGCCTGACAGGGTTGATTTCAA
GBYP-RAD_78	GGTGTGCTGTTAAATCACCTAAGATGGAGCGTTCTCTTGTCTCCTGCAGGTTGGCTATGGCCTCCRGCACGGTTTGTTTTGTCTG[A/G]TAGGTGTTAAGCTCCCACTCCATCCCTGAGATGTACTGAACCATATCTGCAGGAAACACACAGAAATGTGTGAAACTGACACA
GBYP-RAD_79	GGTCTTTTCTTTCTGTTGTAGATCAATCCTGCAGGCTGAATAAATGAAACATGCATGTCCAGTCTGCCTCT[C/T]TTGGAAACACACATACATHRGCGGCWCACARAAGCACACRCATWGAAACTAAACATGTATAGCAACACCTAGTGGACTTAATTTGCTGTTACATTATCAGTATATGGAAACTGCCCTTTGAAACAGTCATGTCACTGTGTGTGTGTGTGTG
GBYP-RAD_81	TTAGTCCTTTCCATTCAAGAGGCAAATGCAGATGCAAATGCACCTCAGTGACATCTTGAAGGAGATCTTGCAGGCTATCCTCGAGTCTTAGTGACCCATCTGCTACCGTAGAGGAGACAGCTGTTGTTGCTGCCTCTCACCAGGACCCAGAGGAGGCAACACCAGCTGCACGGGCATGAACAAACCTCTTTGTCATAATTATCTACAACATGGACCCTCTGATCTGTGCCAAGGTGAGACAGTGAAAACCTGCAGGTGAAGAGGAGAGCCCAAGTCGAGCYCCRAAGCATCCGTCCAACAAAATGAGGAGCAATGASC[A/G]CACTGCAGGCAGGACTGGACATCAGGCCACTTCTCTTGGATCATTTCTTTCTCAGTCCACATAGAACATGCTCCTAACTGGGGAAAGCAGAAAATTTGGTTCAAACTTTCCCCACTGACTCTCCTCATCTGAAGGAGGATGGTATGACTGAGAATCCTCAGAAGGATTCTAGATGTGAAGAGACAACAGCCTCATCATCTTACTGGTCACAGGCTTTAACGGAAATTGATCACTGAATGCAGACTGCAGGTTGCTTTTGGTTGGCTGCACCGGAGGCTTGAAAGTCCAGAGCTGGTGAAGGATGGAGGCGTCTTTATCCGGAGCTACAAGGAATCATGAAGAGGTTGTGGATGAGACGAAAAAAGGATAGAGGCAGTGTGGACCAGATGACAGAGAAGAAGCAAAAAAGTTCAACTGTTTCTCTGTTCTGTGGATGGTGGAAGAAATAACA

GBYP-RAD_82	ACTTCCACCCTAACATTCAATCACACCCTCCTGCTTTTGTTTCTTATTCCTCTTTATTCCCTCCATCATGTTTTCTGCATCCATCTACTTCTCTTCCTCCTTCTTTTCCATCACACTTCTCGCCTCCTCTTATCCCCTCCGCAGTTTGTCCCTCTGATCGTGGAGATGTGCTGCGGTGTGGTGGAAGACACAGGTCTGGAGTACACCGGCATCTACCGGGTGCCAGGGAACAACGCTATGGTGTCCAACCTGCAGGAGCATCTCAA[C/T]AAGGGCATGGACATCAACACTGCTGAGGAGGTGTGGAGGGMATGTCTGTTAWACTGTAGTTTTACTTTACWTTTACCAGGAATTGTTTTGTAATATTAGGGGTGTTGCTTTTATAATTCTACACCAGAAACACTAAATCTTTCCCCCTCCTGTCTCCACAGAGATGGCAGGACCTGAACGTAATCAGCAGCCTGCTCAAATCGTTCTTCCGAAAACTGCCTGAACCACTGTTTACTGATGGTGCGTCCAGTTATTTGTGTATCATGAATCATAATGAACATGTACAATGTATAAGTAAAATTAGATTGCTAATTGATTGTTTTCTTAGTTTGTAGAAAGTTTGTAGAAAATTTTTCTTTTACTTCAAAAATCTGCTTGTTAGCTAAAGATGTCATCTGCATGTGGAAATGACCATTATATTTTTGATTTTCAGACTTTTGTAATATTCCTGGTTTTTCATTTTTCATACACCTTCTCTGTCAGACAAATACAATGATTTCATT
GBYP-RAD_83	TCCTTCCCAGTCCGGCGTCATAGCACGGGGCTGTGTGGGGGAGCAGTAAAAAGGTGGGAGTCTGCTGAAGGAGAAGTTGCTCCGTTTCAACATGGAGAGTGAGGAGCGGACTGGACTGGATCCTCCTGCTGCGGTTCATGTGGCTGCAGTCTGCTGCCACACAGGGAGCTCTGGCGACACCTGCGGCCACAGTAGCGCACCACACCTGCTGCATGGCTCCGAGCTGCGGATCAACTTGATTAATGTGACCTGCAGGCAGCGGCGGAATGTRGCTAAGTACATTTACCCAGGTTGGACAATTTTTAGATGTCTGT[A/G]CTTTATGCKTTATTGAAAGTACTGCTCCACCACAGTCCAGAAGGAAATGTTGTATTTTCTATTTAACAACATTTAATCCGGAATCAGAATCTGTTCATTAGCCAAGTATG
GBYP-RAD_84	TCTCCACAGGAGAGGAACCAAGCGGCAGACCTGCAGGAGGAAGGTDGTTGAGGAAACAGTTCCAWAAGTTATGTGGAGGCAACAGAGTTCAAGCTGGTCCAAACA[C/T]MATCTCTGTAACTGATGGACACCTCTCACCTGGCGATAAGGAACCCCAAAATGGTCAGTTAATGGAGCTAACATCAGA
GBYP-RAD_88	CATATTCTCACAAGTCCAGCTCTCGTGCAAGGAAACATTAGTGCTACACTGAGCACCATGCCATCATTGAATCTGACATCTTATTGTAACCCCACTGTGTTTGGCAATAACCTGTCAAGGAGCAGAGTGTGATATTAGGTCATTATTCTATAACTGTGAATGTTCACACAGTGCCCCTCCTCCAAACCCCCCAAAAGTAGCTAGTGCTCTCACTTTGCAGACGGTTTGCGTGTACTTGCGGCAGTGTTCCTGCAGGTCCCACAGGAGCTTATTAGAGGGAATGGTAGGGCTTCWCACAACCTCAGCACACGC[A/T]TGCTGGCTYCCATCACAACAGCCAGCGGAGAAAGGGGAGAGAGGTTCACAATTACCAGGCTCACGTCACCCGGACTTCAGACACATTCTCACTGCAGTGGCTCTGCAGCATTAAGCAGAAAGGTCACTGGCTTGTTTGAAATTCTGTTTTCAAAGATTCTAATCATAAAGTAGATAATGTTATCCACATTCATGGCCATTATTCGCTTACTGTGCAAGGATACATAAAGAGAGCCACCAGTCAGCGTCTTGTTGGCCTTAACTAATGGCAAAATGTG
GBYP-RAD_91	TTGATAGCTAATCAGTGCCTTCCTAATGTGTCCTCTGCTTCCAGCTGTAAGGAGGACATCTGTCGTGGGGTTGGCAGCCTTCTGGTCTATGTGAAGAGCCTGAAGGGATTGGCGGCCATTAGGGACGCTGTGTGGGACCTCCTGTCCACnGACTCCATCAGTCAGCACTGGAACACTGTGTGCCAGCGGCTGCTGGAGCGCCCCCTGGCTGTCTGGGATGACTTCCTGCAGCAGCTCTTCCTTCAGCGCCTGCAGGTTAGTGTGCTCCAATTTTCATGATCTTGGTGTAACAGAAAATKAAGTCTGCATCTTTAAGCATCTGATCAG[A/G]TCATTCCATTGKCATATTTGTACGTGTTCATGCCTCCTTGAAATTCTGGGTCATGTTCACTCTCACCGTACTCACAGGCCTGCCTTCTTATGCAGTAAAAATTGTGCATATTGTTATATTTCAATGATTCCTTCCTTCCATTCCAAAAGGCCATCACCAAAGATGAAACTGAAGCCATCTCGACGAGCTCCGTCCAGCTCCTCACCTCGGCTGTGAGGGATCTGGAGGGCCAGACCATCCATACTTCTTCAAGTATCAACCCTGGCTCTGGCCGTGGCGCCCAGTACGAAGTAGATGTGGCCTCCTTCTTGTGGTCGGAGTCTTCAGGGGACCTGCTGAGCGATGCAGGGTGGGTCAGTGTTACCCAACGGGGGCAGCAGCAGCAGAGGAGTGGTCTGGCCATGAAGACCCAGGCCCTGACACCCTGCGTTCAGAACTTCTG
GBYP-RAD_94	GTATGTATGTATATGTCAGACACAGATTAAGAGAGGCAGGTAGAGAAAGCAACTGAGTTTGTATTTTTTGCAAATAAGTAAAAGTGCCTGCAGGTAAAYATTTTTTGTGTACTTGTAGAAGTTGAGCTATTTTCTGAGCACAAGAACATGC[C/T]AGCTAAAGAKAGAGAACCAKATTTTYGGTCAGATTTTGAGCTAGAGTAAATACCTGTGCTTGGTATCATTTAAGGCCAGTGAAATCATATCNNNNNNNNNNNNNNAGCATCCAGTTCCTTATGCAGAGTTGTAAAACAGAGAACTTAGGATGTAAATGCATGGACTGTGCTGTCTAATTTGTATTGGGCTGAATGATTATCTGTGATTCTGAAATTACTTCCCAGGAATATATCACTCCTTTCCTGGGATTCCTGGGATTTTTTTTGTTTGGTGAG

GBYP-RAD_95	AAAAATTATGTGTGATGCAACCTCATTTTCTTTTCATCTTTTCTGAGTTTATAATAATTTATCCTTGATTGCTCTCTCCATGCTCAAAAAGATGAGATTGCTGTTGGGAAAATTATATTTTATACTCATTACTTGATAAAATTCCCTTTTATTTAACATGTCCTTATTAGTAACAGCAGTGGACAATCTAATCTGGCTCAAGGTCTGGATCAAAAGCAATTAACAAACACAACCTCTGTGCTATTTCTCCTGCAGGGAGAAGARGATTGACCAGGAAGCSAGGACGAAGACTGGSTTCAGTATGCAAAAGGTCTGGATAGA[A/G]ATCTTTAACCMCACAGAGAATGACCAAGGCCAATACACCCTGGAGATGTTTGATGGCAAAGAGACACACAAACGTGTTCTTAACTTAACTGGACAAGGTGAGAACAAATGGCATTTTGGTTTACAAGTTTGATTTATTTGAAGGATTATGTGTGATGCAACCTCATTTAACAACACAATATAAGATTTGTGAGATGTTTTGAGCTGTCAAAACACAAAACTGATGAGATTATCTTTCTTATTATCTCATATGGACTCAATCTTGAGTGGCACTTTTCTGTTAAGAACTTAATTTGTAGTCGATTAGTAATTTACAAAACCAAATCAAACTAAAATCAAACTAAAGGTAAAGAAAAACTAATGAAACATGAATTAAATGTAAATAATGATTAATATTATTATTTATTTACAGCCTTTGCTGATGCTTTGCTGGAGTACCAGAGGTTGAA
GBYP-RAD_96	GGAAGTTACAACTACAACTTGTCCTGCTAAAGTGATTTTCTGTTTGACTGGCGCTGCACATAACTTTCATTATCTAAGTATTTCCCGGTTAAGTTATTTCTCCAGTTTTATTGACGCAATCTGATATAATATAGATCACTTGAAACCAGCTACTAGTTTACGCACTAGGACTTTCCACACAGATGTAATGCTACAGTAGTAATGATTTTACAAATAGCTGGTGCAGCCCAATCCAGGGTATTCTTGTTCCTGCAGGAGTGCCACCAYAAGAAATTATTATCCCGTCTATTTCACTTGGTAACTTAAATDACTCA[A/G]ATTCTAATTTGGTCTAAGTGCATTATTTTCATGCAAGAGAGTCATTTGGCTTTGTGCACAAAAGTGTTAATGTTTATTTGCCAACCAACCAGGGAAGTTGTTTCTTCTATATGAGGCTGAAAATAGATTTGATACGCTTGAAATAACATTCAATGAATGAACCATAATTGTGCATTACCAAAACAGCCAACTATAATCACTCAATAATAACTGTATTACATGGCCGCCTTCAAAATTGGTGCAGCCAGACATTGAAGCGTCTACATCAGTTATTCTGCCCGCAGGAGTCGCCACGCAAATGCTGCTCTCTTGGAAGAAAGGCATTATGGAAACCTCCCTATCAAAGCTCGGGATCAGAGTTTTTAAAGTGTTTTGCCCCTAAAATGAGCAAGCGAGCCGAGGCTCTGAGGTCGTGTTTACACTCCTCCTCCATGGAAAAGTGGACCCTGCATGTA
GBYP-RAD_98	GTCAGTAAAAAAATGTTGTCCCTCTTAAAGTCTACTCAAAGTGAGAAGCTGACAGCCTACGCCAAGTACAGCTATGATGCACTGGGAAAGCGCTTCCGCATCAGAGAGTTTGGATCTTATAAAAATCAGACCTTCCGTTTTGATGCACTGCTACTCTTCAATCTGGTAATGAAAACAAAGCAATGATATCTGCATTAAGAAATGTCATATACAACATAAATTAATTGAATTGTATAATGCCATTGTGTCCTGCAGGGTGTTATGTATAAGATCAACTACAGGAGAC[A/G]CACGTGTCACAAGAAGCCACTGAGTGTAGACTTCCACCCACTGGCGATACCACAGGATGCTTCCCTGCTTGGCCAGGTTGTATTGGGCAGCTCCTCTGGCCCAGGGCAGGGTATCCTGGTCAACACCTGGGCGGGGGATCTCCAGATGAAGAATGGAACAGGTAAGAGGAAACTAGACTAGGAGATATTAAGACAGAAAAACTGCACAAAGTCATGTGGTGTATGGTAGCACATGACTTTCCCTGATTCATCAATCTAATCGCTGCCCTTGTTTTTATGCTCATGAACCTGCTTGTCTGGTTGTGCTGCTTCAACTTCCTCGTGATCCACTTCTGTTTTCAGCAGCCAAGTACATGAGCACTGTCACTGAGTTTGGATGTATTCCTGTCAGCACTCTGTTTCATACCAACAAAAGTGGATGGGTGGTGACCAGGTTAGTGCATACACAACAAAAAATCTATCTAATCCATCTAGTGTTCACAG
GBYP-RAD_99	TTTATGACCTAAATACTAATAAATCGTCTTCAATGACATTTTAAGACACAACTGGTGTCATACCCATAATACCCGGCCAGGCTAGATCTTCATTATCGTCCCTCTCATGTCCAGGAGCCAGGTGATTAAATCGGTCAAGATGCTCCAGGAGACCAGCCAGGAGAGGGATAGAACCCGTCTCCTGCATCAGACCAGCGTCAATGGTGAGGAGGAGGACGATAGACACCACCAACTCAGGCAGGAGCACTCCTGCAGGAGA[A/G]AAGACCGCAAGTCATYCACAATTTATGYTGCATATACACACTCAGCAAYTTTRAGAGAGGRAATTACCRGTTAGATCTCCTTCAATAACACGAGATACTTCAGCAAAGTGGCGGCGACCGGTAGAAGCAATACTTGTTGCCACTGGGAGGATGTCTCCAATGTGAGTGCACAGCAGGGCAATGTACTTTTTCAACAGGGAACCAACACCCAGAAGCTCAGGATCTACAAAACAGCAGACAAAACTGTCCATTTAGAAGTAATTTTCAAACTTCATCTCTAGTTACTCCAATCTGGAAGACTAGAAAGGTCATTTCAAAGTTGAAATACA
GBYP-RAD_102	CGGCTGGCATATTACTGCCAGGAAATGGGATCTGCAGGTGTGAATTAGAAACCAGCAGTTTACTTTGTCCGCTGTTTCATCCCATATGAACATCCCATAGTTTAGCACTAGTGACTATTCTTAGTGACATTCACTAGTTTCTGGGACGTTCTGAATCAGAATAAGTGTTAACGCAGGTCCATCTTCTTCAGTATTCAACAGTAGTCGAGGTCTCACATGTTATATGAAGTAATGTGTCCATGAAGGGACCTGCAGGA[A/C]TGACAGAGTTATGRSGCCTYGCAGCTTCTTGCTGTTMACAMTGATTAGGAAACAYGTCTGTCACATACRGTTATGACTGCAGGTGAAACGCAGCCAGAGAGTCAGAATGACCTTTCAGACAAACGACTTTATAATCAAAGTTCAGGAATGGATGCAGAGTCACATACAGCAAGCTGGATAATGTCATGTCTTGACGTAAAGCATTACCGTAGTGTTCATCTTCAAGTATAAAGTGTTGATGGAAAGTGGTGCATGTTTTTAAAATCTATATTTAACACAGACATCATGAATCATGTAAAATAAACGGTTAATGGCCAGAATAAAAGACAGAG
GBYP-RA	TACATCTTATTTCATTTAAAAGTGGAACAAATGAGATACAAAGCAAGATCGCTACTTCTTACAGTAAGTTCTTTTTGCACACGCAGTCTTTTGTACGTTTTTCTTTTTACAACTTACCATTCGTACCCTCACCTCGGTGCATCCACACTGTCATTGCTAACGGATGAAAATAACTGTAATTTGTATCATTAGATGTCCTTTCCCACAAGCAGCCTGATGCCTCTCTGAATCCCTGACTGTCAGAAATACCTGCAGGCTCAGCATGAGTCTATGAGTCACTGCTATCTT[C/T]TCAGAGAACAAAGACAAGTACRGAAAAGACTATCTCAAGCTYTCCAAAATGATCGGACACTGTCAGAACATTTAGAGACTGTTAAATGAAATGACACAAATTGTGGTCAAACATATAGAACAAATGATTGAAAACTTGAAAAATGCTTTAAAAATACAGTATATGGCAGCAA

D_104	CACCGTGTGTTGCTATATGTCAGACTTTACACACTCTCTGCCTTAGTGGGAAAGAATGAATCAAGGCGATCCTTAGTTCATAGGGGGAGATAGACAGACAGAGGAACAAAACGAAACGGTGCGAGGAGCTTACTGGCAGTGATGGCAGTGCCAGATGGGAGAGGGAAGAGCTGCCCATGAGAGGCGCCAGTAAGCAGAGACAAGTGGTGCCAGCCCAACTGTGTCTAAAAGGAGGTCCAGCTATTTAATCAAACCCAACACTGAAACCGCACCAGTGCCAGATGCAATTCAAATCCTTATATAACCCAA
GBYP-RAD_106	CTTGCAGGGATAAACAGCCACAATTCACTCGGGGGTTAGTTTCTTGTGTGAAAATGGCAACCTTTCCCCATAACACCTGTATGAATAATTCAGCACTCTGGGCTCTATCAGAGGCTGTCAGAAATGTCAGACGGTTGGAAGTACCCTTGGCCTCCCCCAGAGGATGTTGTCTTAGGGGCTTGCACACACACTCACAACATACACACTTGACCAAATGCCACAGCTTTTTCATTGCCAGAGCTCTACTGCCTGCAGGACACTGAAAGCYGAGCACACCTGCAGTGAGCAAACTGTTGCAGTTTTCCCCYTTTTTTATGGGCTGTTATTG[G/T]TAAATGTGACTTTTTCCACTAAAAGGTGCTACTTCAGTCAGCACTTTAAAACTGAGATAAACAGGCAAGGCTGCACTGGTTAGTGACCATAATTACAGATCATAAGCTGGACATGTTACTTTTGACTGAAACTTGGCTGGACTATAGTGGTAGCTTTACACTAATAGAGGCATCACCGCCAAATTTTAACTTTTTAAATGTTTTTAGGTTTGATAGAAGAGGTAGATGTGTATCTTCTCTGATATATTTTTATGCAGGTAA
GBYP-RAD_107	GAAGTTGGTGATCCACCTGCAGGTACAGTCAGAAAYGTGCAGTTGGTAGAGCTTGTCCTGCAGCAGAGCTGGGATGAT[G/T]GTGTWAAAGGCGGAGCTGAAATCTACAAACAGGATCCTGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGTGAACTGCAGGGGGTCCAGGAGTGGGTCTGTGATGGATCTGAGGTGGTGAGGAGGGGGAACTGGAGATGATTGCTGGAGTCAGGAGGGATGTGTTAGGACTGTCCTTTTGTCTTTCAAATTGAGAGTAGAACTGATTCAGGTTGTTGGACAGGTGTGAGTTGTTAGGAGAG
GBYP-RAD_108	TGCAGGAAGATTCAGCAGACTCAGGAGTGGTGGTGCATCGTTCCACTGTG[C/T]ACAATGCTTGCACAAACAAGACCTTCAAATGAAAGAGTCAGTAGAAGAAAACCTTACCTGC
GBYP-RAD_109	TGCAGGAAATAAAACTGTKCAACTGTTCTGTGAAGCCACAGAAATGTGCTCATYTTAKAYCATTTCATAAACATCCTCTTTGAAT[A/T]ATATTTCAACCATCTCATCAACTTCCAGCCATAATACC
GBYP-RAD_113	GTTATATCCTGCAGGGAAAATTATGAAACAATGAGGT[A/G]AAAATAAAGGAGCTGTTCTTAACATCTCTCCTTTTAAGGCAGAAATTGAATCAAACCATTAAAATTGTAGCTGAACAT
GBYP-RAD	CACACACACACACACACACACACCACTACAAAGAGGGTTAATAGAGTGCTGCAGTTGTCCTGCAGGACAGTC[A/G]GAGGAAGGTAAATAAATCAATGTGACACTGAAATGAGGAAGTGAGTGAAAGAGAGAGAGAGGGKGTGTTAGAGTGDKGATGTGTGTGTGTGTGTCTCTGTCTGCACAGAGATCCGTGTGTTTGTGTGTGTGTGTGTGCGTGTG

_117	
GBYP-RAD_121	CTGTTAAAATGCACACACAGCTGCAACCTGAAAACCCTCCAACCCTCCACCTCTGCAATCTTCTTTCTATGCACCACCGGCTTTTTCTTGTCTGACAACTCATCTCGCACCTGACGCCTTTTACATCAACTTCTACACATTTATGTCAGGTCGAGTTGTTCCTTCGTTCCAGAAACTGTGTCTCCGTGCAGAAGAAACACTCCCGTGTGACACAAAGACGTCAAAATAAAACATTTCTTTACTTCCTGCCTGCAGGA[C/T]TGTACTGAACACCYGTCAGTTCTGGATGTTTGCTGCAMCCDTRACRGTTTCATTTCRCACYTGATTTTCACAMCTTTTCMCTGTGAGGGAACTGAAGTGTTTCTGTCTCAAGCGGCAGGTCTTAACTGTCTGTCAGCGCTCTGAGATGACCCAAAGTCCCTCTAAGACTTTTCCCAGCAGCTCCTGAGCTCGTCATGGTTTCATAAGCTGCTGGAAGAAATGCATGTTGGGAGGATTTTCACTGTCTCAGCGTCTTGTGTGAAGCGTGAGGAATGACAATTATCACCGACGCTGTGGGACGTCTGAAGGCGACAGGACGGAGATACAGACGTAGAATGCTTTGTTACTGCTGCTTCATTAAATTTCACTGTTTTCTATTTATTTTCTTCTTTCTGCAGTTTCCACAGAACAACTTCGCTGGTTCCAGCTTCTCCACTGTGATGATTTACTGCTTTTCTGTTCTGTTTTGTCTGTTTTACAGCGTTGTAAATTTTTGGGGTTTTGGACTGTTG
GBYP-RAD_126	GTTTCCTTCCTCAGTATTTTTCCCTCAGTTTCCCCAAAGAAAACAGGGTCATGTGGGAGTGAGGAGTCATGCTGTGCTCTGTTGTAGTGTCCTAAGATCCCACGTCTAACTATATACTTAACAGAACAACATAAGAAAGTCATTTCCTCTTCCATTAATTAGTTTGCCTGGTATTTAAAGCAAACTCTGATCACATATTGAGAGTCTGTGTTCATCCAGGGGCTGACTTGACCTAGTGGTCAAGGTGACCTGCAGGA[A/C]TGAAATGACATTATGCTCTATTTTCAGCATATACAYAATGTCAGGAAGCCTTTTCAGTGCCGCCAAAGTGTCCTGTCTTGTATTTTTGTCTTCGATCGAATGTCAGTTCATTAACTGCTTTTGCATTTAGTGCTGCACAAAATGTTATAGTCATTATTTTTTTCAAACCAAGGACTTAAAAACCTTCTGTCATTTAGATGTAGTACTTGTTCTATTCATTTAAACTACCGCATTCATGTTTTAAAAATGAAAAAATAATTTGAAACTTCACTTTTTCTTAAGAACTTGTGCAGAACATGTGCTCTGGTGGAGTTTTGAAAGCCTGATCCCCCCTGTCCCCCTACTTTCATCCTTACAGCGTGGATATTTGTCTTTGCAGACAGCCAGCCCAAATCCCTTTGGTGAGTTACACTCAATGACATTTCGGACAGTTATGAGAACAGCTGCAGTGAAATTGTACTTTTTTCTTGGATCAAACATTAGGAAACAAACCCTTCCTCTCCTCCTGGGAG
GBYP-RAD_127	AGGAAGACTATTTCTACCGGAGTGGGAAGCATGAAAGGTGGAGGCATTTGATCCTAGATATCTTAAAGGCTCCAGTGGTGTTCTGTAGCTTTCTAATAAGCTCTTTGAAGACCACCTTCACAGTGTGTCCTTTTACCACAGGGGTCTTAATGCAGCTTTGCCACAAAGAGCGAAATAGGCCTGGGAGGTTTTATCCCTGGTCAAAGCATGACTAAATGGTTCAGATGTTAATGTGTTCGCTCTTCCTACCTGCAGGCTCCATTASCTGAGTTTTTTTTAAACCACCATCCTTTAAGTGATGGAAAAATCTGTTTTGCTGCAGGGAAACAGACAGTC[A/G]CATCCCTCAACCCCCTTGCnCATATCATTTCTAGAATATTTACCTCCTCGATTTGAACTTCTACTGTATATATTTATTCTGCTAAATTGCTGTTGCCACAATAATGGGTTGGACAGAATAATAGAGCAACCGCCTACAATTTGGTGGCTGGACCACTGGAAGACTGCAGGATTTAACGTGAATGAAAACCTGCCTTTTTCCATATAGTTTTAATCAATCACTGAGTGGAGTAACAGAGCATCAGGTGTGCAAG
GBYP-RAD_129	TGTTGTTGTTGTTGTTGTTGTTGTTGTTCAGACTTTTGCAGGTGACGTGGGACATTTGTGGAAAACGTCAGAGTCTCTGCTGGTTTATCAGGAACTGGTGCGAAAAGGAGTTCGTGGTTTAATGTGAGTTGACATCAGACGCTCTGAGTGTTTGTTAACGAGGTGAAAAGTGAATAAAAAACGATCCTGCAGGCAGAAGCTCGAATGACTCAGAGAGCAGATCTGTTCRGATGTGGTTCACTTCCTGTTTGTCTCCAGTTATATAAACAT[C/T]GTTTYYTTTTCACTGACTGGAAGGAAAAATCCTGAAGCCAAACAAAATGATGAATTATTTAGGATAAAGTATCCTGCTTGTCCTCTTTTGCACTTTAACTTCATCATGTTTTCAGTAACTAAACATTTTAACTTTTCACACAAGCATTTGTACATCTTCAGTCCTAGTTAGTGTATATAATTAACCTTTAATTGAATTTGTTTCTTTGACCTTTTTTACCTCTTTGTTTTTGAATTTTGATTAATTTAACTCTGTA
GBYP-RAD_130	AGGCATTATTTAATCCAAATAAATATGTGAAGAGACTTGTATCGCTTAGCTGTGGCCTGTAAGTTAATAACCAACCAGAGTTTGATGTGAAAAATTGGTGGAATTCCCCTTTAAACCACTCATCAAACTAAAAAAATCATCAACTGCCAAATCATCAAGCTCTTCTCTGCGATGTGTTTCTCTTCACAGGAATCAATGCTGGTAGAAGTTCCACGTTTCGAGGAGATCCCCACAGACATACCGCCCAACCTGCAGGAGCGGKTAAATGGYGTCACAGATRTCCTGTCCCGAGTCTCCAAGATGGTGTCTGAGGAC[C/T]TGGAGAAAGCTGTGAGCACCGCTGTGGGTCAGGACAAAGAAGGTAACCGGCCTCCGGGAATGATGTTCACTGTGTAGCGAGTTGCTTCGCTGCAGGTCGTTCCTCACTTTGCTGTGTGTTCTCATGTCGGTCTCCAGGTTCTCCTCAGGACAAGAGGCCGATCCTCGCTGTGGTTCCCAGTCCGGCTGCTCCGTGCCACCCTGGAGGGAAGGAAGGCCTCAGTGCTTGTAAGTCCTGCATTTTTTTCACTAATGTGTTTACCTGATTCTGTGCTTCTTGTGATTATAAGTCAGAGGACAGCAGAGGTCACACAGTGCTTTAGTGTTATTCCTGTGATCATAAAAAATAAGAGAAAAAAAAAGACCTGCATTAACAGTGTCTGCTTCCTCTCTTCCTCATTACAGACCGATGCTCTCTGACCTTCGACCCTCGCACGGCCAACGGGCACCTGTTT
GBYP-RA	TTTTGTGGCACCCGATAAGAGAGCCCTGAATAAATGTGCCTGCATGCATGAAAGACTTGAGAGGGAGAAGTGTTTGCAGGGTAAATATTGCAGTTGGCCTTCGTGCATGTGTACAGAACAATTACATGCTTCATTGTTGTGACAAAAACGGGCCGAGACAGCAGATATTTGCTGCTAATTTAGCTTGAGAAGTCCCCAACGGTGGGGGATAAATCTCATTGGATACTGTATGTCAGCAGTTACACTCTCCTGCAGGCTGCTGGCTGTAAAAGGCACAAGAAGCTCAAATGTAACTCTGCAAGCTGACRGATAAAAATAACTCAGCCRTACTGGACACA[A/T]GGTTTGGTCTAAGTACTGTAATGTGGATCCATTGTGGATGATCAGATCTTTAGGTTAATTTAATAATGGATGTGAGTTTGACTTCTAATGTATTTCTCTACATTGTATTGGCTTCA

D_131	GCCAATTCAGGAACAGCAGCACAAGGTATTCTAACTACTCATAAGTTATCTCTGCTGTAATTGACGATGACATGAGACTGTCTGTAAATCAAGCTGTCGCTTTGTCTTGCCAAGATATAATTTTTCTCACACTCA
GBYP-RAD_132	GTAGTCGAGATGCTGTGATAAGCTTTAATTTCATTGTTTTACAGTTTTAAATGAAGCTTTGTTCAATAAATGCTAATCTTCTCCATCACTCCTGTTATCCAACACTGTCAAAGTCCTTACATTCTCAATTCTCAAGCCAATCAGTCCTTGGATGCCAGAGATGTTTAATGATAATGATTTAATTACAATTATATTTAATTACTGTCATTCTGTCCTTCCACCTCCCCACAACCACCGCAACACAACGACCTGCAGGATGTCCAGAGAGATTCAACRGAGAMTTTCCATCGACTAGYTGCTGGCTTTACTGCACCAGC[A/G]TCTAGMCTCCAGGGGATCMTGTCCTACCTCCTATCTTCACATAGATCTAAGCTTAATGAGCATTTTTCACATCATTAGAATCTTATCACCAAGTCTTTTTTCTGTTGCTAACCTAAATATTGTCATACACTTTCTATTGATCTCGATTGACCTTACTGAAGTGTTGGCAGAGACAGAACAGCACATTTCCAATTATATTCAGCCATGTGTTTAATAGTGCTGATTTTTTACAATGCTGTGGGACACGTGGTATTTTGTTTACTTGCAACACAAGCCATTGATTCAAGTCTGCGTAAGGAGCTTGTGCTGTTTTGTGTGCCTATTTGAAATGAAGTGGAAAGCGTGCCCACCCGAATCAAACTGGCACTGTGCCAGTTGGGTTTTAGAGCGCTGCTGTCAATTAGACCTCTGCTCTTGTTGTGCTCAAGTTGTGAACACATTGACATATCATC
GBYP-RAD_136	TGCCCTTTTTTGCAAATTCTCCAATTATGTTTGTTTGACTGGAAGAGCTGAGGGCGAAGTTTGACTCAGAGGAAACTCAGCACACTATTTAAAAAGTTTCAGCAGTTAGAGAAGACACCGACTGACAAGCAGCAGCAGATGACACGGGTGCCGGTGAGAACTTTTTTTTTTTTGATGGAACTTTTTTTTTTTTTTTTTTGCTGCACAACCTGTCCTCCTCCCTCTGCTGCCGCTGCTGTGATTCACTGCCTGCAGGTTCTGCTGGTAKACAGAGACCA[A/G]GTTCTGGTTTTGTCTCAGCCAGCAGCTCAGYTTACAABAATGTGCYAAATTTKAAGATACGTGACAAACTCAGCTAAACAGTTCGACTACATACAGACAGCTTTTGTTTTAGTTTGTTTGTAAGAA
GBYP-RAD_137	TTTAAGTTTCTCAGCTCTCGACTTCTCCATGTTCTCCAAATCTTGAGGCCATGGCTCCTCCTCCTCTGGCTCCGCCTCCAGCCCAACGTCCTCATCAGATGATAGGTCAATGGTGCTGAGCCCGCCCTCCTGGGCCCGGTTACCGTCAATGACACCTGGCGCTGACTCATCGCCTTCCTCCAAAATCTCGTCACGAGGGTACGGAGGAGGATCCTTCACGAAGACGCTGGATGGAATCTCGTTCTCCTCCTGCAGGAGAACATCAGGGGAATGTCA[A/C]GAGAACGTYAGGAGTAAACACAGGAGAAYGTCAGTGGAACATAAGGAMGCTGGTGGAATTTCCTTAACTGAACCTTAGTGGAACCTCAGGGGAACTTGAGGGGAACCTTAAAGTATGTGGACAGCCAGACTTTGTGTCATGCTGAAACAGGATCAAGCTGCACACACAAAGTTGGAAGACTTTTATCATCAGTCTTTCCTTCATCAAATCTCTGGACACATACTTCTGTCCATATGGTGGTGTGCAGGATATAGTATAGACACAAGTATGTGAACATCCTGTCCTCATACTTGTGTCCCTGTGAAGGTGTAAACTGAGGTTAGTGTGATAAAAAGTGTCTGTAAGAAGATAAAGTTCAGAGAGAAACAAAAAACATGCAGGAAGATGAAGACCAGGAAGCAGAGCTGAGAGCTTCCACAGAGAAAGGCTACGCTGCAAGGGAGGAGCTGCAGCTATGAGGAGAGATCTCACTGCTATGAGAGAGGGACTGATA
GBYP-RAD_139	TGCAAAGAAAAGTATAGATGCATTTTCAGTTCCGTCTTCCTGTACCCACATTTGACATCTTCCGTGTTGCCCTGCTTTCGTCAGGTGTTGGAGTGTGGAGAGGAGAAAGTGCTGACTCTGACAGAAGTGGAGCGTATCAAGGCTCTGGCAGCTCAGCTGGTCAAGCTGCTGCGAGCTCAGAAAAACTCCAGCCTTCCTGTCAACCAGCTGCTCACAGAGTACAGCAAGACCTTTGGTTATGGTCTCCGCCTGCAGGACTATGATGCTA[C/G]CTCCCTGCCTGCTCTGCTGGCCAAACTCTGCCATGTTGTCAAGGTAAAGAACACCTMCAMCMGGATTAATGTTTTTTTCAGTTTGTTTGTGTTAAAAGCATTTGTAGAGCTTCAAGTCATTGGAAATGAAGTTAAATTAAGTTTGCCACAAACAAACTACATGTAATCCTAAATTGATCTTGTTTAGTCAATTTAGCACTGTGGTTATGCATCCCTCACATAGAGTTCATGTCCGTTTTGTTGTCACAAGAGTCTGTTCAGTGCTCCGCTTTACACTATTGCTCCTTCGGCAAGTCTGACTAACTACCAACATAAAAGCTGCCACTTTCTTTCCATTTCAAGGTGGTGGATGGCTCAGAAGGTCGGGAAGTGCTATTGATCAACAGGAAGTCTCTGCGTTCGCTGACCTCACAGCTACTTGCACTACTCATGTCCCAAGAGGAGCAGGTCACTAGGGGTCTTAAGGTGGAGGAGCTGAGTCAGCATTACCTGGCTGTCCAC
GBYP-RAD_142	AGAGTCCAAGCCAGCTAATAAAGATATCTAGGTGACACCGCACTCTTTTTGCTTACAAACATTCGCCTCAGACTCTTAAGATCCCGATAAGCACTCTGCAGTGCCTGAGGGGGGAACTGCAGCCAAAAGCTGTTGGAAAAATCTGGAGTTTAGGAAAGCACCTGGAACCATTCCACTCTCTTGCTAGGGGTCACTGAGTTTTGTCTGGAGGCCTTCCCTACTGTAGCTGTTAACAATGCTGCTGCTTTCCTGCAGGCTATGRCTGCACACACACTCAGAGCTCCCAATAGCGTCAGGGAC[A/G]AATTTGGAAACCATGCTTAGTGTAAAGTGGCACAAAATGGCTGCTGTTATACCTCAGGTGGGTGCAGGGTTACTTGATGCAAGAGGGGAAGTGTTTGTTTTTTGTTTGTTTTTTCTATATTTTGGCAGGAGGGTGAGGGTTGTGTGTGGTGGTTAATATCAGTTGAAGTCAACCCGTTATCACTTCACACATGGAAGACATCTGCCTGGTTCAGTCCGGTGAAATATTTTTAACCATTGTTAAGGGTACCGCTGCATGAACGCACATTTACATGCATATACTGTATTATGTGTCCCTGGTGGATTGCCGTGGAAAGATTGTGTGATGTGGGTACACCAAAACGGGAGCAGGGAGACATGTCCTGCCAGATATGATTTCATGTCTTACGTAAGCCTAAGATGGGGGCAGAGAAGTATTAACCCTGTGTGTGTGAGAGTGTGTGTGAGAGAGTTAGCACCCCTTGAATGAT
GB	ACCAACCATTAGATCCTGATGATTATGACAAGTAAGACTTGATCAAATCTTACTGCTTCTCTTTATGGATGTTATAGAAAAAAAGTCATTATTACCTTAATTTATTACTGGATCACTCCATTACTTGTAAACCAAGCAGTTATTGTCACATAATGTT

YP-RAD_144	CTTCTGGGGAATTACAGCTTGCAATTCAGAAAATAAACACTAGATGGTGACAGTAAGCAACCATTTAAGTCACCGACATGATTCATTGGCACCTGCAGGGAYCTGTCTTTYATCAAGGTGATGAATGTGGGCCGGCGTTTTYGGTGAAYCGGKTGCAGGACTACATCCAGAGCAAGATTGW[C/T]TACTACCTCATGAACATCCATGTGCACTCTCACTCCATCTACCTGTGTCGGCACGGAGAGAGCAACCACAACGTCGAAGGCCGCATCGGAGGAGACTCAGAACTTTCTCCTCGCGGCAAACAGGTACGATTTTAATAGTCTTCATTTTATGAACTGCAAAGCCAGTGTCTTCTCAAAACCCAATTACAAACCTCTCTCAGGGAGATGTAACTGAAATATTATGAACACCTGAGTCCTGACCTTTATCACA
GBYP-RAD_194	TCACGCCTGCACAATAGAGTTGCATTGATTTTGTATCTTCTCCTGTCCTGCAGGGAAAACACATTTTTACTGTGTAGTATTCATWAAGRGA[G/T]GCATAACTGTTGCTAATAACGTATTGAAATTATRTTCMAGCTCCTAATGATGATGCAAGCTTACAACTCCTCCATTACCTCCTAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGCTCGTTCAGGTGAAGTCGGCAGGTTGCAGGTGTGTGGTGTCAGAGAGCACCAGGAGGAGCGCTGACTGAGTACTCAGCCCGGCTGCGTCAGAGTTTGGCCTGCAGTTCTGGCTAAATCTCAGGACCAGCAGTTTATTTTTTGAGCGCCCGCTCCCAACCGCAGCAAAGTTAAAACTGACTGCTCCTGCAAGATTTGCGTTGGGTCCCGCGGGACCCTCGGGATCCCAATCCCAATGCAGTCCTCTAATACATTGGACTCTTGGCTCCAGACACACCTCCCCCACCTGTTATTAGATCATGAGGAAGATGAAGGA
GBYP-RAD_196	GTTCCTCCTCTTTTGCTCTCCACACAAGACTGTTGACCTGCATGCAACCAAAGCCTGCTCAAACGCGATTGGTCAATATTACACGGACTACAAATGAACTTTAAAAAGAAACCAGAATGCTTGCAATACCAAAATCTTATCCTGTTGCCTACAGATTCTGCATTCATATGCAGATATCCATTCATAGAGATTAAAATGTGGCTAACATACTATAGGTGCTAACAGTAGCTGGCTAGTAAGCAAATGTTCCTGCAGGACACTCYGCATGAAGCCTTTATTCTGTCTTGAGC[C/T]TTCAGTCCTSCAGCTCGGCTTAAAACCCTGTGGAACTGCTAATATTCACTGCCTAAGTGTAGACACTGAGACAAAATCCTTACTATGAACAGAGAGGGAACAAAGTTCAGACCCAAAAAGCTACAGAACACGAGTCAGTAGCTCTATAGTTATCCAGAGAGAGACAGAGATGACACAAGCTAAAAAAAAAAAGAAAGAAAGAAAAAAGCACCATTTCATGGATCAGCTGTAAGGCTGGGCGATTAATTGAATTTAATTTTCAATTATGATTTTGGATTCCAATGATTATGAAAACAAGA
GBYP-RAD_198	TTAGCTGATTTAAATGGTGATCTTTTTTGGATCTAATATTCTTTAATGATACCAAATTAACGCATGATGACTCTACATAGCTGGAAGATCTTTGAAATGATAAAGGCACGGTGCGTCTAGATATTATTAGTTGCTGTAGTTGGAGAGCTGCAGTTATTTCTGTTTATTGCAGAAATGAATGAATGTTGTTGACGCATCTCCTTAGGCGGAAGTGATCCACTGTGCGACACGTGCTGTCTCCATAGAAACCTGCAGGTTGTCTGTGCTTCAACACTTTGCTATATAAATTCCTC[C/T]GAGACCTGATCTGTAGCCCAGATGAGAAGAGATGAGAAAAMASAKCGGCTGAAACTCAAGGAGGAGTCTGCATCCTCAAGTTGTCAAATCAATCAGGCATCTGTATGTCGGGTGAACTCAGTGAGAAAGCTGCTGCATATAAGTCCCCTGCATCTTATATATATGTGTGTTTGTGTGT
GBYP-RAD_199	ACTGGGCTGTTCAGCCACAGCAGGCGCTGCAACTCAACCACAGACTAATCCTTGGTGCATACTCCATTGTCTTGTGAGACAGAAGGAAGCCAGTGATGCATTTTTTTTAGTGGACTCAGTACATAATCATTAAAGTATCATGGGCCAATCAATGCATTTATGAACAGTTGTTTGATATTTGATATGAAATATGAATCTTTACTGTCATAAATTTTTAAAAGGAGAATCCTTACCATCTATTTTAGATTCCTGCAGGGGTTAWTAGGG[G/T]CATTTACCTTACTGAAGTAAAAAACCTGAGCRGTATAGTGGTGTCCGATAATTCATTGCCAACAGAATCATGTACTCAAAGTATGTTGCACAAGTGCTGTGGATAAGAAAATACAGGATCATCACTTGCCTCACCAGCTTGTTGAAGTTCTGCATTCAAAACGTATGTAACAGTTAACATTTTATTGGTTAAATGTAGTTTAAATATCATCAGATAAAGTCTTCAACTGTTTCCTACTGTTGGAGGAAAACCTCTGTTAACATATCGTTAAATTTAACAGAGCTGAGCTTACTGTTAAACATCTACTCCTTTCTTGCCTCAG
GBYP-RAD_200	GCTTTCGTAATGAAGTTGTCGAATGACATATTCTTTCAGGACCGCGAGAGGCAACAGGCCCAGATCGGGATCATGGTGGAGTTTGCTATCGCTTTGATTGGCAAGTTGGATGGCATCAACAGACATTCCTTCAATAGCTTCAGGCTTCGTGTGGGTGAGTGCGCTCAGCCGCTTGGCAGCTTCAGCATCGAACTTTCATTGACTGAATACTGCACTGTATCCAGCTCTGTTAGTGCTGACACAATAACCCTGCAGGTTTCCCTGGTTACACTGTGCATGACTGGCACTTATTTACTGTTCTTGYAATGAGAGCAGAAGCATTTACTGA[A/C]AGTCGATWVWHTAGCTGTCATGTCACACTCAGGATCTTCTTAACTGAGTGAAGCCATCTTTTATACGCTAATTTAATCTTTGACAGAAATTTGCTGTATACAGTATTATTAGTAGAGTGGCAACACAGTATCCACCTAACGTGAATGGTCGGTATAAGCCTGCCCCATATACTnATGTTATACTCAAACAATGAGACAGACAGAAAAAATTCACCTCTGTCTATTGTGTCTGCGGTCTTGACACAGTCATCCTCAGCCAGA
GBYP-R	TTTTAACTAAAGATTCATGAATCATTGATAAAAGATGTGAAATATGTGAATAAGTAACATTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATATGTTTTATTCTTGTTATGGAAGGAATACTTAAACTAACCACAAGCTTTGTTTCATATATTCTTGTCCGTTAGAGTACCTTGCAGAGGGTGCAGAGCACATCTATCGCACCAACACCTGTCCCAAGTGTCGGCGTTGCTTCAAGATGCGCTCCCACCTGCAGGAGCAYCTCCA[C/T]TTACATTTCCCTGATCCCAGTCTCCAGTGTCCCACCTGTAAGCGTTAYTTCACMAGYAAGAGTAAGCTACGCATACACAGACTCCGTGAGGCGGGTGAAAAGGTTCATCGC

AD_204	TGCCACTTGTGTGAATATTCTGCTGTGGAGCGGAACGCAATCCGCCGCCACCTTGTCACCGTGCACGCCGACGAGGCAGAAGATGACATCAGCTATCCTTGCCCCACCTGTGGTGAAAGTTTTCGCCAGAGCAGGTTGCTTAAGGCTCACATGAAGACGCACAACATCGCGCCAGATAGCGAGCCGGTGGCCTGCTTCCACGAGGGTTGTTCTTTCCAGAGTTCTTTGCGCAAGGAGCTTCTTAGACACGCCGCCGAAGCGCATGGAGTCAAGGCCGTAGAATGCCGACATCACGCCTGCGGTGCCGTCTTTCAAAACGAGAAGGACATGGAGGCTCATTATCGGACGCACCTCGCCTACCACTGCTCGCTGTGTGATTTCTCTTGCTCCAA
GBYP-RAD_205	ACCCGTCCAGTTCTTTAAATAACATGGTGACATCAGGAAACGGAGCACATGACCTGACCTCAACTCATGACTTGGAGCTCCACACCAGCAGGAAGTGGAAGGATATGACTGAAGCTGCTTTGCGATTTGCTGTCATGGATCTGTTTGGTCATAAACTTGCAGGTATGTGGCGCTTAGGCAGTGCCTGTGTTTTACAAATGTCATCATTTGTATGCTGCAGAAAAAGTTAAACACCTTGCAAAGAAACACCTGCAGGCCAATCAGGKG[C/G]TGTTCTCACTGGGGAATTGAAACAGTGAAGGGAGCTATGTCTCAGGTTTTACCACACYGAGGYAGCTGCAGATTATATTTGAGATTAAATAAAATGATGTTGCCCTTATTATGCCCTGCTATAATAAGTTACAGTTGCACACTCACCTTTAGCTCCCTCTCATGGTCTCCGCTGCAGAGCGTGTTCAAGGAAACTTTGAAGGACTTCCAAACTGGGCTCAGGTTGTTCATGACTGTCTGCGCGTGCACAATACACAAACATCACAGTTATTATTAATCACACACCTCAAATAGTCAATTACATCTATATGTGTTTGCATGTG
GBYP-RAD_207	CAGTAAATACACAGTTCCATTATGCAAAAAGTGTGGTAACAGCATCTGTGACTTTTGACCTTTGTGTAATATAAAGGCCTATTTTTATACAGTCTTAACCAGTGGAAGCAAACCATCATCACCTGTCTAAAAGTTTGACAGAACTCAATGAAATGTTTTATAAAATAGAAAGTTACTTAATTTACTAGTTTAGCAGAGAGTACTGTATAGTTGCGTAGTTGCAGCTTTTTCTTGTCTATTGCTCCAGTCCTGCAGGTGGCGGTGATGCSCTTWTAAGCTGCTTTGCTAACCGCCAATA[A/T]AACCGAGGCAGAAKAAGATATGATTCATTTCCGGCATAAACAAATAACTGCCCTTGTGAATGTTAGTTTCTGTCGATAACTTTAACTGCCATAATGTGTGTCAGAGTCTTTTAAATCACAGGACAGTTTAACTTAAACGTCTGCTGTTAGAAACGGACTTAGAGAATGGCGGCCCCGGCCCATGTTTCCAGAGTCCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCCTGCCGATAGATTTAAGAGCCCTCGGTGACCAGTATGTGAAAGACGAATTCAGAAGACATAAAAATGCATCAGCCGCAGAGGTGACGAACTTCATGACAGAGTGGGAGGTAACATAACATAG
GBYP-RAD_211	TTAGAACARCTGTTTGTCAATCACATTTCTATCAAACCATGGAGTGCTATACCACGTTTTGTTCAGAAGAATGAGGCCTTTCTGGTCAAATCAATCTCACAAGTAATCGGAAATATCTGAAAGCATGACTGCTGAAATAAAAAATACCTGAATTTTGACGAATTGGGAGTTTTCCTGAGTAAACAAACGTCATATTAATTGATTTTTGTTTAGGTGTTATTTTTATATGCCCAGACATGTCTGCCTTGCCTGCAGGTCRYAAGAGGTAATGAATATCTAATCACAGTGGCCCTYGGTGTGTAGGTGCACRTCTKTTATTCTCTGACAT[A/G]TAAGCTCTGGTGGCTCTGTCGTCGTTTTTATTTTTTTCTGCTGTTTGAACTCTCTCGCTTCCTCTTAGTTGTTGGATAACTGACAACACGCACGCAGGTGTTTGTCACATAGAATTATACAAGTTCACTTCTTGGAAACGCCACAATATCTAACCTCATTGTTTTTATACAGATCAAAATGTAATGCCTCCCCTCCCCCTACTAAAATGAGGCATTTTAAGACCTTGAATTACCAAAAACTATGGTAAGACTCTGTAAAGATTCACAGGGACTCTGAATGACAGCTGAAGAATGAAGATTTTACTACGAAATATTTCCTGCATTCACTCATGGAAACCTGTGACTTATGTTGTTTAAATTCATTTTGGACCATCAGCCTTTTAAAATATGCACAAAATGATTACAAATTCCTTTAAGGTGCTGTAGACTATATCTTTTTTT
GBYP-RAD_213	ACGGCTAGTGGCCCTGGTCTAGAGCGGGGCAAGGTCAATGAGGCCGGGTCCTTCACGGTGGACTGCACTAAAGCTGGGGAGGCCGAGCTTACCATCGAGATCCTTTCTGAGTCCGGATCCAAAGCCGAAGTCCACATCCAGAACAACAGTGACGGGACTTATTCCATCACCTACATCCCATCGCTGCACGGCATGTACACCATCACCATCAATTACGGAGGCCACGCGGTGCCCAAGTTCCCTGTCCACCTGCAGGTGGAGCC[A/G]GCTGTCRACACCAGYGGGGTCAAAGTCTAYGGACCAGGAGTGGAACCCAGRGGTGAGGGTCTRWAGATAKCTYYKTATGCAGTTACAGGGTTTTCTTAGGGTTAAATACTCCTTAAAATTTACAAAATAGCATCACAAGAACTTCATTGTTCAACTAGAATATTTTCATTGTCTACCAAATGTTTCATCTTCGCCTCACCGTTTATAAGTTATTGGCTAAAACACAAAGATTTTTATAATTGGCCACAAGGTGGGGCTGTTGGTGCCATGCTTCAATATGTTGTGCACATGCTCAGGGAGAAACTGTGTACCAAGTTTCATTTTATTAAATTAAGGTTCAAATTCAGGGGTTCACCCACAAATTTGGGGTCAATATGATTATATTAATGGGTTGTAAGTTTTTACAGGCTGCAAATTGAGGGATATATGTTCATTTTTTAAGGGGTTTTTAATCTCTGACAAAGCTGTTGAGTTATTTGGTAAATTAAATTCCATTTATATCAGTT
GBYP-RAD_215	ACAGCAACTACAGAAAATAAACCTCTGACGCTTTCTAGTGACATGTTTCAACATGAACATGACTTTCATGTCTCTTGTCTGTTCGGGCTGACCAAAAGAAGTCAACATATCAAGGCCTTAAAATAGTAAATCAGAGCTATTCAAACTGCATGCTGGGATATGAACCTGTAACACGGAGGAATAACAGTACATGCTGGACTTTTCTACAAGTGTGACAGAAACTGTTTTCATCACCTGCAGCTAAAAACCCTGCAGGTGACCAGAACCAGGAA[G/T]GCCAAATCAACTTTCATATTATATTGTCAACMGTTTTKTTTRGCATTTTCAASCCCATAAGTCTAYTCTGTGTCAAATAAATTACATCATGTTAAAGATCAGCTGGTGCTATTTTGTATTTTTGTACTCATTGGGGATCATTGCCTGTGTTTCTCACTGATTCCAGTGTTTTTAGACTCAATATATTTACATTTGACTAGCCCTCAAACCACTAAAATTAGTAAATGAAAGATTTTTCCCACAGGATTTGCAGCCTCGGCAGTTTAAAGAAGGTTTTGGAATAGCATTAAGACCTCTATATTGGAAAATAAAAGTGAGTGAAAATGTGATTGCACAGTTTAATAAATAAAATCTATATAATTCCAAATATTTTAGAGACTTATTTAGGAGTCTGCTCGGGAATTTCTGAGCAGATGTGCATGAGCTCAGTATCTGGCTGAACATCTGCCATGACGATGAAAGACAACTAAAACAATTGTAGTCTGAAGGATATGTAT

GBYP-RAD_216	ACACACACACACACACACACACTCTCTGGTCTGAGCAGTACCTGCAGGCTGTGTYTGTGGTTGCGGTTGAGCTCCAGCAGACTCTCTCTGGAGGCTCGKGTRGACGGGGACAGMGAGAARGCTCT[C/T]TTCATGTTGACCGCTCCCTGACACAACTTCCACTGGATACAATATGTCTCATACAGCTCCTCCACCTGCAGAGACAACAGACAGACAAAGACGTTGTGTGTTCAGACTGAGAACAATACAGTCAAACAATAATCTATTTCTTTACAGCTGCATTAAGACAG
GBYP-RAD_218	CCTCCTGCACACTGGATTCCCACACTGTTATCTGGATGAATATACCTTTTAAATAAAATCTGAAATCAAACCAAAACAATACTGTGATAAAACATACTGACAGCACTGCATATGGAAGAACAAGTATTAGTTGTCACTCCTTACAATAACATGCTGTCATATACACCCTGAGGCAGCTTCACAAGAACAAAGAAAGGTTCACTTCGTTTTTTAAAGGCATATCACAGTCACTGTCACAGTCCATGGATCCTGCAGGGCAACATTAGTTCACTCCCCTG[C/T]CATGTGCCTGGAAATCTAACCCTTTGGCTCTTGTMCCATAACGCATTAWGMTYKSARRMWSAAACCTAATCTTTGATATATGACTGAATCATTAGCATGCACAAGTTAATACAGTGTCACTGTAATGTATTAAAACTTGAAGAAATGAGGTGTCAGCTAAAATTCTAGTTTTTAGGTTTGACATTGAAGATTGAAGACGTGGTATATGGCCGATTTTTTATATTTTTCTTAGCAAATCTTATGTGCAGAGCCAAACCAAC
GBYP-RAD_219	ACTTTCACACAACCCTACAATCATTACTGTCTTTATGAAACTTATAATATTCACAACACTATTAGAGAGAAGTTGATGCAACCCTATAGTCATGTCTGAGGTTATAGTTAGTAGTGGTGTTGTATTACAGCGCAGTATATTGAAGATGTGGCTTATCAAGCCTCATCCACCTCTATAAAAGGGGGACATTAGAAACCTACACTGGCTTCTTTTGTCAAAAATAAACCTGACATGTGATGTTAATTTCACCTGCAGGTTATCRAAAGCARCCCRCAGACAGAAACTACAGCTTCAACCTCC[A/C]CCCTGCCYKGTGCTKCTGGGATTRACATCTCTCTCCRTGATGAAACCTCTGTGTGTCTGAGCAAGCCAGGCCAACTCGTCAGCATCCAACCACAAAATCACAGCAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCGAATCTGCGCCGGACACTGTCATCTCTGCCCACGTTCCCGCATGCTCAGCCGTCATCTCCAACACCGTCAACTCAGCCTCCGCTCTGCCATGCGAGGAGAACGGCATCGCTCTCGACTACAACGAACCAGAGGAGAACCACTACGAGTCTCCCTGTCTGAGCTTGGACGTGCATGACGTGCAGGTGAATGTGGTGCACGTGGCCGAGGAGCCGTCTATCCTTAACCTAGACGGCCAAATCTCAGCACCGCAAGTCAACGGTGAAGCAGCCAGAGAGATCACTTCTGCACC
GBYP-RAD_220	TGCATTTCAGAGAGAGAGTGTGACAGAGAAAGCACTTCACCGTCATCTCTCTCTCTCTGCCTCTGAAATAGGAGTATGCTCTTTCTTTTTATTATTTCGGGTGGGGTTAACGGAGGGCGCGGGAGGGCTCAATGGTCAGTCGGCGCACACTTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGCCTGCAGGTAGAGACGAAACTCCTTCCAGCTGTACTGCAGATGCAGGCCGAACGCCGTCTT[A/C]ACCTGGAGGAACATGGASGAAAGCTCCTGGATGTGGAAGATGTCTGTAAGAGATGGAGGAGGAAGACATTTCACAGAAGTGCATGTGCATATGATACAAACAAAATGAGGACTCCTTCATAAAAACATTGCTGCTAGTGGTCAAAAACCTTCAACAGGAAGTGAACACTGTGCTGGATATTTGATGGATGATGATTCCTTGGGTAGCTGGATTCACACGGTCATAACATCACGTGAGAATCCATCTCAGGCTTCAAGTTATGAGCTTGTGTCTGACCAAG
GBYP-RAD_222	GGGGGGTTCCTACAACCCTTATAGAGATGTTAGTATGCACAACATCATTTGGAAATTCCCATTTACACAAATATGTGGTTTCTTTCTTTGTTGAGTCCCTTATTAGCTGTATAGTCTGTATCTGCACAGTACAGGTTGAACAACTACTGTGGCCAGAAAATTTTGAGATCATAACTTTTTTTTTCTCTCTCTCTTTATAAATGAATAGTTCACATTACATTATGCACAAAACATTAGATGTCAGCTCCTGCAGGAGAGAGGACTTATGATGAAATG[A/G]TTTATCTTYAAGTGATGCTWATCYGTCATCCTGCCCTGATGCAGTCTGACACTGAGYGGTTTGACCGGTTTGTGCAGTTTGGTGTAAACAGTCTTCATAACAGTCAAAACCTCAAAACCACTGAACTCTTCTAAATGACCTCTAAACACTGACGCTGTCGATGCAGCCGCAAGYTAAAGCTCTGTTGTCATGTCACTTAAGATCGTTTAAAGTTATTTGTTAAGTTATAATAACTCATTARAATMATTTATtaTATATATATGTGCTGTTGGAGYTTTGGGAAACACCATCATCAAGAAACAAGAATCTTCAAAACAACAGTCTGATGATAAGAAACAAAATCTCTCACCAGAAGTTTATTATTTAAAACCTTTTTGACTCGACTGACTCAATCATCTTGTTTCTATTTTTTCACTTCACTTCACTTCACTTGCTTGTGTATAATATGTCGTATGTTTATGTATCTCAGTTCAGCTTCGTCGTCCCTGTTT
GBYP-RAD_223	TATACAAAACATCACTATAATAATAGAAGAAATGAACTTTAGCTCCATGATTGGTAAACTGGAGGTAAATTAGTTGCACTCAAAATAAAAAATATTACTGTTTGTTTTTCAAACAGTTCGGTCACTTAGAAAAACTCGACTTGTGGCTGAAGTTAAATAACTCACCGTGATGGGGGCGTAGCGGGCGTAGCCGTCGTGGCGTCTGATGGCTTTTACGGAGAAAACACAGACGGGGACGACGACACAAACCTGCAGGACGAGCAGARCCAGGASGAGACCACGAAGTCCGAACAGAACCACCTGAAACATCCAGAGAAACGACTCA[A/G]CTGTGATCCATCGATCACCGATCGATCGATCGATCGTCTGTCACATCAGnCAGCGTTCAGCAGAGCAGTGATTTAACAAATAAAAACCATCTGCTGGACTGTAGCTGAACACTGGAAGATGTGACGAGAAACAACTGAATAATAACTAATAATAATAATAATATTAATAACTGAATAATAAAATGTTTTACTCACAGCCTGTATTTATCAAACTGATAAAAGTAAAAATTATTCAAACCATCAAACTTGTTTTGAGTGTTAAAA

GBYP-RAD_224	CTGGCAACCTAAGACTCACCTTGTGGACCTGGGAAGCCGTTGGAGGGCCAGCCGAAGGGATGTCCGTCTGTGCCCAGGATAGTGTACTCCTGCTCCATACCGAACCACGGGTGACTATTTTCCACCATGCTCATGATCTGTTTACAGGTTTGGCGCAGATTGGTCTCTGTTGGAACAGCAGGCAGAGATTAGCTGAAATACAAGACAGCTCTAACCCCAGAAATGTTCAGTTTTTAACTGCATTCATACCTGCAGGCTTGCGGTTGTACTTGAGCACTTCACAGAGCACCAGCTTGTTGGGGTCTTTCCTGAACGGGTC[C/T]CTGAACATGGCTGCAGGKATTAGGAACATGTCGCTATTGGAGCCCTCTGACTGGTAGGTGCTGGAGCCGTCGAAGTTCCACTCAGGAAGATCTGACAGAGAAAGACAGCAGAAATCAATGATTAACTTTAAAATCTTACAAAACAATGTTATGGTTGTTGTTACTGATCAGATTGGAGCCAGATCTTACCCTCGATTGTCTTGGGTTCAGAATCCAGCGTCCTGGTCTTGCAGCGCAGTCCTTCTCCAGATCCATCGATCCAGATGTACATGGCTTGGACTTTGTCTCCTTGAGGGAGATCCATGTACTGCTGCTTAACAGCTTTGTTCAGTTTTGAACTTGCTGAGGTGGCCATTTTTTTGACCCAGACACCTACAGAGTAAAGAGATCAGATGATGAGCTTCACTACTGATCACAGTGGAGCCACTATATTTGATTGCGCATGTAAGA
GBYP-RAD_228	AGTTCTAGGACTACTGAAATGGGACTTTCTGACAGTTATTCCTATCCTTGCAGATATATTAGATTATAGTCTAGATATTGTTAAAAGCTAGATTTGTTATGGAGATTTGAGTATGGAGGTGTCAGATAAAGAAGACAGATTTTGGAAGGCAACATAAGGTGAATTAGATTCTTATTTAGATGTAATGGAATAGGGAGATGGAATAACTTTTATAACAGAAAGGAGGTTTGTTTTGTTTTTTTTCCCATCCTGCAGGTTGCAGGCTGGAGAAATGTTCCTGTARGAGAAAATSAGGTYGKGAGATGTTCATATGGAAATG[C/T]ATAGAGGGGTGACTTTTGGCAGAGATTGAGAGAAGCAGATTTCAGCCACTGGTAGGGTTCCAGGTGGCGTGGCTAGCTCGCCTCATTAGAGAATATTATCCAGCATGCCTCACAGCAACCGCCTATGTCCCCCCTTCCAACCCCTCCCACCCATCCACCGCTGACTGCTGGAAGGGACGTTTACCCTGGAAATCAGAGAGGAGAAAGACAGGGAGGGGAAAGGAGGATGACATTAATAGCTAGGAGCTTGACACAATCAAATGTCAGTTT

WebTable 8

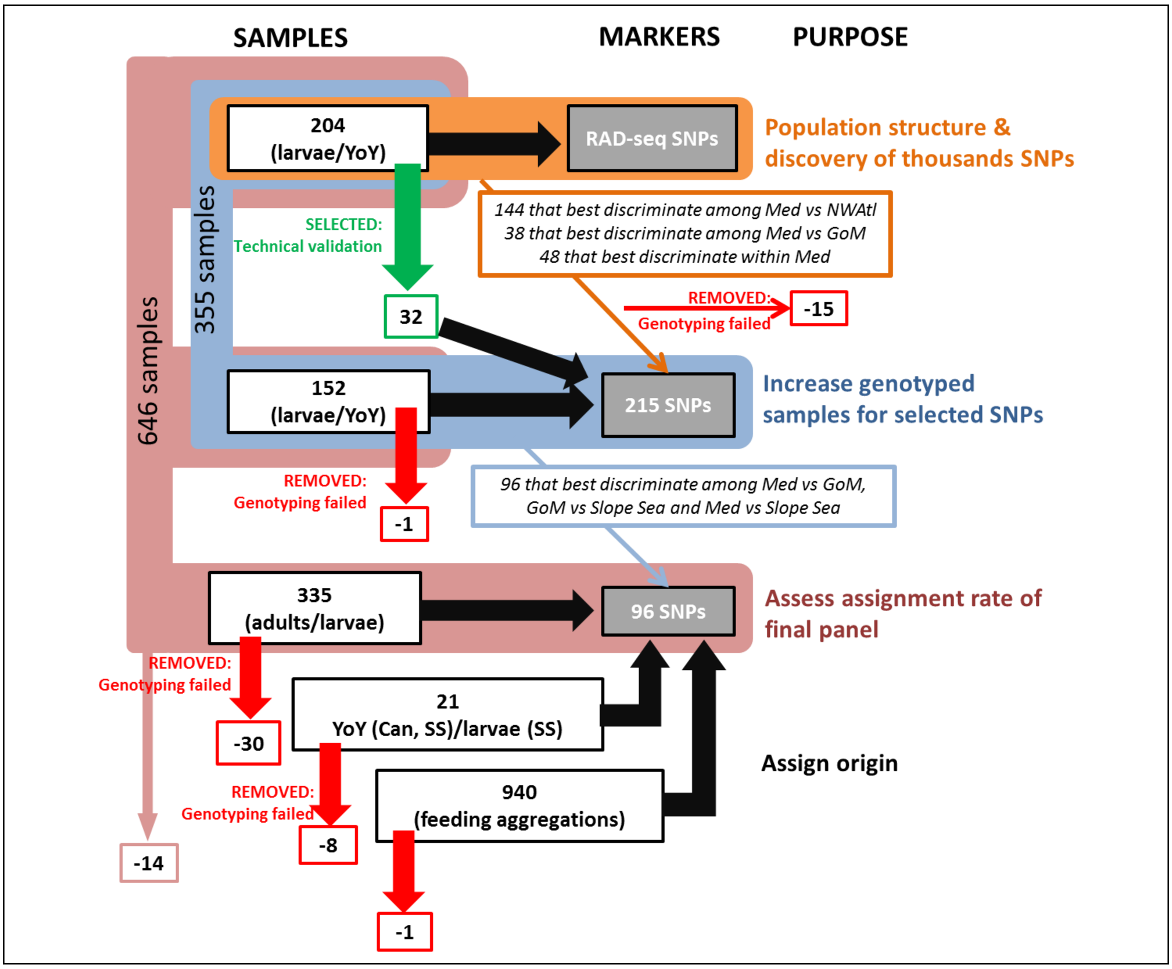
WebTable 8. F_{ST} per group pair calculated for catalogs 1 to 4.

Location Pair	Catalog 1	Catalog 2	Catalog 3	Catalog 4
WMed vs CMed	0.000	0.000	0.000	0.000
WMed vs EMed	0.000	0.000	0.000	0.000
CMed vs EMed	0.000	0.000	0.000	0.000
GOM vs SS	*0.000*	*0.000*	*0.000*	*0.000*
GOM vs CMed	0.004	0.004	0.003	0.002
GOM vs EMed	0.004	0.004	0.003	0.003
GOM vs WMed	0.004	0.004	0.003	0.003
GOM vs MED	*0.004*	*0.004*	*0.003*	*0.003*
SS vs WMed	0.003	0.002	0.002	0.002
SS vs CMed	0.003	0.002	0.002	0.001
SS vs EMed	0.003	0.003	0.002	0.001
SS vs MED	*0.003*	*0.002*	*0.002*	*0.001*
NWATL vs MED	*0.003*	*0.003*	*0.003*	*0.002*

WebPanel 1

Detailed methodological procedures

A detailed schematic view of the methods followed is provided below. First, thousands of SNP markers were discovered using RAD-seq on 204 larvae and young of the year (YoY) samples (orange). From those, the 230 most discriminant were selected and genotyped in 32 already used and 152 new samples (blue). From those, the 96 most discriminant were selected and genotyped for panel validation in 335 spawning adults and larvae (pink). The panel was used to assign origin of Canary island (Can) YoY, Slope Sea (SS) larvae and YoY, and of feeding aggregations. Baseline for assignments is composed of 646 individuals resulting from adding up all reference samples used for panel selection and validation without the Slope Sea young of the year.



Tissue sampling and DNA extraction

Larvae, young of the year, juveniles and medium to large adult ABFT (*Thunnus thynnus*) samples were obtained from scientific surveys and commercial fisheries operating throughout the species distribution range, including spawning grounds (WebTables 1-5). From each fish, a ~1 cm^3 piece of muscle or fin tissue sample was excised and immediately stored in RNA-later or 96% molecular grade ethanol at -20ºC until DNA extraction. Larvae were collected using bongo net tows in the known ABFT spawning areas, and immediately preserved in ethanol. The larvae were identified morphologically (Richards 2005) and/or genetically (Puncher, et al. 2015). Genomic DNA was extracted from about 20 mg of tissue or from whole or partial larvae (eyeballs or tails) using the Wizard® Genomic DNA Purification kit (Promega, WI, USA) following manufacturer's instructions for "Isolating Genomic DNA from Tissue Culture Cells and Animal Tissue". Extracted DNA was suspended in Milli-Q water and concentration was determined with the Quant-iT dsDNA HS assay kit using a Qubit® 2.0 Fluorometer (Life Technologies). DNA integrity was assessed by electrophoresis, migrating about 100 ng of GelRed™-stained DNA on an agarose 1.0% gel.

RAD-seq library preparation and data analysis

Restriction-site-associated DNA libraries of 204 larvae and young of the year samples (WebTable 1) were prepared following the methods of Etter et al (2011). Starting DNA (ranging from 50 to 250ng) was digested with the *SbfI* restriction enzyme and ligated to modified Illumina P1 adapters containing 5bp unique barcodes. Pools of 33 individuals were sheared using the Covaris® M220 Focused-ultrasonicator™ Instrument (Life Technologies) and size selected to 300-500 pb by cutting agarose migrated DNA. After Illumina P2 adaptor ligation, each library was amplified using 14 PCR cycles. Each pool was paired-end sequenced (100 pb) on an Illumina HiSeq2000. Raw sequences are available at NCBI SRA Bioproject # SUB4348994. Generated RAD-tags were analyzed using *Stacks* version 1.32 (Catchen, et al. 2013). Quality filtering and demultiplexing was performed with *process_radtags* truncating all reads to 90 nucleotides to avoid the lower quality bases at the end of the read. PCR duplicates were removed applying *clone_filter* to reads whose forward and reverse pairs passed quality filtering. The following steps were applied to non-clone filtered data (*i.e.*, all forward reads passing quality filtering, even if their reverse pair failed) and to clone-filtered data (*i.e.*, single representatives of each PCR clone). Respectively, only samples with at least 500,000 quality-filter passing forward reads or 100,000 PCR clone representatives were kept. Putative orthologous tags (stacks) per individual were assembled using *ustacks* with a minimum depth of coverage required to create a stack (m) of 5 or 3 and a maximum nucleotide mismatches (M) allowed between stacks of 2 or 4. Catalogs of RAD loci were assembled based on two subsets of individuals (all samples or only Mediterranean Sea samples) using *cstacks* with a number of mismatches allowed between sample tags when generating the catalog (n) of 3 or 6. Matches of individual RAD loci to the catalog were searched using *sstacks*. From each generated catalog, SNPs present in RAD loci found in at least 75% of the individuals under study were selected and exported into *PLINK* format using *populations*. Using *PLINK* version 1.07 (Purcell, et al. 2007), SNPs with a minimum allele frequency (MAF) smaller than 0.05, a genotyping rate smaller than 0.95 and which failed the Hardy Weinberg equilibrium (HWE) test at $p < 0.05$ in at least two areas of study were excluded. Only samples with genotyping rate above 0.8 were retained per dataset. Each genotype dataset was exported to *Structure* and *Genepop* formats using *PGDSpider* version 2.0.8.3 (Lischer and Excoffier 2012). Genotype tables are available at https://sites.google.com/site/naiararodriguezezpeleta/resources.

Genetic diversity and population structure

F_{ST} values per population pair were calculated on each genotype dataset following the Weir and Cockerham Weir and Cockerham (1984) formulation as implemented in *Genepop 4.3* (Rousset 2008). Principal component analyses (PCA) were performed with the R package *adegenet* (Jombart and Ahmed 2011) with no *a priori* population assignment of samples. For each genotype dataset, ten subsets of 5,000 randomly chosen SNPs were created and analyzed with the Bayesian clustering approach implemented in *STRUCTURE* (Pritchard, et al. 2000). For each value of K (number of potential ancestral populations, which ranged from 1 to the number of presumed populations + 1), the genetic ancestry of each individual was evaluated without any prior population assignment, based on the admixture model and a burn-in period of 100,000 iterations followed by 300,000 iterations from which estimates were obtained. The results obtained from the ten subsets considered for each value of K were analyzed with *CLUMPP* (Jakobsson and Rosenberg 2007) to identify common modes, and results were plotted using *DISTRUCT* (Rosenberg 2004). Best K was identified according to the Evanno method (Evanno, et al. 2005) as implemented in *StructureHarvester* (Earl and vonHoldt 2012). Statistical significance among the distributions of belonging to one of two hypothetical ancestral populations was assessed with the Wilcoxon rank sum test.

SNP selection and genotyping

For each catalog based on all samples, the 200 SNPs with the highest F_{ST} values among Northwest Atlantic (Gulf of Mexico larvae and Slope Sea young of the year) and Mediterranean Sea (larvae and young of the year) samples and the 100 SNPs with the highest F_{ST} values among Gulf of Mexico larvae and Mediterranean Sea larvae and young of the year were selected. For each catalog based on only the Mediterranean Sea samples, the 30 SNPs with the highest F_{ST} values among each pair of intra Mediterranean Sea areas (West, Central and East) were retrieved, and from those, the 50 SNPs that provided the highest sum of pairwise F_{ST}s for each catalog were selected. The flanking regions of the 1,400 selected SNPs were obtained by matching their corresponding tags against the ABFT reference genome (Puncher, et al. 2018) using an in-house script (see https://github.com/rodriguez-ezpeleta/ABFT_popgentrace). Obtained sequences were submitted to the Assay Design Group at Fluidigm Corporation (South San Francisco, CA, USA), and from the ones fulfilling the Fluidigm design criteria, the 144 that most discriminate between Northwest Atlantic *vs.* Mediterranean samples, the 38 that most discriminate between Gulf of Mexico *vs.* Mediterranean samples, and the 48 that most discriminate among Mediterranean Sea locations were selected (a total of 230 originating from the 8 catalogs; WebTable 6) and sent for design and manufacture of primers for a SNPtype^{TM} genotyping panel. Genotyping of 184 larvae and young of the year samples (WebTable 2), including 32 already genotyped with RAD-seq, was performed on the Biomark^{TM} HD platform using Flex Six™, 48.48 and 96.96 Dynamic Array IFCs, and the resulting data was analyzed with the Fluidigm Genotyping Analysis Software (one sample was removed for failing for more than 20% of the SNPs). Genotypes derived from RAD and Fluidigm were combined for the 230 SNPs to make a dataset of 355 individuals (204 + 151 [184-32 repeated – 1 failed]). Successfully genotyped SNPs were ranked according to the average F_{ST} values for each of the following pairs: Gulf of Mexico *vs.* Mediterranean Sea, Gulf of Mexico *vs.* Slope Sea, and Slope Sea *vs.* Mediterranean. SNPs were checked for linkage disequilibrium using *Genepop 4.3* (Rousset 2008), and only one per linked group (p-value < 0.001) and/or per genome contig was selected. 96 SNPs with the lowest averaged F_{ST} value-based rank across the three pairs were selected (WebTable 7). 328 adults captured in the Gulf of Mexico and the Mediterranean Sea during the spawning season and 7 larvae from the Gulf of Mexico (WebTable 3), 6 Canary Island young of the year, 1 Slope Sea young of the year,14 Slope Sea larvae (WebTable 4) and 940 feeding aggregations (WebTable 5) were genotyped for the 96 selected SNPs using 96.96 Dynamic Array IFCs, and the resulting data was analyzed with the Fluidigm Genotyping Analysis Software. From them, 39 failed genotyping and were excluded from further analyses.

Origin assignment of samples of known and unknown origin

Self-assignments were performed by calculating assignment scores, *i.e.* probability of belonging to each of the baseline populations, with G*ENECLASS2* (Piry, et al. 2004) using the Rannala and Mountain (1997) criterion (0.05 threshold) of i) 204 individuals (WebTable 1) using the RAD-seq derived genotypes for 169 SNPs (excluding, from the 230 selected, the 15 that failed, and the ones selected for discrimination among Mediterranean areas), ii) 355 individuals genotyped for 230 SNPs (WebTables 1 and 2 minus the 32 already genotyped with RAD-seq and the one that failed) using the RAD-seq and Fluidigm derived genotypes for the 96 final SNP set considering two (Gulf of Mexico and Mediterranean Sea) or three (Gulf of Mexico, Slope Sea and Mediterranean Sea) populations as baseline, and iii) on 165 Mediterranean Sea individuals from WebTable 1 using the RAD-seq derived genotypes for 46 SNPs (48 selected minus 2 that failed) considering three Mediterranean Sea populations as baselines. Samples with assignment scores below 90% were considered “unassigned”.

Using 341 reference individuals (WebTable 1 and 2 minus the 32 already genotyped with RAD-seq, the one that failed and 14 Slope Sea young of the year), loci were ranked according to their discriminative power to assign samples to their known origin following the allele frequency differential method implemented in WHICHLOCI (Banks, et al. 2003). Assignment power of the developed 96 SNP panel and derived subsets was assessed by calculating percentages of correctly and incorrectly assigned of samples of known origin not used for SNP selection. For that aim, assignment scores of each sample were calculated with G*ENECLASS2* (Piry, et al. 2004) using the Rannala and Mountain (1997) criterion (0.05 threshold). Assignments of natal origin (Gulf of Mexico and Mediterranean Sea) were calculated for 305 adults and larvae captured within one of the two spawning areas during the spawning season (WebTable 3) using a leave-one-out approach with a baseline of 646 individuals, that is, the 341 previously genotyped samples (355 minus 14 Slope Sea young of the year) and the 305 spawning adults. True positive stock of origin assignment rate, true negative assignment rate, positive predictive value, negative predictive value and accuracy where calculated for 70, 80 and 90% probability of assignment thresholds. 80% assignment score threshold was selected as being the one providing the largest number of assigned individuals without compromising accuracy. Origin of Canary island young of the year, Slope Sea larvae and young of the year (WebTable 4) and of 940 feeding aggregation samples (WebTable 5) was calculated using the combined set of 646 reference samples as baseline. Samples with assignment score lower than 80% were considered unassigned.

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WebPanel 2

RAD-seq genotyping

The number of RAD-seq reads passing quality filters per individual included in the final analyses ranges from 868,453 to 14,146,731 with an average of 4,430,279. Average number of RAD-tags (loci) per individual is 65,000 and 49,000 for catalogs with and without PCR clones respectively, and overall coverage is 67X and 27X for each case. In total, eight catalogs were created (see Table below) resulting from alternative combinations of orthologous loci identification parameters and removal or not of PCR clones. The number of tags present in at least 75% of the individuals ranges from 31,193 to 41,968 and the number of SNPs after applying selection filters from 7,588 to 13,226. The number of individuals passing inclusion criteria ranges from 180 to 204 in catalogs including all samples and from 146 from 165 in catalogs including only Mediterranean Sea samples.

Catalog	**Sample**	***clone_filter***	***ustacks***		***Cstacks***	**RAD loci (>75% ind.)**	**Final Dataset**	
			M	**M**	**n**		**Individuals**	**SNPs**
1	all	no	5	2	3	39810	204	9871
2	all	no	5	4	6	41968	204	11246
3	all	yes	3	4	6	37089	200	7588
4	all	yes	5	4	6	30077	180	8527
5	med	no	5	2	3	37538	165	11315
6	med	no	5	4	6	40290	165	13226
7	med	yes	3	4	6	36379	162	10496
8	med	yes	5	4	6	31193	146	12613

Details for each catalog constructed using all (Sample:all) or only Mediterranean Sea (Sample:med) samples, removing PCR duplicates (clone_filter:yes) or not (clone_filter:no) and using different m, M and n parameter combinations, and, for each, number of RAD loci present in at least 75% of the individuals and number of individuals and SNPs remaining after catalog filtering.

WebPanel 3

SNP selection and Fluidigm genotyping validation

1400 selected SNPs were successfully mapped to the ABFTnce genome, 929 remained after removing duplicates (those matching to the same contig on the same position), and 423 of them fulfilled Fluidigm specifications. Genotyping of 15 SNPs of the 230 selected for validation in 184 samples was not successful, and one sample failed for more than 20% of the SNPs. Genotyping rate of remaining SNPs and individuals was 99%. Genotyping technical reproducibility, assessed by comparing the Fluidigm and RAD-seq derived genotypes for the 32 repeated samples, was 98%. Most of the mismatches between RAD-seq and Fluidigm derived genotypes are due to homozygous calls in RAD-seq that are heterozygous in Fluidigm (see Table below).

Genotyping technique		**Catalog from which SNPs originate**	
RAD-seq	**Fluidigm**	**With Clones**	**Without Clones**
AA	AB	85.24	76.04
	BB	0.02	0
AB	AA or BB	0.41	0.3
% of mismatches		2.85	1.25

From the average percent of mismatching genotypes between RAD-seq and Fluidigm for each catalog with and without clones, percentage of homozygote (AA) RAD-seq genotypes coded as heterozygotes (AB) or as homozygotes for an alternative allele (BB) in Fluidigm, and percentage of heterozygote (AB) RAD-seq genotypes coded as homozygotes (AA/BB) in Fluidigm

Appendix D

Supplementary Material

(Díaz-Arce et al.)

Supplementary tables

Table S1. Complete list of all the ABFT samples sequenced in this study and available details about capture dates and coordinates, age class, sex and size. Fish length is indicated in cm as fork length (FL), total length (TL) or curved fork length (CFL) when data available. Samples that were included in each RAD catalog are indicated, as well as the probability for each individual captured in the Gulf of Mexico of fitting within the Mediterranean Sea distribution of ancestry values inferred using ADMIXTURE when assuming K=2 ancestral populations. Finally, those samples for which otolith microchemistry information is available and included in Figure S7 are indicated.

SampleID	Library Pool	Location	GrAREA	AGE CLASS	Catch Date [dd/mm/yy]	Length (cm)	Length Type	Lat.	Long.	SEX	Denovo catalog	allSPS mapped catalog	ABFT mapped catalog	Prob (MED-like)	Med-like	Otolith
NOAA-GM-L-4	GBYP10	GOM	NWAtl	A	15/05/2013	245	FL	27.8	-90.1	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-163	GBYP10	GOM	NWAtl	A	15/05/2013	281	FL	28.0	-89.4	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-89	GBYP11	GOM	NWAtl	A	15/04/2010	262	FL	27.6	-88.9	F	INCLUDED	INCLUDED	INCLUDED	0.049	NO	YES
NOAA-GM-L-82	GBYP11	GOM	NWAtl	A	15/04/2010	278	FL	26.0	-91.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-162	GBYP12	GOM	NWAtl	A	15/05/2013	260	FL	28.0	-89.4	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-84	GBYP12	GOM	NWAtl	A	15/05/2010	239	FL	27.1	-90.4	M	FILTERED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-104	GBYP16	GOM	NWAtl	A	15/04/2010	242	FL	27.3	-88.8	M	INCLUDED	INCLUDED	INCLUDED	0.518	MED-like	YES
NOAA-GM-L-74	GBYP13	GOM	NWAtl	A	15/03/2010	252	FL	27.2	-87.6	M	INCLUDED	INCLUDED	INCLUDED	0.341	MED-like	YES
NOAA-GM-L-142	GBYP10	GOM	NWAtl	A	15/05/2014	238	FL	26.9	-90.0	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-111	GBYP10	GOM	NWAtl	A	15/04/2010	243	FL	27.1	-89.2	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-50	GBYP10	GOM	NWAtl	A	15/05/2012	243	FL	27.8	-87.2	F	INCLUDED	INCLUDED	INCLUDED	0.830	MED-like	YES
NOAA-GM-L-88	GBYP10	GOM	NWAtl	A	15/05/2010	238	FL	27.4	-89.0	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-150	GBYP10	GOM	NWAtl	A	15/05/2014	220	FL	28.0	-89.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES

NOAA-GM-L-3	GBYP10	GOM	NWAtl	A	15/05/2013	230	FL	27.8	-90.1	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-83	GBYP10	GOM	NWAtl	A	15/04/2010	249	FL	27.9	-87.1	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-86	GBYP10	GOM	NWAtl	A	15/05/2010	261	FL	27.1	-90.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-135	GBYP10	GOM	NWAtl	A	15/04/2014	221	FL	27.5	-91.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-38	GBYP11	GOM	NWAtl	A	15/04/2012	241	FL	27.9	-86.3	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-149	GBYP11	GOM	NWAtl	A	15/04/2014	228	FL	26.4	-90.9	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-85	GBYP11	GOM	NWAtl	A	15/04/2010	280	FL	27.1	-88.8	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-48	GBYP11	GOM	NWAtl	A	15/05/2012	230	FL	26.6	-89.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-45	GBYP11	GOM	NWAtl	A	15/04/2012	234	FL	27.9	-86.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-22	GBYP11	GOM	NWAtl	A	15/05/2013	244	FL	27.9	-86.4	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-8	GBYP11	GOM	NWAtl	A	15/05/2013	245	FL	27.0	-91.2	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-105	GBYP12	GOM	NWAtl	A	15/04/2010	223	FL	27.4	-91.6	F	FILTERED	INCLUDED	FILTERED	-	-	YES
NOAA-GM-L-94	GBYP12	GOM	NWAtl	A	15/05/2010	230	FL	27.1	-89.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-128	GBYP12	GOM	NWAtl	A	15/04/2014	227	FL	27.7	-89.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-124	GBYP12	GOM	NWAtl	A	15/05/2010	222	FL	26.7	-88.8	F	FILTERED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-172	GBYP12	GOM	NWAtl	A	15/05/2013	259	FL	27.5	-90.2	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-177	GBYP12	GOM	NWAtl	A	15/04/2014	246	FL	27.6	-87.7	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-178	GBYP12	GOM	NWAtl	A	15/05/2014	259	FL	27.7	-87.9	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-166	GBYP13	GOM	NWAtl	A	15/03/2013	232	FL	27.0	-90.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-116	GBYP13	GOM	NWAtl	A	15/03/2010	249	FL	26.7	-89.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-102	GBYP13	GOM	NWAtl	A	15/03/2010	265	FL	27.0	-88.4	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-145	GBYP14	GOM	NWAtl	A	15/05/2014	210	FL	27.4	-92.3	F	FEW TAGS	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-42	GBYP14	GOM	NWAtl	A	15/04/2012	273	FL	28.0	-86.1	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-103	GBYP14	GOM	NWAtl	A	15/04/2010	234	FL	27.2	-89.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-132	GBYP14	GOM	NWAtl	A	15/06/2014	250	FL	27.6	-89.9	M	FEW TAGS	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-170	GBYP14	GOM	NWAtl	A	15/03/2013	228	FL	26.5	-90.5	F	FILTERED	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-108	GBYP14	GOM	NWAtl	A	15/03/2010	233	FL	27.3	-92.0	M	FEW TAGS	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-136	GBYP14	GOM	NWAtl	A	15/04/2014	266	FL	27.5	-89.6	M	FILTERED	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-165	GBYP14	GOM	NWAtl	A	15/03/2013	227	FL	27.8	-89.8	NA	FILTERED	FILTERED	FILTERED	-	-	YES

NOAA-GM-L-141	GBYP14	GOM	NWAtl	A	15/06/2014	199	FL	28.0	-88.9	F	FEW TAGS	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-147	GBYP14	GOM	NWAtl	A	15/01/2014	235	FL	26.3	-90.8	F	FILTERED	INCLUDED	FILTERED	-	-	YES
NOAA-GM-L-36	GBYP15	GOM	NWAtl	A	15/04/2012	239	FL	27.9	-86.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-14	GBYP15	GOM	NWAtl	A	15/04/2013	231	FL	28.3	-88.3	M	FEW TAGS	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-49	GBYP15	GOM	NWAtl	A	15/05/2012	234	FL	27.8	-86.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-106	GBYP15	GOM	NWAtl	A	15/03/2010	262	FL	26.5	-89.1	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-35	GBYP15	GOM	NWAtl	A	15/03/2012	265	FL	26.6	-89.1	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-24	GBYP15	GOM	NWAtl	A	15/05/2013	243	FL	27.0	-91.2	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-13	GBYP16	GOM	NWAtl	A	15/04/2013	231	FL	28.3	-88.3	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-55	GBYP16	GOM	NWAtl	A	15/05/2012	245	FL	27.9	-86.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-78	GBYP16	GOM	NWAtl	A	15/03/2010	262	FL	27.1	-87.1	M	INCLUDED	INCLUDED	INCLUDED	0.001	NO	YES
NOAA-GM-L-92	GBYP10	GOM	NWAtl	A	15/04/2010	257	FL	27.5	-87.8	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-137	GBYP11	GOM	NWAtl	A	15/04/2014	225	FL	27.8	-89.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-90	GBYP12	GOM	NWAtl	A	15/05/2010	220	FL	27.4	-89.0	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-123	GBYP12	GOM	NWAtl	A	15/05/2010	212	FL	27.3	-88.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-164	GBYP15	GOM	NWAtl	A	15/03/2013	227	FL	27.8	-89.8	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
FMAP-MA-L-157	GBYP15	MED	CMed	A	08/06/2012	230	CFL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	YES
FMAP-MA-L-79	GBYP17	MED	CMed	A	10/06/2011	229.5	CFL	35.5	14.0	M	INCLUDED	INCLUDED	INCLUDED	*	-	YES
UNIC-SA-L-46	GBYP17	MED	WMed	A	17/06/2011	180	CFL	39.2	8.4	F	INCLUDED	INCLUDED	INCLUDED	*	-	YES
FMAP-SY-L-83	GBYP13	MED	CMed	A	16/05/12-14/06/12	216	FL	34.0	13.0	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-167	GBYP13	MED	CMed	A	05/06/2015	216	CFL	33.5	13.5	M	FEW TAGS	FILTERED	FILTERED	*	-	NO
FMAP-SY-L-173	GBYP13	MED	CMed	A	05/06/2015	196	CFL	33.5	13.5	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-23	GBYP13	MED	CMed	A	16/05/12-14/06/12	210	FL	34.0	13.0	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-L-78	GBYP13	MED	CMed	A	10/06/2011	237	CFL	35.5	14.0	F	FEW TAGS	FILTERED	FILTERED	*	-	NO
FMAP-SY-L-37	GBYP13	MED	CMed	A	16/05/12-14/06/12	214	FL	34.0	13.0	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-16	GBYP14	MED	CMed	A	16/05/12-14/06/12	225	FL	34.0	13.0	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO

FMAP-SY-L-58	GBYP14	MED	CMed	A	16/05/12-14/06/12	223	FL	34.0	13.0	M	FILTERED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-166	GBYP14	MED	CMed	A	05/06/2015	200	CFL	33.5	13.5	M	FILTERED	INCLUDED	FILTERED	*	-	NO
FMAP-SY-L-155	GBYP14	MED	CMed	A	05/06/2015	218	CFL	33.5	13.5	F	FEW TAGS	FEW TAGS	FEW TAGS	*	-	NO
FMAP-SY-L-4	GBYP14	MED	CMed	A	16/05/12-14/06/12	213	FL	34.0	13.0	F	FILTERED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-2	GBYP14	MED	CMed	A	16/05/12-14/06/12	186	FL	34.0	13.0	M	FILTERED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-47	GBYP14	MED	CMed	A	16/05/12-14/06/12	243	FL	34.0	13.0	F	FILTERED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-152	GBYP14	MED	CMed	A	05/06/2015	219	CFL	33.5	13.5	M	FILTERED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-88	GBYP16	MED	CMed	A	16/05/12-14/06/12	255	FL	34.0	13.0	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-43	GBYP16	MED	CMed	A	16/05/12-14/06/12	219	FL	34.0	13.0	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-80	GBYP16	MED	CMed	A	16/05/12-14/06/12	239	FL	34.0	13.0	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-50	GBYP16	MED	CMed	A	16/05/12-14/06/12	233	FL	34.0	13.0	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-17	GBYP16	MED	CMed	A	16/05/12-14/06/12	217	FL	34.0	13.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-168	GBYP16	MED	CMed	A	05/06/2015	233	CFL	33.5	13.5	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-157	GBYP17	MED	CMed	A	05/06/2015	220	CFL	33.5	13.5	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-169	GBYP17	MED	CMed	A	05/06/2015	223	CFL	33.5	13.5	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-55	GBYP17	MED	CMed	A	16/05/12-14/06/12	251	CFL	34.0	13.0	M	FILTERED	FILTERED	FILTERED	*	-	NO
FMAP-MA-L-77	GBYP17	MED	CMed	A	10/06/2011	252	CFL	35.5	14.0	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-L-71	GBYP17	MED	CMed	A	10/06/2011	225	CFL	35.5	14.0	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-32	ACEITU-03	MED	CMed	L	15/07/2008	0.071	TL	36.7	15.3	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-SI-V-48	ACEITU-03	MED	CMed	L	15/07/2008	0.068	TL	36.7	15.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-54	ACEITU-03	MED	CMed	L	15/07/2008	0.067	TL	36.7	15.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-61	ACEITU-03	MED	CMed	L	15/07/2008	0.061	TL	36.7	15.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO

IEO-SI-V-45	ACEITU-03	MED	CMed	L	15/07/2008	0.067	TL	36.7	15.3	NA	FILTERED	INCLUDED	FILTERED	*	-	NO
IEO-SI-V-36	ACEITU-03	MED	CMed	L	15/07/2008	0.063	TL	36.7	15.3	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-SI-V-42	ACEITU-03	MED	CMed	L	15/07/2008	0.068	TL	36.7	15.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-69	ACEITU-03	MED	CMed	L	15/07/2008	0.076	TL	36.7	15.3	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-SI-V-46	ACEITU-03	MED	CMed	L	15/07/2008	0.064	TL	36.7	15.3	NA	FILTERED	FILTERED	FILTERED	*	-	NO
IEO-SI-V-33	ACEITU-03	MED	CMed	L	15/07/2008	0.077	TL	36.7	15.3	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-SI-V-64	ACEITU-03	MED	CMed	L	15/07/2008	0.065	TL	36.7	15.3	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-SI-V-53	ACEITU-03	MED	CMed	L	15/07/2008	0.073	TL	36.7	15.3	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-SI-V-70	ACEITU-03	MED	CMed	L	15/07/2008	0.062	TL	36.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-39	ACEITU-03	MED	CMed	L	15/07/2008	0.071	TL	36.7	15.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-76	ACEITU-03	MED	CMed	L	15/07/2008	0.059	TL	36.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-40	ACEITU-03	MED	CMed	L	15/07/2008	0.074	TL	36.7	15.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-34	ACEITU-03	MED	CMed	L	15/07/2008	0.074	TL	36.7	15.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-1	ACEITU-04	MED	CMed	Y	10/09/2013	25.2	FL	35.5	14.0	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-4	ACEITU-04	MED	CMed	Y	16/09/2013	23.1	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-5	ACEITU-04	MED	CMed	Y	16/09/2013	21.8	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-8	ACEITU-04	MED	CMed	Y	16/09/2013	22.1	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-9	ACEITU-04	MED	CMed	Y	16/09/2013	23.1	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-10	ACEITU-04	MED	CMed	Y	23/09/2013	26.4	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-13	ACEITU-04	MED	CMed	Y	23/09/2013	27.2	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-17	ACEITU-05	MED	CMed	Y	23/09/2013	23.9	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-23	ACEITU-05	MED	CMed	Y	23/09/2013	21.6	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-29	ACEITU-05	MED	CMed	Y	23/09/2013	22.5	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-31	ACEITU-05	MED	CMed	Y	23/09/2013	26.5	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-33	ACEITU-05	MED	CMed	Y	23/09/2013	22.8	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-34	ACEITU-05	MED	CMed	Y	23/09/2013	20.9	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-35	ACEITU-05	MED	CMed	Y	23/09/2013	23.5	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-36	ACEITU-05	MED	CMed	Y	23/09/2013	25.8	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-37	ACEITU-05	MED	CMed	Y	23/09/2013	26.1	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO

FMAP-MA-0-38	ACEITU-05	MED	CMed	Y	23/09/2013	26.7	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-29	ACEITU-06	MED	CMed	Y	05/10/2012	37	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-4	ACEITU-06	MED	CMed	Y	23/09/2012	31	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-9	ACEITU-06	MED	CMed	Y	23/09/2012	31	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-15	ACEITU-06	MED	CMed	Y	05/10/2012	40	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-10	ACEITU-06	MED	CMed	Y	23/09/2012	30	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-27	ACEITU-07	MED	CMed	Y	05/10/2012	38	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-5	ACEITU-07	MED	CMed	Y	23/09/2012	31	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-6	ACEITU-07	MED	CMed	Y	23/09/2012	32	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-30	ACEITU-07	MED	CMed	Y	05/10/2012	36	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-11	ACEITU-07	MED	CMed	Y	23/09/2012	30	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-1	ACEITU-08	MED	CMed	Y	23/09/2012	29	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-8	ACEITU-08	MED	CMed	Y	23/09/2012	28	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-35	ACEITU-08	MED	CMed	Y	05/10/2012	37	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-12	ACEITU-08	MED	CMed	Y	23/09/2012	28	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-3	ACEITU-08	MED	CMed	Y	23/09/2012	34	FL	37.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-26	ACEITU-08	MED	CMed	Y	05/10/2012	39	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-31	ACEITU-08	MED	CMed	Y	05/10/2012	38	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-36	ACEITU-08	MED	CMed	Y	05/10/2012	38	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-190	GBYP13	MED	EMed	A	28/05/2015	237	FL	36.3	31.5	F	FILTERED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-166	GBYP13	MED	EMed	A	05/06/2015	207	FL	35.6	35.2	M	FILTERED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-178	GBYP13	MED	EMed	A	05/06/2015	222	FL	35.6	35.2	F	FILTERED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-172	GBYP13	MED	EMed	A	05/06/2015	231	FL	35.6	35.2	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-169	GBYP13	MED	EMed	A	05/06/2015	221	FL	35.6	35.2	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-167	GBYP13	MED	EMed	A	05/06/2015	211	FL	35.6	35.2	M	FILTERED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-164	GBYP14	MED	EMed	A	05/06/2015	233	FL	35.6	35.2	M	FILTERED	FILTERED	FILTERED	*	-	NO
ISTA-LS-L-184	GBYP14	MED	EMed	A	28/05/2015	260	FL	36.3	31.5	M	FILTERED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-174	GBYP14	MED	EMed	A	05/06/2015	228	FL	35.6	35.2	F	FILTERED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-199	GBYP14	MED	EMed	A	28/05/2015	210	FL	36.3	31.5	F	FILTERED	INCLUDED	FILTERED	*	-	NO

ISTA-LS-L-200	GBYP14	MED	EMed	A	28/05/2015	208	FL	36.3	31.5	M	FILTERED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-170	GBYP16	MED	EMed	A	05/06/2015	204	FL	35.6	35.2	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-165	GBYP16	MED	EMed	A	05/06/2015	226	FL	35.6	35.2	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-182	GBYP17	MED	EMed	A	05/06/2015	225	FL	35.6	35.2	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-195	GBYP17	MED	EMed	A	28/05/2015	240	FL	36.3	31.5	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-162	GBYP17	MED	EMed	A	05/06/2015	223	FL	35.6	35.2	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-1	ACEITU-01	MED	EMed	L	22/06/2011	0.579	FL	36.1	33.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-26	ACEITU-01	MED	EMed	L	23/06/2011	0.95	FL	36.1	33.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-45	ACEITU-01	MED	EMed	L	24/06/2011	1.26	FL	36.1	33.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-71	ACEITU-02	MED	EMed	L	24/06/2011	1.18	FL	36.1	33.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-317	ACEITU-04	MED	EMed	Y	15/08/2013	21.1	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-318	ACEITU-04	MED	EMed	Y	16/08/2013	23.3	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-320	ACEITU-04	MED	EMed	Y	16/08/2013	22.4	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-325	ACEITU-04	MED	EMed	Y	16/08/2013	24.6	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-327	ACEITU-04	MED	EMed	Y	16/08/2013	23.9	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-334	ACEITU-04	MED	EMed	Y	17/08/2013	23.4	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-336	ACEITU-04	MED	EMed	Y	17/08/2013	24.5	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-337	ACEITU-04	MED	EMed	Y	17/08/2013	24.7	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-369	ACEITU-04	MED	EMed	Y	19/08/2013	22.9	FL	36.2	33.9	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-372	ACEITU-04	MED	EMed	Y	14/08/2013	22.7	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-373	ACEITU-05	MED	EMed	Y	14/08/2013	21.4	FL	36.2	33.9	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-374	ACEITU-05	MED	EMed	Y	14/08/2013	20.4	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-375	ACEITU-05	MED	EMed	Y	06/08/2013	22.8	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-376	ACEITU-05	MED	EMed	Y	06/08/2013	21.5	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-381	ACEITU-05	MED	EMed	Y	04/08/2013	21.7	FL	36.2	33.9	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
CYPR-LS-0-394	ACEITU-05	MED	EMed	Y	16/08/2013	28.5	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-395	ACEITU-05	MED	EMed	Y	13/08/2013	26	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-396	ACEITU-05	MED	EMed	Y	13/08/2013	27.1	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-397	ACEITU-05	MED	EMed	Y	13/08/2013	26.2	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO

CYPR-LS-0-398	ACEITU-05	MED	EMed	Y	13/08/2013	27.1	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-113	ACEITU-06	MED	EMed	Y	29/07/2012	26.1	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-114	ACEITU-06	MED	EMed	Y	29/07/2012	23.1	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-110	ACEITU-06	MED	EMed	Y	03/09/2012	28.7	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-112	ACEITU-06	MED	EMed	Y	29/07/2012	23.8	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-39	ACEITU-07	MED	EMed	Y	24/07/2012	24.9	FL	36.1	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-37	ACEITU-07	MED	EMed	Y	24/07/2012	22.1	FL	36.1	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-52	ACEITU-07	MED	EMed	Y	25/07/2012	21.7	FL	36.1	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-43	ACEITU-07	MED	EMed	Y	24/07/2012	24.5	FL	36.1	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-68	ACEITU-08	MED	EMed	Y	25/07/2012	24.2	FL	36.1	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-111	ACEITU-08	MED	EMed	Y	03/09/2012	30.4	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-56	ACEITU-08	MED	EMed	Y	25/07/2012	24.5	FL	36.1	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-60	ACEITU-08	MED	EMed	Y	25/07/2012	23.2	FL	36.1	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-322	ACEITU-02	MED	EMed	Y	16/08/2013	24.8	FL	36.2	33.9	NA	FILTERED	INCLUDED	FILTERED	*	-	NO
CYPR-LS-0-323	ACEITU-02	MED	EMed	Y	16/08/2013	24.4	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-371	ACEITU-02	MED	EMed	Y	19/08/2013	22.9	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-379	ACEITU-03	MED	EMed	Y	03/08/2013	20.4	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
NOAA-GM-L-15	GBYP10	GOM	NWAtl	A	15/05/2013	194	FL	27.9	-86.5	F	FILTERED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-61	GBYP10	GOM	NWAtl	A	15/05/2012	242	FL	26.9	-90.7	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-153	GBYP10	GOM	NWAtl	A	15/05/2014	210	FL	26.4	-89.1	M	INCLUDED	INCLUDED	INCLUDED	0.385	MED-like	NO
NOAA-GM-L-65	GBYP10	GOM	NWAtl	A	15/05/2011	262	FL	27.1	-89.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-47	GBYP10	GOM	NWAtl	A	15/05/2012	253	FL	27.8	-86.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-7	GBYP10	GOM	NWAtl	A	15/04/2013	233	FL	27.2	-90.7	F	FEW TAGS	FILTERED	FILTERED	-	-	NO
NOAA-GM-L-174	GBYP10	GOM	NWAtl	A	15/04/2014	218	FL	24.5	-84.2	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-37	GBYP10	GOM	NWAtl	A	15/04/2012	283	FL	27.9	-86.3	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-2	GBYP10	GOM	NWAtl	A	15/05/2013	204	FL	26.8	-91.0	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-93	GBYP10	GOM	NWAtl	A	15/04/2010	252	FL	27.2	-91.8	M	FILTERED	INCLUDED	INCLUDED	0.007	NO	NO
NOAA-GM-L-66	GBYP10	GOM	NWAtl	A	15/05/2011	252	FL	27.4	-89.5	F	INCLUDED	INCLUDED	INCLUDED	0.338	MED-like	NO
NOAA-GM-L-59	GBYP10	GOM	NWAtl	A	15/04/2012	259	FL	27.1	-89.0	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO

NOAA-GM-L-56	GBYP10	GOM	NWAtl	A	15/05/2012	271	FL	27.8	-88.8	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-43	GBYP11	GOM	NWAtl	A	15/04/2012	234	FL	27.8	-86.4	M	FEW TAGS	FEW TAGS	FEW TAGS	-	-	NO
NOAA-GM-L-140	GBYP11	GOM	NWAtl	A	15/05/2014	235	FL	27.6	-88.3	F	FILTERED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-87	GBYP11	GOM	NWAtl	A	15/04/2010	238	FL	27.6	-90.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-95	GBYP11	GOM	NWAtl	A	15/04/2010	249	FL	27.6	-86.4	F	INCLUDED	INCLUDED	INCLUDED	0.004	NO	NO
NOAA-GM-L-12	GBYP11	GOM	NWAtl	A	15/04/2013	250	FL	28.7	-88.9	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-9	GBYP11	GOM	NWAtl	A	15/05/2013	255	FL	27.0	-90.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-151	GBYP11	GOM	NWAtl	A	15/05/2014	220	FL	28.0	-89.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-148	GBYP11	GOM	NWAtl	A	15/04/2014	225	FL	27.2	-87.8	M	INCLUDED	INCLUDED	INCLUDED	0.425	MED-like	NO
NOAA-GM-L-52	GBYP11	GOM	NWAtl	A	15/05/2012	243	FL	27.8	-87.2	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-25	GBYP11	GOM	NWAtl	A	15/04/2013	266	FL	28.7	-88.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-70	GBYP11	GOM	NWAtl	A	15/04/2011	251	FL	24.2	-83.0	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-176	GBYP11	GOM	NWAtl	A	15/04/2014	205	FL	28.1	-85.9	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-119	GBYP12	GOM	NWAtl	A	15/04/2010	247	FL	27.7	-87.8	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-118	GBYP12	GOM	NWAtl	A	15/04/2010	249	FL	26.7	-89.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-101	GBYP12	GOM	NWAtl	A	15/04/2010	255	FL	27.7	-90.2	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-122	GBYP12	GOM	NWAtl	A	15/05/2010	240	FL	27.2	-88.6	F	FEW TAGS	FILTERED	FILTERED	-	-	NO
NOAA-GM-L-169	GBYP12	GOM	NWAtl	A	15/05/2013	225	FL	27.0	-90.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-64	GBYP12	GOM	NWAtl	A	15/05/2011	245	FL	27.3	-89.7	M	INCLUDED	INCLUDED	INCLUDED	0.543	MED-like	NO
NOAA-GM-L-81	GBYP12	GOM	NWAtl	A	15/05/2010	262	FL	26.2	-90.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-126	GBYP12	GOM	NWAtl	A	15/04/2014	249	FL	27.0	-89.9	M	FILTERED	INCLUDED	INCLUDED	0.255	MED-like	NO
NOAA-GM-L-161	GBYP12	GOM	NWAtl	A	15/05/2013	224	FL	28.1	-89.3	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-62	GBYP13	GOM	NWAtl	A	15/05/2012	235	FL	27.7	-87.2	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-175	GBYP13	GOM	NWAtl	A	15/06/2014	225	FL	27.7	-87.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-33	GBYP13	GOM	NWAtl	A	15/03/2012	233	FL	28.0	-86.8	M	INCLUDED	INCLUDED	INCLUDED	0.031	NO	NO
NOAA-GM-L-113	GBYP13	GOM	NWAtl	A	15/03/2010	248	FL	27.5	-87.9	M	INCLUDED	INCLUDED	INCLUDED	0.522	MED-like	NO
NOAA-GM-L-154	GBYP14	GOM	NWAtl	A	15/05/2014	213	FL	26.7	-91.4	M	FEW TAGS	FILTERED	FILTERED	-	-	NO
NOAA-GM-L-26	GBYP14	GOM	NWAtl	A	15/04/2013	275	FL	27.9	-89.1	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-112	GBYP14	GOM	NWAtl	A	15/03/2010	265	FL	26.7	-89.5	M	FILTERED	FILTERED	FILTERED	-	-	NO

NOAA-GM-L-110	GBYP14	GOM	NWAtl	A	15/03/2010	240	FL	26.6	-89.4	F	FILTERED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-168	GBYP14	GOM	NWAtl	A	15/03/2013	248	FL	26.6	-89.5	M	FILTERED	FILTERED	FILTERED	-	-	NO
NOAA-GM-L-40	GBYP15	GOM	NWAtl	A	15/04/2012	257	FL	27.8	-88.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-39	GBYP15	GOM	NWAtl	A	15/04/2012	221	FL	28.0	-88.2	M	INCLUDED	INCLUDED	INCLUDED	0.007	NO	NO
NOAA-GM-L-58	GBYP15	GOM	NWAtl	A	15/05/2012	225	FL	27.9	-86.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-139	GBYP15	GOM	NWAtl	A	15/05/2014	253	FL	27.5	-91.3	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-63	GBYP15	GOM	NWAtl	A	15/05/2012	204	FL	27.8	-86.8	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-31	GBYP15	GOM	NWAtl	A	15/05/2013	224	FL	27.5	-90.1	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-54	GBYP15	GOM	NWAtl	A	15/05/2012	263	FL	27.8	-88.8	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-27	GBYP15	GOM	NWAtl	A	15/03/2013	248	FL	27.7	-89.6	M	FILTERED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-173	GBYP15	GOM	NWAtl	A	15/04/2014	218	FL	24.5	-84.2	F	FILTERED	INCLUDED	FILTERED	-	-	NO
NOAA-GM-L-10	GBYP15	GOM	NWAtl	A	15/05/2013	235	FL	27.5	-90.0	M	FILTERED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-41	GBYP15	GOM	NWAtl	A	15/04/2012	255	FL	27.9	-86.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-138	GBYP16	GOM	NWAtl	A	15/05/2014	225	FL	27.4	-92.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-133	GBYP16	GOM	NWAtl	A	15/06/2014	276	FL	27.6	-89.9	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-5	GBYP16	GOM	NWAtl	A	15/06/2013	235	FL	28.0	-89.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-152	GBYP16	GOM	NWAtl	A	15/05/2014	252	FL	27.2	-89.4	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-97	GBYP16	GOM	NWAtl	A	15/04/2010	239	FL	27.2	-91.5	M	INCLUDED	INCLUDED	INCLUDED	0.248	MED-like	NO
NOAA-GM-L-100	GBYP16	GOM	NWAtl	A	15/04/2010	261	FL	27.3	-88.8	M	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-69	ACEITU-01	GOM	NWAtl	L	15/06/2008	-	-	28.0	-89.1	NA	FEW TAGS	FEW TAGS	FEW TAGS	-	-	NO
TAMU-GM-V-72	ACEITU-01	GOM	NWAtl	L	15/06/2008	-	-	28.0	-90.4	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-73	ACEITU-01	GOM	NWAtl	L	15/06/2008	-	-	28.0	-91.5	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-75	ACEITU-01	GOM	NWAtl	L	15/06/2008	-	-	28.0	-89.1	NA	FEW TAGS	FILTERED	FILTERED	-	-	NO
AZTI-GM-V-56	REMAS-04	GOM	NWAtl	L	19/05/2010	-	-	27.0	-94.0	NA	FEW TAGS	FILTERED	FILTERED	-	-	NO
AZTI-GM-V-74	REMAS-04	GOM	NWAtl	L	14/05/2010	-	-	27.7	-89.0	NA	FEW TAGS	FEW TAGS	FEW TAGS	-	-	NO
AZTI-GM-V-71	REMAS-04	GOM	NWAtl	L	14/05/2010	-	-	27.7	-89.0	NA	FEW TAGS	FILTERED	FILTERED	-	-	NO
AZTI-GM-V-75	REMAS-04	GOM	NWAtl	L	14/05/2010	-	-	27.7	-89.0	NA	FEW TAGS	FEW TAGS	FEW TAGS	-	-	NO
TAMU-GM-V-78	ACEITU-01	GOM	NWAtl	L	15/06/2008	-	-	28.0	-89.1	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
AZTI-GM-V-78	REMAS-04	GOM	NWAtl	L	17/05/2010	-	-	26.8	-96.0	NA	FILTERED	INCLUDED	INCLUDED	0	NO	NO

AZTI-GM-V-76	REMAS-04	GOM	NWAtl	L	14/05/2010	-	-	28.1	-90.5	NA	FEW TAGS	FEW TAGS	FEW TAGS	-	-	NO
AZTI-GM-V-81	REMAS-04	GOM	NWAtl	L	17/05/2010	-	-	26.8	-96.0	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
AZTI-GM-V-80	REMAS-04	GOM	NWAtl	L	17/05/2010	-	-	26.8	-96.0	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
AZTI-GM-V-51	REMAS-04	GOM	NWAtl	L	14/05/2010	-	-	28.1	-90.5	NA	FILTERED	INCLUDED	INCLUDED	0	NO	NO
AZTI-GM-V-77	REMAS-04	GOM	NWAtl	L	17/05/2010	-	-	26.8	-96.0	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-80	ACEITU-01	GOM	NWAtl	L	15/06/2009	-	-	26.0	-88.9	NA	FILTERED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-86	ACEITU-01	GOM	NWAtl	L	15/06/2009	-	-	27.5	-91.1	NA	FILTERED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-87	ACEITU-01	GOM	NWAtl	L	15/06/2009	-	-	26.0	-91.1	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-54	ACEITU-02	GOM	NWAtl	L	15/06/2007	-	-	28.0	-89.8	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-55	ACEITU-02	GOM	NWAtl	L	15/06/2007	-	-	27.0	-89.9	NA	FILTERED	INCLUDED	FILTERED	-	-	NO
TAMU-GM-V-57	ACEITU-02	GOM	NWAtl	L	15/06/2007	-	-	27.0	-90.5	NA	FEW TAGS	FILTERED	FILTERED	-	-	NO
TAMU-GM-V-61	ACEITU-02	GOM	NWAtl	L	15/06/2008	-	-	27.0	-88.8	NA	FEW TAGS	FEW TAGS	FEW TAGS	-	-	NO
TAMU-GM-V-62	ACEITU-02	GOM	NWAtl	L	15/06/2008	-	-	27.0	-88.8	NA	FEW TAGS	FEW TAGS	FEW TAGS	-	-	NO
TAMU-GM-V-64	ACEITU-02	GOM	NWAtl	L	15/06/2008	-	-	28.0	-89.1	NA	FILTERED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-67	ACEITU-02	GOM	NWAtl	L	15/06/2008	-	-	28.0	-89.1	NA	FEW TAGS	FILTERED	FILTERED	-	-	NO
TAMU-GM-V-68	ACEITU-02	GOM	NWAtl	L	15/06/2008	-	-	28.0	-89.1	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
AZTI-GM-0-24	ACEITU-04	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-29	ACEITU-04	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-30	ACEITU-05	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-32	ACEITU-05	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-33	ACEITU-05	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-41	ACEITU-03	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_30	GBYP-18	SS	SlopeSea	L	20/06/2016	-	-	37.0	-73.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_19	GBYP-18	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.5	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_25	GBYP-18	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.7	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_23	GBYP-18	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.7	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_41	GBYP-18	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_55	GBYP-18	SS	SlopeSea	L	02/07/2016	-	-	37.3	-72.9	N/A	FEW TAGS	FILTERED	FILTERED	*	-	NO
SlopeSea_20	GBYP-18	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.5	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO

SlopeSea_34	GBYP-18	SS	SlopeSea	L	08/07/2016	-	-	38.9	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_53	GBYP-18	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_37	GBYP-18	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_43	GBYP-18	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_35	GBYP-18	SS	SlopeSea	L	08/07/2016	-	-	38.9	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_17	GBYP-19	SS	SlopeSea	L	19/06/2016	-	-	37.8	-72.6	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_31	GBYP-19	SS	SlopeSea	L	20/06/2016	-	-	37.0	-73.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_32	GBYP-19	SS	SlopeSea	L	20/06/2016	-	-	37.0	-73.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_18	GBYP-19	SS	SlopeSea	L	19/06/2016	-	-	37.5	-73.1	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_46	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_27	GBYP-19	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.7	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_42	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_47	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_22	GBYP-19	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.7	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_21	GBYP-19	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.7	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_54	GBYP-19	SS	SlopeSea	L	02/07/2016	-	-	37.3	-72.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_26	GBYP-19	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.7	N/A	FILTERED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_51	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_40	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_52	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_38	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_15	MESOPE03	SS	SlopeSea	L	18/06/2016	-	-	38.2	-71.4	N/A	FEW TAGS	FILTERED	FILTERED	*	-	NO
SlopeSea_16	MESOPE03	SS	SlopeSea	L	19/06/2016	-	-	37.8	-72.6	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-137	GBYP13	MED	WMed	A	31/05/2015	214	CFL	39.2	8.3	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-136	GBYP13	MED	Wmed	A	31/05/2015	243	CFL	39.2	8.3	F	FILTERED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-134	GBYP13	MED	WMed	A	31/05/2015	247	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-138	GBYP14	MED	WMed	A	31/05/2015	213	CFL	39.2	8.3	M	FILTERED	INCLUDED	FILTERED	*	-	NO
UNIC-SA-L-135	GBYP14	MED	WMed	A	31/05/2015	215	CFL	39.2	8.3	F	FILTERED	FILTERED	FILTERED	*	-	NO
UNIC-SA-L-139	GBYP14	MED	WMed	A	31/05/2015	235	CFL	39.2	8.3	M	FILTERED	INCLUDED	INCLUDED	*	-	NO

UNIC-SA-L-1	GBYP15	MED	WMed	A	21/05/2011	231	CFL	39.2	8.3	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-74	GBYP15	MED	WMed	A	21/06/2012	205	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-40	GBYP15	MED	WMed	A	17/06/2011	181	CFL	39.2	8.4	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-104	GBYP16	MED	WMed	A	21/06/2012	209	CFL	39.2	8.3	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-105	GBYP16	MED	Wmed	A	21/06/2012	209	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-33	GBYP17	MED	WMed	A	17/06/2011	226	CFL	39.2	8.4	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-17	GBYP17	MED	WMed	A	04/06/2011	180	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-78	GBYP17	MED	WMed	A	21/06/2012	198	CFL	39.2	8.3	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-14	GBYP17	MED	WMed	A	04/06/2011	222	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-39	GBYP17	MED	WMed	A	17/06/2011	199	CFL	39.2	8.4	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-2	GBYP17	MED	WMed	A	21/05/2011	193	CFL	39.2	8.3	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-127	GBYP17	MED	Wmed	A	14/06/2013	203	CFL	39.2	8.3	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-131	GBYP17	MED	Wmed	A	14/06/2013	225	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-130	GBYP17	MED	Wmed	A	14/06/2013	225	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-28	ACEITU-01	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-5	ACEITU-01	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-6	ACEITU-01	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-BA-V-90	ACEITU-06	MED	WMed	L	01/07/2013	-	-	38.7	3.0	NA	FEW TAGS	FEW TAGS	FEW TAGS	*	-	NO
IEO-BA-V-91	ACEITU-06	MED	WMed	L	01/07/2013	-	-	38.7	3.0	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-BA-V-88	ACEITU-06	MED	WMed	L	01/07/2013	-	-	38.7	3.0	NA	FEW TAGS	FEW TAGS	FEW TAGS	*	-	NO
IEO-BA-V-92	ACEITU-06	MED	WMed	L	01/07/2013	-	-	38.7	3.0	NA	FEW TAGS	FEW TAGS	FEW TAGS	*	-	NO
IEO-BA-V-94	ACEITU-06	MED	WMed	L	01/07/2013	-	-	38.7	3.0	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-BA-V-73	ACEITU-06	MED	WMed	L	13/07/2013	-	-	38.8	4.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-29	ACEITU-01	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-93	ACEITU-07	MED	WMed	L	01/07/2013	-	-	38.7	3.0	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-BA-V-77	ACEITU-07	MED	WMed	L	07/07/2013	-	-	38.8	0.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-59	ACEITU-07	MED	WMed	L	13/07/2013	-	-	38.8	4.3	NA	FILTERED	FILTERED	FILTERED	*	-	NO
IEO-BA-V-74	ACEITU-07	MED	WMed	L	07/07/2013	-	-	38.8	0.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-76	ACEITU-07	MED	WMed	L	07/07/2013	-	-	38.8	0.7	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO

IEO-BA-V-89	ACEITU-07	MED	WMed	L	01/07/2013	-	-	38.7	3.0	NA	FILTERED	FILTERED	FILTERED	*	-	NO
IEO-BA-V-60	ACEITU-07	MED	WMed	L	13/07/2013	-	-	38.8	4.3	NA	FILTERED	FILTERED	FILTERED	*	-	NO
IEO-BA-V-62	ACEITU-07	MED	WMed	L	13/07/2013	-	-	38.8	4.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-58	ACEITU-08	MED	WMed	L	13/07/2013	-	-	38.8	4.3	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-44	ACEITU-08	MED	WMed	L	01/07/2013	-	-	38.8	3.0	NA	FEW TAGS	FILTERED	FILTERED	*	-	NO
IEO-BA-V-46	ACEITU-08	MED	WMed	L	01/07/2013	-	-	38.8	3.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-30	ACEITU-01	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-22	ACEITU-02	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-23	ACEITU-02	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-24	ACEITU-02	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-25	ACEITU-02	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-31	ACEITU-01	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-7	ACEITU-02	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-10	ACEITU-02	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-11	ACEITU-02	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-14	ACEITU-02	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-32	ACEITU-01	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-1	ACEITU-01	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-2	ACEITU-01	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-3	ACEITU-01	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-4	ACEITU-01	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-92	ACEITU-04	MED	WMed	Y	15/09/2013	30	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-93	ACEITU-04	MED	WMed	Y	15/09/2013	28.9	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-99	ACEITU-04	MED	WMed	Y	21/09/2013	29.4	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-100	ACEITU-04	MED	WMed	Y	21/09/2013	27.6	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-107	ACEITU-05	MED	WMed	Y	12/10/2013	31.7	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-109	ACEITU-05	MED	WMed	Y	13/10/2013	32.7	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-110	ACEITU-05	MED	WMed	Y	17/10/2013	29.3	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-143	ACEITU-05	MED	WMed	Y	15/09/2013	28.7	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO

IEO-BA-0-63	ACEITU-06	MED	WMed	Y	15/09/2012	26	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-59	ACEITU-06	MED	WMed	Y	05/05/2012	48	FL	39.7	3.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-77	ACEITU-06	MED	WMed	Y	16/09/2012	25.1	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-BA-0-72	ACEITU-06	MED	WMed	Y	07/10/2012	-	-	40.9	1.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-69	ACEITU-06	MED	WMed	Y	16/09/2012	28.5	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-67	ACEITU-07	MED	WMed	Y	16/09/2012	25.7	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-66	ACEITU-07	MED	WMed	Y	16/09/2012	28.1	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-BA-0-68	ACEITU-07	MED	WMed	Y	07/10/2012	-	-	40.9	1.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-76	ACEITU-07	MED	WMed	Y	16/09/2012	35.2	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-71	ACEITU-07	MED	WMed	Y	16/09/2012	23.8	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-64	ACEITU-07	MED	WMed	Y	15/09/2012	27.1	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-61	ACEITU-07	MED	WMed	Y	15/09/2012	26.4	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-75	ACEITU-07	MED	WMed	Y	16/09/2012	36.1	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-BA-0-54	ACEITU-07	MED	WMed	Y	07/10/2012	-	-	40.9	1.1	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-60	ACEITU-08	MED	WMed	Y	15/09/2012	26	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-79	ACEITU-08	MED	WMed	Y	16/09/2012	27.5	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-65	ACEITU-08	MED	WMed	Y	15/09/2012	27.2	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-BA-0-56	ACEITU-08	MED	WMed	Y	07/10/2012	-	-	40.9	1.1	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-BA-0-69	ACEITU-08	MED	WMed	Y	07/10/2012	-	-	40.9	1.1	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-BA-0-71	ACEITU-08	MED	WMed	Y	07/10/2012	-	-	40.8	1.1	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-91	ACEITU-03	MED	WMed	Y	15/09/2013	28	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-102	ACEITU-03	MED	WMed	Y	21/09/2013	28.5	FL	39.3	0.0	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-120	ACEITU-03	MED	WMed	Y	28/10/2013	30.2	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-101	ACEITU-03	MED	WMed	Y	21/09/2013	25.5	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-103	ACEITU-03	MED	WMed	Y	22/09/2013	27.6	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-104	ACEITU-03	MED	WMed	Y	22/09/2013	29.6	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-106	ACEITU-03	MED	WMed	Y	12/10/2013	32.8	FL	39.3	0.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-SY-L-165	GBYP16	MED	CMed	A	05/06/2015	166	CFL	33.5	13.5	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-L-76	GBYP17	MED	CMed	A	10/06/2011	231	CFL	35.5	14.0	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO

FMAP-MA-L-72	GBYP17	MED	CMed	A	10/06/2011	230	CFL	35.5	14.0	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-47	ACEITU-03	MED	CMed	L	15/07/2008	0.069	TL	36.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-71	ACEITU-03	MED	CMed	L	15/07/2008	0.064	TL	36.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-SI-V-78	ACEITU-03	MED	CMed	L	15/07/2008	0.063	TL	36.7	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-3	ACEITU-04	MED	CMed	Y	10/09/2013	19.4	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-15	ACEITU-04	MED	CMed	Y	23/09/2013	23.3	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-13	ACEITU-08	MED	CMed	Y	03/10/2012	31	FL	37.9	15.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIB-SI-0-33	ACEITU-08	MED	CMed	Y	05/10/2012	36	FL	37.6	15.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-160	GBYP16	MED	EMed	A	05/06/2015	244	FL	35.6	35.2	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-171	GBYP16	MED	EMed	A	05/06/2015	243	FL	35.6	35.2	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-193	GBYP16	MED	EMed	A	28/05/2015	231	FL	36.3	31.5	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
ISTA-LS-L-201	GBYP17	MED	EMed	A	28/05/2015	198	FL	36.3	31.5	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-46	ACEITU-08	MED	EMed	L	24/06/2011	1.2	FL	36.1	33.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-49	ACEITU-08	MED	EMed	L	24/06/2011	1.2	FL	36.1	33.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-19	ACEITU-01	MED	EMed	L	23/06/2011	1.04	FL	36.1	33.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-52	ACEITU-01	MED	EMed	L	24/06/2011	1.03	FL	36.1	33.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-55	ACEITU-01	MED	EMed	L	24/06/2011	1.25	FL	36.1	33.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-V-62	ACEITU-02	MED	EMed	L	24/06/2011	0.58	FL	36.1	33.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-315	ACEITU-04	MED	EMed	Y	15/08/2013	21.6	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-393	ACEITU-05	MED	EMed	Y	16/08/2013	26.7	FL	35.3	33.3	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-377	ACEITU-02	MED	EMed	Y	27/07/2013	18.2	FL	36.2	33.9	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
NOAA-GM-L-155	GBYP11	GOM	NWAtl	A	15/05/2014	223	FL	27.1	-91.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-156	GBYP11	GOM	NWAtl	A	15/05/2014	233	FL	27.1	-91.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-121	GBYP12	GOM	NWAtl	A	15/05/2010	235	FL	27.0	-88.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-28	GBYP13	GOM	NWAtl	A	15/03/2013	255	FL	27.1	-90.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-1	GBYP15	GOM	NWAtl	A	15/05/2013	248	FL	27.0	-90.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-146	GBYP15	GOM	NWAtl	A	15/04/2014	235	FL	26.3	-90.8	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
NOAA-GM-L-53	GBYP16	GOM	NWAtl	A	15/05/2012	251	FL	27.8	-86.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-74	ACEITU-01	GOM	NWAtl	L	15/06/2008	-	-	28.0	-91.5	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO

TAMU-GM-V-81	ACEITU-01	GOM	NWAtl	L	15/06/2009	-	-	26.0	-88.9	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-82	ACEITU-01	GOM	NWAtl	L	15/06/2009	-	-	26.0	-88.9	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-83	ACEITU-01	GOM	NWAtl	L	15/06/2008	-	-	26.0	-88.9	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-84	ACEITU-01	GOM	NWAtl	L	15/06/2009	-	-	26.0	-88.9	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-85	ACEITU-01	GOM	NWAtl	L	15/06/2009	-	-	27.5	-91.1	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-53	ACEITU-02	GOM	NWAtl	L	15/06/2007	-	-	28.0	-89.8	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-56	ACEITU-02	GOM	NWAtl	L	15/06/2007	-	-	27.0	-90.5	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-58	ACEITU-02	GOM	NWAtl	L	15/06/2007	-	-	27.0	-90.5	NA	INCLUDED	INCLUDED	INCLUDED	0.023	NO	NO
TAMU-GM-V-59	ACEITU-02	GOM	NWAtl	L	15/06/2007	-	-	27.0	-90.5	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-60	ACEITU-02	GOM	NWAtl	L	15/06/2007	-	-	27.0	-90.5	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
TAMU-GM-V-63	ACEITU-02	GOM	NWAtl	L	15/06/2008	-	-	27.0	-87.5	NA	INCLUDED	INCLUDED	INCLUDED	0	NO	NO
AZTI-GM-0-6	ACEITU-04	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-20	ACEITU-04	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-25	ACEITU-04	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-43	ACEITU-05	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-45	ACEITU-05	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-5	ACEITU-03	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-GM-0-42	ACEITU-03	SS	SlopeSea	Y	13/09/2008	-	-	36.4	-74.8	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_24	GBYP-18	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.7	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_36	GBYP-18	SS	SlopeSea	L	08/07/2016	-	-	38.9	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_33	GBYP-18	SS	SlopeSea	L	20/06/2016	-	-	37.0	-73.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_44	GBYP-18	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_28	GBYP-19	SS	SlopeSea	L	19/06/2016	-	-	37.0	-73.7	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_48	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_45	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_50	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-132	GBYP13	MED	Wmed	A	31/05/2015	211	CFL	39.2	8.3	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-103	GBYP17	MED	WMed	A	21/06/2012	222	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO
UNIC-SA-L-100	GBYP17	MED	WMed	A	21/06/2012	191	CFL	39.2	8.3	M	INCLUDED	INCLUDED	INCLUDED	*	-	NO

UNIC-SA-L-102	GBYP17	MED	WMed	A	21/06/2012	192	CFL	39.2	8.3	F	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-75	ACEITU-07	MED	WMed	L	07/07/2013	-	-	38.8	0.7	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-43	ACEITU-08	MED	WMed	L	01/07/2013	-	-	38.8	3.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-26	ACEITU-02	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-27	ACEITU-02	MED	WMed	L	13/07/2012	-	-	38.8	2.6	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-V-9	ACEITU-02	MED	WMed	L	26/06/2012	-	-	38.7	1.2	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
IEO-BA-0-142	ACEITU-05	MED	WMed	Y	15/09/2013	27.5	FL	39.3	0.0	NA	FILTERED	INCLUDED	INCLUDED	*	-	NO
AZTI-BA-0-70	ACEITU-06	MED	WMed	Y	07/10/2012	-	-	40.8	1.1	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
AZTI-BA-0-52	ACEITU-08	MED	WMed	Y	07/10/2012	-	-	40.9	1.1	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
FMAP-MA-0-11	ACEITU-04	MED	CMed	Y	23/09/2013	26.6	FL	35.5	14.0	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
CYPR-LS-0-321	ACEITU-04	MED	EMed	Y	16/08/2013	24.3	FL	36.2	33.9	NA	INCLUDED	INCLUDED	INCLUDED	*	-	NO
SlopeSea_39	GBYP-19	SS	SlopeSea	L	08/07/2016	-	-	39.0	-67.9	N/A	INCLUDED	INCLUDED	INCLUDED	*	-	NO
NOAA-GM-L-144	GBYP10	GOM	NWAtl	A	15/05/2014	223	FL	27.3	-92.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-96	GBYP10	GOM	NWAtl	A	15/04/2010	238	FL	27.2	-92.5	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-51	GBYP10	GOM	NWAtl	A	15/05/2012	233	FL	27.9	-86.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-46	GBYP11	GOM	NWAtl	A	15/04/2012	268	FL	27.9	-86.2	M	INCLUDED	INCLUDED	INCLUDED	0.218	MED-like	YES
NOAA-GM-L-21	GBYP11	GOM	NWAtl	A	15/05/2013	226	FL	27.9	-86.4	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-143	GBYP11	GOM	NWAtl	A	15/05/2014	211	FL	27.5	-91.2	F	FEW TAGS	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-18	GBYP11	GOM	NWAtl	A	15/05/2013	228	FL	27.6	-86.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-71	GBYP11	GOM	NWAtl	A	15/04/2011	232	FL	24.4	-84.5	M	INCLUDED	INCLUDED	INCLUDED	0.003	NO	YES
NOAA-GM-L-6	GBYP11	GOM	NWAtl	A	15/04/2013	235	FL	28.0	-89.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-80	GBYP11	GOM	NWAtl	A	15/04/2010	261	FL	26.1	-91.2	F	FILTERED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-117	GBYP12	GOM	NWAtl	A	15/04/2010	248	FL	26.1	-92.2	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-115	GBYP12	GOM	NWAtl	A	15/04/2010	251	FL	27.1	-89.8	F	FILTERED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-114	GBYP12	GOM	NWAtl	A	15/04/2010	230	FL	26.8	-93.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-120	GBYP12	GOM	NWAtl	A	15/04/2010	272	FL	27.7	-87.7	M	FILTERED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-129	GBYP12	GOM	NWAtl	A	15/04/2014	219	FL	27.7	-90.0	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-179	GBYP12	GOM	NWAtl	A	15/05/2014	268	FL	27.4	-91.2	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-180	GBYP12	GOM	NWAtl	A	15/05/2014	228	FL	27.4	-92.0	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES

NOAA-GM-L-125	GBYP12	GOM	NWAtl	A	15/05/2010	219	FL	26.8	-88.7	F	FILTERED	INCLUDED	FILTERED	-	-	YES
NOAA-GM-L-167	GBYP12	GOM	NWAtl	A	15/05/2013	232	FL	27.0	-90.4	F	FILTERED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-181	GBYP13	GOM	NWAtl	A	15/06/2014	213	FL	27.6	-87.6	F	INCLUDED	INCLUDED	INCLUDED	0.001	NO	YES
NOAA-GM-L-11	GBYP13	GOM	NWAtl	A	15/01/2013	224	FL	26.5	-90.1	M	FILTERED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-131	GBYP13	GOM	NWAtl	A	15/06/2014	235	FL	27.5	-90.1	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-109	GBYP13	GOM	NWAtl	A	15/03/2010	246	FL	27.7	-86.8	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-34	GBYP13	GOM	NWAtl	A	15/03/2012	238	FL	26.7	-88.8	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-98	GBYP13	GOM	NWAtl	A	15/03/2010	244	FL	27.3	-91.9	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-23	GBYP13	GOM	NWAtl	A	15/06/2013	250	FL	27.6	-86.7	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-107	GBYP14	GOM	NWAtl	A	15/03/2010	225	FL	27.3	-92.0	M	INCLUDED	INCLUDED	INCLUDED	0.011	NO	YES
NOAA-GM-L-72	GBYP15	GOM	NWAtl	A	15/04/2011	236	FL	25.2	-85.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-32	GBYP15	GOM	NWAtl	A	15/03/2012	225	FL	27.9	-86.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-44	GBYP15	GOM	NWAtl	A	15/04/2012	241	FL	27.9	-86.1	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-159	GBYP15	GOM	NWAtl	A	15/06/2013	213	FL	27.4	-86.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-158	GBYP15	GOM	NWAtl	A	15/05/2014	227	FL	27.3	-91.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-17	GBYP15	GOM	NWAtl	A	15/05/2013	231	FL	27.6	-86.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-16	GBYP15	GOM	NWAtl	A	15/05/2013	240	FL	27.6	-86.6	M	FEW TAGS	FILTERED	FILTERED	-	-	YES
NOAA-GM-L-60	GBYP15	GOM	NWAtl	A	15/05/2012	248	FL	27.1	-88.9	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-73	GBYP16	GOM	NWAtl	A	15/03/2010	232	FL	27.1	-87.9	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-130	GBYP16	GOM	NWAtl	A	15/06/2014	217	FL	27.5	-90.1	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-57	GBYP16	GOM	NWAtl	A	15/06/2012	243	FL	27.3	-89.4	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-160	GBYP16	GOM	NWAtl	A	15/06/2013	204	FL	27.9	-86.2	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-99	GBYP16	GOM	NWAtl	A	15/04/2010	213	FL	27.1	-89.7	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-79	GBYP10	GOM	NWAtl	A	15/04/2010	276	FL	27.5	-87.6	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-134	GBYP10	GOM	NWAtl	A	15/04/2014	234	FL	26.7	-90.2	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-127	GBYP10	GOM	NWAtl	A	15/04/2014	269	FL	27.2	-90.8	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-171	GBYP10	GOM	NWAtl	A	15/05/2013	251	FL	27.5	-90.3	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-69	GBYP11	GOM	NWAtl	A	15/04/2011	270	FL	24.2	-82.8	M	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-67	GBYP12	GOM	NWAtl	A	15/05/2011	232	FL	25.7	-84.6	M	INCLUDED	INCLUDED	INCLUDED	0.645	MED-like	YES

NOAA-GM-L-91	GBYP12	GOM	NWAtl	A	15/05/2010	246	FL	27.4	-89.0	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES
NOAA-GM-L-157	GBYP16	GOM	NWAtl	A	15/05/2014	240	FL	27.2	-91.5	F	INCLUDED	INCLUDED	INCLUDED	0	NO	YES

Table S2. List of the 173 ABFT adult samples captured in the Gulf of Mexico included in this study and available details about capture dates and coordinates, size indicated in cm as fork length (FL), sex, leading gamete stage, post ovulatory follicle state and reproductive phase when data were available following the standardized terminology described in (Brown-Peterson et al. 2011). Probability for each individual captured in the Gulf of Mexico of fitting within the Mediterranean Sea distribution of ancestry values inferred using ADMIXTURE when assuming K=2 ancestral populations, and those with a probability higher than 0.05 were labelled as "MED-like".

SampleID	Catch Date [dd/mm/yy]	Length (cm)	Length Type	Lat.	Long.	Sex	Leading Gamete Stage	Post Ovulatory Follicle State	Reproductive Phase	RAD-COI-introgressed	Prob (MED-like)	MED-like
NOAA-GM-L-7	15/04/2013	233	FL	27.2	-90.7	F	V3	P0	Spawning capable	NO	-	-
NOAA-GM-L-43	15/04/2012	234	FL	27.8	-86.4	M	SZ	-	Spawning capable	NO	-	-
NOAA-GM-L-143	15/05/2014	211	FL	27.5	-91.2	F	V3	P2	Regressing	NO	-	-
NOAA-GM-L-105	15/04/2010	223	FL	27.4	-91.6	F	V3	P1	Spawning capable	NO	-	-
NOAA-GM-L-122	15/05/2010	240	FL	27.2	-88.6	M	SZ	-	Spawning capable	NO	-	-
NOAA-GM-L-125	15/05/2010	219	FL	26.8	-88.7	F	V3	P2	Spawning capable	NO	-	-
NOAA-GM-L-145	15/05/2014	210	FL	27.4	-92.3	F	LC	P2	Actively Spawning (sub-phase)	NO	-	-
NOAA-GM-L-132	15/06/2014	250	FL	27.6	-89.9	M	SZ	-	Spawning capable	NO	-	-
NOAA-GM-L-170	15/03/2013	228	FL	26.5	-90.5	F	V3	P0	Spawning capable	NO	-	-
NOAA-GM-L-108	15/03/2010	233	FL	27.3	-92.0	-	-	-	-	NO	-	-
NOAA-GM-L-154	15/05/2014	213	FL	26.7	-91.4	M	SZ	-	Spawning capable	NO	-	-
NOAA-GM-L-136	15/04/2014	266	FL	27.5	-89.6	M	SZ	-	Spawning capable	NO	-	-
NOAA-GM-L-165	15/03/2013	227	FL	27.8	-89.8	F	V2	P0	Developing	NO	-	-
NOAA-GM-L-141	15/06/2014	199	FL	28.0	-88.9	F	GVBD	P0	Actively Spawning (sub-phase)	NO	-	-
NOAA-GM-L-112	15/03/2010	265	FL	26.7	-89.5	M	SZ	-	Spawning capable	NO	-	-
NOAA-GM-L-147	15/01/2014	235	FL	26.3	-90.8	M	-	-	0	NO	-	-
NOAA-GM-L-168	15/03/2013	248	FL	26.6	-89.5	M	SZ	-	Spawning capable	NO	-	-
NOAA-GM-L-14	15/04/2013	231	FL	28.3	-88.3	F	V3	P0	Spawning capable	NO	-	-
NOAA-GM-L-16	15/05/2013	240	FL	27.6	-86.6	M	SZ	-	Spawning capable	NO	-	-
NOAA-GM-L-173	15/04/2014	218	FL	24.5	-84.2	-	-	-	-	NO	-	-
NOAA-GM-L-50	15/05/2012	243	FL	27.8	-87.2	M	SZ	-	Spawning capable	NO	0.830	MED-like
NOAA-GM-L-67	15/05/2011	232	FL	25.7	-84.6	M	SZ	-	Spawning capable	NO	0.645	MED-like

NOAA-GM-L-64	15/05/2011	245	FL	27.3	-89.7	M	SZ	-	Spawning capable	NO	0.543	MED-like
NOAA-GM-L-113	15/03/2010	248	FL	27.5	-87.9	M	SZ	-	Spawning capable	YES	0.522	MED-like
NOAA-GM-L-104	15/04/2010	242	FL	27.3	-88.8	M	SZ	-	Spawning capable	NO	0.518	MED-like
NOAA-GM-L-148	15/04/2014	225	FL	27.2	-87.8	M	SZ	-	Spawning capable	NO	0.425	MED-like
NOAA-GM-L-153	15/05/2014	210	FL	26.4	-89.1	M	SZ	-	Spawning capable	NO	0.385	MED-like
NOAA-GM-L-74	15/03/2010	252	FL	27.2	-87.6	M	SZ	-	Spawning capable	NO	0.341	MED-like
NOAA-GM-L-66	15/05/2011	252	FL	27.4	-89.5	F	V3	P2	Spawning capable	NO	0.338	MED-like
NOAA-GM-L-126	15/04/2014	249	FL	27.0	-89.9	M	SZ	-	Spawning capable	NO	0.255	MED-like
NOAA-GM-L-97	15/04/2010	239	FL	27.2	-91.5	M	SZ	-	Spawning capable	NO	0.248	MED-like
NOAA-GM-L-46	15/04/2012	268	FL	27.9	-86.2	M	SZ	-	Spawning capable	NO	0.218	MED-like
NOAA-GM-L-89	15/04/2010	262	FL	27.6	-88.9	F	V2	P0	Developing	NO	0.049	NO
NOAA-GM-L-33	15/03/2012	233	FL	28.0	-86.8	M	SZ	-	Spawning capable	NO	0.031	NO
NOAA-GM-L-107	15/03/2010	225	FL	27.3	-92.0	-	-	-	-	NO	0.011	NO
NOAA-GM-L-39	15/04/2012	221	FL	28.0	-88.2	F	V3	P2	Spawning capable	NO	0.007	NO
NOAA-GM-L-93	15/04/2010	252	FL	27.2	-91.8	M	SZ	-	Spawning capable	NO	0.007	NO
NOAA-GM-L-95	15/04/2010	249	FL	27.6	-86.4	F	CA	P0	Developing	NO	0.004	NO
NOAA-GM-L-71	15/04/2011	232	FL	24.4	-84.5	M	SZ	-	Spawning capable	NO	0.003	NO
NOAA-GM-L-78	15/03/2010	262	FL	27.1	-87.1	M	SZ	-	Spawning capable	NO	0.001	NO
NOAA-GM-L-181	15/06/2014	213	FL	27.6	-87.6	F	V3	P2	Spawning capable	YES	0.001	NO
NOAA-GM-L-15	15/05/2013	194	FL	27.9	-86.5	F	V3	P1	Spawning capable	NO	0	NO
NOAA-GM-L-79	15/04/2010	276	FL	27.5	-87.6	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-61	15/05/2012	242	FL	26.9	-90.7	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-142	15/05/2014	238	FL	26.9	-90.0	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-111	15/04/2010	243	FL	27.1	-89.2	F	CA	P0	Developing	NO	0	NO
NOAA-GM-L-65	15/05/2011	262	FL	27.1	-89.7	F	V3	P3	Spawning capable	NO	0	NO
NOAA-GM-L-144	15/05/2014	223	FL	27.3	-92.5	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-47	15/05/2012	253	FL	27.8	-86.6	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-96	15/04/2010	238	FL	27.2	-92.5	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-88	15/05/2010	238	FL	27.4	-89.0	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-51	15/05/2012	233	FL	27.9	-86.4	F	GVM	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-92	15/04/2010	257	FL	27.5	-87.8	M	-	-	0	NO	0	NO
NOAA-GM-L-174	15/04/2014	218	FL	24.5	-84.2	-	-	-	-	NO	0	NO

NOAA-GM-L-134	15/04/2014	234	FL	26.7	-90.2	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-37	15/04/2012	283	FL	27.9	-86.3	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-127	15/04/2014	269	FL	27.2	-90.8	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-171	15/05/2013	251	FL	27.5	-90.3	F	GVM	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-150	15/05/2014	220	FL	28.0	-89.4	F	LC	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-2	15/05/2013	204	FL	26.8	-91.0	-	-	-	-	NO	0	NO
NOAA-GM-L-59	15/04/2012	259	FL	27.1	-89.0	F	V3	P0	Regressing	NO	0	NO
NOAA-GM-L-4	15/05/2013	245	FL	27.8	-90.1	-	-	-	-	NO	0	NO
NOAA-GM-L-56	15/05/2012	271	FL	27.8	-88.8	F	LC	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-3	15/05/2013	230	FL	27.8	-90.1	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-83	15/04/2010	249	FL	27.9	-87.1	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-86	15/05/2010	261	FL	27.1	-90.4	F	-	-	0	NO	0	NO
NOAA-GM-L-135	15/04/2014	221	FL	27.5	-91.5	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-163	15/05/2013	281	FL	28.0	-89.4	-	-	-	-	NO	0	NO
NOAA-GM-L-38	15/04/2012	241	FL	27.9	-86.3	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-21	15/05/2013	226	FL	27.9	-86.4	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-149	15/04/2014	228	FL	26.4	-90.9	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-140	15/05/2014	235	FL	27.6	-88.3	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-87	15/04/2010	238	FL	27.6	-90.7	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-85	15/04/2010	280	FL	27.1	-88.8	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-137	15/04/2014	225	FL	27.8	-89.6	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-18	15/05/2013	228	FL	27.6	-86.6	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-155	15/05/2014	223	FL	27.1	-91.7	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-48	15/05/2012	230	FL	26.6	-89.7	F	V3	P0	Regressing	NO	0	NO
NOAA-GM-L-12	15/04/2013	250	FL	28.7	-88.9	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-45	15/04/2012	234	FL	27.9	-86.3	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-69	15/04/2011	270	FL	24.2	-82.8	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-6	15/04/2013	235	FL	28.0	-89.5	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-9	15/05/2013	255	FL	27.0	-90.7	F	LC	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-151	15/05/2014	220	FL	28.0	-89.4	F	GVM	P0	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-156	15/05/2014	233	FL	27.1	-91.6	F	LC	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-80	15/04/2010	261	FL	26.1	-91.2	F	V3	P0	Spawning capable	NO	0	NO

NOAA-GM-L-52	15/05/2012	243	FL	27.8	-87.2	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-25	15/04/2013	266	FL	28.7	-88.5	F	V3	P0	Regressing	NO	0	NO
NOAA-GM-L-22	15/05/2013	244	FL	27.9	-86.4	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-8	15/05/2013	245	FL	27.0	-91.2	F	HYD	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-70	15/04/2011	251	FL	24.2	-83.0	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-82	15/04/2010	278	FL	26.0	-91.3	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-176	15/04/2014	205	FL	28.1	-85.9	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-117	15/04/2010	248	FL	26.1	-92.2	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-119	15/04/2010	247	FL	27.7	-87.8	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-118	15/04/2010	249	FL	26.7	-89.5	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-115	15/04/2010	251	FL	27.1	-89.8	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-114	15/04/2010	230	FL	26.8	-93.7	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-101	15/04/2010	255	FL	27.7	-90.2	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-120	15/04/2010	272	FL	27.7	-87.7	-	-	-	-	NO	0	NO
NOAA-GM-L-90	15/05/2010	220	FL	27.4	-89.0	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-123	15/05/2010	212	FL	27.3	-88.3	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-129	15/04/2014	219	FL	27.7	-90.0	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-169	15/05/2013	225	FL	27.0	-90.7	F	H	P3	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-94	15/05/2010	230	FL	27.1	-89.4	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-128	15/04/2014	227	FL	27.7	-89.7	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-162	15/05/2013	260	FL	28.0	-89.4	-	-	-	-	NO	0	NO
NOAA-GM-L-121	15/05/2010	235	FL	27.0	-88.7	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-124	15/05/2010	222	FL	26.7	-88.8	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-172	15/05/2013	259	FL	27.5	-90.2	F	HYD	P3	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-91	15/05/2010	246	FL	27.4	-89.0	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-81	15/05/2010	262	FL	26.2	-90.6	F	LC	P3	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-179	15/05/2014	268	FL	27.4	-91.2	F	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-180	15/05/2014	228	FL	27.4	-92.0	-	-	-	-	NO	0	NO
NOAA-GM-L-177	15/04/2014	246	FL	27.6	-87.7	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-178	15/05/2014	259	FL	27.7	-87.9	F	V	P0	Regressing	NO	0	NO
NOAA-GM-L-84	15/05/2010	239	FL	27.1	-90.4	M	-	-	0	NO	0	NO
NOAA-GM-L-161	15/05/2013	224	FL	28.1	-89.3	-	-	-	-	NO	0	NO

NOAA-GM-L-167	15/05/2013	232	FL	27.0	-90.4	F	GVM	P3	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-166	15/03/2013	232	FL	27.0	-90.4	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-28	15/03/2013	255	FL	27.1	-90.6	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-116	15/03/2010	249	FL	26.7	-89.3	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-62	15/05/2012	235	FL	27.7	-87.2	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-11	15/01/2013	224	FL	26.5	-90.1	M	SZ	-	Regressing	NO	0	NO
NOAA-GM-L-175	15/06/2014	225	FL	27.7	-87.6	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-131	15/06/2014	235	FL	27.5	-90.1	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-109	15/03/2010	246	FL	27.7	-86.8	F	CA	P0	Developing	NO	0	NO
NOAA-GM-L-34	15/03/2012	238	FL	26.7	-88.8	M	ST	-	Developing	NO	0	NO
NOAA-GM-L-102	15/03/2010	265	FL	27.0	-88.4	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-98	15/03/2010	244	FL	27.3	-91.9	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-23	15/06/2013	250	FL	27.6	-86.7	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-42	15/04/2012	273	FL	28.0	-86.1	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-103	15/04/2010	234	FL	27.2	-89.5	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-26	15/04/2013	275	FL	27.9	-89.1	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-110	15/03/2010	240	FL	26.6	-89.4	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-72	15/04/2011	236	FL	25.2	-85.7	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-40	15/04/2012	257	FL	27.8	-88.3	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-32	15/03/2012	225	FL	27.9	-86.3	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-36	15/04/2012	239	FL	27.9	-86.5	F	-	-	0	NO	0	NO
NOAA-GM-L-44	15/04/2012	241	FL	27.9	-86.1	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-159	15/06/2013	213	FL	27.4	-86.7	F	GVM	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-58	15/05/2012	225	FL	27.9	-86.3	-	-	-	-	NO	0	NO
NOAA-GM-L-139	15/05/2014	253	FL	27.5	-91.3	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-49	15/05/2012	234	FL	27.8	-86.6	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-158	15/05/2014	227	FL	27.3	-91.3	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-106	15/03/2010	262	FL	26.5	-89.1	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-1	15/05/2013	248	FL	27.0	-90.6	-	-	-	-	NO	0	NO
NOAA-GM-L-146	15/04/2014	235	FL	26.3	-90.8	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-63	15/05/2012	204	FL	27.8	-86.8	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-17	15/05/2013	231	FL	27.6	-86.6	F	V3	P0	Spawning capable	NO	0	NO

NOAA-GM-L-31	15/05/2013	224	FL	27.5	-90.1	-	-	-	-	NO	0	NO
NOAA-GM-L-54	15/05/2012	263	FL	27.8	-88.8	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-164	15/03/2013	227	FL	27.8	-89.8	-	-	-	-	NO	0	NO
NOAA-GM-L-27	15/03/2013	248	FL	27.7	-89.6	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-35	15/03/2012	265	FL	26.6	-89.1	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-60	15/05/2012	248	FL	27.1	-88.9	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-24	15/05/2013	243	FL	27.0	-91.2	F	HYD	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-10	15/05/2013	235	FL	27.5	-90.0	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-41	15/04/2012	255	FL	27.9	-86.3	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-73	15/03/2010	232	FL	27.1	-87.9	F	V2	P0	Developing	NO	0	NO
NOAA-GM-L-138	15/05/2014	225	FL	27.4	-92.4	F	GVM	P2	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-130	15/06/2014	217	FL	27.5	-90.1	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-133	15/06/2014	276	FL	27.6	-89.9	-	-	-	-	NO	0	NO
NOAA-GM-L-13	15/04/2013	231	FL	28.3	-88.3	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-55	15/05/2012	245	FL	27.9	-86.4	F	V3	P3	Spawning capable	NO	0	NO
NOAA-GM-L-5	15/06/2013	235	FL	28.0	-89.5	F	V3	P3	Actively Spawning (sub-phase)	NO	0	NO
NOAA-GM-L-53	15/05/2012	251	FL	27.8	-86.4	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-157	15/05/2014	240	FL	27.2	-91.5	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-57	15/06/2012	243	FL	27.3	-89.4	F	V3	P0	Regressing	NO	0	NO
NOAA-GM-L-152	15/05/2014	252	FL	27.2	-89.4	M	SZ	-	Spawning capable	NO	0	NO
NOAA-GM-L-160	15/06/2013	204	FL	27.9	-86.2	F	V3	P2	Spawning capable	NO	0	NO
NOAA-GM-L-99	15/04/2010	213	FL	27.1	-89.7	F	V3	P0	Spawning capable	NO	0	NO
NOAA-GM-L-100	15/04/2010	261	FL	27.3	-88.8	M	SZ	-	Spawning capable	NO	0	NO

Table S3. Parwise Fst values estimated from the mapped and de novo catalogs, including and excluding adults from the analysis. P-values estimated performing a 10,000 permutations test are indicated in parenthesis below each Fst value.

	Mapped catalog		**Denovo catalog**	
	All samples	Larvae & YOY	All samples	Larvae & YOY
SS-GOM	0.000505 (0)	0.000972 (0)	0.000260 (0.0199)	0.000750 (0.0169)
SS-MED	0.001834 (0)	0.001863 (0)	0.001587 (0)	0.001698 (0)
MED-GOM	0.002474 (0)	0.00336 (0)	0.002370 (0)	0.003196 (0)

Table S4. F3 statistic for the different tested scenarios of considering Larvae/YOY and adult individuals of each location separately and using both the de novo the mapped catalogs. For each test, the target population is tested to have admixed SNPs from the source populations. Bold values are considered positive for admixture and groups of individuals for which at least one of the tests indicates admixed origin are marked with an asterisk.

Source populations		**Target population**	**Denovo catalog**			**Mapped catalog**		
			F3	**std. err**	**Z**	**F3**	**std. err**	**Z**
GOML	MEDLY	SS*	**-0.00024**	0.000149	-1.617	**-0.000241**	0.000105	-2.304
	GOMA		0.000411	0.000134	3.074	0.000485	0.000099	4.912
	MEDA		**-0.000424**	0.000158	-2.681	**-0.000107**	0.000118	-0.902
MEDLY	MEDA		0.001399	0.000148	9.437	0.001612	0.000124	13.014
	GOMA		**-0.000257**	0.000117	-2.195	**-0.000202**	0.000074	-2.732
MEDA	GOMA		**-0.000273**	0.000121	-2.253	0.000062	0.000087	0.717
SS	GOML	MEDLY	0.001905	0.000164	11.651	0.002012	0.00014	14.38
	GOMA		0.001922	0.000114	16.904	0.001973	0.000102	19.353
	MEDA		0.000239	0.000094	2.546	0.000148	0.000058	2.552
GOML	GOMA		0.002585	0.000142	18.178	0.002703	0.000131	20.677
	MEDA		0.000052	0.000125	0.419	0.000283	0.000073	3.869
GOMA	MEDA		0.000223	0.000075	2.974	0.000414	0.000055	7.571
SS	MEDLY	GOML	0.001391	0.000249	5.591	0.001492	0.000166	8.965
	GOMA		0.000724	0.000232	3.116	0.000742	0.00015	4.952
	MEDA		0.001578	0.000258	6.116	0.001354	0.000172	7.86
MEDLY	GOMA		0.000707	0.000229	3.086	0.000782	0.000155	5.047
	MEDA		0.003256	0.000271	11.996	0.003269	0.000219	14.9
GOMA	MEDA		0.000878	0.000239	3.671	0.000917	0.000158	5.798
SS	MEDLY	GOMA*	0.000518	0.00008	6.471	0.000624	0.000061	10.259
	GOML		**-0.00016**	0.000106	-1.506	**-0.00008**	0.000081	-0.981
	MEDA		0.000534	0.000094	5.698	0.000353	0.000071	4.991
MEDLY	GOML		**-0.000143**	0.000099	-1.437	**-0.000119**	0.000078	-1.532
	MEDA		0.002213	0.000118	18.767	0.002209	0.000107	20.564
GOML	MEDA		**-0.000313**	0.000128	-2.437	**-0.000253**	0.00009	-2.823
SS	MEDLY	MEDA	0.000007	0.000121	0.054	0.000271	0.000076	3.549
	GOML		0.001861	0.000205	9.074	0.002049	0.000162	12.622
	GOMA		0.001707	0.000157	10.868	0.001874	0.000117	15.999
MEDLY	GOML		0.000193	0.000154	1.252	0.000132	0.000091	1.446
	GOMA		0.000023	0.000112	0.205	**-0.000003**	0.00007	-0.046
GOML	GOMA		0.002557	0.000196	13.027	0.002487	0.000146	17.08

Table S5. Results on the five three-dimensional demographic models of divergence tested. All models of divergence were tested both contemplating and supressing migration between location, originating ten different demographic models. Arrows show directional migration between locations when applied. Maximum-likelihood, Akaike information criterion (AIC), the difference in AIC between each model and the best-model, *theta* ($4N_{uA}\mu L$) parameter for the ancestral population estimates for each model after 10 independent runs are presented. The inferred parameters (scaled to theta) for each model are time since splits (where T1 is time since the first split which originates two populations, except for the sim_split models, and T2 is time since the second event which originated the third population), directional migration rate, admixing coefficient as the proportion of the MED admixed component originating the SS and the proportion of correctly orientated variants based on their ancestral state using albacore allele frequencies as reference.

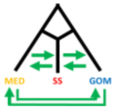
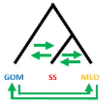
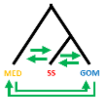
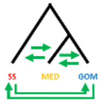
						Population sizes				Time		Directional migration rate						Admixing coefficient	Correct Orientation
	MODEL	BEST LIKE	BEST AIC	Δ_i	Theta	nuA	MED size	GOM size	SS size	T1	T2	MED->GOM	GOM->MED	GOM->SS	SS->GOM	MED->SS	SS->MED	f	O
	sim_split_mig	-3448.16	6918.32	1036.36	2255.75		2.7844	5.6622	9.0977	0.11		8.6004	4.6594	0.5757	0.3433	2.9618	6.9625		0.9855
	sim_split_nomig	-3495.4	7000.8	1118.84	2387.38		18.0564	19.5662	18.405	0.0882									0.9943
	split_admix_mig	-2969.85	5965.7	83.74	1122.1		1.1259	0.6077	3.0124	0.5393	0.7639	1.6287	10.1954	16.7752	0.9989	11.7788	11.2848	0.5946	0.9851
	split_admix_nomig	-3387.73	6789.46	907.5	2251.28		15.904	16.4058	6.2774	0.124	0.0127							0.5068	0.9907
	split_GOM_mig	-3104.02	6234.04	352.08	697.45	0.5107	1.7878	2.0767	2.3844	3.2685	1.3502	0.0632	6.1323	0.2531	5.0141	7.0391	1.2293		0.985
	split_GOM_nomig	-3457.51	6929.02	1047.06	2369.71	17.218	4.6753	19.2694	19.7634	0.0581	0.0227								0.9927
	split_MED_mig	-2927.98	5881.96	0	1212.8	3.2919	3.4983	6.1062	4.9163	0.9724	0.0746	17.1576	0.0544	5.3933	1.6615	11.2704	0.4512		0.9851
	split_MED_nomig	-3461	6936	1054.04	2336.06	18.5728	19.0003	8.0752	3.8226	0.0853	0.0114								0.9909
	split_SS_mig	-3020.06	6066.12	184.16	1689.14	2.1565	10.5726	11.4147	9.6805	0.3849	0.069	0.377	0.2682	2.5975	14.4109	4.5072	3.616		0.9851
	split_SS_nomig	-3482.38	6978.76	1096.8	2354.83	18.2167	2.7548	3.3447	19.4026	0.0637	0.0131								0.9896

Table S6. Number of SNPs per reference scaffold (of the available reference genome of Pacific bluefin tuna (Suda et al. 2019)) with highest 10% loading plots at each of the three principal components (PC1, PC2 and PC3) of PCAs performed using outliers SNPs under selection. Outlier SNPs were seek using two different approaches (PCAdapt and BayeScan, see Material and Methods) on two different catalogs (de novo and mapped, see Material and Methods).

Catalog	Approach	Scaffold	PC1	PC2	PC3
de novo	PCAdapt	BKCK0100075	10		
		BKCK0100111	1		
		BKCK0100005		9	2
		BKCK0100006		1	9
		BKCK0100046		1	
de novo	BayeScan	BKCK0100075	7		1
		BKCK0100076		2	
		BKCK0100100		1	2
		BKCK0100133		1	1
		BKCK0100161		3	3
mapped	Pcadapt	BKCK0100075	15		
		BKCK0100111	8		
		BKCK0100076		1	
		BKCK0100100		12	14
		BKCK0100161		7	5
		BKCK0100173		3	4
mapped	BayeScan	BKCK0100075	12		
		BKCK0100111	7		1
		BKCK0100076		1	
		BKCK0100100		6	13
		BKCK0100101		1	
		BKCK0100161		7	2
		BKCK0100173		4	3

Table S7. Variant positions among individuals of Atlantic bluefin tuna within the COI region. Loci highlighted in yellow are those identified as diagnostic position for introgression from albacore.

SPS	ACC.NUMBER	5630	5759	5792	5795	5834	5837	5933	5999	6002	6008	6041	6059	6071	6170	6173
T. thynnus	MT037075	G	A	C	T	T	A	A	T	T	G	A	C	T	A	C
T. thynnus	MT037084	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037085	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037086	.	G	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037087	.	.	T	C	.	.	.	C	C	A	.	T	.	G	T
T. thynnus	MT037088	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037089	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037090	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037091	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037092	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037093	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037094	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.
T. thynnus	MT037095	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037096	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037097	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037098	.	G	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037099	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037100	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037101	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037102	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037103	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
T. thynnus	MT037104	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037105	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037106	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037107	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037108	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037109	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037110	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037111	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037112	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037113	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037114	.	G	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037115	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037116	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037117	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037118	.	.	.	.	.	.	G	.	.	.	.	.	.	G	.
T. thynnus	MT037119	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037120	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037121	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037122	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037123	.	G	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037124	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
T. thynnus	MT037125	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.

T. thynnus	MT037126	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037127	.	.	T	C	.	.	.	C	C	A	.	T	.	G	T
T. thynnus	MT037128	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037129	A	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037130	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037131	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037132	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037133	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037134	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037135	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037136	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037137	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037138	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037139	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037140	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037141	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037142	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037143	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037144	.	.	.	.	C	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037145	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037146	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037147	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037148	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
T. thynnus	MT037149	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037151	.	.	.	.	.	.	G	.	.	.	G	.	.	.	.
T. thynnus	MT037152	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037153	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037154	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037155	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037156	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037157	.	.	T	C	.	.	.	C	C	A	.	T	.	G	T
T. thynnus	MT037158	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037159	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037160	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037161	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
T. thynnus	MT037162	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037163	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037164	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037165	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037166	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037167	.	.	.	.	.	.	G	.	.	.	.	.	C	.	.
T. thynnus	MT037168	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037169	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. thynnus	MT037170	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
T. alalunga	KT074102	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KT074101	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KT074100	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KT074099	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T

T. alalunga	KT074098	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KT074097	.	.	T	C	.	G	.	.	C	A	.	T	.	-	-
T. alalunga	KT074096	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KT074095	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KT074094	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KP975848	-	-	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KP975847	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KP975846	-	-	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KJ709651	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KC501692	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KC501691	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KC501690	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
T. alalunga	KC501689	.	.	T	C	.	G	.	.	C	A	.	T	.	G	T
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T. orientalis	DQ107631	.	.	T	C	.	G	.	C	C	A	.	T	.	G	T

Table S8. Number of sequenced samples, numbers of individually detected introgressed individuals from each group and percentages of detected introgressed mitochondrial haplotypes. To detect introgression, the diagnostic positions identified by comparing the individually sequenced individuals for the COI region with samples from albacore and Pacific bluefin tuna were used.

	Individually sequenced COI			**RAD-seq**		
Group	n	introgressed n	Introgressed %	n	Introgressed n	Introgressed %
GOM-L	13	0	0.0	38	0	0
GOM-A	21	0	0.0	173	2	1.2
SS-LY	16	1	6.3	52	3	5.8
MED-LY	26	2	7.7	189	8	4.2
MED-A	11	0	0.0	75	3	4.0
TOTAL	87			527		

Supplementary Figures

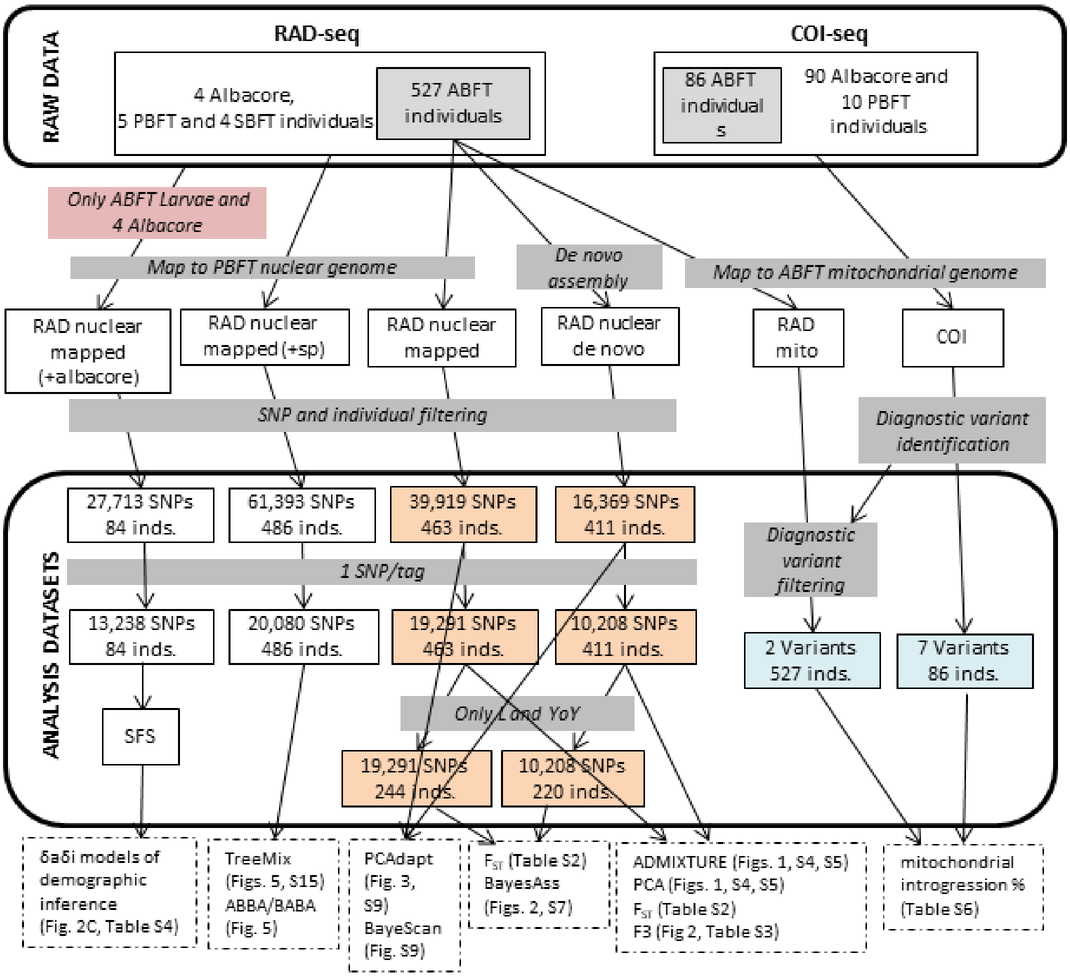

Figure S1. Work-flow of the analyses done in this study, including RAD-seq and COI Sanger sequencing analysis pipelines

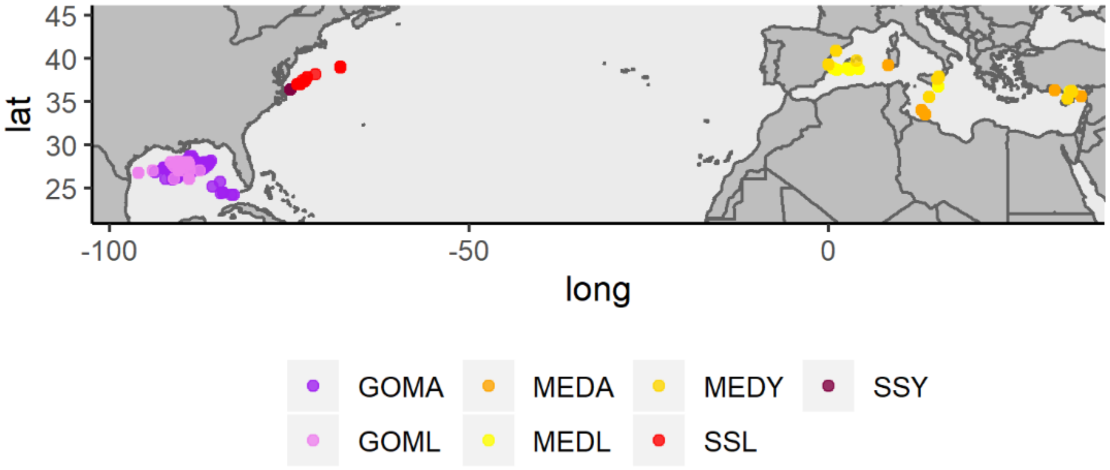

Figure S2. Sampling Locations covering the three known spawning groups of ABFT. Different color points represent different locations (MED, SS and GOM) and age classes (Adults, YOY and Larvae), as shown in the legend.

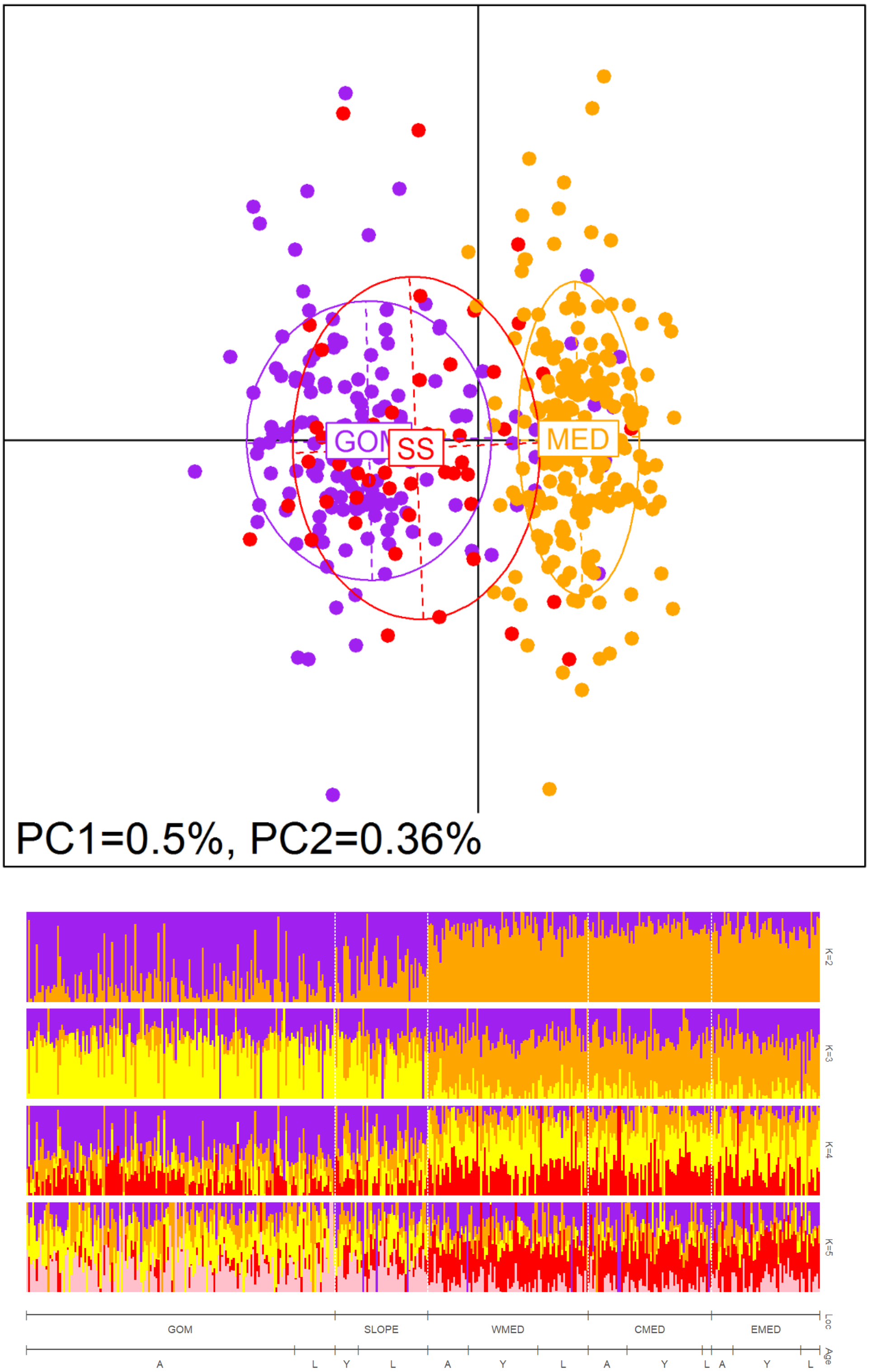

Figure S3. Population structure analysis of ABFT estimated from the de novo RAD-seq catalog. A. PCA, where individuals from the Gulf of Mexico (GOM), the Slope Sea (SS) and the Mediterranean (MED) are represented in purple, red and orange respectively. B. Individual ancestral proportions estimated by ADMIXTURE when assuming 2-5 ancestral populations (K). Cross-validation method described in the ADMIXTURE manual suggest that the more likely number of ancestral populations (K) associated with the lowest error rate is 2.

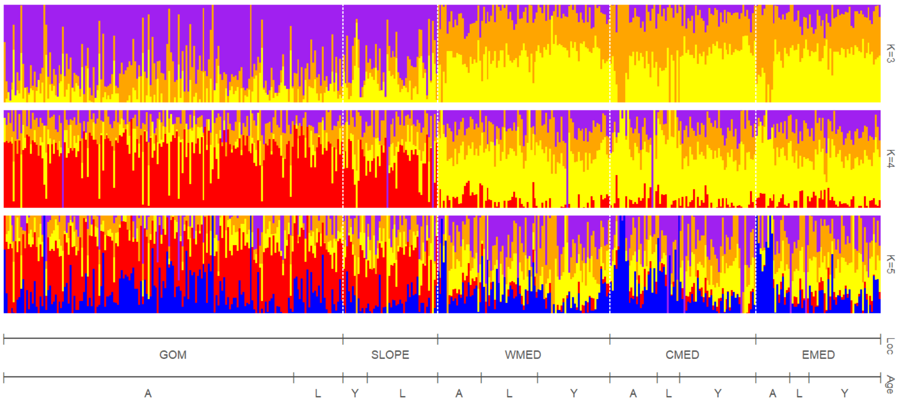

Figure S4. Individual ancestral proportions estimated by ADMIXTURE when assuming 3-5 ancestral populations (K=3,4,5) using the RAD reference mapped ABFT catalog. Cross-validation method described in the ADMIXTURE manual suggest that the more likely number of ancestral populations (K) associated with the lowest error rate is 2.

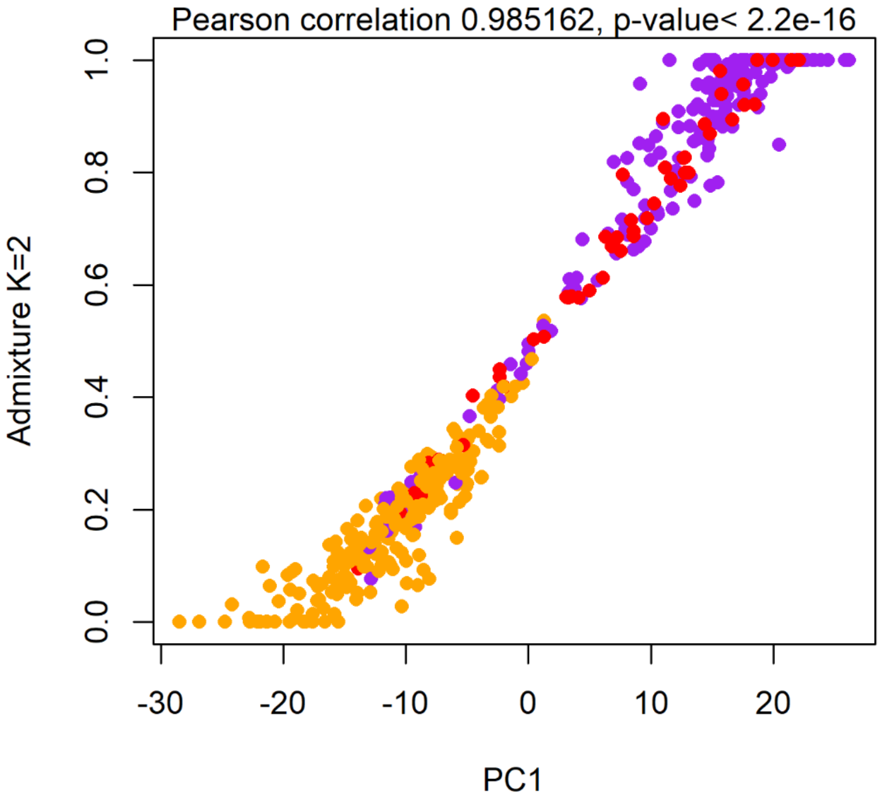

Figure S5. Correlation between PCA and ADMIXTURE results. The x axis show per sample coordinate values estimated for the PC1, and the y axis show ancestry proportions for ancestor 1 when assuming 2 ancestral populations using Admixture estimated based on reference mapped catalog were strongly correlated (Pearson correlation 0.98 p-value 2.2e-16).

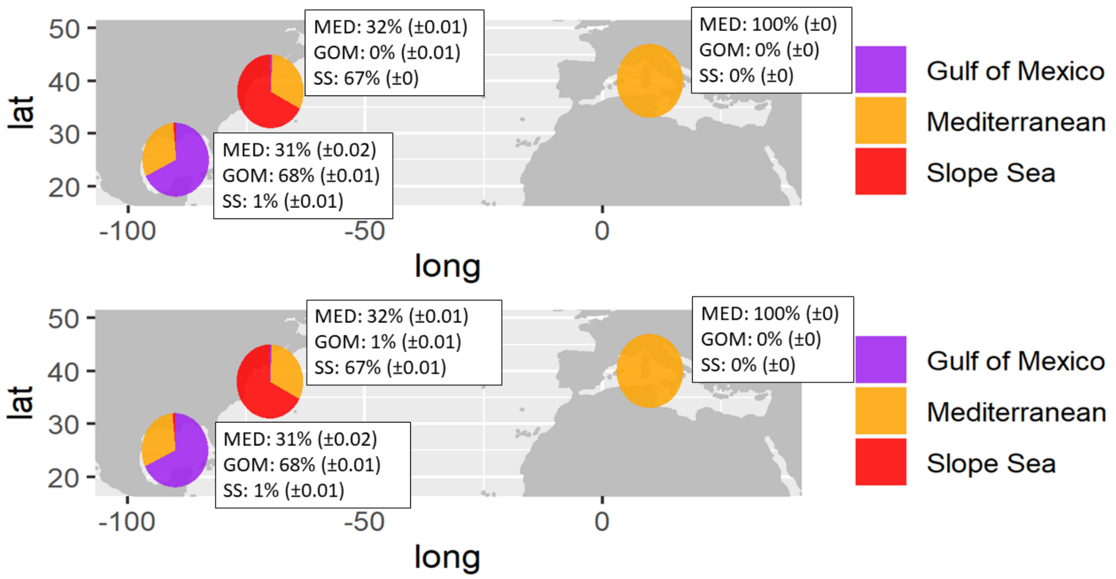

Figure S6. Per location in-migration rates (pie charts) measured as proportion of individuals at each location that are migrants from the other two source locations estimated by BayesAss. Using genotypes derived from the mapped (A) and de novo (B) assembled ABFT catalogs. In the squares are shown percentage values with 95% Confidence Interval in brackets. Proportions estimated using three random subsets of 5000 SNPs per catalogs in different runs were highly similar (± 0.002 and ± 0.0001 difference in proportions estimated from the mapped and de novo catalogs respectively). Result from one run per catalogue is shown.

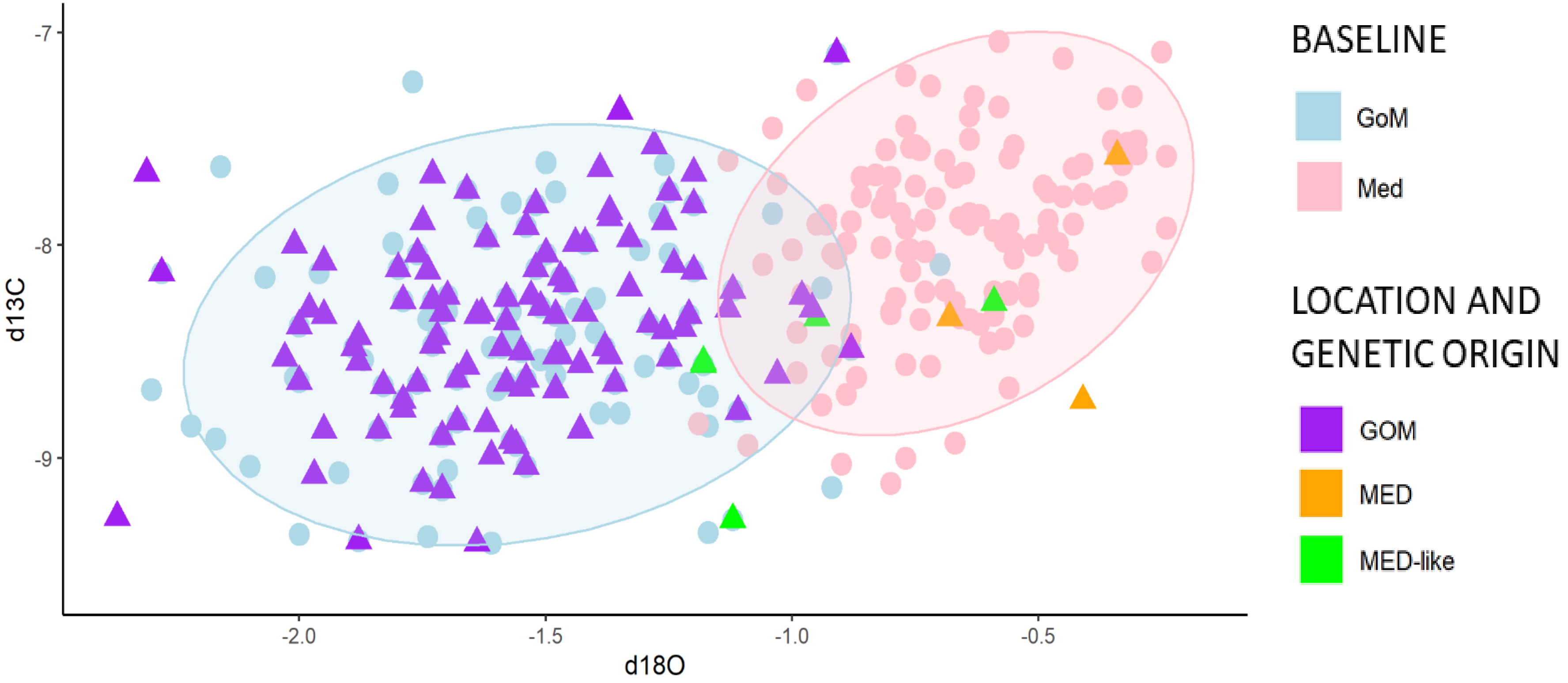

Figure S7. Triangles represent samples included in this study for which otolith isotopic compositions of oxygen (δ^{18}O) and carbon (δ^{13}C) were available. Purple and orange triangles are samples caught in the GOM and MED whose genetic background matched to these locations respectively. Assessment of genetic background was based in the ADMIXTURE results obtained using RAD-seq ABFT reference mapped catalog (Figure 1A,C). We find genetically MED-like individuals caught in the GOM (green triangles), whose otolith signature is intermediate between GOM and MED. Blue and red clouds are respectively the GOM and MED baseline values from Rooker et al. (2014).

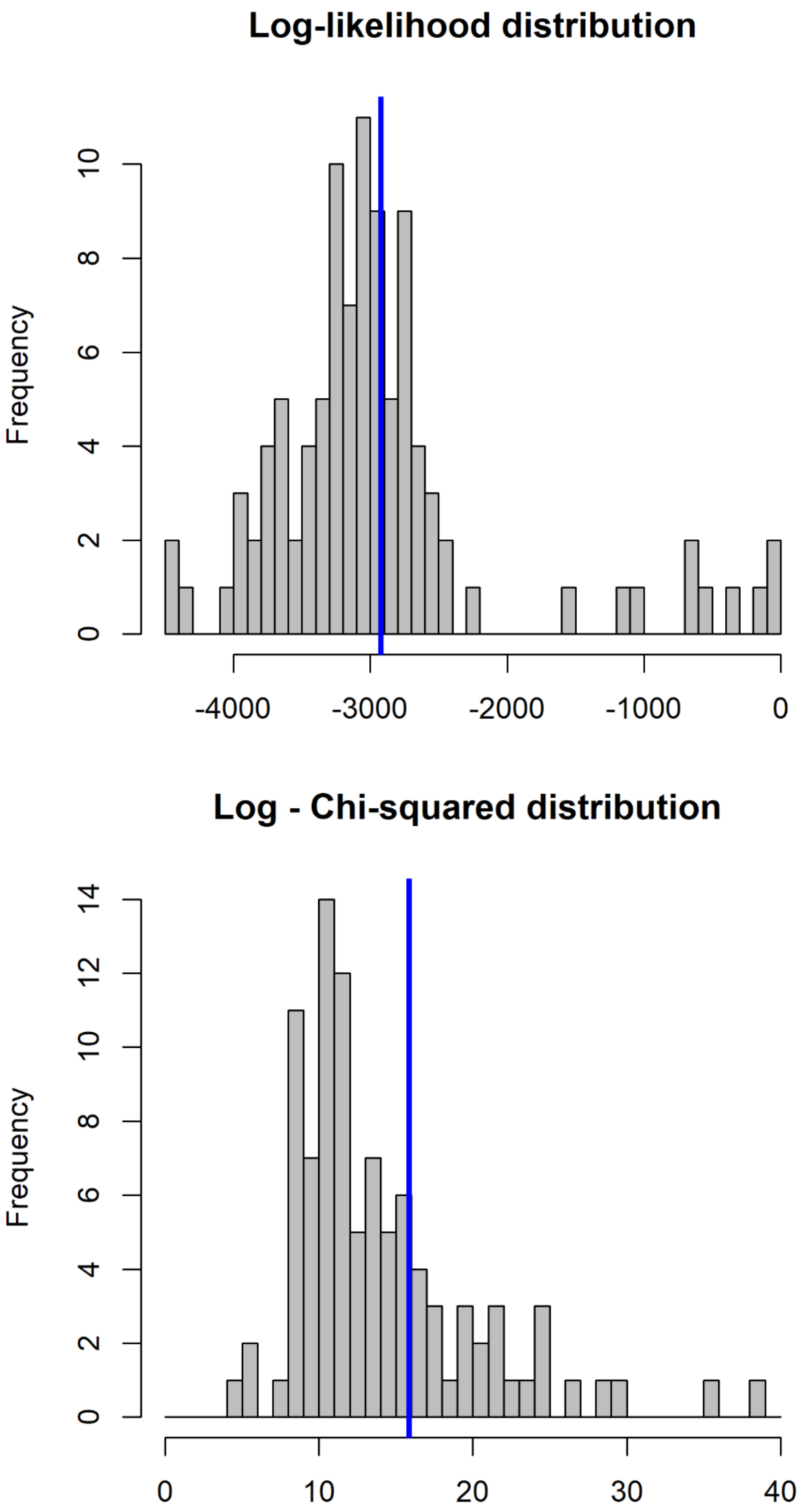

Figure S8. Histograms show the distribution of log likelihood and Pearson's log-transformed chi-squared test statistic values obtained after 100 run simulations. Blue lines represent empirical data.

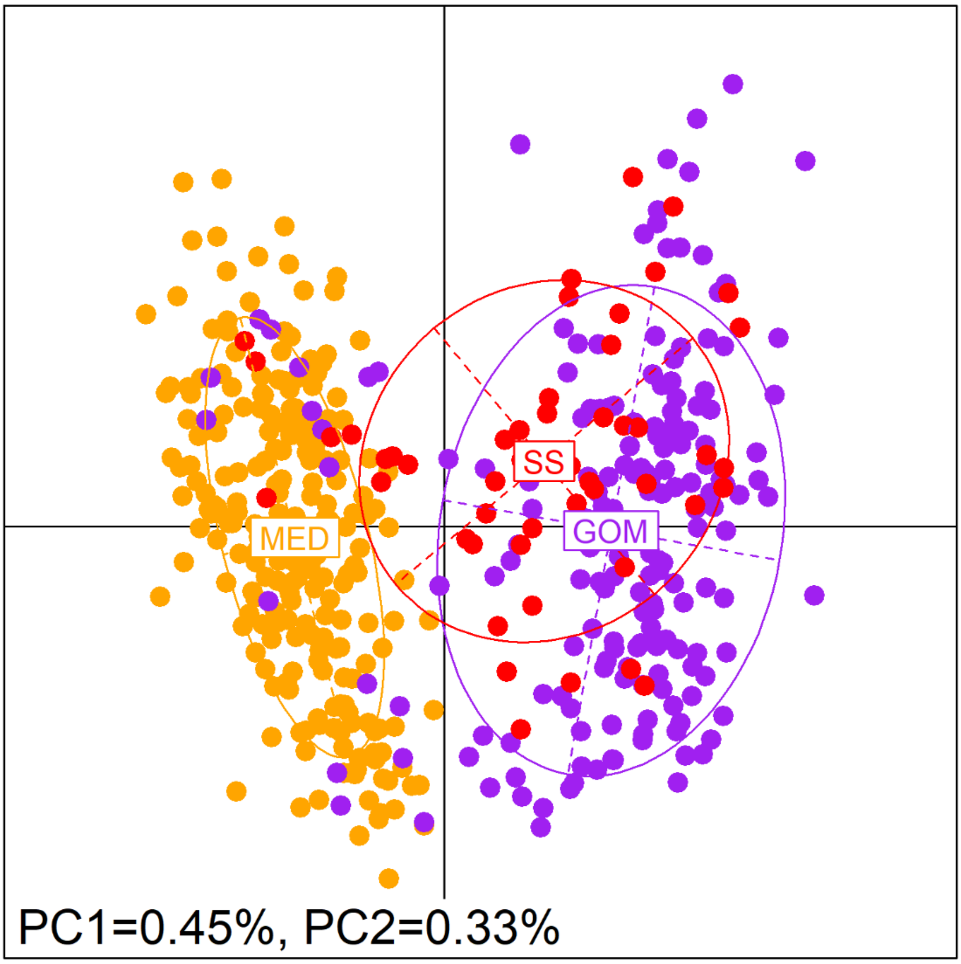

Figure S9. PCA performed using only neutral SNPs, excluding all those outlier SNPs detected by either PCAdapt or BayeScan in the reference mapped catalog.

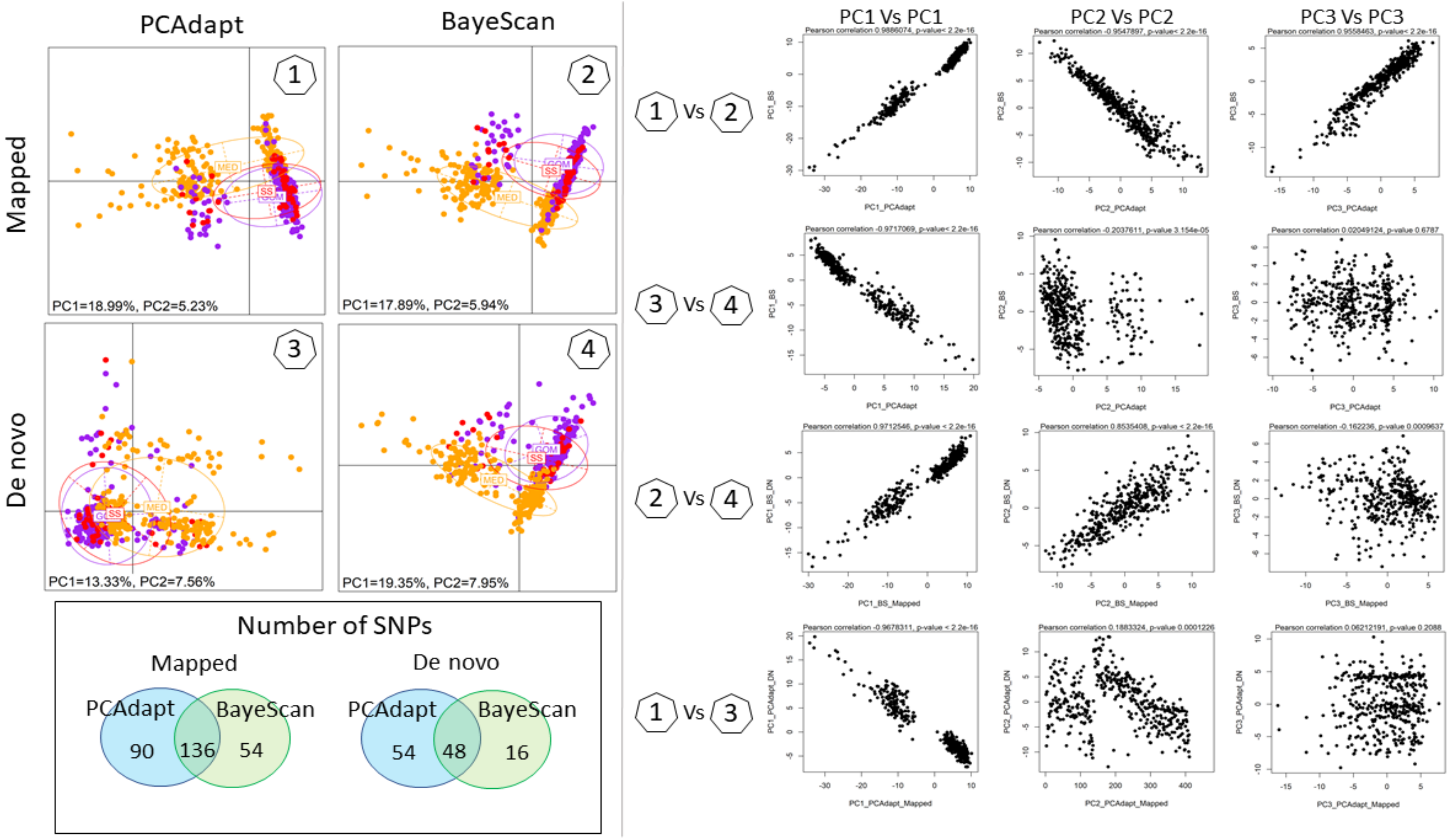

Figure S10. PCA's performed with outliers SNPs selected using approaches implemented in PCAdapt and BayeScan, using both the mapped and the mapped and de novo catalogs. Correlation of sample coordinates along the first three PC between each analysis pairwise comparison is shown. Venn diagrams show the number of candidate SNPs selected using the two different approaches.

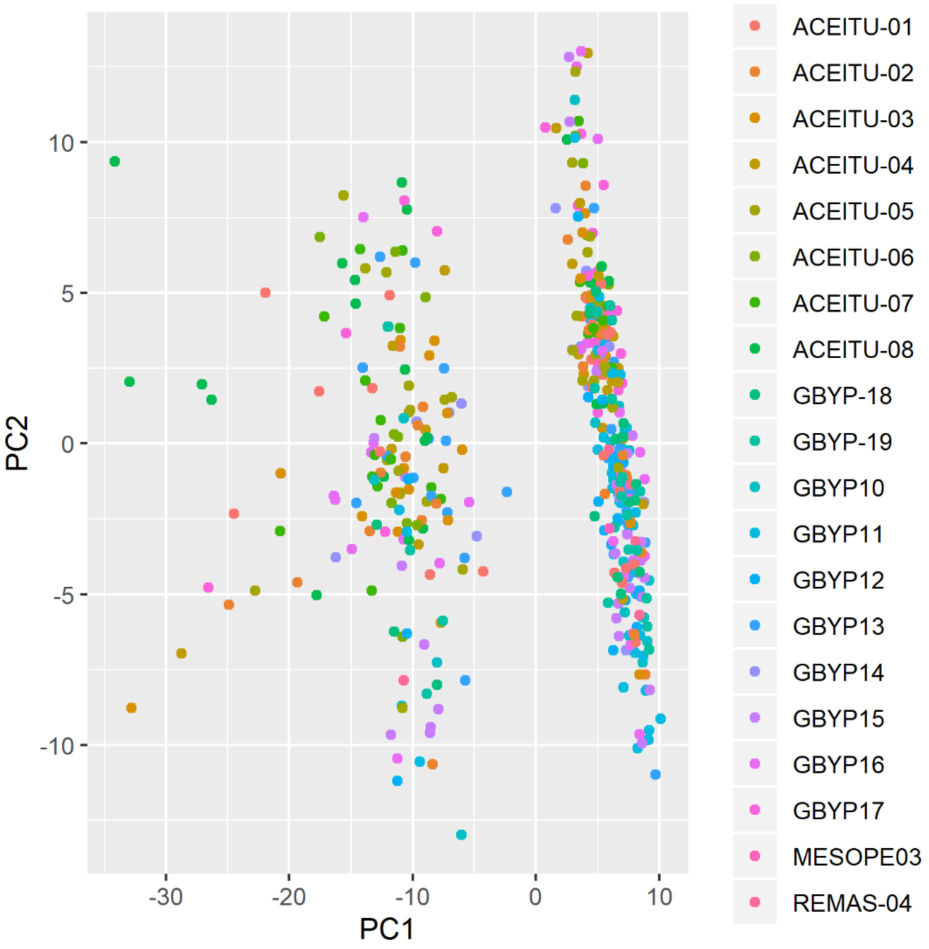

Figure S11. PCA performed using the 226 candidate SNPs selected by PCAdapt including all individuals from the mapped catalog dataset. Different colours indicate different laboratory pools of samples included in different libraries.

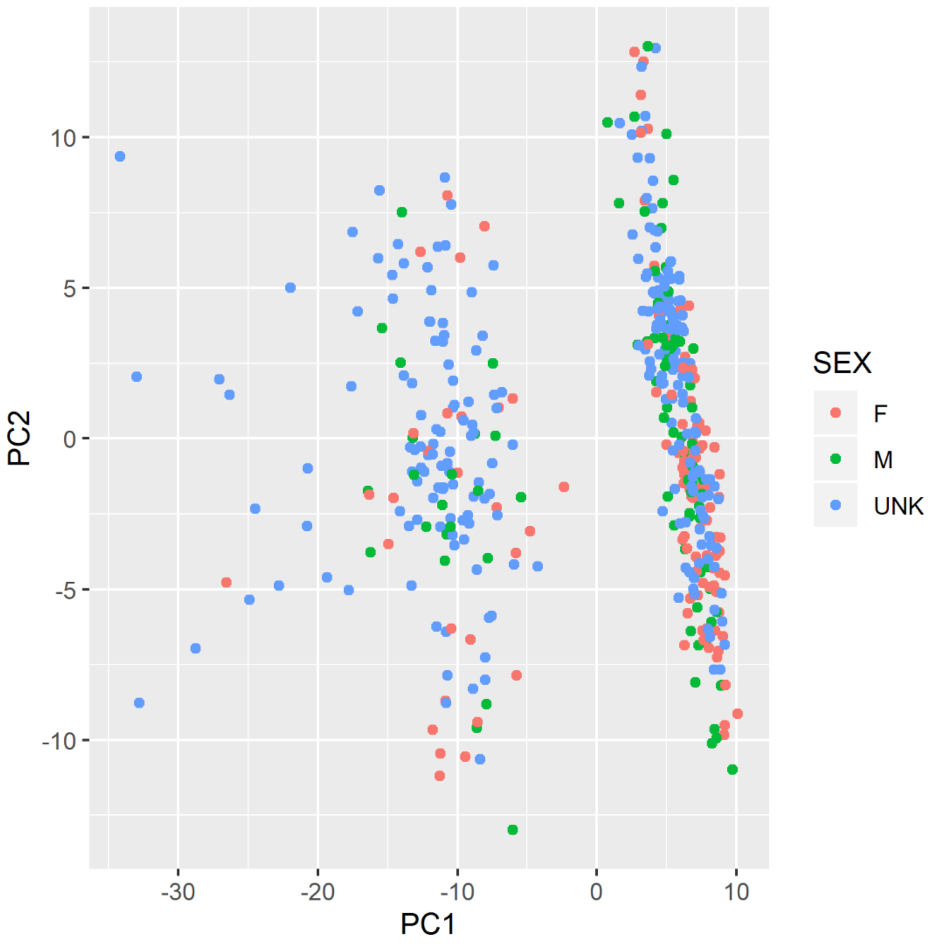

Figure S12. PCA performed using the 226 candidate SNPs selected by PCAdapt including all individuals from the mapped catalog dataset. Different colours indicate sex of the sample: female (red), male (green) or unknown (blue).

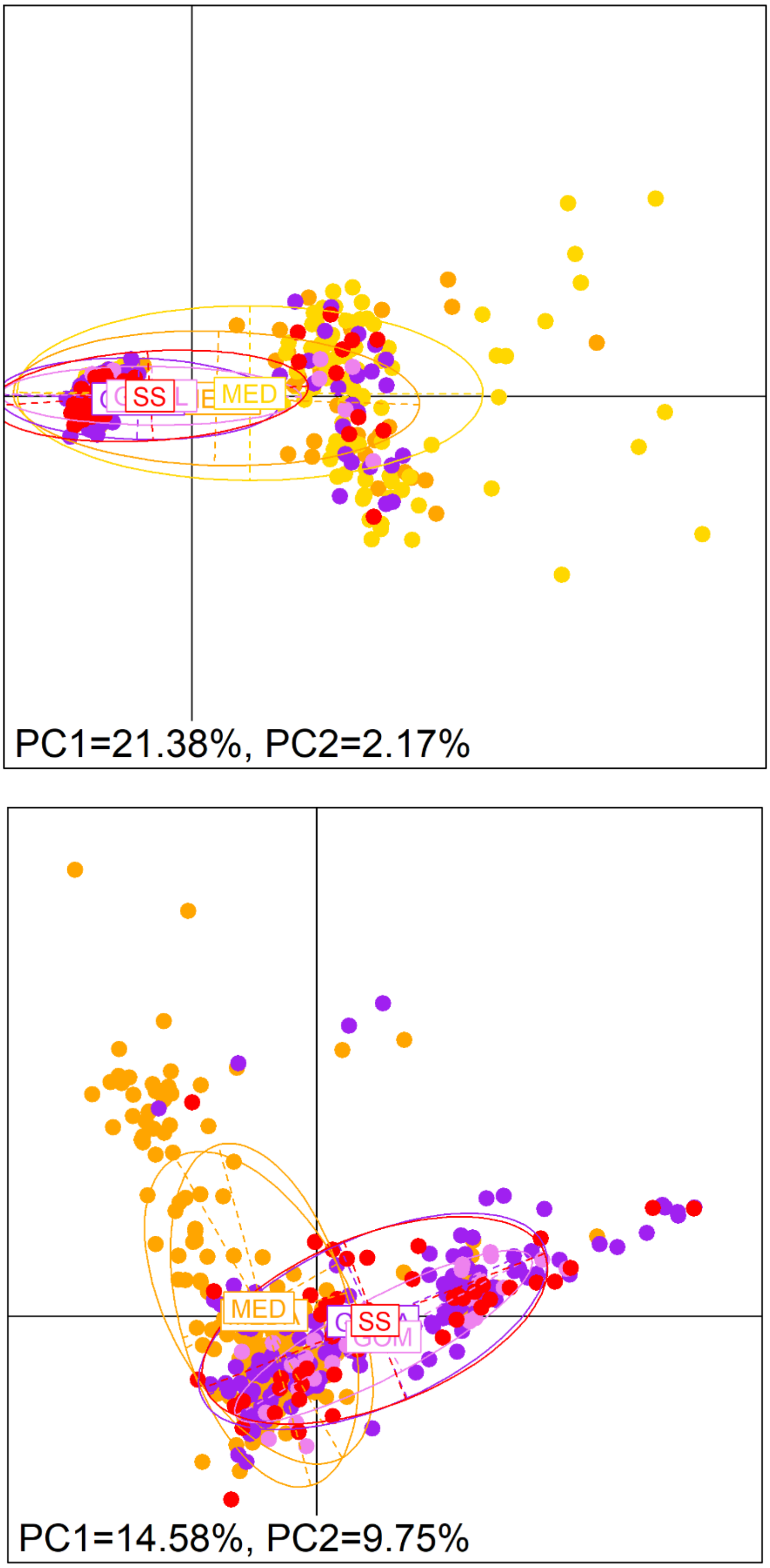

Figure S13. Principal Component Analysis using all filtered SNPs from the mapped catalogue derived from the two linkage groups in which SNPs potentially under selection were found. A. Linkage group 1 is formed by the first 751Kb region of reference scaffold BKCK01000075 and scaffold BKCK01000111, which contained 195 filtered SNPs. B. Linkage group 2 is formed by scaffolds BKCK01000161 and BKCK01000173 and contained 55 filtered SNPs.

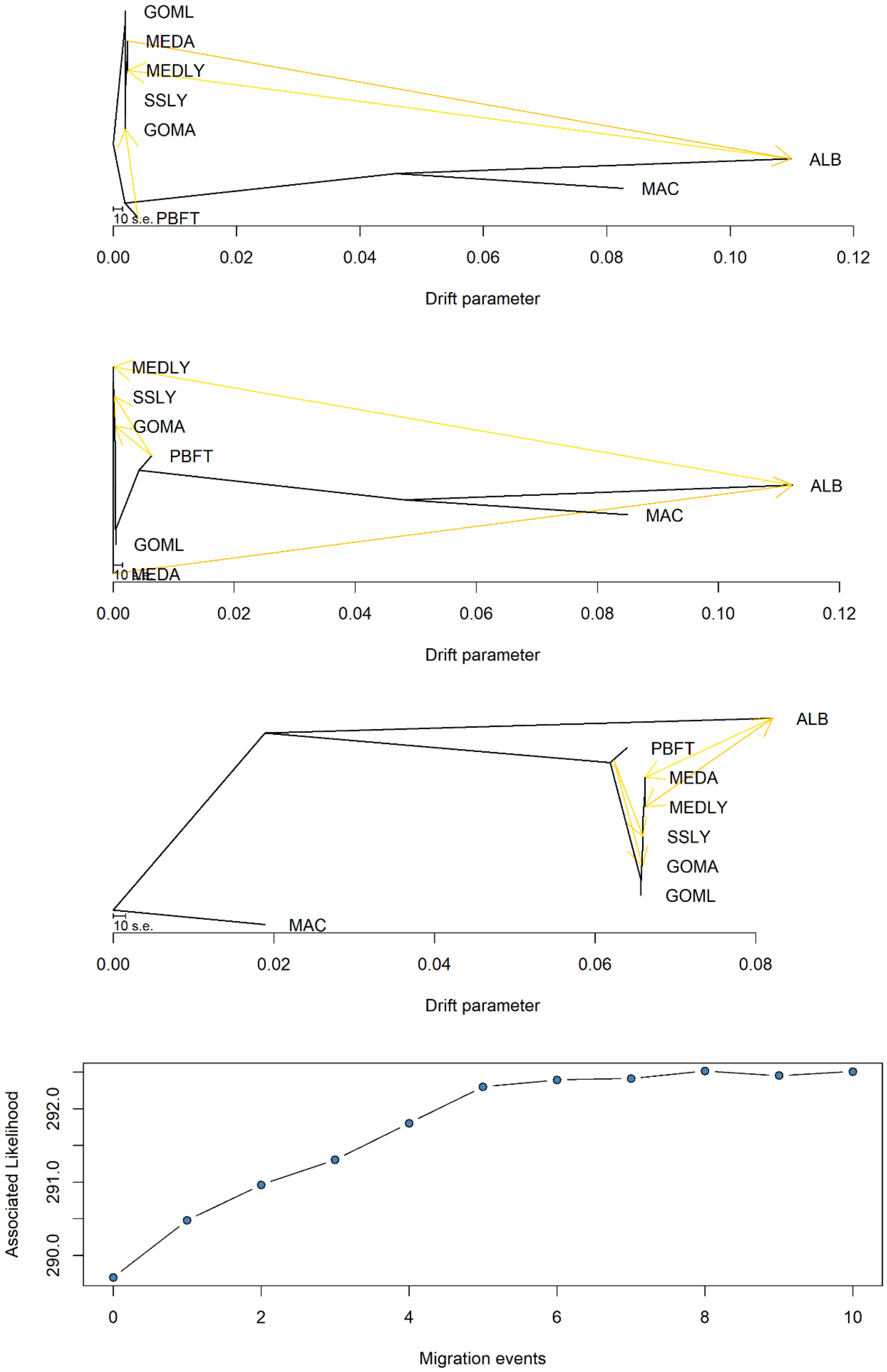

Figure S14. Results of Treemix analysis allowing from three to five migration events (A-C). Associated likelihood values for Treemix analysis allowing for increasing number of migration events from 0 to 10 (D).

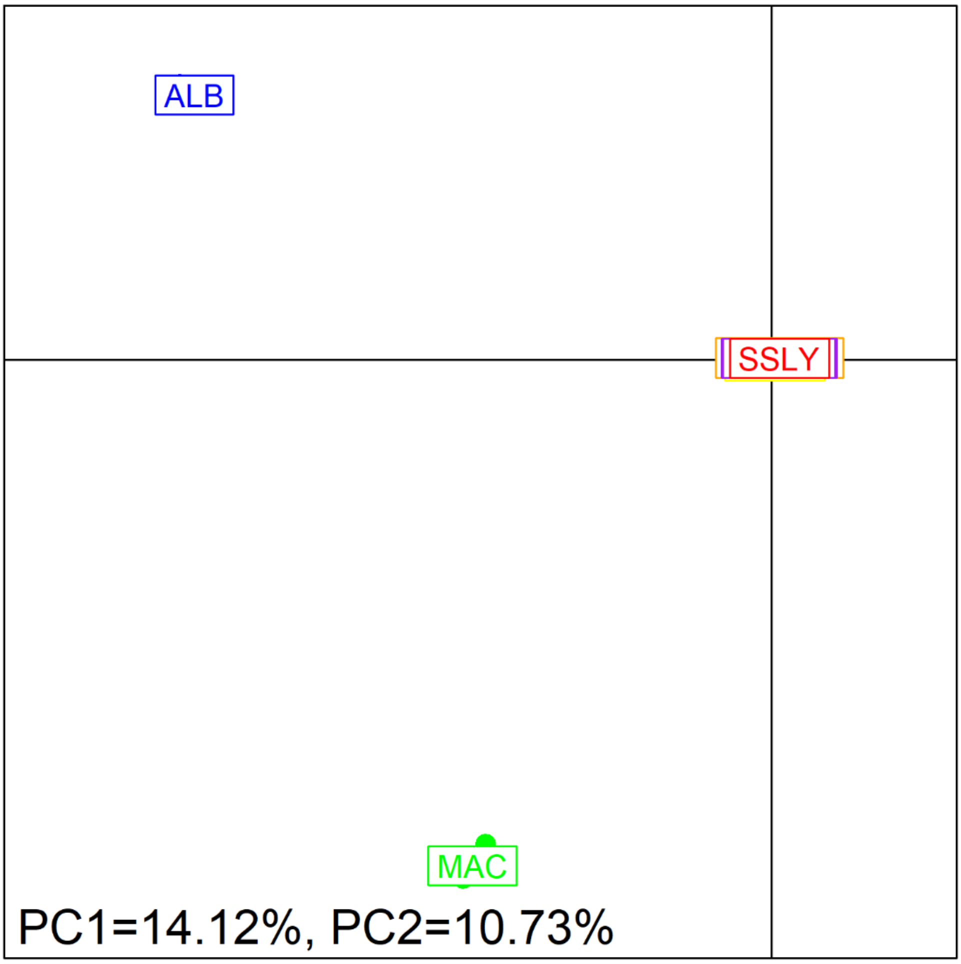

Figure S15. PCA performed using all filtered SNPs from the catalogue including different *T.* species. All samples from the same species clustered together, and Atlantic and Pacific bluefin tuna samples cluster together in a common group. Albacore (ALB), Southern bluefin (MAC) and Pacific bluefin (PBFT) tunas are represented in blue, green and yellow respectively. Atlantic bluefin tuna MED, SS and GOM populations are represented in orange, red and purple respectively.

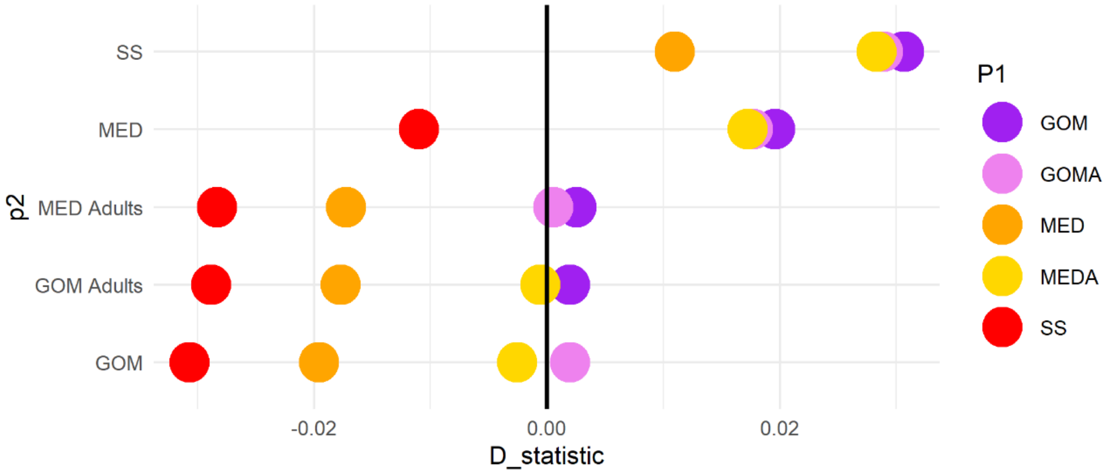

Figure S16. ABBA/BABA test performed using all filtered SNPs extracted from the reference mapped catalog dataset which includes other *Thunnus* species after excluding those located in scaffolds in which highest loading plot SNPs were found. Along the y axis are target groups and colors represent reference groups. The higher the D-statistic, the more introgressed is the target group respect to the reference group. In all the tests Southern bluefin tuna and albacore tuna were used as outgroup and donor respectively.

Brown-Peterson, NJ, DM Wyanski, F Saborido-Rey, BJ Macewicz, SK Lowerre-Barbieri. 2011. A Standardized Terminology for Describing Reproductive Development in Fishes. Marine and Coastal Fisheries 3:52-70.

Rooker, JR, H Arrizabalaga, I Fraile, et al. 2014. Crossing the line: migratory and homing behaviors of Atlantic bluefin tuna. Marine Ecology Progress Series 504:265-276.

Suda, A, I Nishiki, Y Iwasaki, A Matsuura, T Akita, N Suzuki, A Fujiwara. 2019. Improvement of the Pacific bluefin tuna (Thunnus orientalis) reference genome and development of male-specific DNA markers. Scientific Reports 9:14450.