HOX CLUSTER INTERGENIC SEQUENCE EVOLUTION

By

JEREMY DON RAINCROW

A Dissertation submitted to the

Graduate School-New Brunswick

Rutgers, The State University of New Jersey

and

The Graduate School of Biomedical Sciences

University of Medicine and Dentistry of New Jersey

in partial fulfillment of the requirements

for the degree of

Doctor of Philosophy

Graduate Program in Cell and Developmental Biology

written under the direction of

Chi-hua Chiu

and approved by

New Brunswick, New Jersey

October 2010

ABSTRACT OF THE DISSERTATION HOX GENE CLUSTER INTERGENIC SEQUENCE EVOLUTION by JEREMY DON RAINCROW

Dissertation Director: Chi-hua Chiu

The *Hox* gene cluster system is highly conserved among jawed-vertebrates. Specifically, the coding region of *Hox* genes along with their spacing and occurrence is highly conserved throughout gnathostomes. The intergenic regions of these clusters however are more variable. During the construction of a comprehensive non-coding sequence database we discovered that the intergenic sequences appear to also be highly conserved among cartilaginous and lobe-finned fishes, but much more diverged and dynamic in the ray-finned fishes. Starting at the base of the Actinopterygii a turnover of otherwise highly conserved non-coding sequences begins. This turnover is extended well into the derived ray-finned fish clade, Teleostei. Evidence from our population genetic study suggests this turnover, which appears to be due mainly to loosened constraints at the macro-evolutionary level, is highlighted by evidence of strong positive selection acting at the micro-evolutionary level. During the construction of the non-coding sequence database we also discovered that along with evidence of both relaxed constraints and positive selection emerges a pattern of transposable elements found within the *Hox* gene cluster system. The highly conserved Chondrichthyes and Sacropterygii Hox gene clusters have an invasion of type I transposons whereas the Actinopterygii Hox gene clusters have an invasion of type II transposons. Specifically,

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the Tc1 transposon is found throughout the ray-finned fishes *Hox* gene clusters and is highlighted by the presence of two intact Tc1 transposons in and adjacent to bichir's *Hox* gene clusters. Expression in human cell lines suggests that at least one of these Tc1 transposons are active. This combined with simulations ran in our lab point to transposons having a role in past and on-going restructuring of ray-finned fishes genomes.

These findings help shed light on the possible genomic changes that occurred and are occurring within the ray-finned fish clade that help shed light on their past and present species radiations.

Dedication

То

Jim and Patsy Brown

for their tireless support throughout my education

То

Wilder and Angelica Pajares

for giving me a home away from home

То

Maricruz Pajares

for keeping my spirits high

То

Kim Harris

for starting me on the right path

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Introduction- The Unrivaled Teleosts and the Model Meta-Gene 1.1 The Unrivaled Teleosts

1.1.1 Speciose Teleosts

Teleost fishes (division: **Teleostei**) are a highly successful clade both from the species and morphological perspective. Teleosts currently contain ~27,000 species that comprise nearly one-half of all jawed-vertebrates (superclass: **Gnathostomata**) and 99% of all ray-finned fishes (class: **Actinoptergyii**; Nelson 2006). These species are divided into 38 orders with 426 families and 4,084 genera (Nelson 2006).

Along with this taxonomic success is a stunning array of adaptations. Some of the more striking adaptations include fishes that have secondarily lost paired appendages (true eels; **Anguilliformes**), have the ability to inflate their bodies to twice the normal size (pufferfishes; **Tetraodontidae**), have the ability to create their own light (flashlight fish, *Photoblepharon palpebratus*) and even produce electrical fields strong enough to stun or kill (electric ray; **Torpedinidae**, electric eel; **Electrophoridae**, stargazer; **Uranoscopidae**). Teleosts range in size from a 7.9 mm cyprinid (*Paedocypris progenetica*, Kottelat et al. 2006) to a 2-ton ocean sunfish (*Mola mola*, McCann 1961).

The anterior dorsal fin is an example of the variety of adaptations that can be seen even in a single anatomical structure. This single fin has been modified into a lure (**Lophiidae**), camouflage (**Antennariidae**), suction disks (**Echeneidae**), and venom delivery (**Synanceja**, **Trachinidae**, **Thalassophryninae**). As a prime example of the oddity of adaptation seen in teleosts; a recent and very unique phenotype was discovered in the Monterey Bay off the coast of California. A close relative of salmonids, *Macropinna microstoma* is an opisthoproctid fish with a clear skull and rotating tubular eyes that let it take in the dim light from above as well as perform its front-facing predatory role (Robison and Reisenbichler 2008).

Along with anatomical diversity, teleosts also maintain increased variation at the cellular level. One example is coloration. Teleost fishes have a highly complex pigmentation patterning system that involves many pigment cell types known as chromatophores which are all derived from the neural crest. They come in 6 varieties including melanophores (black/brown), xanthophores (yellow/orange), iridophores (iridescent), erythrophores (red), leucophores (white) and even cyanophores (blue; Goda and Fujii 1995). This is in stark contrast to the single pigment cell type in mammals and birds (melanocytes; black/brown/yellow). This increase in chromatophores in teleosts is thought to be partly due to the duplication of color gene pathways both from whole genome duplications as well as lineage specific gene duplications (Braasch et al. 2006, 2009).

1.1.2 Teleost Specific Morphology

Teleost fishes have undergone rapid speciation coincident with an array of adaptive morphologies (Alfaro et al. 2009). They are one of if not the most diverse and successful extant vertebrate lineages. What conditions in the evolutionary history of actinopterygians (ray-finned fishes) underlie both their speciosity and morphological variability?

One hypothesis is that the acquisition of a few shared, advantageous adaptations early in teleost evolution may be necessary to maintain an ecological foothold while facilitating unique adaptations to a variety of habitats resulting in morphological variability (Figure 3; Hulsey et al. 2006). Such a scenario could lead to the phenomenon of adaptive morphological plasticity which we define as a species or group of species that appears to rapidly adapt to a variety of habitats. This plasticity is exemplified by the filling of several ecological niches by cichlid fishes in two separate occasions in Lake Malawi, Lake Tanganyika and Lake Victoria of Africa. All of these rapid speciations occurred independently and in different yet short evolutionary time frames (summary, Koblmüller et al. 2008). Do teleost fishes share such a set of advantageous adaptations?

Teleost fishes diverged from there closest living relative ~250 mya (Figure 2; Hurley et al. 2007). Since that time teleost fishes have evolved into fast, agile fishes able to exploit an almost limitless variety of food sources and habitats. The main adaptations that have contributed to their success have been a reduction in the number and thickness of bones, the amount of bony material in the scales, and fin position and composition allowing for greater flexibility, speed and maneuverability leading to a more dynamic predator/prey relationship (Janvier 1996). Perhaps as important as the increased locomotion is the modification of the feeding structures (Hulsey et al. 2006).

Teleosts have lost many bones in the skull and jaw allowing for the evolution of the extendable front/marginal/oral jaw. The extension of this oral jaw causes negative pressure within the mouth sucking in surrounding water and its contents allowing the fish to better capture prey (Schaeffer and Rosen 1961). However, the oral jaw reduces significantly the bite force and hence the ability of fishes to eat foodstuff containing hard materials such as the chitinous shell of the arthropods and the cellulose cell wall of most plants (Schaeffer and Rosen 1961; Liem 1973). Teleost fishes have developed a second pair of jaws known as pharyngeal jaws that are able to process these harder foodstuffs (Schaeffer and Rosen 1961). Pharyngeal jaws evolved from a dentin surface on the pharynx and eventually developed musculature (Figure 1).

It is hypothesized that the development of the pharyngeal jaw and subsequent partitioning of duties between the oral and pharyngeal jaws has led to a decoupling of their evolution (Liem 1973). This is known as Liem's hypothesis and is thought to be a major reason for the successful species radiation of the teleost division. It is also possible that novel and useful adaptations such as the pharyngeal jaw may be necessary to allow species/groups, such as the teleosts, to maintain a morphological robustness while allowing unique adaptations to a variety of habitats resulting in adaptive morphological plasticity. This would cause a delay in the rapid speciation events following the key innovation as the new innovation allows the species to move into new habitats and increase in number and then subsequently adapt to those habitats resulting in rapid speciation. Alfaro et al. (2009) found this delay between a pharyngeal jaw innovation and rapid speciation in their labrid (Teleostei:Perciformes) fish.

The pharyngeal jaw and other unique features have allowed teleosts to exploit an almost endless variety of habitats (Liem 1973) including water temperatures of -2°C at the polar caps (DeVries and Wohlschlag 1969) to 41°C at the African hot springs (Johnston et al. 1994), from elevations of 3.8 km in the Andean Lake Titicaca (Arratia 1982) to depths of 7.7 km in an ocean trench off the shore of Japan (Jamieson et al. 2009) and various pH, saline, and dissolved oxygen concentrations.

1.1.3 Environmental Change

Another driving factor in teleosts success and uniqueness is their environment. Environmental pressures are known to expedite evolution through natural selection. Were there any environmental factors that may have led to the current state of teleosts?

Teleost fishes' fossil record dates back to the beginning of the Triassic period ~250 million years (my) (Hurley et al. 2007). Shortly after, continental drift was occurring that would lead to the break up of the super continent Pangea into Gondwana and Laurasia (~150 mya, Smith et al. 1994). Eventually (~100 mya) Gondwana and Laurasia would break up into the current continents that have maintained a relatively steady shape over the last 65 my. Plate tectonics occurring during the evolution of the teleost fishes were opening up 1,000s of miles of new shoreline for ocean life. This ocean life includes the evolution of modern corals that host nearly one-half of all extant teleost species and is postulated to have been an aide in the overall diversification of the teleost division (Bellwood and Wainwright 2002; Alfaro et al. 2007). Several mass extinctions also occurred during the evolution of the teleost fishes that would lead to less competition for habitat and resources for those surviving individuals. This may have allowed teleosts to reach great numbers that in turn created competition within the clade driving diversity from within while simultaneously suppressing the success/diversification of other clades.

Coincident with the dawning of the teleost fish division was the largest known mass extinction event in the history of Earth, the Permian-Triassic extinction. During this mass extinction event ~95% of all marine life went extinct. Another major extinction occurred at the end of the Triassic (~200 mya) killing off all marine reptiles except for

Ichthyosaurus. A third mass extinction (Cretaceous-Palaeogene K-P mass extinction) occurred at the end of the Cretaceous period (~65 mya) again resulting in the extinction of all marine reptiles except turtles. Friedman et al. (2010) was able to show that this mass extinction may have led to the Acanthomorph rapid species radiation by allowing the Acanthomorphs to fill the morphological space left void by the extinction of non-teleost vertebrates.

It is unclear if teleosts survived these mass extinctions in greater numbers than other lineages or if they were able to take advantage with the few species that were left. Crow et al. (2005) suggest that the fish specific genome duplication (see section 1.1.4) may have acted as a buffer against extinction for those surviving teleosts. However, Santini et al. (2009) estimated that despite an increase in overall diversification rates in teleosts, teleosts have a 6 times greater extinction rate than non-teleosts gnathostomes. This leads to a one and one-half greater death:birth ratio (of species) in teleosts as opposed to non-teleost gnathostomes. Regardless, teleosts are currently the most successful extant vertebrate lineage. There were also other ray-finned fish lineages that existed prior to the MRCA of living teleosts that were species rich as well that did not survive (Donoghue and Purnell 2005).

Unique and advantageous adaptations, mass extinctions of competitors and vast amounts of new habitat available for niche-filling have helped shape the explosion of teleost fishes' numbers and diversity of species. Are environmental factors and welltimed advantageous adaptations enough or do teleosts fishes have an inherent molecular structure that allows for their success?

1.1.4 Fish Specific Genome Duplication

This species and morphological diversity in teleost fishes has been aided by or at least evolved along side not only environmental factors but also changes in genomic architecture and accelerated molecular evolution. A major genomic change that occurred prior to the divergence of extant teleost fishes is a whole genome duplication dubbed the fish specific genome duplication (FSGD; Meyer et al. 1999, 2005). The best evidence that the FSGD is a whole genome duplication comes from synteny maps from the completed genome of the spotted green pufferfish (*Tetraodon nigroviridis*) showing this taxon has two syntenic regions (paralogons) that correspond to single regions in the human genome (Jaillon et al. 2004). Comparative mapping shows that paralogons of spotted green pufferfish and zebrafish (*Danio rerio*) are homologous, supporting that the FSGD occurred prior to the divergence of the major teleost clades, **Acanthopterygii** and **Ostariophysi** (Woods et al. 2005).

Our labs recent work on *Hox* genes in the goldeye (*Hiodon alosoides*) suggests that **Osteoglossomorpha**, the most basal teleost subdivision, also shares the FSGD with higher teleost fishes (Chambers et al. 2009). Because of the importance of genome duplication in vertebrate evolution (Ohno, 1970; Sidow, 1996) many authors have speculated that the FSGD is directly responsible for the biological diversification (i.e. speciosity) of teleost fishes (Hoegg et al. 2004; Postlethwait et al. 2004; Meyer and Van de Peer 2005).

There are however several lines of evidence that the FSGD is not even coincidental with the teleost species radiation much less a causal agent. Recent examination of the ray-finned fishes fossil record, shows that there are 11 extinct clades between teleosts and their closest living relatives (Donoghue and Purnell 2005). The authors conclude that the character acquisitions normally attributed as synapomorphies of derived teleost fishes arose gradually in ray-finned fish phylogeny with many acquisitions predating the FSGD. Additionally, many of these extinct clades that have been shown to pre-date the FSGD were species rich themselves. Hence fossil evidence suggests that the FSGD is uncoupled to species richness.

Molecular clock analysis between human (*Homo sapiens*) and Japanese pufferfish (*Takifugu rubripes*) estimates the FSGD occurred ~350 mya (Christoffels et al. 2004). Evidence from *Hox* (Crow et al. 2006), Para*Hox* (Mulley et al. 2006), and three nuclear, non-*Hox* genes (Hoegg et al. 2004) supports that the FSGD is coincident with the origin of teleosts in the osteoglossomorphs, after divergence of the bowfin (*Amia calva*). Bowfin fossils suggest this node is ~250 million years old (Hurley et al 2007). Importantly, our work with an Osteoglossomorph has shown that possession of a duplicated genome is not sufficient for species richness (Chambers et al. 2009). It is also important to note that the Actinoptyerygian super-orders (**Ostariophysi** and **Acanthopterygii**) that contain 93% of the present-day teleost species diverged ~135 mya (Benton 2005), much later in ray-finned fish phylogeny than when the FSGD occurred (250-350 mya). Furthermore it has been shown that these species rich super-orders haven't retained many genes as duplicates from the FSGD.

In fact, it is estimated that only ~10% and ~15% of paralogous genes in zebrafish (**Ostariophysi**) and spotted green pufferfish (**Acanthopterygii**) genomes, respectively are a result of the FSGD (Blomme et al. 2006). Interestingly, for both species the

majority of paralogous genes result from lineage specific duplications (~40% of paralogs in zebrafish and ~17% in green-spotted pufferfish (Blomme et. al. 2006). Hence these data demonstrate that the FSGD likely did not play a large role in the diversification of teleost fishes but does suggest gene duplication in general may be important.

1.1.5 Accelerated Evolution

If not the FSGD what was the major molecular contributor to the diversification of the teleost fishes? It is possible that accelerated evolution due to increased mutation rate and increased genetic recombination are factors.

Both coding and non-coding sequences have been shown to be under accelerated evolution in the teleost division of ray-finned fishes. Robison-Rechavi and Laudet (2001) set out to test the Ohno model that one of two duplicate genes should be less constrained by selection and thus be able to acquire a new function (and presumably an accelerated evolution). What they found was that 16/19 genes in fish regardless of their duplication status showed an overall accelerated evolution when compared to mammals. Growth hormone genes have also been found to be under accelerated evolution (5X more substitutions) in teleosts compared to mammals and this acceleration has been shown to be a product of both relaxation of purifying selection and positive selection (Ryynanen and Primmer 2006).

On a genome-wide scale Jaillon et al. (2004) showed that the higher mutation rate held true for 5,082 protein-coding genes when comparing spotted green pufferfish and Japanese pufferfish divergence to the mammalian proxy of human (*Homo sapiens*) and the house mouse (*Mus musculus*). For the 15-25% of genes retained as pairs there is often an asymmetric acceleration of nucleotide substitution (synonymous and nonsynonymous) rate in one of the duplicated paralogs (Wagner et al. 2005; Braasch et al. 2006; Brunet et al. 2006; Crow et al. 2006; Steinke et al. 2006). This pattern is also lineage specific and, for *Hox* genes, also cluster specific (i.e. the *Hox*Aa versus *Hox*Ab clusters of teleosts, Chiu et al. 2004; Wagner et al. 2005).

One signature of molecular adaptation is Ka/Ks >1 (Nei and Gojobori 1986). This means that there is a greater frequency of non-synonynomous changes than synonynomous changes which implies that non-synonomous changes are preferentially fixed in the population. Investigations of duplicated paralogs in teleost fishes have found one paralog to show evidence of positive Darwinian selection; this asymmetry is species specific (Steinke et al. 2006; Brunet et al. 2006). Interestingly, Brunet et al. (2006) suggest that this asymmetric pattern of Darwinian evolution observed is not a result of changes in selective patterns after the FSGD (Vogel 1998; Meyer and Schartl 1999; Volff 2005). Instead, they propose that genes already under strong selective pressure were preferentially maintained as duplicates. Implying that duplication of genes that are advantageous to adaptation leads to greater adaptive success. This is the first insight into possible molecular mechanisms for the success of the teleosts, the accelerated evolution and possibly positive selection on groups of genes in ray-finned fishes prior to the divergence of teleosts that were also advantageous after their divergence.

This accelerated evolution in the teleost fishes has also been observed in conserved non-coding sequences (CNS). Work done by Chiu et al. (2002) showed that conserved non-coding sequences found between human and horn shark (*Heterodontus francisci*) *Hox*A clusters were more often than not absent in the teleost fishes, zebrafish (*Danio rerio*) *Hox*Aa and *Hox*Ab clusters and striped bass (*Morone saxatilis*) *Hox*Aa

cluster. Venkatesh et al. (2007) showed that this loss of CNSs occurred at the genome wide scale as well. They were able to show that between human and elephant shark (*Callorhinchus milii*) there were 4,782 CNSs whereas between human and zebrafish there were only 2,838 and between human and Japanese pufferfish 2,107. This turnover of CNSs in the teleost fish division can be postulated to result in differing expression patterns since CNSs are predicted *cis*-regulatory elements. However conservation of putative or known *cis*-regulatory elements does not always coincide with conserved function. Fisher et al. (2006) show human and zebrafish RET-1 *cis*-regulatory elements have equivalent function in cross-species expression studies, despite no sequence similarity. More research in investigating the effect of *cis*-regulatory element evolution on gene expression changes in ray-finned fishes is urgently needed.

Although the exact mechanisms of the teleosts' success are unknown their radiation is unmatched among extant vertebrates. It is true that fossil records show other lineages that may have been as successful as teleosts (Donoghue and Purnell 2005), however understanding mechanisms that led to the radiation and quite possibly continued radiation of the extant teleosts will give insight into the environmental, phenotypic, and genetic conditions necessary for successful species radiations.

1.2 The Model Meta-Gene

1.2.1 Discovery of Hox Genes

In order to gain more insight into possible molecular mechanisms that have contributed to the teleosts rapid species radiation I focus my study on the *Hox* genes. First, I will give an introduction into *Hox* gene discovery and evolution as well as their clustered nature.

Homeotic mutations are those that transpose whole body parts or segments. Homeotic mutations were first officially described in 1915 in the fruit fly (*Drosophila melanogaster*; Bridges and Morgan 1923). In an effort to isolate the genes responsible for these mutations E.B. Lewis devoted a career to studying them in *D. melanogaster*. In the 1950s, 1960s and 1970s Lewis was able to isolate several clustered homeotic genes that were termed the bithorax complex (BX-C). In a review in 1978 Lewis eloquently laid out a proposal for the rules governing these genes and their expression where each gene had an anterior but not posterior boundary and the expression of each new gene caused the next thoracic or abdominal segment to take on a unique characteristic.

Lewis was incorrect about the number of protein coding genes that were contained within this complex but future insight discovered that micro RNA genes also lie within this complex and help regulate the anterior-posterior patterning in *Drosophila* and thus implementing them as major contributors to the insect body plan (review, Chopra and Mishra 2006). The BX-C contains 3 homeotic genes (Sanchez-Herrero et al. 1985) or as they are known in *Drosophila* Hom-C genes (Akam 1989). The rest of the Hom-C genes were described in a cluster by Kaufman et al. (1980) and were coined the Antennapedia complex or ANT-C. Together the BX-C and ANT-C contain 8 Hom-C genes that are responsible for patterning the anterior-posterior axis of *Drosophila melanogaster*.

The homeotic genes are now defined by a conserved sequence known as the homeobox. McGinnis et al. (1984a) first described the homeobox as a repetitive DNA sequence that was conserved among genes in the BX-C and ANT-C. This 180bp homeobox codes for the 60 amino acid homeodomain. The homeodomain was considered evidence that homeotic genes were transcription factors due to the homology with the *MAT-a1* and *MAT-a2* genes of yeast that are known transcription factors that regulate genes responsible for mate type switching (Shepherd et al. 1984). Evidence of homeotic mutations in vertebrates and the discovery of the conserved homeobox sequence led to rapid isolation of homeotic genes in other animals (chicken; *Gallus gallus*, mouse and human McGinnis et al. 1984b; McGinnis et al. 1984c).

That same year an entire homeobox gene was cloned from the African clawed frog (*Xenopus laevis*) and it was found to have 55 of 60 amino acids conserved in the homeodomain with *D. melanogaster's Antennapedia* (Carrasco et al. 1984) and a homeobox gene from mouse was cloned in the same lab (McGinnis et al. 1984c). Because of the diversity of animal types *Hox* genes were found in, they were looked for in more and more animals to help establish their universality. This was important due to their possible implication as major contributors to the embryological and evolutionary patterning of all animal bauplans.

1.2.2 Evolution of *Hox* Genes

Hox genes are part of a class of helix-turn-helix proteins that are known to bind to DNA and help regulate transcription. The helix-turn-helix motif is one of the most

conserved (oldest) motifs known in living organisms. Giraldo and Diaz-Orejas (2001) found that RepA, which is responsible for DNA replication initiation in *Pseudomonas* (bacteria) and contains a helix-turn-helix motif, was homologous to Orc4p in *Saccharomyces cerevisiae* (eukaryote) and Cdc6p in *Pyrobaculum aerophilum* (archaea) in both sequence and structure making them likely orthologs. This places the origin of the helix-turn-helix motif at or before the most recent common ancestor of all known living organisms.

As mentioned previously, the *Hox*-related family is determined specifically by the presence of the homeodomain, a 60 amino-acid motif. Proteins containing this domain can be found as deep in animal phylogeny as **Cnidaria** (Murtha et al. 1991). Although, to be a true *Hox* family member the gene must be part of a cluster as they are in the BX-C and ANT-C in *Drosophila*. So far *Hox* clusters have been discovered in various states of clustering in both protostomes and deuterostomes, which would date the ancestral *Hox* cluster as far back as the origin of the **Bilateria** (Figure 2).

The **Radiata** (**Cnidaria** and **Ctenophora**) contain *Hox*-related genes but there is no decisive proof that they are clustered in the genome (review; Aboobaker and Blaxter 2003). Among **Bilateria** the oldest known members to contain *Hox* genes would be the phylum **Acoelomorpha**. *Hox* gene orthologs have been found in both classes of **Acoelomorpha**, **Acoela** (Cook et al. 2004) and **Nemertodermatida** (Jimenez-Guri et al. 2006). *Hox* genes have also been found in the other basal Bilaterian phylum, **Chaetognatha** (Papillon et al. 2003). Again it is important to point out that there is no indication that these *Hox* genes are clustered in these sister groups to the superphyla of **Protostomia** and **Deuterstomia**. In protostomes *Hox* genes have been found in the phyla **Nematoda**,

Onychophora (Grenier et al. 1997), **Arthropoda**, **Nemertea** (Kmita-Cunisse et al. 1998), **Platyhelminthes** (overview, Badets and Verneau 2009), **Bryozoa** (Passamaneck and Halanych 2004), **Annelida** (Bleidorn et al. 2009), and **Mollusca** (Degnan and Morse 1993). The nematode *Caenorhabditis elegans* has *Hox* genes but they are not clustered in its genome (review; Aboobaker and Blaxter 2003). This would indicate that the *Hox* cluster was secondarily dispersed in this lineage. The model arthropods *Drosophila* have *Hox* genes in clusters both complete and broken. For deuterostomes *Hox* genes have been found in the phyla **Echinodermata** (Dolecki et al. 1988), **Hemichordata** (Peterson 2004) and **Chordata**. For chordates the first *Hox* genes were discovered in the model organisms chicken, mouse and human (McGinnis et al. 1984b). They have also been found in more basal taxa including **Urochordata** and **Cephalochordata** (Bell et al. 1993; Holland et al. 1992).

Amphioxus (*Branchiostoma floridae*) is thought to contain the ancestral *Hox* gene cluster for the **Gnathostomata** (jawed vertebrates; Garcia-Fernandez and Holland 1994). **Gnathostomata** can be divided into 3 major classes: **Chondrichthyes** (cartilaginous fishes), **Sarcopterygii** (lobe-finned fishes) and **Actinopterygii** (ray-finned fishes). These classes all share the first instance of multiple (4) paralogous *Hox* gene clusters (Kim et al., 2000; Chiu et al., 2002; 2004; Prohaska et al., 2004; Raincrow et al. submitted). These are thought to have arisen via two rounds of genome duplication (Holland et al. 1994) but the cluster count of the intermediate species (lampreys and hagfish) is undetermined. The *Hox* genes in chordates are highly conserved and paralogs are easily discernible. This conservation has proven as useful for phylogenetics in chordates as it

has in determining membership in the protostome superphyla of Lophotrochozoa,

Ecdysozoa and **Platyzoa**. Central to the conservation of *Hox* genes in chordates is the conservation of their clustered formation. Clustering is yet one unique aspect of *Hox* genes.

1.2.3 Evolution of the *Hox* Gene Cluster

As mentioned previously, the first *Hox* gene clusters were discovered in *Drosophila* by E.B. Lewis (1978). Lewis first discovered what is now known as the BX-C or bithorax cluster. The BX-C contains *Hox* genes ultrabithorax, abdominal-A and abdominal-B. The other *Hox* gene cluster found in *Drosophila* was known as the ANT-C or antennapedia cluster. The ANT-C was discovered by Kaufman et al. (1980) and contains *Hox* genes labial (Lab), proboscipedia (Pb), deformed (Dfd), sex combs reduced (Scr) and antennapedia (Ant). The first cluster of *Hox* genes in a vertebrate were found in mouse on chromsome 11 (Hart et al. 1985).

The most primitive animal with an intact *Hox* gene cluster found to date is the nemertean ribbonworm (*Lineus sanguineus*). This ribbonworm has a cluster containing 6 *Hox* genes (Kmita-Cunisse et al. 1998). Other more derived protostomes such as arthropods have evidence of both an intact (red flour beetle; *Tribolium castaneum*, Brown et al. 2002; Shippy et al. 2008, mosquito; *Anopheles gambiae*, Powers et al. 2000) as well as divided (*D. melanogaster*, silk moth; *Bombyx mori*, Yasukochi et al. 2004) *Hox* gene cluster, whereas more primitive protostomes such as nematodes (Burglin and Ruvkun 1993) and platyhelminths (Pierce et al. 2005) have dispersed *Hox* gene clustering.

The same variation in *Hox* gene clustering can be seen in deuterostomes but not to the same extent. The sea urchin (*Strongylocentrotus purpuratus*) has an intact *Hox* gene

cluster but the genes are not in the canonical order (Cameron et al. 2006). Amphioxus, a cephalochordate, contains an intact *Hox* gene cluster that contains 14 *Hox* genes that are all transcribed from the same strand (Garcia-Fernandez and Holland 1994; Ferrier et al. 2000). This is thought to be the archetypal state of *Hox* gene clusters for the chordates. After the divergence of Amphioxus and prior to the divergence of known gnathostomes it is postulated that two rounds of genome duplication occurred giving rise to 4 *Hox* gene clusters (Amores et al. 2004). For accounting purpose Scott (1993) developed a nomenclature system that assigns each of the four paralogous clusters a letter (A, B, C, D) and orthologs to each of the 14 *Hox* genes found in Amphioxus 1-14. For example the gene orthologous to the 9th gene on Amphioxus's *Hox* gene cluster will be known as *Hox*A9 on the A cluster, *Hox*B9 on the B cluster and so on. Each of these clusters is ordered the same as the Amphioxus *Hox* gene cluster but none of them contain the entire complement of 14 genes.

To date intact *Hox* gene clusters homologous to the 4 *Hox* gene clusters have been found in the cartilaginous fish horn shark (*Heterodontus francisci*, Kim et al. 2000), the lobe-finned fishes coelacanth (*Latimeria menadoensis*, Koh et al. 2003; Danke et al. 2004), Western clawed frog (*Xenopus tropicalis*), the domesticated chicken (Richardson et al. 2007), human (Acampora et al. 1989), mouse (Duboule and Dolle 1989), the domesticated dog (*Canis familiaris*), the ray-finned fish, Senegal bichir (*Polypterus senegalus*) and other species with whole genome sequences.

Several gnathostomes lineages have had further genome duplications or tetraploidization events but none of these occurred during a time that allows them to be both shared by many species and still be easily detectable. Over 27,000 species share the

FSGD and all species sequenced to date appear to have between 7-8 intact Hox gene clusters (Figure 3). For accounting purposes these Hox gene clusters follow the Scott (1993) nomenclature with 2 paralogous clusters per original gnathostome cluster (A > Aa, Ab; B > Ba, Bb; C > Ca, Cb; D > Da, Db). To date only fishes of the division **Teleostei** have been found to share the FSGD and it has been proposed that the FSGD is coincident with the base of the teleosts group although there is much evidence to the contrary. There are two main groups of teleosts based on numbers of species: superorder **Ostariophysi** (6,502 species) and superorder **Acanthopterygii** (13,421 species). Only a single fish from **Ostariophysi** has a complete genome and/or complete Hox gene cluster complement sequenced; zebrafish. Several species of Acanthopterygii have been sequenced including medaka (Oryzias latipes; Kurosawa et al. 1999; Naruse et al. 2004), 3-spine stickleback (Gasterosteus aculeatus; Hoegg et al. 2007), spotted green pufferfish (Jaillon et al. 2004), Japanese pufferfish (Kurosawa et al. 2006), Nile tilapia (Oreochromis niloticus; Santini and Bernardi 2005) and African cichlid (Astatotilapia *burtoni*; Hoegg et al. 2007). So far the two separate superorders can be differentiated based on their *Hox* gene cluster content as Ostariophysi has Aa, Ab, Ba, Bb, Ca, Cb and Da clusters and Acanthopterygii has Aa, Ab, Ba, Bb, Ca, Da and Db. This 8 Hox gene cluster architecture is considered the ultimate in *Hox* gene cluster evolution although the number of genes is only slightly higher than states prior (i.e. mouse 39; *Tetraodon nigroviridis* 48). Despite the slight increase in *Hox* gene number they are more tightly clustered and more modular in nature (Duboule 2007), which can lead to a greater flexibility of expression and co-option.

Known *Hox* gene cluster states throughout animal phylogeny leads to the question of what the ancestral state of the *Hox* gene cluster was and why the *Hox* gene cluster exists. There are 2 major theories on the ancestral state of the metazoan *Hox* gene cluster, but they both result in the following groupings. First, the *Hox* gene cluster is divided into 4 major categories: anterior, group 3, central and posterior genes. Anterior genes include group 1 and 2 of deuterostomes and Lb and Pb of protostomes. Group 3 genes appear to have an ancient origin and have been secondarily lost in protostomes, central genes include group 4-8 in deuterostomes and Dfd, Scr, Antp, Ubx and Abd-A in invertebrates and posterior genes include group 9-14 in deuterostomes and Abd-B in protostomes. The origin of each category is thought to lie in a single *Hox* gene. The origin of these 4 *Hox* genes is in question. There are competing theories that there were 2, 3 or 4 original genes. For the 2 and 3 gene models the remaining genes were a result of tandem duplication of a more ancient *Hox* gene. A review of these models can be found in Garcia-Fernandez (2005).

The function of the *Hox* gene cluster has been a topic of debate. It is known that for species with an intact cluster that they show spatiotemporal colinearity with their expression along the anterior-posterior axis of the developing embryo (McGinnis and Krumlauf, 1992; Lufkin, 1996). For this reason it was postulated that the positioning of the *Hox* genes along the cluster and their tight cluster formation, which excludes any other genes, was necessary (although with an unknown mechanism) for proper spatiotemporal patterning. This is not true however as found for animals that do not have intact *Hox* gene clusters yet still maintain spatial patterning such as the fruit fly, the nematode and a tunicate (Seo et al. 2004; review in Ferrier and Minguillon 2003). As described by Monteiro and Ferrier (2006), these species all share rapid development that does not lend itself to the temporal aspect of gene induction. This still allows clustering to be necessary for temporal patterning however. Chambeyron and Bickmore (2004) hypothesized that there could be a structural component to the cluster where the orientation and proximity were needed for proper expression pattern. They were able to show that the anterior portion of the *Hox*B cluster in mice (*Hox*B1-9) underwent chromatin decondensation in response to a known *Hox* gene inducer, retinoic acid. Then in sync with their expression pattern each gene "looped out" from the chromatin structure towards the center of the nucleus. It is possible that the pressures necessary to maintain the cluster formation are different in different lineages and we may never know what the original pressure was. The loss of the clustering formation in some species indicates that it is not essential for bilateral life but its widespread occurrence at least indicates that it is extremely advantageous.

The widespread occurrence of *Hox* genes, their clustered nature and role in the formation of the body plan make them an ideal candidate to study differences and similarities between wide-ranging species and, as we will show in chapter 4, between closely related species. This is especially true in teleosts since many *Hox* genes have been maintained as duplicates and since accelerated and asymmetric rates of nucleotide evolution are thought to be one molecular contribution to the success of this clade.

Chapter 2- Closing the Gap between Teleosts and Non-Actinopterygians 2.1 Introduction

2.1.1 Ray-finned Fish Phylogeny

Comparative genetics has been widely used to help decipher the function of the vast amounts of non-coding DNA in the genome (Lee et al. 2006; Siegel et al. 2007; Sato et al. 2009). In gnathostomes, the predilection towards humans and 'model' organisms has resulted in conducting the majority of long-range comparative genomics between human, mouse, chick (Sarcopterygians), zebrafish, pufferfishes (Actinopterygians) and sometimes sharks (Chondricthyians). While studies of this nature are useful at finding patterns of conservation/loss, it is also important to understand how these patterns arise. To do this a wider taxonomic sample of each order is necessary. In Sarcopterygians the inclusion of reptiles and frogs and possibly even lungfishes and coelacanths will be useful. In Actinopterygians however the knowledge of more basal taxa is limited and therefore we will give a short review.

Actinopterygii (the ray-finned fishes) is subdivided into 4 major clades Polypteriformes (bichir and reedfish), Chondrostei (sturgeons and paddlefish), Holostei (gar and bowfin) and the crown group Teleostei (all remaining ray-finned fishes) (Nelson 1969). Compared to cartilaginous and lobe-finned fishes, the ray-finned fishes have undergone a remarkable number of whole genome duplications, which makes genome comparisons slightly more complicated. The teleosts are by far the most successful extant ray-finned fish clade with 38 orders, 426 families, 4,064 genera and >27,000 species (Nelson 2006). All teleosts share a whole genome duplication dubbed the FSGD (Jaillon et al. 2004). One hallmark of the teleost clade is additional rounds of whole genome duplications in a lineage-specific manner, e.g. salmonids (Ohno 1970; Allendorf and Thorgaard 1984) which have tetraploid genomes and as many as sixteen *Hox* clusters (Moghadam et al. 2005a; Moghadam et al. 2005b). Interestingly, evidence suggests the evolution of basal ray-finned fishes like gar (Ohno 1969) and paddlefish (Dingerkus and Howell 1976) may also be associated with lineage-specific duplication events.

As shown in Figure 2, **Amiiformes**, represented by a single extant species called the bowfin (*Amia calva*) is the closest sister group to the crown group of teleosts (Nelson 1994; Bemis et al. 1997). The bowfin lives in eastern North America and there is no indication of polyploidy in this species.

The next closest order is **Semionotiformes** (Nelson 1994; Bemis et al. 1997) (Figure 2). **Semionotiformes** are comprised of two extant genera with seven species known commonly as gars. Gars can be found in eastern North America and Central America. It has been postulated that gars may have undergone their own genome duplication (Ohno et al. 1969; Dingerkus and Howell 1976).

Order:Acipenseriformes (Figure 2) contains two families (Acipenseridae, Polypdontidae; Nelson 1994) comprised of six genera and twenty-six species known commonly as sturgeons and paddlefish. The twenty-four living species of sturgeons are found throughout the Northern Hemisphere; the two living species of paddlefish are found in the United States and China. Sturgeons have undergone at least three wholegenome duplications that result in phylogeny that can be deduced via chromosome number (Fontana and Colombo 1974; Ludwig et al. 2001; Fontana et al. 2008). Paddlefish appear to have undergone at least 2 whole-genome duplications (Dingerkus and Howell 1976). The most basal ray-finned fish clade is that of the order **Polypteriformes**.

Commonly known as bichirs and reedfish, **Polypteriformes** contains two genera and ten species. Evidence suggests that bichir has not undergone its own genome duplication (Chiu et al. 2004; Mulley et al. 2006; this study). Strikingly, the stem ray-finned fishes comprise ~ forty-four species or less than 1% of all ray-finned fishes. Despite a handful of useful candidate species among the basal ray-finned fishes (such as bichir and bowfin), most authors focus only on comparisons between outgroups to the Actinopterygians (Sarcopterygians; Chondrichthyians) and teleosts. We will present evidence that suggest many patterns and possible hypotheses are missed due to this simplistic approach.

2.1.2 Teleost Bias

The majority of gen(om)e comparison studies that have been conducted comparing Sarcopterygians and/or Chondrichthyians to Actinopterygians have focused on members of the teleost clade (Figure 2). Siegel et al. 2007 compared the Para*Hox* clusters of several teleost fishes to those of human and mouse. In this study they find that teleosts do share some conserved gene order and conserved non-coding sequences with mammals. They also found several non-coding DNAs that are conserved only among teleost fishes. But without more basal **Actinopterygii** in the analysis, there is no way of knowing if these CNS are novel to teleosts or are the result of *cis*-regulatory sequences that evolved in ray-finned fish stem lineages. The lack of phylogenetic depth in this study skews their conclusions about how the Para*Hox* clusters have evolved in the teleosts. This same type of problem arises in phylogenetic comparative work done by other authors as well (Lee et al. 2006).

Sato et al. 2009 conducted loss/retention analysis of 130 genes of taste and olfactory transduction and tricarboxylic acid cycle pathways. Again they compared several teleosts genomes to that of human and determined that one-half of the genes were present prior to the FSGD and 40% of those were maintained as duplicates. Many more genes may have been present prior to the FSGD and subsequently lost after the FSGD although this is unknown given that there is \sim 150 my of evolution missing in the comparison. One may conclude that this missing information is not relevant given that the authors want to compare teleosts to any state prior to their genome duplication. However, without information of how ray-finned fishes evolved prior to the FSGD one has no way of knowing how or why genes are retained or lost after the FSGD and how this has contributed to the evolution of the teleosts. Although the data can stand on its own as far as lost/retention rates, the conclusions drawn from this data are lacking a certain understanding of immediately prior states. This point is argued in Johnston et al. (2007) where the authors find that genes are more likely to be maintained as duplicates if they were undergoing accelerated evolution prior to the duplication.

Another assumption that is made using this type of data is that teleosts have lost several DNA regions including genes and CNSs that are shared between lobe-finned and cartilaginous fishes (Chiu et al. 2002; Venkatesh et al. 2007; Yu et al. 2008). This loss is often contributed to an accelerated mutation rate and/or the FSGD (which may or may not be mutually exclusive events). However, when stem-ray finned fish data is included in these types of studies one finds that this turnover started prior to the teleost radiation (Chiu et al. 2004; this study). Ravi and Venkatesh (2008) addresses this issue as well but still fails to use any stem-ray finned fishes in their study. The lack of data from pre-FSGD stem ray-finned fishes is glaring in phylogenetic studies. For example, a recent study attempted to use EST data to help solve gnathostome phylogenomics for the major clades (**Chondrichthyes**, **Sacropterygii**, **Actinopterygii** and **Tetrapoda**; Hallström and Janke 2008). They contributed lungfish (*Protopterus aethiopicus*) DNA sequence to the study in order to expand the depth of Sarcopterygian sampling, but despite having 4 teleosts, included no stem ray-finned fishes. It is impossible to confidently arrange these major clades without data from pre-FSGD ray-finned fishes. Similar work was done by Martin (2001).

If pre-FSGD stem ray-finned fishes are needed for genome comparison, then which are ideal candidates? Chiu et al. (2004) used bichir, the most basal, extant rayfinned fish. We propose that this is an ideal pre-FSGD ray-finned fish given its place in phylogeny as well as its apparent lack of a lineage specific genome duplication. Comparisons using bichir will add data from a genome that should be similar to Chondricthians and Sarcopterygians structurally, but undergone selective pressures of an Actinopterygian.

2.1.3 Bichir Phylogeny and Anatomy

At the base of the Actinopterygian tree is the genus *Polypterus* (bichir). Despite this phylogenetic position, bichir is not frequently used in studies. Perhaps this is because only recently has bichir held that phylogenetic position.

Polypterus is an enigmatic taxon with many shared and unique features that have given taxonomists constant headaches (Figure 4). Among the shared features are: 1. Lobe-like fins (**Sarcopterygii**) 2. Ganoid scales (**Sarcopterygii**) 3. 2 gular plates (**Coelacanthimorpha:Sarcopterygii** and **Holostei**) 4. Spiracles (**Chondrostei**) 5. Feathery external gills and double ventral lungs as juveniles (**Dipnoi:Sarcopterygi**) andHeterocercal tail (**Chondrostei**) (Janvier 1996).

Among the unique features are: 1. Dorsal fin rays that project horizontally from a vertical spine (Helfman et al. 1997) 2. Recoil aspiration (Brainerd et al. 1989) 3. Heterocercal tail, external gills and lobe-like pectoral fins are due to homoplasy and are anatomically different (Janvier 1996). Early systematists had difficulty classifying bichir using anatomical features and they were placed in at least four separate clades including the **Dipnoi** (lungfishes), **Ganoidei**, three separate groups of **Actinopterygii** (**Teleostei**, **Holostei**, and **Cladistia**) and an entirely separate subclass known as **Brachiopterygii** which was held in equal weight with the **Actinopterygii** and **Sarcopterygii** (Helfman et al. 1997). A consensus was reached in 1982 when Patterson placed **Polypteriformes** as the basal group to the **Actinopterygii**. After the advent of molecular phylogeny much work has been done and today it is accepted that bichir is indeed the most basal rayfinned fish (Inoue et al. 2003; Kikugawa et al. 2004; Figure 2).

Due to the diligent work put into phylogenetically positioning bichir among other fishes we can now use bichir in studies requiring a basal ray-finned fish. But without knowing the ploidy level of bichir we may still incur the issues that arise with other stem ray-finned fishes like the sturgeons, paddlefish and gars. For this reason our lab has put in great effort to help determine whether or not bichir has undergone a lineage specific genome duplication or at the very least chromosomal duplication resulting in greater than 4 *Hox* gene clusters.
2.2 Bichir *Hox* Gene Discovery

2.2.1 PCR Discovery and Sequencing of Hox Genes

Materials and Methods

Degenerate primers were designed from alignments of vertebrate Hox genes for HoxC4 and HoxD9 (C4 Forward 5'-ATG ACG TCG TAT TTG ATG-3'; C4 Reverse 5'-TGA TTT GCC TCT CGG AG-3'; D9 Forward 5'-GTA TTG GTA AAT ATG ATC ACG-3'; D9 Reverse 5'-CKG TTC TGA AAC CAG ATT TT-3'). PCR reactions were setup using reagents from Applied Biosystems[™] AmpliTaq® DNA Polymerase kit (N8080153) in the following concentrations: 1X buffer, 3.5 mM MgCl₂, 0.8 mM dNTP, and 0.5 uM primers. 50 ul reactions were made with 3 ul genomic DNA (unknown concentration), 2.5 units Taq DNA polymerase and diluted with sterile water. Negative controls were made under identical conditions except genomic DNA was not added. The PCR was run using a MJ Research PTC-200 DNA Engine thermalcycler under the following conditions: 95 C for 5 minutes, 30 cycles of (95 C for 1 minute, 47 C (HoxC4) or 52 C (HoxD9) for 1 minute, 72 C for 2 minutes), 72 C for 10 minutes. 5 ul of each PCR reaction was mixed with 1 ul 6X loading dye and loaded onto a 2% agarose gel (1X TAE) along with 4 ul of 1X Invitrogen 1kb DNA ladder (15615-024). Gels were run on an Owl brand electrophoresis unit at 60 milliwatts for 1.5 hours. Bands of correct size were excised from the gel and purified using Qiagen Gel Extraction Kit (28706) under standard protocol except DNA was eluted using 10 ul sterile water. Gel purified DNA was cloned into Promega pGEM®-T Vector System II (A3610) using standard protocol except reaction was incubated at 16 C for 20 hours. 2 ul of ligation reaction was transformed into 25 ul Escherichia coli Promega JM109 Competent Cells (L2001) under

the following protocol: on ice for 20 minutes, 45 C (water bath) for 42 seconds, on ice for 2 minutes, add 240 ul LB broth, 37 C for 1 hour at 200 r.p.m. The transformed cells were plated on to LB agar plates containing 50mg/mL ampicillin, 1M IPTG and X-gal and grown at 37 C for 16 hours. Colony PCR was performed on white colonies under identical conditions as original PCR except in 20 ul reactions. Colonies with band of correct size were grown in 3 mL of LB broth at 37 C for 16 hours at 200 r.p.m. Plasmids containing insert of correct size were purified using Qiagen QIAprep Miniprep Kit (27106) using standard protocol except DNA was eluted using 30 ul sterile water. 300 ng of plasmid DNA was sent for sequencing using the T7 primer to the DNA core facility at the University of Medicine and Dentistry of New Jersey, Pisctaway, NJ.

Chromatograms of the DNA sequences for *Hox*C4 and *Hox*D9 were analyzed for errors. Resulting DNA sequences were then trimmed of vector and primer and blasted against the non-redundant database at http://blast.ncbi.nlm.nih.gov/. Verification of *Hox* paralog identity was based on identity of top matches from this blast. After verification of paralog identity, sequences were analyzed via phylogenetic inference. Alignments were created of all known paralogs using ClustalW algorithm provided by MacVector® 9.5.2. The alignment was corrected by eye so that all sequences started at the same position. Neighbor-joining, Maximum Parsimony, Maximum Likelihood and Bayesian trees were created from these alignments. Neighbor-Joining and Maximum Parsimony trees were created using default parameters in PAUP* v4.0b10 (Swofford 2003). Maximum Likelihood trees were created using GARLI v0.951 (Zwickl 2006), which can be downloaded from www.bio.utexas.edu/faculty/antisense/garli/Garli.html. The starting tree was obtained using heuristic search under the likelihood optimality criterion in PAUP* v4.0b10 (Swofford 2003) with settings as specified by Modeltest (Posada and Crandall 1998, see Model Selection). The same settings were inputted into GARLI v0.951 (Zwickl 2006). Node confidence was assessed by using the bootstrap resampling method with 2,000 replications. The "number of generations without improving topology" setting was changed from 10,000 to 5,000 as suggested in the GARLI manual when doing bootstraps, as it will "shorten the run time without significantly affecting the results". A consensus tree was created using majority rule with a cutoff of 50% in PAUP* v4.0b10 (Swofford 2003). Bayesian trees for the nucleotide alignments were constructed using MrBayes v3.1.2 (Ronquist and Huelsenbeck 2003) and the parallel version of MrBayes v3.1.2 (Altekar et al. 2004) under the settings specified by MrModeltest. Two independent Markov Chain Monte Carlo analyses were run with the following settings: number of generations was set to 1,000,000, sample frequency was taken every 1,000 steps, number of chains was set to 4 and the temperature was set 0.2. 'Burnin' was assessed after the run using the sum parameters command. The 'burnin' for the nucleotide analysis was set to 1 for all 3 datasets, which is equal to the first 1,000 steps or tree topologies. A majority rule consensus tree was created disregarding the 'burnin' trees using the sum trees command with a cut off of 0.50 posterior probability.

2.2.2 BAC Library Screening

Materials and Methods

A 5-fold coverage bichir genomic bacterial artificial chromosome (BAC) library (Chiu et al. 2004) was screened for presence of bichir *Hox* genes using a DNA probe of *Hox*C4 and *Hox*D9. High-density 5 X 5 arrayed filters were made by the RZPD (http://www.rzpd.de). Southern hybridization was performed on these filters. DNA

probes were labeled with a non-radioactive marker, digoxigenin. We DIG (Digoxigenin)labeled the HoxC4 and HoxD9 fragment using Roche Diagnostics DIG DNA labeling kit (11175033910). The DIG labeling reaction includes boiling 800 ng (15 ul) of the HoxC4 or HoxD9 fragment in water for 10', placing on ice (H₂O) for 10', briefly spinning down, then adding 2 ul of the hexanucleotides, 2ul dNTP labeling mix, and 1ul Klenow enzyme provided in Roche kit. We then placed the labeling reaction at 37 C for 20 hrs. Southern hybridization was performed on the 5 X 5 filters in a Lab-Line rotisserie incubator at 65 C. Briefly, filters were "pre-hybridized" at 65 C for 5 hrs. DIG-labeled probe was added to pre-hybridization solution at a concentration of 1ul/ml. Pre-hybridization solution was then replaced with hybridization solution and incubated for 20 hours at 65 C. Filters were then washed with the following steps all at room temperature: rinsed in 2X SSC (300 mM sodium chloride, 30 mM sodium citrate), washed in first hybridization wash (2X SSC, 0.1% v/v SDS-sodium dodecyl sulphate) for 20 minutes while rocking, washed in second hybridization wash (1X SSC, 0.1% SDS) for 20 minutes while rocking, rinsed in diluent buffer (300 mM NaCl, 100 mM Tris ph 8.0) for 20 minutes while rocking. Filters were then saturated by 1% blocking solution (Roche 11096176001) for 1 hour while rocking. Alkaline phosphatase conjugated antibody to DIG (Roche 11093274910) was applied to filters in a 1/1000 ratio in 1% blocking buffer for 30 minutes while rocking. Filters were once again washed in a detergent solution (0.3% v/v Tween in diluent buffer) 3 successive times for 10 minutes while rocking. Filters were then incubated in detection buffer (1mM Tris pH 9.5, 0.1M NaCl) for 5 minutes. Filters were then affixed to old film panel and CDP star substrate (Roche 12041677001) was applied and covered with thin sheet of poly vinyl chloride. The substrate reacts with the alkaline

phosphatase to emit light, which is detected by film in a dark room. Coordinates of positive clones are determined in duplicate on a 2 clone per array basis.

A group of 4 clones were discovered with 1 or both *Hox*C4 and *Hox*D9. Due to the conflicting data from these hybridization experiments the bichir BAC library was screened via PCR for presence of *Hox*C4 containing clones using bichir specific primers (PseC4forward 5'-ATG AGG TCG TAT TTG ATG-3' and PseC4reverse 5'-TGA TTT GCC TCT CGG AG-3').

The bichir BAC library consists of 216 pools each of which contains 384 clones. The PCR reactions were setup similar to that of the genomic DNA isolation except they were scaled to 16 ul. The same PCR program was performed as for the genomic DNA isolation. No pool contained a single distinct band corresponding to the expected product therefore this analysis was not extended.

Earlier, bichir BAC clone CLN84 (AC135508) was isolated that contained the *Hox*D1 gene. This BAC clone was sent to Eric Lander at the Whitehead Institute/MIT Center for Genome Research to be sequenced. Annotation of the clone was performed to yield 3 *Hox* genes; *Hox*D1, *Hox*D2 and *Hox*D3. *Hox*D2 is the first D2 paralog that has been found among bony-fishes and supports the idea that bichir may represent a basal ray-finned fish. Phylogenetic analysis clearly defines *Hox*D1, *Hox*D2 and *Hox*D3 as 'D' paralogs of their specific *Hox* groups (Figure 7). There is no evidence of a *Hox*D4 gene upstream of *Hox*D3 despite 20 kb of sequence. The *Hox*D3 gene has the largest known intron of any vertebrate *Hox* gene. The *Hox*D3 intron is 16,255 bp and contains one intact Tc1 DNA transposon as well as remnants of Rex like non-LTR retrotransposons (see below). Bichir BAC clone M919 (AC138742) was annotated and found to contain 2

of the 3 exons of EVX2 (Figure 7) a vertebrate ortholog of the *Hox* domain containing gene in *D. melanogaster*, even-skipped. A *Hox*B containing bichir BAC clone (AC138147) was also found. This BAC clone contains the entire open reading frame (ORF) of *Hox*B5, *Hox*B8, *Hox*B10, *Hox*B13 and partial sequence for *Hox*B4 and *Hox*B7 (Figure 7). The partial sequences are most likely due to incomplete sequencing of the BAC clone and not due to a pseudogene status for *Hox*B4 and *Hox*B7.

2.3 Hox Gene Data Suggest Bichir is a Basal Ray-finned Fish

Phylogenetic results indicate that *Hox*C4 and *Hox*D9 of bichir were assigned to the correct clusters and paralog groups and each supports bichir's assignment as the most basal living ray-finned fish (Figure 5). Previous work has suggested that bichir does not have its own specific genome duplication (Chiu et al. 2004; Mulley et al. 2006), which is seen in other basal ray-finned fishes such as paddlefish, sturgeon, and gar (Ohno et al. 1969; Fontana and Colombo 1974; Dingerkus and Howell 1976; Ludwig et al. 2001; Fontana et al. 2008). *Hox*C4 is the first discovery of a *Hox*C paralog gene in bichir. *Hox*D9 adds to the annotation of *Hox*D1, *Hox*D2, *Hox*D3, *Hox*D12 and EVX2 in bichir that were found via clone identification and sequencing.

The discovery of several linked HoxB and D cluster genes as well as a HoxC cluster gene has helped verify that bichir has not undergone its own genome duplication (in agreement with Chiu et al. 2004 based on the HoxA cluster) and has also lent information to the evolution of Hox gene clusters in vertebrates as bichir has the first instance of a group 2 gene on the HoxD gene cluster in **Osteichthyes** and also the first instance of a group 1 gene on the HoxD gene cluster in **Actinopterygii** (Figure 6).

2.4 Conclusion

Bichir is in an important phylogenetic position among ray-finned fishes. Diverging from the rest of the ray-finned fishes prior to the FSGD is just one important factor. Bichir also has the distinction of being the most basal living ray-finned fish and according to the data gathered during this and previous work (Chiu et al. 2005; Mulley et al. 2006) does not appear to have undergone a separate lineage-specific genome duplication. Because of these factors it is important and advantageous to include bichir in all analyses determining the effects, or lack there of, of the FSGD on the evolution of ray-finned fishes. As will be presented in the following chapter, data from bichir *Hox* genes and *Hox* gene clusters has lent valuable information to the evolution of *Hox* gene clusters prior to the FSGD that supports the notion the duplication alone is not sufficient in explaining the genomic and phenotypic plasticity seen among the teleost lineage of ray-finned fishes.

Chapter 3- Re-analyzing Teleost Uniqueness

3.1 Introduction

3.1.1 Cis-regulatory Elements

In this chapter we present an argument of why *cis*-regulatory elements are important to evolution, how *cis*-regulatory elements have evolved in the conserved *Hox* gene clusters and how the addition of bichir affects the analyses of the changes observed in the non-coding DNA of teleosts *Hox* gene clusters.

We will start with a background of *cis*-regulatory elements, their detection and their importance. The majority if not all eukaryotic genes contain expression level controlling DNA sequences called *cis*-regulatory elements (CRE). These elements are normally found flanking the transcribed portion of the gene but may also be found within introns and even exons (including the coding region). CREs are supplementary to the promoter sequence that is responsible for binding RNA polymerase and its associated proteins.

The first CRE described was the *lac* operon (Jacob and Monod 1961). This operon is responsible for controlling the response to the presence or absence of glucose/galactose in the environment. From this knowledge came the idea that CREs are switches that could turn on or off the production of a protein. We now know that regulation can occur at many levels from DNA to protein. We also know that CREs are not simply 'on/off' switches. CREs may also work more like a dimmer switch controlling not only if RNA will be made but also how likely and how often RNA will be made. This is possible because CREs are made up of a bundle of transcription factor binding sites (TFBS) that bind proteins responsible for either enhancing or suppressing transcription. CREs respond specifically to the transcription factor environment allowing them to regulate their genes in a context dependent manner, in many instances at specific time-points during ontogeny and in specific tissues.

Complimentary to their role in development and tissue maintenance, CREs are likely to be targets of natural selection at the population level (see 3.1.4) and hence play an important role in genomic (Vavouri and Lehner 2009) and phenotypic evolution (Gompel et al. 2005). Despite their importance, little is known about CREs. This is due to the difficulty in identifying CREs in the genome because they do not code for a specific gene product and may be located far from the gene(s) whose action they control. Multiple methods have been developed to identify CREs. First we will look at traditional wet lab approaches and then computer-based approaches derived from them.

3.1.2 Traditional Approaches to Locating Cis-regulatory Elements

Traditional approaches to finding CREs include DNase footprinting, electromobility shift assays (EMSA) and deletion analysis, which can all be followed by transgenics. The first approach, DNase footprinting, consists of binding specific transcription factors (TFs) to a known sequence and digesting away the exposed, singlestranded DNA leaving behind only the DNA protected by the TF; termed the TFBS (transcription factor binding site), Using this approach, Galas and Schmitz (1978) first reported that TFBS are often clustered in genomes, which is one important trait of CREs.

The second approach, EMSA, involves incubating a specific DNA sequence with either proteins hypothesized to bind to the sequence or whole nuclear protein extracts and identifying DNA-protein complexes by their retarded rate of migration in gels, or 'shift'. While the EMSA procedure alone cannot identify the specific protein that is bound to the known DNA sequence, expansion of this method (supershift; Kristie and Roizman 1986) has proven powerful in identifying CREs of known TFs.

Using these traditional wet lab approaches many TFBS have been identified. Several databases such as TRANSFAC (Matys et al. 2003) and JASPAR (Sandelin et al. 2004) store all these known TFBS and allow one to submit an unknown DNA sequence thought to contain TFBS and have a search algorithm identify any similarities. The search algorithm works by creating a degenerate binding matrix for a transcription factor with known binding sites and then aligning that to the sequence in question. The degenerate binding matrix is designed by giving scores to the presence of one of the four nucleotides (A, C, G, T) at each position relative to the frequency they appear in known binding sites. Sometimes certain nucleotide positions are weighted heavier overall (core sequence) due to their inclusion in most if not all TFBS for their particular TF. These programs can do this for every transcription factor in their database so as to provide one with as complete of an array of possible TFBS for their sequence as possible.

The third approach, deletion analysis, has been used to detect *cis*-regulatory elements for many genes including *Hox* genes (Shashikant et al. 1995; Nonchev et al. 1996; Maconochie et al. 1999). Deletion analysis involves removing portions of the DNA upstream of a gene and looking for indication of loss of expression. After expression is lost the region deleted can be narrowed for higher resolution. All of these methods are, of course, indirect evidence of *cis*-regulatory activity and can be supplemented by transgenics.

Transgenics uses reporter gene assays, which involve placing a putative *cis*regulatory upstream of a minimal promoter and a marker gene (coding for a visible protein; ie. green fluorescent protein or a protein that can be secondarily visualized; ie. β -galactosidase). This construct is then transiently or permanently transfected into a model organism. Via transfection one can test for recapitulation of the endogenous expression pattern of the gene thought to be regulated by the putative *cis*-regulatory element in question and/or identify other possible regulated genes.

3.1.3 Comparative Genomic Approaches to Locating *Cis*-regulatory Elements

In the post-genomic era, comparative genomics has become a powerful approach to identifying CREs. In this method, orthologous non-coding DNA sequences from two to several groups of organisms, which collectively add up to enough evolutionary time that similarities in their sequences can be considered not likely by chance, are aligned. This approach is based on the observation that CREs evolve at a slower rate than surrounding non-coding DNA, presumably because they have a function(s) and are subject to purifying selection (Keightley et al. 2005). Evolutionarily conserved noncoding sequences (CNS; Hardison 2000) are putative CREs. In this approach, the depth of evolutionary time necessary for this analysis differs based on parameters including relative mutation rate, genome size, and generation time (review, Martin and Palumbi 1993). Protocols implementing this method include rVista (Loots and Ovcharenko 2004), TRACKER (Prohaska et al. 2004), and MONKEY (Moses et al. 2004).

Phylogenetic Footprint Clusters (PFCs) are a stringently defined type of CNS with specific methods of detection. PFCs are defined as CNSs that between any two species contain 2 or more "footprints" within 100 nucleotides of each other (Chiu et al.

2002). A footprint is defined as a string of at least 6 nucleotides that are conserved 100% between two or more species being compared that, for mammalian lineages, represent at least 250 million years of additive evolutionary time (Tagle et al. 1988). This method was modeled after DNAse footprinting (see 3.1.2; Galas and Schmitz 1978). Evolutionary biologists determine putative TFBS by allowing evolution to do the "digestion" that can be seen when comparing homologous regions of two distantly related organisms whereby there has been enough evolutionary time that the surrounding non-binding sites have diverged and only the TFBS are still conserved (Tagle et al. 1988).

Phylogenetic footprinting has shown to be a useful method in the search for CREs. The majority of known CREs in *Hox* clusters can be found by this method, although, the amount of false positives has not been assessed due to the amount of time necessary to empirically test each PFC that does not already correspond to a known CRE. A system such as the *Hox* clusters lends itself well to this type of CRE inquiries for several reasons. 1. Identifying orthologous non-coding DNA is highly accurate due to the highly conserved nature of the cluster formation. 2. Because of the importance *Hox* genes have to development, their expression patterns have been well researched and documented. 3. Despite this seeming understanding of the system very few *Hox* genes have had their CREs identified in much detail.

3.1.4 *Cis*-regulatory Elements vs. Transcription Factors

Cis-regulatory element mutations are thought to be responsible for the majority of novelty needed for adaptation in comparison to coding sequence mutations. This hypothesis was first put forth based on the structure and function of CRE vs. coding sequence (Monod and Jacob 1961; Britten and Davidson 1971). *Cis*-regulatory elements

are modular in nature and hence may easily overcome the problem of pleiotropy that acts against changes in protein coding sequences. *Cis*-regulatory elements can drive the expression of a particular gene in many different stages of development as well as in many different tissue types. Depending on which TFs are being expressed in any particular cell or at a given time (developmental, seasonal, etc.), the CRE can respond in kind to either suppress or enhance transcription of the gene it regulates. Because of this cell environmental plasticity, it is possible to change the expression of the gene in one cellular context without affecting the expression in another cellular context (reduced pleiotropy). Coding sequences on the other hand incur mutations that 69% (148/216) of the time change the amino acid sequence that it codes for and thus the protein that it produces.

It is thought that changes in the amino acid sequence would be highly pleiotropic in that a change to the protein structure would affect the function of the protein in all contexts (of course this can be overcome somewhat by alternative splicing and domain specific contexts). Based on these ideas it is proposed that CRE evolution can play a large role in adaptation. There are many experiments to show that this is indeed the case; well-known examples include pigmentation in the fruit fly (Wittkopp et al. 2002; Gompel et al. 2005) and pelvic reduction in sticklebacks (Shapiro et al. 2004). At the population level, CREs have shown to play a role in the adaptation of malaria resistance (Tournamille et al. 1995), lactase persistence (Bersaglieri et al. 2004), and blood clotting in humans (Rockman et al. 2005).

This is an important distinction because all evolution must take place at the population level where changes in allele frequencies cause changes in the species

phenotype as a whole. That CREs would be a more likely source of functional variation/adaptation at the population level is not surprising. As summarized by Wray (2007), expression differences in alleles are independent which means that CREs controlling the expression are co-dominant, whereas coding sequence mutations are more often than not recessive. This is important because for a beneficial allele to reach a frequency in a population that is measurable and effectual it must be selected for in the heterozygote. This is the case because before a sufficient number of homozygotes appear in the population the allele will likely be lost to drift.

There are many good arguments for why CREs play a larger role in adaptation and it appears at first glance that the empirical evidence agrees. But, it is also important to assess the assumption that is made to reach this hypothesis; changes to the amino acid sequence will have pleiotropic effects. This is not necessarily the case. Alternative splicing is one such form that may overcome pleiotropy. Also, proteins have many domains especially transcription factors. Transcription factors in particular have a DNA binding domain that should stay well conserved, changes in this region will almost surely be pleiotropic. But, transcription factors also have protein-protein interaction domains that help them bind to other proteins that are apart of the enhancer/suppressor complex that regulates transcription for the gene they are helping to control. Changes in these regions may or may not be completely pleiotropic such that a transcription factor will not always be binding with the same protein partners in different context.

Lending evidence to this type of modularity are motifs known as Short Linear Motifs (SLiMs) that help regulate these protein-protein interactions (Neduva and Russel 2005). SLiMs are normally 6-10 amino acids in length and often can be modular. Rearrangements of the amino acids can occur giving them a different binding profile and only a few changes can completely inactive or cause a *de novo* binding. In this way, SLiMs can overcome the pleiotropic effects that plague proteins coding mutations and be selected for very much the same way as a CRE.

Despite the possibility of a protein to overcome pleiotropy there is very little evidence that this occurs. There may be other factors that are not considered that keep proteins from overcoming pleiotropy. One reason may have to do with the difficulty to select for these methods at the population level. Which as is pointed out earlier in this paper is necessary to become a contributing allotype. SLiMs may be able to overcome this evolutionary snag but to date very little is known about them and there is no such evidence to support that they do indeed overcome pleiotropy. So until SLiMs or another method is better classified it is still the consensus that the majority of selection on mutations that affect development should occur in CREs.

3.1.5 *Cis*-regulatory Elements and *Hox* Gene Cluster Evolution

CREs are important to the evolution of *Hox* gene clusters. CREs are the most likely targets of natural selection, especially for higher order regulatory genes such as *Hox* genes. This is apparent in how the *Hox* genes accomplish their role. The function of *Hox* genes is to bind to their downstream targets (CREs) and either enhance or suppress the expression of the genes these CREs control. The main result of this transcriptional regulation is locating in space and time the formation of particular structures along an axis. *Hox* genes accomplish this spatiotemporal specificity via overlapping expression profiles setting up specific domains during development of the embryo. For this reason, changing the *Hox* gene's own spatiotemporal expression is the most effective way to alter their function. This is accomplished by altering the CREs of the *Hox* genes themselves thus changing their ability to respond to particular sets of upstream TFs. The result of this alteration will be the *Hox* gene and all of its downstream effectors being expressed in a different location in the embryo and thus altering the positioning along the axis.

The importance of the CREs of *Hox* genes can also be seen via work in the McGinnis lab (McGinnis et al. 1990; Malicki et al 1993) which has shown swapping out the coding region of *Hox* genes between *Drosophila* and mammals still allows them to function normally because they are being expressed at the right time and location. The importance of CREs also comes up in the discussion of the maintenance of the cluster formation. Several evolutionary biologists (Peifer et al. 1987; Kmita and Duboule 2003; Santini et al. 2003) have postulated that one reason the *Hox* genes maintain a clustered formation is because they locally share CREs (Gould et al. 1997). The question of whether or not or how much of a role local CRE sharing plays in maintaining the cluster formation is still open to debate and it is important to understand the maintenance pattern of CREs to determine the likelihood of this hypothesis.

3.2 *Hox* cluster Conserved Non-coding Sequence Database

3.2.1 Need for Comprehensive Database

Previous attempts have been made to catalog the CNSs within the *Hox* gene clusters of gnathostomes (Chiu et al. 2002; Santini et al. 2003; Chiu et al. 2004). These attempts were made in an effort to understand the relationship between species that contain 4 *Hox* gene clusters and those that contain more. In these studies a representative species is chosen from 2 or 3 clades of gnathostomes and then their *Hox* gene clusters are aligned and scanned for CNSs. The issue with these comparisons, which we hope to resolve, was the exclusion of species due to lack of sequencing data or the desire for simplicity.

As described in Chiu et al. (2004) it is important to include basal ray-finned fishes. Also apparent in this study is the knowledge that, at least for the teleost fishes, species thought to be similar may have a quite distinct retention patterns with the same disparately related species. For this reason we have attempted to create a comprehensive database of CNSs for all available gnathostome *Hox* gene clusters in an attempt to better understand the pattern of retention and loss of CNSs in these otherwise highly conserved gene clusters. Understanding this pattern will lead to a better understanding of the forces that act to resolve (or not) redundancies in conserved genetic systems that undergo replication. We also hope that establishing a comprehensive database with an informative and flexible naming system will lead to better communication between labs and help expedite searches for both the function of these CNSs as well as their contribution to the cluster formation of the genes they regulate.

3.2.2 Annotating *Hox* clusters

Materials and Methods

The *Hox* clusters used in this study were constructed by a variety of methods. *Homo sapiens* (human) *Hox*A cluster was taken from a shorter fragment of a contig made from clones with accession numbers AC004079, AC004080, AC010990. Human *Hox*B, *Hox*C, and *Hox*D clusters were taken from genomic DNA from the UCSC genome browser http://genome.ucsc.edu/ (NCBI35/hg17, release May 2004). The *Hox*B cluster is taken from chromosome 17, nucleotides: 43,961,813-44,161,040. The *Hox*C cluster is taken from chromosome 12, nucleotides: 52,618,296-52,735,253. The *Hox*D cluster is taken from chromosome 2, nucleotides: 176,772,385-176,881,142.

Xenopus tropicalis (frog) *Hox* clusters were taken from Ensembl web browser http://nov2005.archive.ensembl.org/Xenopus_tropicalis/index.html (JGI 3, release Jan 2005 v35.1b). The *Hox*A cluster is taken from scaffold 29 nucleotides: 1,777,789-2,133,531. The *Hox*B cluster is taken from scaffold 329 nucleotides: 415,000-1,016,000. The *Hox*C cluster is taken from scaffold 280 nucleotides: 199,492-581,365. The *Hox*D cluster is taken from scaffold 353 nucleotides: 474,676-800,000.

Latimeria menadoensis (coelacanth) *Hox*A cluster from EVX1 to *Hox*A9 was taken from BAC clone VMRC4-19C10 with genbank accession number 147788. The rest of the *Hox*A cluster and the entire *Hox*B, C, and D clusters were isolated from BAC clones and sequenced.

Heterodontus francisci (horn shark) *Hox*A cluster was constructed from two clones with accession numbers AF479755 and AF224262. The *Hox*D cluster was a clone with accession number AF224263.

Polypterus senegalus (bichir) *Hox*A cluster was made from two clones -22F22 and -164C2 with accession numbers AC126321 and AC132195, respectively. The partial *Hox*B cluster is constructed from clone L28995. *Hox*B13 is on segment L28995.23. *Hox*B10 is on segment L28995.7. *Hox*B8 and *Hox*B7 are on segment L28995.17. *Hox*B5 and *Hox*B4 are on segment L28995.1. The partial *Hox*D cluster is constructed from clone CLN84 which includes *Hox*D3, *Hox*D2, and *Hox*D1.

Danio rerio (zebrafish) Hox clusters were made from clones. HoxAa cluster was constructed completely from clone 241117 accession number AC107364, modifications included trimming the first 26,896 and the last 4,176 nucleotides and inserting a C at position 76,071. The HoxAb cluster was made from clone 100019 accession number AC107365 with an alteration of nucleotide 79,324 from T to C to avoid a premature stop codon. The HoxBa cluster was constructed with two clones CH211-72A16 and BUSM1-254O17 with accession numbers BX927395 and AL645782, respectively. Clone CH211-72A16 was spliced to BUSM1-254O17 immediately after the HoxB4a gene. The HoxBbcluster was simply clone BUSM1-227H09 accession number AL645798 used in its entirety with no alterations. The HoxCa cluster was made from clones DKEY 148F24 and clone DKEY 81P22 with accession numbers BX465864 and BX005254, respectively. The *Hox*Cb cluster was taken from a scaffold from the Ensembl genome browser http://nov2005.archive.ensembl.org/Danio_rerio/index.html (WTSI Zv5, release July 2005 35.5b). The HoxDa cluster was clone RP71-78H1 accession number BX322661 used in its entirety.

Oreochromis niloticus (nile tilapia) *Hox*A cluster is the entire clone with accession number AF533976.

Morone saxatilis (striped bass) *Hox*A cluster is the entire clone with accession number AF089743.

Oryzias latipes (medaka) *Hox* clusters were taken from genbank in their entirety. *Hox*Aa, Ab, Ba, Bb, Ca, Da, and Db are under accession numbers AB232918-AB232924, respectively.

Tetraodon nigroviridis (spotted-green pufferfish) *Hox* clusters were all taken from Tetraodon Genome Browser at http://genome.ucsc.edu (Genoscope 7/tetNig1, release Feb 2004). The *Hox*Aa cluster is taken from chromosome 21, nucleotides: 2,878,001-3,153,406. The *Hox*Ab cluster is taken from chromosome 8, nucleotides: 6,506,471-6,727,504. The *Hox*Ba cluster is taken from chromosome Unknown, nucleotides: 37,928,410-38,293,032. The *Hox*Bb cluster is taken from chromosome 2, nucleotides: 1,321,876-1,537,033. The *Hox*C cluster is taken from chromosome 9, nucleotides: 4,083,941-4,353,227. The *Hox*Da cluster is taken from chromosome 2, nucleotides: 10,975,763-11,218,409. An alteration was made at nucleotide position 11,134,740; a T was deleted in order to shift back to correct frame. The *Hox*Db cluster is taken from chromosome 17, nucleotides: 9,471,355-9,694,740.

Takifugu rubripes (Japanese pufferfish) *Hox* clusters were acquired from the http://nov2005.archive.ensembl.org/Fugu_rubripes/index.html (FUGU 2.0, release May 2004 v35.2g). The *Hox*Aa cluster is constructed from the entire scaffold 47. The *Hox*Ab cluster is constructed from scaffold 330.

3.2.3 Create Conserved Non-coding Sequence Database

To obtain PFCs, pair-wise alignments were made between orthologous intergenic regions of human *Hox* clusters and all other species *Hox* clusters, bichir *Hox* clusters and

all ray-finned fish *Hox* clusters, and among all teleost *Hox* clusters using MacVector version 8.0 (Accelrys®) which uses the clustalW algorithm. For PFC analysis the pairwise alignments between acanthomorph 'a' paralog *Hox* clusters were excluded due to their overall high identity. PFCs in this study were defined by the canonical definition of 2 or more sequences with 100% identity over at least 6 base pairs each of which are within 100 base pairs of each other. This analysis consisted of over 900 pair-wise alignments of homologous intergenic regions with an average alignment size of 10 kilobases. Due to the large number of PFCs obtained by this method I further restricted the criteria to include the alignment of each pair-wise PFC to be at least 60% identical and/or contain at least 5 PFs. All *Hox* clusters used in this study were scanned for repetitive and mobile DNA elements using the RepeatMasker database at http://www.repeatmasker.org/. PFCs that corresponded to masked elements were excluded.

In total I identified 563 unique PFCs that fit my criteria. After this I carefully determined which pair-wise PFCs overlapped across other species and numbered according to the relative position in the cluster with 1 starting at the posterior end of the cluster and ascending towards the anterior end of the cluster. This was accomplished by starting with the 'seed' species of human, bichir and zebrafish and determining overlapping PFCs by their overlapping nucleotide positions. After overlapping PFCs were determined, any PFC that existed in more than 2 species was subjected to a multiple alignment that was then trimmed to maintain the criteria of a PFC (Table S1).

PFCs were then broken down into sections based on differential retention of that section in the species that contain that PFC. A section may be as small as an individual

PF or as large as all but one PF. The PFCs were named based on their location in the cluster and for PFCs conserved among more than 2 species, their section content. The name consists of a 3 letter abbreviation for the species that it is found in, followed by 1 or 2 capital letters denoting the *Hox* cluster it resides in, followed by a 2 letter subscript denoting the intergenic region it resides in (see below), followed by the number of the PFC which are roughly ordered by their position along the cluster starting at the 5'end and sometimes followed by a 1-6 letter subscript describing the section content of that PFC (e.g. a PFC that is found between *Hox*A9 and *Hox*A8 in human is named HsaA_{GH}74_{abe} which signifies that it is found in human between genes A9 and A8, it is the 74th PFC on the *Hox*A cluster and it shares sections a, b, and e with other species; Figure 8). For nomenclature purposes *Hox* genes were coded A-O starting with EVX and ending with group 1 genes. We propose that if new PFCs are found within a *Hox* cluster used in this analysis that they be named and numbered based on the following formula:

$$X = \frac{distAP}{distAB} + A$$

X = number of new PFCP = new PFC A = PFC 5' to P B = PFC 3' to P

(e.g. if a new PFC is found 430bp downstream of $HsaA_{GI}103$ and $HsaA_{GI}104$ is 670bp downstream, then the new PFC should be named $HsaA_{GI}103.64$). I then compiled this information into two types of charts. One containing the name, location and sequence of PFCs in each individual *Hox* cluster and the other containing all PFCs in one *Hox* cluster paralog.

3.2.4 Analyze Conserved Non-coding Sequence Database

After the PFC database was created we searched for retention and loss patterns that may be pertinent to the evolution of gnathostomes with special emphasis on the rayfinned fishes and teleosts.

The first pattern looked at was 'deeply' conserved PFCs. 'Deeply' conserved PFCs are defined as found in at least 2 of the following groups, 1) horn shark, 2) \geq 2 lobefinned fish, 3) bichir, 4) \geq 2 teleost fish. This criterion limits 'deeply' conserved PFCs to those that have maintained identity over at least 733 million years of additive evolutionary time. Of the 563 unique PFCs, 78 (13.9%) fit this criterion (Figure 9). Given a random distribution and an average PFC divergence time of at least 270 million years (low end estimate) one would expect 37% of the PFCs to fit the criteria of at least 733 million years so this is a significantly small amount (p-value=0.001). All PFCs were blasted against the expressed sequence tag (EST) database at http://www.ncbi.nlm.nih.gov/BLAST/. If human or zebrafish contained the PFC then their sequence was preferentially used to perform the blast search. All PFCs were also blasted against the n database to identify untranslated regions and microRNAs.

Additionally, PFCs considered 'deeply conserved' were blasted against the non-coding RNA database at http://research.imb.uq.edu.au/rnadb/default.aspx (Pang et al. 2005; Table S2).

Literature searches were done to identify all known *Hox* CREs and micro-RNAs. All known *Hox cis*-regulatory elements and micro-RNAs were detected as deeply conserved PFCs. This speaks to the robustness of this method at detecting conserved functional non-coding sequences. To help determine those PFCs that would be good candidates for *cis*-regulatory elements efforts were made to identify PFCs that existed within sequences of known RNA transcripts. Of the 78 'deeply' conserved PFCs, 8 corresponded to sequences of known function: C8 early enhancer (Shashikant et al. 1995), A2 enhancer (Nonchev et al. 1996), D4 retinoic acid response element (RARE; Morrison et al. 1996), A4 RARE (Doersken et al. 1996), A5 MES enhancer (Larochelle et al. 1999), mir-196b (Yekta et al. 2004), mir-196-2 (Berezikov et al. 2005) and mir-10b (Berezikov et al. 2005). Of the remaining 70 'deeply' conserved PFCs, 22 were found in untranslated regions (UTR) of the RNA transcripts of *Hox* genes, 21 were found in the expressed sequence tag (EST) database and 27 have an unknown function. Of those 27, 6 lie within 500 bp up or downstream of the coding sequence of a *Hox* gene, which implies they could possibly be part of an unsequenced UTR or basal promoter element. That leaves 21 'deeply' conserved PFCs that lie within RNA transcripts and UTRs could also serve a *cis*-regulatory role.

Deeply conserved PFCs seem to have a biased towards the 3' end of the cluster. Between the paralogous *Hox* clusters the only difference that is apparent is the seemingly few deeply conserved PFCs on the *Hox*C cluster which is mainly due to the lack of PFCs with no known function. This may be due to sampling bias as the *Hox*C cluster is the only cluster that contains only 2 of the 4 groups considered (see figure 9 for explanation of groups). The finding of deeply conserved PFCs are not the only pattern worth exploring however, many unique patterns can be found when the phylogeny of the species used in this study are considered. Several patterns of retention/loss of PFCs throughout gnathostome phylogeny can be seen in this database. First we will address the previous findings of Chiu et al. (2004), where it was determined that bichir showed a pattern of 'mosaicism' in its PFC content.

Previous studies found a trend of mosaicism in the retention of PFCs on the *Hox*A cluster of bichir when comparing it to the *Hox*A clusters of non-ray finned fish and teleosts, the more derived ray-finned fish clade. This mosaicism showed alternatives to the apparent pronounced loss of PFCs in teleost fishes, as seen by Chiu et al. 2002, when comparing them to the *Hox*A clusters of human and horn shark whose *Hox* clusters shared a remarkable number of PFCs. In the current study the *Hox*A cluster of bichir shared 17 PFCs exclusively with non-ray finned fishes (lobe-finned fishes and cartilaginous fishes) and 48 PFCs exclusively with teleost fishes which is 26% and 74% respectively.

This appears to be in contrast with the numbers shown in Chiu et al. 2004 because bichir shares much more with the teleosts but still supports the claim of bichir showing a mosaic pattern between non-ray finned fishes and teleosts. When doing this comparison however it is important to take into consideration the number of *Hox* clusters compared in each category. When scaled by the number of pair-wise comparisons made the numbers are a little closer with 47% of the PFCs found exclusively between bichir and non-ray finned fishes and 53% found between bichir and teleosts.

The pattern is different for the *Hox*B cluster where bichir shared 21% of its PFCs with the non-ray finned fishes and 79% of its PFCs with the teleosts even after scaling for number of pair-wise comparisons (Table 4). In order to see if this pattern may be by chance and also to assess the amount of conservation in the derived ray-finned fishes we

also calculated the number of PFCs shared exclusively between human and other non-ray finned fishes and human and teleosts. After scaling, the *Hox*A cluster of human shared 74% of its exclusive PFCs with other non-ray finned fishes and 26% with teleosts. These numbers were comparable on the *Hox*B cluster with 82% and 18% respectively, again showing the conservative nature of non-ray finned fishes *Hox* clusters.

Another category needed to determine the true mosaicism of bichir's *Hox* clusters is the number of PFCs that are shared only among the teleosts species. This becomes a problem however because the **Acanthomorpha**, which consists of all the teleosts in this study excluding zebrafish, are too closely related. This makes it difficult to assign PFCs because of the high identity between their non-coding regions. For this reason the category of "exclusive to teleosts" must be reduced to "shared exclusively between zebrafish and any other teleosts".

The *Hox*Aa cluster of zebrafish shared 49% of its PFCs with non-teleosts (lobe finned fishes, cartilaginous fishes and basal ray-finned fishes) and 51% with teleosts with or without scaling. The *Hox*Ab cluster was 71% non-teleosts and 29% teleosts; *Hox*Ba 29% non-teleosts and 71% teleosts; *Hox*Bb 56% non-teleosts and 44% teleosts all with scaling. For the *Hox*Aa cluster andBb cluster zebrafish appears completely mosaic. For the *Hox*Ab cluster zebrafish appears to be more non-teleost like and for the *Hox*Ba cluster zebrafish appears to be more teleost like. If the 'b' paralog clusters are ignored due to their low number of PFCs (and reduced gene number) then the zebrafish takes on a cluster specific pattern that mirrors that of bichir. The *Hox*A cluster of bichir and its ortholog the *Hox*Aa cluster of zebrafish both share around 50% with non-teleosts and 50% with teleosts. In contrast to the *Hox*A cluster but in agreement with one another, the

*Hox*B cluster of bichir and the *Hox*Ba cluster of zebrafish both share around 25% with non-teleosts and 75% with teleosts (Figure 10).

These patterns and others that will be explained in the following paragraphs show evidence that not only do bichir *Hox* clusters show 'mosaic' patterns but also these patterns are different for different clusters. When one combines this data of turnover in the ray-finned fishes (starting in bichir and continuing into teleosts) with the data that show the lack of retention of ray-finned fish specific PFCs it highlights the dynamic genomic environment that exists in the teleosts that started to take root in the basal ray finned fishes. This is in stark contrast to the extremely conserved nature of the *Hox* cluster regulatory environment seen in and among the sister lobe-finned fishes and more basal cartilaginous fishes.

Combining the information of deeply conserved PFCs with the idea of looking for patterns of gain/retention/loss in the *Hox* clusters we constructed a phylogenetic tree with apparent acquisition and loss numbers for deeply conserved PFCs at each node (Figure 11). The criteria of a deeply conserved PFC requires that the PFC has been conserved for ~1 billion years of additive evolutionary time making this type of analysis very important in identifying large (time) scale changes in non-coding sequence conservation within the *Hox* clusters of the gnathostomes. The identity of whether the PFC was gained or lost in each specific lineage was determined on a parsimony basis. Currently only the *Hox*A cluster can be analyzed using this method because it is the only cluster that we have complete sequences for in horn shark and bichir, two pivotal species in the analysis (Figure 11).

For the *Hox*A cluster it is evident that at least 30 PFCs were acquired sometime before the divergence of the 3 major gnathostome lineages and differential loss of these PFCs can be seen with the majority being absent in the teleosts' HoxAb cluster. 4 PFCs were gained sometime after the divergence of cartilaginous fish but prior to the divergence of the lobe-finned and ray-finned lineages. Again the majority of these are absent in the teleosts' HoxAb cluster. The lobe-finned fish lineage appears to have acquired 2 PFCs at the base which have been maintained throughout lobe-finned phylogeny. The lobe-finned fishes have also maintained all but one of the gnathostome acquired PFCs. The ray-finned fish lineage appears to have gained 7 new PFCs after they diverged from the lobe-finned fishes. They also lost two of the gnathostome PFCs. Bichir does not appear to have lost any of the gnathostome or bony-fish PFCs. The teleosts appears to have lost 7 more of the gnathostome PFCs and 2 of the bony-fish PFCs sometime prior to the genome duplication and did not maintain any PFCs that were gained after the divergence of bichir. The *Hox*Aa cluster is more conservative than the *Hox*Ab cluster in that it only lost 1 more of both the gnathostome PFCs and ray-fin PFCs after the genome duplication. The *HoxAb* cluster appears to be very degenerate in its PFC conservation in that it lost 14 additional gnathostome PFCs, 1 additional bony-fish PFC, and 5 additional ray-fin fish PFCs after the genome duplication. Also the *Hox*Aa and HoxAb clusters appear to have gained 1 PFC each after the genome duplication. It is equally parsimonious to assume that each of these PFCs was gained after bichir diverged but sometime prior to the genome duplication and then subsequently lost in the other paralogous cluster.

These results highlight the turnover of highly and anciently conserved PFCs (putative CREs) that began at the base of the ray-finned fish clade and continued through the derived ray-finned fish clade and the lack of turnover in the lobe-finned and cartilaginous clades.

3.3 Mutation Rate Estimation

Materials and Methods

Intergenic distances analysis was done on select intergenic sequences. I chose intergenic sequences from the 5' and 3' end of each of the 4 *Hox* clusters based on the availability in phylogenetically important taxa. The intergenic sequences chosen for analysis were sequences between *Hox*A13 and *Hox*A11, *Hox*A5 and *Hox*A4, *Hox*B9 and *Hox*B8, *Hox*B3 and *Hox*B2, *Hox*C12 and *Hox*C11, *Hox*C8 and *Hox*C6, *Hox*D12 and *Hox*D11, and *Hox*D4 and *Hox*D3. Comparisons were made between teleost fishes; Japanese pufferfish (Tru) and spotted green pufferfish (Tni), medaka (Ola), and zebrafish (Dre). Comparisons were then made between mammal species with approximately similar divergence dates; human (Hsa) and baboon (*Papio hamadryas*, Pha), dog (Cfa), and opossum (*Monodelphis domesticus*, Mdo). Intergenic sequences were aligned using clustalW algorithm in MacVector version 9.0 (MacVector, Inc.). Jukes-Cantor D-values were calculated from these alignments using Mega version 3.1.

Approximate divergence times between two species that are necessary when performing comparative studies for conservation of non-coding DNA sequences can differ depending on generation times and mutation rates of the taxa selected. For mammals a general time of at least 250 million years divergence was determined by Tagle et al. (1988) for performing phylogenetic footprinting analysis. For other taxa divergence times have not been well worked out. In this study most of the species comparisons fit into the criteria of at least 250 million years divergence except for the comparisons among teleosts (zebrafish, acanthomorphs). For this study it appeared that the intergenic regions of the *Hox* clusters of the acanthomorph species (striped bass, nile tilapia, pufferfishes; diverged ~80-100 mya) were too similar to do a phylogenetic footprint comparison but when aligned with zebrafish which diverged ~135 million years ago (mya) from the acanthomorphs the intergenic regions appeared to be dissimilar enough to do phylogenetic footprint comparisons. For this reason we decided to compare intergenic region distances between teleosts with a mammalian proxy to see if indeed their intergenic regions were diverging quicker.

Figure 12 shows the Jukes-Cantor D-values for teleosts fish versus their mammalian proxies. Immediately apparent is the lesser values for the mammalian proxies which implies that either the teleosts have a much higher mutation rate, much shorter generation time, or the proxies are incorrect due to inaccurate divergence time estimates. The D-values of zebrafish versus Japanese pufferfish allowed us to determine that these species were divergent enough to perform a phylogenetic footprinting analysis. Therefore pair-wise alignments containing zebrafish versus the acanthomorphs were included despite the relatively recent divergence date.

Another pattern that is not as easily noticeable is the difference between the 5' and 3' ends of the clusters. The odd numbers which correspond to the 5' ends of the clusters all have greater D-values than the even numbers which correspond to the 3' ends of the cluster. This greater conservation at the 3' end is also noticeable in Figure 3 where the deeply conserved PFCs are biased towards the 3' end. This data supports the posterior flexibility hypothesis put forward by Ferrier et al. (2000) which states that the posterior *Hox* genes (9-14) are evolving faster than the anterior (1-8) and implies this is occurring, in general, at the posterior end of the *Hox* gene cluster.

3.4 Conclusion

Evolution at the most basic level is change in allele frequency that becomes fixed over time. Empirical and theoretical evidence suggest that selection at the population level is most likely to occur in *cis*-regulatory elements. Because of this it is important to understand the code and evolution of these non-coding elements. Without a standardized code for *cis*-regulatory elements and since they do not code for an identifiable alternative molecule, their identification is not as straightforward as it is for coding DNA.

In an effort to uncover these molecular gems among the other DNA, unique methods have been developed. One such method is detection of evolutionary conservation of non-coding DNA. This method has proved to be advantageous and accurate although not without weaknesses or hurdles. One such hurdle is the fact that sequence conservation may not be necessary for functional conservation (Fisher et al. 2006). Unfornutately, this hurdle cannot currently be overcome. Another such hurdle is finding homologous non-coding sequences to compare since by definition the DNA surrounding the CNSs must not be conserved. A unique molecular phenomenon that can help overcome this issue is the clustering of genes that remains intact over millions of years in disparate species resulting in stretches of definitive homologous non-coding DNA. One such system is the *Hox* gene cluster.

Despite the convenience, few authors attempt to find CNSs within the *Hox* gene clusters and those that have, concentrate on only a few species. In this study, we have done a complete scan of gnathostome *Hox* gene clusters' intergenic regions to identify as many putative CREs as possible while gaining insight into the evolution of these

sequences in jawed-vertebrates with specific focus on the ray-finned fishes and the highly speciose, diverse and derived group, teleosts.

First, it is apparent that CNSs in the gnathostome *Hox* gene clusters adhere to the posterior flexibility hypothesis of *Hox* genes put forth by Ferrier et al. (2000). Second, we have extended the work done by Chiu et al. (2004) showing the mosaicism in basal ray-finned fishes Hox gene clusters. The complete scan of gnathostome Hox clusters has revealed additional data supporting this mosaicism but has also shown that the turnover that causes this mosaicism has been continuous throughout the ray-finned fishes from the basal bichir to the highly derived teleosts family, **Percomorpha**. This is shown by the fact there are no CNSs that are conserved exclusively in teleosts. Zebrafish, an intermediate teleost, appears to be as mosaic as bichir when comparing its conservation to species that diverged before to that of species that diverged after. The turnover of CNSs contributing to this mosaicism is cluster specific indicating that the Hox gene cluster system does not necessarily evolve under the same pressures and circumstances across all clusters. Third, in an effort to formalize the identification of CNSs within the Hox gene cluster system we have proposed a flexible naming system as Scott (1993) did for the *Hox* genes.

Chapter 4- Defining a Cause of Uniqueness

4.1 Introduction

4.1.1 Hindbrain Development

What is happening at the molecular and population level that may explain this turnover in conserved non-coding sequences in ray-finned fishes? To help answer this question we have turned to a well-characterized enhancer controlling the expression of *Hox*A2 in the developing hindbrain. We will start with a brief introduction of hindbrain development and the known expression of *Hox*A2 in vertebrates. We will then perform both macro- and micro-evolutionary studies of the enhancer to help determine possible mechanisms of its seemingly dynamic expression patterns in teleosts.

The vertebrate central nervous system (CNS) develops from neuroectoderm that thickens into the neural plate that rolls into the neural tube. This process occurs in an anterior to posterior pattern. The CNS is ultimately divided into the forebrain, midbrain, hindbrain and spinal cord. During the development of the hindbrain the neural tube is divided into distinct segments called rhombomeres much like the mesoderm is divided into distinct segments termed somites. *Hox* genes are expressed in the developing CNS starting with an anterior border at rhombomere 2 (r2) in the hindbrain and ending at the posterior end of the spinal cord. More specifically group 1-4 genes are restricted to anterior expression limits in the hindbrain whereas group 5-13 genes all have an anterior limit in the spinal cord (Gaunt et al. 1989; Hunt et al. 1991; Keynes and Krumlauf 1994). The peripheral nervous system (PNS) develops from a group of cells that is derived from an area between the thickened neural plate and the overlying ectoderm called the neural crest. Neural crest cells migrate from a dorsal to ventral position and convert from

neuroectoderm into mesenchymal cells which give rise to numerous structures.

Pharyngeal arches (or branchial arches in fish) develop from these migrating neural crest cells. The first pharyngeal arch (PA1) arises from r2, the second pharyngeal arch (PA2) arises from r4 and the third pharyngeal arch arises from r6. The first pharyngeal arch will become the lower oral jaw and the second pharyngeal arch will become the hyoid in tetrapods and structures supporting the lower oral jaw in fish. Pharyngeal arches 3-6 or 7 become parts of the pharynx and trachea in tetrapods and gills and pharyngeal jaws in fish.

4.1.2 Hox A2 Expression

*Hox*A2 is expressed in the developing hindbrain with an anterior limit of expression at the r1/r2 boundary and continues to be expressed through r7 in mouse and chick embryos (Hunt et al. 1991; Krumlauf 1993; Prince et al 1994; Figure 13). Mouse *Hox*A2 has stronger expression in r3, 5 whereas chick has strong expression r3-7. Immediately following the FSGD there were two *Hox*A2 paralogs dubbed *Hox*A2a and *Hox*A2b. Since the FSGD, both paralogs have been independently pseudogenized in fish with a MRCA of 135 mya (zebrafish *Hox*A2a, Prince et al. 1998; medaka *Hox*A2b, Davis et al. 2008) as well as maintained as paralogs with differing expression patterns in fish with a MRCA of ~100 mya (Japanese pufferfish, Amores et al. 2004; Tumpel et al. 2006; striped bass, Scemama et al. 2006; Nile tilapia, Le Pabic et al. 2007). Zebrafish *Hox*A2b gene maintains a near identical ancestral expression pattern in r2-5 with stronger expression in r2, 3 (Prince et al. 1998). The same is true for the *Hox*A2b gene of Japanese pufferfish (Amores et al. 2004, Tumpel et al. 2006). The *Hox*A2a gene of Japanese pufferfish however has lost almost all hindbrain expression and appears in a
small stripe of cells in r1, 2. Striped bass and Nile tilapia *Hox*A2a genes are expressed in r2-7 with stronger expression in r2, 3 similar to the *Hox*A2b genes of zebrafish and pufferfish (Scemama et al. 2006, LePabic et al. 2007). The *Hox*A2b genes of striped bass and Nile tilapia are more weakly expressed. Striped bass *Hox*A2b gene is expressed in r2-5 and Nile tilapia *Hox*A2b is expressed in r2-5, 7 with stronger expression in r3, 5 (Scemama et al. 2006; LePabic et al. 2007; Figure 14).

*Hox*A2 is also expressed in the peripheral nervous system (PNS), specifically neural crest cells derived from r4 that pattern PA2 (Hunt et al. 1991; Krumlauf 1993; Prince et al 1994). This expression is maintained among tetrapods *Hox*A2 genes but again has various patterns in the teleosts' *Hox*A2 paralogs. In zebrafish, which has a pseudogenized *Hox*A2a, only the *Hox*A2b paralog is expressed and maintained in neural crest cells (Prince et al. 1998). The same is true for pufferfish *Hox*A2b expression (Amores et al. 2004; Tumpel et al. 2006). In striped bass and Nile tilapia, both paralogs are expressed weakly at the onset but only *Hox*A2a is maintained in detectable levels (Scemama et al. 2006, LePabic et al. 2007). Medaka, which has a pseudogenized *Hox*A2b, follows the same pattern as striped bass and Nile tilapia (Davis et al. 2008).

Controlling the expression of *Hox*A2 genes are 3 distinct enhancers (Figure 15). Expression in r2 is controlled by an enhancer in exon 2 of the *Hox*A2 gene, expression in r4 is controlled by an enhancer within the intron of the *Hox*A2 gene, and expression in r3, 5 and in r4 derived neural crest cells is controlled by an enhancer ~1-3kb upstream of the *Hox*A2 gene transcription initiation site (Nonchev et al. 1996; Maconochie et al. 2001; Tumpel et al. 2006). Within each of these enhancers are distinct regulatory elements that drive partial expression.

The r3/5 enhancer is the only known *Hox*A2 enhancer that lies outside the transcriptional start and stop sites. The r3/5 enhancer is divided into 5 elements that control rhombomere expression that are known as 'response elements' (RE1-5, Nonchev et al. 1996; Maconochie et al. 2001; Tumpel et al. 2006) and 4 elements that control neural crest and pharyngeal arch expression that are known as 'neural crest elements' (NC1-4, Maconochie et al. 1999). Some upstream transcription factors have been identified that bind to these *cis*-regulatory elements and are necessary for proper HoxA2 expression and rhombomere and pharyngeal arch development. There appears to be 1 specific transcription factor for each of the three compartments where *Hox*A2 expression is driven by the $r_{3/5}$ enhancer. Krox-20 is normally expressed in tissue that will become rhombomeres 3 and 5 (Wilkinson et al. 1989; Nieto et al. 1991; Bradley et al. 1993; Oxtoby and Jowett 1993). Krox-20 (a.k.a. Kruppel, egr2) has two binding sites in the r3/5 enhancer sequence and directly regulates expression of *Hox*A2 in r3 and partially in r5 (Nonchev et al. 1996). Mafb (a.ka. Kreisler, valentino) is normally expressed in and is necessary for r5/6 development (Prince et al. 1998b; Sadl et al. 2003). Mafb has multiple binding sites within the $r_{3/5}$ enhancer and though it has not been shown that it directly regulates *Hox*A2, *Hox*A2 expression is absent in r5 in Mafb^(-/-) zebrafish (Prince et al. 1998b). AP-2 is expressed in the neural crest cells and their derivatives (Mitchell et al. 1991). AP-2 has multiple binding sites in the $r_{3/5}$ enhancer and, though it has not been shown to directly regulate *Hox*A2 expression most likely due to redundant AP-2 family members, the r3/5 enhancer has been shown to drive expression of a reporter gene in the same pattern as AP-2 expression (Maconochie et al. 1999). The combination of these 3 main transcription factors and several co-factors that have not yet been identified are

responsible for the total expression of HoxA2 in r3 and 5 and neural crest cells derived from r4 in the developing hindbrain of all studied vertebrates.

The $r_3/5$ enhancer has been studied in much detail via deletion and swap assays. Deletion assays in mouse done by Nonchev et al. (1996), Maconochie et al. (1999) and Maconochie et al. (2001) identified RE1-4 and NC1-4 as well as two essential Krox-20 binding sites and an element known as Box A. Both Krox-20 sites, Box A and RE1-3 are necessary for proper expression in r3 and 5 although r5 expression is only lost completely in Krox-20 site deletions (Maconochie et al. 2001). RE4 is shown to stimulate r5 expression in the presence of Krox-20 sites. Both RE1 and RE3 contain a TCT motif (TCTNAC) that appears to be the essential binding site for their function (Maconochie et al. 2001). A similar experiment was done for expression in the neural crest cells. NC1, 3 and 4 were shown to be essential for neural crest cell expression but did not affect r3, 5 expression (Maconochie et al. 1999). NC2 was shown to be essential for neural crest cell expression and although it did not affect r³ expression it did lower expression in r⁵ (Maconochie et al. 1999). It is important to note that NC2 and RE4 overlap as well as NC3 and RE3. NC3 and RE3 do not appear to overlap in essential positions though because absence of NC3 does not abolish r3, 5 expression like absence of RE3 (Maconochie et al. 1999; Maconochie et al. 2001). Most likely it is the TCT motif of RE3 that is responsible for driving expression in r3, 5. NC2 and RE4 both give a similar phenotype of reducing or ablating expression in r5.

Swap assays were done in the Japanese pufferfish (Tumpel et al. 2006). The Japanese pufferfish has both a *Hox*A2a and *Hox*A2b paralog although the *Hox*A2a paralog has lost almost all expression (Amores et al. 2004). Tumpel et al. (2006)

assumed that the loss of expression of *Hox*A2a was due to inactive enhancer elements. To take advantage of this they swapped out RE1-4 individually from the functional *Hox*A2b r3/5 enhancer into the non-functional *Hox*A2a r3/5 enhancer to determine how much each individual response element contributed to the overall r3, 5 expression levels. From this analysis they determined the fraction of embryos each response element was able to drive expression in and decided that this was the efficiency of that particular element. The results were as follows: Box A 0%, RE2 6%, RE3 67%, RE4 32% and a newly discovered RE5 33%. Although this percentage was calculated based on the fraction of embryos, the intensity of the staining was directly correlated. Combining these analyses it shows that RE3 is a major factor in r3, 5 expression whereas RE4 and RE5 are minor factors.

4.2 Expression Analysis of *Hox* A2 Paralogs

Materials and Methods

We used *in situ* hybridization using mRNA probes on whole mounted embryo to detect expression of *Hox*A2a and *Hox*A2b in a tissue and stage specific manner. *Hox*A2a, *Hox*A2b and EGR2 were isolated from *F. heteroclitus* gDNA (gift from D. Duvernell) using PCR protocol as described in section 2.2.1 with the following modifications: *Hox*A2a was isolated with *Hox*A2a exon 2 forward (5'-TGACCGAGAGGCAGGTCAAGG-3') and *Hox*A2a exon 2 reverse (5'-AGGGCAGAGGGGCTGTCACC-3') primers at an annealing temperature of 56 C; *Hox*A2b was isolated with *Hox*A2b forward (5'-CCTGACATCTCTCGCTAACC-3') and *Hox*A2b reverse (5'-AGAGGTCAGACGCTGCTGC-3') primers at an annealing temperature of 59 C; EGR2 was isolated with EGR2 forward (5'-CCAGACCTTYACCTAYATGGG-3') and EGR2 reverse (5'-

TGTGTCTCTTYCTCTCRTCGC-3') primers at an annealing temperature of 59 C to yield a 400bp, 250bp and 955bp fragment, respectively. DNA fragments were cloned into the pGEM T-vector (Promega). RNA probes were synthesized using Roche T7 RNA polymerase (10881767001) that primes from the pGEM T-vector T7 site. *Hox*A2a andA2b RNA were synthesized using Roche DIG RNA labeling mix (1127703910). EGR2 was synthesized using Roche Fluoroscein RNA labeling mix (11685619910). RNA was purified using standard Phenol/Chloroform extraction. *In-situ* hybridizations were performed as described (Thisse and Thisse 2008) with the following modifications. Embryos were de-chorionated and de-yolked after rehydration and before digestion. Embryos were then digested in proteinase K for 50 seconds per somite. Antibodies were pre-absorbed in blocking buffer for 2 hours at 4 C while rocking. Following overnight incubation with antibody, embryos were washed 6 times for 30 min each with gentle agitation. Embryos were stained in ceramic spot plates in the dark.

For two-color staining, both EGR2 and the *Hox*A2(a or b) RNA probe were hybridized to the embryo simultaneously. The 1st stain was conducted for EGR2 via Roche anti-fluorscein-AP Fab fragments with Sigma FastTM FastRed (Sigma). The embryo was then washed 2 times for 30 minutes each in 1X PBT followed by a 30 minute wash in AP inactivation solution (0.1 M glycine-HCl pH 2.2, 0.1% Tween 20), followed by 4 times for 30 minutes in 1XPBT. The 2nd stain was conducted for *Hox*A2(a or b) via Roche anti-DIG-AP Fab fragments with NBT/BCIP stain providing a contrasting blue/purple color. Stained embryos were imaged using a Leica DFC290 digital camera attached to a Leica MZ12.5 stereo dissecting microscope.

In-situ hybridization analysis was performed with mRNA of *Hox*A2a and *Hox*A2b genes of mummichog (*Fundulus heteroclitus*) on *F. heteroclitus* embryos from 4 distinct developmental stages to determine the pattern of expression the *Fundulus sp.* group has compared to the patterns seen in other teleosts lineages. Both the *Hox*A2a and *Hox*A2b gene have a similar onset of expression in r2, 3 seen in figures 16m, n respectively. At the 8-somite stage *Hox*A2a and *Hox*A2b show weak expression in r2-4 and PA2 (Figures 16a-d). The strongest expression is seen at the 14-somite stage (as is in other teleosts; Prince et al. 1994; Scemama et al. 2006; Le Pabic et al. 2007; Davis et al. 2008) where *Hox*A2a is expressed in r2-7 with stronger expression in the more anterior rhombomeres and *Hox*A2b in r2-5 with weak expression in r5 (Figures 16e-h). In difference to other teleosts both *Hox*A2a and *Hox*A2b are strongly expressed in PA2 at

the 14-somite stage (Figures 16g, h). Expression was also detected at the 21-somite stage to determine maintenance of expression. At this stage *Hox*A2a and *Hox*A2b are again similar with expression in r2-5 and PA2 although *Hox*A2b appears to have slightly stronger expression in PA2 (Figures 16i-l).

Compared to other teleosts F. heteroclitus maintains the ancestral expression of the *Hox*A2a gene. This is deduced from known expression data where striped bass, Nile tilapia and medaka all have expression in r2-7 with stronger expression more anteriorly and also strong expression in PA2 (Scemama et al. 2006; Le Pabic et al. 2007; Davis et al. 2008). This assumes that the psuedogenization of HoxA2a in zebrafish and the near complete loss of expression in Japanese pufferfish were independent events, which is the most parsimonious conclusion (Prince et al. 1998a; Amores et al. 2004). The HoxA2b paralog however shows continued variation that is seen in other teleosts. In F. *heteroclitus* the *Hox*A2b gene is expressed strongly in r2-4 but weaker in r5 (Figure 16f, h). For the other known teleosts expressions, striped bass has weak expression in r2-5, Nile tilapia has weak expression in r2, 4, 7 and strong expression in r3, 5, medaka has a pseudogene, Japanese pufferfish has strong expression in r2-5 and zebrafish has weak expression in r4, 5 and strong expression in r2, 3 (Scemama et a. 2006; LePabic et al. 2007; Davis et al. 2008; Amores et al. 2004; Prince et al. 1998). Despite the differing expressions among the *Hox*A2b genes of teleosts in the rhombomeres they all show weak expression in PA2 except for F. heteroclitus, which has strong expression. This is the first instance of strong expression of HoxA2b in PA2 and also the first instance of definite and strong expression of both *Hox*A2 paralogs in PA2. Due to the differing expression patterns of *Hox*A2b and the strong conservation of *Hox*A2a expression we

furthered our study to look for evidence of selection in the enhancer sequences of these paralogs.

4.3 Mutation Rate Analysis of *Hox* A2 Loci

4.3.1 Phylogenetics of Hox A2 Loci

Materials and Methods

To determine mutation rates among *Hox*A2 loci we first created phylogenetic trees of each locus. Nucleotide alignments were performed using the clustalW algorithm provided by MacVector® 9.5.2. The alignments were corrected by eye so that all sequences started at the same position. 4 types of gene trees were constructed including neighbor-joining, maximum parsimony, maximum likelihood and Bayesian. Although neighbor-joining and maximum parsimony are considered antiquated there are some cases in which they have been shown to be more accurate (Landan and Graur 2007). For the more sophisticated tree building methods it was necessary to find an optimal model and prior inputs.

ModelTest v3.7 (Posada and Crandall 1998) was used to select the likelihood model for the nucleotide data. The model selected for the *Hox*A2 alignment by the hierarchical likelihood ratio tests (hLRT) (Gaut and Weir 1994) was HKY+G and by the Bayesian information criterion (BIC) (Raftery 1986a, 1986b) was HKY+G. We chose to use the HKY+G model which estimated the following parameters: Base frequencies; A=0.2333, C=0.3466, G=0.2580, T=0.1620. Ti/Tv ratio of 1.4986. Among site rate variation; proportion of invariable sites=0, Gamma distribution shape parameter=0.8828. The model selected for the *Hox*A2 enhancer alignment by the hierarchical likelihood ratio tests (hLRT) (Gaut and Weir 1994) was K80+G and by the Bayesian information criterion (BIC) (Raftery 1986a, 1986b) was K81+G. We chose to use the K80+G model, which estimated the following parameters: Base frequencies; cital frequencies. Ti/Tv ratio of 0.9952. Among site rate variation; proportion of invariable sites=0, Gamma distribution shape parameter=1.0289.

MrModelTest v2.2 (Nylander 2004) was used to select the likelihood model for the nucleotide data that could be implemented by MrBayes. The model selected for the *Hox*A2 alignment by hLRT, hLRT2, hLRT3 and hLRT4 was HKY+G. The model selected by AIC was HKY+G. We chose to use the HKY+G model which when implemented in MrBayes gives a prior state frequency of dirichlet (1,1,1,1) and uses the basic model nst=2 with among site rate variation set to estimate rates based on a gamma shaped distribution. The model selected for the *Hox*A2 enhancer alignment by hLRT, hLRT2, hLRT3 and hLRT4 was K80+G. The model selected by AIC was HKY+G. We chose to use the K80+G model which when implemented in MrBayes gives a prior state frequency of fixed (equal) and uses the basic model nst=2 with among site rate variation set to estimate rates based on a gamma shaped distribution.

Neighbor Joining trees for the nucleotide alignments were constructed using PAUP* v4.0b10 (Swofford 2003). The *Hox*A2 and *Hox*A2 enhancer trees were constructed under the following assumptions; distances were calculated using the Tamura-Nei method (Tamura and Nei 1993), using parameters specified from models selected above. The objective function was set to minimum evolution and TBR was selected as the swapping algorithm. Trees were constructed using the Neighbor Joining method (Saitou and Nei 1987) and then 2000 bootstraps were conducted to assess node confidence. A consensus tree was created using majority rule with a 50% cutoff.

Maximum parsimony trees for nucleotide alignments were constructed using PAUP* v4.0b10 (Swofford 2003). All nucleotide trees were constructed under the

default settings using a heuristic search and node confidence was assessed with 2000 bootstraps. A consensus tree was constructed using majority rule with a 50% cutoff.

Maximum likelihood trees for the nucleotide data of both alignments were constructed using GARLI v0.951 (Zwickl 2006), which can be downloaded from www.bio.utexas.edu/faculty/antisense/garli/Garli.html. The starting tree was obtained using heuristic search under the likelihood optimality criterion in PAUP* v4.0b10 (Swofford 2003) with settings as specified by Modeltest (Posada and Crandall 1998, see Model Selection). The same settings were inputted into GARLI v0.951 (Zwickl 2006). Node confidence was assessed by using the bootstrap resampling method with 2,000 replications. The "number of generations without improving topology" setting was changed from 10,000 to 5,000 as suggested in the GARLI manual when doing bootstraps as it will shorten the run time without significantly affecting the results. A consensus tree was created using majority rule with a 50% cutoff in PAUP* v4.0b10 (Swofford 2003).

Bayesian trees for the nucleotide alignments were constructed using MrBayes v3.1.2 (Ronquist and Huelsenbeck 2003) and the parallel version of MrBayes v3.1.2 (Altekar et al. 2004) under the settings specified by MrModeltest (see Model Selection). Two independent Markov Chain Monte Carlo analyses were run with the following settings: number of generations was set to 1,000,000, sample frequency was taken every 1,000 steps, number of chains was set to 4 and the temperature was set 0.2. 'Burnin' was assessed after the run using the sum parameters command. The 'burnin' for the nucleotide analysis was set to 1 for both datasets, which is equal to the first 1,000 steps or tree topologies. A majority rule consensus tree was created disregarding the 'burnin' trees using the sum trees command with a cut off of 0.50 posterior probability.

Phylogenetic analysis indicated that *Hox*A2a, *Hox*A2b, *Hox*A2a enhancer and *Hox*A2b enhancer sequences isolated from *F. heteroclitus* as well as northern studfish (*Fundulus catenatus*) and the two species that were later used in population level studies, black-striped topminnow (*Fundulus notatus*) and black-spotted topminnow (*Fundulus olivaceus*) were true paralogs and were the result of the same duplication as the rest of the teleosts' *Hox*A2 sequences, FSGD (Figure 17). Overall, gene trees appear to agree with accepted species phylogeny.

4.3.2 Mutation Rate Analysis

Gene trees and alignments were used as input data for a character state tree constructed using MacClade v4 (Maddison and Maddison 1989) for the 156 bp spanning NC2 to RE3 which also encompasses the entire RE4 and 5' half of NC3. From this analysis it is apparent that the 'b' paralog has acquired more changes than the 'a' paralog and at a seemingly steady rate (Figure 18). The changes in the 'a' paralog are concentrated at the base of the teleosts (35) prior to the rapid speciation with significantly (p=0.00468) fewer changes in all of the following internal and terminal branches (34 total) as compared to identical branches in the 'b' paralog (53 base and 122 other). The 'b' paralog however, has a continuous change in characters with no less than 23 on any branch. The *Fundulus sp.* 'b' paralog has acquired more changes than any other 'b' paralog terminal with at least 36 changes. This evidence of continued turnover in the 'b' paralog binding sites well into the *Fundulus sp.* lineage and lack thereof in the 'a' paralog is in contrast to the more conserved nature of the 'b' paralog sequence between the two in-group species of *Fundulus sp.* This is more apparent taking into consideration changes in highly conserved binding sites. When comparing only those sites that have one step in

the tree (those sites where all taxa except for one share the same state) the *Fundulus sp*. 'b' paralogs have at least twice as many steps as any other fish/paralog. This indicates that leading to the *Fundulus sp*. lineage changes in highly conserved nucleotides were at least twice as likely to become fixed then in any other fish lineage. This is further supported by the fact that changes within the *Fundulus sp*. group at the 'b' paralog enhancer are concentrated around functional sites. This same pattern can be seen in the *Hox*A2 coding sequences as well.

4.4 Population Genetic Study of *Fundulus Hox* A2 Enhancer Evolution

4.4.1 Specimen Acquisition

Materials and Methods

To perform a population genetic study on *Fundulus* it was necessary to acquire wild Fundulus fish because no lab strains exist, we needed individuals from two sister species and lab strains are unlikely to maintain the variation that existed before they were institutionalized. For the purpose of the population genetic study we collected individuals from two sister species of killifish, black-striped topminnow and blackspotted topminnow from Mississippi River drainages in Illinois and Missouri with the help of Dr. David Duvernell of University of Southern Illinois-Edwardsville and Robert Lynch (lab member). F. olivaceus was collected from the west side of the Mississippi River (Missouri) from 3 separate locations comprising two separate river drainage systems. These species were chosen due to the glut of knowledge of their phylogeography, well studied relationship, location within the United States and availability of expert on-site help. From the 1st drainage system we collected 93 individuals from one site, which was Rockford Beach at Big River at House Springs (38° 25' 20.27" N, 90° 35' 23.58" W, from here on known as Rockford Beach). From the 2nd drainage system we collected 29 individuals from two sites which were Little Piney Creek (5 individuals) at Highway 44 bridge at Jerome (37° 55' 04.68" N, 91° 58' 16.66" W, from here on known as Little Piney) and Gasconade River (24 individuals) at Jerome (37° 56' 05.34" N, 91° 58' 39.24" W, from here on known as Gasconade River). F. notatus was collected from the east side of the Mississippi River (Illinois) from 3 separate locations comprising two separate river drainage systems. From the 1st drainage system

we collected 42 individuals from one site, which was Salt Creek at Highway 40 bridge east of Effingham (39° 07' 15.49" N, 88° 31' 24.00" W, from here on known as Salt Creek). From the 2nd drainage system we collected 64 individuals from two separate locations which were Kaskaskia River at Highway 2700N north of Vandalia (39° 07' 53.79" N, 90° 35' 23.58" W, from here on known as Kaskaskia River) and Big Creek at Highway 2100E and 2600N intersection north of Saint Elmo (39° 06' 57.32"N, 88° 51' 42.81" W, from here on known as Big Creek). Approximately 12 individuals of an outgroup taxa northern studfish were also collected at Little Piney. The fish were collected on September 16th and 17th, 2006. Collection of individuals was done using seines and hand-nets. We preserved individuals on-site in 95% ethanol. Individuals were later placed into separate, numbered storage bottles in 95% ethanol.

We performed DNA isolation of individuals using fin clips under standard tissue preparation protocols using the AquaPure Genomic DNA Tissue Kit by Bio-Rad.

4.4.2 Gene Isolation

Materials and Methods

We isolated *Hox*A9b, A3a, A2a, A2b and B2a genes; *Hox*A2a and *Hox*A2b r3/5 enhancers as well as phosphoglycerate kinase 1 (PGK1) from *F. notatus* and *F. olivaceus* using PCR protocols as described in section 2.2.1 with the following modifications: *Hox*A9b was isolated with A9b forward (5'-CTTTGGAGACGCACACWCC-3') and A9b reverse (5'-TTCTTCATCTTCATYCTGCGG-3') primers at an annealing temperature of 57 C; *Hox*A3a was isolated with A3a forward (5'-ARTACAARAAGGATCAGAAAGG-3') and A3a reverse (5'-

TTRCCCATTGTGATTGCTCC-3') primers at an annealing temperature of 57 C;

*Hox*A2a was isolated with A2a forward (5'-GAATTCGARCGAGAGAGCG-3') and A2a reverse (5'-ACRGGTCCGTTKGAGATGG-3') primers at an annealing temperature of 56 C; *Hox*B2a was isolated with B2a forward (5'-

CATTTCAAACTTCATCAATCAAGG-3') and B2a reverse (5'-

CTCYTTCATCCAKGGRAACTC-3') primers at an annealing temperature of 58 C; PGK1 was isolated with PGK1 intron 7 forward (5'-

GCRAAGGTGAAAGATAAGATYCAGC-3') and PGK1 intron 7 reverse (5'-

TCTCSGCTTTGGCCATCAGG-3') primers at an annealing temperature of 62 C.

*Hox*A9b and *Hox*A3a were subjected to the same phylogenetic analysis as HoxA2a and HoxA2b to determine their paralog status with the following gene specific input data: Regarding ModelTest v3.7 (Posada and Crandall 1998), the model selected for the HoxA3a alignment by the hierarchical likelihood ratio tests (hLRT) (Gaut and Weir 1994) was HKY+G (Hasegawa et al. 1985) and by the Bayesian information criterion (BIC) (Raftery 1986a, 1986b) was HKY+G. We chose to use the HKY+G model which estimated the following parameters: Base frequencies; A=0.2236, C=0.3432, G=0.2357, T=0.1975. Ti/Tv ratio of 1.4676. Among site rate variation; proportion of invariable sites=0, Gamma distribution shape parameter=0.6010. The model selected for the *Hox*A9b alignment by the hierarchical likelihood ratio tests (hLRT) (Gaut and Weir 1994) was HKY+I+G and by the Bayesian information criterion (BIC) (Raftery 1986a, 1986b) was HKY+I+G. We chose to use the HKY+I+G model which estimated the following parameters: Base frequencies; A=0.2923, C=0.2753, G=0.2391, T=0.1933. Ti/Tv ratio of 1.4986. Among site rate variation; proportion of invariable sites=0.2648, Gamma distribution shape parameter=1.7812. Regarding

MrModelTest v2.2 (Nylander 2004), the model selected for the *Hox*A3a alignment by hLRT, hLRT2, and hLRT4 was HKY+G, hLRT3 was GTR+G (Lanave et al. 1984). The model selected by AIC was GTR+G. We chose to use the HKY+G model which when implemented in MrBayes gives a prior state frequency of Dirichlet (1,1,1,1) and uses the basic model nst=2 with among site rate variation set to estimate rates based on a gamma shaped distribution. The model selected for the *Hox*A9b alignment by hLRT2, hLRT3, and hLRT4 was HKY+I+G, hLRT was GTR+I+G. The model selected by AIC was HKY+I+G. We chose to use the HKY+I+G model which when implemented in MrBayes gives a prior state frequency of dirichlet (1,1,1,1) and uses the basic model nst=2 with among site rate variation set to estimate not be basic model nst=2 with a gives a prior state frequency of dirichlet (1,1,1,1) and uses the basic model nst=2 with among site rate variation set to estimate rates based on a gamma shaped distribution and proportion of invariable sites.

To empirically link the *Hox*A2 enhancers to the genes they regulate the entire intergenic region of *Hox*A3a to *Hox*A2a was isolated in *F. catenatus*. We used Takara LA Taq due to its ability to amplify longer DNA fragments with the following volumes and concentrations of reagents: 5.0 ul 10X buffer, 4.0 ul MgCl₂ (25 mM), 4.0 ul dNTP (10 mM), 1.0 ul each of primers (25 pmol/ul), 1.0 ul gDNA (250 ng/ul), and 1.0 ul LA Taq (5 U/ul). We conducted the PCR reaction under the following conditions: 95 C for 2', 30 cycles of (95 C for 30'', 55 C for 1', 68 C for 4'), 68 C for 5' and 10 C hold. Due to unknown product size and multiple bands we performed a southern blot and hybridization.

We performed the southern blot procedure by transferring the PCR reaction from a 1% agarose gel to Amersham pharmacia biotech's Hybond-N+ nylon membrane. We performed transfer of DNA from the agarose gel to the nylon membrane as follows: Soaked gel in southern denaturation solution (0.2 M NaOH, 0.6 M NaCl) for 30' on a rocker. Soaked gel in neutralization solution for 30' on a rocker. Placed two sheets of Whatman's paper cut to size of gel in a glass dish, filled to top of Whatman's paper with 20X SSC (3.0 M NaCl, 0.3 M sodium citrate), place gel on top of paper, place Hybond-N+ membrane on gel, place two more pieces of Whatman's paper followed by 5 inches of paper towels and a ~11b weight, add 20X SSC 1 hr later, wrapped entire assembly in plastic wrap and let sit overnight. We cut all paper and membrane to the exact size of the gel. We then let the membrane dry and pre-hybridized overnight in 10ml hybridization solution (5X SSC, 0.1% ν/ν N-Lauroylsarcosine, 0.2% ν/ν sodium dodecyl sulfate, 1% w/ν blocking solution (Roche Diagnostics Blocking reagent)) at 65 C in rotisserie incubator along with a positive filter consisting of *Hox*A3a fragment on the nylon membrane. We prepared the positive filter by placing 1 ul (100 ng/ul) of fragment on a nylon membrane, drying, then floating in southern denaturation solution for 3' followed by floating in neutralization solution for 3'.

We used the 451 bp *Hox*A3a fragment isolated from *F. catenatus* genomic DNA as a probe. We DIG (Digoxigenin)-labeled the *Hox*A3a fragment using Roche Diagnostics DIG DNA labeling kit (11175033910). The DIG labeling reaction includes boiling 800 ng (15 ul) of the *Hox*A3a fragment in water for 10', placing on ice (H₂O) for 10', briefly spinning down, then adding 2 ul of the hexanucleotides, 2ul dNTP labeling mix, and 1ul Klenow enzyme provided in Roche kit. We then placed the labeling reaction at 37 C for 20 hrs.

After pre-hybridization and probe labeling we re-boiled the probe for 10' and chilled on ice for 10'. We then added the 20 ul of probe to 10 ml of hybridization

solution and hybridized membranes overnight in rotisserie incubator. We then washed the membranes briefly in 2X SSC followed by 2 washes in 2X SSC, 0.1% v/v SDS for 20' at room temperature on a rocker followed by 2 washes in 0.5X SSC, 0.1% v/v SDS for 20' at 65 C in rotisserie incubator. We then rinsed filter in diluent buffer (300 mM NaCl, 0.1 M Tris pH 8.0). We followed this by a "blocking" step by placing membranes in 40 ml of diluent buffer, 4 ml 10% blocking solution for 1 hr on a rocker then an "antiblocking" step by placing membranes in 30 ml of diluent buffer, 4 ml 10% blocking solution, 3 uL of Roche Diagnostics Anti-DIG-AP Fab fragments (0.75 U/ul). We followed this with 3 washes in a tween solution (150 ul tween 20, 50 ml diluent buffer) for 10' on a rocker. We followed this with washing in 50 ml of detection buffer (100 mM Tris pH9.5, 100 mM NaCl) for 5' on a rocker. We then prepared the membranes for exposure to Kodak Biomax light film. We prepared the membranes for exposure by adding Roche Diagnostics CDP-star to their surface. We then exposed the membranes to the film for 10' and then the film was developed on a Kodak developer.

Following identification of correct band (~6.5 kb) by southern hybridization we followed the protocol explained above to sequence the fragment. We had to create 3 sets of species-specific nested primers to sequence the entire fragment We used Takara LA Taq with the following volumes and concentrations of reagents: 5.0 ul 10X buffer, 4.0 ul MgCl₂ (25 mM), 4.0 ul dNTP (10 mM), 1.0 ul each of primers (25 pmol/ul), 1.0 ul gDNA (250 ng/ul), and 1.0 ul LA Taq (5 U/ul). We conducted the PCR reaction under the following conditions: 95 C for 2', 30 cycles of (95 C for 30'', 55 C for 1', 68 C for 4'), 68 C for 5' and 10 C hold.

4.4.3 Population Level Gene Sequencing

Materials and Methods

*Hox*A2a enhancer, *Hox*A2b enhancer and a shorter fragment of PGK1 intron 7 were isolated from ~100 individuals of the *F. olivaceus* populations. These were done with Finnzymes Phusion Taq due to its 50 times greater accuracy over AB amplitaq. Phusion Taq PCR reactions, volumes and concentrations were as follows: 10.0 ul 5X HF buffer, 4.0-7.0 ul MgCl₂ (25mM), 1.0 ul dNTP (10 mM), 1.0 ul each of primers (25 pmol/ul), 1.0 ul gDNA (250 ng/ul), 0.5 ul Phusion Taq (2 U/ul) and sterile water to 50 ul. The PCR reaction for Phusion Taq was conducted under the following conditions: 98 C for 1', 30 cycles of (98 C for 30'', annealing temperature (see table 2) for 30'', 72 C for 30''), 72 C for 5' and 10 C hold. All PCR reactions were carried out in an Eppendorf Mastercycler® ep thermocycler. Following PCR, the PCR products were sent directly from the gel purification step to be sequenced. Approximately 70 ng of purified PCR product was sent. This method of direct PCR sequencing reduces the effect of base pair mispairing that can occur with DNA polymerases due to the fragments with the mispairing representing a minority of the fragments in the sequencing reaction.

4.4.4 Tests of Selection

We conducted both interspecies and intraspecies tests of selection on the *Fundulus sp.* group (Table 1). For interspecies comparisons we calculated the Ka/Ks ratio (Nei and Gojobori 1986). This test was performed on all coding regions that were sequenced (Table 1). These results were directly compared with the Kb/Ki ratio (Hahn 2007, see materials and methods), which was implemented for the non-coding *Hox*A2 enhancers. These ratios are an indicator of selective forces acting at these loci. A ratio of

one is an indicator that there is no selection and the nucleotides are neutrally evolving. More than one denotes positive selection and less than one denotes negative or purifying selection. The majority of loci indicate negative or purifying selection.

Since the *Hox* loci are master regulatory genes found throughout the animal kingdom, selection to maintain nucleotide sequence and thus protein function is likely. The non-*Hox* locus PGK1 also appears to be under purifying selection. The lone exception to the neutral theory of evolution is the comparison between in-group species *F. olivaceus* and *F. notatus* at the *Hox*A2b enhancer. This comparison yields an exceptionally high Kb/Ki ratio of 7.78 (p=0.03) indicating strong positive selection as described in Hahn et al. (2004). The positive selection is isolated to this node as the Kb/Ki ratios between either of these two sister species and the out-group species, *F. catenatus*, is close to and not significantly different than 1. Further indication of positive selection can be noted by comparing the non-coding/non-binding percent difference for each locus, which is an indicator of neutral evolution at each site.

As seen in table 1 the two sister species, *F. olivaceus* and *F. notatus* have a lower percent difference than either do to the out-group, *F. catenatus*, most likely due to the divergence dates of these species. The more notable difference is the divergence seen between sister species when comparing the two *Hox*A2 enhancers; *Hox*A2b enhancer 0.48% and *Hox*A2a enhancer 2.02%. Compared to the *Hox*Ab cluster genes which are 2.63% and 2.95% and the *Hox*Aa cluster genes which are 0.66% and 0.90% there seems to be an inverse relationship between enhancer and gene neutral mutation rates at the 'a' and 'b' paralog loci (Figure 19). This inverse relationship is not seen however in the comparison between either of the sister species to the out-group species. At this level the

*Hox*A2a enhancer is more conserved at 4.03% for both comparisons than is the *Hox*A2b enhancer, 4.76% and 5.24%.

Also, between the sister species no other locus has more than 1 fixed difference in the functional region whereas the HoxA2b enhancer has 4. This evidence that the neutral mutation rate was slowed at the non-binding sites in the HoxA2b enhancer between *F*. *olivaceus* and *F*. *notatus* strengthens the claim that nucleotides at binding sites were preferentially fixed in the population (positive selection) at this enhancer.

Following the method used by Hughes and Nei 1988, we also applied the Kb/Ki ratio test to the F. olivaceus within species data. The HoxA2a enhancer had a Kb/Ki ratio of 0.00 (p=0.59) indicating purifying selection. The HoxA2b had a Kb/Ki ratio of 1.94 (p=0.63) suggesting balancing selection although neither test was statistically significant. The neutral polymorphism at these two sites was less than the non-Hox locus with the HoxA2a enhancer at 0.76%, the HoxA2b enhancer at 0.48% and intron 7 of the PGK1 gene at 2.4%. We also performed conventional intraspecies tests of selection using the software programs Neutrality Test v1.1 (Li et al. 2003) and DnaSP v4.0 (Rozas et al. 2003) on the *Hox*A2b enhancer. These test were not performed on the *Hox*A2a enhancer because alleles could not be confidently assigned to individuals. These programs gave a Tajima's D score of 1.681 and 1.13474 standard deviations from the mean for the *Hox*A2b enhancer indicating an excess of high frequency polymorphisms that is interpreted as balancing selection, which was shown to not be significant. Fu and Li's D and F statistics were 0.68090 and 0.96107 respectively without an out-group and changed less than 0.001 when an out-group was included. Again these tests did not have significance (p > 0.05) but fell in the direction of balancing selection. In order to take

advantage of the multiple loci and species an HKA test was performed (results not shown) but the results again were not statistically significant. It appears that within species the *Hox*A2b enhancer is evolving under no or slightly balancing selection but between *F. olivaceus* and *F. notatus* there was strong positive selection.

We also performed a Hardy-Weinberg (H-W) equilibrium test on the *Hox*A2b enhancer of the *F. olivaceus* population to show that our sample was a random set of the population. This is an important step as many tests of selection assume random sampling. The *F. olivaceus* population has two distinct sub-populations gathered from three sites. The first sub-population was gathered from two sites along the same river drainage that are named Little Piney and Gasconade River (see materials and methods). The second sub-population was gathered from one site and is named Rockford Beach. The Little Piney/Gasconade River sub-population showed no allele variants at the *Hox*A2b enhancer. The Rockford Beach sub-population had two allele variants that were distinct from the one found in Little Piney/Gasconade River for a total of three alleles. These three alleles were found to be in Hardy-Weinberg equilibrium within the Rockford Beach sub-population (p=0.62). This verified that our sample of the population was not biased which could alter tests of selection that assume random mating.

Given the data we collected and the lack of information about the divergence dates between our two sister species we performed a divergence date estimation. The nuclear gene estimate of the divergence date between *F. olivaceus* and *F. notatus* was calculated by calculating the distance between 7 homologous regions (*Hox*B2a exon 1, *Hox*A9b exon 1, 2 and intron, *Hox*A2b exon 1, *Hox*A3a exon 2, and *Hox*A2a exon 1, *Hox*A2a enhancer and *Hox*A2b enhancer) totaling 1,395 bp. Divergence date estimations for the three *Fundulus sp.* involved in this study were performed based on the % difference of the sequences accumulated. This was then compared to two pufferfish species (*Tetraodon nigroviridis* and *Takifugu rubripes*) with a known divergence date to estimate divergence date for the *Fundulus sp.* assuming an equal rate of mutation for these two **Acanthomorpha** clades. Overall *F. olivaceus* and *F. notatus* appear to have diverged around ~4.76 mya. This is the first nuclear data used to estimate divergence dates for these two species to our knowledge and agrees with the date derived from mitochondrial data ~2.75 mya (personal communication, Brian Kreiser).

4.4.5 In-silico Detection of Upstream Binding Factors

To better understand the expression patterns and evidence of selection it is necessary to know the nature of the enhancer. The *Hox*A2 R3/5 enhancer consists of 7 modules. RE2-5 help code for expression in r3 and 5 and NC1, 2 and 3 code for expression in neural crest cells derived from r4 and their derivative (PA2) (Nonchev et al. 1996; Maconochie et al. 2001; Tumpel et al. 2006). Three main transcription factors are thought to control *Hox*A2 expression via the R3/R5 enhancer: Krox-20, which controls expression in r3, 5 (Nonchev et al. 1996); Mafb, which control expression in r5 (Prince et al. 1998); and AP-2, which controls expression in PA2 (Maconochie et al. 1999). Since the domains of the enhancer that code for both r3 and 5 expression (RE4) and neural crest cell expression (NC2) overlap in the area of strong positive selection it is possible that we are seeing strong purifying selection elsewhere in the enhancer (RE2, 3, 5) (see divergence comparisons above) to maintain rhombomere expression in the presence of strong positive selection (RE4/NC2) to increase expression in the neural crest cells and their derivatives. This is supported by Tumpel et al. 2006, who showed RE4 is 32% efficient at driving R3/5 expression and RE3 and RE5 were 67% and 33% efficient, respectively with RE1 and RE2 contributing negligible amounts. So maintaining strong purifying selection in RE3 and RE5 could compensate for the loss of expression in RE4 due to its overlap with the strong positive selection to modify NC2. It is also possible that upstream factors that normally bind to RE4 to drive expression in r3 and 5 have coevolved with the nucleotide changes to maintain expression. A third possibility that compensatory mutations elsewhere in the enhancer are compensating for the loss of specificity at RE4 seems less likely since the rest of the enhancer is so well conserved. To help differentiate between the three possible scenarios TFBS prediction program JASPAR was used to analyze possible TFBS changes between F. notatus and F. olivaceus at the changes within RE4/NC2 (Sandelin et al. 2004; Figure 20). All 4 fixed differences resulted in different TFBS profiles and this region is flanked by two RUSH- 1α sites (5' site and 3' site) that are present in all 4 species (Figure 20). Both 5' and 3' RUSH-1 α sites have shifted toward each other by 2 nucleotides in the two sister species due to two mutations shared by these species that are not present in either F. heteroclitus or F. catenatus (Figure 20). Despite these mutations both sites have maintained similar scores in the JASPAR database. RUSH-1 α is a SWI/SNF-related matrix-associated protein, which possesses nucleosome remodeling activity and may be necessary for basal transcription of target genes (Hewetson et al. 2002). RUSH transcription factors also contain a RING finger domain at the c-terminal end that plays a role in protein-protein interactions (Mansharamani et al. 2001). RUSH-1α binding sites share sequence similarity with FOXL1 and FOXC1 binding sites.

FOXL1 and FOXC1 are forkhead family transcription factors that play roles in anterior segment development (Hacker et al. 1995). All four species maintain either 1 FOXC1 or FOXL1 at both 5' and 3' sites but *F. notatus* has binding sites for both forkhead family member at both 5' and 3' sites (Figure 20). The 3' site also has affinity for Ultrabithorax (Ubx). Ubx is orthologous to HoxA7 in vertebrates and although there is no evidence that HoxA7 regulates hindbrain development it is worth noting that F. *olivaceus* loses this Ubx TFBS at the 3' site but gains it back at the 5' site. Both F. olivaceus and F. notatus independently gain an HMG-1 binding site. HMG-1 helps regulate transcription, differentiation and DNA repair (Bianchi and Beltrame 2000; Mitsouras et al. 2002). HMG-1 contains two DNA binding sites along with a C-terminal protein interaction domain that has been shown to interact with *Hox* proteins and enhance their DNA binding and transcriptional activation (Zappavigna et al. 1996). The Ubx and HMG-1 site are of importance due to the discovery that Hox genes often auto and crossregulate (Hafen et al. 1984; Kuziora and McGinnis 1988). The most pertinent TFBS change occurs in F. notatus midway between the 5' and 3' site. At this site all species except for F. notatus maintain an Mafb binding site. Mafb also known as kreisler (mouse) or valentino (zebrafish) is expressed in the developing hindbrain and is essential for r5, 6 development and patterning (Prince et al. 1998b; Sadl et al. 2003). The 1 fixed difference between F. olivaceus and F. notatus that lies outside of any known functional element causes F. notatus to have an Mafb binding site that the other three Fundulus sp. do not. From this data there is evidence of both positive selection to gain binding sites as well as compensatory mutations to maintain them.

If we subject all other vertebrate HoxA2 enhancer sequences to the same type of analysis for Mafb binding sites as well as AP-2 and Krox20 binding sites a unique pattern emerges. Comparing binding sites of all three major R3/R5 enhancer transcription factors across vertebrate phylogeny allows us to see that RE3 is the most well conserved response element, whereas RE4 appears to be less conserved (Figure 21). This is in agreement with the idea that RE3 is responsible for a more basal expression whereas RE4 can act as a "fine-tuning" element. Tumpel et al. (2006) also showed this in their swap assays where RE3 recapitulated 67% whereas RE4 recapitulated 32% of the normal expression. Despite RE3 being the more conserved region the *Fundulus sp.* appear to be more variable than other species, specifically in the loss of highly conserved AP-2 binding sites. The two sister species have both lost an AP-2 binding site that is conserved among all enhancers except the HoxA2a enhancers, including the two other members of the *Fundulus sp.* group. It also appears that all of the Fundulus sp. have lost another AP-2 binding site in RE3 that is shared among all ray-finned fish including both 'a' and 'b' paralogs and also with chicken, frog and coelacanth. The region between the Krox-20 binding site and RE4 has been shown to be non-functional in both deletion analysis and swap assays (Maconochie et al. 2001; Tumpel et al. 2006). In this region a mutation in F. notatus adds back an Mafb binding site that no other Fundulus sp. member has. Also, the entire *Fundulus sp.* group lacks any AP-2 binding sites. This is possibly due to the ability for spurious binding sites to 'sequester' transcriptions factors away from the functional binding sites since the *Fundulus sp.* group specifically has lost 2 well-conserved AP-2 binding sites in RE3.

4.5 Discussion

*Hox*A2 is the most anteriorly expressed *Hox* gene in anterior-posterior patterning. The expression pattern of this gene has been shown for many vertebrates including birds, mammals and fish. In ray-finned fishes the expression pattern is made more complex due to the retention of two paralogs following the FSGD. Much work has gone into discovering the CREs responsible for driving expression of *Hox*A2 in the developing nervous system and derived structures. From this work a detailed map of the CREs has emerged. In this study we set forth to gather data that would help shine light on the evolution of one of these particular CREs. From this study we have discovered that the r3/r5 enhancer of the *Hox*A2 gene has undergone different rates of mutation throughout gnathostome evolution. More specifically, the retention of *Hox*A2 paralogs in the teleosts resulted in asymmetrical evolution. The *Hox*A2a r3/r5 enhancer appears to have undergone an accelerated rate of mutation fixation after the FSGD but prior to the **Ostariophysii/Acanthomorpha** species radiations. In contrast, the *Hox*A2b r3/r5

throughout the teleost species radiation. The highest r3/r5 enhancer mutation rate is maintained in the *Hox*A2b locus of the *Fundulus* sp. complex. Classification of these mutation fixations indicates that the mutations in TFBS were preferentially retained. Evolutionary maintenance of the r3/r5 enhancers along with support from earlier expression assays indicates there are certain elements that may be more important to basal expression whereas other elements may act as 'fine-tuning' mechanisms. The *Fundulus* sp. complex is again unique with more loss of TFBSs in the basal elements than any other species/group.

In an effort to discover why/how the *Fundulus* sp. complex has so much nucleotide turnover in the otherwise more conserved and seemingly more basal regions of the r3/r5 enhancer we performed micro-evolutionary tests. From these test we discovered support for evidence of strong positive selection occurring within this group between two closely related sister species. More specifically we saw 4 fixed differences within 38 base pairs in the RE4/NC2 region. TFBS analysis indicates these changes resulted in the two sister species each independently gaining the same *Hox* protein-binding partner. The loss of a *Hox* protein-binding site was regained in one species but the loss of the TFBS for Mafb (a TF necessary for HoxA2 expression in r5) in the other species was not regained. This shows that turnover of CREs at the macro-evolutionary level that appear to be due to relaxation of constraint and probable neutral evolution may actually be driven at least in part by strong positive selection at the micro-evolutionary level. This reiterates the need for more research into the evolutionary mechanisms that are shaping our CREs rather than research aimed at detecting the results of those mechanisms. Emphasis on the level at which evolution actually occurs may help shed a brighter light on how non-coding DNA contributes to adaptation and ultimately lead us to a more accurate and useful genetic code for regulatory DNA.

If the selective pressure is indeed due to the need to increase PA2 expression of *Hox*A2b, then what might be the possible phenotypes on which selection is acting? *Hox*A2 has been shown to directly regulate bone morphogenetic protein 4 (BMP4; Smith et al. 2009). BMP4 is expressed in the lower oral jaw (LOJ) and is directly associated with altering the ratio between flexibility and bite force of the oral jaw (Albertson et al. 2005).

Liem's Hypothesis contains the idea, that since the adaptation of posterior pharyngeal arches into a pharyngeal jaw, that oral and pharyngeal jaws have become uncoupled and may evolve independently (Liem 1973). While we are not testing this hypothesis in this study it does help explain how such adaptations can occur without detriment to the species and how such a variation in *Hox*A2 expression could be tolerated within the teleosts.

Fundulus olivaceus and *F. notatus* have been well studied in their physical characteristics and habitat distribution (Petifils 1986). The only defined distinguishing characteristic between the two species is the presence of dark regular spots above the lateral line in *F. olivaceus* (Thomerson 1966). A possible explanation for the phenotypic difference that may be driving the positive selection for altered expression of *Hox*A2b in PA2 has to do with courtship. *F. olivaceus* males have been seen defending a 3m² territory from other males (Harper 1992). During this defense the male will flare its opercles and gular area when a female and another male are present (Baugh 1981). This behavior is not seen in *F. notatus*. It is possible that differing PA2 development could lead to the ability/inability to flare this area. Albertson et al. (2005) state the lever mechanism that is directly correlated with BMP4 expression is reliant on the ligament attaching the lower jaw to the opercle. QTL mapping in cichlids has also shown a correlation between directional selection at the genetic level and phenotypic effects in the LOJ (Albertson et al. 2003).

Other possible explanations include bite speed/force or digging ability for egg depositing. *F. olivaceus and F. notatus* both feed at the same trophic level on the same food stuff so the need for bite speed/force differences is unlikely (Thomerson and

Wooldrige 1970). The two sister species do prefer habitats with different floor surfaces although neither bury their eggs. Since *Hox*A2 is both partially responsible for the musculature and innervation of the LOJ several other phenotypes may also be affected.

In conclusion, we have found evidence of positive selection followed by balancing selection acting at the microevolutionary level in an enhancer that is differentially driving expression between two paralogs at the macroevolutionary level. Coincident with this selection is evidence of compensatory mutations. To our knowledge, this is the first study to research the evolutionary forces acting on a *Hox cis*regulatory element within and between sister species.

Chapter 5 - Independent Evolutionary Mechanisms of Teleosts Uniqueness

5.1 Introduction

5.1.1 Transposable Elements Role in Genomic Evolution

Transposable elements (TE) were discovered by McClintock (1956) and are endogenous sequences of DNA that have the ability to transpose from place to place within the genome. There are two main classes of transposable elements. Class I transposons (a.ka. retrotransposons) transpose by the copy and paste method. First RNA is transcribed and then reverse transcribed by a reverse transcriptase encoded for by the element itself. Finally, the new DNA sequence is integrated back into the genome by an integrase also coded for by the element itself. Class II transposons (a.k.a. DNA transposons) transpose by the cut and paste method. A transposase protein coded for by the element itself excises the element, or any other element that contains the correct repeat sequences, from the genome and integrates it somewhere else in the genome.

Class II but not class I transposons have been found to be positively correlated with areas of high recombination within the genome (Duret et al. 2000). This association is theorized to be a cause-effect relationship rather than an exploitation of the endogenous double stranded DNA repair process, but not all class II transposons seem to have this ability. In a study done on class II transposable elements in *C. elegans*, Tc1 transposon family members were found in areas of high recombination whereas closely related Tc3 and Tc5 transposons were not (Rizzon et al. 2003).

The introduction of transposable elements near a gene can interrupt or in some cases introduce *cis*-regulatory sequences (McClintock 1956). TEs can also become exons

or introduce alternate splice sites within a gene (Kim et al. 2006; Huh et al. 2009). TEs can also contribute to the overall size of a genome. In some cases TEs compose nearly 50% or more of the entire genome (Lander et al. 2001). Because of the ability to affect genetic structure at both the gene and genome level, TEs are considered a major force in genomic evolution. Because TEs have the ability to reorganize, lengthen intergenic regions, as well as create general havoc to gene sequences it has been theorized that they would be preferentially excluded from well-organized and conserved gene clusters such as the *Hox* gene cluster (Fried et al. 2004).

5.1.2 Tc1 Transposons

As mentioned in the previous section Tc1 transposons have been found to associate with areas of high recombination (Duret et al. 2000). Despite this we found them to be prevalent in ray-finned fishes *Hox* clusters. For this reason we pursued several methods aimed at detecting their possible role in *Hox* cluster evolution that relies on a basic understanding of their mechanism of action.

The Tc1 transposable element was originally found in a species of worm, *Caenorhabditis elegans* (Emmons et al. 1983, X01005.1). This Tc1 was found to be a high copy number transposable element with precise excision from the DNA sequence in which it was residing (Emmons et al. 1983). It was later discovered that Tc1 not only had sites of precise excision but also sites of imprecise excision resulting in the element leaving remnants of its own insertion or taking small sections of DNA from its insertion site (Ruan and Emmons 1987). The Tc1 transposable element also differs not only in its excision precision but also in its excision prowess i.e., the rate at which it excises or inserts. This difference in excision rate is apparent when comparing germ line excision rate to the rate of excisions in somatic tissue. Excisions occur more than 1,000 times more often in somatic than in germ line tissue (Eide and Anderson 1988). This is important because the number of excisions has a direct effect on the mutagenic ability of the element, also only germ line "jumps" can be seen in the next generation. Earlier in the same decade Eide and Anderson (1985) found that Tc1 transposition was strain specific. This shows that the response to Tc1 differs between cell types as well as between individuals within the same species.

The structure of the Tc1 transposable element and the Tc1 transposase and their interaction were discovered not long after the Tc1 sequence itself was obtained. Tc1 is known to be a 1,610 base pair transposable element with 54 base pair terminal inverted repeats (Liao et al. 1983; Figure 23). There is one continuous open reading frame that codes for a 343 amino acid transposase (Vos et al. 1993). Structurally Tc1 transposase contains a bipartite DNA binding domain. The first domain is from amino acids 1-68 and the second domain is from amino acids 68-142 (Vos and Plasterk 1994). There is also the catalytic domain, characterized by its DDE (Aspartate, Aspartate, Glutamate) motif at positions 157, 247 and 282 respectively (Doak et al. 1994). The bipartite DNA binding domain of the Tc1 transposase binds the Tc1 transposable element by first binding to nucleotides 12-26, with the amino-terminal domain and then binding nucleotides 7-13 with the carboxy-terminal domain, if and only if the amino-terminal domain binds first (Riddle et al. 1997).

Upon excision the Tc1 transposable element inserts preferentially nearby and in some cases to specific sequences (Luo et al. 1998). In the case of Tc1, that integration site has been shown to be a TA/AT palindrome sequence (Rosenzweig et al. 1983b). A

preference has also been shown for the TA palindrome to be flanked by specific nucleotides. The consensus sequence for Tc1 integration is GARATATGT (the R represents A/G) (Mori et al. 1988).

In order for the transposable element to insert into the target sequence it must bring its 5' and 3' ends into close proximity. This can be accomplished by forming an intermediate loop, as some introns excised from mRNA do. This is known to occur in the Tc1 excision reaction (Rose and Snutch 1984). Proteins from the host cell can also be involved in Tc1 transposition. Since there are differences in the "jumping" abilities of Tc1 transposable elements in germ line and somatic tissue, it is fair to assume that different cell types differentially regulate its transposition. Shortly after Tc1 was discovered, it was shown that Tc1 elements in 5 different loci on different chromosomes were more active in the somatic tissue opposed to the germ line tissue. The study also showed that this was caused by tissue-specific factors that either activated or suppressed the transposition (Emmons et al. 1986). Although there may be factors that help suppress or up-regulate transposition, they are not necessary for transposition. The Tc1 transposase, itself along with the terminal 26bp of the repeat region, are sufficient for activity (Vos et al. 1996).

Although Tc1 was originally found in *C. elegans* and most of the early research went into the mechanisms of transposition, recent effort has been invested in characterizing the phylogenetic extent of this transposable element. Tc1 has been found in fungi (Langin et al. 1995), nematodes (Emmons et al. 1983), arthropods (Jacobson et al. 1986) and vertebrates (Radice et al. 1994). Tc1 also shares its DDE motif with bacterial IS transposases and retroviruses (Fayet et al. 1990), leading to the theory that

Tc1 is a very ancient and conserved transposon. The discovery of the mariner transposable element in *Drosophila mauritiana* led to the realization that Tc1 and mariner constituted a 'family' (Jacobson et al. 1986). Transposable elements belonging to this family subsequently have been discovered in species representing several lineages, several with Tc1 elements that are still active. One lineage shown to lack such a Tc1-like element is the ray-finned fish clade. Almost all remnants of elements found have been shown to have stop codons within their open reading frame. There is evidence, however, for activity in a few species. In zebrafish, active transposition of Tc1-like elements have been shown to occur, although no Tc1-like element with a complete open reading frame has been found to date (Lam et al. 1996). There have also been transcribed Tc1-like transposable elements have premature stop codons and have not been shown to be translated into functional transposases (Krasnov et al. 2005).
5.2 Transposable Elements in *Hox* Clusters

Transposable elements were originally thought to be excluded from gnathostome *Hox* gene clusters due to their ability to cause genomic rearrangements, alter intergenic distances and ablate or introduce *cis*-regulatory elements (Fried et al. 2004). But, recent work has shown there are indeed TEs within the *Hox* gene clusters (Di poï et al. 2009). We have systematically searched *Hox* gene clusters of the following gnathostomes for transposable elements: horn shark, human, coelacanth (*Latimeria menadoensis*), bichir, zebrafish, medaka, Nile tilapia, spotted-green pufferfish, Western clawed frog, and chicken (Figure 24).

From this analysis we discovered that TEs do reside in and around *Hox* gene clusters of gnathostomes although the type of TEs differs between lineages. Human and shark and for the most part coelacanth *Hox* clusters contain class I transposons whereas the ray-finned fishes including bichir *Hox* clusters contain mostly class II transposons that increase in frequency in the teleost division. This shows a distinction between ray-finned fishes and cartilaginous/lobe-finned fishes. This distinction becomes relevant in terms of how these two types of transposons transpose. Class II transposons "cut and paste" to adjacent regions of DNA with sloppy precision taking with and leaving behind DNA sequences whereas class I transposons "copy and paste" resulting only in insertions. Because of this class I transposons have a greater ability to alter intergenic distances.

One specific class II transposon was of interest due to finding two open reading frames in and immediately flanking the bichir *Hox* cluster. The Tc1/mariner family of DNA transposons is found throughout animal phylogeny from *C. elegans* to Drosophila

to frog (Emmons et al. 1983; Harris et al. 1988; Lam et al. 1996). It is also found among many teleosts fishes (Radice et al. 1994). However a Tc1 with an intact open reading frame has never been found in a vertebrate. We have found two Tc1 transposons in and around the bichir *Hox* clusters. The first is found flanking bichir's *Hox*A cluster just downstream of *Hox*A1. The second is found within the 16,254 base pair intron of *Hox*D3. This is the largest intron found to date for a canonical *Hox* gene. A typical *Hox* gene intron is ~25X smaller (200-700 base pairs). These two Tc1 transposons both contain complete open reading frames that code for amino acid sequences that share homology with known functional Tc1 transposons including the DDE active motif, glycine rich box, nuclear localization signal and paired DNA binding domains (Figure 25). They also contain the inverted repeats flanking the open reading frames that are necessary for self-excision. Although these two Tc1 transposons both appear functional they do differ from each other significantly and do not appear to be the result of a recent transposition from one location to the other (Figure 25).

Tc1 family members are grouped into different sub-families. Within the teleost division Tc1-like transposons are grouped into A, B and C subfamilies with A and B being more closely related (Ivics et al. 1996). Other, more ancient, Tc1-like sequences from a diverse array of organisms (*C. elegans*, frog, fungus, etc.) group outside of the recent teleosts expansions and appear more closely related to one another than to any of the 3 teleost subfamilies (Figure 26). The Tc1-like transposon flanking bichir's *Hox*A cluster (bichir *Hox*A Tzf) groups with subfamily C, which is mainly composed of zebrafish Tc1-like sequences. The Tc1-like transposon found with bichir's *Hox*D3 intron (bichir *Hox*D Tc1) groups with the seemingly more ancient clade. The *Hox*D Tc1 also

differs in the spacing of its catalytic domain. Tc1 family members normally have a DD34E catalytic domain with 34 amino acids between the second aspartate and the glutamate (Shao and Tu 2001). Other variations have also been found for related transposons such as the DD35E motif shared by the bacterial insertion sequence (IS) and human immuno-deficiency virus (HIV, Plasterk et al. 1999). DD37E transposons have also been found (Shao and Tu 2001). The *Hox*D Tc1 has 36 amino acids between the second aspartate and glutamate (Figure 25). The only other transposon with the DD36E configuration is the Tc1-like transposon *Maya*2 found in the African clawed frog (Sinzelle et al. 2005). *Hox*D Tc1 also shares the short inverted repeats with *Maya*2 and the original Tc1 found in *C. elegans*.

Tc1-like sequences are found in and around *Hox* clusters of the teleost fishes as well (Figure 27). They maintain the pattern seen in bichir where subfamily C members flank the *Hox* gene clusters and the seemingly more ancient Tc1 transposons are located within *Hox* gene clusters. In zebrafish, 4 subfamily C members are found within 100 kilobases upstream of the *Hox*Aa cluster and 2 are found within 50 kilobases downstream and all contain inverted repeats. This is significant because Tc1-like transposons normally transpose to an area within 100 kilobases from where they are excised (Fischer et al. 2001; Carlson et al. 2003). Also, intact inverted repeats within 12.5 kilobases of each other are all that are necessary for the Tc1 transposon protein to excise and transpose DNA (Fischer et al. 1999). At first glance this may not seem an issue in zebrafish since no intact Tc1 has been found that is capable of producing a full-length protein. However, as previously mentioned it has been shown that zebrafish has Tc1 transposon activity (Lam et al. 1996). Whether there is another transposon capable of

utilizing the Tc1 inverted repeats is unknown, but it is also possible that the intact Tc1 has yet to be annotated due to the incompleteness of the genome sequence. There is also a subfamily C member flanking the anterior end of the zebrafish *Hox*Da cluster. Within the *Hox* clusters are only members that group with the seemingly more ancient clade. There is one between zebrafish's *Hox*A11a and A9a, *Hox*B13a and B10a, *Hox*B2a and B1a, *Hox*C3a and C1a and medaka's Eve1 and *Hox*D13a and *Hox*D13a and D9a. It appears that at the time the more ancient Tc1-like transposon entered the teleost fishes' genomes the *Hox* gene clusters were more amenable to invasion but during the more recent expansion of the teleosts-specific Tc1-like transposon expansion they have been excluded.

5.3 Testing Tc1 Transposon Activity

Since we found two intact Tc1 transposons in and around bichir's *Hox* clusters we decided to develop both theoretical and functional tests to determine the ability of these sequences to create a functional transposase as well as their ability to alter the structure of the *Hox* clusters in which they reside.

First, we determined if there was a difference in the likelihood that a Tc1 would jump into Hox clusters of different species since we had previously determined that there is a difference in the types of transposons that invade ray-finned fishes Hox clusters and lobe-finned and cartilaginous fishes *Hox* clusters. In order to perform this analysis we implemented the ProTIS program developed by Liu et al. (2005). In this program 4 types of Tc1-like insertion sites are given weights based on empirical frequencies of insertion. The four categories are 13, 5, 4, and 1 where 13 is 13 times more likely to incur an insertion than 1. This script was run in Perl on the *Hox*A clusters of horn shark, human, mouse, coelacanth, bichir, zebrafish (Aa and Ab) and Japanese pufferfish (Takifugu *rubripes*; Figure 28, 29). From this analysis it is apparent that it is twice as likely that a Tc1-like transposon will jump into an intergenic or intronic region rather than an exonic region. It is also apparent that the species that actually have Tc1-like sequences in an around their Hox clusters are twice as likely to have an additional insertion of a Tc1-like transposon within their *Hox* clusters. Bichir and zebrafish have a relative average weight of 0.40 for their non-coding regions whereas mouse and human have a relative average weight of 0.15. This discrepancy disappears outside of the HoxA cluster where bichir and zebrafish have a relative average weight of 0.25 and mouse and human 0.22. From this data we can conclude that the reason ray-finned fishes have invasions of class II

transposon where lobed-finned fishes do not is partly due to their respective *Hox* cluster sequence preference. It appears that mouse and human actively maintain an environment that is not conducive to Tc1 transposon insertion (average weight of 0.15 inside cluster to 0.22 outside cluster) and bichir and zebrafish are maintaining an environment that is conducive to Tc1 transposon insertion (average weight of 0.40 inside cluster to 0.25 outside cluster).

Second, we determined what would be the results of a Tc1-like transposon jumping in and out of the bichir *Hox*A cluster. For this analysis a program was written in Perl and JAVA with the help of lab members (Yu-Kang Cheng, Richard David-Rus and Robert Lynch). In this implementation the program takes into consideration the location of the ORF of the transposon, the inverted repeats, *Hox* coding regions and pattern of insertion sites (obtained by previously mentioned script). Variables for the program include rate of fixation in generations, nucleotide mutation rate, population size, number of fixation events and number of runs to execute. For our analysis we started out with the following parameters:

Fixation Rate: 1

Mutation Rate: 0.000624855

Population Size: 500

Fixation Events: 25

Current number of runs used: 1000

In summary the algorithm would jump the transposon and check for sequence differences. If the mutation was in an exon then it was considered inviable and a new mutation was performed. If the mutation hit in a PFC it was considered inviable with an 80% rate of survival. If the mutation hit another area of the *Hox* cluster it was considered 100% viable and continued. In order to multiply the class II Tc1 transposon must jump

in front of the replication fork thus copying itself. We considered this would happen 1 out of every 1000 jumps. In order for the transposase to transpose it must find two inverted repeats within 12.5 kilobases of each other and in the correct orientation (Fischer et al. 1999). Once these are found the transposase will cut this sequence out and jump it either to the right or left with a 50% probability. If the transposition is outside of the reference sequence then it will be considered missing and the run will start over. When a transposition occurs there are 8 types of footprints left behind. Which type was considered with the frequency of the empirical weights given by van Luenen et al. (1994). Based on this program there appears to be no preference of any specific intergenic or intronic region in which the Tc1 transposase integrates (Figure 30). Also, the major changes in *Hox* gene cluster architecture were due to spacing and not sequence alteration.

Third, we developed an *in vitro* system to test the ability of the Tc1 *Hox*A and Tc1 *Hox*D transposons from bichir to mediate transposition. The first step of this experiment was to construct vectors (Figure 31). Two vectors contain the transposase coding sequence of each bichir Tc1 transposon. Four vectors contain reporter genes with inverted repeats from either transposase sequence. As a backbone pFastBac1 vector (GenBank accession number: AY598466.1) was used that contains its own polyhedron promoter, SV40 polyadenylation site as well as an F1 origin of replication, gentamicin-resistance gene and ampicillin-resistance gene. Before each vector was created we first integrated a multiple cloning site (synthesized by IDT) developed to specifically integrate our genes and promoters between the polyhedron promoter and SV40 polyadenylation site. The multiple cloning site also included the short inverted repeats of the Tc1 *Hox*D

transposon. To each reporter gene vector all additional sequences were added between the inverted repeats. We spliced in the EF1α eukaryotic promoter (GenBank accession number: EF203084.1) as well as the EM7 prokaryotic promoter (synthesized by IDT) to vectors 1-4. For vector 1 we added the reporter fusion gene HcRed-Blasticidin (GenBank accession numbers: AY92935.1 and AB364162.1, respectively) and for vector 2 we added Hygromycin-green fluorescent protein (GenBank accession number:

AB289768.2) downstream of the two promoter sequences. For vector 3 and 4 we replaced the Tc1 *Hox*D inverted repeats of vectors 1 and 2, respectively, with Tc1 *Hox*A inverted repeats. For the expression vectors we added all sequences outside of the inverted repeats specifically downstream. We added a CAG promoter (GenBank accession number: EF59149.1) to both vectors 5 and 6. To vector 5 we added the Tc1 *Hox*D transposase coding sequence downstream of the CAG promoter. For vector 6 we replaced the Tc1 *Hox*D transposase coding sequence with the Tc1 *Hox*A transposase coding sequence. The total size of each vector was approximately and did not exceed the 7,000 -8,000 base pair range. The vectors are identified as follows: vector 1-pFBEEHcRed, vector 2-pFBEEHygroGFP, vector 3-pFB5EEHcRed3, vector 4-pFB5EEHygroGFP, vector 5-pFBCAGpTc1 and vector 6-pFBCAGpTzf.

Vector design, pFastBac1 vector and reporter gene mother vectors were obtained from Rick Cohen's lab of the W.M. Keck Center for Collaborative Neuroscience at Rutgers, The State University of New Jersey. The multiple cloning site and EM7 promoter were synthesized each as two single stranded DNA molecules by IDT. We annealed the sense and anti-sense strands of these sequences via the following protocol: 1. Dilute DNA oligo crystals in Fermentas 1X PNK Buffer A to a final concentration of 0.001 M. a. Add 20 ul of each strand of the multiple cloning site (50 ul each of EM7 promoter) to a 1.5 mL tube, hand shake and quick spin. b. Add 3 inches of water to a 150 mL beaker and bring to a boil, remove from heat and place on desktop. c. Place 1.5 mL tubes in a float and place in water, let come to room temperature (~45 minutes). 2. Phosphorylate double stranded oligos. a. add the following to a 1.5 mL tube (20 uL dsDNA oligo, 4 uL 10X PNK Buffer A, 0.4 uL 100uM dATP, 13.6 uL pure water, 2.0 uL T4 polykinase (Fermentas). b. incubate in 37 C water bath for 20 minutes. 3. Follow protocol for Enzyme reaction cleanup (Qiagen MinElute Kit 28204). Use spectrophotometer to measure concentration of purified DNA. Run 1% agarose gel to check for proper annealing.

The next step is to amplify the promoters, reporter genes and Tc1 transposons from their respective vectors. Each of these sequences are amplified from their vectors using primers specific for the sequence with additional sequences that can be cut by restriction enzyme to produce overhangs for insertion into vector. They were amplified with the following primers, annealing temperatures and extension times:

Ef1α (58 C, 45"), Ef1-alpha-ClaI-F (5'-ATATATCGATGTTTGCCGCCAGAACACAGGTAAGTGC-3') and Ef1-alpha-SphI-R (5'-GTATGGCATGCTTTGGCTTTTAGGGGGTAGTTTTCACGACAC-3'); HcRed-Blasticidin (58 C, 45"), HcRed-BSD-5-SalI-F (5'-

CATACGTCGACCCACCATGGTGAGCGGCCTGCTGAAG-3') and HcRed-BSD-3-SbfI-R (5'-GTATGCCTGCAGGTTAGCCCTCCCACACATAACCAGAG-3'); Hygromycin-green fluorescent protein (57 C, 1'), HygroGFP-5-SalI-F (5'-

CATACGTCGACCCACCATGAAAAAGCCTGAACTCACCGCGACG-3') and HygroGFP-3-SbfI-R (5'-GTATGCCTGCAGGTTACTTGTACAGCTCGTCCATGCCGAG-3'); CAG promoter (57 C, 1'), CAGpromoter-5-AscI-F (5'-CATACGGCGCGCCCTAGTTATTAATAGTAATCAATTAC-3') and CAGpromoter-3-NsiI-R (5'-GTATGATGCATTTTGCCAAAATGATGAGACAGCAC-3'); Tc1 *Hox*D (57 C, 1'), Tc1-5-NsiI-F (5'- CATACATGCATCCACCATGCGGCAGTCGTGTGGGCGAAAATGC-3') and Tc1-3-XmaI-R (5'-GTATGCCCGGGCTAACACGGTGTTTGACCCCCTTTCG-3'); Tc1 *Hox*A (57 C, 1'), Tzf-5-NsiI-F (5'- CATACATGCATCCACCATGTCAGAGCACAAACCAAGCATG-3') and Tzf-3-XmaI-R (5'- GTATGCCCGGGTCAATACTTTGTCGATGCACCTTTG-3'); Tc1 *Hox*A 5' inverted repeat (55 C, 30"), 5IVRTzf-5-NotI-F (5'- CATACGCGGCCGCTACAGTGCATCCGGAAAGTATTCA-3') and 5IVRTzf-3-ClaI-R (5'-GTGATATCGATAGCAAAGGCTGTGAATACTTATGTA-3'); Tc1 *Hox*A 3' inverted repeat (55 C, 30"), 3IVRTzf-MluI-F (5'-

CATACACGCGTGCAAAGGCTTTGAATACTTATGTA-3') and 3IVRTzf-AscI-R (5'-GTATGGGCGCGCCTACAGTGCATCCGGAAAGTATTC-3').

The PCR reactions were setup with the following volumes: 5.0 uL 10 X LA Taqbuffer (Takara), $4.0 \text{ uL } 25 \text{mg/mL } \text{MgCl}_2$, 4.0 uL 10 mg/mL dNTP, 2.5 uL 10 pmol/uLforward primer, 2.5 uL 10 pmol/uL reverse primer, 30-60 ng DNA template, 0.5 uL LATaq (Takara), dilute to 50 uL with pure water. The PCR reactions were ran through PCR in a Eppendorf EP gradient S thermalcycler with the following program: initial denaturation 95 C 2' 30 cycles of (95 C 30'', variable annealing temperature for 1', 68 Cfor variable extension time), final extension 68 C 5'. PCR reactions were purified using Quiagen Gel Extraction Kit 28704 under standard protocol conditions.

The next step is to end digest the amplified sequences. Each sequence is digested with specific restriction endonucleases that will allow them to be ligated to the vector in a particular location. The following enzymes were used to end digest each sequence: Ef1alpha, 10 units ClaI (New England Biolabs, NEB) and 10 units SphI (NEB) with 1X bovine serum albumin and NEB buffer 4; HcRed-Blastocidin, 20 units SalI (Fermentas, F) and 20 units SdaI (F) with Fermentas buffer SdaI; Hygromycin-green fluorescent protein, 20 units SalI (F) and 20 units SdaI (F) with Fermentas buffer SdaI; CAG promoter, 20 units AscI (F) and 20 units NsiI (F) Fermentas buffer R; Tc1 *Hox*D, 20 units NsiI (F) and 20 units XmaI (NEB) with Fermentas buffer SdaI; Tc1 *Hox*A, 20 units NsiI (F) and 20 units XmaI (NEB) with Fermentas buffer SdaI; Tc1 *Hox*A 5' inverted repeat, 15 units ClaI (NEB) and 10 units NotI (NEB) with NEB buffer 3; Tc1 *Hox*A 3' inverted repeat, 20 units AscI (F) and 20 units (F) MluI with Fermentas buffer R. Each reaction consists of 5.0 ug of DNA (except Tc1 *Hox*A 5' and 3' inverted repeats which uses only 500 ng) along with the restriction enzymes and buffers diluted to 100 uL with pure water. Reactions are placed in a 37 C for 1 hour. Reactions are then purified using Qiagen Enzyme Reaction Cleanup Kit 28204 under standard protocol.

The next step is to ligate the inserts to the vector. First the vector must be digested to receive the proper insert. For any particular insert digest the vector in the same reaction conditions including the same enzymes. Also set up 2 test digestions (10 uL total) one for each enzyme independently. Dephosphorylate the main digestion by the following protocol: 1. Add 5.0 uL 10X Fast AP buffer (Fermentas), 4.0 uL Fast AP (Fermentas), 43 uL sterile water to a 1.5 mL tube and mix. 2. Add mix directly to digestion reaction after digestion and place in 37 C water bath for 10'. Run gel of uncut, single digestions and main digestion on 1% agarose gel to check for proper digestion. Second the insert should be ligated to the vector. The insert to vector ratio should be 3:1. The ligation should be setup under the following conditions: 100 ng vector, variable amount of insert, 2 uL 10X ligase buffer (Fermentas), 1 uL T4 DNA ligase (Fermentas #EL0014) and dilute to 20 uL with sterile water. Place at room temperature for 1 hour. Vector can be transformed into JM109 competent cells ((Promega) using protocol outlined in chapter 4. Colony PCR and sequence verification are performed using protocol outlined in chapter 4.

After the 6 vectors were created they were transformed into human embryonic kidney cell (HEK) 293 cell lines and grown in ampicillin to test for the presence of vector. The vectors have been transformed into the HEK 293 cell lines in the following combinations: 1. negative control-unrelated vector with no expressed genes 2. pFBEEHygroGFP, pFBCAGpTc1 3. pFB5EEHygroGFP3, pFBCAGpTzf. The HcRed-Blastocidin reporter gene has yet to be used because transformation of both transposons simultaneously has yet to be performed.

After initial growth in ampicillin surviving cells were transferred to hygromycin plates and scored for fluorescence. Initial results suggest that the Tc1 *Hox*D transposase was able to mediate transposition of the reporter gene via its inverted repeats into the nuclear genome of the cell.

5.4 Conclusion

Transposable elements are themselves mutations (change in DNA sequence) but they also cause mutation. Because of this and the frequency at which they occur they are considered drivers of genome evolution (review, Biémont and Vieira 2006). The Hox gene cluster was thought to be devoid of such elements due to the abilities of these elements to cause large and small-scale genomic rearrangements that would seemingly disrupt the orderly and clustered nature. Shockingly, TEs were discovered in the Hox gene clusters of several species of gnathostomes. However, the types of TEs found in *Hox* gene clusters seem to be lineage specific. The ray-finned fishes have undergone an invasion of class II transposons that tend to associate with greater recombination rates as opposed to the lobe-finned and cartilaginous fishes, which have an invasion of class I transposons. One particular class II transposon that is highly associated with areas of high recombination, the Tc1 transposable element, is found in great frequency in and around the ray-finned fishes' Hox gene clusters. This invasion seems to have been specific to a particular type of Tc1 element and perhaps to a particular period in geological time. Closer inspection of these Tc1 elements in and around the ray-finned fishes *Hox* gene clusters reveals two intact transposons in the basal living ray-finned fish, bichir. Present knowledge indicates that these are the only known intact Tc1 elements in all of **Vertebrata**. Experiments show that discrimination between types of transposable elements found in *Hox* gene clusters of different species/lineages is the result of presence/absence of insertion sites within those clusters. These patterns are likely

maintained through purifying selection. This implies that invasion of the *Hox* gene clusters coincide with relaxed constraints on purifying selection.

As we have shown previously with the higher rate of turnover of CNSs and the faster rate of mutation in the r3/r5 enhancer of the *Hox*A2 gene, the ray-finned fishes and to a greater extent the derived teleost clade have what can best be described as an 'evolvable' *Hox* gene cluster system. This evolvability is apparent at both the molecular level as well as the phenotypic level and can be seen at both the micro as well as macroevolutionary levels. Such a system was likely to arise in a fashion similar to the following scenario.

For the ray-finned fish lineage to develop an "evolvable" genome based on Lynch (2007) it is likely that there was a bottleneck in population size(s) that allowed mutation and drift to act as the major evolutionary forces, which led to more complex genes. Following this bottleneck a population expansion necessarily occurred leading to an increase in heterozygotes, which is synonymous with an increase in standing variation. Either following or co-occurring with the population expansion was an increase in natural selection as the major evolutionary force due both to strong extrinsic factors (i.e. niche filling, resource competition, etc.) and to the increase in the effectiveness in selection due to the large population size. Strong extrinsic factors that coincide with the diversification of ray-finned fish include large continental plate movements exposing 1,000s of miles of new shoreline, rise of current coral reef species, sea level changes, etc. (Bellwood and Wainwright 2002). Species diversity associated with these extrinsic factors has been studied in pufferfishes and was shown to be significantly correlated with species number (Alfaro et al. 2007).

Chapter 6 – Overall Conclusions

6.1 Questions Addressed

My thesis has addressed the evolution of the intergenic sequences of *Hox* gene clusters among jawed-vertebrates. Specifically it has concentrated on the current state of *Hox* gene cluster intergenic sequences in the ray-finned fishes to obtain a better understanding of how these sequences changed starting at the base of the lineage leading into the duplicated paralogs of the crown group, teleosts. I found that the intergenic sequences of cartilaginous and lobe-finned fishes have maintained a relatively stable set of PFCs as has been reported previously. Chiu et al. (2004) found that the ray-finned fishes, however, have had a considerable turnover of PFCs in the HoxA cluster starting at the base of the lineage and this turnover continues well into the teleost division. My work extends this to the *HoxB* and *HoxD* clusters by adding data from the phylogenetically important ray-finned fish, bichir. I found that this rate of turnover appears to be different but steady for each *Hox* gene cluster paralog. This restructuring of *Hox* gene cluster intergenic sequences of the ray-finned fishes appears to be mostly the result of relaxed constraints on the conservation of PFCs due to the loss of several deeply conserved PFCs although positive selection for novel PFCs cannot be ruled out as a few novel ray-finned fish specific PFCs were also found.

Though the macro-evolution of the *Hox* gene clusters in the ray-finned fishes appears to be undergoing mostly relaxed constraints it is unclear what is happening at the micro-evolutionary level to obtain this result. To date and to my knowledge the question of what forces are acting at the micro-evolutionary level within *Hox* gene cluster intergenic sequences has not been addressed. To address this, at least for one specific CRE, I performed a population level study. Curiously, the strong evidence of relaxed selective constraints seen at the macro-evolutionary level for this CRE appears to be partially the result of strong positive selection at the micro-evolutionary level.

Directional selection on CREs is just one possible force shaping the architecture of the *Hox* gene cluster intergenic sequences. To address what other possible genetic mechanisms have helped shape these non-coding sequences I also cataloged all of the mobile elements and remnants of mobile elements. I found that the conserved *Hox* gene clusters of cartilaginous and lobe-finned fishes contain mostly class I (retro-) transposons, but ray-finned fishes with their high rate of PFC turnover contain mostly class II (DNA) transposons.

6.2 Contribution to the Field

My work has provided the field of *Hox* gene cluster evolution with an important database to begin the cataloging of PFCs and other CNSs. My hope is this database will lead to a large consensus database that can be expanded upon as well as studied in a collaborative effort between evolutionary and developmental biologist. Specifically I have contributed to the knowledge that large turnover of PFCs seen in the ray-finned fishes *Hox*A cluster that appears to be steady from the stem to the crown is not confined only to the *Hox*A cluster and that this turnover proceeds at various rates between the *Hox* gene cluster paralogs. I have also contributed to the recent work done by Di poï et al. (2009, 2010) in lizards that shows mobile elements have invaded the *Hox* gene clusters. My work specifically adds data from the ray-finned fishes, which were not included in these studies. Finally, my population level study was the first such work done at the micro-evolutionary level for any *Hox* gene locus. I hope that my population level research will spur initiatives into similar studies for other regions of the *Hox* gene cluster system and open a door to a deeper understanding of its evolution.

6.3 Questions Raised

The findings of my work raise several intriguing questions. 1. What are the function of the 21 deeply conserved PFCs not associated with any known transcripts? The discovery of these deeply conserved PFCs with no known function desperately calls for research into their possible roles in the *Hox* gene clusters. 2. What are the roles of transposable elements in *Hox* gene cluster evolution? Research into the correlation between transposable element invasions, PFC turnover and morphological variability will help not only further the knowledge of *Hox* gene clusters but genome evolution in general. 3. What knowledge can be gained by studying the micro-evolution of the *Hox* gene clusters? Evidence of strong positive selection at the micro-evolutionary level in an enhancer of a gene that appears to be under relaxed constraints at the macro-evolutionary level brings into question what forces are acting at the micro-evolutionary level in other parts of the *Hox* gene clusters (microRNAs, coding regions, introns, etc...)

6.4 Future Research

Further work is necessary to further realize the impact of the findings of my work. Expression vector studies need to be done to obtain at least a rudimentary knowledge of the function of the deeply conserved PFCs with no known function. While these PFCs may be maintained for reasons other than *cis*-regulation this is the first logical step. Complete sequencing of *Hox* gene clusters of species in phylogenetically important positions (such as hagfish, lamprey, lungfish, bowfin, gold eye, etc...) needs to be completed to obtain a better picture of the evolution of the vertebrate *Hox* gene cluster system. This is exemplified in the recent work in lizards (Di poï et al. 2009, 2010). Collaborative efforts between the fields of mobile element evolution and *Hox* gene cluster evolution could result in the enrichment of both as each provides a unique mechanism for research and could enrich the other.

To follow up on the evidence of strong positive selection between the sister species of killifish there is a need to first establish the effects on expression of these nucleotide differences and then to link this to a phenotypic difference. Functional analyses of the nucleotide differences in the CRE proved difficult. Perhaps this is due to the relatively few differences between the sister species. It is possible that these changes do not alter whether or not a protein will bind but at what strength and length of time it will bind. If the differences are this slight then binding conditions would have to be optimal to maintain pristine protein structure. Freckleton et al. (2009) have designed one type of analysis that may help overcome this problem. In this study genomic DNA is fragmented and ligated into bacteriophages. These bacteriophages will produce amino acid sequences from the genomic DNA inserts and present these molecules on their capsid. These phages can then be selected for by binding to a specific DNA sequence (*cis*-regulatory element). The genomic DNA sequence can then be amplified and either bound to a micro array or sequenced. This would allow the possible production of proteins that are normally only produced in developmental stages of species such as *F*. *olivaceus* and *F. notatus* where lab strains have not been established. After establishing expression differences, phenotypic correlation studies should also be performed to see if there is a correlation between genotype and phenotype in these fish. The possibility of a connection between the selection seen at the *Hox*A2b enhancer and the ability to flare the opercle in mate defense are intriguing. Bone morphometrics and behavior studies in these two species could help resolve the results of this selective pressure.

6.5 Concluding Remarks

Less than 10 years ago was an idea that the gnathostome *Hox* gene cluster intergenic sequences, specifically the CNSs, were as conserved as the genes themselves. This was challenged by Chiu et al. (2002) where they showed that in the teleosts Hox gene clusters intergenic sequences had lost several PFCs. This was then attributed to the FSGD. This was again challenged by Chiu et al. (2004) where they showed that the actual turnover of PFCs started well before the FSGD in the basal ray-finned fish, bichir. My research has shown that these changes exist across all *Hox* gene cluster paralogs although with varying rates of turnover. It was also the convention that mobile elements would be absent from the *Hox* gene clusters due to their ability to disrupt the order and orientation of the genes in the cluster as well as the spacing between them. My research in ray-finned fishes along with work done by the Duboule lab (Di poï et al. 2009, 2010) in lizards has shown that *Hox* gene clusters do in fact have mobile elements throughout and that the types of mobile elements that have invaded the clusters are lineage specific. Finally, prior to my research, there has never been a population level study of a *Hox* gene cluster locus. My findings, specifically the evidence of strong positive selection at the population level along with the unique evolution of ray-finned fishes *Hox* gene clusters, should focus attention not only on the macro-evolution of this unique system but also on its micro-evolution.

7. Legends

7.1 Table Legends

Table 1-Tests of Selection

A. Interspecies comparisons. Shown are the percent differences found between F. olivaceus, F. notatus and F. catenatus at several loci. Total differences is the number of differences seen for each comparison and the total length of that comparison followed by the percent difference. *Coding/in element* is the number of differences seen among nucleotides that either change the amino acid coded for or reside within a known response element. *Non-coding/out element* is the number of differences seen among nucleotides that either do not change the amino acid coded for or reside outside of a known response element. Ka/Ks-Kb/Ki is the results of synonymous/non-synonymous or within binding site/outside binding site ratio tests. The highest ratio is 7.78 seen between sister species F. olivaceus and F. notatus for the Hox A2b Enhancer. B. Intraspecies comparisons. Shown are the percent polymorphisms for each category within F. olivaceus populations as well as their Kb/Ki ratios for the Hox A2a and Hox A2b enhancers as well as a portion of intron 7 of the PGK1 gene. Also shown are the alleles for each locus and their percent in each population. There are no known binding elements within PGK1 intron 7 therefore no Kb/Ki ratio was done. Note the relatively high number of polymorphism within PGK1 intron 7. C. Hardy-Weinberg Test. Shown is the Hardy-Weinberg test for assortative mating for the Hox A2b enhancer within the Rockford Beach sub-population of F. olivaceus. Note that the observed deviation from expected frequencies is 61% probable to happen by chance thus this population is shown to be in Hardy-Weinberg equilibrium.

Table 2-Primers

List of primer names and sequences that were used to amplify regions of interest used in this study. Annealing temperatures are listed to the right. AB/LA stands for annealing temperatures used for Applied Biosystems Taq polymerase and Takara LA Taq polymerase. Phusion refers to annealing temperatures used for Finnzymes Phusion Taq polymerase.

Table 3-Divergence Estimation between Fundulus sp.

Divergence date estimations for the three *Fundulus sp.* involved in this study along with percent difference between two pufferfish species with an estimated divergence date of 5-30 my. Personal communication with Michael Alfaro. Table 4-Exclusive PFC Patterns in *Hox* A and *Hox* B Clusters

Percentage of PFCs shared exclusively between indicated groups. Each comparison was also scaled to the number of pair wise comparisons made for that group of comparisons.

7.2 Figure Legends

Figure 1-Oral and Pharyngeal Jaws

Teleosts fishes have two sets of jaws. The oral or frontal jaws have mostly lost the ability to grind or smash foodstuffs. The pharyngeal jaws evolved secondarily and mostly grind and smash foodstuffs. Liem's Hypothesis states that this partitioning of work allows the two jaws to evolve independently.

Figure 2-Metazoan Tree

The Metazoan tree shown here has families as the terminal branches and an emphasis on the ray-finned fishes (Actinopterygii). Two insets show alternative phylogenies for the Actinopterygii.

Figure 3-Gnathostome Phylogeny and Hox Gene Cluster Content

This phylogenetic tree is shown to emphasize the gnathostome species that contain 4 *Hox* gene clusters versus those that contain 8 *Hox* gene clusters as a result of the FSGD. For each species or group a summary of known Hox genes are shown to the right. Paralogous group Hox genes are aligned vertically with the corresponding group number at the top (E = even skipped homologs). For every group/species their Hox clusters are labeled according to accepted nomenclature. A colored pie piece indicates presence of intact Hox gene, a gray pie piece indicates a pseudogene, a white pie piece and/or no pie indicates absence of Hox gene/s. For killifish and striped bass known and verified Hox gene content is listed. See figure 2 for scientific names corresponding to common names.

Figure 4-Bichir Anatomy

The bichir is a unique organism that shares traits with many different orders as well as some unique features.

Figure 5-Bichir *Hox* Gene Trees

Bootstrap or Bayesian posterior probability support is indicated for each branch. Protein trees clockwise from top left, neighbor joining, maximum parsimony and Bayesian. Nucleotide trees from top left, neighbor joining, maximum parsimony, maximum likelihood and Bayesian.

Figure 6-Bichir *Hox* Gene Content

Hox gene cluster size is roughly to scale. *Hox* genes are indicated by boxes with their paralog identity indicated by number. *Hox* genes in blue were previously annotated and those in yellow were annotated during this work. Curved lines on either side of a gene indicate incomplete sequencing of that gene. Unconnected *Hox* genes indicate unsequenced intergenic regions. *Hox* D3 has a 16,255 bp intron indicated by a line connecting the two coding regions.

Figure 7-Bichir *Hox* Gene Trees

Bootstrap or Bayesian posterior probability support is indicated for each branch. Protein trees clockwise from top left, neighbor joining, maximum parsimony and Bayesian. Nucleotide trees from top left, neighbor joining, maximum parsimony, maximum likelihood and Bayesian.

Figure 8-Phylogentic Footprint Clusters Naming Scheme

Proposed nomenclature for naming phylogenetic footprint clusters. The name consists of a 3-letter abbreviation for the species consisting of the first letter of the genus and first two letters of the species. A capital letter representing the Hox cluster, two subscript capital letters represent the position along the cluster, an identification number specific for each PFC, and 1-6 lower case subscript letters representing the section content of that species.

Figure 9-Deeply Conserved PFCs

A map of the locations of deeply conserved phylogenetic footprint clusters on reconstructed gnathostome ancestor HoxA, B, C, and D clusters. Black boxes denote Hox genes; open boxes denote Hox genes that are found in only 1 extant gnathostome to date. Red lines represent PFCs that are found within untranslated regions (UTRs) of Hox gene mRNAs. Blue lines represent PFCs that are found within 500 nucleotides of a Hox gene proper region but have not been identified as UTRs. Green lines represent PFCs that have high or identical sequence identity to sequences in the EST library. Yellow lines represent PFCs that are not found in any databases or published papers. Black lines are sequences with known function and labeled accordingly. 'Deeply Conserved' refers to PFCs conserved between at least 2 of the following groups, 1) horn shark, 2) \geq 2 lobefinned fish, 3) bichir, 4) \geq 2 teleost fish. The C8 early enhancer does not qualify as deeply conserved but has been found by the PFC method with the 5' end conserved in lobefinned fish and the 3' end conserved in teleost fish. Information on blast results and PFC number for each PFC represented in this figure is available in supplementary table 1. Numbers in the figure refer to the following references: 1. Larochelle et al. 1999. 2. Nonchev et al. 1996. 3. Berezikov et al. 2005. 4. Shashikant et al. 1995. 5. Morrison et al. 1996. 6. Yekta et al. 2004. 7. Doersken et al. 1996.

Figure 10-PFC Retention Mosaicism

Select species showing the pattern of PFC retention with species containing 4 *Hox* gene clusters (red) or 8 *Hox* gene clusters (blue) for the *Hox* A (left) and *Hox* B (right) gene clusters. As you can see from the pie diagrams human retains mostly PFCs that are shared with other 4 *Hox* gene cluster species whereas bichir has a greater turnover sharing more PFCs with 8 *Hox* gene cluster species. The same pattern can be seen for zebrafish 'a' paralogs indicating further turnover within the teleosts. Also the rate of turnover is greater for the *Hox* B gene cluster than for the *Hox* A gene cluster. Figure 11-*Hox* A Gene Cluster Retention

A simplified phylogenetic tree of the *Hox* A clusters. Solid circles denote acquisition of a new PFC in that lineage. Open circles denote loss of PFCs in that lineage. Color of open circles denote where the lost PFCs were originally acquired. Numbers indicate the amount of PFCs gained or lost. I only used PFCs that met the criteria of being conserved between at least 3 species. Notice that there is no apparent gain of any PFCs at the base of the teleost but there is evidence of 7 new PFCs gained before the divergence of bichir at the base of the ray-finned fish clade. This puts acquisition of new elements prior to FSGD at a ratio of 7:2. If the two gains in the teleost Aa and Ab clusters are considered to be gained prior to the divergence of the paralogous clusters and then lost in each of the paralogs; the acquisition of new elements in the rayfinned fish clade is in favor of pre-FSGD with a ratio of 9:0.

Figure 12-Intergenic Distances with Mammalian Proxies

Comparison of Hox cluster orthologous intergenic region distances between teleost fish with proxies from mammals. The random bar consists of an average distance for comparisons of 10 random intergenic regions, distances greater than distances between random sequences are considered by chance and therefore are not considered informative. No HoxC cluster is currently available for opossum, *Monodelphis domestica*. Notice the greater distances for teleost fish opposed to the mammalian proxies. This is either due to an overall increased mutation rate and/or incorrect divergence dates for teleost fishes resulting in incorrect proxies.

Figure 13-*Hox* A2 Gene Expression Pattern

In mammals and birds the *Hox* A2 gene is found to be expressed in rhombomeres 2-7 of the developing hindbrain as well as in neural crest cells derived from rhombomere 4. *Hox* A2 has the most posterior expression of any *Hox* gene.

Figure 14-Hox A2 Paralogs Expression Patterns

Expression patterns of the *Hox* A2a and *Hox* A2b paralogs in various teleost fishes. The *Hox* A2a paralog maintains a mores ancestral expression pattern in the Acanthomorpha but has been independently pseudogenized in both zebrafish and pufferfish. The *Hox* A2b paralog has a more varied expression with pseudogenization in medaka.

Figure 15-Hox A2 Gene Regulation Schematic

Hox A2 gene expression is controlled by 3 *cis*-regulatory elements. The r3/r5 enahncer lies 1-3 kb upstream of the translational start site and controls expression in rhombomeres 3 and 5 as well as neural crest cells derived from rhombomere 4. The r4 enhancer lies within the intron and controls expression in rhombomere 4. The r2 enhancer lies within the 3' portion of exon 2 and controls expression in rhombomere 2. Figure 16-*In-situ* Hybridization of *Fundulus heteroclitus* Embryos

Hox A2 gene expression in *Fundulus sp.* was discovered using RNA *in-situ* hybridization assays. *Hox* A2a expression is on the left in each developmental stage and and *Hox* A2b expression is on the right. Dorsal views are on top and lateral views are on bottom. An arrow indicates the otic vesicle, which lays overlapping rhombomeres 4 and 5. An arrowhead indicates pharyngeal arch 2. EGR2, a krox-20 ortholog, stains rhombomeres 3 and 5 and is used to show location of rhombomeres in early embryos. M and N are 2-4 somite stage embryos with EGR2 staining in red and *Hox* A2 staining in

blue/purple. A-D are 8-somite stage embryos. E-H are 14-somite stage embryos. I-L are 21-somite stage embryos.

Figure 17-Fundulus sp. Hox Gene Trees

Nucleotide trees are shown. Bootstrap or Bayesian posterior probability support is indicated for each branch from top left, neighbor joining, maximum parsimony, maximum likelihood and Bayesian. The branch that supports paralog status for *Fundulus sp.* is circled. *Fundulus sp.* are circled.

Figure 18-Charater State Trees

This character state tree of the *Hox* A2 r3/r5 enhancer from NC2 to RE3 including RE4 and 5' portion of NC3 shows the number of nucleotide changes on each branch and branch lengths are proportional to number of changes. 'a' following common names refers to the *Hox* A2a enhancer and 'b' to the *Hox* A2b enhancer. Total number of changes on each branch is inside squares and number of single-step changes is in diamonds. The *Hox* A2b enhancers show significantly more changes among teleosts and those changes are continuously steady moving from the stem to terminal branches. The *Hox* A2a enhancers share the majority of their changes and have very few terminal branch changes. Killifish *Hox* A2b enhancers have the most number of changes as well as twice as many single-step changes as any teleost *Hox* A2 enhancer. The same pattern is seen for the *Hox* A2 gene region.

Figure 19-Ka/Ks Ratio and Synonymous Percent Difference

This figure shows the Ka/Ks ratios and synonymous percent differences between *F. olivaceus* and *F. notatus* for the *Hox* A2a an *Hox* A2b r3/r5 enhancers and surrounding genes.

Figure 20-RE4/NC2 *Hox* A2b r3/r5 Enhancer Variable Region

All 4 fixed differences and one polymorphism are located within 38 bps of each other in the RE4/NC2 region of the r3/r5 enhancer of the *Hox* A2b gene in the *Fundulus sp. F. notatus* has 4 differences that result in slight alteration of RUSH1- α site strength and loss of the Mafb binding site with gain of an HMG-1 binding site. *F. olivaceus* has 4 differences that result in slight alteration of RUSH1- α site strength and loss relocation of an Ubx site with. *F. olivaceus* allele #5 has an additional polymorphism that results in the loss of the RUSH1- α site and does not appear in the population in the homozygous state.

Figure 21-Master TFBS Retention

Shown are the TFBS for krox-20, AP-2 and Mafb. These three transcription factors control 3 major aspects of *Hox* A2 gene expression in the developing hindbrain. Response elements 2-5 are also indicated. Triangles indicate AP-2 binding sites and circles indicate Mafb binding sites. Dark color represents TFBS located in the same orientation as transcription and reddish color represents TFBS located in the opposite orientation of transcription.

Figure 22-Fundulus sp. Tree

3 major groups of *Fundulus* are shown along with their possible phylogenetic relationships. Pictures of *F. olivaceus* and *F. notatus* are also shown showing the presence or absence of spots above the lateral line. Approximate divergence dates are given.

Figure 23-Tc1 DNA Transposon Schematic

Schematic of the original Tc1 DNA transposon found in *C. elegans*. D refers to the aspartate amino acid and E to the glutamate amino acid. The Tc1 transposon bind directly to its own inverted repeat sequences as a dimer bringing the two inverted repeats within close proximity.

Figure 24-*Hox* Gene Cluster Transposon Content

The *Hox* gene clusters of 9 species are represented. The top line represents the *Hox* gene cluster of amphioxus which contains the most *Hox* genes of any cluster. The next four lines represent the *Hox* A, B, C and D gene clusters (respectively) of bichir (light blue), horn shark (red), coelacanth (green) and human (pink). The last four lines represent the *Hox* Aa/Ab, Ba/Bb, Ca/Cb and Da/Db gene clusters (respectively) of pufferfish (light blue), Nile tilapia (purple), medaka (green) and zebrafish (fuchsia). The bars indicated the percentage of the intergenic region that is composed of transposons. The bars are color coded to each species and designate 3 types of transposons; Class II transposons (solid bar), Class I LTR transposons (striped bar) and Class I non-LTR transposons (open bar).

Figure 25-Tc1-like Transposons in Bichir

Amino acid alignment of the artificially constructed and functional *sleeping beauty* Tc1-like transposon, the consensus reconstructed ancestral salmonid Tc1-like transposon, the intact Tc1-like transposon found flanking bichir's *Hox* A gene cluster and the intact Tc1-like transposon found within the intron of bichir's *Hox* D3 gene. 4 functional domains are highlighted; two DNA binding domains (Paired-like domain with Leucine Zipper and Homeo-like Domain), nuclear localization signal, glycine-rich box and DDE active motif. The DDE active motif is well conserved between the functional *sleeping beauty* transposon and the two bichir Tc1-like transposons although the *Hox* D Tc1-like transposon has a hereto for unseen DD36E motif. Although the DNA binding domains do not appear to be conserved, the two Tc1-like transposons in bichir still are reported as having a Tc1-like DNA binding domain by NCBI protein-blast domain searching algorithm.

Figure 26-Tc1-like Transposon Tree

The Tc1-like transposons found in teleosts are separated into 3 main groups labeled A, B and C. The Tc1-like sequences found during this study are circled in red. Figure 27-Tc1-like Tranposons in *Hox* Gene Clusters

All Tc1-like transposons found within the *Hox* gene clusters either group or have a greater similarity with Tc1-like sequences that group outside the three main teleosts groups. All Tc1-like transposons found flanking the *Hox* gene clusters group within teleosts group C. Tc1-like transposons that still maintain an identifiable inverted repeat are identified with a star.

Figure 28-Hox A Gene Cluster Tc1 Insertion Sites

Shown is the relative amount of Tc1 insertion sites found in intergenic regions of 8 *Hox* A gene clusters. The amount is based on the number and weight of insertion sites. Figure 29-*Hox* A Gene Cluster Tc1 Insertion Sites supplement

A-D. Shown is the relative amount of Tc1 insertion sites found in intergenic regions of 8 *Hox* A gene clusters. These figures show the relative amount divided into the 4 weight categories. E and F. Shown is the relative amount of Tc1 insertion sites found in intron and exon regions, respectively, of 8 *Hox* A gene clusters.

Figure 30-Simulation Results of Tc1-like Transposition in Bichir Hox A Gene Cluster

Shown is the number of base pair alterations after 25 simulated fixations or "jumps" of the Tc1-like transposon found flanking bichir's *Hox* A gene cluster. There appears to be no discernable pattern or preference for location of base pair alteration. Figure 31-Schematic of Tc1-like Activity Confirmation Vectors

All vectors used a pFastBac1 backbone with an integrated multiple cloning site designed by Rick Cohen. P_{PH} indicates the polyhedron promoter; SV40 polyA indicates location of the poly A signal. 1-6 shows the different multiple cloning site regions used to make the 6 types of vectors used in this study.

8. Tables and Figures 8.1 Tables

Table 1.

A. Interspecies Comparisons

1.	PGK1 locus	Total Differences	coding/in	element non-	-coding/out element	Ka/Ks-Kb/Ki	p-value
	F.olivaceus/F. notatus	58/1615 (3.59%)	0/92 (0	.00%) 5	58/1523 (3.81%)	0.00	. 0.06
	F. catenatus/F. olivaceus	124/1635 (7.58%)	1/92 (1	.09%) 1	23/1543 (7.97%)	0.14	0.02
	F. catenatus/F. notatus	103/1652 (6.23%)	1/92 (1	.09%) 1	02/1560 (6.54%)	0.17	0.04
	A3a locus (exon 2)						
	F.olivaceus/F. notatus	2/451 (0.44%)	1/300 (0	0.33%)	1/151 (0.66%)	0.50	0.62
	F. catenatus/F. olivaceus	13/451 (2.88%)	4/300 (1	.33%)	9/151 (5.96%)	0.22	0.01
	F. catenatus/F. notatus	15/451 (3.33%)	5/300 (1	1.67%)	10/151 (6.62%)	0.25	0.01
	T nigroviridis/T rubrines	23/436 (5 28%)	5/290 (1	1 72%)	18/146 (12.3%)	0.14	<0.001
	A2a locus (exon 1)	20/100 (0.20/0)	0,200 (10/110 (12:070)	0.11	40.001
	Folivaceus/E potatus	2/333 (0.60%)	1/222 ((1 45%)	1/111 (0.90%)	0.50	0.62
	E catenatus/E olivaceus	3/333 (0.00%)	2/222 (0	0.45%)	1/111 (0.90%)	1.00	1.00
	E estenatus/F. pototus	5/333 (0.3078)	2/222 (0	1.259/)	2/111/1 0.00/)	0.75	0.75
	F. Catenatus/F. notatus	5/333 (1.50%)	3/222 (1.30%)	2/111(1.00%)	0.75	0.75
~	A Challen and A Sintrem	13/304 (3.57%)	1/243 (0	J.40%)	12/121 (9.9%)	0.04	<0.001
Ζ.	Asb locus (exon1,2 intron)	12/507 (2 100/)	1/100 //	520/)	12/407 (2 05%)	0.19	0.06
	F catenatus/F olivaceus	27/597 (4.52%)	1/190 (0) 53%)	26/407 (6.39%)	0.18	0.00
	F. catenatus/F. notatus	22/597 (3.69%)	0/190 (0	0.00%)	22/407 (5.40%)	0.00	0.001
	T. nigroviridis/T. rubripes	23/285 (8.07%)	12/190 (6.32%)	11/95 (11.6%)	0.55	0.14
				intr	on 86/243 (35.4%)		
	A2b locus (exon1)						
	F.olivaceus/F. notatus	2/227 (0.88%)	0/151 (0	0.00%)	2/76 (2.63%)	0.00	0.05
	F. catenatus/F. olivaceus	3/227 (1.32%) 5/227 (2.20%)	3/151 (1	1.99%)	0/76 (0.00%)	N/A 0.75	0.22
	T. nigroviridis/T. rubrines	8/216 (3.70%)	4/144 (2	2.78%)	4/72 (5.56%)	0.50	0.32
	B2a locus (exon1)				(,)		
	F.olivaceus/F. notatus	1/209 (0.48%)	1/138 (0).72%)	0/71 (0.00%)	N/A	0.47
	F. catenatus/F. olivaceus	3/209 (1.44%)	2/138 (1	1.45%)	1/71 (1.41%)	1.03	0.98
	F. catenatus/F. notatus	4/209 (1.91%)	3/138 (2	2.17%)	1/71 (1.41%)	1.54	0.70
2	I. nigroviridis/ I. rubripes	26/478 (5.44%)	6/319 (1	1.88%)	20/159 (12.6%)	0.15	<0.001
э.	Aza Ennancer	0/530 (4 670/)	4/4 44 /0	740/)	0/207 (2.020/)	0.40	0.20
	F. catenatus/F. notatus	9/536 (1.07%) 17/538 (2.97%)	1/141 (() 71%)	0/397 (2.02%) 16/397 (4.03%)	0.40	0.30
	F. catenatus/F. notatus	16/538 (2.97%)	0/141 (0	0.00%)	16/397 (4.03%)	0.00	0.02
	T. nigroviridis/T. rubripes	49/555 (8.83%)	3/181 (1	1.66%)	46/374 (12.3%)	0.13	<0.001
4.	A2b Enhancer						
	F.olivaceus/F. notatus	5/318 (1.57%)	4/108 (3	3.70%)	1/210 (0.48%)	7.78	0.03
	F. catenatus/F. olivaceus	16/318 (5.03%)	6/108 (5	5.56%)	10/210 (4.76%)	1.17	0.77
	T nigroviridis/T rubrines	18/318 (5.67%)	6/108 (t 17/172 (0.00%) 9.88%)	12/210 (5.71%) 44/248 (10.3%)	0.97	0.96
	1. Higrovindio/1. Tubripeo	01/420 (14.070)	11/11/2 (0.0070)	44/240 (10.070)	0.00	0.04
в.	Intraspecies Comparisons						
В. 1.	Intraspecies Comparisons A2a Enhancer						
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism						
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population	Total Pol	ymorphism	in elements	out elemen	nts Kb/Ki	p-value
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney	Total Pol	ymorphism 519	in elements 0/141	out elemen 0/397	nts Kb/Ki 0.00	p-value
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach	Total Pol 0/: 1/:	ymorphism 519 519	in elements 0/141 0/141	out elemen 0/397 1/397	nts Kb/Ki 0.00 0.00	<i>p-value</i> 0.56
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total	Total Pol 0/ 1/ 	ymorphism 519 519 519 (0.6%)	in elements 0/141 0/141 0/141 0/141	out elemer 0/397 1/397 0/397 0/397 (0 76	nts Kb/Ki 0.00 0.00 0.00	<i>p-value</i> 0.56
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles	Total Pol 0/ 1/ 0/ 3/519	ymorphism 519 519 519 (0.6%)	in elements 0/141 0/141 0/141 0/141 (0.00%	out elemer 0/397 1/397 0/397 6) 3/397 (0.76	nts Kb/Ki 0.00 0.00 0.00 %) 0.00	<i>p-value</i> 0.56 0.31
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele	Total Pol 0/ 1/: 	ymorphism 519 519 (0.6%) Piney	in elements 0/141 0/141 0/141 0/141 (0.00% Rockford Bea	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F	nts Kb/Ki 0.00 0.00 0.00 %) 0.00 River	<i>p-value</i> 0.56 0.31
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1	Total Pol 0/ 1/ 0/ 3/519 Little	ymorphism 519 519 (0.6%) Piney 00%	in elements 0/141 0/141 0/141 0/141 (0.00% Rockford Bea 0%	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100%	nts Kb/Ki 0.00 0.00 0.00 %) 0.00 River	<i>p-value</i> 0.56 0.31
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 1330, -177G, -300A	Total Pol 0/ 1/; 0/ 3/519 Little 10	ymorphism 519 519 (0.6%) <i>Piney</i> 00%	in elements 0/141 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73%	out elemer 0/397 1/397 0/397 5) 3/397 (0.76 ch Gasconade F 100% 0%	nts Kb/Ki 0.00 0.00 0.00 %) 0.00 River	<i>p-value</i> 0.56 0.31
В. 1. а.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G	Total Pol 0/ 1/: 3/519 Little 100 0	ymorphism 519 519 (0.6%) Piney 10% 9% 6	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 149	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0%	nts Kb/Ki 0.00 0.00 %) 0.00 River	<i>p-value</i> 0.56 0.31
B. 1. a. b.	Intraspecies Comparisons A2a Enhancer F- olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F- olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer	Total Pol 0/ 1// 3/519 Little 10 0 00	ymorphism 519 519 (0.6%) <i>Piney</i> 10% 1% 6	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42	nts Kb/Ki 0.00 0.00 %) 0.00 River	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer E olivaceus Polymorphism	Total Pol 0/ 1/ 0/ 3/519 Little 10 0 0	ymorphism 519 519 (0.6%) <i>Piney</i> 0% 9% 6	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148	out elemer 0/397 0/397 5) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42	kb/Ki Kb/Ki 0.00 0.00 0.00 0.00 %) 0.00 %iver	<i>p-value</i> 0.56 — 0.31
 B. a. b. 2. a. 	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population	Total Pol 0/ 1/ 0/ 3/519 Little 10 0 0 0 Total Pol	ymorphism 519 519 519 (0.6%) Piney 0% 0% 6 5 ymorphism	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 cu elemer	nts Kb/Ki 0.00 0.00 0.00 %) 0.00 River	<i>p-value</i> 0.56 — 0.31
B. 1. a. b. 2. a.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney	Total Pol 0/ 1/ 3/519 Little 100 0 Total Pol 0/	ymorphism 519 519 (0.6%) Piney 00% 9% 6 ymorphism 318	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148 in elements 0/108	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 : out elemer 0/210	nts Kb/Ki 0.00 0.00 %) 0.00 %) 0.00 River nts Kb/Ki N/A	<i>p-value</i> 0.56 – 0.31
B. 1. a. b. 2. a.	Intraspecies Comparisons A2a Enhancer F- olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F- olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach	Total Pol 0/ 3/519 Little 10 0 Total Pol 0/ 2/	ymorphism 519 519 (0.6%) <i>Piney</i> 10% 9% 6 6 <i>ymorphism</i> 318	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 0% 42 : out elemer 0/210 1/210	nts Kb/Ki 0.00 0.00 %) 0.00 River	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a.	Intraspecies Comparisons A2a Enhancer F- olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F- olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F- olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River	Total Pol 0/ 1/ 3/519 Little 10 0 0 Total Pol 0/ 2/ 0/	ymorphism 519 519 (0.6%) Piney 00% 9% 6 ymorphism 318 318 318	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 27% 148 in elements 0/108 1/108	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 6) 3/397 (0.76 100% 0% 0% 42 42 c out elemer 0/210 1/210 0/210	nts Kb/Ki 0.00 0.00 0.00 %) 0.00 %) 0.00 %iver nts Kb/Ki N/A 1.94 1.94	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total E. olivaceus Alleles	Total Pol 0// 1// 0// 3/519 Little 10 00 0/ 0/ 2// 2/318	ymorphism 519 519 519 (0.6%) Piney 00% 9% 6 5 ymorphism 318 318 318 318 318	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 0/108	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 6) 3/397 (0.76 6) 0% 0% 0% 0% 42 42 5: out elemer 0/210 0/210 6) 1/210 (0.48	nts Kb/Ki 0.00 0.00 %) 0.00 %) 0.00 %iver nts Kb/Ki NA 1.94 %) 1.94	<i>p-value</i> 0.56 0.31 0.63 0.63
B. 1. a. b. 2. a.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele	Total Pol 0/ 3/519 Little 100 0/ 2/318 Little 100 0/ 2/318	ymorphism 519 519 519 (0.6%) Piney 00% % % % 6 ymorphism 318 318 318 (0.63%) Piney	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 0/108 1/108 0/108	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade R 100% 0% 0% 42 : out elemer 0/210 1/210 0/210 6) 1/210 (0.48	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A 9%) 1.94	<i>p-value</i> 0.56 0.31 0.63 0.63
B. 1. a. b. 2. a.	Intraspecies Comparisons A2a Enhancer F- olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F- olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromesome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1	Total Pol 0/ 3/519 Little 100 0/ 2/ 2/318 Little 100 2/318	ymorphism 519 519 (0.6%) Piney 00% 6 ymorphism 318 318 318 (0.63%) Piney 00%	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92%) Rockford Bea 49%	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 c out elemer 0/210 1/210 0/210 5) 1/210 (0.48 ch Gasconade F 100%	nts Kb/Ki 0.00 0.00 %) 0.00 River	<i>p-value</i> 0.56 0.31 0.63 0.63
B. 1. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 133C, -177G, -300A #3 - 133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G	Total Pol 0/ 3/519 Little 10 0 0/ 2/ 2/318 Little 2/318 Little	ymorphism 519 519 (0.6%) Piney 00% 9% 6 ymorphism 318 318 318 (0.63%) Piney 10%	in elements 0/141 0/141 0/141 (0.00% 73% 27% 27% 148 in elements 0/108 1/108 (0.92% Rockford Bea 49% 13%	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 6) 3/397 (0.76 100% 0% 42 42 5: out elemer 0/210 1/210 (0.48 ch Gasconade F 100% 0%	nts Kb/Ki 0.00 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A %) 1.94 River	<i>p-value</i> 0.56 0.31 0.63
B. 1. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A	Total Pol 0// 1// 0// 3/519 Little 10 0/ 0/ 2// 2/318 Little 10 0/ 0/ 2/318	ymorphism 519 519 (0.6%) Piney 00% 9% 6 ymorphism 318 318 318 318 318 (0.63%) Piney 10% 9%	in elements 0/141 0/141 0/141 (0.00% 73% 27% 148 in elements 0/108 1/108 0/108 1/108 (0.92% Rockford Bea 49% 13% 38%	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 c out elemer 0/210 1/210 0/210 5) 1/210 (0.48 ch Gasconade F 100% 0% 0%	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A %) 1.94 River	<i>p-value</i> 0.56 0.31 0.63
B. 1. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count	Total Pol 0/ 3/519 Little 100 0/ 2/318 Little 2/318 Little 100 0/	ymorphism 519 519 519 (0.6%) Piney 00% 6 ymorphism 318 318 318 (0.63%) Piney 00% 9% 10	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 0/108 1/108 0/108 1/10 1/10	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 42 : out elemer 0/210 1/210 0/210 1/210 0/210 5) 1/210 (0.48 ch Gasconade F 100% 0% 28	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A %) 1.94 River	<i>p-value</i> 0.56 0.31 0.63
B. 1. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count	Total Pol 0/ 3/519 Little 100 0/ 2/318 Little 0/ 2/318 Little 100 0/ 2/318	ymorphism 519 519 519 (0.6%) Piney 00% 6 ymorphism 318 318 318 (0.63%) Piney 00% 9% 9% 10	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92%) Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 cout elemer 0/210 1/210 0/210 1/210 0/210 5) 1/210 (0.48 Gasconade F 100% 0% 0% 28	kb/ki Kb/ki 0.00 0.00 0.00 0.00 %) 0.00 River N/A 1.94 N/A %) 1.94 River Siver	<i>p-value</i> 0.56 0.31 0.63
B. 1. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 133C, -177G, -300A #3 - 133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count B PGK1 intron7	Total Pol 0/ 3/519 Little 10 0/ 2/318 Little 10 2/318 Little 10 0/ 2/318	ymorphism 519 519 (0.6%) Piney 00% 1% 6 ymorphism 318 318 318 (0.63%) Piney 10 9% 10	in elements 0/141 0/141 0/141 (0.00% 73% 27% 148 in elements 0/108 1/108 (0.92% Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 Gasconade F 100% 0% 0% 42 cout elemer 0/210 0/210 5) 1/210 (0.48 ch Gasconade F 100% 0% 0% 28	nts Kb/Ki 0.00 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A %) 1.94 River	<i>p-value</i> 0.56 0.31 0.63
B. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 133C, -177G, -300A #3 - 133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 F. olivaceus Polymorphism PGK1 intron7 F. olivaceus Polymorphism Population	Total Pol 0/ 1/ 3/519 Little 10 0/ 2/ 2/318 Little 10 0/ 2/318	ymorphism 519 519 519 (0.6%) Piney 00% 1% 6 ymorphism 318 318 318 318 (0.63%) Piney 10% 10 Vmorphism	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92% Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 c out elemer 0/210 0/210 0/210 6) 1/210 (0.48 ch Gasconade F 100% 0% 0% 28	nts Kb/Ki 0.00 0.00 %) 0.00 %) 0.00 ?// ?/ ?/ N/A 1.94 N/A N/A N/A 1.94 ?/ ?/ ?/ ?/ ?/ ?/ ?/ ?/ ?/ ?/ ?/ ?/ ?/	<i>p-value</i> 0.56 0.31 0.63 0.63
B. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 133C, -177G, -300A #3 - 133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #1 #1 #1 5 A218G #7 T68A Chromosome count 5 PGK1 intron7 F. olivaceus Polymorphism Population Little Piney	Total Pol 0/ 1// 0/ 3/519 Little 10 0/ 2/ 2/318 Little 10 0/ 2/318	ymorphism 519 519 519 (0.6%) Piney 00% 9% 6 ymorphism 318 318 318 318 (0.63%) Piney 10% 9% 10 ymorphism 333	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92% Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 : out elemer 0/210 1/210 0/210 5) 1/210 (0.48 ch Gasconade F 100% 0% 28	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A %) 1.94 River	<i>p-value</i> 0.56 0.31 0.63
B. 1. a. b. 2. a. 5.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 133C, -177G, -300A #3 - 133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #1 #5 A218G #7 T68A Chromosome count FOIvaceus Polymorphism Population Little Piney Rockford Beach Chromosome count	Total Pol 0/ 3/519 Little 100 C Total Pol 0/ 2/318 Little 10 C C C C Total Pol 6/ 8/	ymorphism 519 519 519 719 719 710 710 710 710 710 710 710 710	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92% Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade R 100% 0% 42 : out elemer 0/210 1/210 1/210 0/210 6) 1/210 (0.48 ch Gasconade R 100% 0% 0% 28	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A %) 1.94 River	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a. 5.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #5 A218G #7 T68A Chromosome count F. Olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count F. Olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River	Total Pol 0/ 3/519 Little 10 0/ 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 6/ 8/ 8/ 8/ 8/ 6/	ymorphism 519 519 (0.6%) Piney 00% 0% 0% 6 ymorphism 318 318 (0.63%) Piney 10% 0% 10 ymorphism 333 333 333	in elements 0/141 0/141 0/141 (0.00% 73% 27% 148 in elements 0/108 1/108 (0.92% Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 Gasconade F 100% 0% 42 cout elemer 0/210 0/210 5) 1/210 (0.48 ch Gasconade F 100% 0% 0% 28	nts Kb/Ki 0.00 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A %) 1.94 River	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total #1 #2-133C, -177G, -300A #3-133C, -177G, -300A #3-133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count PGK1 intron7 F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total PGK1 intron7 F. olivaceus Polymorphism Population Chromosome count PGK1 intron7 F. olivaceus Polymorphism Population Gasconade River Total T. olivaceus Rolymorphism Population Colivaceus Rolymorphism Population Casconade River Total	Total Pol 0/ 1/ 3/519 Little 10 0/ 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 0/ 2/318	ymorphism 519 519 519 (0.6%) Piney 00% 1% 6 ymorphism 318 318 318 (0.63%) Piney 10% 10 Piney 10% 10% 10 21% 21% 21% 21% 21% 21% 21% 21%	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92%) Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 c out elemer 0/210 1/210 0/210 0/210 0/210 6) 1/210 (0.48 ch Gasconade F 100% 0% 0% 28	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki NA 1.94 %) 1.94 River	<i>p-value</i> 0.56 0.31 0.63 0.63
B. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total #1 #2 -133C, -177G, -300A #3 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Chromosome Count A2b Enhancer F. olivaceus Alleles Allele #1 #5 A218G #1 #5 A218G #1 #5 A218G #1 F. olivaceus Polymorphism Population F. olivaceus Polymorphism Population Entraspective BACH Intron7 F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele	Total Pol 0/ 3/519 Little 10 0/ 2/ 2/318 Little 10 0/ 2/318 Little 10 0/ 0/ 2/318	ymorphism 519 519 519 519 70% 90% 9% 9% 6 9% 9% 10 9% 10 9% 10 9% 10 9% 10 9% 10 9% 10 9% 10 9% 10 10 10 10 10 10 10 10 10 10	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92%) Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 42 c out elemer 0/210 1/210 0) 1/210 (0.48 ch Gasconade F 100% 0% 28	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A %) 1.94 River	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a. b. 3. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 133C, -177G, -300A #3 - 133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count F. Olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1	Total Pol 0/ 3/519 Little 100 0/ 2/318 Little 100 0/ 2/318 Little 100 0/ 6/ 8/ 8/333 Littl	ymorphism 519 519 519 (0.6%) Piney 00% 0% 0% 6 ymorphism 318 318 318 (0.63%) Piney 0% 10 ymorphism 333 333 333 (2.4%) ie Piney/Gascod 13%	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92% Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 42 c out elemer 0/210 1/210 1/210 0/210 6) 1/210 (0.48 ch Gasconade F 100% 0% 28 Rockford Be 65%	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 N/A N/A N/A N/A River	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a. b. 3. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count F. Olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 A455GT, G62T, C68T, A72C, A88	Total Pol 0/ 3/519 1/ 0/ 3/519 10 0/ 0/ 2/318 10 0/ 2/318 10 0/ 0/ 2/318 10 0/ 0/ 2/318 10 0/ 0/ 2/333 10 10 0/ 0/ 2/333 10 10 10 10 10 10 10 10 10 10 10 10 10	ymorphism 519 519 9 9 9 9 9 519 10 9 9 9 6 9 9 9 5 6 9 9 9 5 6 9 9 9 5 6 9 9 9 5 6 9 9 5 9 9 5 9 9 5 9 5 9 5 9 5 9 5 9 5 9 5 9 5 9 5 9 5 9 5 6 5 9 5 9 5 6 5 9 5 9 5 6 5 9 5 5 5 5 5 5 5 5 5 5 5 5 5	in elements 0/141 0/141 0/141 (0.00% 73% 27% 148 in elements 0/108 1/108 (0.92% Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 Gasconade F 0% 0% 42 cout elemer 0/210 0/210 6) 1/210 (0.48 ch Gasconade F 100% 0% 0% 28 Rockford Be 65% 22%	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki NA 1.94 N/A %) 1.94 River ach	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 -133C, -177G, -300A #3 -133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count F. Olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 AA55GT, G62T, C68T, A72C, A8 CCGA264TCTT	Total Pol 0/ 3/519 Little 10 0/ 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 0/ 2/318 Little 10 0/ 0/ 2/318 Little 8/ 3/333 Littl	ymorphism 519 519 519 519 70% 7% 6 7% 7% 7% 7% 7% 7% 7% 7% 7% 7%	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements 0/108 0/108 1/108 (0.92% Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 0% 42 c out elemer 0/210 0/210 0/210 6) 1/210 (0.48 ch Gasconade F 100% 0% 28 Rockford Be 65% 22%	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki NA 1.94 %) 1.94 River ach	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 133C, -177G, -300A #3 - 133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 AA5SGT, G62T, C68T, A72C, A8 CCGA264TCTT #3 C179T	Total Pol 0/ 1// 0/ 3/519 Little 10 0/ 2/318 Little 10 2/318 Little 10 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 2/318 Little 10 0/ 2/ 3/ 5/ 9/ 10 0/ 2/ 3/ 5/ 9/ 10 0/ 2/ 3/ 5/ 9/ 10 0/ 2/ 3/ 5/ 9/ 10 0/ 2/ 2/ 10 0/ 2/ 2/ 10 0/ 2/ 2/ 10 0/ 2/ 2/ 10 0/ 2/ 2/ 3/ 5/ 9/ 0/ 2/ 2/ 10 0/ 2/ 2/ 10 0/ 2/ 3/ 5/ 9/ 0/ 2/ 2/ 3/ 5/ 9/ 0/ 2/ 3/ 5/ 9/ 0/ 2/ 2/ 2/ 3/ 5/ 9/ 0/ 2/ 2/ 3/ 5/ 9/ 0/ 2/ 2/ 3/ 5/ 9/ 0/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 9/ 2/ 3/ 5/ 3/ 5/ 2/ 3/ 5/ 3/ 5/ 2/ 3/ 5/ 5/ 2/ 3/ 5/ 5/ 5/ 5/ 5/ 5/ 5/ 2/ 3/ 5/ 5/ 5/ 5/ 5/ 5/ 5/ 5/ 5/ 5/ 5/ 5/ 5/	ymorphism 519 519 519 519 70% 9% 9% 6 ymorphism 318 318 318 318 (0.63%) Piney 0% 9% 10 ymorphism 333 333 (2.4%) le Piney/Gasccc 13% 86% 0%	in elements 0/141 0/141 0/141 (0.00%) Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 (0.92%) Rockford Bea 49% 13% 38% 142	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 42 c out elemer 0/210 1/210 0/210 5) 1/210 (0.48 ch Gasconade F 100% 0% 28 Rockford Be 65% 22% 8%	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki N/A 1.94 %) 1.94 River ach	<i>p-value</i> 0.56 0.31
B. 1. a. b. 2. a. b. 3. b.	Intraspecies Comparisons A2a Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 - 133C, -177G, -300A #3 - 133C, -177G Chromosome Count A2b Enhancer F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #5 A218G #7 T68A Chromosome count F Olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Polymorphism Population Little Piney Rockford Beach Gasconade River Total F. olivaceus Alleles Allele #1 #2 AA55GT, G62T, C68T, A72C, A8 CCGA264TCTT #3 C179T #4 C235T Chrome count	Total Pol 0/ 3/519 Little 100 0/ 2/318 Little 100 0/ 2/318 Little 100 0/ 8/ 8/ 333 Littl 8/333 Littl	ymorphism 519 519 519 719 719 710 710 710 710 710 710 710 710	in elements 0/141 0/141 0/141 (0.00% Rockford Bea 0% 73% 27% 148 in elements 0/108 1/108 0/108 1/108 0/108 1/108 0/108 1/108 1/108 1/108 1/108 1/108 1/108 1/108 1/108 1/108	out elemer 0/397 1/397 0/397 6) 3/397 (0.76 ch Gasconade F 100% 0% 42 c out elemer 0/210 1/210 0/210 1/210 0/210 1/210 (0.48 ch Gasconade F 100% 0% 28 Rockford Be 65% 22% 8%	nts Kb/Ki 0.00 0.00 %) 0.00 River nts Kb/Ki NA 1.94 NA %) 1.94 River ach	<i>p-value</i> 0.56 0.31

Table 2.

		Annealing
Primer Name	Primer Sequence	AB/LA-Phusion
A9b forward	5' CTT TGG AGA CGC ACA CWC C 3'	57 C
A9b reverse	5' TTC TTC ATC TTC ATY CTG CGG 3'	
A2b forward	5' CCT GAC ATC TCT CGC TAA CC 3'	59 C-60 C
A2b reverse	5' AGA GGT CAG ACG CTG CTG C 3'	
A3a forward	5' ART ACA ARA AGG ATC AGA AAG G 3'	57 C
A3a reverse	5' TTR CCC ATT GTG ATT GCT CC 3'	
A2a forward	5' GAA TTC GAR CGA GAG AGC G 3'	56 C-60 C
A2a reverse	5' ACR GGT CCG TTK GAG ATG G 3'	
B2a forward	5' CAT TTC AAA CTT CAT CAA TCA AGG 3'	58 C
B2a reverse	5' CTC YTT CAT CCA KGG RAA CTC 3'	
A3a-A2a int 1 forward	5' AAT GTG AAG CCG TCC GTC C 3'	
A3a-A2a int 1 reverse	5' CAG TAG CTC TCA TAT TTA GGC 3'	
A3a-A2a int 2 forward	5' CCA TGC CAC TAG ATT GCA AGC 3'	
A3a-A2a int 2 reverse	5' ACG TCT ACG TCT CCA AAT CCG 3'	
A3a-A2a int 3 forward	5' AAC AAA TGC TGG ATA TAG ATG GC 3'	
A3a-A2a int 3 reverse	5' CAC GTA ACA GTA ACA TGA AGG C 3'	
A2b enhancer forward	5' AAC ACC CAC TCA CCT CAG C 3'	56 C-60 C
A2b enhancer reverse	5' GTG TGA TCA ATC TTT CHM GCC 3'	
A2a enhancer forward	5' CAA AGA TAA GTG TGC AGA ACG C 3'	56 C-67 C
A2a enhancer reverse	5' TGG CTT GTT GAG TAA GAA GAG G 3'	
PGK1 intron 7 forward	5' GCR AAG GTG AAA GAT AAG ATY CAG C 3'	N/A-62 C
PGK1 intron 7 reverse	5' TCT CSG CTT TGG CCA TCA GG 3'	
PGK1 intron 7 short forward	5' CTG TTT CCA CCA CGA TCT CC 3'	N/A-60 C
PGK1 intron 7 short reverse	5' TCA AAA GAT TGC AAC CAA CG 3'	
A2a exon 2 forward	5' TGA CCG AGA GGC AGG TCA AGG 3'	56 C
A2a exon 2 reverse	5' AGG GCA GAG GGG CTG TCA CC 3'	
EGR2 forward	5' CCA GAC CTT YAC CTA YAT GGG 3'	59 C
EGR2 reverse	5' TGT GTC TCT TYC TCT CRT CGC 3'	

Table 3.			
A3a locus (exon 2)	non-coding/out element	5	30
F.olivaceus/F. notatus	1/151 (0.66%)	0.27	1.61
F. catenatus/F. olivaceus	9/151 (5.96%)	2.42	14.5
F. catenatus/F. notatus	10/151 (6.62%)	2.69	16.1
T. nigroviridis/T. rubripes	18/146 (12.3%)	2.46/my	0.41/my
A2a locus (exon 1)		600000000000000000000000000	10000000000000000000000000000000000000
F.olivaceus/F. notatus	1/111 (0.90%)	0.45	2.73
F. catenatus/F. olivaceus	1/111 (0.90%)	0.45	2.73
F. catenatus/F. notatus	2/111(1.80%)	0.91	5.45
T. nigroviridis/T. rubripes	12/121 (9.9%)	1.98/my	0.33/my
A9b locus (exon1,2 intron	1)	38962005859630300	
F.olivaceus/F. notatus	12/407 (2.95%)	1.27	7.76
F. catenatus/F. olivaceus	26/407 (6.39%)	2.75	16.8
F. catenatus/F. notatus	22/407 (5.40%)	2.33	14.2
T. nigroviridis/T. rubripes	11/95 (11.6%)	2.32/my	0.38/my
A2b locus (exon1)			
F.olivaceus/F. notatus	2/76 (2.63%)	2.37	13.8
F. catenatus/F. olivaceus	0/76 (0.00%)	0	0
F. catenatus/F. notatus	2/76 (2.63%)	2.37	13.8
T. nigroviridis/T. rubripes	4/72 (5.56%)	1.11/my	0.19/my
B2a locus (exon1)	1. Contraction (Contraction (Contraction))		
F.olivaceus/F. notatus	0/71 (0.00%)	0	0
F. catenatus/F. olivaceus	1/71 (1.41%)	0.56	3.36
F. catenatus/F. notatus	1/71 (1.41%)	0.56	3.36
T. nigroviridis/T. rubripes	20/159 (12.6%)	2.52/my	0.42/my
A2a Enhancer		555555 F4186554	
F.olivaceus/F. notatus	8/397 (2.02%)	0.82	4.93
F. catenatus/F. olivaceus	16/397 (4.03%)	1.64	9.83
F. catenatus/F. notatus	16/397 (4.03%)	1.64	9.83
T. nigroviridis/T. rubripes	46/374 (12.3%)	2.46/my	0.41/my
A2b Enhancer	1035-11-1 AUE 0-10-10-10-10-10-10-10-10-10-10-10-10-10	5.8 .56	1941 - 1947 - 688
F.olivaceus/F. notatus	1/210 (0.48%)	0.23	1.41
F. catenatus/F. olivaceus	10/210 (4.76%)	2.31	14
F. catenatus/F. notatus	11/210 (5.24%)	2.54	15.4
T. nigroviridis/T. rubripes	44/428 (10.3%)	2.06/my	0.34/my
TOTAL	(d. 1954 - 57	ai 93	S S
F.olivaceus/F. notatus	25/1423 (1.76%)	0.79	4.76
F. catenatus/F. olivaceus	63/1423 (4.43%)	2	12
F. catenatus/F. notatus	64/1423 (4.50%)	2.03	12.2
T. nigroviridis/T. rubripes	155/1395 (11.1%)	2.22/my	0.37/my
Table 4. Human

Г	٦	u	I	I	I	d
C	2	2	ι.		,	

Raw	4 c	luster	teleost		
HoxA	48	46%	57	54%	
HoxB	30	60%	20	40%	

Scaled	4 cl	uster	teleost		
HoxA	16 74%		5.7 26%		
HoxB	15	82%	3.33	18%	

Bichir Ra

Raw	4 cluster		Tel	eost	Both		
HoxA	17	20%	48	56%	21	24%	
HoxB	3	8%	22	59%	12	32%	

Scaled	4 cl	uster	Tele	eost	Both		
HoxA	4.3	40%	4.8	45%	1.6	15%	
HoxB	1	17%	3.67	61%	1.3	22%	

Scaled	4 c	luster	Teleost		
HoxA	4	47%	4.8	53%	
HoxB	1	21%	3.7	79%	

Zebrafish _____

Raw	4 cl	uster	teleost		
HoxAa	18	49%	19	51%	
HoxAb	12	80%	3	20%	
HoxBa	23	43%	30	57%	
HoxBb	5	71%	2	29%	

Scaled	4 cl	4 cluster		teleost		
HoxAa	3.6	49%	3.8	51%		
HoxAb	2.4	71%	1	29%		
HoxBa	5.8	28%	15	72%		
HoxBb	1.3	56%	1	44%		

Figure 1.



Credit: Zina Deretsky, National Science Foundation (after Rita Mehta, UC Davis)







Figure 4.



(Nile <u>Bichir</u> ("Polypterus bichir bichir") from Günther, A.C.L.G., 1880. "An introduction to the study of fishes". Today & Tomorrow's Book Agency, New Delhi. <u>Category:Polypteriformes</u>)









Figure 7. (continued)









LmeHoxD3







Figure 7. (continued)

















Figure 17.









Figure 19.

4-5kb













Pse Tzf HoxA		1	$\label{eq:m-kskelsvdlrdrivsrkksgegyrkalkvpmstvvstsrkwkkfettrtlpragrpsklsdrgrralvre} M-kskelsvdlrdrivsrkksgegyrkalkvpmstvvstsrkwkkfettrtlpragrpsklsdrgrralvre}$	71
Pse Tcl HoxD		1	MRQSCGLIQADRRATLTE	33
			helix helix Nuclear Localization Signal	
SB10		76	VQINPRTTAKDLVKMLEETGTKVSISTVKRVLYRHNLKGRSARKKPLLQNRHKK-ARLRFATAHGDKDRTFWR	147
Salmonid Tc1	ancestor	76	eq:vqinprtakdlvkmleetgakvsistvkrvlyrhnlkgrsarkkpllqnrhkn-arlrfatahgdkdrtfwr	147
Pse Tzf HoxA		72	$\tt VTKNPIVTELQRSSVESGEPSRRTTISATIHQSGLYGRVARRKPFLSKRHMAARLEFAKRHLKDFQAIRN$	141
Pse Tcl HoxD		34	ITTRYNRGMQQSICEATT-RTTLRQMGYNSRRPHRVPLISTTNRKKGLQFAQA-HQNWTEDWKN	95
			Glycine-Rich Box	
SB10		148	NVLWSDETKIELFGHNDHRYVWRKKGEACKPKNTIPTVKHGGGSIMLWGCFAAGGTGALHKIDGIMRKENYVDIL	222
Salmonid Tc1	ancestor	148	NVLWSDETKIELFGHNDHRYVWRKKGEAYKPKNTIPTMKHGGGSIMLWGCFAAGGTGALHKIDGIMRKENYVDIL	222
Pse Tzf HoxA		142	$\tt KILWTDETKIKLFGVNARCHVWRKPGTAHHQANTISTVKHGGGSSIMLSGFFSAAGTGRLVRTKGKMTAAMYRDIL$	216
Pse Tcl HoxD		96	$-VVWSD\underline{BSRFLLF} \\ HSNGRVRIWRKQNENMDPSCLVTTVQAGGGGVMVWGMFSRQTLGSIVPIGHRLNATGYLSIV$	169
			DDE Motif-	
SB10		223	KQHLKTSVRKLKLGRKWVFQMDNDP-KHTSKVVAK-WL-KDNKVKVLEWPSQSPDLNPIENLWAELKKRVRARR-	293
Salmonid Tc1	ancestor	223	KQHLKTSVRKLKLGRKWVFQMDNDP-KHTSKVVAK-WL-KDNKVKVLEWPSQSPDLNPIENLWAELKKCVRARR-	293
Pse Tzf HoxA		217	DENLLQSALDLRLGRRFIFQQDNDP-KHTANI-SKEWL-QDNSVNVLEWPSQSSDLNLIEHLWRDLKMAVH-RRF	287
Pse Tcl HoxD		170	SDHVHPFMTTMYPSSDGYFQQDNAPCHKA-RIISNWFLEHDNEFTVLKWPPQSPDLNPIEHLWDVVERELRALDV	243
SB10		294	-PTNLTQLHQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGNATKY 340	
Salmonid Tc1	ancestor	294	-PTNLTQLHQLCQEEWAKIHPTYCGKLVEGYPKHLTQVKQFKGNATKY 340	
Pse Tzf HoxA		200	- DOMINELEDOCKEEWAKIAKDOCAKLEAOVOKDLEAVIAAKCACTKY 334	
100 101 1101111		200	F SNEMEDERCCREEWARDARDROADEAD I SIRCEAV TAARGASTRI 554	

Figure 26.



Figure 27.





Figure 28.



Figure 29.





Figure 29. (continued)





Figure 29. (continued)





9. Appendices

Table S1-PFC Database

Each folder contains an "All species" file that contains a list of all PFCs for that particular Hox cluster paralog. For each PFC there is a name in the cell corresponding to the species that contains that particular PFC. For each individual Hox cluster there is a file that contains all PFCs contained within that Hox cluster, the distance to the 3' Hox gene, the length of the PFC in that Hox cluster, and the sequence of the PFC from that Hox cluster. For the Human Hox cluster files and asterisk has been placed next to the name of all PFCs that also correspond to conserved non-coding sequences found between human (Homo sapiens) and pufferfish (Takifugu rubripes) by Lee et al. (2006).

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 | Coelacanth A | Human A

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 | Nile Tilapia A | Medaka AA
 | Tetraodon AA | Takifugu AA | Zebrafish AB
 | Medaka AB | Tetraodon AB | Takifugu AB
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| 28 | | XtrA _{AC} 28
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| 30 | HfrA _{AC} 30 _{ab} | XtrA _{AC} 30 _{ab}
 | LmeA _{BC} 30 _b | HsaA _{AC} 30 _{bc}

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 | OniA _{AC} 30 _{ab} | OlaAA _{Ac} 30 _{ab}
 | TniAA _{AC} 30 _{abc} | TruAA _{AC} 30 _{abc} | DreAB _{AC} 30 _{abc}
 | OlaAB _{AC} 30 _{bc} | TniAB _{AC} 30 _{bc} |
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| 31 | HfrA _{AC} 31 _{abolf} |
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 | PseA _{AC} 31 _{abolef} | DreAA _{AC} 31 _{bdef} |
 | | OhAA _{AC} 31 _{acter}
 | TniAA _{AC} 31 _{adef} | TruAA _{AC} 31 _{abder} | DreAB _{AC} 31 _{al}
 | ObAB-32 | TniAB-32 |
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 | OlaAB _{CE} 33 | TniAB _{CE} 33 |
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 | OlaAB _{CE} 34 | TniAB _{CE} 34 |
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| 36 | | (I.)
 | | HsaA _{CE} 36

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 | OniAcu36 |
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 | LmcAcx38 | HsaA _{CE} 37
HsaAcr38

 | | DreAA _{CE} 37 |
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 | | HsaA _{CE} 39

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 | | HsaA _{CE} 40

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DreAAcre41 | V/////////////////////////////////////
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 | TniAA-41 | |
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| 41 | |
 | | HsaAcr42

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 | OniAcm42 |
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| 43 | HfrA _{CE} 43 _a | XtrA _{CE} 43 _{ab}
 | | HsaA _{CE} 43 _{ab}

 | PseA _{CI} 43 _{ab} | |
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 | PseA _{CE} 45 | DreAA _{CI} 45 | <i>\////////////////////////////////////</i>
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 | | HsaA _{CE} 47
HeaA_48

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 | | OlaAA _{CE} 47
 | | TruAA 48 |
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 | | HenA51

 | | DreAA _{CE} 50 |
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HeaAcc54

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 | OniA-54 |
 | | TruAA _{CE} 53 |
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 | PseA _{CE} 55 | |
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 | | TruAA _{CE} 55 |
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 | PseAct56
PseAct57ab | |
 | OniAcu575 | OlaAAcr575
 | TniAAcr575 | TruAAcr57 _b | DreAB _{CE} 56
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 | | | DreAB _{CE} 58
 | OlaAB _{CE} 58 | |
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| 59 | HfrA _{CE} 60 _{al} | XtrA _{CE} 60 _{aole}
 | LmeA _{CE} 60 _{abok} | HsaA _{CE} 59
HsaA _{CE} 60 _{abale}

 | PseA _{CE} 60 _{abd} | DreAA _{CE} 60 _{abc} |
 | OniA _{cm} 60 _{abod} | OlaAA _{ce} 60 _{abol}
 | TniAA _{cu} 60 _{abol} | TruAA _{CE} 60 _{abol} | DreAB _{CE} 60 _{abc}
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 | OlaAB _{EF} 61 | | TruAB ₁₀ 61
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| 63 | HIN _B 02 |
 | LineA _{II} 02 | HsaA ₁₂ 63

 | PseAge63 | |
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 | PseAgr65 _{bc}
PseAgr66 | DreAApg03 _{bc} |
 | OntAgroom | OBAAE 05bcd
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 | OlaAB _{EF} 65 _{acds} | TniAB ₁₂ 65 | TruABgr65acde
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 | LmcA ₁₂ 69 | HsaA ₁₂ 69
HsaA ₁₂ 70

 | PseAgr68 | DreAA _{EG} 70 |
 | Nile Tilania A | Madalar A A
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 | OlaABgr68 | Tatana dan AR | Tubifum AD
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PFC
71 | Hornshark A | Frog A
 | LmcA ₁₂ 69
Coelacanth A | HsaA ₁₂ 69
HsaA ₁₂ 70
Human A
HsaA ₁₂ 71

 | PseAgrof
PseAgrof8
Bichir A | DreAA _{EG} 70
Zebrafish AA | Striped Bass A
 | Nile Tilapia A | Medaka AA
 | Tetraodon AA | Takifugu AA
TruAAt#71 | Zebrafish AB
 | OlaABg168
Medaka AB | Tetraodon AB | Takifugu AB
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PFC
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73 | Hornshark A
HfrAsr73 | Frog A
 | LmcA ₁₂ 69
Coelacanth A | HsaA ₁₂ 69
HsaA ₁₂ 70
Human A
HsaA ₁₂ 71
HsaA ₁₂ 72
HsaA ₁₇ 72

 | PseAge07 PseAge68 Bichir A | DreAAgg70
Zebrafish AA | Striped Bass A
 | Nile Tilapia A
OniAgy72 | Medaka AA
 | Tetraodon AA | Takifugu AA
TruAAge71 | Zebrafish AB
 | OlaABgr68
Medaka AB | Tetraodon AB | Takifugu AB
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PFC
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74 | Homshark A
HfrAgr73 | Frog A
 | LmcA ₁₂ 69
Coelacanth A | HsaA ₁₂ 69
HsaA ₁₂ 70
Human A
HsaA ₁₂ 71
HsaA ₁₂ 72
HsaA ₁₂ 73

 | PseA _{EP} 74 | DreAA _{EG} 70
Zebrafish AA | Striped Bass A
 | Nile Tilapia A
OniAgy72 | Medaka AA
 | Tetraodon AA | Takifugu AA
TruAAgy71 | Zebrafish AB
DreAB _{EF} 74
 | OlaABg168
Medaka AB | Tetraodon AB | Takifugu AB
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PFC
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76 | Hornshark A
HfrAgy73
HfrAgy75 _{bor} | Frog A
XtrAgy75 _{shels}
 | LmcA ₈₂ 69
Coelacanth A
LmcA ₈₂ 75 _{Note} | HsaA ₁₂ 69
HsaA ₁₂ 70
Human A
HsaA ₁₂ 71
HsaA ₂₇ 72
HsaA ₂₇ 73
HsaA ₁₂ 75 _{bok}

 | PscAgr74
PscAgr75 _{scie}
PscAgr76 | DreAA _{BG} 70
Zebrafish AA | Singed Bass A
 | Nile Tilapia A
OniAer72
OniAer75 _{acte}
OniAer76 | Medaka AA
OlaAA2275 _{sok}
 | Tetraodon AA
TniAAgr75 _{ok} | Takifugu AA
TruAAg71
TruAAg75 _{sole} | Zebrafish AB
DreAB _{E7} 74
DreAB _{E7} 75 _{abc}
 | OlaAB _{E2} 68
Medaka AB
OlaAB _{E2} 75 _{abc} | Tetraodon AB
TniAB _{IF} 75 _{abot} | Takifugu AB
TruAB _{ET} 75 _{dod}
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PFC
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77 | Homshark A
HfrAgr73
HfrAgr75 _{ba} | Frog A
XtrAg/75 _{abcds}
XtrAg/77
 | LmcA ₂₂ 69
Coelacanth A
LmcA ₃₂ 75 _{Nole} | HsaA ₄₂ 69
HsaA ₃₂ 70
Human A
HsaA ₃₂ 71
HsaA ₃₂ 71
HsaA ₃₂ 73
HsaA ₃₂ 75
Nok
HsaA ₅₂ 75
Nok

 | PscAgr74 PscAgr75 pscAgr75 pscAgr76 | DreAA _{EG} 70
Zebrafish AA | Striped Bass A
 | Nile Tilapia A
OniAer72
OniAer75 _{aole}
OniAer76 | Medaka AA
OlaAA ₂₂ 75 _{sok}
 | Tetraodon AA
TniAAgr75 _{ob} | Takifugu AA
TruAAgr71
TruAAgr75 _{sole} | Zebrafish AB
DreAB _{E7} 74
DreAB _{E7} 75 _{abc}
 | OlaAB _{E2} 68
Medaka AB
OlaAB _{E2} 75 _{abc} | Tetraodon AB
TniAB _{IP} 75 _{abol} | Takifugu AB
TruAB _{EP} 75 _{abol}
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PFC
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79 | Hornshark A
HfrAgy73
HfrAgy75 _{hos}
HfrAgy75 _{hos} | Frog A
XtrA _{B2} 75 _{abole}
XtrA _{B2} 77
XtrA _{B2} 77
XtrA _{B2} 78 _{bel}
XtrA _{B2} 78 _{bel}
 | LmcA ₂₇ 69
Coelacanth A
LmcA ₂₇ 75 _{Not}
LmcA ₂₇ 75 _{Not} | HsaA ₁₂ 69
HsaA ₁₂ 70
Human A
HsaA ₁₂ 71
HsaA ₁₂ 71
HsaA ₁₂ 72
HsaA ₁₂ 75 _{bok}
HsaA ₁₂ 75 _{bok}

 | PscAgr68
Bichir A
PscAgr74
PscAgr75w
PscAgr76
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PscAgr76 | DreAA _{EG} 70
Zebrafish AA
DreAA _{EG} 79 _{al} | Striped Bass A
 | Nile Tilapia A
OniA _{E7} 72
OniA _{E7} 75 _{sole}
OniA _{F7} 76
OniA _{F7} 79 _{bik} | Medaka AA
OlaAA ₃₂₇ 75 _{shk}
OlaAA ₇₂₇ 79 _{shk}
 | Tetraodon AA
TniAAgr75 _{ole}
TniAAgr79 _{ole} | Takifugu AA
TruAAge71
TruAAge75 _{solo}
TruAAge75 _{solo} | Zebrafish AB
DreAB ₁₂₇ 74
DreAB ₁₂₇ 75 _{abc}
DreAB ₁₂₆ 79 _{bil}
 | OlaABgr75dc | Tetraodon AB
TniAB _{IE} 75 _{abal}
TniAB _{IE} 79 _{bal} | Takifugu AB
TruAB _{E7} 75 _{dool}
 |
| 67
68
69
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PFC
71
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77
78
79
80
81 | Hornshark A
HfrA ₈₂ 73
HfrA ₈₂ 75 _{ba}
HfrA ₈₂ 75 _{ba}
HfrA ₈₂ 79 _{ba} | Frog A
XtrAp:75 ₈₀₄
XtrAp:77
XtrAp:78 ₈₆
XtrAp:78 ₈₆
 | LmeA ₁₂ 69
Coelacanth A
LmeA ₁₇ 75 _{hole}
LmeA ₁₇₇ 78 _{de}
LmeA ₁₇₇ 78 _{de} | HsaArg69
HsaArg70
Human A
HsaArg71
HsaArg72
HsaArg73
HsaArg75 _{bole}
HsaArg77
HsaArg77
HsaArg77
HsaArg77
hsaArg79 _{bole}

 | PseAgg65
Bichir A
Bichir A
PseAg774
PseAg75
pseAg75
pseAg75
pseAg76
PseAg76
bseAg76
bseAg76
bseAg76
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bs | DreAA _{rci} 70
Zebrafish AA
DreAA _{rci} 79 _{st} | Singed Base A
 | Nile Tilapia A
OniA ₅₂₇ 72
OniA ₅₂₇ 75 _{ade}
OniA ₅₂₇ 76
OniA ₅₂₇ 79 _{ble} | Medaka AA
OlaAA _{TE} 75 _{80.8}
OlaAA _{TE} 79 _{60.8}
 | Tetraodon AA
TniAAg75 _{ab}
TniAAg75 _{ab} | Takifugu AA
TruAAgg71
TruAAgg75 _{totk}
TruAAgg75 _{totk} | Zebrafish AB
DreAB ₁₂ 74
DreAB ₁₂ 75 _{de}
DreAB ₁₅ 75 _{de}
 | OlaAB _{EI} 75 _{abc} | Tetraodon AB
TniAB ₁₂₇ 75 _{abol}
TniAB ₁₂₇ 79 _{bol}
TniAB ₁₂₇ 79 _{bol} | Takifugu AB
TruAB ₁₀ 75 ₄₆₄
TruAB ₁₀ 80
TruAB ₁₀ 80
 |
| 67
68
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PFC
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79
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81
82 | Hornshark A
HfrA ₃₂₇ 73
HfrA ₅₂₇ 75 _{Na}
HfrA ₇₀₇ 78 _{ab}
HfrA ₇₀₇ 79 _b | Frog A
XtrAg:75 ₈₀₄₆
XtrAg:77
XtrAg:77
XtrAg:78 ₈₆
XtrAg:78 ₈₆
 | LmeA ₂₁ 69
Coelacanth A
LmeA ₁₇ 75 _{N/6}
LmeA ₁₇₇ 78 _{de}
LmeA ₁₇₇ 79 _b | HsaArg69
HsaArg70
Human A
HsaArg71
HsaArg72
HsaArg73
HsaArg75 _{bole}
HsaArg77
HsaArg77
HsaArg77
hsaArg77
hsaArg77
hsaArg79 _{bol}

 | PacAgg07
PacAgg68
Bichir A
Bichir A
PacAg74
PacAg74
PacAg75_ab
PacAg75_bb
PacAg75_bb
PacAg75_bb
PacAg75_bb
PacAg76bb
PacAg76bb | DreAA ₈₆₇ 70
Zebrafish AA
DreAA ₈₆₇ 79 _{a1}
DreAA ₆₆₇ 82 | Striped Bass A
 | Nile Tilapia A
OniA ₅₂₇ 72
OniA ₅₂₇ 75 _{hdf}
OniA ₅₂₇ 76
OniA ₅₂₇ 79 _{hdf} | Medaka AA
OlaAA ₁₀ 75 _{00k}
OlaAA ₁₀ 79 _{00k}
 | Tetraodon AA
TniAAgr75 _{ob}
TniAAgr79 _{obb}
TniAAgr82 | Tskifugu AA
TruAAg271
TruAAg275 _{sole}
TruAAg279 _{sole} | Zebrafish AB
DreAB ₁₀ 74
DreAB ₁₀ 75 _{abc}
DreAB ₁₀ 79 _{bl}
DreAB ₁₀ 59 _{bl}
 | OlaAB _{EE} 68
Meduka AB
OlaAB _{EE} 75 _{abc}
OlaAB _{EE} 81 _b | Tetraodon AB
TniAB ₁₇ 75 _{abd}
TniAB ₁₇₂ 79 _{bol}
TniAB ₁₇₂ 81 _@ | Takifugu AB
TruAB _{EF} 75 _{acci}
TruAB _{EF} 80
TruAB _{FG} 80
 |
| 677
68
699
700
PFC
711
722
733
744
755
766
777
78
799
800
811
823
84 | Hornshark A
HfrAsz73
HfrAsz75 _{No}
HfrA _{F0} 78 _{ab}
HfrA _{F0} 78 _{ab} | Frog A
XtrApp75 ₈₀₄₆
XtrApp77
XtrApp77
XtrApp79 ₈₀
 | LmeA ₃₂ 69
Coelacanth A
LmeA ₃₇ 75 _{Nob}
LmeA ₃₇₅ 75 _{Nob} | HsaArg769
HsaArg70
Human A
HsaArg71
HsaArg72
HsaArg72
HsaArg72
HsaArg72
HsaArg77
HsaArg77
HsaArg77
HsaArg78 _{bob}

 | PacAgg07
PacAgg08
Bichir A
PacAgg74
PacAgg74
PacAgg75
PacAgg75
PacAgg76
PacAgg76
PacAgg76
PacAgg76
PacAgg76
PacAgg76
PacAgg78
PacAgg80
PacAgg83
PacAgg83 | DreAAcc70
Zebrafish AA
DreAAcc79 _{ad}
DreAAcc79 _{ad}
DreAAcc982 | Strined Bass A
Strined Bass A
MsaAye ₂ 76
MsaAye ₂ 76
 | Nile Tilapia A
OniAey72
OniAyy75 _{actic}
OniAyy75 _{bclic}
OniAyy79 _{bclic}
OniAyy78 | Medaka AA
OlaAAgg75 _{sok}
OlaAAgg79 _{sok}
 | Tetraodon AA
TniAAg75 _{ab}
TniAAg75 _{ab}
TniAAg79 _{abb}
TniAAg82
TniAAg82 | Takifugu AA
TruAAgr71
TruAAgr75 _{toth}
TruAAgr79 _{toth} | Zebrafish AB
DreAB ₁₂₇ 74
DreAB _{1275 da}
DreAB ₁₂₇ 75 _{da}
DreAB ₁₂₇ 79 _{bil}
 | OlaAB ₂₂ 68
Meduka AB
OlaAB ₂₂ 75 _{abc}
OlaAB _{7C} 81 _b | Tetraodon AB
TniAB ₁₇₇ 75 _{abol}
TniAB ₁₇₅ 79 _{bol}
TniAB ₁₇₅ 81 _{ab} | Takifugu AB
TruAB ₁₂ 75 ₄₆₋₀
TruAB ₁₇₀ 80
TruAB ₁₇₀ 81 ₄
 |
| 67
688
699
700
711
72
73
74
75
76
77
78
80
80
811
82
83
84
85 | Hornshark A
HfrAgr73
HfrAgr75 _{ba}
HfrAgr78 _{ba}
HfrAgr78 _{ba} | Frog A
XtrAgr75 _{book}
XtrAgr77
XtrAgr78 _b
XtrAgr79 _b
 | LmcApp69
Coelacanth A
LmcApp75 _{tode}
LmcApp78 _{de}
LmcApp79 _{to}
LmcApp79 _{to} | HsaAr269
HsaAr270
Hsraar7
HsaAr271
HsaAr271
HsaAr273
HsaAr273
HsaAr277
HsaAr277
HsaAr277
HsaAr277
HsaAr277
HsaAr277
HsaAr278
hsaAr278
hsaAr278
hsaAr285

 | PacAgg07
PacAgg08
Bichir A
Bichir A
PacAg774
PacAg774
PacAg775 ₆₀₆
PacAg75 ₆₀₆
PacAg75 ₆₀₆
PacAg75 ₆₀₆
PacAg75 ₆₀₆
PacAg83
PacAg83
PacAg83 | DreAA _{ter} 70
Zebrafish AA
DreAA _{ter} 79 _{al}
DreAA _{ter} 82 | Striped Base A
Striped Base A
MsaAye_76
MsaAye_76
 | Nile Tilapia A
OniArg72
OniArg75 _{adi}
OniArg76
OniArg79 _{ade}
OniArg79 _{ade} | Medaka AA
OlaAAyg75 _{kok}
OlaAAyg79 _{kok}
 | Tetraodon AA
TnikAqp75 _{ab}
TnikAqp79 _{able}
TnikAqp82
TnikAqp82 | Takifugu AA
TruAAgr71
TruAAgr75 _{oole}
TruAAgr79 _{oole} | Zebrafish AB
DreAB ₁₂ 74
DreAB ₁₂ 75 _{de}
DreAB ₁₂ 79 _{bi}
DreAB ₁₂ 81 _{ab}
 | OlaAB ₂₂ 68
Medaka AB
OlaAB ₂₂ 75 _{ab} | Tetraodon AB
TniAB _{IT} 75 _{abol}
TniAB _{ITG} 79 _{bol}
TniAB _{ITG} 81 _{ab} | Takifugu AB
TruABgr75 _{6c4}
TruABgr75 _{6c4}
TruABgr80
TruABgr81 _{ab}
 |
| 67
68
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72
73
74
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78
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81
82
83
84
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86
86 | Hornshark A
HfrAgr73
HfrAgr75 _{ho}
HfrArq78 _{Ja} ,
HfrArq78 _{Ja} , | Frog A
XtrAp:75 ₈₅₆
XtrAp:77
XtrAp:78
XtrAp:78
XtrAp:79 ₈₆
 | LmcAgr69
Coclacanth A
LmcAgr75 _{Not}
LmcAgr78 ₂₆
LmcAgr78 ₂₆
LmcAgr85 | HsaAr269
HsaAr270
Human A
HsaAr271
HsaAr271
HsaAr273
HsaAr273
HsaAr277
HsaAr277
HsaAr273
hsaAr273
hsaAr273
hsaAr273
hsaAr235
HsaAr255
HsaAr285

 | PacAgg07
PacAgg07
Bichir A
Bichir A
PacAg74
PacAg774
PacAg775
PacAg775
PacAg775
PacAg775
PacAg775
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Pac | DreAA ₈₀ 70
Zebrafish AA
DreAA ₈₀ 79 _{al}
DreAA ₈₀ 82 | Striged Base A
 | Nik Tilapia A
OniAgr72
OniAgr75 _{adt}
OniAgr676
OniAgr679 _{adt}
OniAgr683 | Medaka AA
OlaAAyy75 ₀₀₀
OlaAAyy75 ₀₀₀
 | Teiraodon AA
TeirAAgr75 _{ab}
TeirAAgr75 _{ab}
TeirAAgr79 _{abb}
TeirAAgr82
TeirAAgr84 | Takifuru AA
TruAAgr71
TruAAgr75 _{adt}
TruAAgr79 _{abb} | Zebrafish AB
DreAB ₁₇₇ 74
DreAB ₁₇₇ 75 _{de}
DreAB ₁₇₇ 75 _{de}
DreAB ₁₇₇ 81 _{de}
 | OlaABg268
Medaka AB
OlaABg275 _{de}
OlaABg275 _{de}
OlaABg281 _b | Tetraodon AB
TeiAB _{IE} 75 _{abal}
TniAB _{IC} 79 _{bal}
TniAB _{IC} 81 _a
TniAB _{IC} 86 | TruAB ₁₇ 75 ₆₀₄
TruAB ₁₇ 75 ₆₀₄
TruAB ₁₇ 80
TruAB ₁₇ 80
TruAB ₁₇ 86
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HEAq773
HEAq775 _N
HEAq775 _N
HEAq775 _N | Frog A
XtrA ₁₂ 75 ₀₋₀₀
XtrA ₁₂ 77
XtrA ₁₂ 77
XtrA ₁₂ 78
XtrA ₁₂ 79 _b
 | LmeA ₂₂ 69
Coekseanth A
LmeA ₂₂ 75 _{hole}
LmeA ₂₂ 78 ₂₆
LmeA ₂₂ 78 ₂₆
LmeA ₂₂ 85 | HaaAra60
HaaAra70
Human A
HaaAra71
HaaAra72
HaaAra73
HaaAra75 ₅₀₀
HaaAra75 ₅₀₀
HaaAra78 ₅₀
HaaAra78 ₅₀
HaaAra785
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Bschir A
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psc | DreAA _{ec} 70
Zebrafish AA
DreAA _{ec} 79 _{st}
DreAA _{ec} 82 | Striped Base A
Striped Base A
Msa Ayu 76
Msa Ayu 79 ₆₆
 | Nile Tilapia A
OniAe272
OniAe275 <u>solit</u>
OniAe276
OniAe276
OniAe278
OniAe283
OniAe288 | Medaka AA
OlaAAgr75 _{kok}
OlaAAgr79 _{kok}
 | Tetraodon AA
TniAAgr75 ₅₆
TniAAgr79 ₆₆₆
TniAAgr29 ₆₆₆
TniAAgr282
TniAAgr84 | Takifuru AA
TruAAgr71
TruAAgr75 _{ade} | Zebrafish AB
DreAB ₁₂₇ 74
DreAB ₁₂₇ 75 _{.00}
DreAB ₁₂₇ 79 _{.01}
DreAB ₁₂₇ 81.00
DreAB ₁₂₇ 86
 | OlaABgr68
Mcduka AB
OlaABgr75 ₆
OlaABgr81 _b
OlaABgr81 _b | Tetraodon AB
TniAB _{IT2} 75 _{abat}
TniAB _{IT2} 79 _{bat}
TniAB _{IT2} 81 _@
TniAB _{IT2} 86 | Takifugu AB
TruAB ₁₇ 75 ₂₆₀
TruAB ₁₇ 80
TruAB ₁₆ 80
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990 | Hornsbark A
HEAgr73
HEAgr75 ₆₆
HEAgr75 ₆₆
HEAgr75 ₆₆ | Prog A χμτλ ₁₀ /25 ₂₀₂₆ Χμτλ ₁₀ /27, χρ. Χμτλ ₁₀ /27, χρ. Χμτλ ₁₀ /28, χρ.
 | LmeA ₁₂ 69
Coelacanth A
LmeA ₁₂ 75 _{N/6}
LmeA ₁₂ 75 _{N/6}
LmeA ₁₂ 78 _{N/6}
LmeA ₁₂ 78 _{N/6} | HasAgr60
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Bichira A
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Zebrafish AA
DreAAcc79 _{ad}
DreAAcc79 _{ad} | Singa Ibas A
Singa Ibas A
MasAng76
MasAng79 ₄₀
 | Nile Tilapia A
OniA ₄₇ 72
OniA ₄₇ 75 ₈₀₈
OniA ₆₇ 83 | Meduka AA
Meduka AA
QiaAAgg75 _{ook}
QiaAAgg79 _{ook}
 | Tetraodon AA
TaiAAgr75 _{ab}
TaiAAgr79 _{abb}
TaiAAgr82
TaiAAgr84 | Takifuru AA
TruAAgr71
TruAAgr75 _{toth}
TruAAgr79 _{toth} | Zebrafish AB
DreAB ₁₀₇ 74
DreAB ₁₀₇ 75 _{.06}
DreAB ₁₀₇ 81 _{.06}
DreAB ₁₀₇ 81 _{.06}
 | OhaAB ₀₇ 68
Mrchika AB
OhaAB ₉₇ 75 ₈₆
OhaAB ₉₇ 81 ₃
OhaAB ₉₇ 81 ₃
OhaAB ₉₇ 86
OhaAB ₉₇ 86 | Tetrandon AB
TmAB ₁₀ 75 ₂₀₄
TmAB ₁₀ 75 ₂₀₄
TmAB ₁₀ 78 ₁₀
TmAB ₁₀ 81 ₀ | Takifugu AB
Takifugu AB
TauABug 75 _{Kot}
TauABug 80
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HEAg73
HEAg75a
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HEAg75a | Frog A
XtrA ₁₀ 73 ₂₀₀₀
XtrA ₁₀ 77
XtrA ₁₀ 77 ₂₀₀
XtrA ₁₀ 77 ₂₀
 | LmcAgt99
Creleanth A
LmcAgt75 ₃₀₀
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 | Nik Tianja A
Orahyr?2
Orahyr?5 ₈₀₆
Orahyr?5 ₈₀₆
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Orahyr?5 ₈₀₆ | Medaka AA
OlaAA ₁₇₇ 75 <u>~~0</u>
OlaAA ₁₇₇ 79 _{00.0}
 | Tetrasdon AA
TeidAkgr75 _{ab}
TeidAkgr79 _{ab}
TeidAkgr29 _{ab}
TeidAkgr22
TeidAkgr24 | Takifugu AA
TruAAgr71
TruAAgr75 _{oolo}
TruAAgr79 _{oolo} | Zebrafish AB
DreABig/74
DreABig/75 _{ab}
DreABig/75 _{ab}
DreABig/75 _{ab}
DreABig/75 _{ab}
 | OlaAB ₀₇ 68
Mrdaka AB
OlaAB ₀₇ 75 ₂₆
OlaAB ₀₇ 81 ₃
OlaAB ₀₇ 87 | Tetrandon AB
TmAB ₁₀ 75 ₂₀₀
TmAB ₁₀ 75 ₂₀₀
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TruAB ₁₀ 75 ₂₆₄
TruAB ₁₀ 80
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Hitchar 73
Hitchar 75
Hitchar 75 ₃₆
Hitchar 75 ₃₆
Hitchar 93 ₃₆
Hitchar 91
Hitchar 91 | Frog A
XrrA ₁₀ 75 ₀₀₀₀
XrrA ₁₀ 77
XrrA ₁₀ 72 ₀₀
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Dre AA ₀₂ 93 ₄
Dre AA ₀₂ 95
Dre AA ₀₂ 95
Dre AA ₀₂ 95
 | Stepel Base A | Nile: Tiliptia A OniAq;72 OniAq;72 OniAq;72 OniAq;72 OniAq;72 OniAq;72 OniAq;73 OniAq;74 OniAq;75 | Medda AA OlaAAyr75xxx
 | Тенлодов АА
ТанАА ₁₀ 75 ₀
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130	HfrAu130ab	XtrAu130ab	LmeAu130ab		PseAu130a										
131					PseAJK131										TruAB _{GN} 131
132	HfrA _{IK} 132 _K	XtrA _{IK} 132 _{sc}	LmeA _{IK} 132 _{ac}	HsaA _{JK} 132 _{ac}	PseA _{IK} 132 _{ac}	DreAA _{cax} 132 _{abat}	MsaA _{ttk} 132 _{abod}	OniAcax132abcd	OhAA _{IK} 132 _{abol}	TniAAGK132abol	TruAA _{GK} 132 _{abcd}				
133			LmeA _{KL} 133	HsaA _{KL} 133	PseA _{KL} 133										
134	1		LmeA _{KL} 134	HsaA _{KL} 134	PseA _{KL} 134										
135					PseA _{KL} 135							Dre AB _{GN} 135			
136	HfrA _{KL} 136 _{abc}	XtrAg136abc	LmeA _{KL} 136 _{abc}	HsaA _{KL} 136 _{ab}	PseA _{KL} 136 _{ac}	DreAAsz 136ac	MsaAaz 136abc	OniAsz_136abc	OlaAA _{KL} 136 _{ab}	TniAA _{KL} 136 _{ab}	TruAA ₈₂ 136 _{abc}				
137	1		LmeA _{KL} 137	HsaA _{KL} 137											
138	HfrA _{KL} 138 _b	XtrA _{KL} 138 _{abc}		HsaA _{KL} 138 _{abc}											
139	•			HsaA _{KL} 139			MsaAaz139								
140	HfrA _{KL} 140 _{cde}	XtrA _{KL} 140 _{bcde}	LmeA _{KL} 140 _{bode}	HsaA _{KL} 140 _{bcde}	PseA _{KL} 140 _{bole}	DreAA ₈₂ 140 _{ade}	MsaA _{KL} 140 _{abede}	OniA ₈₁ 140 _{abode}	OhAA _{KL} 140 _{abole}	TniAA _{KL} 140 _{abcde}	TruAA ₈₂ 140 _{abcd}				
PFC	Hornshark A	Frog A	Coelacanth A	Human A	Bichir A	Zebrafish AA	Striped Bass A	Nile Tilapia A	Medaka AA	Tetraodon AA	Takifugu AA	Zebrafish AB	Medaka AB	Tetraodon AB	Takifugu AB
141												Dre AB _{GN} 141		TmAB _{GN} 141	
142		No. 1. 142		W. A. 142	PseA _{KL} 142	D 11 142		0.11.110	01.1.1.142	T 14 4 142		Dre AB _{GN} 142			
143	HITA _{KL} 143 _{abc}	AllA _{KL} 143 _{abc}	LmeA _{KL} 143 _{ab}	HSLA _{KL} 143 _{abc}	PseA _{KL} 145 _{bc}	DreAng 145bed	MSLAg_14.5bol	OnDA _{RL} 145 _{bcd}	OBAA _{KL} 145 _{bed}	InDAA _{KL} 14.5 _{bod}					
144				H A 145	PSCA _{KL} 144	DreAAg_144		OniA 145							
143				HstAL145				OnitA _{RL} 145	Oha A 146						
140	UGA 147			HstAge 147					OLPARE 140						
148	HfrA., 148			HsaA., 148											t
149	HfrAv: 149.	XtrAss 149.5	I meAve 149-au	HsaAss 149.	Pse Avi 1495	DreA Ava 149.	MstArt 149t.	OniAva 149t.	ObA Avi 149.	TniA Avr 149-1	TruAAss 149sed				1
150	1		LmeA _{k1} 150	HsaA _{k1} 150											
151	1			HsaA _{KL} 151				OniA ₈₂ 151							
152	HfrA _{KL} 152			HsaA _{KL} 152											
153				HsaA _{KL} 153								Dre AB _{GN} 153			
154				HsaA _{KL} 154				OniAsz_154							
155	HfrA _{KL} 155			HsaA _{KL} 155											
156	i i		LmeA _{KL} 156	HsaA _{KL} 156											
157	HfrA _{KL} 157 _{bc}	XtrAg157bc	LmeA _{KL} 157 _{bc}	HsaA _{KL} 157 _{bc}	PseA _{KL} 157 _{abc}	DreAA _{KL} 157 _{abc}	MsaA _{KI} 157 _{abc}	OniA ₈₂ 157 _{abc}	OhAA _{KL} 157 _{abc}	TniAA _{KL} 157 _{abc}	TruAA ₈₂ 157 _{abc}				
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159					PseALM159		<i>\////////////////////////////////////</i>					DreAB _{GN} 159			l
160			LmeA _{LM} 160	HsaA _{LM} 160			<i><u> </u></i>								<u> </u>
161	HfrA _{LM} 161			HsaA _{LM} 161			<i>\////////////////////////////////////</i>								l
162			LmeA _{LM} 162	HsaA _{LM} 162											
16.5		AuALM103		Headraul 64		DmAA164	¥/////////////////////////////////////								1
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166	HfrA. u166			HsaAcu166		ALC: NO									1
167	HfrA1M167			HsaAr M167											
168	HfrA _{LM} 168		1	HsaALM168											
169				HsaA _{LM} 169		DreAA _{LM} 169									
170	•			HsaA _{LM} 170	PseALM170										
171					PseALM171									TniAB _{GN} 171	
172					PseA _{LM} 172			OniA _{LM} 172	OhAA _{LM} 172	TniAA _{LM} 172	TruAA _{LM} 172				
173		No. 1. 174		HsaA _{LM} 173				OniA _{LM} 173							
1/4		AtrA _{LM} 1/4		HSLALMI /4				OniA 175							
175				Headaul 76	Prn A 176			Only M175							
177	HfrArsel 77			HsaAcul 77	1 screative										
178				HsaALM178		DreAALM178									
179	HfrA1M179abc	XtrA _{LM} 179 _{ac}	LmeALM179abc	HsaALM179ab	PseALM179abc			OniA _{LM} 179 _{ab}	OhAA _{LM} 179 _{ab}	TniAA _{LM} 179 _a	TruAALM179ab				
180	HfrA _{1M} 180				PseALM180										
181	HfrA1M181bode	XtrA _{LM} 181 _{bole}	LmeALM181bcde	HsaA _{LM} 181 _{ce}	PseALM181M	DreAALM181abc		OniA _{LM} 181 _{abcde}	OhAA _{LM} 181 _{abcd}	TniAA _{LM} 181 _{abole}	TruAA _{LM} 181 _{abole}				
182				HsaA _{LM} 182					OhAA _{LM} 182						
183						DreAALM183					TruAA _{LM} 183				
184	110 1 100		LmcA _{LM} 184	Hsan _{LM} 184											
185	HITALM185			HeaA 186							TruAA 186				
187				HeaA 187							THE DI MIGO				
188	HfrA188	XtrA., 188									TruAA187				
189			LmeA _{1M} 188	HsaA _{t M} 188							TruAA _{1M} 187				
190		Len	LmeA _{LM} 188	HsaA _{LM} 188	PseArm189				OlaAA _{1M} 189		TruAA _{LM} 187				
191)	100	LmeA _{LM} 188	HsaA _{LM} 188 HsaA _{LM} 190	PseA _{LM} 189			OniA _{LM} 190	OlaAA _{LM} 189		TruAA _{1M} 187				
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192		1.00	LmeA _{LM} 188	HsaA _{LM} 188 HsaA _{LM} 190 HsaA _{LM} 191 HsaA _{LM} 192	PseA _{LM} 189			OniA _{LM} 190 OniA _{LM} 191 OniA _{LM} 192	OhAA _{LM} 189		TruAA _{1M} 187				
192 193	HfrA _{1M} 193 _{cd}	XtrA _{tM} 193 _{cd}	LmcA _{LM} 188	HsaA _{LM} 188 HsaA _{LM} 190 HsaA _{LM} 191 HsaA _{LM} 191 HsaA _{LM} 192 HsaA _{LM} 193 _{cd}	PseA _{LM} 189 PseA _{LM} 193 _{bed}	DreAA _{tM} 193 _{ab}		OniA _{LM} 190 OniA _{LM} 191 OniA _{LM} 192 OniA _{LM} 193 _{abci}	OlaAA _{LM} 189 OlaAA _{LM} 193 _{shol}	TniAA _{tM} 193 _{abd}	TruAA _{LM} 187 TruAA _{LM} 193 _{aM}				
192 193 194	HfrA _{1M} 193 _{cd} HfrA _{1M} 194 _{bde}	XtrA _{LM} 193 _{cd} XtrA _{LM} 194 _{bole}	LmcA _{LM} 188 LmcA _{LM} 194 _{hole}	HsaA _{LM} 188 HsaA _{LM} 190 HsaA _{LM} 190 HsaA _{LM} 191 HsaA _{LM} 192 HsaA _{LM} 193 _{cd}	PseA _{LM} 189 PseA _{LM} 193 _{hol} PseA _{LM} 194 _{shole}	DreAA _{EM} 193 _{ab} DreAA _{EM} 194 _{abol}		OniA _{LM} 190 OniA _{LM} 191 OniA _{LM} 192 OniA _{LM} 193 _{abcl} OniA _{LM} 194 _{sol}	OlaAA _{LM} 189 OlaAA _{LM} 193 _{abol} OlaAA _{LM} 194 _{sol}	TniAA _{tad} 193 _{abd} TniAA _{tad} 194 _{abd}	TruAA _{1M} 187 TruAA _{1M} 193 _{ab} TruAA _{1M} 193 _{ab}	D. 40			
192 193 194 195	HfrA _{1M} 193 _{ct} HfrA _{1M} 194 _{Me}	XtrA _{LM} 193 _{cd} XtrA _{LM} 194 _{bole}	LmcA _{LM} 188 LmcA _{LM} 194 _{bole}	HsaA _{kM} 188 HsaA _{kM} 190 HsaA _{kM} 191 HsaA _{kM} 192 HsaA _{kM} 192 _{cd} HsaA _{kM} 194 _{cok}	PscA _{LM} 189 PscA _{LM} 193 _{bol} PscA _{LM} 193 _{bol} PscA _{LM} 194 _{abols} PscA _{LM} 195 DscA _{LM} 195	DreAA _{LM} 193 _{ab} DreAA _{LM} 194 _{abot}		OniA _{LM} 190 OniA _{LM} 191 OniA _{LM} 192 OniA _{LM} 193 _{2bcl} OniA _{LM} 194 _{2bcl}	OlaAA _{LM} 189 OlaAA _{LM} 193 _{abol} OlaAA _{LM} 193 _{abol}	TniAA _{LM} 193 _{abd} TniAA _{LM} 194 _{abol}	TruAA ₁₂₄ 187 TruAA ₁₂₄ 193 _{abd} TruAA ₁₂₄ 193 _{abd}	DreAB _{GN} 195			
192 193 194 195 196	HfrA _{1M} 193 _{cd} HfrA _{1M} 194 _{bde}	XtrA _{LM} 193 _{od} XtrA _{LM} 194 _{bole}	LmcA _{LM} 188 LmcA _{LM} 194 _{Nde}	HsaA _{6.M} 188 HsaA _{6.M} 190 HsaA _{6.M} 191 HsaA _{6.M} 192 HsaA _{6.M} 192 _{0d} HsaA _{6.M} 194 _{hok}	PscA _{LM} 189 PscA _{LM} 193 _{bol} PscA _{LM} 194 _{abole} PscA _{LM} 195 PscA _{LM} 196	DreAA _{tM} 193 _{ab} DreAA _{tM} 194 _{abot}		OniA _{LM} 190 OniA _{LM} 191 OniA _{LM} 192 OniA _{LM} 193 _{abd} OniA _{LM} 194 _{ast}	OlaAA _{1M} 189 OlaAA _{1M} 193 _{shol} OlaAA _{1M} 194 _{sol} OlaAA _{1M} 194 _{sol} OlaAA _{1M} 196 OlaA_1M107	TniAA _{1M} 193 _{abd} TniAA _{1M} 194 _{abd}	TruAA _{1M} 187 TruAA _{1M} 193 _{ab} TruAA _{1M} 194 _{abot}	DreAB _{GN} 195			
192 193 194 195 196 197	HfrA ₁₃₄ 193 _{cd} HfrA ₁₃₄ 194 _{bde}	XtrA _{LM} 193 _{od} XtrA _{LM} 194 _{bole}	LmcA _{LM} 188 LmcA _{LM} 194 _{Nob}	HsaA _{6.01} 188 HsaA _{6.01} 190 HsaA _{6.01} 191 HsaA _{6.01} 192 HsaA _{6.01} 193 _{0.01} HsaA _{6.01} 193 _{0.01}	PscA _{LM} 189 PscA _{LM} 193 _{bol} PscA _{LM} 193 _{bol} PscA _{LM} 195 PscA _{LM} 196 PscA _{LM} 196	DreAA _{tM} 193 _{ab} DreAA _{tM} 194 _{abel} DreAA _{tM} 197		OniA _{LM} 190 OniA _{LM} 191 OniA _{LM} 192 OniA _{LM} 193 _{3bd} OniA _{LM} 194 _{sol}	OlaAA ₁₃₄ 189 OlaA ₁₃₄ 193 _{3bod} OlaA ₁₃₄ 193 _{mod} OlaA ₁₃₄ 194 _{mod} OlaAA ₁₃₄ 196 OlaA ₁₃₄ 197	TniAA _{1M} 193 _{abd} TniAA _{1M} 194 _{abol}	TruAA _{1M} 187 TruAA _{1M} 193 _{abi} TruAA _{1M} 194 _{abol}	DreAB _{GN} 195			
192 193 194 195 196 197 198 199	HfrA _{1M} 193 _{cd} HfrA _{1M} 194 _{bde} HfrA _{1M} 198 _{bbc} HfrA _{1M} 198 _{bbc}	XtrA _{LM} 193 _{of} XtrA _{LM} 194 _{bole} XtrA _{LM} 198 _{se} XtrA _{LM} 199 _{se}	LmcA _{LM} 188 LmcA _{LM} 194 _{bok} LmcA _{LM} 198 _{bok} LmcA _{LM} 198 _{bok}	HsaA _{4.84} 188 HsaA _{4.84} 190 HsaA _{4.84} 191 HsaA _{4.84} 192 HsaA _{4.84} 193 _{cd} HsaA _{4.84} 193 _{cd} HsaA _{4.84} 198 _{bbc} HsaA _{4.84} 198 _{bbc}	PscA _{LM} 189 PscA _{LM} 193 _{Nol} PscA _{LM} 193 _{Nol} PscA _{LM} 195 PscA _{LM} 195 PscA _{LM} 198 ₂₀ PscA _{LM} 198 ₂₀	DreAA _{kM} 193 _{ab} DreAA _{kM} 194 _{abat} DreAA _{kM} 197 DreAA _{kM} 197		OniA _{1M} 190 OniA _{1M} 191 OniA _{1M} 192 OniA _{1M} 193 _{abd} OniA _{1M} 194 _{ad}	OlaAA ₁₃₄ 189 OlaAA ₁₃₄ 193 _{abol} OlaAA ₁₃₄ 193 _{abol} OlaAA ₁₃₄ 196 OlaAA ₁₃₄ 197 OlaAA ₁₃₄ 199	TniAA _{tM} 193 _{abd} TniAA _{tM} 194 _{abot} TniAA199	TruAA ₁₃₄ 187 TruAA ₁₃₄ 193 _{abd} TruAA ₁₃₄ 193 _{abd} TruAA ₁₃₄ 194 _{abd}	DreAB _{GN} 195			
192 193 194 195 196 197 198 199 200	HfrA _{1M} 193 _{cd} HfrA _{1M} 194 _{bde} HfrA _{1M} 198 _{sbc} HfrA _{1M} 198 _{sbc}	XtrA _{1M} 193 _{vd} XtrA _{1M} 194 _{bole} XtrA _{1M} 194 _{bole} XtrA _{1M} 198 _{bo}	LmeA _{LM} 188 LmeA _{LM} 194 _{Nob} LmeA _{LM} 194 _{Nob} LmeA _{LM} 198 _{80c}	HsaA _{4,34} 188 HsaA _{4,34} 190 HsaA _{4,34} 191 HsaA _{4,34} 191 HsaA _{4,34} 192 _{cd} HsaA _{4,34} 192 _{cd} HsaA _{4,34} 198 _{abc} HsaA _{4,34} 198 _{abc}	PseA _{LM} 189 PseA _{LM} 193 _{bol} PseA _{LM} 193 _{bol} PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 199 _{bol} PseA _{LM} 199 _{bol}	DreAA _{EM} 193 _{ab} DreAA _{EM} 194 _{abol} DreAA _{EM} 197 DreAA _{EM} 199 _{bol}		$\begin{array}{l} & \text{OniA}_{LM}190\\ & \text{OniA}_{LM}191\\ & \text{OniA}_{LM}192\\ & \text{OniA}_{LM}193_{3bd}\\ & \text{OniA}_{LM}193_{3bd}\\ & \text{OniA}_{LM}199_{3bd}\\ & \text{OniA}_{LM}199_{3bd}\\ \end{array}$	OlaAA _{1M} 189 OlaA _{1M} 193 _{abol} OlaA _{1M} 193 _{abol} OlaA _{1M} 194 OlaA _{1M} 196 OlaA _{1M} 197 OlaA _{1M} 199 _{bol}	TniAA _{LM} 193 _{abd} TniAA _{LM} 194 _{abot} TniAA _{LM} 199 _{bod}	TruAA _{1M} 187 TruAA _{1M} 193 _{abd} TruAA _{1M} 193 _{abd} TruAA _{1M} 199 _{Nol} TruAA _{1M} 290	DreAB _{GN} 195			
192 193 194 195 196 197 198 199 200 201	HfrA ₁₃₄ 193 _{cd} HfrA ₁₃₄ 193 _{cd} HfrA ₁₃₄ 194 _{bde} HfrA ₁₃₄ 198 _{bbc} HfrA ₁₃₄ 199 _{bbd} HfrA ₁₃₄ 199 _{bbd}	XtrA _{LM} 193 _{od} XtrA _{LM} 194 _{bode} XtrA _{LM} 198 _{ac} XtrA _{LM} 199 _{acd} XtrA _{LM} 290	LmeA _{1M} 188 LmeA _{1M} 194 _{hole} LmeA _{1M} 194 _{hole} LmeA _{1M} 198 _{bb} LmeA _{1M} 199 _{bol}	HsaA _{cal} 188 HsaA _{cal} 190 HsaA _{cal} 191 HsaA _{cal} 191 HsaA _{cal} 192 HsaA _{cal} 194 _{bab} HsaA _{cal} 194 _{bab} HsaA _{cal} 198 _{ab} HsaA _{cal} 198 _{ab}	PseA _{LM} 189 PseA _{LM} 193 _{bol} PseA _{LM} 193 _{bol} PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 29 _{bol} PseA _{LM} 200	DreAA _{LM} 193 _{ab} DreAA _{LM} 193 _{ab} DreAA _{LM} 194 _{abol} DreAA _{LM} 197 DreAA _{LM} 199 _{bol}		OniA _{LM} 190 OniA _{LM} 191 OniA _{LM} 192 OniA _{LM} 193 _{Job} OniA _{LM} 194 _{Job}	OlaAA _{1M} 189 OlaAA _{1M} 193 _{abcl} OlaAA _{1M} 194 _{ocl} OlaAA _{1M} 196 OlaAA _{1M} 197 OlaAA _{1M} 199 _{bcl}	TniAA _{LM} 193 _{abi} TniAA _{LM} 194 _{abit} TniAA _{LM} 199 _{bot}	TruAA ₁₃₄ 187 TruAA ₁₃₄ 193 _{abd} TruAA ₁₃₄ 194 _{abd} TruAA ₁₃₄ 199 _{bd} TruAA ₁₃₄ 199 _{bd}	DreAB _{ON} 195			
192 193 194 195 196 197 198 199 200 201 201	HfrA _{1M} 193 _{cd} HfrA _{1M} 194 _{bd} HfrA _{1M} 194 _{bd} HfrA _{1M} 198 _{ab} HfrA _{1M} 199 _{abal} HfrA _{1M} 29201 HfrA _{M0} 202	XtrA _{1M} 193 _{od} XtrA _{1M} 194 _{bala} XtrA _{1M} 194 _{bala} XtrA _{1M} 198 _{ac} XtrA _{1M} 199 _{act}	LmcA _{1M} 188 LmcA _{1M} 194 _{bole} LmcA _{1M} 194 _{bole} LmcA _{1M} 199 _{aol} LmcA _{1M} 199 _{aol}	HsaA _{kkl} 188 HsaA _{kkl} 190 HsaA _{kkl} 191 HsaA _{kkl} 191 HsaA _{kkl} 192 HsaA _{kkl} 193 _{5d} HsaA _{kkl} 193 _{5d} HsaA _{kkl} 193 _{6d} HsaA _{kkl} 193 _{6d} HsaA _{kkl} 193 _{6d} HsaA _{kkl} 201 HsaA _{kkl} 201	PseA _{tM} 189 PseA _{tM} 193 _{bol} PseA _{tM} 193 _{bol} PseA _{tM} 194 _{bol} PseA _{tM} 195 PseA _{tM} 196 PseA _{tM} 196 _{bol} PseA _{tM} 196 _{bol}	DreAA _{LM} 193 _{ab} DreAA _{LM} 194 _{abat} DreAA _{LM} 194 _{bbat} DreAA _{LM} 199 _{bat}		OniA ₃₃₄ 190 OniA ₁₃₄ 191 OniA ₁₃₄ 192 OniA ₁₃₄ 193 OniA ₁₃₄ 194 _{set} OniA ₁₃₄ 199 _{bet}	OlaAA _{1M} 189 OlaAA _{MM} 193 ₀₀₁ OlaAA _{MM} 194 ₀₀₁ OlaAA _{MM} 196 OlaAA _{MM} 197 OlaAA _{MM} 199 ₀₀₂	TniAA _{3M} 193 ₆₆ TniAA _{3M} 194 ₆₆₀ TniAA _{5M} 199 ₆₆₁	TruAA ₁₃₄ 187 TruAA ₁₃₄ 193 _{abd} TruAA ₁₃₄ 194 _{abd} TruAA ₁₃₄ 199 _{bbd} TruAA ₁₃₅ 199 _{bbd}	DreAB _{GN} 195			
192 193 194 195 196 197 198 199 200 201 202 203	HfrA _{1M} 193 ₀₀ HfrA _{1M} 194 _{bit} HfrA _{1M} 194 _{bit} HfrA _{1M} 194 _{bit} HfrA _{1M} 199 _{abot} HfrA _{1M} 201 HfrA _{MD} 201	XtrA _{LM} 193 _{cd} XtrA _{LM} 194 _{bole} XtrA _{LM} 194 _{bole} XtrA _{LM} 198 _{bol} XtrA _{LM} 199 _{bol} XtrA _{LM} 201	LmcA _{1M} 188 LmcA _{1M} 194 _{hob} LmcA _{1M} 194 _{hob} LmcA _{1M} 198 _{bo} LmcA _{1M} 198 _{bo} LmcA _{1M} 199 _{bol}	HsaA _{kal} 188 HsaA _{kal} 190 HsaA _{kal} 191 HsaA _{kal} 191 HsaA _{kal} 193 _{id} HsaA _{kal} 194 _{isd} HsaA _{kal} 194 _{isd} HsaA _{kal} 194 _{isd} HsaA _{kal} 29 _{is}	PseA _{tM} 189 PseA _{tM} 193 _{bol} PseA _{tM} 193 _{bol} PseA _{tM} 194 _{bol} PseA _{tM} 194 PseA _{tM} 196 PseA _{tM} 198 _{bol} PseA _{tM} 198 _{bol}	DreAA _{tM} 193 _{ab} DreAA _{tM} 194 _{abd} DreAA _{tM} 197 DreAA _{tM} 199 _{bol}		OniA ₃₃₄ 190 OniA ₁₃₄ 191 OniA ₁₃₄ 192 OniA ₁₃₄ 193 _{hol} OniA ₁₃₄ 193 _{hol} OniA ₁₃₄ 193 _{hol} OniA ₁₃₄ 199 _{hol}	OlaAA _{3M} 189 OlaAA _{3M} 193 _{dod} OlaAA _{3M} 194 _{ad} OlaAA _{3M} 194 OlaAA _{3M} 196 OlaAA _{3M} 199 _{bod}	TniAA _{tM} 193 ₂₆₁ TniAA _{tM} 194 ₂₆₀ TniAA _{tM} 194 ₅₆₁	TruAA ₃₃₂ 187 TruAA ₃₃₂ 193 ₂₀₂ TruAA ₃₃₂ 194 ₂₀₂ TruAA ₃₃₂ 194 ₂₀₂ TruAA ₃₃₂ 199 ₂₀₂₄	DreAR _{EN} 195			
192 193 194 195 196 197 198 199 200 201 201 202 203 204	HfrA _{1M} 193 ₀₆ HfrA _{1M} 194 _{b6} HfrA _{1M} 194 _{b6} HfrA _{1M} 198 ₈₆ HfrA _{1M} 199 _{3b01} HfrA _{M0} 201 HfrA _{M0} 202	XirA _{1M} 193 _{.01} XirA _{1M} 194 _{bolic} XirA _{1M} 194 _{bolic} XirA _{1M} 199 _{boli} XirA _{1M} 199 _{boli} XirA _{1M} 201 XirA _{M0} 201	LmcA _{1M} 188 LmcA _{1M} 194 _{Nok} LmcA _{1M} 194 _{Nok} LmcA _{1M} 198 _{pol} LmcA _{1M} 199 _{pol} LmcA _{1M} 201	HsaA _{kal} 188 HsaA _{kal} 190 HsaA _{kal} 191 HsaA _{kal} 192 HsaA _{kal} 193 ₅₆ HsaA _{kal} 194 ₅₆ HsaA _{kal} 194 ₅₆ HsaA _{kal} 194 ₅₆ HsaA _{kal} 194 ₅₆ HsaA _{kal} 296 HsaA _{kal} 201 HsaA _{kal} 203 HsaA _{kal} 203	PseA _{LM} 189 PseA _{LM} 193 ₃₆₄ PseA _{LM} 193 ₃₆₆ PseA _{LM} 193 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 204 PseA _{LM} 204 _{abd}	DreA4 _{6M} 193 _{ab} DreA4 _{6M} 194 _{abal} DreA4 _{6M} 197 DreA4 _{6M} 199 _{bol}		OniA _{3,M} 190 OniA _{3,M} 191 OniA _{3,M} 192 OniA _{1,M} 193 _{,bol} OniA _{1,M} 193 _{,bol} OniA _{1,M} 199 _{,bol} OniA _{4,M} 199 _{,bol}	OlaAA _{3M} 189 OlaAA _{3M} 193 _{abol} OlaAA _{3M} 194 _{oct} OlaAA _{3M} 196 OlaAA _{3M} 196 OlaAA _{3M} 197 OlaAA _{3M} 199 _{bol}	TniAA _{1M} 193 ₆₆ TniAA _{1M} 194 ₆₆ TniAA _{1M} 194 ₆₆ TniAA _{1M} 199 ₆₆	ТгиАА ₁₃₄ 187 ТгиАА ₁₃₄ 193 ₂₆₄ ТгиАА ₁₃₄ 194 ₂₆₆₄ ТгиАА ₁₃₄ 199 ₃₆₆₄ ТгиАА ₁₃₄ 199 ₃₆₆₄ ТгиАА ₁₆₂ 200	DreAB _{GN} 195 DreAB _{GN} 204 _{bod}	OlaAB _{0x} 204 ₈₅	TniABox204 _{sd}	TruABox204 _{nd}
192 193 194 195 196 197 198 199 200 201 202 203 204 204	HfrA _{1M} 193 ₀₁ HfrA _{1M} 194 _{bdr} HfrA _{1M} 194 _{bdr} HfrA _{1M} 198 _{abs} HfrA _{1M} 199 _{abst} HfrA _{1M} 201 HfrA _{MP} 201	XirA _{LM} 193 _{od} XirA _{LM} 194 _{bod} XirA _{LM} 194 _{bod} XirA _{LM} 199 _{ad} XirA _M 201 XirA _{M0} 201	LmcA _{1M} 188 LmcA _{1M} 194 _{toth} LmcA _{1M} 194 _{toth} LmcA _{1M} 199 _{toth} LmcA _{1M} 199 _{toth}	HsaA ₁₃₁ 188 HsaA ₂₃₁ 190 HsaA ₂₃₁ 191 HsaA ₂₃₁ 192 HsaA ₂₃₁ 193 ₅₆ HsaA ₂₃₁ 193 ₅₆ HsaA ₂₃₁ 193 ₅₆ HsaA ₂₃₁ 193 ₅₆ HsaA ₂₃₂ 01 HsaA ₂₃₂ 01 HsaA ₂₃₂ 01 HsaA ₂₃₂ 03 HsaA ₂₃₂ 03	PscA _{1A1} 189 PscA _{1A1} 193 _{bol} PscA _{1A1} 194 _{bolo} PscA _{1A1} 194 PscA _{1A1} 195 PscA _{1A1} 195 PscA _{1A1} 195 PscA _{1A1} 195 PscA _{1A1} 195 PscA _{1A2} 195 PscA _{1A2} 200 PscA _{2A2} 200	DreAA _{tM} 193 ₃₀ DreAA _{tM} 194 _{abat} DreAA _{tM} 197 DreAA _{tM} 197 DreAA _{tM} 199 _{bat}		OniA ₁₃₄ 190 OniA ₁₃₄ 191 OniA ₁₃₄ 193 Jud OniA ₁₃₄ 193 _{Jud} OniA ₁₃₄ 193 _{Jud} OniA ₁₃₄ 193 _{Jud} OniA ₁₃₄ 293 OniA ₃₃₆₂ 203 OniA ₃₃₆₂ 204 _{ded}	OlaAA _{1M} 189 OlaAA _{1M} 193 _{abd} OlaAA _{2M} 193 _{abd} OlaAA _{3M} 194 _{bad} OlaAA _{3M} 196 OlaAA _{3M} 197 OlaAA _{3M} 197 OlaAA _{3M} 199 _{bad}	TniAA _{1M} 193 _{dol} TniAA _{1M} 194 _{dol} TniAA _{1M} 194 _{bol} TniAA _{1M} 199 _{bol}	TruAA ₁₃₂ 187 TruAA ₁₃₄ 193 ₂₆₂ TruAA ₁₃₄ 194 ₂₆₆₂ TruAA ₁₃₄ 199 ₅₆₂ TruAA ₁₄₆ 209 TruAA ₁₆₆ 204 ₆₆₆	DreAB _{GN} 195 DreAB _{GN} 204 _{bal} DreAB _{GN} 204 _{bal} DreAB _{GN} 205	OlaAB _{CN} 204 _N	TniABcx204.st	TruAB _{GN} 204 _{bod}
192 193 194 195 196 197 198 199 200 201 201 202 203 204 205 206 205	HfrA ₁₃₄ 193 _{.06} HfrA ₁₃₄ 194 _{bic} HfrA ₁₃₄ 194 _{bic} HfrA ₁₃₄ 199 _{abat} HfrA ₁₃₄ 199 _{abat} HfrA ₁₃₅ 201 HfrA ₃₅₅ 201	XtrA _{LM} 193 _{od} XtrA _{LM} 194 _{hade} XtrA _{LM} 199 _{hade} XtrA _{LM} 199 _{nod} XtrA _{LM} 201 XtrA _{M0} 201	LmcA _{1M} 194 _{N00} LmcA _{1M} 194 _{N00} LmcA _{1M} 194 _{N00} LmcA _{1M} 199 _{N01} LmcA _{1M} 201	HsaA _{1,21} 185 HsaA _{2,21} 190 HsaA _{2,21} 191 HsaA _{2,21} 192 HsaA _{2,21} 192 ₅₆ HsaA _{2,21} 193 ₅₆ HsaA _{2,21} 194 ₅₆ HsaA _{2,21} 194 ₅₆ HsaA _{2,22} 01 HsaA _{2,22} 01 HsaA _{2,22} 01	PacA _{LM} 189 PacA _{LM} 193 _{bol} PacA _{LM} 193 _{bol} PacA _{LM} 194 _{doot} PacA _{LM} 195 PacA _{LM} 199 _{bol} PacA _{LM} 199 _{bol} PacA _{LM} 204 PacA _{LM} 204 PacA _{LM} 204 PacA _{LM} 205 PacA _{LM} 205	DreAA _{kM} 193 _{ab} DreAA _{kM} 194 _{abat} DreAA _{kM} 194 _{abat} DreAA _{kM} 199 _{bat}		OniA ₁₃₁ 190 OniA ₁₃₁ 191 OniA ₁₃₁ 192 OniA ₁₃₁ 193 _{Jost} OniA ₁₃₁ 194 _{Jost} OniA ₁₃₁ 194 _{Jost} OniA ₁₃₂₀ 203 OniA ₁₃₂₀ 204 _{dot}	OlaAA _{1M} 189 OlaAA _{1M} 193 _{abst} OlaAA _{1M} 193 _{abst} OlaAA _{1M} 194 _{wst} OlaAA _{1M} 196 OlaAA _{1M} 196 OlaAA _{1M} 199 _{bst}	TniAA _{tM} 193 ₂₀₁ TniAA _{tM} 194 ₂₀₁ TniAA _{tM} 199 ₂₀₁ TniAA _{tM} 204 ₂₀₁	ТлиА4 ₁₄₁ 193 _{ай} ТлиА4 ₁₄₁ 193 _{ай} ТлиА4 ₁₄₁ 194 _{асс} ТлиА4 ₁₄₁ 194 _{асс} ТлиА4 ₁₄₁ 199 ₅₆₇ ТлиА4 ₁₄₂ 200	DreAB _{EN} 195 DreAB _{EN} 204 _{bot} DreAB _{EN} 204 _{bot} DreAB _{EN} 205	OlaAB _{CN} 204 _N	TniAB _{CN} 204 _{cd} TniAB _{CN} 206	TruAB _{GN} 204 _{hod}
192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 206 207	HirA _{1M} 193 _{od} HirA _{1M} 194 _{bb} HirA _{1M} 194 _{bb} HirA _{1M} 198 _{bb} HirA _{1M} 199 _{bb} HirA _{1M} 201	XtrA _{1M} 193 _{od} XtrA _{1M} 194 _{od} XtrA _{1M} 194 _{od} XtrA _{1M} 198 _{od} XtrA _{2M} 199 _{od} XtrA _{2M} 201 XtrA _{M2} 201	LmcA _{1M} 188 LmcA _{1M} 194 _{hole} LmcA _{1M} 198 _{bo} LmcA _{1M} 199 _{bol} LmcA _{1M} 199 _{bol}	HsaA ₁₄₁ 188 HsaA ₂₄₁ 190 HsaA ₂₄₁ 91 HsaA ₂₄₁ 92 HsaA ₂₄₁ 93 ₅₆ HsaA ₂₄₂ 03 HsaA ₂₆₂ 03 HsaA ₂₆₂ 03 HsaA ₂₆₂ 03 HsaA ₂₆₂ 03 HsaA ₂₆₂ 03 HsaA ₂₆₂ 04 ₅₆	PseA _{4.84} 189 PseA _{4.84} 193 _{20.64} PseA _{3.84} 194 _{20.66} PseA _{4.84} 195 PseA _{4.84} 195 PseA _{4.84} 195 PseA _{4.84} 198 ₂₀ PseA _{4.84} 200 PseA _{4.86} 205 PseA _{4.86} 205 PseA _{4.86} 207	DreAA ₆₄₀ 193 ₀₀ DreAA ₆₄₀ 194 ₀₀₀ DreAA ₆₄₀ 197 DreAA ₆₄₀ 199 ₀₀₁		OniA ₁₃₁ 190 OniA ₁₃₁ 191 OniA ₁₃₁ 193 ₂₆₆ OniA ₁₃₁ 193 ₆₆ OniA ₁₃₁ 193 ₆₆ OniA ₁₃₁ 199 ₆₆ OniA ₁₃₁ 199 ₆₆ OniA ₁₃₀₂ 203 OniA ₁₃₀₂ 203	OliaA _{1,0} 189 OliaA _{1,0} 193 _{doct} OliaA _{1,0} 193 _{doct} OliaA _{1,0} 196 OliaA _{1,0} 196 OliaA _{1,0} 199 _{bol} OliaA _{1,0} 199 _{bol}	TniAA _M 193 _{Ad} TniAA _M 193 _{Ad} TniAA _M 199 _{Ad} TniAA _M 204 _{Add} TniAA _M 204 _{Add}	ТпиАА ₁₃₄ 187 ТпиАА ₁₃₄ 193 ₂₆₄ ТпиАА ₁₃₄ 194 ₂₆₆ ТпиАА ₁₃₆ 194 ₂₆₆ ТпиАА ₁₃₆ 290 ТпиАА ₁₆₆ 200	DreAB _{ON} 195 DreAB _{ON} 204 _{Red} DreAB _{ON} 205	OlaAB _{CN} 204 _N	TniAB _{GX} 204 _{cd} TniAB _{GX} 206	TruAB _{GN} 204 _{bol}
192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 206 207 207	HfrA ₁₃₁ 193 _{od} HfrA ₁₃₁ 194 _{bb} HfrA ₁₃₁ 194 _{bb} HfrA ₁₃₁ 198 _{abc} HfrA ₁₃₁ 198 _{abc} HfrA ₁₃₀ 201 HfrA ₃₀₀ 201	100 XtrA _{1M} 193 ₃₀₁ XtrA _{1M} 194 ₅₀₆ XtrA _{1M} 194 ₈₆ XtrA _{1M} 199 ₈₆ XtrA _{1M} 199 ₈₆ XtrA _{1M} 201 XtrA _{M0} 201	LmcA _{1M} 194 _{not} LmcA _{1M} 194 _{not} LmcA _{1M} 194 _{not} LmcA _{1M} 198 _{not} LmcA _{1M} 199 _{not}	HstA _{1,21} 188 HstA _{1,21} 190 HstA _{2,21} 191 HstA _{2,21} 191 HstA _{2,21} 192, HstA _{2,21} 192, HstA _{2,21} 192, HstA _{2,21} 194, HstA _{2,21} 194, HstA _{2,22} 201 HstA _{2,22} 203 HstA _{2,22} 204, HstA _{2,22} 204, HstA _{2,22} 208 HstA _{2,22} 208	PseA _{LM} 189 PseA _{LM} 193 _{bol} PseA _{LM} 193 _{bol} PseA _{LM} 194 _{bol} PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 195 PseA _{LM} 200	DreAA _{cM} 193 _{ab} DreAA _{cM} 193 _{ab} DreAA _{cM} 194 _{abat} DreAA _{cM} 199 _{bat} DreAA _{cM} 199 _{bat}		OniA ₁₄₁ 190 OniA ₁₄₁ 191 OniA ₁₄₁ 193 ₃₀₄ OniA ₁₄₁ 193 ₄₀₄ OniA ₁₄₁ 193 ₄₀₄ OniA ₁₄₁ 193 ₄₀₄ OniA ₁₄₁ 193 ₄₀₄	OlaAA _{1M} 189 OlaAA _{1M} 193 _{2bol} OlaAA _{2M} 193 _{2bol} OlaAA _{2M} 194 _{bol} OlaAA _{2M} 197 OlaAA _{2M} 197 OlaAA _{2M} 199 _{bol}	TniAA _{1M} 193 ₂₀₁ TniAA _{1M} 194 ₂₀₀₁ TniAA _{1M} 199 ₂₀₁ TniAA _{1M} 199 ₂₀₁ TniAA _{1M} 204 ₂₀₁	TruAA _{1M} 193 _{A1} TruAA _{1M} 193 _{A1} TruAA _{1M} 194 _{A0} TruAA _{1M} 194 _{A0} TruAA _{1M} 204 _{A0} TruAA _{1M} 204 _{A0}	Dre AB _{GN} 195 Dre AB _{GN} 204 _{bod} Dre AB _{GN} 204 _{bod}	OlaAB _{CN} 204 _N	TniABox204 _{al}	TruAB _{GN} 204 _{bot}
192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 206 207 208 209 209 210	HfrA ₁₀₁ 193, ₀ HfrA ₁₀₁ 194 ₀₀ HfrA ₁₀₁ 194 ₀₀ HfrA ₁₀₁ 198 ₀₀ HfrA ₁₀₁ 199 ₀₀₀₁ HfrA ₁₀₂ 201 HfrA ₁₀₂ 201	100 XtrA _{1M} 193 ₀₀ XtrA _{1M} 194 ₀₀₀ XtrA _{1M} 199 ₀₀₀ XtrA _{M0} 201 XtrA _{M0} 201 XtrA _{M0} 201	LmcA ₁₃₄ 188 LmcA ₁₃₄ 194 ₀₋₀₀ LmcA ₁₃₄ 194 ₀₋₀₀ LmcA ₁₃₄ 194 ₀₋₀₀ LmcA ₁₃₄ 194 ₀₋₀₀ LmcA ₁₃₄ 201 LmcA ₁₄₅ 201	HsaA ₁₂₄ 188 HsaA ₁₂₄ 190 HsaA ₁₂ 191 HsaA ₁₂ 191 HsaA ₁₂ 192 HsaA ₁₂ 193 ₆₄ HsaA ₁₂ 193 ₆₄ HsaA ₁₂ 193 ₆₆ HsaA ₁₂ 193 ₆₇ HsaA ₁₂ 203 HsaA ₁₂₂ 203 HsaA ₁₂₂ 203 HsaA ₁₂₂ 203 HsaA ₁₂₂ 208 HsaA ₁₂₂ 208 HsaA ₁₂₂ 208	PseA _{1Al} 189 PseA _{1Al} 189 PseA _{1Al} 193 _{Aud} PseA _{1Al} 194 _{Aud} PseA _{2Al} 194 PseA _{2Al} 199 PseA _{2Al} 199 _{Bod} PseA _{2Al} 209 PseA _{2Al} 200 PseA ₂ 200 PseA _{2Al} 200 PseA ₂ 200 P	DreAA _{LM} 193 _{ab} DreAA _{LM} 194 _{abat} DreAA _{LM} 194 _{abat} DreAA _{LM} 199 _{bat} DreAA _{LM} 199 _{bat}		OniA ₁₄₁ 100 OniA ₁₄₁ 101 OniA ₁₄₁ 102 OniA ₁₄₁ 103 _{dot} OniA ₁₄₄ 104 _{dot} OniA ₁₄₄ 109 _{hot} OniA ₁₄₄ 109 _{hot}	OlaAA ₃₄ 189 OlaAA ₃₄ 193 _{Aud} OlaAA ₃₄ 193 _{Aud} OlaAA ₃₄ 196 OlaAA ₃₄ 196 OlaAA ₃₄ 197 OlaAA ₃₄ 199 ₅₀	TniAA _{tM} 193 _{dat} TniAA _{tM} 194 _{dat} TniAA _{tM} 199 _{bat} TniAA _{tM} 204 _{dat} TniAA _{tM} 207	TruAA ₁₃₄ 197 TruAA ₁₃₄ 193 ₂₆₄ TruAA ₁₃₄ 194 ₆₆₆ TruAA ₁₃₄ 194 ₆₆₆ TruAA ₁₃₄ 199 ₂₆₆ TruAA ₁₃₆ 200 TruAA ₁₆₅ 200	DreAB _{GN} 195 DreAB _{GN} 204 _{hod} DreAB _{GN} 205	OlaABex204 _{ir}	TriABco204 _{ad}	TmAB ₀₂ 204 ₆₄
192 193 194 195 196 197 198 200 201 202 203 204 205 206 207 208 206 207 208 209 200 201 0 7 7 208 209 200 201 200 201 202 203 204 205 206 207 200 200 201 202 203 204 205 200 201 202 203 204 205 200 201 200 201 200 201 200 201 200 201 200 201 200 201 200 201 200 201 200 201 200 201 200 201 200 201 200 201 200 200	HfrA ₁₃₄ 193 _{cd} HfrA ₁₃₄ 194 _{bd} HfrA ₁₃₄ 194 _{bd} HfrA ₁₃₄ 198 _{abs} HfrA ₁₃₆ 29 _{abst} HfrA ₁₃₆ 201 HfrA ₁₃₆ 202 HfrA ₃₆₅ 210 _b HfrA ₃₆₅ 210 _b	XirA ₁₃₄ 193 _{af} XirA ₁₃₄ 193 _{af} XirA ₁₃₄ 195 _{af} XirA ₁₃₄ 195 _{af} XirA ₁₃₄ 200 XirA ₁₃₆ 201 XirA ₁₃₆ 201 XirA ₁₃₆ 201 bir Fing A	LmcA ₃₄ 188	HsaA _{3,11} 188 HsaA _{3,11} 190 HsaA _{3,11} 90 HsaA _{3,11} 91 HsaA _{3,11} 92 HsaA _{3,11} 92 ₁ , HsaA _{3,11} 93 _{5,1} HsaA _{3,11} 93 _{5,2} HsaA _{3,11} 93 _{6,2} HsaA _{3,12} 93 _{6,2} HsaA _{3,12} 93 _{6,2} HsaA _{3,12} 03 HsaA _{3,12} 07 HsaA _{3,12} 0 HsaA _{3,12} 0	Peck ₁₄ 189 Peck ₁₄ 189 Peck ₁₄ 193 ₅₆₇ Peck ₁₄ 195 Peck ₁₄ 195 Peck ₁₄ 195 Peck ₁₄ 195 Peck ₁₄ 205 Peck ₁₆ 200 Peck ₁₆ 205 Peck ₁₆ 205 Peck ₁₆ 206	DreAA _{1M} 193 _M DreAA _{1M} 194 _{dot} DreAA _{1M} 197 DreAA _{1M} 199 _{bol} DreAA _{1M} 199 _{bol}	Stoped Base A	Chik _{kik} 190 Chik _{kik} 192 Chik _{kik} 192 Chik _{kik} 193 ₅₆ Chik _{kik} 293 ₅₆ Chik _{kik} 293 ₅₆ Chik _{kik} 293 Chik _{kik} 203 Chik _{kik} 203 Chik _{kik} 203 Chik _{kik} 203 Chik _{kik} 203 Chik _{kik} 204	OlaAA ₁₆₁ 189 OlaAA ₁₆₁ 183 OlaAA ₁₆₁ 193 _{And} OlaAA ₁₆₁ 196 OlaAA ₁₆₁ 197 OlaAA ₁₆₁ 199 _{And} OlaAA ₁₆₁ 199 _{And}	TniAA ₂₀ 193 ₂₀ TniAA ₂₀ 194 ₂₀ TniAA ₂₀ 199 ₂₀ TniAA ₂₀ 199 ₂₀ TniAA ₂₀ 204 ₂₀ TniAA ₂₀ 207	ТпаА4, ₁₄ 197 ТпаА4, ₁₄ 193 ₂₆₁ ТпаА4, ₁₄ 194 ₂₆₆₁ ТпаА4, ₁₄ 194 ₂₆₆₁ ТпаА4, ₁₆ 200 ТпаА4, ₁₆ 204 ₆₆₁	Dre AB ₀₀ 195 Dre AB ₀₀ 204 ₅₀ Dre AB ₀₀ 205 Zebrafish AB	OlaABex204v	TmABco204_d TmABco204_d TmABco206	TmABcs204 _{ml}
192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 209 209 209 209 209 209 209 209 200	НЕА ₁₄₁ 93 ₁₄ НЕА ₁₄₂ 94 ₆₀ НЕА ₁₄₂ 94 ₆₀ НЕА ₁₄₂ 98 ₆₆ НЕА ₁₄₂ 99 ₆₆₁ НЕА ₁₆₂ 201 НЕА ₁₆₂ 201 НЕА ₁₆₂ 210, НЕА ₁₆₂ 210,	Sar XirA ₁₄ 193 _{al} XirA ₁₄ 194 _{bat} XirA ₁₄ 198 _{bat} XirA ₁₄ 298 _{bat} XirA ₁₆ 201 XirA ₁₆ 201 XirA ₁₆ 201 XirA ₁₆ 201 XirA ₁₆ 201 XirA ₁₆ 201	LmcA ₃₄ 188 LmcA ₃₄ 194 ₄₆ LmcA ₁₄ 194 ₄₆ LmcA ₁₄ 194 ₆₆ LmcA ₁₄ 299 ₆₆ LmcA ₁₆₂ 201 LmcA ₁₆₂ 201 Crobasth A LmcA ₁₆₂ 210 ₂₆	ItaA ₁₀ 2188 ItaA ₁₀ 2189 ItaA ₁₁ 219 ItaA ₁₁ 219 Ita	PecA ₁₄ 189 PecA ₁₄ 193 _{ad} PecA ₁₄ 194 _{adm} PecA ₁₄ 194 _{adm} PecA ₁₄ 195 _a PecA ₁₄ 195 _a PecA ₁₄ 195 _a PecA ₁₆ 201 PecA ₁₆	DreAA ₃₄ 197 ₀ DreAA ₃₄ 197 ₀ DreAA ₃₄ 197 ₀ DreA ₄₄ 197 ₀ DreA ₄₄ 199 ₀₀ DreA ₄₄₀ 299 Zebrafish AA	Stepel Bas A	OniAya100 OniAya101 OniAya101 OniAya102 OniAya102 OniAya103 OniAya103 OniAya103 OniAya103 OniAya103 OniAya103 OniAya203 OniAya204 OniAya204 OniAya214	ClarA ₁₄₂ 139 ClarA ₁₄₂ 133 ₂₆₄ ClarA ₁₄₂ 133 ₂₆₄ ClarA ₁₄₂ 136 ClarA ₁₄₂ 136 ClarA ₁₄₂ 136 ClarA ₁₄₂ 139 ClarA ₁₄₂ 234 ClarA ₁₄ 234 ClarA ₁₄ 234 ClarA ₁₄ 234 ClarA ₁₄ 234 ClarA ₁₄ 2	TniAA _{1M} 193 ₂₆₂ TniAA _{1M} 194 ₂₆₂ TniAA _{1M} 194 ₂₆₂ TniAA _{1M} 199 ₂₆₂ TniAA _{2M} 294 ₂₆₂ TniAA _{2M} 204 ₂₆₂	TruAku2157 TruAku2157 TruAku2159 _{ad} TruAku2159 _{ad} TruAku2209 _{ad} TruAku2204 _{ad}	Dre AB ₀₀ 195 Dre AB ₀₀ 204 _{6.0} Dre AB ₀₀ 205 Dre AB ₀₀ 205 Zebrafish AB Dre AB ₀₀ 211 ₄₀ 0	OlaAB ₀₂ 204 ₆	TasABcs204.st TasABcs204.st TasABcs205	TraABco204oct
192 193394 1955 1966 1977 1988 1999 2000 2011 2022 203 204 2050 2070 2088 2099 2100 2072 2088 2099 2100 2072 2088 2099 2112 2099 2112 2099 2112 2099 2112 2095 2095 2095 2005 2005 2005 2005 200	HEA ₁₃₂ 193 ₂₄ HEA ₁₃₂ 194 ₆₆ HEA ₁₃₂ 194 ₆₆ HEA ₁₃₂ 199 ₂₆₇ HEA ₁₃₂ 201 HEA ₁₆₂ 201 HEA ₁₆₂ 201 HEA ₁₆₂ 210 ₆ HERA ₆₆₂ 210 ₆	XirA ₁₆₁ 193 ₁ XirA ₁₆₁ 193 ₁ XirA ₁₆₁ 198 ₆₀ XirA ₁₆₂ 198 ₆₀ XirA ₁₆₂ 201 XirA ₁₆₂ 201 XirA ₁₆₂ 201 XirA ₁₆₂ 201 XirA ₁₆₂ 201 ₆₀	LmeA ₃₄ 188 LmeA ₃₄ 194 ₅₆₈ LmeA ₃₄ 194 ₅₆₈ LmeA ₃₄ 194 ₅₆₈ LmeA ₃₄ 201	Harkud 88 Harkud 90 Harkud 90 Harkud 91 Harkud 92 Harkud 92 Harkud 92 Harkud 92 Harkud 93 Harkud 93	Peck ₁₀ 189 Peck ₁₀ 199 Peck ₁₀ 195 ₁₆₁ Peck ₁₀ 195 ₁₆₁ Peck ₁₀ 196 Peck ₁₀ 196 Peck ₁₀ 296 Peck ₁₀ 206 Peck ₁₀ 216 Peck ₁₀	DreAA ₁₀ 193 ₂₀ DreAA ₁₀ 193 ₂₀ DreAA ₁₀ 194 ₂₀₁ DreAA ₁₀ 199 ₂₀₁ DreAA ₁₀ 199 ₂₀₁ DreAA ₁₀ 2199 ₂₀₁	Stepel Bas A	0 0 0 0 0 0 0 0 0 0 0 0 0 0	OlaAA ₁₀ 139 OlaAA ₁₀ 139 OlaAA ₁₀ 139 OlaAA ₁₀ 136 OlaAA ₁₀ 195 OlaAA ₁₀ 195 OlaA ₁₀ 195	TaiAA ₀₀ 193 ₂₆ TaiAA ₀₀ 194 ₂₆ TaiAA ₀₀ 195 ₄₆ TaiAA ₀₀ 204 ₂₆ TaiAA ₀₀ 207 TaiAA ₀₀ 207 TaiAA ₀₀ 211 ₂₀₄	TmAA ₁₀ 193 ₄₀ TmAA ₁₀ 193 ₄₀ TmAA ₁₀ 194 ₄₆₄ TmAA ₁₀ 194 ₄₆₄ TmAA ₁₀ 294 ₄₆₄ TmAA ₁₀ 294 ₄₆₄	DecABox195 DecABox204os1 DecABox204os1 DecABox205 Zebrußch AB DecABox211os2	OlaABcc204, Medula AB OlaABcc21,	TaiABco204_d TaiABco206 Tetraodon AB Tetraodon AB	TraAB ₀₀ 204 ₀₀
192 1933 1944 195 196 197 1988 1999 200 202 203 204 205 206 207 208 209 210 212 213 213 213 213 213 213 213 213 213	HEA ₁₃₂ 193 ₂₄ HEA ₁₃₂ 194 ₃₆ HEA ₁₃₂ 194 ₅₆ HEA ₁₃₂ 199 ₅₆ HEA ₁₃₂ 192 ₅₆ HEA ₁₃₂ 210 HEA ₁₆ 210 HEA ₁₆ 210	56 ХигА ₁₀₄ 193 ₄₀ ХигА ₁₀₄ 194 ₂₀₀ ХигА ₁₀₄ 198 ₂₀ ХигА ₁₀₅ 201 ₂₀ ХигА ₁₀₅ 201 ₂₀ ХигА ₁₀₅ 210 ₂₀ ХигА ₁₀₅ 211 ₂₀	Lanch ₁₄₁ 188 Lanch ₁₄₁ 194 ₅₀₆ Lanch ₁₄₁ 194 ₅₀₆ Lanch ₁₄₁ 195 ₅₀ Lanch ₁₄₁ 195 ₅₀ Lanch ₁₄₂ 195 ₅₀ Lanch ₁₄₂ 10 ₅₆ Cordscath A Lanch ₁₄₂ 210 ₅₆	Hash _a ul 88 Hash _a ul 90 Hash _a ul 90 Hash _a ul 91 Hash _a ul 92 Hash _a ul 93 _{ba} Hash _a ul 95 _{ba}	Peck ₁₀ [89 Peck ₁₀ [93, ₁₀ Peck ₁₀ [93, ₁₀ Peck ₁₀ [95, ₁₀ Peck ₁₀ [10, ₁₀	DreAA ₁₀ 193 ₀ DreAA ₁₀ 194 ₀₀ DreAA ₁₀ 194 ₀₀ DreAA ₁₀ 197 DreA ₁₀ 199 ₀₀ DreA ₁₀ 209 Zzhrafuk AA	Super Base A	كَلَّبْلَ اللَّهُ اللَّهُ المَانَ اللَّهُ اللَّهُ اللَّهُ اللَّهُ الللَّهُ اللَّهُ اللَّهُ اللَّهُ اللَّهُ اللَّهُ اللَّهُ اللَّهُ اللَّ اللَّهُ اللَّهُ اللَّ اللَّهُ اللَّهُ اللَّ اللَّاللَّهُ اللَّهُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّهُ اللَّهُ اللَّهُ اللَّهُ اللَّهُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلُولَةُ اللَّالِيلَّةُ اللَّالِيلِيلَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ مُنْتَلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّالِيلَةُ اللَّ	OlaAA ₂₀ 139 OlaAA ₂₀ 139 OlaAA ₂₀ 139 ₂₆₁ OlaAA ₂₀ 139 OlaAA ₂₀ 19 OlaAA ₂₀ 19 OlaAA ₂₀ 19 ₂₆₁ OlaAA ₂₀ 219 ₂₆₁	TaiAA ₀₄ 193 ₆₆ TaiAA ₀₄ 194 ₆₆ TaiAA ₀₄ 199 ₆₆ TaiAA ₀₆ 20 ₆₆₆ TaiAA ₀₆ 207 TaiAa ₀₆ 211 ₀₀₀	TmAA ₁₀₂ 157 TmAA ₁₀₂ 153 ₃₆₂ TmAA ₁₀₂ 153 ₃₆₂ TmAA ₁₀₂ 53 ₃₆₂ TmAA ₁₀₂ 53 ₅₆₂ TmAA ₁₀₂ 53 ₅₆₂ TmAA ₁₀₂ 53 ₅₆₂	DreABco.2045cf DreABco.2045cf DreABco.2045cf DreABco.215 DreABco.215 DreABco.215 DreABco.215 DreABco.215 DreABco.215 DreABco.215 DreABco.216 DreABco.2	OlaABec204c	TasAB ₀₂ 204 ₂₁ TasAB ₀₂ 206	Tin AB ₀₀ 204 ₆₀ Tin AB ₀₀ 208 Takinga AB
1922 1933 1955 1955 2000 2011 2022 203 2000 2010 2020 203 2000 2000	HEA ₁₃₁ 93 ₄₆ HEA ₁₃₁ 93 ₆₆ HEA ₁₃₁ 98 ₆₆ HEA ₁₃₁ 98 ₆₆ HEA ₁₃₁ 99 ₆₆ HEA ₁₃₂ 99 ₆₆ HEA ₁₃₂ 20 HEA ₁₃₂ 210 HEA ₁₃₂ 210 HEA ₁₃₂ 210 ₅	а ХигА ₁₄₁ 193 ₁₄ ХигА ₁₄₂ 193 ₆₆ ХигА ₁₄₂ 195 ₆₆ ХигА ₁₄₂ 195 ₆₆ ХигА ₁₄₂ 295 ₆₆ ХигА ₁₄₂ 210 ₆ Гига ₁₄₂ 210 ₆ Гига ₁₄₂ 210 ₆	LmcA ₂₄ 188 LmcA ₂₄ 194 ₅₀₆ LmcA ₂₄ 195 ₅₀₆ LmcA ₂₄ 195 ₅₀₆ LmcA ₂₆ 201 LmcA ₂₆ 210 ₂₆ Crecksorth A LmcA ₂₆ 210 ₂₆	HarAyd 88 HarAyd 90 HarAyd 90 HarAyd 90 HarAyd 92 HarAyd 92 HarAyd 92 HarAyd 92 HarAyd 92 HarAyd 92 HarAyd 92 HarAyd 93 HarAyd	Pech ₃₀ 189 Pech ₃₀ 189 Pech ₃₀ 193 ₃₆ Pech ₃₀ 195 ₃₆ Pech ₃₀ 196 Pech ₃₀ 198 ₂₀ Pech ₃₀ 298 ₂₀ Pech ₃₀ 298 ₂₀ Pech ₃₀ 298 ₂₀ Pech ₃₀ 298 Pech ₃₀	DecAd ₁₀ 193 ₀ DecAd ₁₀ 193 ₀ DecAd ₁₀ 194 ₀₀ DecAd ₁₀ 197 DecAd ₁₀ 199 ₁₀ Zerzfish AA	Sept Iba A	OniAya100 OniAya101 OniAya102 OniAya102 OniAya103 OniAya104 OniAya104 OniAya104 OniAya104 OniAya104 OniAya104 OniAya104 OniAya204 OniAya204 OniAya204 OniAya204 OniAya204 OniAya204	04AA ₃₄ 189 04AA ₃₄ 193 04AA ₃₄ 193 ₂₆₄ 04AA ₃₄ 193 ₂₆₄ 04AA ₃₄ 195 04AA ₃₄ 195 04AA ₃₄ 195 04AA ₃₄ 193 ₂₆ 04AA ₃₄ 193 ₂₆ 04AA ₃₆ 214 ₂₆₄	TaiAA ₂₀ 193 ₂₆ TaiAA ₂₀ 195 ₂₆ TaiAA ₂₀ 195 ₂₆ TaiAA ₂₀ 295 ₂₆ TaiAA ₂₀ 295 ₂₆ TaiAA ₂₀ 297 TaiAA ₂₀ 211 _{20,26}	TmAA ₁₂₁ 82 TmAA ₁₂₁ 82 mAA ₁₂₁ 93 ₄₀ TmAA ₁₂₁ 94 ₄₆₄ TmAA ₁₂₁ 99 ₄₆ TmAA ₁₂₂ 99 ₄₆ TmAA ₁₂₂ 99 ₄₆ TmAA ₁₂₂ 91 ₄₆₄ TmAA ₁₂₂ 914	DecAB ₀₀ 195	OlaAB _{co} 204 ₆	TmARton204.g	Tar All ₂₀ 204 ₂₀
1922 1933 1944 1951 1956 1977 1988 2001 2012 2033 2044 2055 2066 2077 2089 2099 2100 2099 2102 2111 2122 2133 2144 2155	HEA ₁₃₂ 193 ₂₄ HEA ₁₃₂ 194 ₃₆ HEA ₁₃₂ 194 ₃₆ HEA ₁₃₂ 198 ₃₆ HEA ₁₃₂ 020 HEA ₁₆ 2020 HEA ₁₆ 2020 HEA ₁₆ 2020 HEA ₁₆ 211 ₁₆₄ HEA ₁₆ 211 ₁₆₄	20 XirA ₁₀ 193 ₂₄ XirA ₁₀ 194 ₅₆ XirA ₁₀ 198 ₆₆ XirA ₁₀ 299 ₆₆ XirA ₁₀ 201 XirA ₁₀ 204 ₆₀₇ XirA ₁₀ 201 ₆₀₇	Lanch ₁₄ 188 Lanch ₁₄ 194 ₅₀₀ Lanch ₁₄ 195 ₅₀ Lanch ₁₄ 195 ₅₀ Lanch ₁₄ 195 ₅₀ Lanch ₁₄ 295 ₅₀ Lanch ₁₄ 201 Lanch ₁₄	Hark ₁₀ 188 Hark ₁₀ 190 Hark ₁₀ 191 Hark ₁₀ 192 Hark ₁₀ 192 Hark ₁₀ 195 Hark ₁₀ 195 Hark ₁₀ 195 Hark ₁₀ 195 Hark ₁₀ 295 Hark ₁₀ 295 Hark ₁₀ 295 Hark ₁₀ 295 Hark ₁₀ 21 Hark ₁₀ 201 Hark ₁₀ 201 Hark ₁₀ 205 Hark ₁₀	Pech ₃₀ 189 Pech ₃₀ 189 Pech ₃₀ 195 ₃₄ Pech ₃₀ 195 ₃₄ Pech ₃₀ 195 ₃₄ Pech ₃₀ 295 Pech ₃₀ 295 Pech ₃₀ 205 Pech ₃₀ 205 Pech ₃₀ 205 Pech ₃₀ 207 Pech ₃₀ 205 Pech ₃₀ 207 Pech ₃₀ 205 Pech ₃₀ 207 Pech ₃₀ 215 Pech ₃₀ 211 Pech ₃₀ 214	DreAA ₁₀ 193 ₀ DreAA ₁₀ 194 ₀₀ DreAA ₁₀ 194 ₀₀ DreAA ₁₀ 199 ₀₀ DreAA ₁₀ 199 ₀₀ Zzbrafish AA	Nipel Bas A	004Aga100 004Aga101 004Aga101 004Aga102 004Aga102 004Aga103 004Aga103 004Aga103 004Aga103 004Aga103 004Aga103 004Aga103 004Aga11	044A ₃₀ /39 044A ₃₀ /39 ₅₀ 044A ₃₀ /39 ₅₀ 044A ₃₀ /20 ₄₀₀	TaiAA ₀₂ 193 ₆₆ TaiAA ₀₂ 193 ₆₆ TaiAA ₀₂ 196 ₆₆ TaiAA ₀₂ 19 ₆₆₆ TaiAA ₀₂ 207 TaiAA ₀₂ 211 ₆₆₆	TmAA ₁₀₂ 157 TmAA ₁₀₂ 153 ₃₆₂ TmAA ₁₀₂ 153 ₃₆₂ TmAA ₁₀₂ 53 ₃₆₂ TmAA ₁₀₂ 53 ₃₆₂ TmAA ₁₀₂ 530 TmAA ₁₀₂ 530 TmAA ₁₀₂ 530 TmAA ₁₀₂ 51 TmAA ₁₀₂ 51 TmAA ₁₀₂ 51 TmAA ₁₀₂ 51	Dre AB ₆₀ 195	OlaABco204,	TaiABo204_ TaiABo204_ TaiABo2206	TruABco204cc
1922 1933 1944 1955 1966 1977 2000 2010 2020 2033 2044 2055 2060 2070 2088 2099 2100 2072 2088 2099 2110 2122 2133 2044 2155 2066 2072 2088 2099 2101 2122 2133 2044 2055 2067 2072	НЕА ₁₃₂ 193 ₂₆ НЕА ₁₃₂ 195 ₂₆ НЕА ₁₃₂ 195 ₂₆ НЕА ₁₃₂ 195 ₂₆ НЕА ₁₃₂ 195 ₂₆ НЕА ₁₃₂ 210 ₅ НЕА ₁₃₂ 210 ₅ НЕА ₁₃₂ 210 ₅ НЕА ₁₃₂ 210 ₅ НЕА ₁₃₂ 210 ₅	10 XirA ₁₄ 193 ₂₄ XirA ₁₄ 193 ₂₆ XirA ₁₄ 198 ₂₆ XirA ₁₄ 199 ₂₆ XirA ₁₄ 293 ₂₆ XirA ₁₆ 201 XirA ₁₆	Lunch ₁₄₁ 198 Lunch ₁₄₁ 194 ₅₀₀ Lunch ₁₄₁ 195 ₅₀ Lunch ₁₄₁ 195 ₅₀ Lunch ₁₄₁ 195 ₅₀ Lunch ₁₄₁ 210 ₅₀ Lunch ₁₄₀ 210 ₅₀ Lunch ₁₄₀ 210 ₅₀ Lunch ₁₄₀ 210 ₅₀	Hash _a 188 Hash _a 2190 Hash _a 2190 Hash _a 2192 Hash _a 2192 Hash _a 2192 ₁ Hash _a 219 ₂ Hash _a 219 ₂ Hash _a 219 ₂ Hash _a 219 ₂ Hash _a 210 Hash _a 203 Hash _a 215 ₁ Hash _a 215 ₁	Peck ₁₄ 199 Peck ₁₄ 193 Peck ₁₄ 195 Peck ₁₄ 195 Peck ₁₄ 195 Peck ₁₄ 195 Peck ₁₄ 198 Peck ₁₄ 198 Peck ₁₄ 198 Peck ₁₄ 298 Peck ₁₆ 201 Peck ₁₆ 205 Peck	DecAA ₁₀ 193_ DecAA ₁₀ 193_ DecAA ₁₀ 194 ₀₋₁ DecAA ₁₀ 197 DecAA ₁₀ 199 ₀₋₁ DecAa ₁₀ 299 Zebrafish AA	Stypel Jacob	004Aga100 004Aga100 004Aga102 004Aga102 004Aga102 004Aga103 004Aga103 004Aga103 004Aga103 004Aga103 004Aga11Aga1 004Aga1 004Aga11Aga1 004Aga10 004Aga10 004Aga10 004Aga10 00	004A ₃₀ 189 004A ₃₀ 193 ₂₆₇ 004A ₃₀ 193 ₂₆₇ 004A ₃₀ 195 004A ₃₀ 195 004A ₃₀ 195 004A ₃₀ 294 ₂₆₇ 004A ₃₀ 292 ₃₆₇ 004A ₃₀ 292 ₃₆₇ 004A ₃₀ 292 ₃₆₇ 004A ₃₀ 292 ₃₆₇ 004A ₃₀ 004A ₃	TaiAA ₂₀ 195 ₂₆ TaiAA ₂₀ 195 ₂₆ TaiAA ₂₀ 195 ₂₆ TaiAA ₂₀ 295 ₂₆ TaiAA ₂₀ 295 ₂₆ TaiAA ₂₀ 207 TaiAA ₂₀ 21 TaiAA ₂₀ 21 TaiAA ₂₀ 21 TaiAA ₂₀ 216	TmAA ₁₀ 197 TmAA ₁₀ 193 ₄₀ TmAA ₁₀ 193 ₄₀ TmAA ₁₀ 193 ₄₀ TmAA ₁₀ 293 ₄₀ TmAA ₁₀ 200 TmAA ₁₀ 200 TmAA ₁₀ 200 TmAA ₁₀ 204 TmAA ₁₀ 214 TmAA ₁₀ 214	Dec AB ₀₀ 204 ₆₂ Dec AB ₀₀ 215	OlaAB ₀₂ 204 ₀	TmAB ₀₀ 204,g TmAB ₀₀ 206 Tetraodon AB Tetraodon AB	Tan AB ₀₀ 20H ₀₀ (
1922 1933 1944 1955 1966 1977 1988 2000 2010 2020 2033 2044 2055 2066 2007 2033 2044 2055 2066 2072 2033 2044 2055 2066 2072 2033 2044 2055 2066 2077 2088 2099 2000 2010 2017 2017 2018 2055 2066 2077 2088 2099 2000 2017 2018 2055 2066 2077 2088 2099 2000 2017 2018 2055 2066 2077 2088 2099 2000 2017 2078 2078 2078 2078 2078 2078 2078 2078 2078 2078 2078 2078 2079 2079 2070 2078 2079 2079 2070 2079 2070 2079 2070 2079 2070 2079 2070 2079 2070 2079 2070 2079 2070 2079	HEA ₃₃₂ 193 ₂₆ HEA ₃₃₂ 195 ₂₆ HEA ₃₃₂ 195 ₂₆ HEA ₃₃₂ 195 ₂₆ HEA ₃₃₂ 201 HEA ₃₃₂ 210 ₅ HEA ₃₃₂ 210 ₅	20 XirA ₁₀ 193 ₂ XirA ₁₀ 194 ₅₀ XirA ₁₀ 198 ₆ XirA ₁₀ 299 ₆₁ XirA ₁₀ 204 ₆₀ XirA ₁₀ 204 ₆₀ XirA ₁₀ 210 ₆ Ping A XirA ₁₀ 210 ₆	Lanch _{ad} 188 Lanch _{ad} 194 ₅₀₀ Lanch _{ad} 195 ₅₀ Lanch _{ad} 195 ₅₀ Lanch _{ad} 295 ₅₀ Lanch _{ad} 201 Lanch _{ad} 201	Hark ₁₀ 188 Hark ₁₀ 190 Hark ₁₀ 191 Hark ₁₀ 192 Hark ₁₀ 192 Hark ₁₀ 192 Hark ₁₀ 195 Hark ₁₀ 195 Hark ₁₀ 195 Hark ₁₀ 195 Hark ₁₀ 295 Hark	Peck ₁₀ 199 Peck ₁₀ 193 Peck ₁₀ 193 ₃₄ Peck ₁₀ 195 ₃₄ Peck ₁₀ 195 ₃₄ Peck ₁₀ 295 Peck ₁	DreAA ₃₂ 193 ₀ DreAA ₃₂ 194 ₀₄ DreAA ₃₂ 194 ₀₄ DreAA ₃₂ 197 DreA ₃₂ 197 DreA ₃₂ 209 Zebrafish AA	Stepel Bas A	004Aga100 004Aga101 004Aga101 004Aga102 004Aga102 004Aga103 004Aga103 004Aga103 004Aga103 004Aga103 004Aga103 004Aga110	044A ₃₀ /189 044A ₃₀ /193 ₂₆₄ 044A ₃₀ /195 ₂₆₄ 044A ₃₀ /195 044A ₃₀ /195 044A ₄₀ /195 ₆₆ 044A ₄₀ /195 ₆₆ 044A ₄₀ /215 ₄₆₆ 044A ₄₀ /216 044A ₄₀ /216	TaiAA ₁₀ 193 ₆₆ TaiAA ₁₀ 193 ₆₆ TaiAA ₁₀ 194 ₆₆ TaiAA ₁₀ 19 ₅₆ TaiAA ₁₀ 207 TaiAA ₁₀ 207 TaiAA ₁₀ 21 TaiAA ₁₀ 216	TmAA ₁₀₁ 157 TmAA ₁₀₁ 153 ₃₆ TmAA ₁₀₁ 153 ₃₆ TmAA ₁₀₁ 59 ₃₆ TmAA ₁₀₂ 59 ₃₆ TmAA ₁₀₂ 500 TmAA ₁₀₂ 500 TmAA ₁₀₂ 500 TmAA ₁₀₂ 500 TmAA ₁₀₂ 510 TmAA ₁₀₂ 511 TmAA ₁₀₂ 511 TmAA ₁₀₂ 511 TmAA ₁₀₂ 511	Dre AB ₆₀ 195	Modala AB	TeiraBea004_ TeiraBea004_ Teirabea AB Teirabea AB Teirabea AB Teirabea AB	TruABco204cc
1922 1933 1944 1955 1966 1977 1989 2000 2010 2020 2033 2044 2055 206 2077 2088 206 2077 2088 2067 2072 2088 2072 2088 2072 2087 2087 2087 2097 2087 2097 2097 2007 2017 20	HEA ₁₀₁ 193 ₂₁ HEA ₁₀₁ 193 ₂₂ HEA ₁₀₁ 195 ₂₀ HEA ₁₀₁ 195 ₂₀ HEA ₁₀₂ 201 HEA ₁₀₂ 201 HEA ₁₀₂ 210 HEA ₁₀₂ 210 HEA ₁₀₂ 210 HEA ₁₀₂ 210 HEA ₁₀₂ 210 HEA ₁₀₂ 210	20 XirA ₁₄ 193 ₂₄ XirA ₁₄ 193 ₂₆ XirA ₁₄ 195 ₂₆ XirA ₁₄ 195 ₂₆ XirA ₁₄ 195 ₂₆ XirA ₁₄ 205 ₂₆ XirA ₁₆ 201 XirA ₁₆ 201 Xir	LmcA ₁₄ 198 LmcA ₁₄ 194 ₅₀ LmcA ₁₄ 195 ₅₀ LmcA ₁₄ 195 ₅₀ LmcA ₁₄ 195 ₅₀ LmcA ₁₄ 295 ₆₁ LmcA ₁₄ 210 ₅₀ LmcA ₁₀ 201 LmcA ₁₀ 210 ₅₀ LmcA ₁₀ 211 ₅₀ LmcA ₁₀ 211 ₅₀ LmcA ₁₀ 211 ₅₀	Hash _a ul 88 Hash _a ul 90 Hash _a ul 90 Hash _a ul 90 Hash _a ul 92 Hash _a ul 93 ₅₀ Hash _a ul	Peck _{MI} 199 Peck _{MI} 199 Peck _{MI} 195 _{MI} Peck _{MI} 195 _{MI} Peck _{MI} 195 _{MI} Peck _{MI} 195 _{MI} Peck _{MI} 295 _{MI} Peck _{MI} 295 _{MI} Peck _{MI} 205 Peck _{MI} 205 Peck _{MI} 205 Peck _{MI} 205 Peck _{MI} 205 Peck _{MI} 201 Peck _{MI} 201 Peck _{MI} 201 Peck _{MI} 201 Peck _{MI} 211 Peck _{MI} 214 Peck _{MI}	DecAd ₁₀ 193_ DecAd ₁₀ 193_ DecAd ₁₀ 194 ₂₀₄ DecAd ₁₀ 197 DecAd ₁₀ 199 ₂₀₄ Zelvzifish AA DecAd ₁₀ 216 DecAd ₁₀ 216	Styleiderek	004Aga100 004Aga100 004Aga102 004Aga102 004Aga102 004Aga103 004Aga103 004Aga103 004Aga103 004Aga103 004Aga104 004Aga114	04AA ₃₄ 189 04AA ₃₄ 193 ₂₆₄ 04AA ₃₄ 193 ₂₆₄ 04AA ₃₄ 193 ₄₆ 04AA ₃₄ 195 04AA ₃₄ 195 04AA ₃₄ 195 04AA ₃₄ 195 04AA ₃₄ 216 04AA ₄₆ 216 04AA ₄₆ 278	TaiAA ₂₀ 193 ₂₆ TaiAA ₂₀ 194 ₂₆₄ TaiAA ₂₀ 194 ₂₆₄ TaiAA ₂₀ 194 ₂₆₄ TaiAA ₂₀ 204 ₂₆₄ TaiAA ₂₀ 201 ₂₆₄ TaiAA ₂₀ 201 ₂₆₄ TaiAA ₂₀ 211 ₂₆₄ TaiAA ₂₀ 216 TaiAA ₂₀ 216	TmAA ₁₀₂ 157 TmAA ₁₀₂ 153 ₂₆₁ TmAA ₁₀₂ 153 ₂₆₁ TmAA ₁₀₂ 159 ₂₆₁ TmAA ₁₀₂ 159 ₂₆₁ TmAA ₁₀₂ 216 ₂₆₂ TmAA ₁₀₂ 216	Dec AB ₀₀ 204 ₆₄ Dec AB ₀₀ 21 Dec AB	OlaAB ₀₀ 204 ₀	TrisAB ₀₀ 204g TrisAB ₀₀ 205 Tetraoden AB TrisAB ₀₀ 205	TaxAB ₀₀ 208 TaxAB ₀₀ 208 TaxAB ₀₀ 208
1922 1933 1955 1966 1977 1988 1999 2000 2010 2022 2033 2044 2055 2066 2077 2088 2099 2010 2022 2033 2045 2055 2066 2072 2085 2095 2017 20 20 20 20 20 20 20 20 20 20	HEA ₁₂₁ 93, ₂₁ HEA ₁₂₁ 93, ₂₆ HEA ₁₂₁ 93, ₂₆ HEA ₁₂₁ 93, ₂₆ HEA ₁₂₁ 93, ₂₆ HEA ₁₂₂ 93, ₂₆ HEA ₁₂₂ 210, HEA ₂₂₂ 210, HEA ₂₂₂ 210, HEA ₂₂₂ 210, HEA ₂₂₂ 210, HEA ₂₂₂ 210, HEA ₂₂₂ 219, HEA ₂₂₂ 219	SarrAng 193, a XirAng 193, a XirAng 194, and XirAng 194, and XirAng 291, and XirAng 201, and XirAng 201, and YirAng 201, and YirAng 21 Inac	LmcA ₁₀₂ 188 LmcA ₁₀₂ 194 ₅₀₀ LmcA ₁₀₂ 194 ₅₀₀ LmcA ₁₀₂ 195 ₆₀ LmcA ₁₀₂ 201 LmcA ₁₀₂ 210 ₆₀ Crobusth A LmcA ₁₀₂ 210 ₆₀ LmcA ₁₀₂ 219	Hark ₁₄ 188 Hark ₁₄ 190 Hark ₁₄ 190 Hark ₁₄ 192 Hark ₁₄ 192 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 2195 Hark ₁₄ 218 Hark	Peck ₁₀ 199 Peck ₁₀ 193 Peck ₁₀ 195 ₃₀ Peck ₁₀ 195 ₃₀ Peck ₁₀ 195 ₄₀ Peck ₁₀ 195 ₄₀ Peck ₁₀ 195 ₄₀ Peck ₁₀ 205 Peck ₁₀ 205 Peck ₁₀ 205 Peck ₁₀ 205 Peck ₁₀ 205 Peck ₁₀ 205 Peck ₁₀ 210 Peck ₁₀ 211 Peck ₁₀ 211 Peck ₁₀ 211 Peck ₁₀ 211 Peck ₁₀ 214	DreAA ₁₀ 193 ₀ DreAA ₁₀ 194 ₀₀ DreAA ₁₀ 194 ₀₀ DreAA ₁₀ 197 DreAA ₁₀ 299 Zebrafish AA	Supel Bas A	OniAya100 OniAya101 OniAya102 OniAya103 OniAya103 OniAya104 OniAya105 OniAya104 OniAya105 OniAya104 OniAya105 OniAya105 OniAya104 OniAya105 OniAya201	044A ₃₀ /39 044A ₃₀ /39 044A ₃₀ /39 044A ₃₀ /39 044A ₃₀ /39 044A ₃₀ /39 044A ₄₀ /39 ₅₀ 044A ₄₀ /39 ₅₀ 044A ₄₀ /39 ₅₀ 044A ₄₀ /31 ₆₀ 044A ₄₀ /31 ₆₀ 044A ₄₀ /31 044A ₄₀ /31 044A ₄₀ /31 044A ₄₀ /31 044A ₄₀ /31 044A ₄₀ /31 044A ₄₀ /31	TaiAA ₂₀ 193 ₂₆ TaiAA ₂₀ 193 ₂₆ TaiAA ₂₀ 19 ₅₆ TaiAA ₂₀ 29 ₅₆ TaiAA ₂₀ 207 TaiAA ₂₀ 217 TaiAA ₂₀ 216 TaiAA ₂₀ 216	TmAA ₁₀ 197 TmAA ₁₀ 193 ₃₆ TmAA ₁₀ 193 ₃₆ TmAA ₁₀ 19 ₃₆₇ TmAA ₁₀ 19 ₃₆₇ TmAA ₁₀ 29 ₃₆₇ TmAA ₁₀ 200 TmAA ₁₀ 200 TmAA ₁₀ 211 TmAA ₁₀ 211	Dre AB ₆₀ 195	Medula AB	TaiABo204_ TaiABo204_ TaiABo2206	TauABoo204ac
1922 1933 1955 1966 1977 1988 1999 2000 2011 2022 2033 204 2055 2066 2077 2022 2033 2046 2072 2032 2046 2072 2032 2046 2072 2032 2046 2072 2032 2046 2072 2032 2046 2072 2032 2046 2072 2	HEA ₁₀₁ 93, ₄ HEA ₁₀₁ 93, ₆ HEA ₁₀₁ 95, ₆ HEA ₁₀₁ 95, ₆ HEA ₁₀₂ 99, ₈₀₁ HEA ₁₀₂ 201 HEA ₁₀₂ 210, HEA ₁₀₂	20 XirA ₁₄ 193 ₂ XirA ₁₄ 193 ₂ XirA ₁₄ 195 ₂ XirA ₁₄ 195 ₂ XirA ₁₄ 195 ₂ XirA ₁₄ 195 ₂ XirA ₁₄ 201 XirA ₁₆ 201 XirA ₁₆ 201 XirA ₁₆ 210 ₂ XirA ₁₆ 210 ₂ XirA ₁₆ 210 ₂ XirA ₁₆ 210 ₂	LmcA ₁₄₁ 188 LmcA ₁₄₁ 194 ₅₀₀ LmcA ₁₄₁ 195 ₅₀ LmcA ₁₄₁ 195 ₅₀ LmcA ₁₄₁ 195 ₅₀ LmcA ₁₄₁ 210 ₅₀ LmcA ₁₄₀ 210 ₅₀ LmcA ₁₀₀ 211 _{6.04} LmcA ₁₀₀ 211 _{6.04}	Hash _a ul 88 Hash _a ul 90 Hash _a ul 90 Hash _a ul 90 Hash _a ul 92 Hash _a ul 93 ₅₀ Hash _a ul 93 ₅₀	Peck _M 199 Peck _M 199 Peck _M 195 _M Peck _M 195 _M Peck _M 195 Peck _M 199 _M Peck _M 295 Peck _M 295 Peck _M 295 Peck _M 205 Peck _M 20	DecAA ₁₀ 193_ DecAA ₁₀ 194 ₀₋₀ DecAA ₁₀ 194 ₀₋₀ DecAA ₁₀ 197 DecAA ₁₀ 197 DecAa ₁₀ 207 Zetrafish AA	StyleiderA	004Aga100 004Aga120 004Aga122 004Aga122 004Aga123	004A ₃₀ (39 004A ₃₀ (35 _{Aut}) 004A ₃₀ (35 _{Aut}) 004A ₃₀ (36 004A ₃₀ (36 004A ₃₀ (36 004A ₃₀ (37) 004A ₃₀ (3	TaiAA ₂₀ 193 ₂₆ TaiAA ₂₀ 195 ₂₆ TaiAA ₂₀ 195 ₂₆ TaiAA ₂₀ 195 ₂₆ TaiAA ₂₀ 29 TaiAA ₂₀ 217 TaiAA ₂₀ 216 TaiAA ₂₀ 219	TmAA ₁₀ 197 TmAA ₁₀ 193 ₆₆ TmAA ₁₀ 193 ₆₆ TmAA ₁₀ 193 ₆₆ TmAA ₁₀ 193 ₆₆ TmAA ₁₀ 200 TmAA ₁₀ 201 ₆₆	Dec AB ₀₀ 205 ₄₄	OlaAB ₀₀ 204 ₀	TmAR ₀₂ 204 ₂₂ TmAR ₀₂ 205	Tau Aligo 208 Tau Aligo 208 Tau Aligo 208 Tau Aligo 208
1922 1933 1955 1966 1977 2010 2010 2010 2020 2030 2044 2055 2060 2077 2088 2090 2020	HEA ₁₀ 193, _d HEA ₁₀ 193, _d HEA ₁₀ 198, _{b0} HEA ₁₀ 198, _{b0} HEA ₁₀ 200 HEA ₁₀ 200 HEA ₁₀ 200 HEA ₁₀ 210, HEA ₁₀ 210, HEA ₁₀ 215 HEA ₁₀ 219	SarrAyal 93, a XirAyal 94, a XirAyal 94, a XirAyal 99, a XirAyal 99, a XirAya 90, a	LmcA ₁₀ 198 LmcA ₁₀ 194 ₅₀₀ LmcA ₁₀ 195 ₅₀ LmcA ₁₀ 195 ₅₀ LmcA ₁₀ 295 ₆₀ LmcA ₁₀ 201 LmcA ₁₀ 201 LmcA ₁₀ 210 ₂₀ LmcA ₁₀ 219 LmcA ₁₀ 219	Hark ₁₄ 188 Hark ₁₄ 190 Hark ₁₄ 190 Hark ₁₄ 192 Hark ₁₄ 192 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 195 Hark ₁₄ 295 Hark ₁₄ 295 Hark ₁₄ 295 Hark ₁₄ 201 Hark ₁₄ 20 Hark ₁₄ 20 Hark ₁₄ 201 Hark ₁₄ 20 Hark ₁₄ 20 H	Perkyu199 Perkyu193 _{bat} Perkyu193 _{bat} Perkyu193 _{bat} Perkyu195 _{bat} Perkyu195 _{bat} Perkyu195 _{bat} Perkyu195 _{ba}	DerAA ₁₀ 193 ₀ DerAA ₁₀ 194 ₀₄ DerAA ₁₀ 194 ₀₄ DerAA ₁₀ 197 DerAA ₁₀ 299 Zehrlich AA		000443100 000443010 000443012 000443012 000443012 000443012 000443012 00044301 000044301 000044301 000045000000000000000000000	044A ₃₀ /39 044A ₃₀ /39 ₂₆₁ 044A ₃₀ /39 ₂₆₁ 044A ₃₀ /39 044A ₃₀ /39 044A ₄₀ /39 ₅₀ 044A ₄₀ /39 ₅₀ 044A ₄₀ /39 ₅₀ 044A ₄₀ /39 ₄₀ 044A ₄₀ /31 ₄₀₀ 044A ₄₀ /31 ₄₀₀ 044A ₄₀ /31 ₄₀₀ 044A ₄₀ /31 044A ₄₀ /31 044	TaiAA ₁₀ 193 ₂₆ TaiAA ₁₀ 193 ₂₆ TaiAA ₁₀ 194 ₂₆ TaiAA ₁₀ 294 ₂₆ TaiAA ₁₀ 294 ₂₆ TaiAA ₁₀ 294 ₂₆ TaiAA ₁₀ 207 TaiAA ₁₀ 211 ₂₀₀₇ TaiAA ₁₀ 211 ₂₀₀₇ TaiAA ₁₀ 211 TaiAA ₁₀ 211 TaiAA ₁₀ 219 TaiAA ₁₀ 219	ТанАл ₁₀ 197 ТанАл ₁₀ 193 ₆₆ ТанАл ₁₀ 193 ₆₆ ТанАл ₁₀ 19 ₆₆ ТанАл ₁₀ 29 ₆₆ ТанАл ₁₀ 204 ₆₆ ТанАл ₁₀ 204 ₆₆ ТанАл ₁₀ 214 ТанАл ₁₀ 214 ТанАл ₁₀ 216	Dre AB ₀₀ 195		Teradon AB Teradon AB Teradon AB Teradon AB Teradon AB Teradon AB Teradon AB Teradon AB Teradon AB Teradon AB	TruABc.204

PFC	Dist. To 3' gene	Length Sequence	CTA		
HfrA _{AC} 24	9,775	54 TITAAACACAT			
HfrA _{AC} 25	9,493	13 CATCTAGTGGGAA			
$HfrA_{AC}30_{ab}$	3,064	34 GGCTAGACTGCAACTTTCAACTTGACCTTGGCCT			
		CTTTGCATATCATGTGATCATCTCGCAGCCAATGAGGAGGG GTTTCAGCGACACTGGCGCGTCAATGCTGCTAAGTCTGAG	CAA AGA		
115-4 04		CTCAGTATCTCTTTTCAGTCTTAGGGGGCTTTTAAAACGGCC	ACT		
HITA _{AC} 31 _{abodf}	150	141 ADICICAATO			
HfrA _{CE} 43 _a	10,846	44 TTAAACCTTGACCTTGACGAAAACTGATAGTCTTTGACCTT	GAC		
HfrA _{CE} 52	8,880	24 GATTAACCTGGTTTATTGTAAAAA			
		TGTCAATTTCTCCAGGCATCTGGTCACATGACTGGCTTGTC	CCT		
HfrA 60	101	GCGATGTATGGAGATACATTTCCACGTCAGCTTACGTTTCC	AAA		
CEOUad	191				
HfrA _{EF} 62	9,010	40 TIGAACTICIGITGCGCCATGGACGTCACCTCTAACCTTG			
HfrA _{EF} 73	1,534	20 GGGAGGGTGTGGGGGGGGGGGGG A TTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	TC A		
		TACTCAGCGTGTTTGCACAAGAAATGTCAGCCTGAACTGG.	ATAT		
HfrA _{EF} 75 _{bce}	337	105 CTTCTGCTTTCGCCAAA			
		ATCTATITAAATATTACCTAGACGGTCGTAATTTGTCTGGG	CTAT		
		ATAGCAATGGTGCTGTAACGTTTGTCGGCTTTTGTTGAGTT GACTTGCTAGTATATCTGGGTTGTTGCTGTCTTGGACGAGT	TAT GGTT		
$HfrA_{FG}78_{abc}$	6,925	170 TCAGTTGAGCGAACAGCCACGAAGACAGAGGAAGC			
HfrAre 79	5 761	AGGTAGTTTCATGTTGTTGGGGGCTCAAGTCTATCTCTACAA 54 GAAACTGCCT	CAC		
in the obc	0,701				
HfrA _{FG} 91	416	TTTTATGTGAAGGTTAACGGTTTTAAGGTGTTCGTTAAAAA 79 CGAGCATCTGATGGGAAGATTGATTATGATATAAAA	AAA		
		CATA A A A CATA CCC A CTTCC TATATA A A ATTATCTC TAT.			
		AGATTGACTCTGTTACAAGCTGCGGATTGATTTATATTTTA	TIGT		
		TGTTTTTTGAATCACGTGAGTAACTTAGCCAATGGCATGGA GCTTCTGCACCATATTAGTAGACTGTACTTGTCGCGGGGGGG	AGT AAG		
$HfrA_{FG}92_{acdef}$	237	203 TIGITACATIGAAATCIGCTCTITCAT			
HfrA _{GI} 97	6,493	23 TACCTCGCGTCATATTGACCAAA			
HfrA _{GI} 98 _b	5,339	37 ATAAAAGAAAATGACTGCTGTAAGCGTTTATGGGGTG	ree		
		GAGACTTGCAATAAAATGAAGGGTCTGGCAAGCCGTCTGC	TAT		
HfrA _{GI} 103 _{ac}	5,105	99 TCAGGTTTTAATG			
		CACCTGTGATGTGGAATGCTATTGGGGGACGGGATCACAT	GGT		ATGTTCTAGTTCACAGTATGTATGCCTGGATACCACGGTGTAGC
		CGGGTCACGTGAATAGAAATAAGTCGGACTGAAGGAAAA GTGTTTGGTGTAAATCGGGGGGTGTAATGCTGCCATATATCA	IGG		TGTGCTGCTTTGTTCAATTTTCCTGTCGTTAATAAATCACCATCT CTTACATGCGCAGGGCTGAGAGGCAACTGTAGGCAGCAGCGTT
HfrA _{GI} 111 _{ab}	184	171 TATCTCGTAAAAACCGACACTGAAGAGCCTTGGCCAACAAA	TC	12 007	TGGAAATAAAGAGGCATAAGCTAAATTCCTCTATGATTCATTA
		A TOCOCTOTA COA COTOCOTA A TA OTO A TOCOCO A A A T	TITALM167	12,281	18 CAAGAGCAACACAAATAC
		ATAAATCCGTTGTTGTTGTTATGAAAATTTACAACTTTGCAA	TAG	12,201	
		AACTITACGAGTIGTICGGTITTICCATIGGCCGCTGAAAG GTGGAGTGTAACCGTGAACATGAACTITTTATAATTICCCT	ICAT IGC		AATTCCATGCATCACTCAATTGGCAGAAAACGTGTAAGCACAC ATTTCGCATGAGGGTCCCTATAGACACGATTTACGATTCCACTG
$HfrA_{IJ}119_{abcd}$	5,493	187 GACTATAGAGC			GAAAAAAATCACAATCATTACATCGCTGTCAAGTACACTCCT CACCCTGTGCTATACTCACTAAAATCACCTAAGCTTTCTATGAC
HfrAu124	3 635	TTCCCCACAATTAGTTATTGGATCCTGATTGATCGTTAGTA. 46 AG	AAT	0.440	ACTGCTTTGCCTTTGTCAGGTAATTATAAACCTTTTCTGGGTTCA
	0,000		HITA _{LM} 177	8,118	AAATAAAAGGATTTAAGTTGACGTATGACCACGTGAGCACATA
		GATCAGCTGGTTATATTTGCTGCTGTCGCTTTGGCGCTCGG CCTGAAACAAACCACCTCGATGACTACTAATAGCTAAAC	CAT HfrA _{LM} 179 _{abc}	7,472	70 ATACAGCGCATTATTGTGGCATTTGGA
HfrA _{IJ} 130 _{ab}	136	111 TIGTGTACTAATACATAACAAAAT			ATGGATTITATTITGAGGTATTICAAATACTICCGTTGATIGTIC
		TGCCCCCAAGGACAACCCAAAGCTACTACAGGAGCCG	HITA _{LM} 181 _{bcde}	7,253	85 ATTAATATGGGGGGGTTATGCTGTGCAGGGAAAGGTCAG ATATAAAATTGCACCCACCAGTGAGTCCTGCTCAGCAAAGGTC
		GCGCGCCCCGTGCGCGTGCCCCACGTTCTTCCTTCCACG	CAAC HfrA _{LM} 180	6,306	68 AGGGTGTTGCGATTTGATTTATGTT
		TTTCCAATTTGTATCACAGTGCACGGATTTACCTCTAGAGG TCAGCGAGAATTTACGACTGGACAACAAAAGCACGTGAT	TCA		GTCCAGACTTGGTGCAAATTTGACAAGGCTAAAACAGACATAA
Life 122	204	AGTCGTACCCCATATTTGGGCGCCTACGTAGGAGGGAACG	_{AAG} HfrA _{LM} 185	5,757	95 ATAATA GCAATA AGCGATA GGAGCA AGTGTTTTCTCTTTAGTCCTCTGTT
HIIA _{JK} 132 _{ac}	324	297 IACATOICCCAOICATTICCATAATICATCATAATIO	116-1 100		TACAGCCTTAGTGCATGCATGCATGAAGTCATAAATCTTACGTAGCCATAA
		AAACTTTTATACACCTCAGTTCCGGCTTTATGACATTTGGG	IGC	4,340	110 ACGACAGAAGCATIGGTATGCAT
		CATAGCACAGACTGATAGCCTCACTGGCTATAAAAAAC	CGT Hfra 193	2 664	AATATTCATAAGAAACATACCCCATTTCTTTGGTATTAGATAAG 76 AGCAGCCAGGAAAGCTGATAGCAGTCTTATCT
HfrA., 136	10 279	GGTGTCATTAAAGTAAGTTTTATGGTTTTGGGGAGTTGACA 210 AACAGTATATTCTACATAAACATATAATCTCACTGA	ACC	5,004	GAGTTTATGTCCCAGTGATTTATGACCATATGACTTAAATGTCG
HfrA _{kl} 138 _b	9.028	12 AACTITATGGCC	HfrA _{LM} 194 _{bde}	3,295	GTTCAAGAAGAGTTCACATGCTATAGCTTCCTTTCACATCGTGA 95 CTGATAC
NL		ATCTGCACACTCTGCGACTCACCAGCAGAGCTCGCTTTAG	ACC		
HTFA _{KL} 140 _{cde}	5,906	49 AAGTIC			CTATTATCGTTCGGTTGGAAGAAAAGTTCACACCGTGGTCATAA
		AGGTCAAAAAGTTGAGGGTCAAAAGTTTACGTTTTGCACG	ACTT HfrALM198 _{shc}	1,285	AGAAGAACGCCAGTTTTTCAGGTTCCTGGTGCTTTCCGATCCAT 153 CATGCTTTTAGCAGGTAGAATT
		GTAATCATCTGCTCAGACAGAGTTTGATGTCAATGTTATAG GATCTTGACTATCAGCACAAAAGATAAAATAGCTTTGAGT	CGC TACT		
$HfrA_{KL}143_{abc}$	5,397	162 CGTGTATCATACTATGGACTCCAGGTGAAC			AATATTGCTGCACACTTTTTATGGCTTTTCATGTCAGTTGCTATT GAGAGTAAGATGGATTTGTACCATTTCGCCATTATGGTTTTGTTT
HfrA _{KL} 147	4,073	21 GGATCAATAAATAAAAAAAAAA			CTTGTAACCCCAGGTCTACCCGAAGAGGCCATTGGAAGAAAAG AGTCACGTGACACAGGGCGCCAATGTTATTCTATAAGGGTGTC
HfrA _{KL} 148	3,281	14 AATTAATTICAAAT	HfrA _{LM} 199 _{abcd}	219	213 AAGACCCTGTCAGTTTGCGAAATAAATATTGGGAAAC
		CTTTTAGAAATGGCTAAGTCCAAGGCCGAGGTGAAATTCA	GGT		
		CACCGCGTCTAACAAATATGAAAATGTCGCCTCACGAATG CGCCTTGTTACTTAACAAAGACTGTCAATGTATAAGATTAA	GCA ATAA		AACAGGGTATATGAACAAATTTTCTAAAAATTACTTAAACGTG AATTTGTTCGTGCTTTATTTTTCCTTGCGAGGAACAGTAAAATGG
$HfrA_{KL}149_{abc}$	2,989	153 GAAACAAAACGCACACGGTGTCA			TITATATTIGCACTTCTITACATTGAATGGTTAAACAAGATCAAA GCGCTTTTACAGGGTCTCCCTGGGCAAATAAGAGTTCTTGTCCA
		TTTGATATCAGCTCTTAAAACATACACGTTTTGGAAATGTC	GTA LIKA OOA		TCTTTCAGTATGTGTGTGTGTGTGTGGTGAACATTCAAATTTATTT
		AAAAGCGCTATCTTTGCCCTTCGCTTTAAAATGGCTGTAAA	TCT	4,347	288 HIGCLEHIGCAAAGGAGAAAAAAGGACCCAGTTCTGCCCC
HfrA _{KL} 152	2,336	163 CACTTGGGGGTCCTGGCTCCATCTCTGTTTAT	HfrA _{MN} 202	3,536	53 ACGCAAGAAA
116-0 455	4.450	AGAAGGCATATTGCATATGACTACTTTGAAGAAATAACGT	GCA		GTGTCAAAACTTTGAAGATTAATGGATTACTTTGTTAATGACTC
I IIIA _{KL} 155	1,459	GGAGGGTTTTATGGAACAGAAAAACGACAACGCGAGAAA	HITA _{MN} 210 _b AAT	559	78 LAGGCGTUAGATTTAGGTGCAAGATGATTTGTGA GAGGCGTTTCTCTCCGACTTTTTGGATCAATCACATGACAGTG
$HfrA_{KL}157_{bc}$	66	66 TAGTATTTTGCACTTCAGAAATTA			CCTTCTTTTGATTAAACCCCAAATTGCATCGGCAGACGAAT
		GAATCATTAATCACCTCATTCAATAAATACTTCTTTGTATA	CTTC		ATTICAATAGUTAATAGUTAATTICAACCTIGICUCAATGA ATTICAATAGUTAATAGUAGGACGGUCCCATACGGCUGTAATC
HfrA _{LM} 161	15,251	79 AACAGCAAGTCTGAAGGGCGTTCTTTTGGAAAAGT	HfrA _{MN} 211 _{bcdef}	279	178 AG
		GATAAAGGGTCACGCGTCTCCTCTGTGTATGTATTGAAATT	TTA	4,290	AATAAAATTGAGCAGTCTGGTCAGTCTCGTTCTTTACTTTTTCA
	10	ATCTCCCTAGTCACGTGACTCATTAAATAATTAATGCAGC	GGT HfrA _{NO} 218	3,924	59 TATCAGCATTTATT
100 ULV	13,538	124 COMMINISTIATORACICOLAGIATICOCACIAG	1111A _{NO} ∠19	∠,804	01 CICAIAAAICAAAICCCIIIIAIGAAIGAGA

Heterodontus francisci horn shark Hox A

23 047	TCTCTGTAATAATAAAACAGTACCTTGTAATTGATCCCAACTAA GATATAATTAATCCTTATTGGAGGGAAAACAATCCTACTGGGTT TAATTAATGTTTTATTGATTTTTAGTAGACTTAAGGTATGGTGAT 147 CCAAATTATGGAA			
15 204	20 CAGGTACATGTATGGACTCC			
13,284	24 TGTAAACACTTCTGAGCTTTTAAT			
12,711	44 TAGTTTTTGCCACTGATGTTTAAAAATTTCATTTTCACTTTCTA			
1,773	35 TGGCTAGACTGCAGCTTTCAACTTGAACTTGGCCT			
10,652	CTGCTCAGGTAAATTATACATATAACTATCTACATTCTACATTCTACATAC 49 ATTTT			
10,217	ТАПТААААТПОСАБТААТСНОГИСАПТИТАПТСОВОТВААТ СБАЛАААСАБССАБТСБАГСТАБСАПТИТААТСААААТБА ТАПТБААСАААТСАЯТТАПТИССТБОСТИАТСАСТААААТБ GTATCHTGTAAATAATTAATTAATGAGCACCGTGACGTGTTTTG 205 ГОСАСААТТААТТСАТИТИТТАСТАА			
0.660	TTAAACCTTGACCTTGACGAAAAGACACAATTTTTGACCTTGAC ACTGTCAACTCAAGTATAGGGCATCATTTCTATTAATGGAGGAA OO TATCGCCACCT			
2,671	AGAATTTGTTTTCCTTACCAGAGGCGGGGGGGGGGGGGG			
175	TGTCAATTTCCCCGGTGTGATCACATGACCAGCACCTCCCTOCTA AGGATGGGGATGGATTTCCACGTCAGCTACGTCTTTCCAATTC TACTTCACGGATCTGCTTCAAAGAGGCAGCTGCATTAGGGAT 169 GATGTTAAGCTCAGCTAATCCGGACAGCCCGAGGTAGC			
	GGGAGGGGTTGCTGGGAGCTAGCGAGCTTCCATTGGCTGCGTG CATTTGCCGTGGTGCAGGGGTATCTCTAATCATATTCAGCATGT TTTGCACAAGAAATGTCAGCCAGAAAGGAATATCTGCTCTCTTC			
150	137 GCCAAA GACAAGCACCCGCAAGCTCCACTCTTTCCTTGTCTCTTTAAAT			
5,446	67 СТААТСТІТТІСССТААТСТІТТТ			
	ATACIATITAAATATTACCTAGACAGICGIAATTIGICIGGGCCTT ATAGCAATGGAGCTGGAAGGGTGATCGGCTTITGTGTAGTTTTA TGACTTGCTCGCATATCGCTTTGCTTGCAACCCAGGGGG			
4,600	AGGTAGTITTATGTTGTTGGGCATTCACCTTTCTCTCTACAACAA			
4,255	55 GAAACTGCCT			
	CATAAAAACATATGGCTCTGCTATAAAAATGATGACTGCAAA ACAGTGACCCATTAATAGCCTGCGGACTGATTTATACCTTATTG TTCTGCTGCACGTCACATGGCCCGGGACTGAT AGGCTGCCTTCAACTTATTAGGTGACTGTACTTCTTTGTAGGAC			
230	204 CAAGTIGITACATGAAATCIGCAGTITICAT			
4,224	Z3 IACTICAIGGCUAAIGACCAAA			
3,038	ACGCCCTCTGTTGTTCCAGACAGAAAGAGACTTCAAAGAATGG GCACTAAAAGTGTGTAATAAATGGCTGGCTGCAAACTGTCTG 129 GAATICGCTCCTTAATGATTTTATGGCTGTCCTGCAGCAATTA	$\rm XtrA_{\rm KL}157_{\rm bc}$	74	GGAGGGTTCTGTGCAGAACAGAAAAACGACAACGGCGAGAAAA 74 ATTAGTATTITTGTGCACTTGCACAAATTA TGCCCTTTGCTAAGGCAACCAGGGTTCACAGGAGGAGGACACGTT TGCCCTTGCCAATGCATGCTTTTTTCTGGAAAGAGGCAACGTT
2,004	12 TIGAAATTITAT	XtrA _{IM} 163	13,031	106 TCAAACCCTTGACCTTTA
1,237	33 GTTTATGGTGTGCAATATACTGGGGTTGTAAAA	XtrA _{LM} 174	7,764	17 CAGTGTAAATCTGGTGA
	CACCTGTACGGTGCAATCAGATTGGACGGGGCGGTCAGATGGT GGCAGATCACGTGGCCCAGGCAGCCAGCCAGTGCAAAGGAA AAGATGGGGTTTTGTGTAAATGTGGGGGTTAGTGCTGCCATAT ATCACTGCCGCCTCGTAAAACCGACACCGGAGCTACCGGAC	XtrA _{LM} 179 _{ac}	6,224	AAATAAAAGGATTTAAGTTGACGTAGGACCACGTGAGCCCATA 70 ACACAACGCATTATTGTTGTATTTGGA ATGGATTATATTTTAAGGTATATCCGTTGATTGTTCCTAAAAGG
193	179 ACAAATC	XtrA _{LM} 181 _{bcde}	6,016	76 GGTGAGTTATTGCTGTGCACGTCAGAGGTCAG
5,451	28 CATAATATATTTTTTTGTTAAACATAAT			GCAATAAGCAGTAAGTAGCAAATGTGTCCTGTTTTAATGCAAC
	ATGGCGGCTAGGAAGGACCTGCCTCCTGTAAGTGATGAGGCAA TGGCTATAAATCCGTTGTTGTTATGAAAATTTACAACTTTGCA ATACAAGTTTATGAGTTGCTGGGATATTCCATTGGCCGCGCTGTG	XtrA _{LM} 188	4,053	GTTTACAGCATTCGTACATAGGGCTATAAATCTTTCCTAGCCAT 113 AAATGACAAAACCCATTGGTATGCAT
5 000	GTCATGTGAATGGGAACCGAGAACATGAAGTTTTTTATCATTCC 102 CCCTGCGAGGATAGAGC	XtrA 193.	3.035	AATATTTGTAAGAAACATACCCATGTTGTGTGTGGACTACACT 76 TGGAAAGCCCTGTGAGTTGATAGCTCTTATCT
5,009	192 ссетасалаалианае	Man LM roocd	0,000	TCGTCAGAAACTAAGGTAAGCAGGCCAGAAATCTTCTATCACT
4,612	CCTGGCTCATTTCCTGCTCTTCCTGGCACCAAACCGGGCTCTAT 77 ACTTCTCTATGCAACCAGCCACAAGCTGTCAG GATCAGCTGCTCAGATTTGCCTCTGTCGCTTTTGGCTCCCGGCCA	XtrA _{LM} 194 _{bode}	2,715	TCTCAATGGTGGAGTTTATGTCCCAATGATTTATGGCCATAGTCT TAAATCTCGGTTCAAGCAGAGTTCACAAGCTCAAGCTTCCTTTC 148 AAGAAGTGACTGATAC
104	TCCAGAAACAAACCAGTTGGATGAGTGCTAATAGTTATAGGCA			TGACCCCCATACATCAAACGACAGAGCAGTTGCAAAGACAGA
134				ACCTATTATCGTTGGGACTGCACAGAAAGTTCATGCCGTGGTCA
	TGGCGCAAGAGGCTGCTCAAAAGCTTCCAGCTCTACACGGGGC CGCGCACAAACGCTCGCTCCCTTAGCAGCCTCCCTGCTCCCCC ACTAGTACACCCAGTTTACCTCTAGAGGTCATCAGCCGGGATTTA CGACTGGCAGACAA AGCACCTGGTTCCAAGTCGAGGCATTG	$\rm XtrA_{LM}198_{ac}$	1,474	155 CATCATGTTTAACAGGTAGAATT AATATIGCTGAAGACTTTTTCCTTTCTGGCTTTCATGTCACTTAG
207	TTTGGGTGCCTACGTAGGAGGGAACCAAGTACATGTCCCAGTC			CCATTGTAAGTAAGATGGATTTGTCCTACTTCTTCACTGTACTGT GCTTCTCATCCACCACAGGTCTGACCAGCGAGGCCATTGGAGG
307	207 AITICCATAATICATCATAAATIOIOCAAOOOTOCIATA	XtrA199	225	AGGAACGCCACGTGACAGAGGGGGGGCCAATGTTATTCTTTACG 210 GGTGTCAAGACCCTGTCAGTTTGTGAAATAAATATTGGGAAAC
	AAACTITIATAAGCTCTAGTTCCGGCTATGTGACATTIGCTTGCC AAATGAATAGGGTTTTGTCTATGAATTACATCGTAAAAATCCTCC ATAGCACAGACAGATAGGCTCACTGGCTATAAAAAGTCACGTG GGCTATTAAACTAAGTTTATGTTTTAGGGACTAGACGACCA		220	AACAGGGTATAGCAACAATTITTATATGGGGAACAAATTCTTCT
8,170	209 ACATTATATAGTACATATCATATAATCTCACTGA			TACATGTGAATTTGTTTGCACATTTTCTTAACCCACAGGGAACC CATTTAAATTATTATTGCACTTCTATTCAATTGCTAGCCAAATAT TAAAAAAAAAA
7,296	88 GCAGTGTGATTAGTCAGCAATGAACTTTATGGCCAGAATTAACT	XtrA _{MN} 201	4,619	308 GTTAATTATTATATTTTCATGGAAAAAAAGAAT
5,144	AAGATAAATCTGCAAACCCCAGGAATCACCAGCAGAGCTCGCT 56 TTATACCAAGTTC	XtrA204	1 800	AGAAGCTTTAAATGTGATCTTTAGGGCCAGTAGCTGTCAAGCCA TTTGGCAAGCAAGATTGATCACACGCAGACTTCCTCCCAGCTTT 92 GTTT
	AGGTCAAAAAGTTAGAGGTCAAAAGTTACTTCTCCAAGTCAT	··· win - S abod	1,000	
	CTATCAGGCAAAAGTTIGATGTCAATGTTATAGTAGAAATTTTG CCTATCAGCACAAAAGATAAAACGTGTTTGAGTTAGGCAAGCA			GIGTCAAAACTTIGAAGATTAATGGATTACTTIGTTAATGACTT AAGGCGTCAGATTITGGTCCTTAAATGATTIGTGAGGTGTAAAA
4,712	154 CCATAGACTGGACTCCTGGTGAAC	$XtrA_{MN}210_{bc}$	564	114 CGCCTTCCTGACAGACAGACAGACAATG
	CTITTAGAAAAGCTTAAGTCCAAGGGCGAGGTGAACTTCAGGT CACCGAGTCTAACAAATATGAAAATGTCGCCTGGTGAACTGCG AGGCTACTTAATTAACAAAGACTGTCAATGCGCGAAGATTAATA			GAUGEGITECTICTINACTITITTGGATCAATCACACAGACAG TGGCTTCTTTGATTAAACCCCAAATTGTCATCGGCAGGAGCA ATCATGTGACAACCAATTCGGTCCAATTTCAACCTTGTCCCAT GAATTCAATAGTTTAATAGTAGGACGACGCCCATACGCCTTTA
3,549	153 TGAAACAAAATGTGCGCAGTGTCA	XtrA _{MN} 211 _{bcdef}	303	180 ATCAG

 Xenopus tropicalis western clawed frog

 PFC
 Dist. To 3' gene
 Length
 Sequence

 XtrA_{Ac}3
 55,355
 20
 CATTATTGCCATGACAACTG

37,794

54,155 25 TTCAAAAATAAGCACCTGTTTTGAG

31 AAATGTTAAACGCATCAAGAATTGTTCTGAG

 $\rm XtrA_{AC}4$

XtrA_{AC}15

 $\begin{array}{c} XtrA_{AC}23\\ XtrA_{AC}26\\ XtrA_{AC}27\\ XtrA_{AC}28\\ XtrA_{AC}30_{ab}\\ XtrA_{CE}35 \end{array}$

XtrA_{CE}39 XtrA_{CE}43_{ab} XtrA_{CE}57_{cd}

 $\rm XtrA_{CE}60_{acde}$

XtrA_{EF}75_{abcde} XtrA_{FG}77

XtrA_{FG}78_{ac} XtrA_{FG}79_{bc}

XtrA_{FG}92_{abcdef} XtrA_{GI}97

XtrA_{GI}103_{acd} XtrA_{GI}105 XtrA_{GI}110

XtrA_{GI}111_{ab} XtrA_{IJ}118

XtrA_{IJ}119_{abcd} XtrA_{IJ}122 XtrA_{IJ}130_{ab}

XtrA_{JK}132_{ac}

XtrA_{KL}136_{abc} XtrA_{KL}138_{abc} XtrA_{KL}140_{bcde}

XtrA_{KL}143_{abc}

 $XtrA_{KL}149_{abc}$

Latimeria menado	oensis coelacanth	Hox A				
PFC	Dist. To 3' gene	Length	Sequence			
			TCTGGGAGGGATCACCATTGCCCCTTCTTTCTAAACTGTCATT CTTAATGGTGCAGTCGTCATTACAGTACCACTGGTGACGCCA			
1 mo A 2	74 500	420	CTCATTGATTGCAAGTGGATAAATAGAAACGTCTGCCACCGT			
LINEAABZ	71,523	139	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA			
			TCCTGGAACCAAAATGGCCTGTACAGTTCGCCAAACACTCG			
			CTGAGCTGCTGGAGCTGCCTGGGGACCTGCGGCTGCAGCGT CCCTGGGTCTTCCAGGATGAGAGGGGGGCGCCGCTGGGCCGC			
			CTATATGGAGAGGGTAAGTACCCAAGATGTCTGCTGTGTGTG			
LmeA _{AB} 29	25,959	245	GT			
LmeA _{BC} 30 _b	2,389	24	CAACTITCAACITGACCTTGGCCT			
LmeA _{CE} 38	14,071	24	GAATGAACCACCTTTGTGCTGAAA			
			AAGCTGAAGTTGACTGCCAAATGTGCTATAAAACCGCAGGT			
			ATTATAGCTTAAAAGCCCTAATACAAGTGCAAGAATTTGTCT			
1 mo \ 57	2 1 2 1	172	GCGTTCAAGCAGAGGCGGGGGGAAGCCTCTGTGATGGTGGCG CCTTIGT			
Efficince abcd	3,121	175	TGTCAATTTCAGCATCTGATCATGTGACATGCACCTCCCTGA			
			GATGGCTGTAGATGGATCTCCACGTCAGCTTACGTCTCCAAA			
			GAATCATGTTGAGCTCAGCTAAAGTGGAGATCCAAAGGTAG			
LmeA _{CE} 60 _{abcde}	171	168	с			
LmeA _{EF} 62	6,797	40	TIGAACTICIGGATITATACGGACATCACCTATAACCTIG			
1 mgA 60	4.500		COTACA ACA ACCACTOTOTOTO A COTO A TACATTOTTA			
LINEAEF09	4,530	0 30	ATTGGCTTTAAACTCTTGCTGTGGTATGGGGTATCTCTAATCA			
1 m a A 75		405	TATTCAGCATGTTTTGCACAAGAAATGTCAGCCAGAAAGGG			
LineA _{EF} /S _{bcde}	118	105	ATCTATUTA A ATATTACCTAGACAGTCGTA ATUTGTCTGGGC			
			CATATAGCAATGGTGCTCTAAGGTTTGTCGGCTTTTGTTCAGT			
			TITATGACTIGCTAGTATAGCTGGATTGTAGCTGTCTTGGACG AGAGGTTTCAGTTGAGTGAAGAGCTGGAAAGACAGAGGAAG			
LmeA _{FG} 78 _{abc}	4,812	170	с			
LmeA _{FO} 79 _{bo}	4.124	55	AGGTAGTTTCATGTTGTTGGGGGCTCCAAATTTATCTCTATAAC AAGAAACTGCCT			
- FG - DC	.,		GGGCGCCAGCATTCCATTGAGCCTGAATGCACAACAGCGAC			
LmeA _{FG} 85	3,504	44	CTC			
			CATAAAATAATAATAAAAAAATATGGCTTCTACATTGAAATT			
			ATGACTGCAAAACATTGACCCTCTAATAGACTGCGGACTGA			
			ACCAATTGAATGGTAGGCAGTACTGAACTTAATAGCTGACT			
LmeAcc92	247	213	CCACTTGTTCACGCGGCCAAGTTGTTACATGAAATCCGCTGT TTCAT			
LmeA _{GI} 97	7,064	23	TACCTCGTTGCCTATTGACCAAA			
			ACGCCCTCTGTTGTTGCAGATAGAAGGAACTTCAAAGACTTA GCCCAGAGACTGCAATAAATGAAGGGTCTGGCATGTTGTCT			
			GGAATTCAGCTITTAATTAGTTTACAACAGCCTAGCTTCACT			AAAGTTAAGTACTTGCTGAAGATAGCAATCACTTACAAAGG
LmeA _{GI} 103 _{ace}	5,638	207	TTCAGACAAAGGGTCCGCGGAAATAACTGTCTTTATTG			GTATTCACATGCACGAATGCACTGCACTGCACTGCACGAGTGACTT
LmeA _{GI} 110	1,514	33	GTTTATGGTGTGTAATATAGCACGGCAGTAAA			TITAAAAGTATITITTCTCTTTICATAATGACCTTTTGGACTTC AATGAGCAGCACAATATCCTTGCAAACTCTTTAAAGCAACT
			CACCTGAAATGCAAGAAGAAGATTGGGTGAAACGGTCATATG	1 mg A 160	20.805	CTTTATGATTCTAAAGAAACTATTTTATTTTCTTGTTCCTAAC
			GTATATCACGTGTATAAAACGGCTCAGACCAAAAGAAAATG GGGTTTGGTGTAAATCTGGGGTGTAATGCTATCATATATCAA	LmeA 162	20,895	254 IAC 18 CCAACTCCTGCTTTGATT
I meA111 .	191	169	GCTACCTCGTAAAACCGACACTGAAGCGTCCTGGCCAACAA ATC	LINEALMIOZ	19,007	16 centercertermann
Enterigititiab	101	100		LmeA _{LM} 184	8,692	38 TCCTTTTTTTCCTTCTTTATCGTAGTTTCCTAAAAGAT
			ATGGCGCCTCTCAAAGAACGACTCTTCACAGGGAAGAGGAA	LmeA _{LM} 179 _{abc}	6,986	70 TAATACAGGGCATTATTGTAGCATTGGA
			GTAATACAAGTTTATGAGTTGTTCAGTTTCTCCATTGGCCGCC			A TOO A THEFA THEFY A COT A THEORY A TROTTO A TEA A TOT
I meA119	4 898	190	GCTGGTCATGTGGATIGTAACCGTGAACATGAACTTTTTATA ATTTCCCTTACGAGAATAGAGC	LmeA _{LM} 181 _{bode}	6,749	76 GGTGAGTTATTGCTGTTCAAGGCAAAGGTCAG
Enter (j 110 abcd	4,000	150				
I meA122	4.510	77	CCTGGCTAATTTCCTGCTTCTCTTGGCATGCAGAGGAAAGGT TTCTTCTGAGTACAACCAACAGGACAGCTGTCAG			GCAATAIGCCGIAAGGAGCIAGIGITTICIGITTIAGIGCICI GTTTACAGCTTTGGTGCATGAAGCCATAAATCTTGCGTAGCC
LINGAUIZZ	4,510	, ,,		LmeA _{LM} 188	4,048	114 ATAAATGACAAAAATGCATTGGTATGCAT
			GATCAGCTGATTGTATTTGCTGTCGTCGCTTTTGGCGTTACGC			TCGTCAGAAACTAAGGTAAGCAGGCCAGAAATAGGCAATC
LmeA _{IJ} 130 _{ab}	135	5 110	CTAGATGTACTAATACCATTICCATGACTACTACTACTAGTATAG			AGTIGIGAATGGCGGAGTITATGTCCTAGTGATTTATAGCCA
				LmeA _{LM} 194 _{bode}	2,874	149 GCTTCCTTTCACGCAGTGACTGATAC
			TGGCGCAAAAGTATAATTCAAAACTAGAACTTTAAGGCGGG GACGCGCCACTAGTACGCGCTTCTTCCCTCCGGCATCAACCC			
			TGCCTTCTCATTTGTGCACGAGTTTACCTCCAGAGGTCATCA			TGACCCCCATACATCAAATTACAGAGCAGTTTCAGAGACAG AACCTATTATCGCTAGGTTGAGAGAAAAGTTCAAGCCGTGG
			GUAGGATTIACGACIGGACAACAAAACGCACGIGATTCAAA GTCGTACCCCATATTTGGGTGCCTACGTAGGAGGGAACCAA	1 400	4 000	TCATGGAGATGATCGCCAGTTTTTCAGGTTCCTGGTGTTTTCC
I meA132	320	203	GTACATGTCCCAGTCATTTCCATAATTCATCATAAATTGTGC AAGGGT	LmeA _{LM} 196 _{abc}	1,238	155 COARCEATERIOTTIAACAODIAOAATI
Entor (jk rozac	020	200	AATAGCTCCAAGCTGTCAGGAAATAATTTACTTTTAAACTAC			AATATTGATGGCCTTTTTTTTTTTTTTTTTTTTTTTTTT
LmeA _{KL} 133	16,559	45	СТА			AGCTATTGAGACTAAGATGGATTTGTAGTTCTATTTCTCCACT ATAGTAAGCGTCTTGTAATTCCAGGTCTAGCCGAAGAGGCC
			GTGCCTITGTATAGCTCTITGCACGAACTTCAATAAGTGTCTC			ATTGGAGGAAAGACGTCACGTGAAAGGGGGGGGCCAATGTT ATTCTATAAGGGTGTCAAGACCCTGTCAGCTTGTGAAATAAA
LmeA _{KL} 134	16,393	72	TTATAAGCGCAGCTTCAGTGATGTATGTT	LmeA _{LM} 199 _{acd}	228	222 TATTGGGAAAC
			AAACTITATTACCCCGAGTTCCGGCTATATGACATTTGGGTG			
			CCAAATGAATAGGGTTTTGCCTTTGGATAAGATCGTAAAAATC ATCCATAGCAGAGAGAGAGAGAGCTCACTCCCTTATAAAAATC			AACAGGGTATATGAACACATTTTAAAGGTTATATAAATGTG AATTTCTTCGAACTTTATTTATCCCATGAAACCAATTAATT
			CACGTGGTGCCATTAAAGTAAGTTTTATGGTTTTGGGGAGTT			ATTITATIGCACTICICTGGTITITAAATGGACAGAACAAACT GAAAGGCGCITIGAACAGGGTCCCTGGACAATTATCGATATT
LmeA _{KL} 136 _{abc}	15,637	207	GACATCCAACAGTATATGCCACATAACATATAATCACTGA			TGTACGTCTTTCATTGTGTGTGTGTGGTGGAACATTCAGATTT
LmeA _{KL} 137	15,105	13	AAGULAAAGUAAA AAGATAAATCTGCACACCCTGGGAGCCACCAGCAGAGCTCG	LmeA _{MN} 201	4.657	ATTIATTIGICUTIGCATAAATAGAATATTCTAAGTGTTTAAA 284 GT
$LmeA_{KL}140_{bcde}$	9,436	56	CTTTAGACCAAGTIC		1,007	-
$\rm LmeA_{\rm KL}143_{ab}$	8,950	27	AGGTCAGAGTTGAGGGTCAAAAGTTTA			TICTCCTGGTGTGTTGGTTCTTATGTGGCTAGGATGTGGGGGGT CTGGGTGTCAAAACTTTGAAGATTAATGGATTACTTTGTTAA
			CTTTTAGAAAAAGCTAAGTCCAAGGCCGAGGTGAATTTCAG	1 mo A 010		TGACTCAAGGCGTCAGATTTAGGTGCTTAAATGATTTGTGAG
			GTCACTATGTCTAACAAATATGAAAATGTCGCCTGCTGAAC	LINEA _{MN} Z1U _{abc}	567	101 OTOTAAAGCOTCTTCCCGACAGICAGAAACAAIG
LmeA _{KL} 149 _{abc}	3,004	151	GGCACGCCTTGTTATTAACAAAGACTGTCAATGTGTAAGAT TAATAAGAAACAAAGTGCACAGTGTCA			TGTAAATAAAGCACTGCTGGTCCAGAATGAGGCGTTCCTTCC
LmeA _{KL} 150	6,987	31	ACATTICTGAAGIGICTITCTTTTTTTTCTCA			IGACTITITITIGGATCAATCACACAGACAGTGGCTTCTTTTG ATTAAACCCCCAAATTGTCATTGGGCAGAGGCAATCATGTGA
LmeA _{KL} 156	4,887	13	TICTACATTAGCT	ImeΔ. 211	200	CAACCAATTCGGTCCAATTTCAACCTTGTCTCCATGAATTCA 200 ATAGTTTAATAGTAGCACGGTCCCCATACGGCTGTAATCAC
LmeA _{va} 157.	76	60	GGAGGGTTTTACATAGACCAGAAAAACTACAACGCGAGAA AAATTAGTATTTTTGCACTTCACAAATTA	Lme _{vo} 219	3 061	32 CTCATAAATCAAATTGCTTTTTATGAATGAGA
NL · + · DC	10	05	· · · · · · · · · · · · · · · · · · ·	- 140	5,001	

Homo sapiens human H	ox A			
PFC Dist t	o 3' gene	Length	Sequence	
			CTCCTGCTGCAATCGTCATTACAGTACCGCTGGTGACGCCACT	
HeaA 2*	40 707	120	CGGCGAGCGCAAGTGGATAAATAGAAACGTCTGCCACAGCGA AGATGAAAGG	
HsaA3	42,121	139	CATTATTACAACTG	Hao A 70
HsaA _{Ac} 4	41,245	21	TTCAAACTGACCCTTTTTGAG	HSaAFG/9bc
AC .	11,000			HsaA _{FG} 85
			TTATTGAGAAGAGATTGGAGTGGGGGTCAGGGGAGGATATGTTT	HsaA _{FG} 86
			ATCCTTTCCAAGCACTGGGCTATCCAAGGGCCAGACAAACCT	HsaA _{FG} 88
			GACCACCTTGCTCCCCTACTCCCAGTCCCCTGCCATGGGGGCA CCATCTCCACCCTCTTCCACCCCTGCACTGTAAGAGGGAACCT	HsaA _{FG} 89
HsaA _{AC} 5	36,891	227	GCCCACTGCAGC	HsaA _{FG} 90
HsaA _{AC} 6	32,134	26	TTTTGTAAAGAATTCTACAGAATGAA	
HsaA8	30.093	45	GAAAAAGAAAAATCCCATGTGCTCTGGCTCTAAGTCTTATAAC AA	HsaA _{FG} 91
HsaA _{Ac} 9	29 255	20	ATAAATAACTACAGAGCAAA	
HsaA _{AC} 10	29,122	32	TCCAGGATTTTGTGTCCTTTTTGCAAAAGACA	
HsaA _{AC} 11	28,926	20	TACTTAAATTAGACTGCTTG	
HsaA _{AC} 14	28,729	18	ACTGAAAGGAAGAGGAAT	HsaA _{FG} 92 _{abcdef} *
HsaA _{AC} 15	27,827	28	AAATGTAAGTTTCCCAAGTCTTTCTGAG	HsaA _{GI} 96
HsaA _{AC} 16	27,563	26	AATAAAACGTTTTTCTGGAGATAGAA	HsaA _{GI} 97
HsaA _{AC} 22	23,227	16	TATTATTCACTCTTTT	HsaA.,98.*
			TCTCTGGCTAATAGAAAACAGAAAGCCAAAGAATGAGCACAA GACTTCTAGGAAAAGATTTAAATGAGGCTCCAATTTTCCTAGG	Tioux (Gloop
HsaA _{AC} 23	15,760	106	CAGGCAAACCAAATCTGGAAA	
HsaA24	10 752	54	GATTAAAGTTTAATCCGAGGTGTGTGCTCAGACTTGCCATGTTA TTTAAACACAT	
HsaA25	10,752	13	CATCTAGTGGGAA	Hsa4103*
HsaA ₄₀ 26	8 804	16	CAGGTAGGAAGACTCC	HsaAq104
HsaA _{4C} 27	7,466	25	TGTAAAAGCATCCCAGATATTTAAT	HsaAgi105
HsaA _{AC} 28	7,033	35	TAGTITAATCATTAGAAATTTCTTTIGTGTTTCTA	
				HsaA _{GI} 106
			TCCTGGGTGGCACGGGCCCCTGCAGTCCAGCAAGCCGGTGTCC CCCGCGGGCTGGCCGCGCACTGCGAGAAGGCGTTTCCTCCTTC	HsaA _{GI} 107
			CAGCCGAGCCCTTCACCAAGCTCCCTCTGCTTCTAACGCATGC	HSAA _{GI} 110
HeaA 20	E 1E0	102	TCCGGTCCTTTCCGCGAAGGCTGTTTCCAGCTCCAGTGAAGAG CGATCAGTGGCACTGTCGGGG	
HsaA _{AC} 25	2 062	193	CAACTTTCAACTTGACCTTGGCCTCCAGCCG	
TIOUN (ACOODC	2,002	01	CTGCTCAGGTAAATCTTAGTGAAATTCCTACCGTTGTTGTACGT	HsaA _{GI} 111 _{ab} *
HsaA _{CE} 35	12,608	59	TCTGCAAAACATTTT	HeaA 114
HsaA _{CE} 36	12,393	26	CCGGGTCGGTAATGTCTTTTTAAGAA	HsaA _N 114
HsaA _{CE} 37	12,360	20	TAATTGCITATAACAAGCAT	HsaAu118
HsaA _{CE} 38	12,082	24	GAATGAAAATICATICCCCIGAAA	
			TATTAAGGGATTAGTATTTTTCCATGTTTATTGTGTTATCAGAGT	
			CAAGCAGTTATTTCAACCAGCACATTCGTTTTGTTCATATTCAC	Hea/ 110
Han A 20	40.007	040	TATAGAATGATATCTTGTAAATAAAGACATTCAGCACACTGTG	I San J I Sabcd
HsaA _{CE} 39	12,027	210	CATCITICACAGCACATTITITAATCAAGCAGT	11 4 400
HsaA _{ce} 40	11,901	23	ATTATTATTCAGTACTTCTTTTG	HSaA _{IJ} 122
LIGGINGE 12	11,002	20	TTAAACCTTGACCTTGACGAAAAAAAAGACAATTTGTGACCTT	HsaA,124
Han A 42	44.000	404	GACTTTTGACAGCTCATGAATTGGCCTTAGCTGGATTAGTAGAT	1130/10124
HSBACE43ab	11,330	101	CAAOOOCOCCACCI	HsaA _{IJ} 125
			ACCACAGGATTGGATACAGAACGAGAGTTATCCTGGATAACT	HsaA _{IJ} 126
HsaA _{CE} 47	10,585	80	CAGAGCIGAGIACIGCICCAGGGIGGIGIGCAAICIIA	HsaA _{IJ} 127
HSaA _{CE} 48	10,227	26		HsaA _{JJ} 129
HsaA 51	0.807	21	TGTGTGTTTAAGAACAGCTCCAA	
HsaA _{CE} 57*	9,007	23	GATTAAAGTATTTTTTTTTTTTTAAAAA	
HsaAce53	9,292	24	TTAAAACAACCTAGTTGAAATCTTTTCTTAAAAAT	
	5,007	55		
HsaA _{CE} 54	4,355	40	GCCTGTCAAGTGACGATCCTTGCAGCTCACGTCCCTTGAA	HsaA _{JK} 132 _{ac} *
			AAGCIGAAGTTGACTGCCAAAACTGCTATAAAACCGCAGGTC TGTCTAGAACTGTTTTCGGTTTTCCTAGACGCCCCCGGGTTCAA	HsaA _{k1} 133
			TTATGGTCTTAAAAGCCCTAATACAAGTGCAAGAATTTGTTTG	
HsaAcr57abod*	2.744	175	TTGT	HsaA _{KL} 134
HsaA _{CE} 59	2,045	21	GTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
			1G1CAATTTCAACATCGGGTCACATGACCAGCACCTCCCTGCT AAGGATGGGGATAGATTTCCACGTCAGCTTACGTCTCCAAATT	
			TCTACTTCACGGATCCGCTTCAAAGAGGCAGCTGCAGTGGAGA	HsaA _{KL} 136 _{ab} *
msaA _{CE} bU _{abcde} *	175	169	ATCATGTTAAGCTCGGCTACTGCGGGGGGGGGCCCAAGGTAGC	HsaA _{KL} 137
HsaA _{EF} 62	6,367	41	TTGAACTTCTGCCTTAAAATTGGACATCACCCATAACCTTG	
HsaA _{EF} 63	5,802	35	GATTTCTTAGATGTAAAAATGAGATCTCAATAGCA	HsaA _{KL} 138 _{abc}
HsaA69	1 310	47	CCTACAATGCCAGAGCCGCCTCCAGTTCTAAGGCCAGAGGCT GTTTA	HsaA _{KL} 139
HsaA _{FF} 70	3,537	16	AGAAATTTAGTAGCTG	HsaA _{KL} 140 _{bcde} *
HsaA _{EF} 71	3,041	20	TTTATTACAAGGGGGAAAAA	
	.,	20	CTCTGAAGCTTTTCTGCACTCAGGTTCGTCCGTCTCATGGGCCT	
HsaA _{EF} 72	2,150	65	AGAGGGIAGAAATTTGCCTT	Head 143 *
HsaA _{EF} /3	1,158	20	UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU	Head 145
			GTATTCAGCATGTTTTGCACAAGAAATGTCAGCCAGAAAGGGC	HsaA _w 146
HsaA _{EF} 75 _{bcde} *	119	106	TATCTGCTCCCTTCGCCAAA	HsaA _{vi} 147
HsaA _{FG} 77	5,580	70	TAAATCGCCTTGAACAAAAAGTTTTT	HsaA _{KL} 148
			ATCIATITAAATATTACCTAGACGGTCGTAATTTGTCTGGGCCC TATAGCCCTGGTGCCGTAAGGTTTGTCGGCTTTTGTTCAGTTTT	
Hao A 70 *			ATGGCTTGCTAGTATATCTGGATTGTGGCTGTCTTGGACCAGTG	HanA 140 *
risaA _{FG} /8 _{abc}	5,037	170	AT ITCAULIDAUAUUUUUUUUULIACATAUACAUAGGAAGC	risaA _{KL} 149 _{abc}

4,091	AGGTAGTTTCCTGTTGTTGGGATCCACCTTTCTCTCGACAGCAC 54 GACACTGCCT	
3 750	GGGCGCCCGCTTCCATCCTGAGCCTCCCACTGGAGGCCTGCGC	
3,758	14 CAAGGCCTCGGTTA	
0.040	ATACAGCACCTTTGTGCAGCTGGGTGCTGGAGAAGGGGACCCT	
2,843	16 GTAACTCTCTTATTTT	
1,921	28 CAGGACGGGGCCATTICGGAGTICATIG	
	TTTTATGTGAGGGGCTCCGCTGGCCGCACTCGCACGCGGGACC	
461	80 CGCGCCTTCTTGATGGCGTGATTAATTGTGATATAAAA	
	CATAAAAACATATGGCTTTTGCTATAAAAATTATGACTGCAAA	
	ACATCGGACCATTAATAGCGTGCGGAGTGATTTACGCGTTATT GTTCTGCTGGACGGGCACGTGACGCGCACGGCCAATGGGGGGC	
252	GCGGGCGCCGGCAACTTATTAGGTGACTGTACTTCCCCCCCGG 207 TGCCACCAAGTTGTTACATGAAATCTGCAGTTCAT	
6.293	16 CTATATAGTCCTGTCT	
5,974	23 TACCTCAAGGCCTACTGACCAAA	
5,246	37 ATAAAAGAAAATGAGGGCTGTTACCGTTTATGGGGTG	
	GCAGTAAGAGTGTGCCATAAAGCCGGGTCTGCGAACTGTCTG	i
	GAATICGICCCTTAAIGAGITTACAACIGICCAGCCCCAATIA GGATATICCACCAAAGCCCTTICATTIGTICATTIGTICIGTCT	
4,970	211 GCCGCCGATAAAGCGGCTGCGGAAACACCTCTTTTATTG	
3,880	18 TIGAAAGCCTGATITTAT	
2.044		
∠,014 1.896	45 CENTRETETTICENETITICE TO CONTRACT CLARGE	
1,448	33 GTTTATGGTGTGTAATCGAGCTGAGCAGTAAAA	
	CACCTIGIGAGGACTICCTGAGATTICGCGGAGGCCGTCATGTIGGG	
	CGGTCACGTGCTGCGGCGAGCCCGCCAAAGAAAATGGGG	
182	169 CCTCGTAAAACCGACACTGAAAGCTGCCGGACAACAAATC	
6 864	CAAAATACTACCTAGCACAGGCCTCTGCTCGAGGCACCCCCA 52 AACTACCTAT	
5,835	18 TGTCATGTATCTTTTTAA	
5,711	36 CATAATIGGGTGCATGTGTTTTTGTGTGTCCATAAT	
	ATGGCGCCGGTGTAAGAGCTGCCTCCTCTCAGTGATGGGGAAA	
	GGGTCATAAATCCGTTGTTGTTATGAAAATTTACAACTTTGCA ATACAACTTTATGAGTTGTTCGGCCCTTCCATTGGCCGCTGTCG	
5.027	GTCATGTGGATGAGAACCGTGAACATGAACTTTTTTATAATTTC 102 CCTTGCGAGAATAGAGC	
0,021	132	
4,651	79 ATTCTTCTCCGGGCTGCCCAAGCAACAGCAGCAAGAGGACA	
3,943	24 GAAAAACTTACTAATTCAGCCAGA	
3,822	29 TGTTGGAGGAGAGGATGGGATTAATTGGG TTCCCCAACTTGAGACAATATCTTGGTATGGATTCGATAAATA	
3,428	44 G	
2,663	14 CCCTCCAGGCTGGC	
2,401	TITTAAAAGTCCCTTTTAATTTTTTGACTCGAGTTTTCATTTTCA	
2,016	55 CCTATTGAAT	
	TGGCGCTCGAGTCCGGCTGAACGGCGGCAACTGGCGGCGGGG	
	ACCCCCTATTAGTGCACGAGTTTACCTCTAGAGGTCATCAGG	
	CAGGATTTACGACTGGACAACAAAAGCACGTGATTCGAAGTC GTACCCCATATTTGGGTGCCTACGTAGGAGGGAACCAAGTACA	
312	292 TGTCCCAGTCATTTCCATAATTCATCATAAATTGTGCAAGGGT GTGCCTTTATAGGACCCTTTGCACGAACTCTGGAAGTGGCTCTT	
10,536	71 ATAAGCGCAGCTTCAGTGATGTATGTT	
10,696	43 AATAGCTCCAAGCTGTTAAAGATATTTTTATTCAAACTACCTA	
	AAACTITATAAGCCCCAGTTCCGGCTATATGACATTTGGGTGC	
	CAAATGAATAGGGTTTTGTCTATGAATTAGATCGTAAAATCAT CCATAGCACAGACAGATCGCTTCACTGCCTATAAAACGTCAC	
	GTAGGCACATAAGTAAGTTTTATGGTTTTGGGGAGGTTGACAT	
9,690	13 AAGGCAGAGCAAA	
2,200	CTGTTTGCCTGCATGTTCTTTTTTTTTTCGGCGGGACTGTTCTCAG	
8,556	90 CT	
7,803	35 CAAATTCTCCTACTGCATTCAGAAATGAAACAAAA	
5,879	AAGATAAATCTGCACACCCTAGGAATCGCCAGCAGAGCACGC 56 TTTAGTACAAGTTC	
	AGGTCAAAAAGTTGAGGGTCAAAAGTTTACATTSTCCACTSC	
	CTTAGTCATCTGCCCAGACAGAGTTGATGTCATGTCAGGC	
5,424	161GATCTIGACTATCAGCACAAAAGATAAAATGGCTCAGAGT 163 GACGCGTGTATCACGGTATGGACTCCAGGTGAAC	
4,340	24 ACTGAAGAGCTAAACAATATTTTA	
4,292	30 TAAGTGTTGGTGCTGTAAGAATCTATTTTC	
4,222	16 AATTAATTGGTCAAAT	
0,010		
	CTTITAGAAGCGCAAAGTCCAAGGCCGAGGTGAACTTCAGGTC AGTGCGTCTAACAAATATGAAAATGTCGGCTAGTGAAGGGCG	;
3,214	CGCCTTGTGATTTAACAAAGACTGTCAATGTGTAAGATTAATA 152 AGAAACAAAATGCACACGGTGTCA	

HsaA _{KL} 150	2,707	28	ACATTTCAGGGCATCCCATCTTTTCTCA			
	0.040	40	TTATTAATTGAGTTAGTTTCTTCCTGGCTTTACTTTGGTGTCTTG			
HSAA _{KL} 151	2,048	40				
			TTTGATTCAATGGAATGATGCTATGGTTTGCAAAGGGAGATTG AGGAAGGTTCAGAAAAGGTACTGAGATTGTTTATTACAGCCAT			
1000 450	0.554	450	AAATCTTGCAGTAAAATGTCAAAATGTCGGTGTTGAGATAACA			
HsaA _{KL} 152 HsaA _{in} 153	2,551	159	TAAAGATTACACTCAGTGTTGATTTC			
HsaA _{KL} 155	1,756	18	CCTTTTTAACCTCTTTTC			
			AGAAGGCTGTTTATACTGCTCTTTGAAAAATCAACTAAGGTGC			
HsaA _{KL} 155 HsaA 156	1,536	46	TICTACCCTTAGCT			
HSAA _{KL} 150	1,020	14	GGAGGGGCCTCGGCAAGCCCAGAAAAAACGACAACGCGAGA			
HsaA _{KL} 157 _{bc} *	71	71	AAAATTAGTATTTTTGCACTTCACAAATTA			
			AAAGTTGAAACCATGCAGTGCTGTGGGCCCAGGAGTTTCTGCA			
			GCTGTTCTACACACTGAACTCTGAGCACACTTGGAAAGAAGTG GTCTCTTTCGTATTTGGTATTTGTTGCACCCTTCACACTTAATCTG			
			CCTGTTTCCCAGGAGATAAAAAATAGTTGTGCAAAGGGTTGA			
HsaA _{LM} 160	17,551	223	GATTAGITTTIGITICCIGGCIGTICITAAGGICCICTICACIAA CTAC			
			CAATCATTAATCACCTCAAACAATAAATACTICTTAATC			
HsaA _{LM} 161	16,478	77	AACAGCAATICTGAAAGGCATTCTCTGGGAAAAGT			
HsaA _{LM} 162	16,053	15	CCAACTGTATTGATT			
			TGCCCTTTGCTAGGGCAACCATAAGAGTTCACCGAGAGGACA			
11			AATTTTCTATCTCATTAATTGTTTTTTTTTTTTTAAGCAAACCCTA			
HsaA _{LM} 163	15,877	113	TTAAAGACAGTATTTTGTGTGTAAGCTCTATAATTTT			
IISaA _{LM} 104	15,767	30				
			GATAAAGGTGTAGCGCCTGTGCAAGGGAGATATTGAAATTGTA ATCTTTGAGGTCACGTGACTCATTAAATAATTAATGCAGATCG			
HsaA _{LM} 166	14,125	121	TCAGGAATGGATCGGAGTCGTCAGGGCCTCACTAG			
			ATGTTCTGATTCACGCTGGGGAAGGCTGCAGAGATACCACAGG			
			ACCGCGCCGGCGAGCGAGCGAGCGAGCGAGCGAGCGAGC			
			CGCGGAGAGAGAGGCCACGGCGGCGGCGGCAGCCATTGTAAA GTGAGAGACCTGGGCAGCATCTCTCTGTGACTCATTAGTCTGA			
HsaA _{LM} 167	13,715	220	ACGATITA			
HsaA _{LM} 168	12,807	20	CAAGAGAGGGTTGCAAATAC			
HsaA _{LM} 169	12,405	19	ATTCACATTCTCCAAGTTG			
HsaA173	11,622	26	TCCTATTTGAAACAAG			
HsaA_174	9.462	19	CAGTGTGAATGATTGGTGA			
HsaA _{LM} 175	8,495	25	CAATTAGATCATTTCCTCTGATATT			
	9 462	50	TTAGAAACTTATAATTCCATGTATCACTCAGTTGTGCACTGAG			
HSAALM176	8,462	50	GAAAGC			
			AATTCCATGTATCACTCAGTTGTGCACTGAGGAAATGCTTAAG TGCAAGTTTAGTCAGGCACTAGGTITCCTAGGATTTGCAAA ACCCGGACCCACCACTATAGCCAAGCACACTTTTCCTAGTG GGCTCCCCACTGAACAAAACCAACTGGACTGG			
HsaA _{LM} 177	8,450	258	GTCTGTAGTGTATGGTGTGGGGGTGTTAGCAAACTCCATAC			
HsaA _{LM} 178	8,391	23	GCACTAGGTTTCTCTAGATTTTG			
HsaA _{LM} 179 _{abc} *	7,797	70	AAATAAAAGGATTTAAGTIGACGTATGACCACGTGAGCACAT AATACAGCGCATTATTGTGGCATTTGGA			
HeaA 181 *	7 515	69	TATTITAAGGTATTICCGCCGATTGTTCATATCTAGAGTGAGTT ATGGCTGTGAGAGAGACAAAGGTCAG			
I ISAALM I D I CE	7,515	00	GGAAGAGGGAAATCGATGAGGGAAATGTGCAGATGCGCTGCC			
HsaA _{LM} 182	7,025	71	ATTTTATTGATGATGCTTCCAGGCACTTT			
HsaA _{LM} 184	7,403	40	TCCTTTGTTTCTCTTTTAGAACCGAAACCATTTGAAAGAT			
			TITAATTGCTGFTCAATTACTTGTCAGCATTTCATAGATTTATG			
HsaA _{LM} 185	6,153	93	таата			
HsaA _{LM} 186	5,530	13	CGGGGATTTGGGG			
HsaA _{LM} 187	5,051	34	GTTTTGCCCGGCAGGGTCTTGGCGCCAGTGGAAA			
			GCAATATGCCATAAGGAGCAAGTGTTTGCTGTTTTGTGCTCTGT			
HsaA188	4 714	112	TTACAGCTITIGGGGCGCCGAGTCATAAATCTTGCCCAGCCATA AATGACAAAAACCATTGGTATGCAT			
HsaA _{LM} 190	4,555	13	GGCTTTGTTTTTG			
	4.004	50	CTCAGCGTTACTCCATCCCACTAATGAGGAAAATATGTATATA			
HsaA192	4,284	28	GCATAATTTTCCTGGACTTTCGTGACGC			TGCT
1 JULY LW 1 J Z	3,003	20	AATATTCATAAGAAACATACCCAAGTCGGTGCCACTAGCCCA	HsaA _{MN} 202	4,273	56 GTGC
HsaA _{LM} 193 _{cd}	3,373	74	GGCAGAGCCCGGCGCCGCACTAGCGCTTATCT	HsaA _{MN} 203	3,403	40 CAGA
			TCGTCAGAAGTTAAGGTAAGCAGGGCCGCAACCGGCCGCTCC			AAAT
			CGGCGCTGAATGGCGGAGTTTACGTCTCGGTGATTTATGGCTG CAGACTTAAATCTCGGTTCAAGAAGAGTTCACAAGCCGGAGC	HsaA _{MN} 204 _{bcd} *	2,238	84 GCAA
HsaA _{LM} 194 _{bcde} *	2,999	151	TTCCTTCCCGGCAGTGACTGATAC	HsaA _{MN} 208	1,377	42 ACAG
			TGACCCCCATACATCAAATTACATAGCAGTITCTAAGACAGAA	HsaA _{MN} 209	1,752	16 TTAA
			CCTATTATCGTTAAGTTGGAAGGAGAGTTCAAACTGTGGTCAT			TTCT
HsaA _{LM} 198 _{abc} *	1,245	166	CCCCCTCTAATCCATCATGTTTTAACAGGTAGAATT			CTCG GACT
				HsaA _{MN} 210 _{abc}	726	162 GCGA
			AATATIGCIGACCACITIFICITITATGGCTTTCATGTCACTTAG CTATTGAGAGTAAGATGGATTTGCGCGGAGCCCTCACCGCGCT			TGTA
			GCGCTTCTCGCCCACCAGGTCTGCGCGGGGGGGGGGCGATTGGCG GCGGAGTGTCACGTGACCGCGGGGGGGGGG			GACT
HsaA _{LM} 199 _{ac} *	227	197	CACGGGTGTCAAACCCCTGTCAG	HeaA 211 *	254	AATT
				HsaA _{NO} 215	351 4,771	207 AATA 12 TGCC
			AACAGGGTATATGAACAAATTTTCTAGTCGAGTTTTCAATGTG	HeaA 219	4 205	AATA
			AATTIGTTCTTACATTATGGCTCCCGAGGGGAAGCGATTACTTT TTTTAATTITAAATTTTTTTTTTTTTTTTTT	HsaA _{NO} 219	4,385 3,195	31 CTCA
			GAGAAAAAAAATCAAAGGCGCTTTGAAACAGGGGCTCTCTGT GCAAGGATGACTAAGTGTACGTCTTTCCGTGTGTGTGTATGCTGGT	HsaA _{NO} 220	1,579	22 TAAA
HsaA _{MN} 201*	5,116	304	GAACAGTCAGATTTATTTTATATTTTTTTGCAAGCATT	HsaA _{NO} 221	826	32 GAAG

56	TGCTGCGGAGGCAGGCTGAGGGCGCAGGGGCTGCCGAGTGCT GTGCACGGAAGAAA
40	CAGAGACAGAAGTGGAAAATGTCGCCATTTTGTTTGCAAT
84	AAATGTGTTCTTAAGGGCTAGAAGCTGTCAAGGCTTTTGGTGA GCAAGATTGATCGCGCCCCAGACTTCCTTTGGAGCTTTGTTT
42	ACAGACTTCCTGGAAATCGGAAATACTCACCGCACCCGAGCC
16	TTAAAAATTATTTTTT
162	TICTCCTGCTITAACAGAACTIATGTGGCTGGGACGCAGGGCC CTCGGGTGTCAAAACTITGAAGATIAATGGATIACTITGTTAAT GACTGCAGCGTCTAACTGAGGTGCTAAATGATTGTGAGGT GCGAGGCGTCTTCCCCGACAGTCCCAAACAATG
207	ТОТАААТАААGCCTCGCTGGCCCCCAATGAGGCGTTCCTTCCC GACTTTTTTGGATCAATCAACCAGACAGTGGCTTCTTTGATTA AAGCCCAATTTGTCATTGGCGGAGAGCATCATTGTGACAGC AATCGGTCCAATTICAACCTIGTCTCCATGAATTCAATAGTT AATGGTACGCGGTCCCCATCAATCGG
12	TGCCTTCTTTTA
51	AATAAAATICGTCACAATTTATCCTCTTTTTTCAATTTTAATAC ATTTATT
31	CTCATAAATCAAACGCTTTCTATGAATGAGA
22	TAAACAACAATTTAACGACCTC
32	GAAGTTTCTTTCTTGCCCTCGTCTCCTTCAC

Delunterus cons	aalua biabir Hay I	、 、				
POlypierus serie	Dist to 3' gene	1 I enath	Sequence	PseA _{IJ} 121	1,266	
	Dist to o going	Longui	TCTGGGAGGGATCACCATTGCCCTTCTCTTTCTAAGCTGTCAT	PseA _{IJ} 128	1,680	:
			TCTTAATGGTGCGCTCGTCATTACAGTACTGCTGGTGACGCCA CTCATTGATTTCAAGTGGATAAACAGAAACAGCTACTACCCGA	PseA _{IJ} 130 _a	140	
PseA _{AC} 2	100,256	140	GAAGATGAAAGG	Dec.4 121	4 077	
PseA _{AC} 1	97,071	16	CTGTCCTTTTIGCGCCC	FSEAJKIST	1,077	'
PseA _{AC} 6	64,905	27	TTTTGTAAGGAAGCTGTAAGGAATGAA			
PseA _{AC} 7	55,564	39	TTTAAACAAAAAACATTTAAAAATGTGCAGGACATATAGA			
PeoA 12	4.059	44	ATATTTCTATTGTTGCGATGTCATGATACTAGAATTTAA			
PseA _{AC} 12	4,958	41	ATGGATA AATGT	PseA 1x132ac	328	2
PseA _{AC} 13	4,536	12	TAAATTCAAAGAACAATTCCCAT	5 4 400		
I SEACT	3,790	23	CAATAAACAGTTGGTAAAACTTGTGCTTAAATATTGCAAATA	PseA _{KL} 133	6,532	:
Real 10	2 222	155	CAAATCTCAAACGTATCTTAGCATACTATATTTTTGCTGTAAG CAATTCTTCATGTTGAGCTAACATAAACAGTTATTCCAATTTA ATTTCA A AACTATAAATCACGCCAATCA	PseA _{KL} 134 PseA _{KL} 135	6,356 5,900	
ProA 22	2,233	100	таттататстит			
PseA _{AC} 22	55,617	10	CATCTAGTOGGAA			
PseA _{AC} 25	6,478	13	TEGETAGACTECAACTTEACCTEGCCT			
r Ser _{AC} SU _{ab}	1,501	30	is de monter de mierren andre moster	PseA _{KL} 136 _{ac}	5,599	2
			CTITIGCATATCACGTGGCTTGCCTCAGCCAATGATTTCTTCTC	Dec 4 140	4 269	
			CCTAATGTACACAGGCGCGTCAGTGCTGGTAAGTCCCTGAGA TICAGTATCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	PseA 140	4,200	
PseA _{AC} 31 _{abcdef}	153	147	CAGAAGTCTCAATGTTGGA	1 30AKL 142	3,911	
10 40000			TTAAACCTTGACCTTGAATGAAAAAAGAGCCTTTGACCTTGA	PseA _{KL} 143 _{bc}	3,707	ł
PeoA 43	9 6 4 1	100	CTGTAATAGTAGTTAATGAATAGACATAGCAGGGATTGTTGA AGCAAGCTTGCCACCT	PseA., 144	3 034	
Peod 44	0,041	100	AATAAGAAATGAAATGAA	KL	0,004	
PacA 45	4,333	10	AGTGTATTGAAGTAACAAAAATGTAA			
PSEACE45	3,752	20		PseA _{KL} 149 _{bc}	2,084	1
PSeA _{CE} 55	2,656	24	ATAAACAACTATGAAATTATTAAA	142 00		
PseA _{CE} 56	2,400	41	TTTTTAAGAAATGATTAATTAATTGTATTTTATTTCATTTT			
			AAGCTGAAGTTGATTGCCAAAAGTGCAATAAAACCGCAGGT	PseA _{KL} 157 _{abc}	165	1
			CAGTCCAGTCCTGTTTTTGGGGTTTTGGTGCAGCCCTGTGTTCAA TTATGGCTTGAAAGCAAGAATACAAGTGCAAGAATGTGTTTG	PseA159	7 636	
PseA _{CE} 57 _{abc}	1,892	144	CAGTCACAAAGAGGCGG	PseA170	10 595	
				1 CONLM 11 C	10,000	
			TGTCAATTTCTGCATCTGGTCACATGACCCGCACCTCCCTGTA ATGGATGGAGATGGATCTCCACGTCAGCTTACGTCTCCAAAT			
PseA _{CE} 60 _{abd}	176	113	TTTTACTCCGCGGATCTGCTTCAAAGAG			
Dec A 62	2.075	40	TIGA ACTECA ATATECCTATICA ACATCA CCTATA ACCTEC			
PseA _{EF} 62	3,875	40				
PseA _{EF} 03	5,604	25		PseA _{LM} 171	5,653	3
PSeA _{EF} 04	4,293	31	AIGGAAACACAIGIAICAAIGIAAAAIAIIG	PseA _{LM} 172	5,260	ł
			CCTAATTACAACACATCCTCCGTGTTGCTGTGGCAACTTGGTC	D 470	5 070	
DooA 65	2 522	440	ATAAAAACTGTCTGAGTCTGGTGCATTTGTAGAATTGGAGAG CCTGCAATAAAATGTCTGAGACCAAGGTTAT	PSEA _{LM} 176	5,876	
PseA _{EF} 05 _{bc}	3,532	116		PseA _{LM} 179 _{abc}	5,111	
PSeA _{EF} 00	3,271	31	GCACAGTGAAAAGCTGTTCACATGTAAATAATAATAATAATAATA	Dec. 191	4.096	
PseA _{EF} 67	1,257	47	ATAAT	- SEALM TO T _{bd}	4,960	:
PseA _{EF} 68	936	15	AAAGTAACAACAAAA	PseA _{LM} 180	4,313	
PseA _{EF} 74	1,110	19	CACTGAACTCTTCAGTTAT	PseA _{LM} 189	3,359	
			GGGAGGAGCTGCTGCTCGTCCGGGTTTCATTGGCCCTCCGC TTCTACCGTGCAGTGGGGGGTATCTGTAATGATATTCAGCATGT TTTCCACAAAATCTCACCCAGAAAGGCCTATCTTCTCCT			
PseA _{EF} 75 _{acde}	149	136	TCGCCAAA	PseA193	2 573	1
PseA _{FG} 76	3,390	12	AGTTTTATGACT	LM - Bcd	_,	
			ATCTATTTAAATATTACCTAGGCAGTCGTAATTTGTCTAGGCC			
			ATATAGCAATGGTGCTGTAAGGTTTGTCTCCTTTTGTTAAGTTT			
Pse4 78	3 472	144	TATGACTIGCTAGTATATCTAGACTATIGCTGTCTTGGGCGAG TGGTTTCTGTIGAG	PseA _{LM} 194 _{abcde}	2,216	1
. son _{FG} / O _{ab}	3,472	144	AGGTAGTITCATGTTGTTGGGGGCTCCATTTTCAATCCCTACAA	PseA _{LM} 195	1,039	:
PseA _{FG} 79 _{bde}	2,848	71	CACGAAAGTGCCTTAATTGCTCCAGTTA			
PseA _{FG} 80	1,633	28	AAGCAGGGTGTAGGGCACCGATATTTTG	PseA _{LM} 198 _{ab}	955	1
PseA _{FG} 83	1,392	22	AAGAATTGAAATTCCATAATTT	D 4 400		
PseA _{FG} 84	1,260	23	ATATTTTATATTAAATAGCACT	- SEALM 190	889	
			CATA A A ATC AT A TGCCTTTAC A ATA A A A A ATTATCACTCA A A			
			AATGCTGACCCCCATTTTTACTGGTTTGCGGACTGATTTATAT			
			TITATIGTICTGCTTGGCGATCACGTGTTCTGCACCAGCCAAT	BeoA 100	100	4
PseA _{EG} 92 _{short}	254	209	TIGTGAAGCGAACTIGCTACTIGATIGTACAGTICICT	PeeA 200	189	1
PseAo.94	3 806	200	ACTACCTTTATGGCTGCACA	PSEA _{MN} 200	3,484	
PseA _{ci} 100	3,592	25	GTAAAACGCAAGTTCTGTGAGTATT	5		
Pse4 - 101	2 865	37	AATATTATCTCATACGTAAATCATATTCAGGTTTCAT	PseA _{MN} 204 _{abcd} PseA _{MN} 205	1,532	
PseA 102	2,000	30	TGCTGTATATGCAGTAGCTTTGTTAGATCCACTAAATAA	PseA _{MN} 206	1,215	:
1 00/10/102	1,720	00		F SEAMNZON	954	
D. 4 100			ACGCCCTCTGTTGCAGATGGAAGAAACATCAAAGACTTGTCC AGGGATTGTCCCATAAAACGAAGGGTCTGACAAACTGTCTG AATCTGACTTTTAATGAGTTACAACTGTCGCAGCTACAATTAA GTTGTTTTCAGGAAAGACCATCCGTTTGCTGCGTTTTTCGGGTGT TTTLAGGAAAGACCATCCGTTTGCTGCGTTTTTGCGGGTGT	PseA _{MN} 210 _{ab}	594	1:
r seA _{GI} 103 _{abcde}	1,952	207	AGTATATTTGCTGCCTAACTGGCTAACAAATTACCACCAATA			
PseA _{GI} 108	944	44	AT	PeoA 214	000	
PseA _{GI} 109	461	13	TGGCAATTCATCT	PSPA 212	290	1
PseA _{IJ} 112	4,935	24	TATATTTTTGTTCGGTTGTTAATG	PseA213	4,220	
D. A. MA			TTAATGTTTTAAGTTGTTTTTAGAAATAAACATGCCACTGTAA		0,000	
PseA _{IJ} 113	4,041	55	AIGIGTAATTTT			
			ATGGCGCCTATCTGTGACCTGCCCCTCGGAGAGAGGAAAA GGCCATAAATCCGTTGTTGTTATGAAAATTTACAACTTTGCA ATACAACTTTACGAGTTGTTCGGTATTTICCATTGGCCACTCTT			
Deed 110			GGTCATGTGGATTGTAACCATGAACATGAACTTTTTTATAATA	PseA _{NO} 214	2,881	2
rseA _{IJ} 119 _{abcd}	3,100	189	ICCCIAICUAUAAIAUAUC	PseA _{NO} 222	237	:

15	TITITATGITAATIT
23	ATITTTGAGGTGAAAGTTTTAAA
60	ATCTAGAAACAAACCA
63	CAATATGCCCACTTGATAATTAAATTAAGTAGAGCTCCTAAAC AATTAACACAATTTTTGTTTA
292	ТОБСОСАНСАЛИМСА МОВСААМ ТАЛАМ ТТГА МОСЛОВОС GECTETC 2002/COCGUTT CATTITE X00C ATTC X00C ATTC TTTTTTETETTTTTTTTTTTTTTTTTTTTTTTTTT
50	АЛТАӨСТССААӨССАССАӨАААӨАААСАААСАТТӨТТТТАА ААСТАССТА
72	GTGCCTTTGTATGACTTTTTGCACGAACTCCAATAAGTTGCTC TTAAAAGCGCAACTTCATTGATGTATGTT
31	ATTICAGECTIIGICIAACAATATTIACTI
207	AAACTITATTAGCCETCABTTCCGGCCTATATGACATTGGGTGC CAAATGAATGAGGGTTTGGCTGATGAATGAATGAA TCCATAGAAGAAGCAGATAGGCTTACTGGCTATAAAAAGTC ACGTGAAGCAATAAAGTTAAGTT
30	TTAAGAAAGTAGACAAGATGTTTTAAAAAT
56	ACAAAAGATTAAACAACTITGCATCATTCAGATATCTCTCTG GACTCGAGGTGAAC
36	TAGCTATATCCTGGGTAAGAAAAACAAACTGATTTGT
135	ITCAAGUCUAUUUAAA ITCAUUCAA UUCUT LACAAAI ATGAAAATGCCCCTCCTGATATGACCACGCCTTGTTATGAAC AAAGACTGTCAATGCTTAAGATTAATAAGAAACAAAATGCA CAAGGTGTCA
165 51	CCATTGGCGCGTATGCTTACACTGTTGGCAGCTTGTTTCTGT GATTGGTAGGAAGGCCACGTGATTATACAACTTTCTACATT TGCAGTGAATGGGGGGCGTTTATTGGACGAGAAAAAAA ACAAGAGGGAAAAATTAGTATTTTGCCTCCACAAATTA AACATTACCTTATTCATTTACTGGATGTTAAACAAAATATAA AATAAAAC
26	CAAACAGAGGACAGTTTTTCACTTCA
	GTITGAGTCTAGAGCACGCCTTAATTCAATAGCGGTTTGAAG AGGCAAGTATAGTGCAGTATAGTAATGAACCTACCGGTAGGG GTTICCTTTGCAAGATGAATGATCGTCGGGAAAATATGTTACGT TTAAGACTGTGTTACAAATATGCACAGAAAATATGGTACGCT TAATGCCATATGAAGTATGAAACTATTAACTATGAGATGCATGC
326	CC TTAATGATTCACAAATTCAAATAAAAGGATTTAAGTTGACGT
56	ATGACCACGTGAGC TTAGAAACCCATAATTGCAAGCCGCGAGCCTATAGGAAATG
42	C AAATAAAAGGATTTAAGTTGACGTATGACCACGTGAGCGCAT
70 58	AATACAACGCATTATTGTGGCATTTGGA ATGGATTTAATATTTTGAGGTACTTCCTTTGATTTTTCGCTTTT GATGTTAGTTATTG
68	ATATAAAATTGCATCCCAGAGTGAGTCCAGCTTTGAAAGGGT CATAATGCTGAGATTTGATTT
14	GGATTIGTTTTTC
178	GCATAATITTICHTCHCACAGTGACGCCTGTTTCGGGGGGGTT CACACAGTGCCTGTACAAGACTICTTGAGTGAGACTGTCTTTT AAACGAAAGTGTTATGTTA
198	ATCGATTTIGCTGCTGAATGAGAAAATATTATGTCGTGTTCTG CATTGTCGTCAGAGGCTAAGGTAAGCAGGCCAGAAATAGG CATTAGTGTAAATGCGGGTGTTTATGTCCCAGTGATTTATG ACCATATGACTTAAATGCGGTCAGAAGAGTTCACAAGGCT AGAGGCTTCTTCAAACACAGAATGATAC TGATTIGCTTCGCTAGTAACACTTAA
20	TGACCCCTATACATCAAATCTGAGCAATTTTAAAGACAGATA CCATTATTGCTAAAGGTTGGAAGAAAAGTTCAAACTGTGGTC
105 70	ATGGAGATGAAGACTGTITTT AAAGTICAAACTGTGGTCATGGAGATGAAGACTGTTITTCTTT CTTICTTICTTICTTICTTICTT
-	TGTC & GTTGC CT & TTC & & & & GTT & A C A TGC A TOTO TOTO TOTO CO
183 34	INICAD INCC IN TRANSMOLANDINE OF CONTROL CONTROL THATAACAGTEGOTIGHTITTAACCCTAGGTCTUTTCCAGGTA GCCATTGGTGGAGAGGAGTCACCTGACAGAGGGGTGCCAAT GTIATICCATAAGGGTGTCAAGACCCTGTCAGTTATGAAAT AAATATTGGGAAAC CATTCCATGCTGCTCCCGGTTTTCAGAAATAAATA
	AGAAGCTGTAAATGTGTTCTTAAGGCTAGAAGCTGTCAGACC GTTTGGCAAACAAGATTGATAGCACACATGCTTCCTTGCTGC
91	TTIGTTT
22 33	AAAA LATTICACAGAAATGTTT CCACAATCTAATCACGTACACTTTATCCAAAAT
18	GTATTTTTGATTAATCAA
126	TICTECTIGIGIGIAAATECTTAAGTAGITGATATETAGAGIT CCTIGIGICAAAACITIGAAGAITAATIGGATTACTIGITAAT GACICCAGCGCGCAGAGAITAAGGAATIGGAATGATHIGIGA GAGCCGTICCACACCGAGGITHIGGATCAATEACCACAGACAG GAGCCTITCCACACCGAGGAITHIGGATCAATEACCACAGACAG GACICTIGIGAACCAATEGGATCAATTGACCAGAGAAGI AACTAGIGGACAACCAATEGGATCAATTGACCTIGGATC
178	CATGAATTCAATAGTTTAATAGTAGCGCGGGTCCCCATACGGC TGTAATCAG
16	TACAATTTGTTTGCTA
20	AAAATATGAAATAGAAAGTA
219	AGAAAACAAATTAAAGTATAAGTTACAGTITICGAGATITAA AAAGTGGTCAACATITITICGAATAATTAATAATCAGTITITGATT GACIGTGAATTAATTGTAAAACAATAAATTATTATTGCTTA ATGGTITGCTAAGATAAATCGAACGGCAATITICCCAAGCGATT TGTTAATATAATGCAAATCGCGTITCTAAATATGTTATCAGTIT GGCATT

36 GCGTCACCTTGATACAACAGAGCGTGGAATTTAAAT

Danio rerio zebra	fish Hox Aa		0			
DreAA _{AC} 1	Dist to 3 gene 6,297	Length 16	CTGTCCTCGTGCGCCC			
DreAA _{4C} 7	3.144	39	TTTAAACAAAATATATTTTATATATACTGATAATATAGA			
DreAA ₄₀ 9	5 842	21	ATAAATATATTTTTGAGCAAA			
DreAA _{AC} 11	5,590	17	TACTTAGTAGCTGCTTG			
DreAA _{AC} 12	4,907	42	ATATTTTTTACAGTGTGCAGATAATTTGAAAATGTAATTTAA			
DreAA _{AC} 13	4,482	18	AIGGATTTTAGTAAAIGT CTTGTTATTGCAGTGTTTTATAACAATGAGTTTTAGATGTTTCCAG			
DreAA _{AC} 18	4,430	48	AA			
			AAATATTTAAAACAACTIGTAAAAACGCIATTATIACA AAATATTTAAAACAACTIGTACGTCATGTTTAGATTTTAAAAACGA			
	0.050	450	AACAAATTTGTAAATGTTAATAAACCGTTATTTACGATAAGTTTT GATAGTTCATCTTTTACAATGA			
DIEAA _{AC} 19	2,258	158	GATAGITCATCHTTACAATGA			
			TGTTAATAAACCGTTATTTACGATAAGTTTTGATAGTTCATCTTTT			
			ACAATGAAAAATAACACGCAAAAAAAAAACATATAAAAATGTAA			
			CAAAGCGTTTGGCTTGATGGACCGTCCATTCACACCAGATATTG			
	2 153	202	AAATAAATTTAGGCTCCTATCATTTTGCTATTTTGGTGTGTTAAGA AATATTTTACTATAATGCTTTTTTTCAGT			
DIGITIN	2,100	202				
			AAAATACAAAATCAGAAGGAAACCATGTTAAGTTAAAACTACA			
			TCTGTTTTCACCAAAGATTTCTCAACAAACAACAAGCTTTTAGAC TGGCCATCAAAGTCAGAATAGGCCAACAGGCACTGTGTCGCGGG			
			AAGACGGCAACTTTCAACTTGACCTTGGCCTGCAGACGCGTCAG			
DreAA ₄ 21	1.044	238	CCICGCGCGIAAAATACAGACAAATATAGGGGGGGGGGGG			
DreAA _{AC} 30 _b	905	24	CAACTITCAACTIGACCTIGGCCT			
ACTO			GCCAATCGAGACGTGATTCTGGATGTACGAGGGTGCGTCAGAGT			
	112	103	CAACTGTCTCCCCTTTTCAGTGTCTAAGCTTCACAAAAAAGAGCC ACACGTCTCAATGT			
DroAA 37	6 026	103	TAATTGAAACAAAAGCAT			
DreAA _{ce} 40	5,020	33	CATCTTCTGATGIGCGTTTGTAAGTGAAGCAGT			
DreAAce40	3 163	16	ACATTIGGITTTAAAA			
DreAA _{er} 45	2 799	10	AGTGTATTTACAAATGTAA			
DreAA _{or} 50	1 151	18	CTTGAGGCATTTGGCAGA			
	1,101	10				
	200	00	TGTCAATTTCTTCACATGATCACGTGACCCTGGCCTCAGTTGGAG			
DIEAACEUUabc	200	09				
			CCTAATTACGGGGACATCCTCCTTGTTGCTTCAGCAACACGGCCA			
DreAA_65	10 155	119	TAAAAGCTGTCTGTGTGTGTGGAGCATTTGGGCAATTGCAGCGTGGT GCCATAAACTGTCTGAGAACCAAGGTTAT			
DreAA _{EQ} 70	11,248	16	AGAAATTTAGTAGCTG			
20	, .					
DreAA= 79	2 565	77	GACTGTCGAGTGGTTTAGGTAGTTTCATGTTGTTGGGATTACATTC AAACTCTGCAACGTGAAACTGTCTTAATTGC			
DreAA=_82	1,000	26	TAATGTACTCTTCAAGAGTATAATIT			
Diorotegoz	1,000	20	CACGTGGTCACTTCACCCAATCAAATGGCACTTTGCTCTCAACTT			
	404	400	ATTATCTGACTGGGGCTTTGAGAGGGGGAAGTTGCCTCTCCATTT TCACATATTGCTATTTTG			
DreAA_95	7 679	30	TITATIGAATAATAAAAAGCATTICATATCT			
DIEAAGK90	7,070	30	TGTTAGCCGCATCCAGCCATAAAAGACAATTACTGCTATAACCG			
D. 44 00			TTTATGGTGTGCAAAGCGCTGCGAGGCGAGAAAACGCAACACA			
DreAA _{GK} 98 _{abcde}	6,861	113				
DroAA 100	6,587	20	GTAAAAAGGAAATTATTTAAGTATT			
DIEAAGKIUU	0,220	20	CAAAATGTGGCCTAAGAACTGGCTTTTGTAATGTCATTACCACTA			
DreAA _{GK} 114	7,953	50	CCTAT			
DreAA _{GK} 115	6,173	13	CGTCCAAACACAA			
DreAA _{GK} 116	3,947	35	TGTTTTAGAGCAAAAACATAATTTAGAAAAAAAGT			
			ATGGCGCCTGACTGCAATCCAGCCCCCTTCTCAGCCAGCGTCTC	DreAA _{kt} 157	163	16
			ATGAGAAGCTATAAATCTGTTATTGTTATGAAAAATTTACTACTTT	abc	100	
			GUCATACAACTITACGAGCTGCCGCTGGTTCTCATTGGTTACAAG TCAGTCACGTGTTTTAAGACCACATAAACGTTAACTTTTTATGCG	DreAA _{LM} 158	7,072	6
DreAA _{GK} 119 _{abd}	3,603	205	TGTGCACCCCAACCCAAAATAGAGC	DreAA _{LM} 164	6,728	З
DreAA _{GK} 120	2,489	21	TTAAATAGAAAGAAAAACCTT	DreAALM165	5,813	1
DreAA _{GK} 127	2,230	23	AACATGCTAATTCGTGTCTTCAA	DroAA 179	4,278	1
			TOCOCCACCOCTACCATOTACAAACAACCCATTTAACTCCTACT	DreAA _{LM} 178	1,141	1
			TCGCCAAAACTGTTGTTGCGCGCCTCCCGTGTCCTAACAATTCCAC			
			CCTGATTTCCTGCTTACGTCTGAGTTTACCGCTGGAGGTCACAGA	DreAA _{LM} 181 _{abc}	4,699	9
			ATAGCCCATATTTGGAAGCCTACGTAAGGGTGCATTAAGTCTGTG			
DreAA _{GK} 132 _{abcd}	378	376	TCTCACTCATTTCCATAATTCATCATAAATAG			
			AAACTITACTAGACCCTTTACCATTCTGGATCCACGACATTGGCT	DreAA _{LM} 183	3,833	16
			GGTAAGATAAATAATGAGTGTTTGGTCCACGAATTAGATCGTAA	D 44 400	0.050	
			AATTCACICGGACIGAGACIGCAGATAGGCICACTIGCCATAAA ACAGTCACGTGGTGGCAATTAAAGTCAGTTTTATGGTTTTGGGGA	DreAA _{LM} 193 _{ab}	2,058	e
DreAA _{KL} 136 _{ac}	5,701	216	GTCGACACTATATGGCATATAAAGTTAAATCGCACTGA			
			GGTTCACCGTGAGGTCAGTGGCGGCAGGAAGATGAATGTCCACA			
DreAA _{KL} 140 _{ade}	4,105	84	CGCCATAAACCACCAGCAGAGCTCGCTTTTGGCCAAGTTC	DreAA _{LM} 194 _{abcd}	1,624	16
				DreAA _{LM} 197	766	1
			GGTCAAAAGTTTAAAGCAGAACAAGTAGCTGTCATCTGTTCTTGT AGAGCGCAGTGCCACTTTTATAATGGCACAAAAGATGGAATAGC			
			TGTGAATCCCGTGAGTTCTGGTCTAACCTCGCGATGAACCCTGCA			
			AGCTGGGTGACCCTAGGTTAGCATCCCAAGAGACTACCTAC		101	
DreAA _{KL} 143 _{bcd}	3,640	287	TTGGTGAATTTCCTCTGAATAAATAGTATTTG	DreAA_000	191	18
DreAA _{KL} 144	2,968	35	TAGCTAAAAACCTTCCGAGAAAAGGTATCAATTTGT	DroAA216	2,217	1
				DreAA	3,073	2
			GAAAATGTCACATTTTCAGAGGGCACGCCTTGTTTAACAAATAT		1,922	4
	4 004	405	ACTGTCAATGAACAAGATTAATAAGCGGCGAAATGGACACTGA GTCACTAAGAGGTCAAACCGAAGTTATCTCTCT		0.40	_
Dicnn _{KL} 149 _{bde}	1,821	105		DIENNMOZZO	243	

163	CCATTGGTGCTTGTTTACACGATGCCCACAGGAGGCGCTGATTGG TCGCATTTCTCACGTGACCGAGCAACTTTGTACATTGACAGAG AGTAGGTGGGTTTTGGAGAGTCAGAATACGACAGCACCATAAA AATTAGAATTGTTGCACTTTTTCAAATTA
62	AAATTTTAATTGACTGGCTCACATGACCTTATTAAATAATAGATA CCCCTTGGTTAGAAATA
31	TTAAAGTTTAATTGTGAATCACAGTAATTTT
15	TGACGGAAAACAAGC
14	ATTCACTCAAGTTG
15	GCACTATTGATTTTG
96	CTGTCATGGACGGATATGTTTTTCCACACTGAAAAAGACAAAGT CCTGCGCACCATGAGGATGGATTTTATTTT
166	AGCAGTGGCGGCCCGTTTGTTGCGGAGCCTCGCTTGGGAAACGA GGATATAATAAGGAGTATCATCCAGAAGCACGCTGCGCACG GGGTCACGACGCCGCGGGCTTAGG GGGCCGCTGCTCGAGGCTAATGACTATTGGAT
62	AAGGCGCTTAATTTGCATAATTTTTCTTGTCTACGGTGACGCTCTG TTTCGAGGGAGTTCAC
161	АТСGАТТІСТGССGСТGААТGAGAGAAGCICGCGCGGGTGCTGCG СGCTGCTCGTCAGAGAGGAAGTAAGCTGGACGAGAGGCAGGGT СГССААТGCTGTTAAATGGCGAGTTGTGGATTATGACCGCGCG GCGAAATCTCGGTTCAGGGGAGATTCA
17	GGTTTTTCAGGTTTTCT
	TGTCAGCCGAGCTTTGAAAAGTAAGATGGATAGGCCTTATTTCA CCCGCTCACCGTGTCTTCTCTCACCGTAGGTTACCCGTAGAGCC CATTGGCGAAGAGGTGTCACGTGACTACGTTGAGCCAATGTTCTT CTACAAAGTGGTCAGGACCTTGTCAGAAAGTGAAATAAACATTG
185	GGAAAC
17	TTAAAAGTTCATTTTTT
25	GTCAGACCTITTGGCAAGTAAGATT
28	TTTATGTAATTACGGTTGATGGAAAAAA

Morone saxatilis	striped bass Ho	x Aa				
PFC	Dist to 3' gene	Length	Sequence			
MsaA _{FG} 76	3,451	12	AGTTTTATGACT			
$MsaA_{FG}79_{bde}$	3,064	69	AGGTAGTTTCATGTTGTGGGGGTCCATTTCTAACTCTGC AACATGAAACTGTCTTAATTGCCCCAGTTA CACGTGTGTCTGCTACCCAATAGCATGGCAGCCTGACT			
MsaA _{FG} 93 _{abcdef}	222	127	CCCCATTACTAGCCCACTGTAGTTCTCTGTGGGGCCAA GTTGCTACTTGATTTCTCCACATTGTTATTTTGCGAGGC TGGGTTTACTGC			
			TGTTAGCTGTATACAGCCATAAAAGACAATTACCGCTA TAACCTTTTATGGGGTGCAAAGCGCTGCGAGGCGAG			
MsaA _{GI} 99 _{abcde}	2,714	116	AGCTG			
MsaA _{GI} 103 _{bodef}	2,111	288	GCAGATGGACACAAACTTCAAAGGCTCGACCAGAGAC AGTGCAATAAAACGCCTGGTCTGCTATACTGTCTGGCA TTCCAGTTTTAATGGCCTTTATGGCCGTCCAGACACAAT TAGGCCGTTTCCAGAATGGACCCCATTGTTTTTCTTC TCTTTCTGTGAGACTGCGCTCTGGACAAAAGGCCGAGC GGAAATGATCAGCTTTATTGGATCCCCCCCGACGGGGA CCCACAGGACTCACGGTCATTTGGAGC			
MsaA _{GI} 107	1,620	22	TAACTTTTAGCTGGTATTTTAT			
			AGTATATTTATTGTCATTATTATTATTAGTATTAGTA			
MsaA _{GI} 108	943	45	ATAAT GTITIGGTGTAAATCTAGGGTGTATTGCTGTCATATATCA CACTACCTCGTAAAAACGACACTGAGGATTCTGGGCC			
MsaA _{GI} 111 _b	97	84	AACAAATC			
MsaA _{GI} 115	2,012	13	CGTCCAGACACAA			
MsaA _{lK} 117	4,578	18	TGTCATACGTGTTTTTAA			
			ATAAATCCGTTGTTCGTTTAGTGAAAATTTACAACAGT GGTCAATACAACTCTTAACGACCCGGCTCGACATCAT ATTGGCCCCAGCTGTGTCACGTGACACCGACCGTGAA CATGAACTTTTCTATATATAATTTCCAATAGAGGAGAT			
MsaA _{IK} 119 _{bod}	3,891	155	AGAGC			
MsaA _{IK} 123	3,033	26	GAAAAATICATIGGAIGGIGGCCAGA			
MsaA _{IK} 128	1,229	23	ATTITITACATTAAACATTITAAA			
Mean 132	201	290	TGGCGCACCACGACAATTCAAAACACCCAAGCCCTGG CTCTGAGTTGCCCTAGCCACGAGCGCATGGAGCGC GCACCTTCACATCCACCCCAGCAGTATTCCTCTGTGCAC GAGTTTACCTCTGGAGGTCACCAAGCAGGATTTACGAC TGGTCAACAAAGCACGTGATTCTCCGCCGTACCCAA ATTTGGGTGCCTACGTAAGAGAATCCAAGTCAAGT			
WS20 YK YS2 abcd	331	303	AAACTITATTAGGGCCGATTCTGGCTCTCTGACATTTG GGTGCTAAATGAATGGGGGTTTTGTCTATGAATTAAA TCGTAAAATCATCCGGGCCGGCCCAGTAGGCTCA CTGGCAATAACGGTCACGTGGTAGCCCATTAAAGTAA GTTTATGTGTTTGGGGGGTGAGCCATTAAAGTAA			
MsaA _{KL} 136 _{abc}	7,562	206	ACATATAATCGCACTGA			
MsaA _{KL} 139	5,859	46	CAAATTCCGCTCATTGTCATGCAAAGATGTCTCCCTCT TAACAAAA GGTTCATCTGGAGGTCAGCCACAGCACCAAGATAAAAT			
MsaA _{KL} 140 _{abcde}	5,621	84	CTGCATCTTCTCAGAGCCACCAGCAGAGCTCGCTTTAG GCCAAGTTC			
			GGTCAAAAGTTTACGCOCTGAACAAGTCTCCGTCATCT GTTCACTCGGAGCTTGATGCCAGCCTTATAATAGCGAT CTTGACTCCGCGCAAAAAGACAGAATAGCTTTGAATT ACATATGTTGCACGGTGCACTCCAGGTGAACCCCTGAA AGCGCGGTGACCTCCGCGTTGGGACCCGGGGAGGGGGA CCCCCCTGCGTGCCCAGGTAACAAGATTGACTGGCTG			
MsaA _{KL} 143 _{bcd}	4,952	315	GCGTTTTATTAGGGCGGTTGATTGGTGAAT			
MsaA _{KL} 149 _{bcde}	1,855	170	TCCAAGTCCGGGGTGAACCCAGGTCACTGCGTCTAAC AGATATGAAAATGTCGCCTCTTTGGAAAAAAAGGGCA CGCCTTGTTGTTTAACAAAGGCGAACCGTCGAATGGCCAAGAT TAATCAGAAACAAAATGGAAACGGTGTCACGTTGGGG TCAGGCAGAAGTTATCTCTGT			
			CCATTGGTTCCTGTTTACATGATGCCCACAGGACACGC GGTGATTGGTGGCCCTTTCACACGTGACCAGGCACTTT GTACATTGACAGGAGGTGGGGGGTTTGTGGGAGATC AGAAAAACGACACGCCGATAAAAATTAGTATTGTTCC			
MsaA _{kl} 157 _{abc}	164	164	ACTTCACAAATTA			
Oreochromis niloticus N	lile tilapia	Hox Aa	C			
---	----------------	--------	---	--	--------	---
PFC Dist to	3' gene	Length	Sequence TEECTAGACAGCAACATTCAACTTGACCTTEECCT			
OniA _{AC} 30 _{ab}	10.027	24	CCGGGTCTTATCGACGTGGAAGAA			
OniAcr42	9.408	24	ATTATTATTATTATTTCTTTTG			
OniAcr54	3,400	38	GCCTGTAGTAAAGCTTTGAGCTTTTTCTTTTCCTTGAA			
	0,010	00				
OniA _{CE} 57 _{bc}	2,236	120	GCTATAAAAACCCAGGTCTGTGCAGTGCTGGCTTGGTTTTCCTGG GCATCCTGTCCTCAATTACAGCTTAAAAGCTTCGGCACAACTCTTA GAATTTGTCTGGATTGACCGAGAGGCGG			
			TGTCAATTTCTGCCGTGTGGTCGGTCACGTGACCTCCTCCGTG			
${\sf OniA}_{\sf CE}60_{\sf abcd}$	206	118	GAGTGGATGGAGATGACTCTCCACGTCAGCCTACGTCTCCCAATTT CTGCTTAGCGAACCTGCTTCAAAGAG			
			CCTAATTACGGGACATCCTCCCCGTTGCCGCAGCAACGCGGCCAT			
OniA _{FF} 65 _{hod}	3.627	128	TGCAATAAACCGTCTGAGAGCCAAAGGTATTAACTGTG			
	- / -		CTCTGAAATTTTATGCACACAGGTTTTATATAAAAATTAAGAAAGTG			
OniA _{EF} 72	1,161	50	CCIT			
			GGGAGGGACTGCCCATCTTCCAGCTTTTCCATTGGTTTCACAGTCT			
OniAFF75acte	150	137	GCICGGCGGAGAGGGGGGGCCICTAAICATAICCAGCAIGITTIGC ACAAGAAATGTCAGCCAGAAAGGGCTACCTTCTCTCTCTC			
OniA _{EG} 76	3.273	12	AGTTTTATGACT			
			AGGTAGTTTCATGTTGTTGGGGGTCCATTTCTAACTCTGCAACATGA			
OniA _{FG} 79 _{bde}	2,879	69	AACTGTCTTAATTGCCCCAGTTA			
OniA _{FG} 83	1,374	20	AAGAATTATGCATTTAATTT ATACAGTATATTAAATGTATCCTGGTGCAGGCCATTCCCCGCGCCA			
OniA _{FG} 88	1,721	58	TTTCCTTTTAAA			
			CACGTGTGTCTGCTACCCAATGGCATGGCAGCCTGTCTCCCCATTA CTTTCCCACTGTAGTCTCTCTGTGGAGCGAAGTTGCTACTTGATTTCT			
OniA _{FG} 93 _{abdef}	219	127	CCACATIGHTATTTGIGAGGCIGGGITTACIGC			
OniA _{GK} 94	10,308	19	CTATATTIGETCGCCC			
OTIIAGK96	10,140	19	TGTTAGCTGTATACAGCCATAAAAGACAATTACCGCTATAACCTTT			
OniA _{GK} 98 _{abcd}	9,217	73	TATGGGGTGCAAAGCGCTGCGAGGCGA			
			TAAAACGCCTGGTCTGCTATACTGTCTGGCATTCCAGTTTTAATGG			
			CTITATGGCCGTCCAGACACAATTAGGCCGCTTCCAGAATGGCAC CCATTGTTTTTTCTCTCTCTGTGAGACTGCGGTCTGGACAAAA			
OniA _{GK} 103 _{bcdef}	8,610	289	GGCCCGAGCGGAAATGATCAGTTTTATTGGATTCTCCTCGACGGGG ACGCGCAGGACTCACGGTCATTTGGAG			
			GTTTGGTGTAAATCTAGGGTGTATTGCTGTCATCTATCACACTACCT			
OniA _{GK} 111 _b	6,657	84	CGTAAAAACGACACTGAGGATTCTGGGCCAACAAATC			
			A TEGECOCTE A CECTE A CETECOCTE CETECOCTE CETETITITE TET			
			CTCTCTCTCCCCCCGTCCCTCTCCCTCCAGCTCTGGGCCATAAA			
			GACGCGGCCCGGGTTCCCATTGGCCGCAGCTTGTCACGTGGCTGG			
OniA _{GK} 119 _{abc}	3,871	200	GAGCCATGAACATGAA			
			TECCERACEACEACEA A ARCA COCA A A COCCECCIÓN CA			
			GTTTGCCCTAGCCACGAGCGCAGGGAAAGCGCGCACCCCTTATAT			
			CCCACCCAGTATTTCCTGCGTGCACGAGTTTACCTCTGGAGGTCAC CGAGCAGGATTTACGACTGGTCAACAAAAGCACGTGATTCTTCGC			
			CATACCCCATATTTGGGTGCCTACGTAAGAGAGAATCAAGTCCAT			
OniA _{GK} 132 _{abcd}	484	392	GICCCACICATHCCATAATICATCATAAA			
			AAACTTTATTAGGGCCGTTTCTGGCTCTCTGACATTTGGGTGCTAA			
			ATGAATGGGGGGTTTGTCTATGAATTAGATCGTAAAAATCATCCGG AGAGCGGCCAGATAGGCTCACTGGCCATAAACGGTCACGTGGTAG			
			CCATTAAAGTAAGTTTTATGGTTTTGGGGAGGTGACAGTATATTGC			
OniA _{KL} 136 _{abc}	7,537	205	ACATAACATATAATCGCACTGA			
			GGTTCATCTGGAGGTCAGCCACAGCACCAAGATAAATCTGCATCC			
OniA _{KL} 140 _{abcde}	5,596	84	TCTCTGAGCCACCAGCAGAGCTCGCTTTAGGCCAAGTTC			
			GGTCAAAAGTTTACGCGCTGAACAACTCTCCGTCATCTGTTCACTC			
			GGAGCCTGATGCCAGCCTTATAATAGCGATCTTGACTCTCCACAC			
			AGGTGAACCCTGGATGCGCAGTGACCTCGCGTTTGAAACCGGGGG			AAGGCGCTACTTCATTTGCATAATTTTTCTTGTCTATGGTGACGCTC TCGTTCGCGCCAGTTCACTCCATGCTACTAGTGAACGCAT
OniAri 143hort	4.958	311	AGGAGACCCCCCACCCGTCCCCAGCAACAAGATTGAGTGGTTGGC GTTTTATTAGGGCGGCTGATTGGTGAAT			CACATACACCAGCATAGCCTTGGCCGACTTTAATATTGCTATGAA
OniA _{rt} 145	2,825	21	ACTGAATACTTTGACATTTTA	OniA _M 193 _{abor}	2.455	GCCCTGGTCATTGCTCTATAGCAGGACGATACATTCAATCTTGGGG 201 CCAGATAAGTCTTATCT
et in RE	_,			- Dw - abcu	_,	
			TCCAAGTCCGGGGTGAACCCCGGGTCACTGCGTCTAACAGATATG AAAATGTCGCCTCTTTGGAAAAAGGGCACGCCTTGTTGTTAACAA			ATCGATTTCGTCGCTGAATGAGAAAATATTGCTTGGTGCTCTGCAT TCGTCGTAAGAGGATAAGGTAAGCAGGCCAGGAATAGGCTCCCTC
			AGACTGTCAATGGGCAAGATTAATCAGAAACAAAATGGAAACGG	0.11.101		GGTTGTAAATGGCTGAGTTTGTATGTCGCGCGGTGATTTATCACCG
OniA _{KL} 149 _{bcde}	1,758	169	TGTCACTATGGGGTCAGGCAGAAGTTATCTCTGT	UniA _{LM} 194 _{acd}	2,028	169 TATGACHAGATCICGGHCAGGAAGAGHCA TGTCAGGGCTGCATTGAAAAGTAAGATCGCACCACCATTTCTTC
OniA _{KL} 151	1,254	45	TTATTATTACTATTATTATTATTATTATTATTATTATGGTTTCTTGG			TCCTCACAGTGCTTCTTGTAACCCTAGGTTCACCCAAGGAGGCCAT
OniA _{KL} 154	497	17	CCTTTTCTTTTCTTTTC			TGGCGGAGAGGCGTCACGTGACCACGGGGTGCCAATGTTATTCTA CAAGGGTGTCAAGACCCTGTCAGTTTCTGAAATAAATATTGGGAA
			CCATEGGETCCEGETEAC ATGATGCCC AC A CCAC A CCCCCETC A TEX	OniA _{LM} 199 _{bcd}	190	184 AC
			GTGGCTCTTCACACGTGACCAGGCAACTTTGTACATTTGACAGGGA	OniA _{MN} 203	2,658	45 CAGAGACACAGCTGGAGCTAAAAGACTACACTTTGGGTGTGCAAT
OniA _{ki} 157 _{ahn}	164	164	GIAUUAUGUITTIGIUGAGATUAGAAAAACGACAGCGCGATAAA AATTAGTATTGTTGCACTTCACAAATTA			
			TTAATGATTCACGGGCTCAAATAAAAGGGATTTAAGTTGACGTTGC	OniA _{MN} 204 _{abcd}	1,720	91 GGCGAGTAAGATTGATCGCGCGCAGGCTTCCAGGACTCTTGTTT
UniA _{LM} 172	5,729	57	GICACGIGAG	OniA _{MN} 216	1,686	25 GTCAGACCTTTTGGCGAGTAAGATT
OniA _{LM} 173	8,368	16	CAATTAGGACTTGGGGGCGATATT			TITAAATATAAACAGTIGTCCCCCCCAGCTGAGCGAGGCCTTCT
UNIA _{LM} 175	6,224	24	AAATAAAAGGGATTTAAGTTGACGTTGCGTCACGTGAGCGCGGCG			TCACCAGAGTTTTGGATCAATCAGGCAGACAGTGGCTTCTTTTGAT
OniA _{LM} 179 _{ab}	5,711	53	CATAATAC			TAAACCCCAAATTGTCATTGGGCAGAGGTAATCATGTGACAGGCA ATTCGGTCCAATTTCAACCTTGTCTCCATGAATTCAATAGTTTAAT
			CTGTCACGGACGGATATGTTTTTCCACGCGGACGGAGTCAGAGCT	OniA _{MN} 211 _{abcd}	el 344	213 AGCAGCTCGGTCCCCATACGGCCGTAATCAG
0-14 484	F 16-		CGAGCTTTGGGAGGATGGATTTTATTTTGAGGTATTTCCGCTGATTG	OniA _{NO} 212	3,601	16 TACAATTAACTTGCTA
OniA190	5,469 2,470	135	GCTTTCTTTTG	OniA 213	3,472	20 AAAATAATITITAAAAAGTA 20 CTCATAAAATCACTCCCTCCCCATCAATCACA
OniA191	3,178 2 079	13	CTCAGCTATTTGAAAGCACAACTATATATACATATAT	OniA _{ve} 221	2,919	30 GAAGTTTTCTGTCTTTTGCTTCTCCTCAC
OniA _{LM} 192	2,438	28	GCATAATTTTTCTTGTCTATGGTGACGC	OniA _{NO} 222	282	36 GCGTCACCTTGATCGACGAGTGCTTGGAATTTAAAT

Oryzias latipes me PFC	daka Hox Aa Dist to 3' gene I	enath Sequence			
OlaAA _{AC} 1	5,762	16 CTGTCCTTGTGCGCCC			
		ТGTTAATTATCTTGATTTCAAAACAATCTGAATCAAATCA	r r		
OlaAA _{AC} 20	1,772	287 CCAATTITTICIGTAACAATAIGITICIAATTITAIGGGGA			
OlaAA _{AC} SU _{ab}	921	42 IOUCHIGAEAGEGICACGTGCCGGCGCCCTGACCAATCAG AGCCCGAGCTGCCGGCTCTTGTGCCCGCGCAGGCGCTTACCA TCTTTGCAAGCGCTGCCGCCTTGTGCCCCGTCAGGCGCTTT			
OlaAA _{AC} 31 _{acdef}	167	157 TAAAAAAGAGCCAGAAAGCTTCAATGTTGGA ACCACAAACTCCAGACAGAATCTTTGGCTIGTGTTTTGTTCATT			
OlaAA _{CE} 47	6,877	66 ATTTACCACGGTGGTTAATCTTA			
OlaAA _{CE} 49	6,475	17 AGAAATAAAGATTTTGC			
OlaAA _{CE} 57 _{bc}	2,146	GCTATAAAAAGCGCAGTTCAGTGCAGAGCTGGCTTTGGTTTTC CTGAGCATCCTGTCCTCAATTACAGCTTAAAAGCCTCAGTAC 120 AACTCGTAGAATTTGCCTGGATTGACTAAGAGGCGG			
OlaAA _{CE} 50	1,266	23 CTTGAGACCATTTTTTAGGCAGA			
OlaAA _{CE} 60 _{abod}	204	TGTCAATTTCTGCCGCGTGATCACGTGACCCTCCTCCTCAGTC GAGTGGATGGAGAGGGCTCTCCACGTCAGCTTACGTCTCCAA 115 ATTTCTGCTTAGCGAACCTGCTTCAAAGAG			
	0.000	CCTAATTATGGGACATCCTCCCCGTTGCCGCAGCAACGCCGC CATAAAAGCTGTCTGAGAGTCTGGAGCATTTGTACAATTGGA GTCCAGTGCAATAAACCGTCTGAGACCCAAGGTTATTAACTC	- -		
OlaAAEF05bcd	3,082	GGGAGGGACCTCCTCTTTTCCAGTCTTTCATTGGTCTGGGGC			
OlaAA _{EF} 75 _{acde}	147	СТАСССТЕGAGAGGGGGGCCССТААТСАТАТССАGCATGTT ТГБТАССАGAAATGTCAGCCAGAAAGGGCTATCTTCTTCCTT 134 ССССААА			
		GACTGTCGAGTGGTTTAGGTAGTTTCATGTTGTTGGGGTCCAT			
OlaAA _{FG} 79 _{abcde} OlaAA _{FG} 89	2,645 904	85 ТТСТААСТСТGСААСАСGАААСТGCCTTAATTGCCACAGTTA 17 GTAACTGTTTTTATTTT			
OlaAA _{FG} 93 _{abcdef}	223	CACGTGACTCTGCTGACCAATGGCAGGGGCGTCTGTCTCCCC ATTACTTTCCCACTGTAGTTCTGTGTGGGGGCCAAGTTGCTACT 127 TGATTTCTCCCACATTGTTATTTTGTGAGGCTGGGTTTACTGC			
OlaAA _{GI} 94	3,952	19 ACTACCTICATITIGCACA			
OlaAA _{Gi} 98 _{abcd}	3,113	TGTTAGTTGTATGCAGTCATAAAAGACAATTACCGCCATAAC 73 CTTTTATTGGGTGCAAAGCGCCGCAAGGCGA			
OlaAAci103bote	2,638	GCAGATGGACCCAAACTTCAAAGACTCGCCCAGAGACAGT CAATAAAACGCCTGGTCTATCTGTCTGCGCTTCCAGT TAATGACTTTATGGCAGTCCAGACAAATAGGCCGTTCCA GAATGACACCCCATTGTTCTTCTTCTTTCTGTGACTGAC ATTTCCACAAAAGGCTGGCGCAAAGATACAGCTTATTGGA TCCTGCCCGCCGGGGGCGCAGGACTCACGGTCATTCTGAC 288 C	: 7 3		
Gi - bulei	_,	GTTIGGIGTAAATCTAGGGTGTATIGCTGTAATATATCACACI		070 50	AAATAAAAGGGATTTAAGTTGACGTTGCGTCACGTGAGCAGG
OlaAA _{GI} 111 _b	98	84 ACCTCGTAAAAACGACACTGGGGATTCTGGGCCAACAATC ATGGCGCCTCACCCCTCCCCT	Саалаци (7 Sab 4,	625 115	CTGTCAGGGACGGATATGTTTTTCCACGCGGACAGAGTCGGA GCCCAAGCTATGGGAGGATGGATTTTATTTT
OlaAA _w 119 _{aba}	3.725	TTGGCCACAGCGCATCACGTGGGAGGGACCCGTGAACATGA 170 A	Glav (LM To Tabed 4,	025 115	GGAAGAAAACCGGAGCCCTGGTCTGGCCATACGATGCAGAT
OlaAA _{IK} 120	2,375	21 TTAAATAAAAAACACAACCTT	OlaAA _{LM} 182 5,	026 64	TATATGCTGGTTACCCCCACTTT
OlaAA _{IK} 126	1,416	14 GGCTAATAAAAGAT	OlaAA _{LM} 189 3,	199 14	GGAITHAITHC
		TGGCGCAGCGCGACAATTCAAAACAGCAAAGCCCTGCCTTC TCGCTCGCCTTAGCCCAGAGCGCGGGAGGCGCGCCCCCT ACATCCCACCCAGTATTTCCTGCGTGCGGGGTTAACCTCTG AGGTCACCGAGCAGGATTTACCACGGTGGTCAACAAAAGCACG TGATTCCCCGCCGACACCCATATTGGGGCCCTACGTAAGA	OlaAA _{LM} 193 _{abod} 2,	249 201	AAGGCCGCGACTTCATTTGCATAATTTTTCTTGTCATGGTGAC GCTCTGGTTCGGGCAGTTCACTGGTGTCTGCATGGATCGGT GAAGGATCTCATAGTCAAGCATGCCTCGGCTGGCAGCGACGATAA TTGCTATGAAGCACTGGTCCACTGCTCCATAGCATGACGATAC ATTCAGTCTTCAGGCCCAGATAAATCTTATCT
OlaAA _{IK} 132 _{abcd}	384	AGAATCAAGTCCATGTCCCACTCATTTCCATAATTCATCATA 382 AATT			ATCGATTICGTCGCTGAATGAGAAAGTATTGCACGGTGCTTTG CATTCATCGTGAGAGGATAAGGTAAGCAGGCCAGAAATAGG CTCCCTCAGTTGTAAATGGTGGAGTTTGTGTGTCGCGCAGTGA
		AAACTITATTAAGGGGTTGATTCTGGCTCCCTGACATTTAGGT GCTAAATGAATGGGGGTTTGTCTATGAATAGATCGTAAAA ATCATCCGGGGACCGGCCAGATAGGCTCACTGGGCCATAAAC CCTCACCGGCCACCGCCAGATAGGCTCACTGGGCCATAAAC	OlaAA _{LM} 194 _{acd} 1,	819 169	TTTATCACCGTATGACTTAGATCTCGGTTCAGGAAGAGTTCA
OlaAA _{KL} 136 _{ab}	6,756	199 GTEACOIGGIAGCCATAAAGTAAGTATAAT GGTEACAGGAGGTCAGCCGCAGCAGCAGGAGAAAAATCTGC ATCCTCTCGGGAGGCCACCAGCAGGCGCGCTTTAGGCCAAGT	OlaAA _{LM} 196 OlaAA _{LM} 197	826 72 784 17	GGITTTICIGGITTICTTIGGTAATTICTT GGITTTICIGGITTICT
OlaAA _{KL} 140 _{abcde}	5,016	84 C GGTCAAAAGTTTACGCACTGAACAAGTCTCAGTCATCTGTTC			TGTCAGGTCTGTATTGAAAAGTAAGATGGATCGCCACCATTT CTCCTCCTCACAGTGCTTCTTGTAACCCCAGGTTCACCCAG GAAGCCATTGGAGGAGAGCGTCACGTGACCACGGGGTGCC AATGTTATTCTACAAGGGTGTCAGGACCCTGTCAGTTTCTGA
		ACTCAGAGCCTGATGCCAGCTTTATAATAGGATCTTGACTC TCCACACAAAAGGCAGAATAGCTTTGCATTACATATGTTGCA CGGTGCACTCCAGGTGAACCCTGGAAGCCCGATGACCTCGC GTTTGGGACCGGGGGGGGGG	OlaAA _{LM} 199 _{bcd}	190 184	AATAAATATTGGGAAAC AGAAGCCTTAAATGTGTTGCGAGGGCACCGAGCTGTCAGACC TTTTGCGAGTAAGATTGATCGCGCACAGGCTTCCAGGACTC
OlaAA _{KL} 143 _{bcd}	4,450	292 GCA	OlaAA _{MN} 204 _{abcd} I,	403 91 360 25	GTCAGACCTTTTGGCGAGTAAGATT
OlaAA _{KL} 146	2,512	19 TAAGTGTICTGTTATTTIC TCCAAGGCCGGGGTGAACCCCCGGTCACTGCGTCTAACAGA ATGAAATGTCGCCTCTTTGGGGAAAAAAGGGAGGGAAAA GCCTTGTTGTTTAACAAAGACTGTCAATGAGTAAGATTAATC	Г	20	TGTAAATAAAAGCAGTCGTGCCCCAGCTGAGAGAGGGGATA TTCACCAGAGHTTTIGGATCAATCAGGCAGAACAGTAACTTT TGATTAAAACCCCAAATTGTCATTGGGCAGAAGTAATCATGT GACAGGCAATTCGGTCCAATTGAACTTGTCCCATGAATT
OlaAA _{KI} 149 _{hode}	1.744	AGAAACAAAATGGAAACGGTGTCACTTTAGGGTCAGGCAGA 178 AGTTATCTCTGT	OlaAA _{MN} 211 _{abcrief}	334 211	G
NL DODE	.,+		OlaAA _{NO} 219 3,	083 30	CTCATAAATCACTCCGTGGCATGAATGAGA
		CCATTGGTTCCTGTTTACATGATGCCCACAGGACAGCCGGTG ATTGGTGGCTCCTCACACGTGACCAGGCAACTTTGTACATTTC	, OlaAA _{NO} 217 1,	840 29	TTTATGTATCTCTTGGAAACTTGAAAAAA
Ola44 157	164	ACAGGGAGTAGGAGGGTTTTGTGGAGATCAGAAAAACGACA 164 GCGCGATAAAAATTAGTATTGTTGCACTTCACAAATTA	OlaAA _{NO} 220 1,	434 24	TAAACATCAAGTCTGCTTGACCTC
OlaAA _{LM} 165	5,943	15 TGACGGAAAACAAGC	OlaAA _{NO} 222	283 36	GCGTCACCTTGATCGACGAGCGCTTGGAATTTAAAT
OlaAA _{LM} 172	5,117	TTAATGATTCACGGACTCAAATAAAAGGGATTTAAGTTGACG 57 TTGCGTCACGTGAGC	OlaAA _{NO} 223	194 74	ACTGGCTGACCCTGGCCCACGTGACAGCACCCGTTCATTGAT ATCACCCCACGCGCCCTCCTTCCCTTACTGAT

Tetraodon nigrovii	ridis spotted green	n pufferfish Hox Aa		
PFC	Dist to 3' gene	22 TCCAGGAATGTCTTTAAAGACA		
TniAA16	0,007 1 783	22 AATAAAGTTTATCACTGGGTAATAGAA		
ThiAA _{AC} 10	4,783	27 TAAAATTTAAAGATTTAAAATCCCAT		
CTUD O VAC T	0,040	CTTGTTGCGCATCTGTAACGACCGCACTAGGTGAT		
TniAA _{AC} 18	3,170	44 CGTCCAGAA TGGCTAGACGGCAACTTTCAACTTGACCTTGGCCT		
TniAA _{AC} 30 _{abc}	893	42 CCAGCCG		
		CTTTGCATAGCCAGACCACGTGACACCAGCCCGAC CAATGACAGCGCGACCTCGGCGCTCCTGTGCGCGCT		
ToiAA 21	170	CAGAGTGGCAGTACTCCCTGGGAACGCGTATCTCC		
ThiAA _{AC} ST _{acdef}	8.070	16 ACATITAAGGTTAAAA		
TniAA _{or} 59	1 843	22 GTGGTGTCGCCTGGCCGGAGAG		
THE RECEIPT	1,040	GCTATAAAAACACAGGTCTGTGCGGAGCCGGCTTT GGTTTTTCTGGGCATCCTGTGCTCAATTACTGCTTA		
${\rm TniAA_{CE}57_{bc}}$	1,789	120 TGACTGAGAGGGGG TGTCAATTCTGCCGCGGGTCACGTGATCTCCTCC		
T=: 4.4 CO	000	TCTATGGAGTGGATGGATGGATGGCTCTCCACGTCAG CTTACGTCTCCAAATTTCAGCATAGCAAACCTGCT1		
I NIAA _{CE} 6U _{abcd}	203	114 GAAAGAG CCTAATTACGGGACATCCTCCCTGTTGCCGCAGCA		
		ACGTGACCATAAAAGCCGTCTGAGAGTCTGGGGCA TTTGTACAATTGGAGTGCAGTGC		
TniAA _{EF} 65 _{bc}	3,721	120 GAGAACCAAGGTTAT GCACAGTGAAGGGTGAACCAAATAAAACAGGTTT		
TniAA _{EF} 67	1,239	46 TTTAAAAATAAT ATTGGTTTTACAGTCCGCACAGTGGAGAGGGGGGGC		
		GCCTCTAATCATATCCAGCATGTTTTGCACAAGAA ATGTCAGCCAGAAAGGGCTACCTTCTCCCCTCGCC		
TniAA _{EF} 75 _{cde}	121	108 AAA		
T :		GACTGICGAGIGGITTAGGTAGTTICATGTIGTIGG GGTCCATTTCAAACTCTGCAACATGAAACTGTCTT		
ThiAA _{FG} 79 _{abde}	2,514	85 AATIGCCCCAGIIA		
ThiAA _{FG} 02	1,045			
TTIAA _{FG} 04	914	24 AIATTITOGAAACIAIAIAGCACI		TCCAAGTACGGGGTGAACCCCCAGGTCAGCGCGTCT AACAGATATGAAAACGTCGCCCCTTAGAAAAATG
		CACGTGTGTGCGCTGCCCAATGAGAGCGCGCCTTG		GCACGCCTTGTTGTTTAACAAAGACTGTCAATGGG
		GCTCCCCATTACAAGCCCACTGTAGTTCTCTGTGGC GCCAAGTTGCTACTTGATTTCTTCACATTGTTATTTT	TniAAv 149 1.6	CAAGATTAATCAGAAACAAAATGGAAGCAGTGTC 67 161 ACTTTTGGGTCAGGCAGAAGTTA
TniAA _{FG} 93 _{abcdef}	214	127 GTGAGACTGTGTTTACTGC		
		TGTTAGCTGTTTACAGCCATAAAAGACAATTACCG CCATAACCTTTTATGGGGTGCAAAGCGCTGCGAGG		CCATTGGTTCCTGTTTACATGATGCCCACGGGAGA
TniAA98	6 866	CGAGAGGAGAAAAAGACGCGGAGGACGA 112 AGACAGCTG		CGCGCIGATIGATIGGTGGCTITTICACACGIGACCAGGC AACTITGTACATITGACAGGGGGTAGGAGGGGTATT GTCCACCACCACAAAAACCCACCACCCCCATAAAAA
GROCabcde	0,000	112	TniAA _{KI} 157 _{abc} 1	64 164 TAGTATTGTTGCACTTCACAAATTA
		GCAGATGGACTCAAACTTCAAAGACGGCCAGAGA		
		CAGCGCAATAAACCCGCCTGGTCTGCTACTCTGTC TGGCATTCCAGTTTAAATTGTTTTATGACCGTCCAG	TniAA _{LM} 158 7.1	AAATTITAATTCGCCATGTTCACGTGACTTGTTGAA 61 62 TAATGAATGCCCTGGGGTCAGAAATA
		ACACAATTAGTCCGTTTCCAGAATGGCACCCATTT GTTTTTTTCTCCTCTTTCTGTGAGACAACGCTCTGGA	TniAA_172 4.8	TTAATGATTCACGGGCTCAAATAAAAGGGATTTAA 92 57 GTTGACGTTGCGTCACGTGAGC
		CAAAAGGCTCGGCGGAAATGATCAGTTTATTGGA TTCCACCGACGGGGACGCGCAGGACTCACGGTCAT	TniAA_179_ 4.8	AAATAAAAGGGATTTAAGTTGACGTTGCGTCACGT 74 39 GAGC
I nIAA _{GK} 103 _{bcdef}	6,402	287 TIGAAGAG GTTTGGTGTAAATCTAGGCAGTATTACTGTCATATA		
TniAA111.	4 968	TCAAGCCACCTCGTAAAAACGACACTGAGGATTCT 84 GGACCAACAAATC		AGTGGGCTTCGGGAGGATGGATTTTATTTTGAGGTA
GKTTB	4,300	04 concentration	ΤρίΔΔ 181 4.5	TTTCCGCCTATTGTTCATTACCACCGTGAGTTATTG
Toi 4 4 112	E 21E	TTAATGAATTCAGTTCCTTATAAAAATCTGCAAATT	TITIAA _{LM} TOT _{abcde} 4,5	09 IZI clockookoockoooleko
THAAGK 113	5,215	00		AAGGCGCTGCTGATTTGCATAATTTTTTTGTTCGTG
		ATGGCGCCTGGTGGTGCCCCCCCTCCTCCCTCCT		GCGTGGTCCCCGGTGAAGGATAACAGAGCAACATA
		CAGGCTCTGGCTCATAAATCTGCTGTTGTTATGAA		GCCTTGGCTGAGTTTGATATTGCCATGAAGCCCTGG
		AATTTACAACACAGCGACGTAACTTTACGACCGTA	TniAA _{LM} 193 _{abd} 2,0	69 197 GGCCCAGATAACTCTTATCT
TniAA _{GK} 119 _{abc}	2,714	198 ACGGAGCCGTGAACATGAA		
T-: 1 1 100		AGTAATTGTCTTTAGATTGACAACATATGTTCAACC		ATCGATTTCGTCGCTGAATGAGAAAATATCGCCCG GTGCTCTGCATTGGTCGTCAGAGGATCAGGTAAGC
ThiAA _{GK} 129	2,004	52 CORACIOARIGECCIG		GGGCCAAAAATAGGCTCCCTCGGTTGTGAATGGCG
		TGGCGCACCACGACAATCCAAAACAAGGGAGTTT	TniAA _{LM} 194 _{abcd} 1,6	46 169 ACTTAGATCTCGGTTCAGGAAGAGTTCA
		GTTCTGGCTTTGGGAGCGCGCAGGCGCACATCCTC CACATCCCACCCAGTAGTTGCTCCGTACTCGAGTT		
		ACCTCTGGAGGTCACCAGGCAGGATTTACGACTGG		TGTCAGCCCTGCATTGAAAAGTAAGATGGATCGCC ACCATTTCTTCTCCCTCACAGTCCTTCTTGTAACCCT
		TCAACAAAAGCACGTGATTCTCCGGCGTACCCCAT ATTTGGGTGCCTACGTAAGAGAGAATCAAGTCCAT		AGGTTCACCCGAGGAGGCCATTGGCGGAGGGGGCGT
T-: 0.0 400		GTCCCACTCATTTCCATAATTCATCATAAATTGTGC		CACGTGACCACGGGGTGCCAATGTTATTCTACAAG GGTGTCAAGACCCTGTCAGTTTCTGGAATAAATATT
I NIAA _{GK} 132 _{abcd}	372	370 AAGGGIGCT	TniAA _{LM} 199 _{bcd} 1	90 184 GGGAAAC
		AAACTITATTAAGGCCGAATCTGGCTCTGACATTTC		A CAA COOTTAA A TOTOTTOOCACCOCACCOACOTO
		GAAGCTAAATGAATGGGGGGGCTTTTGTCTATGAAT TAGATCGTAAAAATCATCCGGAGTGCCGCCAGATA		TCAGACCTTTTGGCGAGTAAGATTGATCGCGCACA
		GGCTCACTGGCCATAAACGGTCACGTGGTAGCCAT	TniAA _{MN} 204 _{abcd} 1,4	68 91 GGCTTCCAGCACTCTTIGTTT
TniAAva 136-	6.066	TAAAGTAAGTTTTATGGTTTTGGGGAGTTGACAGTA 197 TATTGCACATAACATATAAT	TniAA _{MN} 216 1,4	32 25 GTCAGACCTTTTGGCGAGTAAGATT
rin o (_{KL} roo _{ab}	0,000	GGTTCATGTGGAGGTCACCAAGATAAATCTGCATC	TniAA _{MN} 207 9	18 19 GTATTTTAGCCATAATCAA
To: 0.0 140	4.000	CTCTCGGAGCCACCAGCAGAGCTCGCTTTAGGCCA		TGTAAATAAAAGCAGTCGTTACCAGCTGAGAGAGG
111AAKL 14Uabcde	4,632	10 Adrie		CGATCTTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTGATCAATCA
		GGTCAAAAGTTTACCACTGAACAAGACTCCGTCAT		CAGACAGIGGCTTCTTTTGATTAAACCCCAAATTGT CATTGGACAGAGGTAATCATGTGACAGGCTATTCG
		CTGTTCACTTGGAGCTCGATGCCAGCCTTATAATAC CGATCTTGACTCACAAAAGACAGAATACCTTTG		GTCCAATTTCAACCTTGTCTCCATGAATTCAATAGT TTAATAGTAGCTTCGTCCCCACACGACGACGATAATCA
		AATTACATATGTTGGACTGTGCACTCCAGGTGAAC	TniAA _{MN} 211 _{abcdef} 33	37 216 G
		CUIGGAAGUGUGGIGAUUIUGUGIUGAAGACCGG GGGATGGGACCCCCGCCCGCCCCAGCAACAAGA	TniAA _{NO} 219 2,5	36 30 CTCATAAATCACTCGGTGGCATGAATGAGA
TniAA., 143	4 092	TTGAGTGCCCGTCGTTTTATTAGGGCGGCTGATTGG 306 TGAATTTCCT	TniAA	GCGTCACCTCTATCGATGAGGCCCTGGAATTTAAA 81 36 T
KL + Obcd	4,003	000		

Takifugu rubripes 、 PFC	Japanese pufferfish Hox Dist to 3' gene Length	Aa Sequence		
Ταιδά 5	7 175 102	TTATTGGCCTCCCTTTCGGGTTGCGGGTTACGTGG AAACCCTGCATCTTTGGCGCATGCAAATTTACATCC AGGCTGATATGCTATGTGAGGGACTCATTATCCAAG GGAGCGAAAACATTCTTGGTGGTTGAGTTACACACAG GAGGCTCGAGCGGCACCGTGTTCAATGGAGAGAG ACAGCTTGFGAGC		
	5 423 16	CTGTCCTTGTGCGCCC		
TUARACT	5,425 10			
TruAA _{AC} 8	1,704 34	GAAAAAGAGAAGTCATATCAACAGTAAATAACAA		
TruAA _{AC} 14	625 15	ACTGAAAAAAGGAAT		
TruAA _{AC} 21	1,030 235	AAAATAAAGGGTAAAAACATAATGATTGTAAAAGT TAATGTCCTTCAATGGCTCTCAATGGGGCAGGAATT CTCACCCCTCTTCCGCTCCTTCAAGGCATGCAGAG GTTCCTTTAAAGCCTGGATTGCCGGACAGCCTGGGT GGCTAGACGGCAACTTTCAACTTGACCTTGGCCTCC AGCCCGTCCTATGGAGGAAAAAGCAGGAGTATTTCCA GTGTTTTGCATGCTGTGAAACA		
TruAA _{AC} 30 _{abc}	888 42	CAGCCG		
		CTTTGCATAGTCGGGTCACGTGGTACAACCCTGGCC AATGACGCGCGTCCTCGGCGCCCTCTGGCACGTCA GAGTGGCAATACTCCCTGGGAACCATATCTTTTT	TruAA _{KL} 136 _{abc}	3,67
		TTCAGTCCCTGGGCTTTTTAAAAAAGAGCCACAAGC		2,0
TruAA _{AC} 31 _{abdef}	165 156	CICAAIGIIGGA		
TruAA _{CE} 48	7,169 26	TAATITAGTICIAIGGTIGTAGGAAA		
TruAA _{CE} 53	6,132 29		Tru 0.0 140	1.0
	4,880 4.20	GCTATAAAAACGCAGGTCTGTGCAGAGCTGCCTTTG GCTTTCCTGGGCATCCCTGTGCTCAATTACAGCTTAAA AGCTTCAGCACAACTCGTAGAATTIGTCTGAATTGA CTGAGAGCCGG	HUAAKL Hobed	1,04
TUAACEOT	1,009 120	TGTCAATTTCTACCGCGCGGGTCACGTGATCTCCTCCT		
		CCATGGAGTGGATGGAGATGGCTCTCCACGTCAGCT	TruAA _{KL} 157 _{abc}	16
TruAAce60abod	203 114	TACGICICCAAATTICAGCATAGCAAACCIGCTIGA . AAGAG	TruAA _{LM} 172	4,83
ТгиАА65	3 300 128	CCTAATTACGGGACATCCTCCCTGTTGCCCCAGCAA CGCGGCCATAAAAGTCGTCTGAGAGTCTGGGGCATT TGTACAATTGGAGTGCAGTGGCAATAAACCGTCTGAG AACCAAGGTTATTAACTGTG	TruAA _{LM} 179 _{ab}	4,81
TruAA _{rr} 71	1 325 15	TTTATTGCGGAAAAA	T 44 464	
THAN ULEFT	1,020 10		I ruAA _{LM} 181 _{abcde}	4,56
TruAA _{EF} 75 _{acde}	150 137	GGGAGGACCCCTTATCTTCCACTATTTCCATTGTT TTACAGTCCGACAGTGGGAGAGGGGCCCCCTCTAAT CATATCCAGCATGTTTIGCACAAGAATGTCACCA GAAGGGCTACCTTCTCCCCTCGCCAAA GACTGTCGAGTGGTTTAAGTAGTTTCATGTGTGGG GTCCATTGCAACCTGCAACATGAACTGTCTTAA	TruAA _{LM} 183	3,99
TruAA _{FG} 79 _{abde}	2,700 85	TTGCCCCAGTTA	TruAA _{LM} 186 TruAA _{LM} 187	3,87 3,52
TruAA _{FG} 93 _{abcdef}	212 127	CTCCCCATTACAAGCCCACTGTAGTTCTCTGTGGGG CCAAGTTGCTACTTGATTTCTCCACATTGTTATTTTGT GAGACTGTGTTTACTGC		
TruAA _{GK} 95	7.934 30	TTTATTTATTAAATAAAAACAAATTATATCT		
TruAAcr/99	7 590 98	ATAAAAGACAATTACCGCCATAACCTTTTATGGGGT GCAAAGCGCTGCGAGGCGAG	TruAA _{LM} 193 _{abd}	2,01
TruAA _{GK} 100	6,809 20	CCTTTGCTTAGCCAGTCCTA		
GR	-,		TruAA _{LM} 194 _{abcd}	1,59
		GCAGATGGACTCAAACTTCAAAGACGGCCAGGAGA AGCGCAATAAAACGCCTGGTCGGCTGTACTGTCG GCATTCACAGTTTAATGGTTTTATGGCCGTCCAGAC ACAATTAGCCCGTTTCCAGAATGGCACCACTTTGT TTTTCTCTTTTTTGGTGGACAACACCCTCTGGACAAA AGGCCCAGCGGAAATGATCAGTTTTATTGGATTCCC GCAGCGCCAGCGGAAATGATCAGTTTTTATTGGATTCCC	T 11 100	
TruAA _{GK} 103 _{bcdef}	7,098 285	GAG	I ruAA _{LM} 199 _{bcd}	19
		GTTTGGTGTAAATCTAGGCTGTATTACTGTCATATAT	TruAA _{MN} 200	3,05
TruAA _{GK} 111 ₅	5,556 83	CAAGCTACCTCGTAAAAACGACACTAAGGATTCTG GCCAACAAATC		
ind block in the	0,000 00		TruAA _{MN} 204 _{abcd}	1,43
TruAA _{GK} 116	4,073 35	TGTTTTATATCAAAATGTCTAAAAAAAAAAAAAAAGT	TruAA _{MN} 216	1,39
TruAA _{GK} 119 _{abc} TruAA _{GK} 125	3,321 197 3,254 15	ATGGCGCCCGGTGGTGGGTGACCCCCCCTCTTCTT TCTCTCCTCCACCCAGTTCACCAGCTCTCCCTCC GGCGTGGCTCATAAATCGGCTGTTGTTATGAAAA TTACAACAGCGGCGTACTTTACGAGCGGACTC GTCTCCCTATTGGTCGCAGCCGATCACGTGGCGGAG GACCCTGAACATGAA	TruAA _{MN} 211 _{abcdef}	33
		TGGCGCGCCACGACAATACAAAACAAGCGAGTTTG TCCTGCCTTTGAGCGCACGGAGGCGCGCACCCTCCA CATCCACCCAGTATTTGCCTCTGTGCATGAGTTTACC TCTGGAGGTCACCAGGCAGGATTACGACTGGTCAA CAAAAGCACGTGATTCACCGGCGTACCCCCATATTTG GTTGCCTACGTAAGAGAGAATCAAGTCTATGTCCCA	TruAA _{NO} 214	2,73
Tru & 400	070 07	CTCATTTCCATAATTCATCATAAATTGTGCAAGGGT	Τημά Δ 222	-
TTUAAGK132abcd	376 374	001	IIUAA _{NO} 222	28

3,673	AAACTITIATTAAGGCCGATICTGGGTCTGACATITG GACGCTAAATGAATGGGGGGTTTTGTCTATGAATTA GATCGTAAAAATCATCCGGAGCGCGGCCAGATAAG CTCACTGGCCATAAAACGGTCACGTGGTAGCATTAA AGTAAGTITTATOGTITTGGGGAGTTGACAGTATATT 204 GCACATAACATATAATCGCACTGA
2,046	GGTTCATGTGGAGGTCATCTCCGGCACGAAGATAAA 63 TCTGCATCCTCTCAGAGCCACCAGCAG
1,641	TCCAAGTACGGGGTGAACCCCAGGTCAGTGCGTCTA ACAGATATGAAAACGTCGCCCCCTAGAAAAATGGC ACGCCTTGTTGTTACAAAAGCTGCAATGGGCAA GATTAATCAGAAACAAAATGGAAGCAGTGTCACTTT 161 TGGGTCAGGCAGAAGTTA
164	CCATTGGTTCCTGTTTACATGATGCCCACGGGAGGC GCGGTGATTGGTGGCTTTTCACACGTGACCAGGCA CTTTGACATTTGACAGGGAGTAGGAGGGGTTTTGTG GAGATCAGAAAAACGACAGCGCGGATAAAAATTAGT 164 ATTGTTGCACTTCACAAATTA
4,830	TTAATGATTCACGGGCTCAAATAAAAGGGATTTAAG 57 TTGACGCTGCGTCACGTGAGC
4,812	AAATAAAAGGGATTTAAGTTGACGCTGCGTCACGTG 53 AGCGGGGCGCATAATAC
4,567	CTGTCACGGACGGATATGCTTGTTCAACGCGGACCG AGTGGGCTTCGGGAGGATGGATTTTATTTGAGGTAT TTCCCCCCATTGTTCATTACCACCGTGAGTTATTGCT 128 GCAGGAGGCAGAGGTCAG
3,996 3 871	AGCAGTGAACGTGTTGTGTGATTGTGTCCCCCCCGG GGAAAACGAGCATATAATGGAAGACGAGTGCCAT CTAGGACCGCCCGCCCATGCTGGGGACACGACGACGTC TCCCTTGATTATGGCCCCGGGGACTTGGGGAAGAT 171 GGTGTGCGAGACCTAATGGACGACTATTCGAT 13 CGGGACTTGGGG
3,520	30 GTTTTGTTCATGTATGGGCGCCGTTGGAAA
2,012	AAGGCGCTGCTGATTIGCATAATTITTITGTTCGTGG TGACGCTCAGGTTCGGGGCAGTTCACTGCTGTCGC GTGGTACTGGTGAAGGATCACATAGCCCAACATAG CCTTGGCTGGTTGATATTTCCATGAAGCCCTGGC ATTGCTCCTTACCTAGCGGACGATACATTCAATCTCGGG 199 CCTAGATAACTCTTATCT
1,591	ATCGATTTCGTCGCTGAATGAGAAAAATATCGCCAGG TGCCCTGCATTGGTCGTCAGAGGATCAGGTAAGCAG GCCAGAAATAGGCCGCCTCGGTTGTGAATGGCGGAG TTTGTGTGTGTCGTGCGTGATTTATCACCGTATGACTT 169 AGATCTCGGTTCAGGAAGAGTTCA
100	TGTCAGCCCTGTATTGAAAAGTAAGATGGATCGCCA CCATTTCTTCTCCCCACGTCGTTCTTGTAACCCTAG GTTCACCCGAGGAGGCCATTGGAGGAGGAGGGCGTCA CGTGAAACACGGGGTGCCAATGTTATTCTACAAGGGT GTCAAGACCCTGTCAGTTTCTGAAATAAATATTGGG 40 AAAC
190	104 8880
3,053	34 CATTCCATGCTGCTCCAGTTCGAAGAAATAAATA AGAAGCCTTAAATGTGTTGCGAGGGCACCGAGCTGT CAGACCTTTTGGCGAGTAAGATTGATCGCGCACAGG
1,431	91 CTTCCAGCACTCTTTGTTT
1,397	25 GICAGACCITITIGGCGAGTAAGATT
332	ТGTAAATAAAAGCAGTCGTCCCAGCTGAGCGAGGC GATCTTCATCTGAGTTTTTTTGGATCAATCATGCAG ACAGTGGCTTCTTTGATTAAACCCCAAATTGTCATT GGCCAGAGGTAATCATGTGACAGCCTATTCGGTCCA ATTTCAACCTTGTCTCCATGAATTCAATAGTTTAATA 212 GTAGCTTGGTCCCCACACGACCATAATCAG
	AGAAAACTAAAATGAAATTAGTAGAGTAAATAGAG AGCCGTATGCAAATTCTCAACAGGTTGGCAATGAA TATAATTIGATAATCGGGGGGCACTGTGATGACAC AGGTTCACTTITTACAATTCTTTTAATTGCATTGTA AATCTTAATGCGTACATCGCATTATTGGGATGCATA TAAAGTAAATACTAAGATAAAAATCTAAGAACGCT
2,735	ZZZ AGCATTI

36 GCGTCACCTTGATCGACGAGCGCCTGGAATTTAAAT

175	
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Danio rerio zebra	fish Hox Ab				
PFC	Dist to 3' gene Le	ength Sequence			
DreAB _{AC} 30 _{abc}	828	39 CTAGACTGCAACTTTCAACTTGACCTTGGCCTCCAGCCG			
B 45 64		CTITICCATGTCACGTGCCTGCTCTCGTCCAATAACAGTTGGATCCTGAC GCACGCGGGGCGCATGGGTATCTGTTACTCCACTGATCCACAGCTTCT			
DreAB _{AC} 31 _{ad}	151	106 CITICAGIC			
DreAB _{CE} 44	4,069	19 AATAAGTTGAGGAAATGAA			
DreAB _{CE} 56	2,131	40 TTTTTACGAACTTGGTCTTGTTCACAAATTCTTACATTTT			
DreAB _{CE} 58	813	17 GCTCTTTAACATTTITA			
DreAB _{CE} 60 _{abc}	183	TGTCAATTTCTGCCCTTGGTCACATGACTGGCGCTCTCTGGAATGGATG 87 GAGATGGATCTCCACGTCACGTCACGTCTCAAAATTTC	<i>Oryzias latipes</i> PFC	medaka Hox Ab Dist to 3' gene L	ength Sequence
DreAB _{EF} 64	3,127	32 ATGGAATTATTATTATTATTATTAACGAATATTG	$OIaAB_{AC}30_{bc}$	663	31 CAACTITICAACTIGACCITIGGCCTCCAGCCG
DreAB65	2 421	GCATECTTTGAGGCTCGATGGAATTTCGCCCTAATTACGGCACATCCCC CCGTTGCTGCAGCAACTCAGTCATAAAACCTGTCTTAGTCTGGAGCACT TGTAGAATTGCAGTGAGGTGCCATTAAACCGTCTGAGAACCAAGGTTAT 171 TAACTGGACTAAGAGCTGGAAAAC	OlaAB _{CE} 32	3,911	ТАТААТІТАТТАСАТІАТІGACAGCTITCATGTCGCCTGAGTGGCT СПЭТІТGAACTAAACATITCCCATCTCACGTITTAATIGGAACCAG 116 TCGATGCGGGCTGTTGACAGAAGA
DreAB 66	2 126	31 CCACTGGATGGCGCACTTTAGATCAATGTCA		2.067	44 AAGCCAACGUUTGACAATAAATGAUTGAGAUATGCAGUGUGU
DreAB 74	102	10 CACTGAGTIGTATAGTTAT	Oland _{CE} 55	3,207	44 / //////////////////////////////////
DICADEFIT	105	GGGAGGAGTCATCGGTGCTCGTTGCGATTTAATTGGCTGTTAGCTCACA	OlaAB _{CE} 34	1,814	39 CAGITTITIGTICTICTITITITICICATAATCACTITAAA
		CTGAGTTGTATAGTTATCAGTAATTATATTCAGAATGTTTTGCACAAGA	OlaAB _{CF} 58	790	17 GCTCTTTTTCCCTTTTTA
DreAB _{EF} 75 _{abc}	150	105 AATGTCA	0211		TGGAAATCAGACCTGCAGCAGTTAATATTTGATATCCATGACAAA
DreAB _{FG} 79 _{bd}	2,019	AGGTAGTITTATGTIGTIGGGCTCTATTTTATATCCCCGCAACACGAAA 62 CTGTCTTAATTGC	OlaAB _{EF} 61	3,781	60 AGGCCCCCTTCATTT
DreAB _{FG} 86	1,724	14 CAAGGCCTCGGTTA			GCATCCTGCCAGGCTCCCCAGGAATTCCACTTTGATTGCTGCACAT
DreAB _{EC} 81	1.650	GCCGGATGCGTCTGCTGGGCCGGAGAAAAAAAAAAAAAGGCTTTATT 93 GGCCATATTCAAGCCAGACAGCCAAGTTACAACCCGAAGAAAAAC	Ola4865	3 336	CCTCCCAGTIGCTTCAGTGACTTGGCCATAAAAGGCGGATTCGTC TGGAGCATTTGCAGTGCGGTGCAATAAAGCGTCTGAGACCAAGG 170 TTATTAACTGTGACTCCGGGGGGGGGGGGGGGGGGGGGG
DreAB _{E0} 92	281	37 CATAAAAGCGTATGACTCTACCGTTAAAAATATGACT	OlaAB66	3 050	21 CCACTGGATGGCGCTCCTTAGATCAATGTCA
ro au				3,050	15 44407444446744444
DreAB _{GN} 98 _{bc}	9,448	44 ATAAAACACAATCACAGTCTTAACTGTTTATAGGGTGCAAAGCG	OlaAD _{EF} 00	659	GGGAGGAGTCAGTCTCCTGCTGTTTTAATTGGCTGCAGACTTCAGT
DreAB _{GN} 102	4,893	40 TGCTGTATAGGCCACCGATTTTGTTTATTGCAAAAAATAA			GAGAAGCGTGAGTATCAGTAATTATCCGGCAATGTTTTGCTCAAG
DreAB _{GN} 135	6,703	31 ATTTTCAAGTTATGTTCAGCAAACTTTACTT	OlaAB _{EF} 75 _{abc}	144	99 AAATGTCA
DreAB _{GN} 141	4,750	29 TTGTTTGAGGCCAAATTTTGGTCTAATAT	OlaAB _{FG} 86	867	14 CAAGGCCTCGGTTA
DreAB _{GN} 142	4,701	32 TTAAGATCGTAAATTTGAATAATTGTAAAAAT			TTATTGGGTATATITAGCTTAGACAGCTCTAGGTTGTAACCTTAAG
DreAB _{GN} 153	1,598	25 TAAAGATACATCCTTGTTTGATTTC	OlaAB _{FG} 81 _b	763	52 AAAAAC
DreAB _{GN} 159	7,285	44 AACATTATTTATTAAGTTTTATAATACAAAACAACTGGTAAAAC			AAATCATGTTTATTGCTTATAAAAGAAGATATTTGCCAATAAAAG
DreAB _{GN} 195	978	24 TGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT			CGCAGGGATTTGCTATTAAAATATGGTGAGGAAAATGGTGGCCAT TTAGCTGAGCAGCAAAAGGCTGATTTATTATTATTGTTCAGTCCCA
DreAB _{GN} 204 _{bcd}	1,159	AAATGTGTTCTTAGGGCACTAAGCTGTCAGACCTTTTGGCGTGTAAGAT 82 TGATAGCGTGCAGGCTTCCAGGGCTCTTTGTTT			CGGTCACGTGTTTGGGGCCCCTATCCAGCATTGACAAGCTCA GCTTTCTGGGCCCATGAGCATGTAGGGTGCACAAAAAGCGACA
DreAB _{GN} 205	1,362	23 AAAATATAACACAAATAATGTTT	OlaAB _{FG} 87	340	241 CTTACCATGCAATGAA
			OlaAB _{GN} 104	1,640	31 TTTAATGTTTAAAAAAACTTACAAACACACC
		GAGGCGTTCCTCTCGGACTTTTTCGATCAATCACACAGAGCAGTGGCTT CTTTTGATTAAACCCCAAATTGTCATTGGACAGAGGTAATCACAGTGGAC AAGCAATACGGTCCAATTTCAACCTTGTCCCCAGAAACCCAATACGTT	OlaAB _{GN} 204 _{hc}	805	AAATGTTCTCTAAGGGCAAAGAGCTGTCAGAGCTCTTGGCTGGAA 53 AGATTGAT
DreAB 211	271	179 AATGGCACCGCGGTCCCCCATACGGCCGTAATCAG	OlaAB _{GN} 211	171	23 TCATTGGGCAGATATCATGTGAC
Giv Doder			314 0		

Tetraodon nigro	viridis spotted gree	n pufferfish Hox Ab			
PFC	Dist to 3' gene L	ength Sequence			
TniAB _{AC} 30 _{bc}	844	31 CAACTITITAACTIGACCTIGGCCTCCAGCCG			
			Takifugu rubripe	es Japanese puffe	erfish Hox Ab
TniABas 32	3 003	ACGCTGTTTGACCTACACATTICCTTCCTTTCTTTAATTGGAACC 117 AGTCCGAGCGCCCGTTGGCAGAAGA	PFC	Dist to 3' gene	Length Sequence TGGAAATGCGATCTACTGCAGATGTTATTTGATATCC
THIN IDGEOL	0,000	AAGCCAAGGGTTTTTTTTTTTTTTAATAAATAAACGTTTCAGAAACGC	TruAB _{EF} 61	2,733	59 ATTACAAAGAGTTCCTTCATTT
TniAB _{CE} 33	3,293	52 AATGTGTT			
TniAB _{CE} 34	1,808	39 CAGTTIGITITIGGGATTITITITAAAAACATGTTITAAA			GCATCCTGTGAGGTTCCGAGGAATTCCGCCCTGATGG CTGCACATCCTCCCAGTGCTCCAGTAACTTGGCCAT
TniAB _{CE} 51	1,736	23 ТСТСТСТТТТСТСТААТСТССАА	T 40 05		AAAACGCGGACTCGTCGGACGACGAGCAGC GCAATAAAGCGTCTGCGACCAAGGTTATTAACTGTG
		GCATCCTGTGGGGGCTTTGAGGAATTCCGCCCTGATTGCTGCACA	I ruAB _{EF} 65 _{acde}	2,263	163 ACIGAGAGGIIGAAAAC
		TCCTCCCAGTIGCTCTAGTAACTIGGTCATAAAACGCGGATTCGT CTGAAGCATTIGGGAACCAGCGCCATAAAGCGTCTGCGACCAA	TruAB _{EF} 66	2,029	31 CCACTGGGTGGCGCCCCTCAGATCAATGTCA GGGAGGAGTCTATAGCCGCCTAGTGTTTTAATTGGCT
I niAB _{EF} 65 _{acde}	2,287	163 GGITATTAACIGIGACIGAGAGGIIGAAAAC			GCAGGCTACAGTCAGAAGCGTGAGTATCAGTAATTA
TniAB _{EF} 66	2,026	31 CCACTGGGCGGCGCCCCTCAGATCAATGTCA			TTCAGCAATGTTTTGCACAAGAAATGTCAGCCAGAA
		GGGAGGAGTCTGTAGTCGCCTAGTGTTTTAATTGGCTGCAGGCT ACAGTGAGAAGCGTGAGTATCAGTAATTATTCAGCAATGTTTTG	TruAB _{EF} 75 _{abcd}	147	112 AGG
TniAB==75abod	147	112 CACAAGAAATGTCAGCCAGAAAGG	TruAB _{FG} 80	1,492	28 AAGCAGGATGTTTTGTTTTTGTATTTTG
21 4000		AGGTAGTCTCATGTTGTTGGGTTCTAATATTTCTCCCACAACAGG			
TniAB _{FG} 79 _{bcd}	1,233	54 AAACTGCCT			GCCGGATGCGTCTGCCTCGGCAAGAAAAGGGACACA
		GCCGGATGCGTCTGCCTCCGCAAGAAAAGGGACACAAAAGCTA		906	AAAGCIGAACITTATIGGIGATATITAGCITAGACAG
TniAB _{EC} 81 _{ab}	779	97 AAAGAAAAAC	TTUAD _{FG} OT _{ab}	806	
TniABro86	862	14 CAAGGCCTCGGTTA	IruAB _{FG} 86	859	14 CAAGGCCICGGIIA
-FG	002				
TniAB _{GN} 101	3,571	38 AATATTGCAGTAAAGTTTGATCAGCAATCTAGTTTCAT			AAATCATAACCTITATAGCITATAAAAAGTCATATTT TCCCCAATAAATGCGCGCGAATTTGCTATTAAAAATAT
					GGTGGTGGGGGGGGAAGGGGGATGGTGGCCATTGAGT
		GTCCAAAATTTCTACCAGAAGGTGACGGAATATTTGCCTTTTGTC TGTGTCGGAGATAAAGGTGTGAGCCTGAATGGAATCGCTCCTAC			TGAGCAGCAGGCTGATTTATTATTATTGTTCTGTCCC
		AGCCAACACCCACTCACCTCAGCGGACAATCGATCCTGCACAA			ACGGTCACGTGTTTGGGGCGCCCTATCCAGTCTTGGG
		AAGATGGTCCATACGTTTCTATACCATTACACAAAACCATTCCC	TruAB 87	206	245 GGTGCAGAAAGGCACGCAATGAA
TniABou106	1.083	323 AAAACGCGCCAGTTTCGTTTGGAAGTGATTTTC	Trui AD 00	500	
TniABou121	569	14 TITITAATGAATTT	TruAB _{FG} 90	864	28 CAGGACAAGGCCICGGIIAIGAICAIIG
TniABou141	4 536	28 TIGTTTIGGTIGTTTTTTTTTTTTTTTAATAT	TruAB _{GN} 109	890	13 IGGCAAATCATCT
GNI	4,000	20	TruAB _{GN} 112	4,295	24 TATATTTGAGTATCATTGTTAATG
		GTTTGAGCCGGAGCGCGCTGGATTCCCACGATGGCGAATTTGGG	T 45 464		CAATATGGTGTGATATATGATACAGCAGCCATAAAT
		AGATCATTTTATCCACCTTCCTGCCCTTCTTCTTTGTTTCCTTCAC	TruAB _{GN} 131	2,260	56 AATTIAGAAACTICIGITIA
		TTTTACATCTCATTACTTCGGTATCATTTGTTCCATAAACICACATC TTTTACATCTCATTACTTTCGGTATCATTTGTTCCATAAACAGCA			AAATGTGTTCTTAGGGCAGGGAGCTGTCAGACCTTTT GGCGTGAAAGATTGATCACACTCAGGGACCGAGGTC
		CACTCGCCCGGAAAACAATAATCCTCTGATGGCTTTCGTTGATTT	TruABou204	1 027	80 TTIGTTT
TniAB _{GN} 171	3,117	313 TATTAATATCAAGTATTGCAACTGTTCCAG	IT GNEO 1000	1,027	ACAGACTTTCGTCTATAAATGAATTTCTCAATCATAA
TniAB. 204	1.007	AGCTGTCAGACCTTTGGGCGAGAAAGATTGATCACACTCAGGCT 60 ACCGAGGTCTTTGTTT	TruAB _{GN} 208	1,217	44 TCGAGCC
ThiAD 206	1,007				
I IIAD _{GN} 200	1,426	30 cenerationaloionaatioiceaaati			TGTAAATAAAGCAACCCCTACCCCGGAATGAGGCG
		TGTAAATAAAGCAATCCCTACCCCGGAATGAGGCGTTACCCCT			TTACCTCTCCGACGTTCTCGATCAATCACAGGGGACA
		CCGACGTTCTCGATCATTCACAGGGACAGTTGCTTCTTTTGATAG			GTGGCTTCTTTTGATAGAGGAAAAAAAACCTCAAATT GTCATTGGGCAGATTTAATCATGTGACAACCAACAC
		AGAAAAAAACCCTCAAATTGTCATTGGGCAGATTTAATCATGTG ACATGCAACGAGCTCTCATTCCAACCGCATCCTTGTGAAAGCAA			GTCTAATTCCAACCACCATCCTTGTGAAAGCAACAC
TniAB _{GN} 211 _{abce}	298	199 TAGTTTATGGCACAGAGGTCCC	TruAB _{GN} 211 _{abce}	297	201 TTATGGCACAGGGGTCCC

PFC	Frog B	Coelacanth B	Human B	Bichir B	Zebrafish Ba	Medaka Ba	Tetraodon Ba	Zebrafish Bb	Medaka Bb	Tetraodon Bb
1					DreBA _{AC} 1		TniBA _{AC} 1			
2				PseB _{AC} 2			TniBA _{AC} 2			
3				PseB _{AC} 3		OlaBA _{AC} 3				
4				PseB _{AC} 4			TniBA _{4C} 4			
5				1.0		OlaBA5	TniBAcc5			
6					DreBArc6	OlaBAcc6				
7					DieDitFG0	OlaBA7	TniBA7			
/ 0						OlaDA _{CG} /	ThiDA _{CG} /			
0					DIEBA _{CF} o		TIIDA _{CG} o			
9					DreBA _{CF} 9		TniBA _{CG} 9			
10					DreBA _{CF} 10		TniBA _{CG} 10			
11					DreBA _{CF} 11		TniBA _{CG} 11			
12					DreBA _{CF} 12	OlaBA _{CG} 12				
13						OlaBA _{CG} 13	TniBA _{CG} 13			
14						OlaBA _{CG} 14	TniBA _{CG} 14			
15						OlaBA _{CG} 15	TniBA _{CG} 15			
16				PseB _{CF} 16		OlaBA _{CG} 16				
17				PseB _{CF} 17	DreBA _{CF} 17					
18				PseB _{CE} 18		OlaBA _{CG} 18				
19				PseB _{CE} 19	DreBA _{CE} 19	cu				
20				PseBor20	DreBA _{cr} 20					
21				PseB _{cr} 21	Diebii(ji20	OlaBA as 21				
22	XtrB22		HeaB 22	1 SCDFH21		0.001.0621				
22	D(G22	I meB 23	HsaB 23							
23		LmeB 24	HeaR 24							
24		LineD _{CF} 24	118aD _{CG} 24		<u> </u>					
25		LINEB _{CF} 25	HSaB _{CG} 25							
26		LmeB _{CF} 26	HsaB _{CG} 26		D D4		m m +			
27					DreBA _{FG} 27		TniBA _{CG} 27			
28			HsaB _{CG} 28				TniBA _{CG} 28			
29		LmeB _{CF} 29	HsaB _{CG} 29						▐▋▋▋▋▋	
- 30			HsaB _{CG} 30			OlaBA _{CG} 30				
31		LmeB _{CF} 31	HsaB _{CG} 31							
32		LmeB _{CF} 32	HsaB _{CG} 32							
33		LmeB _{FG} 33	HsaB _{CG} 33							
34		LmeB _{CF} 34	HsaB _{CG} 34							
35	XtrBcg35		HsaBcg35							
36	XtrBcc36		HsaBcc36							
37	XtrBcc37		HsaBcc37							
38	XtrB38		HeaB 38							
30	AdD _{CG} 50		H3aD _{CG} 50			OlaBA 30	ThiBA 30			
39					D==DA 40	OlaBA _{GH} 39	THIDAGH39			
40				D D 40	DrebA _{GH} 40	OlaBA _{GH} 40				
42				PseB _{FH} 42		OlaBA _{GH} 42				
43			HsaB _{GH} 43			OlaBA _{GH} 43				
44			HsaB _{GH} 44				TniBA _{GH} 44			
45			HsaB _{GH} 45		DreBA _{GH} 45	OlaBA _{GH} 45	TniBA _{GH} 45			
46			HsaB _{GH} 46		DreBA _{GH} 46					
47					DreBA _{GH} 47		TniBA _{GH} 47			
48					DreBA _{GH} 48	OlaBA _{GH} 48				
49			HsaB _{GH} 49	PseB _{FH} 49						
50	XtrB _{GH} 50 _{abcdef}	LmeB _{GH} 50 _{abc}	HsaB _{GH} 50 _{abcdef}	PseB _{FH} 50 _{abef}	DreBA _{GH} 50 _{bcf}					
51	XtrB _{GH} 51 _{ab}	LmeB _{GH} 51 _{abcd}	HsaB _{GH} 51 _{abc}	PseB _{FH} 51 _{abcd}	DreBA _{GH} 51 _{bcd}					
52	XtrB _{GH} 52 _{bole}	LmeB _{GH} 52 _{abode}	HsaB _{GH} 52 _{bcde}	PseB _{FH} 52 _{acd}	DreBA _{GH} 52 _{acd}					
53						OlaBA _{GH} 53	TniBA _{GH} 53			
54						OlaBA _{HI} 54	TniBA _{HI} 54			
55			ĺ		DreBAur55	••**	TniBAur55			
56				1	DreBAur56	l	TniBAur56			
57			HsaBur57			OlaBAur57			▐▋▋▋▋	
58			- Jones Fills, I	PseB ₁₀ 58		- and all /	TniBA58			
50			1	PseB _m 59				DreBB59	╞╞┼┼┼	
60	XtrB60	I meB60	HsaB60	PseB60	DreBA60	OlaBA60				
	GHOU _a	EncoHIOOab	1 2000 HIOUa	DeaR 61	LICDI HIOUab	Surpr HI00ab		DraBB 41		
01		LmoP (2	HaaD 62	DeeP 62	DroPA (2			DICDDHJ01		
02		LineD _{HI} 02 _{abc}	HsaD _{HI} 02 _{abc}	n sed _{HI} 02 _{abc}	DiedA _{HI} 02 _b			<u> </u>		
03		LineD _{HI} 03 _{ab}	risan _{HI} 03 _{ab}	r sen _{HI} 03 _{ab}	DrebA _{HI} 03 _b					
64	V: D . (5	L D (5	nsaBu64		D D4 65	01.04.77		DIREBBHJ64		
65	AITB _{IJ} 03 _{abc}	LineB _{IJ} 05 _{abcd}	risaB _{IJ} 05 _{abcd}		DreBA _{IJ} 05 _{abcd}	UIABA _{HJ} 65 _{bc}		DreBB _{HJ} 65 _{cd}		
66		LmeB _{IJ} 66	HsaB _{IJ} 66							
67					DreBA _{IJ} 67		TniBA _{HJ} 67			
68					DreBA _{IJ} 68		TniBA _{HJ} 68			
69					DreBA _{IJ} 69		TniBA _{HJ} 69			
70	XtrB _{IJ} 70 _{ab}	LmeB _{IJ} 70 _{ab}	HsaB _{IJ} 70 _{ab}		DreBA _{IJ} 70 _{ab}	OlaBA _{HJ} 70 _{ab}	TniBA _{HJ} 70 _{ab}	DreBB _{HJ} 70 _b	OlaBB _{IJ} 70 _b	TniBB _{IJ} 70 _b
71		LmeB _{IJ} 71	HsaB _{IJ} 71							
72									OlaBB _{JK} 72	TniBB _{JK} 72
73									OlaBB _{JK} 73	TniBB _{JK} 73
74									OlaBB _{IK} 74	TniBB _{IK} 74
75						OlaBA _{1K} 75	TniBA _{1K} 75			
76			ĺ			OlaBAn 76	TniBAn/76			
77				1	DreBA _{IV} 77		TniBA _W 77			
78			1	PseB _w 78	JN, ' /	1			OlaBBrr 78	
70	XtrB ₁₂ 79.	LmeB ₁₂ 79.	HsaB _W 79.	PseB _w 79.	DreBA _{IV} 79.	1	1	DreBB _W 79.	OlaBBry 79	TniBB _w 79.
80	- JK / Jab	LmeB80	HsaB ₁₁ , 80	- Jose IK / Jabe	- · · · · · · JK / /bc			JK / Jbc	JK / Zabc	JK / Zabc
01		LINCOJKOU	LISUD KLOU						OlaBB 01	TniBB 01
02									OlaDD _{KM} 81	TaiDD 82
- 62			1			1	1		Olabb _{KM} 82	1 IIIDD _{KM} 82

02		1	1	DD 92	D==DA 92		1			
0.5				r se B _{KL} 03	DIEBAKL05					
84			HsaB _{KL} 84	PseB _{KL} 84						
85				PseB _{KL} 85	DreBA _{KL} 85					
86	1			PseB _{KL} 86	DreBA _{KL} 86					
87	XtrBy 87hadaf	LmeB _{FI} 87 _{andef}	HsaBy 87 abodat	PseB _{FT} 87 _{abadaf}	DreBAy 87abadaf	OlaBArt 87hodef	TniBArt 87hodof	DreBBro87#	OlaBByyy87da	TniBB _{KM} 87 _{do}
88	KL OCCEI	KL * acder	HsaB 88	KL abcder	KL abcder	KL OCCEI	KL Ocder	DreBB	KM de	Kivi - uc
00			IIsaD _{KL} 88	D D 00			1	DICDDK000	<u> </u>	
89			HsaB _{KL} 89	PseB _{KL} 89						
90		LmeB _{KL} 90 _{abcd}	HsaB _{KL} 90 _{abcd}	PseB _{KL} 90 _{abcd}	DreBA _{KL} 90 _b			DreBB _{K0} 90 _{abcd}	OlaBB _{KM} 90 _{abc}	TniBB _{KM} 90 _{bc}
91	1			PseB _{KL} 91	DreBA _{KL} 91	OlaBA _{KL} 91	TniBA _{KL} 91			
92								DreBB _{vo} 92	OlaBB _{VM} 92	
03			1					DreBB 03	OlaBB 03	TniBB 03
,,				D D 04	D D1 01			DICDD _{K0} 95	Olabb _{M0} 95	TIBD _{M0} 95
94				PseB _{KL} 94	DreBA _{KL} 94					
95				PseB _{KL} 95			TniBA _{KL} 95			
96	1		HsaB _{KL} 96			OlaBA _{KL} 96				
98			HsaB _{KI} 98		DreBA _{k1} 98					
99			HsaB99		nu.				OlaBB	
100		L	HanD 100						Old D _{KM}	
100		LINEB _{KL} 100	HSaD _{KL} 100							
101		LmeB _{KL} 101	HsaB _{KL} 101							
102		LmeB _{KL} 102 _{ab}	HsaB _{KL} 102 _{ab}	PseB _{KL} 102 _{ab}	DreBA _{KL} 102 _{ab}	OlaBA _{KL} 102 _b	TniBA _{KL} 102 _b			
103					DreBA _{KL} 103	OlaBA _{KL} 103				
104			HsaBra 104	PseB., 104.	DreBA ₁₀ 104	OlaBArr 104	TniBA., 104	DreBB _{wo} 104		TniBB ₁₀ 104
105			rioub _{KL} ro i _{bcde}	Dee P 105	DroPA 105	OlaPA 105	ThiDA 105	DICDDK010 Tabce		THEDDMOTOR
103			+	D D I C	D. D. L. 103abc	OraDA _{KL} 103 _{ac}	THIDA _{KL} 103 _{bc}		───	ł
106	'	 	<u> </u>	rseB _{KL} 106	DreBA _{KL} 106				───	
107		<u> </u>	HsaB _{KL} 107		DreBA _{KL} 107				L	
108	I	LmeB _{KL} 108	HsaB _{KL} 108	PseB _{KL} 108	DreBA _{KL} 108			L	L	L
109			1			OlaBAr M109	TniBAr 109		Γ	
110	XtrB., 110	I meB., 110	HsaB110		DreBA., 110	-LM-02	TniBA 110		t	t
110	KL110abc	LmaD 111	II. D 111		LMITUabe		· mon KL110bc		t	ł
111	l'	LIIEDLMIII	risaD _{LM} 111				<u> </u>		───	ł
112	l'	LmeB _{LM} 112	HsaB _{LM} 112							L
113	XtrB _{KL} 113 _{ab}	LmeB _{LM} 113 _{ab}	HsaB _{LM} 113 _{ab}		DreBA _{LM} 113 _{bc}	OlaBA _{LM} 113 _{bc}	TniBA _{LM} 113 _{bc}			
114	XtrB _{KL} 114 _b	LmeB _{LM} 114 _{ab}	HsaB _{LM} 114 _{ab}		DreBA _{LM} 114 _{ab}					
115			HsaB _{1M} 115					DreBBro115		
116		I meB116	HsaB116					RO -		
117		LINCOLMITO	IIsaD _{LM} 110						Ol-DD 117	
117			HsaD _{LM} 117						Olabb _{KM} 117	
118	XtrB _{LM} 118 _{abcde}	LmeB _{LM} 118 _{abcde}	HsaB _{LM} 118 _{abcde}		DreBA _{LM} 118 _{abcd}	OlaBA _{LM} 118 _b	TniBA _{LM} 118 _{bc}			
119					DreBA _{LM} 119	OlaBA _{LM} 119				
120					DreBA _{LM} 120	OlaBA _{LM} 120				
121						OlaBAry 121	TniBA ₁₁ 121		1	
122			1			$Ol_{a}BA = 122$	TniBA 122			
122			-			OLDA 122	T IDA 122			
125						OIABA _{LM} 125	IniBA _{LM} 123			
124						OlaBA _{LM} 124	TniBA _{LM} 124			
125						OlaBA _{LM} 125	TniBA _{LM} 125			
126						OlaBA _{LM} 126	TniBA _{LM} 126			
127					DreBA., 127	OlaBA, 127	TniBA., 127			
128			HeaB 128		LMIT	OlaBA 128	- mar - LM /			
120			HanD 120		D DA 120	Olabri LM120			ł	
129			HsaB _{LM} 129		DreBA _{LM} 129					
130		LmeB _{LM} 130	HsaB _{LM} 130							
131	1		HsaB _{LM} 131							TniBB _{KM} 131
132			HsaB _{LM} 132		DreBA _{IM} 132					
133		LmeB133	HsaB133		LITT					
124	· · · · · · · · · · · · · · · · · · ·	LmcD _{LM} 133	HoaD_124		D DA 124		T.:DA 124			
1.54	l'	LINCD _{LM} 134 _{acd}	IISaD _{LM} 134 _{abcd}		DICDALM134abed	01.01.10	1 IIIDALM134 _{bc}		ł	ł
135		LmeB _{LM} 135	HsaB _{LM} 135			OlaBA _{LM} 135				
136						OlaBA _{MN} 136	TniBA _{MN} 136			L
137						OlaBA _{MN} 137	TniBA _{MN} 137			
138						OlaBA _{MN} 138	TniBA _{MN} 138			
130	XtrB,139	LmeB139	HsaB139		DreBA139	OlaBA 139	TniBA139	1	1	t
140	Nu D 140	LineD _{MN} 139 _{bcd}	II. D 140		D DA 140	OLDA 140	Third MN139 acde		<u> </u>	ł
140	AUD _{MN} 140 _b	LINCD _{MN} 140 _{bc}	risaD _{MN} 140 _{bc}		DICDA _{MN} 140 _{abc}	OIADA _{MN} 140 _{abc}	1 IIIDA _{MN} 140 _{abc}		───	l
141	'	LmeB _{MN} 141	HsaB _{MN} 141		DreBA _{MN} 141	OlaBA _{MN} 141	TniBA _{MN} 141		 	
142				<u> </u>	<u> </u>	OlaBA _{MN} 142	TniBA _{MN} 142			
143	1					OlaBA _{MN} 143	TniBA _{MN} 143			
144				V/////////////////////////////////////	DreBA _{MN} 144		TniBA _{MN} 144			
145			1		DreBA145	1	TniBA145	1	1	t
146	i'	<u> </u>	†		DreBA 146		TniBA 146		<u> </u>	<u> </u>
140	'	<u> </u>	+		D DA 147	01.04.147	1 IIIDA _{MN} 140		 	<u> </u>
147	'	 	───	¥/////////////////////////////////////	DreBA _{NO} 147	UIaBA _{NO} 147			───	
148	 '	ļ	ļ		DreBA _{NO} 148	OlaBA _{NO} 148	ļ		└───	
149				<u> </u>	DreBA _{NO} 149	OlaBA _{NO} 149				
150		LmeB _{MN} 150	HsaB _{MN} 150							
151	l l	LmeB _{x0} 151	HsaB _{MN} 151				İ		1	1
152	1	I meB 152	HsaB		1				t	t
152	l	LmoP 152	Loop 152				1		<u> </u>	ł
153	l'	LINED _{MN} 153	risaD _{MN} 155		D D IS	01.01.1.1	T 'D4 15'		╂─────	ł
154	'	LmeB _{NO} 154 _b	HsaB _{NO} 154 _{abc}		DreBA _{NO} 154 _{bc}	UIABA _{NO} 154 _{ab}	1 niBA _{NO} 154 _{ab}		┥────	<u> </u>
155			L		DreBA _{NO} 155	OlaBA _{NO} 155			L	L
156				V/////////////////////////////////////		OlaBA _{NO} 156	TniBA _{NO} 156			
157					DreBA _{NO} 157		TniBA _{NO} 157			
158					DreBA _{NO} 158		TniBA _{NO} 158			
159		1	HsaBvo159		NO	1	10	1	OlaBB. 159	1
1.00		<u> </u>	LoaD 160			OlaPA 1/0			Sand Mo139	<u> </u>
160		<u> </u>	nsaB _{NO} 160	<i>\////////////////////////////////////</i>		UIABA _{NO} 160			+	l
161	XtrB _{NO} 161 _{ab}	LmeB _{NO} 161	HsaB _{NO} 161 _{abc}	V/////////////////////////////////////	DreBA _{NO} 161 _{abc}	OlaBA _{NO} 161 _{abc}	TniBA _{NO} 161 _{ab}	DreBB _{K0} 161 _{bc}	OlaBB _{MO} 161 _{bc}	TniBB _{M0} 161 _{bc}

Xenopus tropica	lis western clawed	d frog Ho	ox B
PFC	Dist. To 3' gene	Length	Sequence
XtrB _{CG} 22	95,671	23	CCACTGCAACTCACTAACCTITA
XtrB _{CG} 35	11,212	22	GGCCCTAGAGGAGTGTAGGGGC
XtrB _{CG} 36	3,460	22	GTAAATATGCTTTGCGCTTATT
XtrB _{CG} 37	1,248	22	AGTACAGAATGGCAACACTCAG
XtrB _{CG} 38	179	116	CCGATIGATGAATAGCCCTCTGACGCTTTATCAGGCACACGG AGAAAGTITGACCAATCATTIGCCAGGAGCTCACACCCCAGC AGCCCAAGTGCACCGAGTTGGCGAGCAAGTTG
			СТСЭТАААСТССТААСАGСТІТІАТАТАССІGСАБТАТАААСАА САТСААСАТСТСОБСТІТАТАБСІСІТІТАТАБІТІСОСТАААСА СТІТАСОБСБІТІТІТІБОССАТТАСАААСССААТГІССІТІСАТ СОБААТАБІТАААССТІТАТСААТААТАБОБОБОБАЛАТІБА ТСАТТААААЛАГБІТАААТАТГАБСТБОБСТСБІТІБІТІТІААААТ
XtrB _{GH} 50 _{abcdef}	9,020	352	ATGTTTCAGCCTAAGAAACGGTATGATTTGATAACTTGTA
$XtrB_{GH}51_{ab}$	8,352	30	TGATTTGTTGTAAGGAGAGAGAGATCTCATTA
XtrB _{GH} 52 _{bcde}	8,209	153	CCAATAGGAGCAGGCTITGCTAATAGATGCAAACGTTCCTGA AAAGACACAGCAAAATATGAAAGAACTCATTTGCTGGGAAG TAAATCACAGAAAACTGTTTAGAACTGGCAACCCTTCTTGG AAATGTAAAGCGAGAAAGTCTTTAAGTG
XtrB _{GH} 60 _a	7,472	17	CAACATGAAACTGCCTA
			AGATGGCGGCGGAGGAAAGGCTGCACTTAAAGCAGTCATGA AGAAATGCAATAAATTCCTTGTTGTTTATGAAAATTACAAC TITGTGTTAGAAGTTATGAGTGGCTGGGGTCGGGCCC AGGGCCGGTCATGTGGACCTTGTAGCCTGGAACATGAACTTTTC
XtrB _{IJ} 65 _{abc}	5,298	179	TCATTTCCC
XtrB _{IJ} 70 _{ab}	90	61	ТААААСАСААСАААТСАТА
XtrB _{JK} 79 _{ab}	250	192	CCTAACGATTCTCAGATCGTCATTATTTGTAACCATAGAGCAT GGATACCTCTTGAGGTCATCAGTGAGAATTTACGACTGGTCA ACAAAGCAGTGGATTTCCAAAGCGACCCACACCCCCATATT TGGCCGCATACATAGCAAAAACCAAGTACAGTGTATGGGGAT AATTCATTAATACATCATAAAT
			TGACATTTCCATGTCAAATGGATTGGGTTTATGTAGAAGTTC CATGGTACAAATGGCCCAGACCTCAGGCTCAGACCCCCCTCAC TGGCTCGCAAAAGTCACGTGTGCCTCCATAAAGTTAGTTTTATG GTTTTAGGGAGTGACAATGTACAATATTTCACAATCTCCA
XtrB _{KL} 87 _{bcdef}	11,748	193	GAATGTTAAGTGACAAGTTTAAC
XtrB _{KL} 110 _{abc}	18,135	71	CAAACCCTGGCCCATTIGTCATGTTTAC
			ACAGATGTTCCTCGGTAAATCCAGGTTTTCCCTGTGTTTTTATG TTACAAAGGCACCGGCCACTGCAATAGCTCAACTCTGACAA GCAAAAAGATAATCAAAATGACAAATGAGTTCTTTTGTGAGA
XtrB _{KL} 113 _{ab}	17,291	156	CACAGATCTTGTATTAATTTTCATTTTC
XtrB _{KL} 114 _b	16,696	39	AAGAAAAATGAGAGAATTATACAGAAAATCATTAATCAC
			GGTCATAGTGGTCCTGAGTGGATGGATGCAGCCCCCCCATC CCCCCCCCCC
XtrB _{LM} 118 _{abcde}	13,264	362	GAGCC
XtrB _{MN} 139 _{bc}	4,026	20	TTAACGTGAATACAGGGTAT
XtrB _{MN} 140 _b	3,795	19	TIGCACITACAGTITACAT
XtrB _{NO} 161 _{ab}	266	39	TCAGATTGATGGGCCGGGTTTGATTGAAGTCTCTTTGTC

Latimeria menadoensis co	pelacanth Ho	DX B			
PFC Dist. To LmeBcs23	3' gene Lei 78.400	ngth Sequence 19 TATITACACTITATAAAAA			
LmeB _{CF} 24	69,457	TAAAGGAGGCATTAAAAAACAAATTTGAGACGGGGAAAAA 69 GAAGAATTGGTTGTATTGTAAATGAAGTA			
l maR 25		20 TTC ATTA TTA ATTCC AT ACACATA CA ATCTT ATCCCTCA			
LineB _{CF} 25	64 023	18 GAGCTCAATGTCAATAAG			
LmeB _{CF} 29	36.877	22 GAAAATATAGAAAATGGCTGCT			
LmeB _{CF} 31	34,567	17 CACTGTGTAGTGGCCTG			
LmeB _{CF} 32	10,740	24 GTCAGTTGGATTCTTCCTCTTTCT			
LmeB _{FG} 33	14,696	26 AAAACCTATGCAAGTTCATTTTCAAA			
LmeB _{CF} 34	5,467	TTAAATATGTTTTATAATAAATATGCAATTATGCATAAACAT 67 GGTGAATTGTCTCAAGTCATTTGAT			
-		СТСОТААААТТСТААСАGССТТІТТІГІЛДГАДТАТДАТАТАААС ААСААСАĞĞССТĞĞĞĞТТТАТТĞСАСТТТАТАДТІГДТААА ТАСТТТАСТĞССТПТГІĞĞТАТТАСААСТĞĞACITÇССССТС АТБТААТАĞТТАААССТТТАТСАЛТААТААĞĞAAATTĞĞ ТТААААТĞГТĞĞĞTATĞAACACCTCGTTGTTTAAAATATĞ			
$\rm LmeB_{GH}50_{abc}$	916	CTTTAACCGGGAAGTTGCATGATTCCATAAAACGTATTAAAA 338 TA			
ImeBau51	461	TGATTTGTTGTAAAGCACCAGATATCTCATTAATGATGGTGG 74 TCGAATATATTATGTATTATATTCTCCCCTCC			
Efficience GHO Tabed	401	GTCCGTGTGGAGTAAGAGAAGCCAATAGGATTTGGTTTTGGT			
		AACAACTCATTTGCGGTGAAGTAAATCACAGAAAACTGTTT			
I meBau52	309	ATGAACTGGCACCTCTTCTTGGAAATGTAATGCGAGAACTCT 173 TTAAGTG			
LmeBul60	1.643	24 CAACATGAAACTGCCTATTTATGC			
Emobridoab	1,010				
I meBur62	1 278	AGCATGCGCACATTGCAAAGATCAGTTGTAAAGTGATCCTA TAAGTITACTGTGCAAAGAATGATGATACTGTATACGGATT ACTTATGAGGGACCTGATGATATATTTATGTTCTCACCA CTITGTTCTATTGTCTAAACCTGGAAACGGCGGAAGAAAG GGTACAATAAAAGTTTACAACCGGGAAACGGCGGAAGAAAG 272 GCTTGCCTCCTCATT			
EmobrioLabo	1,210				
L	220	ΑΤΓΑΤΓΤΑΤΟΤΙΚΑΤΤΕΥΑΤΛΑΘΤΟΘΑΟΥ ΑΤΑΤΑΛΑΤΤΗ ΤΓΟΛΟΑΤΤΑΛΟΚΑΘΟΑΛΟΚΟΘΕΑΛΟΥ ΑΘΟΥΤΗΛΑΛΑΤΤΙΚΟΑΤ ΓΓΟΤΤΑGΑΑΤΓΑΛΟΓΙΟΓΙΑΛΟΚΟΛΑΟΥ ΑΘΟΥΤΗΛΑΤΙΚΟ ΓΓΟΤΤΑGΑΑΤΓΑΛΟΓΙΟΤΗΠΙΟΘΙΤΟΓΑΛΑΤΙCΙΘΟΛΙΕΓΙΑΑΤΙCΙ ΟΓΑΛΑΛΟΘΟΘΟΙΟ ΤΑΛΟΓΙΟΓΙΑΛΑΙCΙΑΙ ΑΛΑΟΓΙ ΤΟ ΑΛΑΟΓΙΑΛΟΓΙΑΤΑΛΟΓΙΑΛΑΛΟΓΙ			
Lined _{HI} o3 _{ab}	230	Z36 CCCGGCCIACAAAICACCCAGCCAAAII			
I meB. 65	6 670	AGATGGCGGCTGAAAGAAGACTGCTGTTAAAGCAGTCATGA AGAATGCAATAAATTCCTTGTTGTTTATGAAAATTACCA CTTGTGATAGAACTTTAGGTGGCTGGGTACTGGGATGG CCAGGGCCGGTCATGTGGACGGGTAACCGGTAACACTGAACT 200 TTTTATGATTUTCCATGTGCTTATATTCGCGTCATCTTTTGG			
LmeB.66	5 523	16 ATTITTA AATATTAAA			
Ellebijoo	0,020	CCAATCTCCGATAAACTACTAATAGCTAAACCACTTGGACT			
LmeB _{IJ} 70 _{ab}	91	61 ATAAAACACAAAATCATA			
LmeB ₁ 71	2.270	ACTACCTAGAAGGACGCAGAAGGTTATAGTTCAATAATTTTG 68 TATGTGACTGTGTTTGTAGTTTGTCT			
~		CCTAACGATTCTCAGCTCGTCATTATTTGTAACCATAGAGCA TGAATTACCTCTTGAGGTCATCAGTGAGAATTTACCACTGGT CAACAAAAGCACGTGATTCCCAAACGCACCCCCCCCCC			GGTCATAGTGGTCCTTTGAGTATGGAACAGAGGAGACCCCCTT CCCCCTCCTGATCACGTGATTCATTAATAATAATGCAGAG GTTGCAGAATAGATATGTATTCGTCAGGAAATCGCAGAC TGGTCTCTTGTGTCTGACGTGAAATTCAACTGTCCTTTTAAA AACAAGCCTTATGCGAGAAAAAGGAGGGGGAAAAAG
LmeB _{JK} 79 _{abc}	252	231 ATAACGACCAAGATCCACAAATC	LmaD 110		GAGGCTGCAATAAAACAATTTTGGAAGCAGAGCCACACCGT
LmeB _{.ik} 80	15,285	36 GCATGTTTTATGTGAGATGTTATAACTTATTTATAA	LMB _{LM} 118 _{abcde} 1	16,226	356 GGGCIGG
		AAAAGTAGGTATGGCATTTAGATGTCAAATGGATTGGGTTT ATCTAGAAGTTAGATCGTAAAAATCCCACGGACCTCAGACA GATATCCCTCACTGGCTCTCAAAAAGTCACCTGGGATCCTA ACTTATCTTTPTTCTCTCTCACTACAAGTCACCTGGGATCCTAA	LmeB _{LM} 130	7,572	TITTATGTATTTGGAGGCAATCAAAACTACTICCGTTGATTG ATCATTAATCAGGGGGGTGAGTTATTACTCCTCTCAAGCAAAGGCCA 11 TTGGGGAAAGACGCCTATATCTGTCA CAGAGGCCATTGTTATCAGTGAGCAGGGCGTACCAGTCTAT
LmeB _{KL} 87 _{acdef}	13,956	203 ATTECACATECTAGAATGITAAGTGACACTTAAC ATTECACATECTAGAATGITAAGTGACACTTAAC	LmeB _{LM} 133	3,335	51 AGGCCAACCA CTCGTCAGAGGCTAAGGTAAGCTGGACTCAAATAGGCTATC
LmeB _{kl} 90 _{abo} -	9,749	TCTCATCAATAATTCATAGGAAACCGGGATCATTCTGAGGTC 85 A	1 moR 134	2.044	ACTITIGTGAATGGCGGAGTATATGTCCCAGTGATTTATGACC ATATGACTTCAATCTCGGTTCAAGAAGAGTTCACAAGCTTTA ACACTTCC
LmeB., 100	8 594	CTGTAACACCACAAAACCACCAGCAGAGCCCGCTTCAGACCA	LINEBLM 134acd	3,041	132 AOCTICE
L. B. (a)	0,004	ATGGAATTTCTTAACCCGTGACCACGATTGATGATGAATAT	LmeB _{LM} 135	202	41 CCTATICATGICATGIGCITTICACTATATAAGATGGAT
LmeB _{KL} 101	5,255	52 HIGGACHTH	LmeB _{MN} 139 _{bcd}	3,907	38 TCTTGACTTAACGTGAAAACAGGGTATCTTTGAACAAA
	1 100	AAGTAATGACCTGGGCAAAATTCAATATGACCGAGCATGCT TTGCGACTGCATTATGGAAGCTGTGAGTGGGAGAGCCCGGG AGGGGGGGAACCCCAGGGTCAGCCGCTGTAACAAATATA AATGTTCAGAGGACGCATGACACGCCTAGCTGTTTAACAAA			TIGCACTTAGAGTITACATTIGATGGGGGAAACAACCTIGAA AGGCGTITAGCCAGTICAATCGIGACGTCTTICGATACGTGT GIGTICTGGIGAACATTCATATATTATTGGTGTATAGCCAG TITAAATATTTTCTTIGTGATTATTATTACCCCCAAACATTAGTA
LINEDKLIUZab	4,488	AAACGAGTAAGGGTTAGGAATAAATTTAGTATATTTTGTG	LmeB _{MN} 140 _{bc}	3.794	TITATATTAAGAAAGAGACAAACTGTACTTTTTAGTATTTA 217 CCTG
LmeB _{KL} 108	60	59 TGCAATTCAAAGAAATT	LmeB _{MN} 141	3,325	17 ААСААТТСТТДААТААА
I meB110	22 843	CAGATITIGGCGAAGATGGATCCTTGTTTCATCTTTAATCACA 71 CCAAACTCTGCCCCATTTGTCATGTTTAC	LmeB _{MN} 150	2,960	ICACGIGFIGICCAGAGIGAACCTITATIGGACCTAAAAGGA 53 AAACAAAGAAA
LmeB _M 111	22,010	26 TGTACATAGTGGTAATAGAAATAAAT			
	,=0.	TTGTGTTTAGCAAAGCTGATTTATACATAGGCATGGGTCTTTA	LmeB _{MN} 151	2,500	36 AATIGTATACAATGTTTGCGTTTTGGCGTTTAATTA
LmeB _{LM} 112	21,871	64 ATAACAAAGGACATGTGTGGGT			ATCAATTACCAATACTCAAGGGTTTTTCTGAATACAATTTTCT
		ACAGATGTTCCTTGGTGTTTGCAGGTTTTGTGTGTATTTTTAT	LmeB _{MN} 152	2,253	85 G
$LmeB_{LM}113_{ab}$	21,521	АССАСАААGGАGCАСТБСААТАССТОААСТСТБАСААG СААЛТАGAТААТСААБАСАААТБССТГСТТТБГБАСА 153 СБСАБСТГГГБТАТААТТГСАТТТГС АААGTГСАСАБССАТТАТТГБТАБАСАБАБССААБААААТ			CTCTGGAGTTGTAGATCGATTGAAGAAAATAATGCTTTCTTT
$LmeB_{LM}114_{ab}$	20,567	71 GCGAGAATTATACAGAAAATCATTAATCAC	LmeB _{NO} 154 _b 1	250 19,653	21 TATITATIGTATATTATTTTC
LmeB _{LM} 116	19,673	CACGTITITCAAACCGATTACCTCAGTICTATAGTAACAGACT 78 GACCTCTGAAACCCTTGACCTTITITAGACTGGACA	LmeB _{NO} 161 _a	264	TCAGATTGATGGGCAGGGTTTGATTGAAATCCCTTTGTCATG 64 CAAATGTCAAGCACTTGATGGA

Homo sapiens hui	man Hox B				
PFC	Dist to 3' gene	Length	Sequence		
HsaB _{CG} 22	96,213	23			
HsaB _{CG} 23	95,483	28			
			TAAAGGGGAGATCTAAGCAAATGATATGAACGGTCAGGTCAAG		
			AATIGGCCACACAATIGAACGAAGIACATITITIAGCAIGTIGGT AGATATCCCATTGAAAATGCTTGGCATGGAAGCATGGGAATTG		
HsaB _{CG} 24	84,917	159	AGGAAACTGGTTAGAGATCCCCCTACGGA		
HsaB _{CG} 25	80,145	36	TTGATTTCCCAAGGGCAGGTACCCTTGGCAGCCTGA		
HsaB _{CG} 26	78,392	21	GAGCTCGTTGACTTTAATAAG		
HsaB _{CG} 28	51,295	31	CATAAAGAACTTTCTAGTGCATCCTTGGGCC		
HsaB _{CG} 29	46,437	29	GAAAATTTTTAAAAGCATCTTTTGCTGCT		
HsaB _{CG} 30	44,661	21	CTTATTGATGAGTTGGATAAA		
HsaB _{CG} 31	43,671	16	CACTGTGCCTGGCCTG		
HsaB _{CG} 32	14,496	29	GTCAGTTTACGTAGGTCTTCACCCTTTCT		
			TTAAATTTAAATTTAAAAAAAAAAGGGATACATTTCAGTAATCCATT AAACATCAGGGGTGAATTGTAACAGAATCCAATTCCATATTTGA		
HsaBco33	30.201	89	Т		
HsaB _{co} 34	14,496	29	GTCAGTTTACGTAGGTCTTCACCCTTTCT		
HsaB _{co} 35	11.355	23	GGCCCTGGACGTTTCTGAGGGGC	HeaR 00	7 070
HsaBcc36	3.545	22	GTAAATTTCAGCTAAGCTTATT	IISAD _{KL} 99	1,213
HsaB _{co} 37	1.319	24	AGTACAGGAGGGCTGAAAACTCAG	HsaB _{KL} 100*	7,248
00				HeaR 101	4 5 1 1
			CCGATTGATTTATGTCGGAGCTGACGCTTTATCAGGCAGTCGGA	I ISaD _{KL} IOI	4,511
HsaB _{CG} 38*	264	118	GCTCCACTGTACTTTGTTGGCTGAGAAGTTG		
HsaB _{GH} 43	8,164	15	TCTTCCCCATCTCAC		
HsaB _{GH} 44	5,323	19	TCATTAGGGATGCAAAATG		
GI				HsaB _{KL} 102 _{ab} *	4,357
HooP 45*	4.045	0.4	GCAATAAAATAATATGACCGCTATAAAAGTTTATAGCGTATAA	HsaB _{er} 104	1.606
Head AF	4,945	84	AGACGTCTGGGCGCGGGCCAGCCTCTTGATTCTTTACA	HsaB _{kl} 107	1.472
Hsab _{GH} 40	4,502	38		1 IGGD KE 101	.,2
nsab _{GH} 49	2,390	35	monaadeereeaemiondereaaaami	HsaB _{KL} 108*	59
			CTCGTAAAATGCTAACAGCTTTTATGCGCTGCGGCATAAACAAC	HsaB _{LM} 110 _b *	23,888
			AACAGACTCCGGCTTTATTGCGTTTTATAGTTTCTTAAAGAGTTT	HsaB _{LM} 111	23,080
			ACAGCCGTTTTTTGGGGGGGCCGGTTATCCAGCCAATTCCCTCCA CACGATAGTTAAACCTTTATCAATAATAAGGAAATTGATCATTA		
			AAGCTTTAAATATGACTACCTCGTTTGTTTGAAAAATACGTTTAGG	HsaB _{LM} 112	22,942
HsaB _{GH} 50 _{abcdef} *	1,227	342	AGAGGAAGCTGTATGATTTGATAACTTGTATTA		
HsaBou51abo	748	71	AACAGATTTAATCCGTATTCATTCTC		
011 400					
			CCAATAGGATGCGGGGTCTCTAATGGATGCAAATGATCATGAA	HsaB _{LM} 113 _{ab} *	22,517
			ATCACCGAAAACTGTTTATGAACTGCATCCCTTCTTCGAAATG	HsaB _{LM} 114 _{ab} *	21,660
HsaB _{GH} 52 _{bcde} *	480	153	TAAAGCGAGGACCTCTTTAAGTG	HsaB _{LM} 115	21,308
HsaB _{HI} 57*	1,889	34	ATTTCTGCTAAGTTCTCCCAACAACATGAAACTG		
$HsaB_{HI}60_{a}$	1,868	17	CAACATGAAACTGCCTA	HsaB116	20 477
			AGCATGCGCGCTGTGGGCAATTGTTACAAGTGTTCTTAGGTTTA	HsaB117	19,434
			CTGTGAAGAAGAATGTATICTGTATCCGTGAATTGCTTTATGGGGG	LINGUED	10,404
			GGAGGGAGGGCTAATTATATATTTTGTTGTTGTTCCTCTATACTTTGT		
			GGAGGGAGGGCTAATTATATATTTTGTTGTTGTTCCTCTATACTTTGT TCTGTTGTCGCGCCTGAAAAGGGCGGAAGAGTTACAATAAAGT		
HsaB 62	1 623	222	GGAGGGAGGGCTAATTATATATTTTGTTGTTGTTCCTCTATACTTTGT TCTGTTGTCTGCCGCCTGAAAAGGGCGGAAGAGTTACAATAAAGT TTACAAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT		
HsaB _{HI} 62 _{abc}	1,623	223	GGAGGGAGGCCTAATHATATHTITGTIGTICCICTATACHTGT TICTGTIGTICCCCCCGAAAAGGGCGGAAGGGTIACAATAAAG TIACAAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TI		
HsaB _{HI} 62 _{abc}	1,623	223	GGAGGGAGGGCTAATIATATATTITTITGITGTCCTCATACTTIGT TCTGTTGTCCCCCCCGAAAAGGCGGAAGAGTTACAATAAAT TTACAAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT ATTATTGATCATATTITATAAATCCAACGCCACACAATTITTTCC	HsaBut118storts*	16.792
HsaB _{HI} 62 _{abc}	1,623	223	GGAGGGAGGGCTAATTATATATATTITTITGITGTCCTCATACTTIGT TCTGTTGTCGCCGCCGGAAGGGCGGAAGGTTACAATAAAT TTACAAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT ATTATTGATCATATTTTATAAATCCAACGCCCACACAATTITTCC ACATTACCGGGACCCTGGGGGAGACGGCCCGGCCATTGGCGGAG	HsaB _{LM} 118 _{abcde} * HsaB128	16,792 12,557
HsaB _{HI} 62 _{abc}	1,623	223	GGAGGGAGGGCTAATTATATATATTITTITGITGTCCTCATACITTG TCCTGTTGTCCCCCCCGCAAAGGGCGGAAGAGTTACAATAAGT TTACAGCAAGCAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT ATTATTGATCATATTTTATAAATCCAACGCCACAACAATTITTICC ACATTACCGGGACCCGTGGGGAGACGGCCCCGGCCATTGGCGGA GGGGACCTTACGTGGGCCGGGGTCACGTGGGCCAGGAGAAA AGGGGGTCCTTTTGGTGTAACTCGGAACTAATTCGGAACTA	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129	16,792 12,557 10,193
HsaB _{HI} 62 _{abc}	1,623	223	GGAGGGAGGGCTAATTATATATATTITTITGITGTCCTCTATACTTIGT TCTGTTGTCCCCGCCGAAAGGGCGGAAGAGTTACAATAAGT TTACAAGCAAGCAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT ATTATTGATCATATTTTATAAATCCAACGCCCCACAATTITTCC ACATTACCGGACCCGTGGGGAGACGGCCCGGCCATGGCGGA GGGGACCTTACGTGGGGGGGGGCACGTGGCCGGGAAAA GGGGGGTCCTTTTGGTGAAATCGGACTAATTCGTAATAT ATCAAGGAATCTCGTAAAACCGACACTAAAACGTCCCTGCCTA CAAATCATCCGTCGCACA	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129	16,792 12,557 10,193
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB 64	1,623 238 9.547	223 238 238	GGAGGGAGGGCTAATIATATATITITITIGTICTCTCTATACTITIG TICTGTIGTICCCCCCGCAAAGGGCGGAAGAGTTACAATAAGT TACAAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT ATTATIGATCATATITITATAAATCCAACGCCCACCAATITITICC ACATTACCGGGAGCCGTGGGGGGACGCGCCGGCCATTGGCGGA GGGGACCTCACGTGGGCCGGGGTCACGTGGGCCGGGCATTGGGGGA GGGGGCTCTTTITGGTGTAAATCGGGACTCTAATICTGTAATAT ATCAAGGAAATCCGTAAACCGGCACTAAAACGCCCCCGCCTA CAAATCACGGGGGTTCTAAATC	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB_120	16,792 12,557 10,193
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64	1,623 238 9,547	223 238 23	GGAGGGAGGGCTAATTATATATATTITITIGTIGTICCTEATACTITIG TICTITIGTICGCCCCGCAAAAGGGCGGAAAGTTACAATAAAT TTAATGGATAATATTITATAAATCCAACGCCCGCCAGCGCTCCTCAT TT ATTATIGATCATATTITATAAATCCAACGCCCACCAATTITITCC ACATTACCGGGACCCGTGGGGAGACGGCCCGGCCATTGGCGG GGGGACGTCACGTGGGCCGGGGAACGGCCCGGCC	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB_L31	16,792 12,557 10,193 7,873 7,873
HsaB _{HI} 62 _{abc} HsaB _{HI} 63 _{ab} HsaB _{IJ} 64	1,623 238 9,547	223 238 23	GGAGGGAGGGAGGAGCTAATTATATATATTITTITTITTITTITTETTETTETTATAATTAAT	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB_132*	16,792 12,557 10,193 7,873 7,665 4,562
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64	1,623 238 9,547	223 238 23	GGAGGGAGGGAGGACTAATTATATATATTITTITGITGITCCTCATACTTIGI TCCTGTTGITCCCGCCCGGAAAGGGCGGAAGAGTTACAATAAGT TTACAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT ATTATTGATCATATTITATAAATCCAACGCCCACACAATTITTICC ACATTACCGGGACCCGTGGGGGGGACACGGCCCGGCC	HsaB _{LM} 118 _{abcse} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132*	16,792 12,557 10,193 7,873 7,665 4,597
HsaB _{HI} 62 _{abc} HsaB _{HI} 63 _{ab} HsaB _{IJ} 64	1,623 238 9,547	223 238 23	GGAGGGAGGGCTAATTATATATTITTITGITGITCCTCTATACTITGI TCCTGTTGTCCCCGCCGAAAGGGCGGAAGAGTTACAATAAGT TTACAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT ATTATTGATCATATTITATAAATCCAACGCCCGCCATGGCGG GGGACCTCACGGGGCCCGTGGGGGGAGCGGCCCGGCC	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133	16,792 12,557 10,193 7,873 7,665 4,597 3,473
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _H 64 HsaB _H 65 _{abcd} *	1,623 238 9,547 7,032	223 238 23 209	GGAGGGAGGGCTAATTATATATTITTITGITGITCCTCTATACTITGI TCTGTTGITCCCCCCCGCAAAGGGCGGAAGAGTTACAATAAGT TTACAGCAAGCAAGAACCCGAGAGCGCGCAGCGCTCCTCAT TT ATTATIGATCATATTITATAAATCCAACGCCCACCAATTITTICC ACATTACCGGGACCCGGGGGGAGCGGCCCGGCCATGGCGGA GGGACCTCACGTGGGGGGGACGCCCCGGCCATGGGGGAGAAA AGGGGGTCTTITTIGGTGAAATCGGACTAATTICGGACTATA ATCAAGGAATCCGGCAAAACCGCCACTAAAACGTCCCTGCCTA CAAATCAATCCGGCCAAATT TTAAATGAAAGGAGTTTATAAAACC AGATGGCGACTGAGAAAAAGGGTGCCGGTGGGACCAGCCATGAA GGAATGCCATAAATCCTGTGTTTATGAAAATTTACAACTT GGAATGGCAATAAATCCTGTGTGTTATGAAAATTTACAACTT GGAATGGCGCGCGGGGTTAATGGGACTACACACACTTTTATCAA	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133	16,792 12,557 10,193 7,873 7,865 4,597 3,473
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64 HsaB _U 65 _{abcd} * HsaB _U 66	1,623 238 9,547 7,032 5,717	223 238 23 239 209 15	GGAGGGAGGGCTAATTATATATATTITTITGITGITCCTCATACITTGI TCTGTTGITCGCCGCCGGAAAGGGGGGAAGAGTTACAATAAGT TACTAGCGAGAACCCGAGACTGGCCCGGCCAGCGCTCCTCAT TT ATTATTGATCATATTITATAAATCCAACGCCCGGCCAGCGCTCGCGGA GGGACCCTCACGTGGGCGGGGAGACGGCCCGGCC	$\begin{split} &HsaB_{LM} 118_{abcde} ^{*} \\ &HsaB_{LM} 128 \\ &HsaB_{LM} 129 \\ &HsaB_{LM} 130 \\ &HsaB_{LM} 131 \\ &HsaB_{LM} 132 ^{*} \\ &HsaB_{LM} 133 \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64 HsaB _U 66 HsaB _U 66 HsaB _U 70*	1,623 238 9,547 7,032 5,717 103	223 238 23 209 15 61	GGAGGGAGGGCAATTATATATATATTITTITGITGITCCTCATACITTGI TCTCTTGITGITCCCCCCGCAAAAGGGCGGAAGAGTTACAATAAGT TI ATTATIGATCATATTITATAAATCCAACGCCACCACAATTITTCC ACATTACCGGAACCCGTGGGGAGACGGCCCGGCCATGGCGGA GGGACCGTCACGTGGGCGGGGCACGTGGGCCGGCCATGGCGGA GGGACGTCACTITGGTGTAATCGGACTATA ATCAAGGAATCTCGTAAAACCCACCACAAAACGTCCTGGCCA GAATGACGCCAGGCAATTITGGAATCAAGTCGTGGAGGAGACAACCTG GAAGAAGCCATCAGTTAAAAACC AGATGGCGACTGAGAAAAGGGTTGCTGGGGGAGCAGCCATGAA GAATGCCCGCGAATT TTAAATGAAAGGAGTTTATGAGGGTGGGAGCAGCCATGAA GAATGCCCGTGGGCGAGCGGCGGGGGGGGGG	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abcd} *	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072
$HsaB_{H}62_{abc}$ $HsaB_{H}63_{ab}$ $HsaB_{L}64$ $HsaB_{L}65_{abcd}^{*}$ $HsaB_{L}66$ $HsaB_{L}70_{ab}^{*}$	1,623 238 9,547 7,032 5,717 103	223 238 23 209 15 61	GGAGGGAGGGCAATTATATATATATTITITITGITGITCCTEATACTITGI TCICTITGITCCCCGCCGCAAGAGGCGGAAGAGTTACAATAAGT TTACAAGCAAGAAACCCGAGACTGGCCCGGCCACGCCTCCTCAT TT ATTATTGATCATATTITATAAATCCAACGCCCGCCATGCGGGG GGGACCTCACGTGGGGGGGGCACGTGGCCGGCATTGGCGG GGGACCTCACGTGGGCGGGGTCACGTGGTCCGGGGGGAGAAA AGGGGGTCTTITTGGTAAAATCCAACGTCCCTGCCGG GGGACCTCACGTGGGCGGGGTCACGTGGGCCGGGCACGTGGGAGAAA AGGGGGACTTITTGGTAAAAACC ACAATCATCCGGCCAATT TTAAATGAAAGGAGTTGCTGGTGGGGGGGCACCCTGACGA GAATGGCCGCCATGT TTAAATGAAAGGAGTTTAAAAACC AGATGGCGGCCGGCGCTCTGTGGTGGAGCACCCATGAA GAATGGCGGCGCGGC	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abcd} *	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 65 _{abcd} * HsaB _U 66 HsaB _U 70 _{ab} *	1,623 238 9,547 7,032 5,717 103	223 238 23 209 15 61	GGAGGGAGGGCTAATTATATATATTITTITGITGITCCTCTATACTTIGI TCCTGTTGTCCCGCCCGCAAGGGGGGGAGAGGTTACAATAAGT TTACAGCGAGAACCCGAGAGTGGCCCGGCCAGCGCTCCTCAT TT ATTATTGATCATATTITATAAATCCAACGCCCGGCCATGGCGG GGGACCTCACGGGGCCCTGGGGGGGGGCACGGCGCGGCCATGGGGG GGGACCTCACGTGGGCGGGGCACGTGGTCCGGGGGGAGAA GGGGGTCCTTITTGGTGAAATCAATTCGTGACTTA ATCAAGGAATCCGGCCAACTAAAACGGCCCGGGCACGGGGCACGGGGCACGGGGGGCACGTGGGGGAGAGGGCGCGGGGCACGTGGGGGGGCACGTGGGGGGGG	$\label{eq:linear_state} \begin{split} &HsaB_{LM} 118_{abcde}^* \\ &HsaB_{LM} 128 \\ &HsaB_{LM} 129 \\ \\ &HsaB_{LM} 130 \\ &HsaB_{LM} 131 \\ \\ &HsaB_{LM} 132^* \\ \\ &HsaB_{LM} 134_{abcd}^* \\ \\ &HsaB_{LM} 135^* \end{split}$	16,792 12,557 10,193 7,873 7,865 4,597 3,473 3,072 248
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _L 65 _{abcd} * HsaB _L 66 HsaB _L 70 _{ab} *	1,623 238 9,547 7,032 5,717 103 2,259	223 238 23 209 15 61 87	GGAGGGAGGGCTAATTATATATATTITTITGITGTCCTCTATACTTIGT TCTGTTGTCCGCCCGCAAAAGGGGGGAAAGATTACAATAAGT TT ATTATTGATCATATTTTATAAATCCAACGCCCGCCAGCGCTCCTCAT T ATTATTGATCATATTTTATAAATCCAACGCCCGGCCATGGCGGA GGGACCCTCACGTGGGCGGGGGACGGCCCCGGCCATGGCGGA GGGACCTCACGTGGGCCGGGTCACGTGGCCCGGGCAATGGCGGA GGGGGCCTTITTGGTGTAAATCCGGACCTAAAACGTCCTGCCA AGGGGGTCTTTITGGTGTAAAACC CAATCATCCGGCCAAT TTAATGAAAGGAGTTTAAAAACC AGATGGCGGACTGAGAAAAGGGTTGCTGGTGGAGCAGCCAGC	$\label{eq:linear_state} HsaB_{LM}118_{abcde}^*$ $HsaB_{LM}128$ $HsaB_{LM}129$ $HsaB_{LM}130$ $HsaB_{LM}131$ $HsaB_{LM}132^*$ $HsaB_{LM}133$ $HsaB_{LM}134_{abcd}^*$ $HsaB_{LM}135^*$ $HsaB_{MM}139_{abcd}^*$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581
HsaB _H 62 _{abc} HsaB _H 63 ₄₀ HsaB _U 64 HsaB _U 66 HsaB _U 70 _{ab} *	1,623 238 9,547 7,032 5,717 103 2,259	223 238 23 209 15 61 87	GGAGGGAGGGAGGACTAATTATATATATTITTITTGTTGTTCCTTATACTTIGT TCTGTTGTTCCCGCCCGCAAAAGGGGGGAAAGTATTACAATAAGT TT ATTATTGATCATATTITATAAATCCAACGCCGCCAGCGCTCCTCAT TT ATTATTGATCATATTITTATAAATCCAACGCCCGCGCCATTGCCGGG GGGACCCTCACGTGGGCGGGGCACGTGGCCCGGCCATTGCCGGA GGGGACCTTTTTTGGTGTAAATCCGACCTAATTTCTGTAATAT ATCAAGGGATCTTTTGTTGTAAAAACC AGGGGGTCTTTTTGGTGTAAAACC AGAATGCCGCCGCCATTTGTGTTATGAAAATTCGAACATA TTAATGAAAGGAGTTTAAAAACC AGATGGCGACTGAGAAAAAGGGTTGCTGGTGGAGCAGCCATGAA GAATGCCGCCAATT TTAATGAAAGGAGTTTAAAGCGCGGGGGCGGCGCGCGCAGCAACAACTT TGAATGAAAGGAGTTTATAGATGGTTGTGTGTGAACCAACGACTAGAA AAACCAACAACTATCATAAAACC AGATGGCGACTTAAATGCCTGGTGAACCAGCCATGAA ATTTTGGAAATTAAA CCAATCCTCGGAAGAAGAGGAGCCTCAGAGAAAACAAAG TCTATTTTAAATTAAA	$\begin{split} &HsaB_{LM}118_{abcde}^{*}\\ &HsaB_{LM}128\\ &HsaB_{LM}129\\ &HsaB_{LM}130\\ &HsaB_{LM}131\\ &HsaB_{LM}132^{*}\\ &HsaB_{LM}133\\ &HsaB_{LM}134_{abcd}^{*}\\ &HsaB_{LM}135^{*}\\ &HsaB_{MN}139_{abcd}^{*}\\ \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64 HsaB _U 65 _{abcd} * HsaB _U 66 HsaB _U 70 _{ab} *	1,623 238 9,547 7,032 5,717 103 2,259	223 238 23 209 15 61 87	GGAGGGAGGGAGGACTAATTATATATATTITTITGITGITCCTETATACTITAG TICTGITGITGICGCCCGCCAGAAGGGGGGAAGAGTTACAATAAGT TI ATTATIGATCATATTITATAAATCCAACGCCCGCCAGCGCTCCTCAT TI ATTATIGATCATATTITATAAATCCAACGCCCGCCATGGCGGA GGGACGTCACGTGGGGGGGACGGCGCGCCGCGGGGGGAGAG GGGGACCTTTIGGGTAATGCGGCCAGCGGCCATGGCGGAGAAA GGGGGTCCTTITTIGGTGTAATGCGGCTGGGGGGGCACGTGGGGAGAAA AGGGGGCCTTITTIGGTGTAATGCGGCTGGGGGGCACGCGCCATGA GAATGCACGCCGAATT TTAAATGAAAGGAGTTGCTGGTGGGGCGCCGCCATGAA GAATGCCCGGCAATT TTAAATGAAAGGAGTTTAAAAACC AGATGGCGACTGGGAAAAGGGTTGCTGGTGGGAGCAGCCATGA GAATGCAATGATCCTGTTGTGTTATGAAAATTACAAACTTT CGCTGGGGGATTATATGGCGGCGGGCGTGGGAGCAGCCATGA ATTITTGGAAATAAATCCAGCAGCATGGAACAAGCATGCAACGCG CGGGGCATGTGGCGGGGGGCGTGGGAACAGCAACTATA AAACAACAAAATACATA AACACACAAAATCATA ACCACTAGAAGTAAGGAGGAGGCGCCGCGGCGCCGGGACTATA AAACACAAAAATCATA	$\begin{split} &HsaB_{LM}11B_{abcde}^{*}\\ &HsaB_{LM}128\\ &HsaB_{LM}129\\ &HsaB_{LM}130\\ &HsaB_{LM}131\\ &HsaB_{LM}132^{*}\\ &HsaB_{LM}133\\ &HsaB_{LM}134_{abcd}^{*}\\ &HsaB_{LM}139_{abcd}^{*}\\ \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64 HsaB _U 65 _{abcd} * HsaB _U 66 HsaB _U 70 _{ab} *	1,623 238 9,547 7,032 5,717 103 2,259	223 238 23 209 15 61 87	GGAGGGAGGGCTAATTATATATATTITTITGITGITCCTCATACTTIGT TCTCTTITGITCGCCCCGCCAGAGGCGGAAGAGTTACAATAAGT TTACAGCGAGAACCCGAGAGCGGCGCAGCGCTCCTCAT TT ATTATTGATCATATTITATAAATCCAACGCCCGGCCATGCGCGG GGGACCTCACGGGGCCCGGGGGGCACGGGCCCGGCCATGGCGG GGGACCTCACGTGGGCGGGGCACGTGGTCCGGAGAGAAA AGGGGGTCTTITTGGTGTAATCGGACTCAATTCGTGATAT ATCAAGGGATCTTGGTAAAACCGCCCGGCCATGGCGG AAATCACTCCGCCCAAT TTAAATGAAAGGAGTTTATAAAACC AGATGGCGGCCTGAGGAAAAGGGTTGCTGGTGGAGCAGCACCATGAA GAATGCCGCCGCAATT TTAAATGAAAGGAGTTTATGAAAAACGCCCGGCCCTGGAC GGGGCACTTTATGAGAGGAGTTCACGGGGGCACGCGCGCG	$\begin{split} &HsaB_{LM} 11B_{abcde}^{*} \\ &HsaB_{LM} 128 \\ &HsaB_{LM} 129 \\ &HsaB_{LM} 130 \\ &HsaB_{LM} 131 \\ &HsaB_{LM} 132^{*} \\ &HsaB_{LM} 133 \\ &HsaB_{LM} 134_{abcd}^{*} \\ &HsaB_{LM} 135^{*} \\ &HsaB_{MM} 139_{abcd}^{*} \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581
HsaB _H 62 _{sbc} HsaB _H 63 _{sb} HsaB _U 65 _{sbcd} * HsaB _U 66 HsaB _U 71	1,623 238 9,547 7,032 5,717 103 2,259	223 238 23 209 15 61 87	GGAGGGAGGGCTAATTATATATATTITTITGITGITCCTEATACITTAG TECTGITGITCGCCGCCGCGAGAGGGGGGGAGAGTATTACAATAAG TI ATTAATGATCATATITTATAAATCCAACGCCCGGCCATGCGCTCCTCAT TT ATTATIGATCATATITTATAAATCCAACGCCCGGCCATGGCGG GGGACCTCACGGGGCCCTGGGGGGGGGCACGTGGGCGGGGCACTGGGGGGGG	$\label{eq:linear_states} \begin{split} &HsaB_{LM}11B_{abcde}^*\\ &HsaB_{LM}128\\ &HsaB_{LM}129\\ \\ &HsaB_{LM}130\\ &HsaB_{LM}131\\ \\ &HsaB_{LM}132^*\\ \\ &HsaB_{LM}134_{abcd}^*\\ \\ &HsaB_{LM}135^*\\ \\ &HsaB_{May}139_{abcd}^*\\ \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581
HsaB _H 62 _{abc} HsaB _H 63 ₄₀ HsaB _J 64 HsaB _J 66 HsaB _L 70 _{ab} * HsaB _J 71 HsaB _J 79 _{abc} *	1,623 238 9,547 7,032 5,717 103 2,259 267	223 238 23 209 15 61 87 246	GGAGGGAGGGAGGACTAATTATATATTITTITTITTITTITTITTITTETTETTETTAAATAGA TICTITTITTICGCCCCGCAGAAAGGGGGGAAGAATTAATTAAATTA	$\begin{split} & HsaB_{LM} 118_{abcde} * \\ & HsaB_{LM} 128 \\ & HsaB_{LM} 129 \\ & HsaB_{LM} 130 \\ & HsaB_{LM} 131 \\ & HsaB_{LM} 132 * \\ & HsaB_{LM} 134_{abcd} * \\ & HsaB_{LM} 135 * \\ & HsaB_{MN} 139_{abcd} * \\ & HsaB_{MN} 140_{bc} * \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64 HsaB _U 65 _{abcd} * HsaB _U 70 _{ab} * HsaB _U 71 HsaB _{JK} 79 _{abc} *	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558	223 238 23 209 15 61 87 246 53	GGAGGGAGGGAGGACTAATTATATATATTITTITTGTTGTTCCTCTATACTTIGT TCTGTTGTTGCCGCCCGCCAGAGGGGGGAGAGTAGTTACAATAAGT TA ATTATTGATCATATTITATAAATCCAACGCCGCCAGCGCTCCTCAT T ATTATTGATCATATTITATAAATCCAACGCCGCCATGCGGGG GGGACGTCACGTGGGGGGGGGG	$\begin{split} & HsaB_{LM} 118_{abcde}^{*} \\ & HsaB_{LM} 128 \\ & HsaB_{LM} 129 \\ & HsaB_{LM} 130 \\ & HsaB_{LM} 131 \\ & HsaB_{LM} 132^{*} \\ & HsaB_{LM} 133 \\ & HsaB_{LM} 134_{abcd}^{*} \\ & HsaB_{MM} 139_{abcd}^{*} \\ & HsaB_{MM} 140_{bc}^{*} \\ & HsaB_{MM} 140_{bc}^{*} \\ & HsaB_{MM} 141^{*} \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 65 _{abcd} * HsaB _U 66 HsaB _U 70 _{ab} * HsaB _U 71 HsaB _U 79 _{abc} *	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483	223 238 23 209 15 61 87 246 53 19	GGAGGGAGGGAGGACTAATTATATATATTITTITGITGITCCTEATACTTIGT TCTGTTGITCGCCGCCGCAAGAGGGGGAAGAGTTACAATTAAGT TACTAGCGAGAACCCGGAGAGTGGCCGGCGCAGCGCTCCTCAT T ATTATTGATCATATTITATAAATCCAACGCCGCCATGCGGG GGGACCGTCAGGGGGGGGGG	$\begin{split} & HsaB_{LM} 11B_{abcde}^{*} \\ & HsaB_{LM} 128 \\ & HsaB_{LM} 129 \\ & HsaB_{LM} 130 \\ & HsaB_{LM} 131 \\ & HsaB_{LM} 132^{*} \\ & HsaB_{LM} 133 \\ & HsaB_{LM} 134 \\ & HsaB_{LM} 135^{*} \\ & HsaB_{LM} 139_{abcd}^{*} \\ & HsaB_{LM} 140_{bc}^{*} \\ & HsaB_{LM} 140_{bc}^{*} \\ & HsaB_{LM} 150 \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64 HsaB _U 65 _{abcd} * HsaB _U 70 _{ab} * HsaB _U 71 HsaB _{JK} 79 _{abc} * HsaB _{KL} 80 HsaB _{KL} 84	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483	223 238 23 209 15 61 87 246 53 19	GGAGGGAGGGAGGACTAATTATATATATATTITITITGITGITCCTEATACITTAG TICTGITGITGICGCCCGCCGAGAGGGGGGAGAGAGTATACAATAAGT TICATTAGCGGGAACCCGGAGAGTGGCCCGGCCACGCGCTCCTCAT T ATTATTGATCATATITITATAAATCCAACGCCCGCCATGCGGGG GGGACCTCACGTGGGGGGGGCACGTGGGCCGGGGCATGGGGGGAGAA GGGGGTCCTTITTGGTGTAATTICGGACTCAATTICTGTAATTA ATCAAGGGATCTITGGTGTAATACC CAATCATCCGGCCAATT TIAATGAAAGGGGTTTATAAAACC AGATGGCGGCCTGGGGAAAGGGGTGCCGGGGGCACGGGCACGGGCACTG GGGACCTGGGGAACTGGTGGAGCAGCCACCAGAA AAATGACCGGCCAATT TIAATGAAAGGGGTTTATAAAACC AGATGGCGGCCTGGGAAAGGGGTGCCGGGGGCACGGCGCCGGGG GGGACATGGCCGGCGGGTGGGACGACCCATGAA GAATGCCGGACATGGTGTGTTTATGAAAATTTACAACTTT GTGATAGAAGGGTTTATGAGACATGCACGGCGCCGCGGC GGGGCATGGGCCGGGCGACGTGGAACGGACACTTTTACCACCTTG GTGATAGAAGTTTATGAGGGCGACGACGCGGCGCCGGGCCTGGGACATGA AAATGCCAACAATACTTC TTCCCGGGGTATAATGCCACGATCGTTGTGTGTGT TTCCCGGGGGTATAATGCAGCATCGTTGTGG TTTTGGAATTACTACTAT ACCACCAACAAATCATTA AACCAACAAATCATTA	$\begin{split} & HsaB_{LM} 11B_{abcde}^{*} \\ & HsaB_{LM} 128 \\ & HsaB_{LM} 129 \\ & HsaB_{LM} 130 \\ & HsaB_{LM} 131 \\ & HsaB_{LM} 132^{*} \\ & HsaB_{LM} 133 \\ & HsaB_{LM} 134_{abcd}^{*} \\ & HsaB_{LM} 135^{*} \\ & HsaB_{MM} 140_{bc}^{*} \\ & HsaB_{MM} 140_{bc} \\ & HsaB_{MM} 151 \\ \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 65 _{abcd} * HsaB _U 65 HsaB _U 70 _{ab} * HsaB _U 71 HsaB _{JK} 79 _{abc} * HsaB _K 80 HsaB _{KC} 84	1,623 238 9,547 7,032 5,717 103 2,259 267 13,658 13,483	223 238 23 209 15 61 87 246 53 19	GGAGGGAGGGAGGACTAATTATATATATTITTITTGTTGTTCCTTATACTTIGT TCTGTTGTTGCCGCCGCGCAGAGGGGGGAGAGTATTACAATAAGT TT ATTATTGATCATATTITATAAATCCAACGCCGCGACGCCTCCTCAT T ATTATTGATCATATTITATAAATCCAACGCCCGGCCATGGCGGG GGGACCCTCACGTGGGGGGGGGCACGTGGCCGGGCATTGGCGG GGGACCTCACGTGGGCCGGGTCACGTGGTCCGGGGGGAGAAA AGGGGTCCTTITTGGTGTAAATCCGGACTAAAACTTCGGAATTA ATCAAGGAATCTCGGAAAAACGCGCAGCACAAAACGTCCGGCCATG GGGGGCCTTITGGTGTAAAACC AAATCATCCGGCCAAT TTAATGAAAGGAGTTTAAAAAC AGATGGCGCCGCGCTTGGTGGAGCAGCCACCATGAA GAATGGCGCCGCGCTTGTGTGGAGCAGCCACCCATGAA GAATGGCGCGACTTGTTGTGTATATGAAAATTTACAACCTT TTCCCTGGGGGCGGAGTTATAGAGCATGGTGGAGCAGCCACCATGAA GAATGGCCGACTTATATGAGCATGTTGTGGAGCAGCCACCATGAA AAACCACACAAATCATA ACCAACGAATCATA ACCACCACAAATCATA ACCACCACAAATCATA ACCACCACAAATCATA ACCACCACAAATCATA ACCACCACAAATCATA ACCACCACAAATCATA ACCACCACAAATCATA ACCACCCAGAAGTACCACCACCACAAAACGAGTGCCACGC CCCCCCCCTATTGGATCCCCGCGCCCCCCCCCC	$\begin{split} & HsaB_{LM} 118_{abcde}^{*} \\ & HsaB_{LM} 128 \\ & HsaB_{LM} 129 \\ & HsaB_{LM} 130 \\ & HsaB_{LM} 131 \\ & HsaB_{LM} 132^{*} \\ & HsaB_{LM} 133 \\ & HsaB_{LM} 134_{abcd}^{*} \\ & HsaB_{LM} 135^{*} \\ & HsaB_{AM} 149_{abcd}^{*} \\ & HsaB_{AM} 140_{bc}^{*} \\ & HsaB_{AM} 140_{bc} \\ & HsaB_{AM} 150 \\ & HsaB_{AM} 151 \\ \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _J 64 HsaB _J 66 HsaB _J 70 _{ab} * HsaB _J 71 HsaB _J 79 _{abc} * HsaB _{JK} 79 _{abc} *	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483	223 238 23 209 15 61 87 246 53 19	GGAGGGAGGGAGGACTAATTATATTATTITTITTITTITTITTITTITTETTETTETTITTI TECTTITTITCCGCCCCGCAAAAGGGGGGAAAGTATTACAATAAAT T ATTATTGATCATATTITTATAAATCCAACGCCGCCAGCGCTCCTCAT T ATTATTGATCATATTITTATAAATCCAACGCCGCCATGCGCCTCCTCAT T ATTATTGATCATATTITTATAAATCCAACGCCGCCATGCGGGAGAGA GGGGACCTTAGTGGGGGGGGCACGTGGGCCGGCCATGCGGGA GGGGACCTTGGTGGGGGGGCACGTGGGCCGGCCATGCCGGA GGGGGCCTTTTGGTGGAAAACCGACACTAAAACGTCCGGCGGCATT ATCAAGGGATCTTTTGGTGGAAAACCGCCCACAAAACGTCCGTGGCAG GGGAGCCGCCGATT TTAATGAAAGGAGTTTATAGAGGTGCTGGTGGAGCAGCCACCATGAA GAATGCCCGCCAATT TTAATGAAAGGAGTTTATAGAGGTGGTGGGAGCAGCCATGAA GAATGCCGCGACTTATGGGAGTGCTGGTGGAGCAGCCACCATGAA GAATGCCGCGACTTATATGGCGGGGGCTGGGACAGCCATGAA AAACCACAACAATTACAACTTTGGAATCAACGCAGCGCCTGGACAACTTT TTCCGTGGTGGAGTATAATGCAGCATTCTTTTGGAAAAATTACAA TTCCCTGGGGAGCTATAATAGCAGCATTCTTTTGAACAATTACCAACTTT GCCTGGGGGAGTATAATGCAGCGGGCGCCGGGGCTGGGACTATA AAACCACAAAATTACA CCAATCCTCGGAAGTAAGAAGGAGGCCCCGGGGCTGGGACTATA AAACCACAACAAATTACAAGAGGGGGCCCCGGGGCTGGGACTATA AAACCACAACAAATTACATATAGGGGGGGCCGGGGCTGGGACTATA AAACCACAACAAATTACTATTATTGTAACCATAGGAGCATG AATTACCTTGGGATGCGTCATCATTATTGTAACCATAGAGCAGG GGTGTCAACGAAGTAAGCAGGAGCCCCCCCCACCCCCCCC	$\begin{split} & HsaB_{LM} 118_{abcde}^{*} \\ & HsaB_{LM} 128 \\ & HsaB_{LM} 129 \\ & HsaB_{LM} 130 \\ & HsaB_{LM} 131 \\ & HsaB_{LM} 132^{*} \\ & HsaB_{LM} 134_{abcd}^{*} \\ & HsaB_{LM} 134_{abcd}^{*} \\ & HsaB_{LM} 139_{abcd}^{*} \\ & HsaB_{LM} 140_{bc}^{*} \\ & HsaB_{LM} 140_{bc}^{*} \\ & HsaB_{LM} 150 \\ & HsaB_{LM} 151 \\ \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64 HsaB _U 66 HsaB _U 70 _{ab} * HsaB _U 71 HsaB _{JX} 79 _{abc} * HsaB _{XX} 80 HsaB _{XX} 84	1,623 238 9,547 7,032 5,717 103 2,259 267 13,658 13,483	223 238 23 209 15 61 87 246 53 19	GGAGGGAGGGAGGACTAATTATATTATTITTITGITGITCCTEATACTTAAG TICTGITGITCGCCGCCGCCAGAGGGGGAAGAGTTACAATAAGT TI ATTATIGATCATATTITATAAATCCAACGCCGGCCATGCGCTCCTCAT T ATTATIGATCATATTITATAAATCCAACGCCGGCCATGCGGGA GGGACGTCACGTGGGGGGGGGG	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abcd} * HsaB _{LM} 139 _{abcd} * HsaB _{LM} 140 _{bc} * HsaB _{LM} 140 _{bc} * HsaB _{LM} 151 HsaB _{LM} 151	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 65 _{abcd} * HsaB _U 65 _{abcd} * HsaB _U 70 _{ab} * HsaB _{JK} 79 _{abc} * HsaB _{JK} 80 HsaB _{KL} 87 _{abcd} *	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483 13,483	223 238 23 209 15 61 87 246 53 19 204	GGAGGGAGGGAGGACTAATTATATTATTITTITGITGITCCTEATACTTIGT TCTCTITGITCGCCGCCCGCCAGGCGGAGAGGTATAACAAAGCAGGAGACCCCGCGCCGCGCCACGCCTCCTCAT T ATTATTGATCATATTITATAAATCCAACGCCCACACAATTITTICC ACATTACCGGGACCCGTGGGGGGGGACGCGGCCGCCATGGCGG GGGACCTCACGTGGGCGGGGCACGTGGGCCGGGCATTGCGGGA GGGGACCTTTTTGGTGAAAATCGGACGCCCGGGGCATTGCGGGA GGGGGCCTTTTTGGTGAAAATCGGACACGCATGCGGGACACG GGGGGCCTTTTTGGTGAAAAATCGGACACCATGAA GGGGGGCCTTTTTGGTGAAAATCGGCACGCATGAC GGGGGCCTTTTTGGTGAAAATCGGACACCATGAA GAATGCCGCCAATT TTAAATGAAAGGAGTTTAAAAAC AGATGGCGGCCGCGCTCTGTGTGGGGCACCCCTGAC GGGGGCCTTTTGGTGTAAAACC GGGTGCCTTGGGGGACAGCGCGCGCCCCGGGC GGGGCACTGGGGAAAAGGGTTGCTGGTGGGAGCACCCATGAA GAATGCCATAAATTCCCTGTTGTTTTGGAAAATTTACAACTTT GGTAGAAGTTATGAGTGGTGTGAACCAGCACTGGACAACTTAC GGTATGGCAGGACTGCTGACTGGGGGGGCCGCCGGGCC GCGCCAATTACCTGTGTGTTATGAAAATTTACAACTTT TCCCTGGGGGTATAATGCAGCATTCTTTGG TTTTGGAATTATAA CCACCTGGAGGATATATAGCGCGCGGCGCCCGGGCCTCGGACTATA AAACACAAAAATTCATA CCACCTGGAAGTAAGAAGAGGAGCCTCAGAAGAAACAAAG TCCTCTGGGGTATAATGCGCAACTATGGAGAGAAACAAAG TCCTCTGGAGTCTCAGGGGGGACCTCCAGAAGAAACAAAG TCCTCTGGGGTATAATTCGGGATGGGGGAGCTCGCAACTGGAACACGAGGGCCTC CCAACGATTCCCGGGCCGCCCCCCCCCC	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abcd} * HsaB _{LM} 135* HsaB _{LM} 140 _{bc} * HsaB _{MM} 140 _{bc} * HsaB _{MM} 150 HsaB _{MM} 151 HsaB _{MM} 152*	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 65 _{abcd} * HsaB _U 65 _{abcd} * HsaB _U 70 _{ab} * HsaB _U 71 HsaB _K 80 HsaB _{KL} 87 _{abcd} * HsaB _{KL} 87 _{abcd} *	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483 12,115 12,418	223 238 23 209 15 61 87 246 53 19 204	GGAGGGAGGGAGGACTAATTATATTATTITTITTITTITTITTCTCTTTTTTC TCTTTTTTCCCGCCCGCAAAAGGGGGGAACATTTACTAAATAAGT TT ATTATTGATCATATTTTATAAATCCAACGCCCGGCCATGCGCTCCTCAT T ATTATTGATCATATTTTATAAATCCAACGCCCGGCCATGCGCGCA GGGACCCTCACGTGGGCGGGGCACGTGGCCCGGCCATGGCGGA GGGACCTCACGTGGGCCGGGCACGTGGCCCGGCCATGCCGGA GGGGGCCTTTTGGTGTAAATCCGAACGACATTCCGGACATA ATCAAGGGATCTTTGGTGTAAAACC AGGGGGCCTTTTGGTGTAAAACC ACAATCATCCGGCCAAT TTAATGAAAGGAGTTTAAAAACC AGAATGCCGCCAAT TTAATGAAAGGAGTTTAAAAACC AGAATGCCGCCAAT TTAATGAAAGGAGTTTAGAGGGTGCGGGGAGCAGCCATGA GAATGCCGCCAAT TTACATGCATAAATCCCTGTGGAGCAGCCACCATGA GAATGCCGCAATTTTTGGTGTATGAAGCATGCAGGCG CCGGTCATGTGCCGGGCGCGCGGGACAGCCATGA AAATCATCCCGGGAGTATAATTACAACTTT TCCCGGGGGCGTATAATGCAGCATTCTTTGG ATTTTTGGAAATTAAA CCAACCTCGGAATAATTACAAGCCATGGAGCAGCCATGA AAACCACACAAAATCATX ACCAACCAACAATCATX ACCACCAGAAGTAAGAGGGGGCCCCAGGAGAAAACCAAG TTCTTTTTGAAATTAAATT	$\begin{split} & HsaB_{LM} 118_{abcde}^{*} \\ & HsaB_{LM} 128 \\ & HsaB_{LM} 129 \\ & HsaB_{LM} 130 \\ & HsaB_{LM} 131 \\ & HsaB_{LM} 132^{*} \\ & HsaB_{LM} 134_{abcd}^{*} \\ & HsaB_{LM} 134_{abcd}^{*} \\ & HsaB_{LM} 135^{*} \\ & HsaB_{LM} 149_{abcd}^{*} \\ & HsaB_{LM} 140_{bc}^{*} \\ & HsaB_{LM} 141^{*} \\ & HsaB_{LM} 151 \\ & HsaB_{LM} 151 \\ \\ & HsaB_{LM} 152^{*} \end{split}$	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _J 64 HsaB _J 64 HsaB _J 66 HsaB _J 70 _{ab} * HsaB _J 71 HsaB _J 79 _{abc} * HsaB _{KL} 80 HsaB _{KL} 87 _{abcdel} * HsaB _{KL} 87 _{abcdel} *	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483 12,115 12,418 11,577	223 238 23 209 15 61 87 246 53 19 204 40 35	GGAGGGAGGGAGGGCTAATTATATATATATTITTITTITTITTITTITTETTETTETTITTI TECTTITTITCICCECCCGCAAAAGGGGGGAAAGATTATACAATAAGT TT ATTATTGATCATATTITTATAAATCCAACGCCCGCCATGCGCTCCTCAT T ATTATTGATCATATTITTATAAATCCAACGCCACACAATTITTICC ACATTACCGGGACCCGTGGGGAGACGGCCCGGCCATTGGCGGG GGGACCTCACGTGGGCCGGGGTCACGTGGGCCGGCCATTGCCGGA GGGACCTCACGTGGGCCGGGGTCACGTGGGCCGGCCATTGCCGGA GGGGCCCTTTTTGGTGAAAACCCAACGTCCTGGCGGAGAGAAA AGGGGGTCCTTTTTGGTGAAAACCCAACGTCCTGGCGGAGCAGCCACCACGA GGGAGCCGCGCAATT TTAAATGAAAGGAGTTTAAAAACC AGAATGCCGCGACATT TTAAATGAAAGGAGTTTATGAGGGTGGGAGCAGCCACGAA AAATCATCCGGCCGAGCCTGGGACAGCCACCATGAA GAATGGCGGCCGGCGCTCTGGTGGAGCAGCCACCATGAA GAATGCCGTGGGTATAATGCAGCGTGGGACAGCAGCAACAACTT TGCCGTGGTGGTATAATGCAGCATTCTTTTGGAAAATTTACAACTTT TCCCGTGGGGGTATAATGCAGCGGCGCGCGGCGCG	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abcd} * HsaB _{LM} 139 _{abcd} * HsaB _{MM} 140 _{bc} * HsaB _{MM} 140 _{bc} * HsaB _{MM} 150 HsaB _{MM} 151 HsaB _{MM} 152*	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 65 _{abcd} * HsaB _U 66 HsaB _U 70 _{ab} * HsaB _U 71 HsaB _{KL} 89 HsaB _{KL} 87 _{abcdef} * HsaB _{KL} 89 HsaB _{KL} 89 HsaB _{KL} 89	1,623 238 9,547 7,032 5,717 103 2,259 267 13,658 13,483 12,418 11,577 9,043	223 238 23 209 15 61 87 246 53 19 204 40 035 18	GGAGGGAGGGAGGACTAATTATATTATTITTITGITGITCCTEATACITTAG TICTGITGITGICGCGCCGCGAGAGGGGGAGAGAGTTACAATAAGT TA ATTATIGATCATATTITATAAATCCAACGCCGGCCATGCGCTCATTAT T ATTATIGATCATATTITATAAATCCAACGCCGGCCATGCGGG GGGACGCTCACGTGGGGGGGGGG	HsaB _{LM} 118 _{abode} * HsaB _{LM} 128 HsaB _{LM} 120 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abod} * HsaB _{LM} 139 _{abod} * HsaB _{LM} 140 _{bo} * HsaB _{LM} 140 _{bo} * HsaB _{LM} 151 HsaB _{LM} 151 HsaB _{LM} 152*	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732 328
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _J 64 HsaB _J 65 _{abcd} * HsaB _J 70 _{ab} * HsaB _J 71 HsaB _{JK} 79 _{abc} * HsaB _{KL} 80 HsaB _{KL} 84 HsaB _{KL} 87 _{abcdet} *	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483 12,115 12,418 11,577 9,043	223 238 23 209 15 61 87 246 53 19 204 40 35 18	GGAGGGAGGGCTAATTATATTATTITTITGITGITCCTEATACTITGI TCICTITGITCGCCGCCCGCAGAGGCGGAAGAGTTACAATTAAGT TI ATTATIGATCATATTITATAAATTCAAACGCCGGCCAGCGCTCCTCAT T ATTATIGATCATATTITATAAATCCAAACGCCACACAATTITTICC ACATTACCGGGACCCGTGGGGGGGGCACGTGGCCGGCATTGCCGGG GGGGACCTCACGTGGGCGGGGGCACGTGGGCCGGGCATTGCGGGAGAAG GGGGGCCTTTITGIGTGAAATCCGGCCAGCAGCACTGACGG GGGGACCTCACGTGGGCCGGGGTCACGTGGGCGGGCACTGGCGGAGAAA AGCGGGGCCTTTITGIGTGAAATCCGGCACAGCACCATGAA GGGGGTCCTTITTGIGTGAAAACCCGCCACTAAAACGTCCTGCCGG CAAATCATCCGCGCCAATT TTAAATGAAAGGAGTTTAAAAAC AGATGGCGCCGCGGCATCTGGTGGAGCACCCATGAA GAATGCCGCGCAGTTTTTGGTGTTATGAGAATTTCAAACTTT GGATGAGAGTATATAGCGCGTGGTGGAGCACCCATGAA GAATGCCATAAATTCCACGTGGTGAACATGAACTTTTATCAT TTCCCGGGGTTATAATGCACGATGCTTGTGGAGCAGCCGCGGCCGCGGCCGCGCGCG	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abcd} * HsaB _{LM} 139 _{abcd} * HsaB _{LM} 140 _{bc} * HsaB _{MM} 140 _{bc} * HsaB _{MM} 151 HsaB _{MM} 151 HsaB _{MM} 153*	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732 328 11,844
HsaB _H 62 _{abc} HsaB _H 62 _{abc} HsaB _U 65 _{abcd} HsaB _U 65 _{abcd} HsaB _U 70 _{ab} HsaB _U 70 _{ab} HsaB _K 87 _{abcd} HsaB _{KL} 87 HsaB _{KL} 87 HsaB _{KL} 88 HsaB _{KL} 89 HsaB _{KL} 96 HsaB _{KL} 96	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483 12,115 12,418 11,577 9,043 8,297	223 238 23 209 15 61 87 246 53 19 204 40 35 18 84	GGAGGGAGGGAGGACTAATTATATATATTITTITTITTITTITCTCTTTTTC TCTTTITTICCCCCCCC	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 134 _{abcd} * HsaB _{LM} 134 _{abcd} * HsaB _{LM} 139 _{abcd} * HsaB _{LM} 140 _{bc} * HsaB _{LM} 140 _{bc} * HsaB _{LM} 151 HsaB _{LM} 151 HsaB _{LM} 152* HsaB _{LM} 153*	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732 2,732 328 11,844 5,635
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _J 64 HsaB _J 64 HsaB _J 70 _{ab} * HsaB _J 71 HsaB _J 77 _{abc} * HsaB _{KL} 80 HsaB _{KL} 87 _{abcd} * HsaB _{KL} 88 HsaB _{KL} 89 HsaB _{KL} 90 _{abcd}	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483 12,115 12,418 11,577 9,043 8,297	223 238 23 209 15 61 87 246 53 19 204 40 35 18 84	GGAGGGAGGGCTAATTATATATATTITTITTITTITTITTITTETTETTETTACATTAAGT TECTTITTITCCGCCCGCCAGAAGGGGGGAAAGTATTACAATTAAGT T ATTATTGATCATATTITTATAAATCCAACGCCCGCCAGCGCTCCTCAT T ATTATTGATCATATTITTATAAATCCAACGCCCGCCATGCGCTCCTCAT T ATTATTGATCATATTITTATAAATCCAACGCCCGCCATGCCGGAGAGAA AGGGGGTCCTTITTGGTGAAAACCGACGCCCGGCCATGCCGGGAGAAG AGGGGGTCCTTITTGGTGAAAACCGACGCCAGGAGAAGAAACAAGGGCTTCGTAAAACCGCCGCGGCAATT ATCAAGGGAACTCTTITGGTGAAAACCGCCCTGCAGAGGAGACACCCATGAA GAATGGCCGCCAGAGTATCTGGACTCAAGTGCCGGGGACACCTGGAGAAGAAACGGCCTTGGTGAAAACGGGCGAATT TTAATGAAAGGAGTTTATAGAGGGTGCTGGTGGAGCAGCCATGAA GAATGGCCGCCGAGAT TTAAATGAAAGGAGTTTATAGAGGTGTGGTGGAGCAGCCATGAA GAATGGCCGCAGAGTATATTAGAAAATTTACAAACTTI TGGATGAAAGTATTAAGAGCGTGGAACAAGGACTTGCAGCGG CCGGTCATGTGGCCGGCGCGCGCGGCGGCGGGACAACCTAGA AAACCAACAAATTACA CCAATCTCGGAAGTAAGAAGAGGAGCCTCAGAAGAAACAAAG TTCTATTTTAAATTTTCTATGTGGTGTGTGTGTGTGTGTG	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abcd} * HsaB _{LM} 134 _{abcd} * HsaB _{LM} 139 _{abcd} * HsaB _{MM} 140 _{bc} * HsaB _{MM} 140 _{bc} * HsaB _{MM} 151 HsaB _{MM} 151 HsaB _{MM} 152*	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732 2,732 328 11,844 5,635 2,483
HsaB _H 62 _{abc} HsaB _H 63 _{ab} HsaB _U 64 HsaB _U 64 HsaB _U 64 HsaB _U 70 _{ab} * HsaB _K 70 _{abc} * HsaB _K 80 HsaB _{KL} 87 _{abcdel} * HsaB _{KL} 89 HsaB _{KL} 89 HsaB _{KL} 89 HsaB _{KL} 96 HsaB _{KL} 90 _{abcd}	1,623 238 9,547 7,032 5,717 103 2,259 267 13,558 13,483 12,115 12,418 11,577 9,043 8,297	223 238 23 209 15 61 87 246 53 19 204 40 35 18 84	GGAGGGAGGGCTAATTATATTATTATTITTITTITTITTITTITTITTETTECTEATTACATTAAG TICTITTITTICCGCCCGCAGAAGGGGGGAAGAGTTACAATTAAGT TI ATTATTGATCATATTITTATAAATCCAACGCCCGCCATGCGCTCATCAT T ATTATTGATCATATTITTATAAATCCAACGCCCGCCATGCGCGCATGCCGG GGGACCGTCAGGGGGGGGCACGTGGGCCGGCCATGCGGGAGAG GGGCACCTCACGTGGGCGGGGGCACGTGGGCCGGCCATGCCGGAGAGAA AGGGGGTCTTTTTGGTGTAATCGGACTCAATTCGTGATATTA ATCAAGGAATCCTCGTGGGGGAGACGCCCCGGCCATGCGGGA GGGCGCCTGAGGAAAACGGCTGCGGGGGGCGCCGCGCC	HsaB _{LM} 118 _{abcde} * HsaB _{LM} 128 HsaB _{LM} 129 HsaB _{LM} 130 HsaB _{LM} 130 HsaB _{LM} 131 HsaB _{LM} 132* HsaB _{LM} 133 HsaB _{LM} 134 _{abcd} * HsaB _{LM} 135* HsaB _{MM} 140 _{bc} * HsaB _{MM} 140 _{bc} * HsaB _{MM} 151 HsaB _{MM} 151 HsaB _{MM} 152* HsaB _{MM} 152*	16,792 12,557 10,193 7,873 7,665 4,597 3,473 3,072 248 4,581 4,478 3,994 3,495 3,013 2,732 328 11,844 5,635 2,483

51	CTGTAACATCCCGGAGCTGCCAGTAGAGTCCGCCTTAGACCAA GTTCACAG
51	ATGGAAAATCAAAACAGGGGCGTGGCCGACTGACTCCTATCCG
55	AATGGGACITTT
	A ACTA ATCACCTACCCA A A ATTCA ATATCACCCACC
	GCGAGCATATTATAGTAACTGCCTGCTCGTGGGGGGGGGG
	GAGAGGTGAACCGCAGGTCACGGCGTCTAAAAATTATTAAAAT
200	GTTTGAGAGCCTCGTGACGCGCCTAGCTGTTTAACAAAGACTGC CAAAGTATGAGATTAACACGGAAAACT
200	TACCCTGTAGATCCGAATTTGTGTAAGGAATTTTGTGGTCACAA
69	ATTCGTATCTAGGGGAATATGTAGT
34	TTTCTGAATGAGGACAGTCTGGTGACTGGCCACA
50	AAACGAGTCAGGGGTCGGAATAAATTTTAGTATATTTTGTGGGC
12	CATCHITAATCAC
13	TGTACAGAGTGACAATAGAAATAAAT
20	
90	TTGTGTGTGGTTGAAGAGTTTTTTTCAAAGAGTCTGATGGGAATTT TTATCTCAGAGGACTCCAAATTGTGGGGGGCTGGTTTGTTT
	ACAGATGTTTCTGGGTGTTTGCAGGTTTTCAGAGTATTTTTATATT
	ACAAAGAAGCTAGCCAGTGCCATAGCTCAAACTCTGACAAGCA AATAGATAATCAAGAAGACAAATGGCCTCTTTTGTGAAGCCTTG
156	CTCCAGTATTAATTTTCATTTTC
	AAAGTTCACAGCCATTCTGTGTAGACAAGAGCTAAGAAAAATG
12	CACAACTGAAAGAAGAAGAACA
20	
	CACGTTTTCTAGGCGATTAGCTCAGTATTAGAACCACAAAATGA
79	TIGGTITIGCATTINITA A ATTENTIC
20	
	GGTCATAGTGGTCCTTTGAGCCTGAAATCGAAAGACCCCCTTCC
	CCCTCCCGGTCACGTGATTCATTAAATAATTAATGCCGAGGTTG CAGAATAGATATGTATTCGTCAGGAAAATCGCAGGCTCGGTCTC
	CCTGTTTCTGACGTGCAATTCAACTGTCCTTTGAAAAACAAGCC
202	TGTACCCCGAGAAAAAAAAAAAGAGAGGGGGGGAGAGAGA
22	TCCTCCCTCAAACTCCCAGCCT
27	TAATTTAATTGATTTTATCATAAATCA
	TTTTATATTTGGAGGCAATTCGGAAGGCCTTTCGCTGATTGGTCA
400	TTAATCCACTGAGTTATTGTCTGCTAAACAGAGGTCACTGGGAG
100	
20	TGCAGACACCTACATTITITGGCTCCTGTCTTCCTCC
50	CAGAGGCCATTGTTACGGAGAGTAGGGCGTACCAGTCTTATAGG
51	GCAACCA
	CTCGTCGGTGGCTAAGGTAAGCTGGACTGAAATAGGCTATCAGT TTGTGAATGGCCGGAGAGTATGTCTCAATGATTTATGGCCCATAT
	GACTCCAATCTCGGTTCAAGAAGAGTTCACAAGCTTTAAGCTTC
133	С
40	CCTATTGATGTCAGTTCCCTTTTCAGTTCCTAAGATGGAT
20	TOTECA OTTA A COTCA A A A CACCOTATA TETECA A CA A A
38	
	TTGCACTTAGAATTTACATTTTAATGGATGTAAAAAACAACTGTG
	AGAGATGTCTGGGCCTGCAGAAGTCCAGCATTGCTCAAAAAAG
	CTGTTAAAATATTTTCTTTTTTGTATTATTTATCCCCCTACATTAT
222	GTATTTATATGAGGGAAAAAAAGGAAAAAATTGTACTTTTTAG TATTTACCTG
232	AACAATTCTTGAATAAA
.,	TCACGTGACCCGAAGCCCAACCACCATTGGGTCTAAAATGAAA
52	ACAAAGAAA
33	AATTGTAAGCGATGTGCCCGCATTGCTTAATTA
	TATAATTTAAAGGCATAAGAGCGTGCAAAGTTTGATTGGGATCA AATAACGCTCAAGGGTTTTCTTTCTTTTCT
107	TTGAATAACATTTTCTG
	CTCTGGTGTTTTTGAATCAATTAAACCAAATAATGCTCTCTGTTT TCCACCAGGCCCAGACGAGCGATTGCCGGAGCCCGGTCCCCGG
	ACCACGAATTCCCTGTAATTTCGCTGGAGTCCTGGGGTTTAATAG
190	AGAGAGTCCCCATACGCTTGTATTTATCAGCAATATACAATTAT
180	
	TATITATTAAAATTCTITAATAATAGGAAAAGGGGAAAGTATTT
73	
20	
25	TCAGATGGATGGGCTGCGGGGGGATTGAAGTGTCTTTGTCATGCT
64	AATGCTTGGGGGGTGATGGA

23 CGCTGCTCTGGACCAGAGGCAGA

Polypterus senegalus	bichir Hox	B	Seguence
PFC Dist PseB ₄₀ 2	16 089	Length 26	AAACAACGTCACCTTTCTGGAGAAAT
PseB _{AC} 3	5,963	28	AATTAAATTAGTCAATACGATTAGTGCT
PseB _{AC} 4	3,355	22	TTTAATGTCACGTTGAATACAT
PseB _{CF} 16	-107	14	TITITGCTTITGTT
PseB _{CF} 17	-1,106	27	AAATCAGTGTTTAACCTTGACCTTGAA
PseB _{CF} 18	7,372	27	TTTGTTACGTTACTGCGGTTCATCAGT
PseB _{CF} 19	336	24	TIGAAATGGTCAATGTGTACATTT
PseB _{CF} 20	53	53	CCCAGCA
PseB _{FH} 21	in 10	16	TGATCTGATTCATATT
PseB _{FH} 42	2,782	26	ATGAAACCTGTATTTGAGAATGCAGA
PseB _{FH} 49	2,104	34	TTTGTAATGTTTCATTAAGTTTCCGCAGAATTTT
			CTCGTAAAAATTTAACAGCTIGTGTTCCTTIGCATTCCTGTATAAAC AACGCGCAACCTTGCCGTTTATGGGATTTGTTAAACCATTTACCGC TTTATTTTCTATACGGCAGATACAATATCCACGGGTATACAACT AATATTACCATGAAACCATATTTATAACAATCATTAAAACGTT AATATTACCATGAAACCATATTTATAACAATCATTAAAACGTT AATATGACCACCITCGTTGCTTTATTAAAAACGTTTACTGGTGGAATA
PseB _{FH} 50 _{abef}	986	342	CIGCGTTTTCATAAGATGTTCTA TGATTTGATGCAAAGCGGCAGATATCTCATTAACTAACCCGGTTGA
PseB _{FH} 51 _{abcd}	528	74	ACATATTAATGCGCATATTCTCCCCTCC
PseB. 52	352	162	GTCCGTGTGGAAAACCTGAAGCCAATGGGATGGAGATCCGGTAAT AGATGCAAATTATCATGAAAAGACTCTGCAAAATATGAAACAACT CATTICGGCGGGAGTAAATCACAGAAAACTGTTTATGAACTGGCA CCCCTTCTTGGGAAATCAATCCAGGAAAC
PseB 58	1 944	27	TTGGTGTGTGAAGAAACAAAGAACTGA
PseB _H 59	1,815	36	AAATGTGAAACTTTTTATTAGAATGGTTTCTTAATT
PseB _{HI} 60 _{ab}	1,680	24	CAACATGAAACTGCCTATTTATGC
PseB _{HI} 61	1,624	16	AAATCAAGATATTTTT
PseB _{HI} 62 _{abc}	1.586	219	AGCATGCGCACAGTTAAAAAAAATGTAACGTGACCCTCTGTTTACT GTGAAAAGAATGTATACTGTACTCGTGAATTACTTTATGGGGACTC CGTGATATACTCTGTTGTTTTGCGCACACTTTGTCTATTGTCTAAACC TGGAAGCACGCGAAAAAGGGCACAATAAAGTTTACAAGCAG AATCCGTGACACTCATTGCTCGCGCCTCFGGTTCATTT
			ATTATTAGACATATTTAACATTTAAACTGTATTACAAATTTRCA CATTACTGGAGCTGCAGGGATCCCGAATTCTATTGGATCAGCGAGA AGCACGTGTCTTGTCACGTGTCTCCACAAGAAAAAGGGGTGCTTT TGGTGTAATTCTGGACTCTAATTCGTGATCTATATCACCGGTACATTG
PseB _{HI} 63 _{ab}	233	233	ATT
PseB _{IK} 78	779	25	CATTTGGCTGACTTTATATATGTTT
			CCTAACAATTCTCATCGGTCATTATTIGTAACCATAGAGCATGAA TTACCTCTTGAAGTCATCAGTGAGAATTTACGACTGGTCAACAAA GCACGTGATTCCCTAACGCACCCCCCCATATTTGGCCGCATA CATAGCAAAAACGAAGTACAGTGCATTGCTATAATTCAATTAATAC ATCATAAATCGGAACGACAGCGTTATAAGCACCAAGATCTACA
PseB _{IK} 79 _{abc}	252	231	ATC
PseB _{k1} 83	12,413	65	AACATTATICCAAGICIGGAGIACIGIAAAAGCACCITTIGGCAIG CTCGTGATGTTATAGGCAT
PseB _{KL} 84	12,176	17	GTTTCATGTGAACTTCT
PseB _{KL} 85	12,239	133	GTIGTTATCGTTATAAATCTTATGIGACAAGT0CGATGTTGATGCTT ТСТТАААGTCGGCATGTTTCATGIGAACTTCTAAGTGTATAACTT АТГГССААГСТАТАССААСТGTATAATTTTAAGTTTACA
PseB _{KL} 86	11,914	222	GTICATIGTGTGTATACTITTACTCGAATAACAAATGTACAATATGT ATTATTCATGTGCGAAAAAGTIGTAAATAATTATACATTTTAATG TGATCAAGAATATTIGTAGTAAGCAGTGTGAATAATGACAAGCATICTG TGGAAAATGGCATCTGTCATGTGCGACTGCCACTTAGTATTTTGCG AATAAGCATTTTTTGTAGTTTGTAGCTTAACTTG
			AAAAGTAGGTATGACATTICGATGTCAAATGGATGAGGGTTTTATC TAGAAGTTAGATCGTAAAAATCCCCCCAGACCATAGACAGATACCC CTCACTGGCTCTCAAAAGTCACCGTGGGCACTAGACTAG
PseB _{KL} 8/ _{abcdef}	10,865	201	GGGAAAAGATTTTTGTCATTTATGCTCCCT
FSED _{KL} 09	10,359	31	double and the second se
D D 00			ATAATGTGGTTTGCATATTGATAGGAGTAATCTGCGCTCATATCTCA
PseB	8,221 6 920	84	CAGAGCCCGCTTCAGACCA
F SED _{KL} S I	0,030	19	character in the content
PseB _{KL} 94	5,703	39	AAGTTTATGTGGTGTGTGTATTCCTGTATACTATTATTATT
PseB _{KL} 95	1,593	20	ATTTITTTACTGTTIGTICA AAGTAATGACCTGGGCAAAATTCAATATGACCGAGCAAGCGGTAT GCATTACTATAGAAGTGGCAAGTGGGAAGGCCTCTAGAAGGGGT GAAACGCAGGTCAGCGCGTCTAACAAAGTATTAAAAGTACTGGGA TGCATGACACGCCTAGCTGTTTAACAAAGACTGCGCAAAGTATTAG
PseB _{KL} 102 _{ab}	3,824	195	ATTAATACGAAAACT
PseB _{KL} 104 _{abcde}	1,219	77	TCACAAATTCGTATCTAGGGGAGTATGTAGT
PcoR 10F	604	7-	GTGATTTAGGAGCTTGGTATCCCGAATTAGTTGATGAATTTTTTATC GATCCAAACAAGCCCAGATTTATCTCTG
PseB _{in} 106	21م 4/1	15	TTTTCATGAACAC
DD 400			AAACGAGTAAAAGGGATAGAAATAAATTTTAGTATATTTTTGTGTGC
LPSG PKI 100	61	60	aauxaaddaaau

Danio rerio zebrafish PFC Di	n Hox Ba ist to 3' gene	Length	Sequence			
DreBA ₄ c1	2.734	42	AAACAAGTACACATTTAATCCGTTAAGAAACTTATATTCCAG			
DreBA _{EC} 6	1.621	12	AGAATATTAACA			
DreBAcr8	12 954	14	ATTAATCTTATCAC			
DreBA _{er} 9	10,950	10	TCACAGTTGAACTTGAGAC			
DreBA _{er} 10	4 962	25	CTTACAGTCCTAATTAAATATTTAA			
DreBA - 11	4,502	13	CATGAAATTCACA			
DreBA12	2 225	22	GTTAGTCAGAAAATGGCATTCAG			
DroBA 17	2,000	23	AAATCAGCTETTAACCTIGACCTIGAA			
DreBA _{CF} 17	12,020	27	ATTGAAATAGTGTGTATAGTGAGATTT			
DreBAcr20	268	55	TIGAAAAGCCAATIGAAAGGGACACTATIGCCTIGGCCCAAA ATATGCTCCAGCA			
DreBA ₌ 27	1 863	30	TAGATATTTTTTCCAAGATACTAGCATTAT			
DreBA40	5 275	26	TGTAATAAATTAATGCATACAGAAAA			
DICD/GH40	5,275	20	GCAATAAAATAATATGACTGTAATAAAACTTTATAGGGTATAA			A ACTA ATCA COTOCOTA CA ATTCA ATATCA COCA CO
DreBA _{GH} 45	4,705	83	ATTTCTGAAGGTTAAGAACTAAATGGCTGTAAAGCAAACA			GCATGCATTACTATAGAACTTTAGAGTGGGAGAGACCCAGAGT
DreBA _{GH} 46	4,300	35	AGACGTCTGGGATGACCAACGTTAATTTGTTTACA			AGGGGTGAACCGGAGGTCAGTGCGTCTAACAAATATTAAAAT GTACTGGGACTCGTGACACGCCTCGCTGTTTAACAAAGACTGC
DreBA _{GH} 47	2,445	14	CAGTCGCTCTTCAT	DreBA _{KI} 102 _{ab}	4,301	197 CAAAGTGCGAGATTAATATGAAAACT
				DreBA _{KL} 103	1,024	19 AACATTTGGTTTGTTATTG
			AACATGCACCACGTGTTTCTATATTTAAAAAGTAAAAAGTAA ACAGCCTTIAGTTCGATGTGACGTTTTTGTTTTCCATGTTACT TAGATATATATTGCGATGTTTTTTAATACGAATCTAGTTTCAT TACAACAATTGGACATCTGCAATTTTAACCTCACCAGAACCCA CACCCACCACATGTTTAAGCATGTTAACGAATGTAGCACCTGGTT	DreBA _{KL} 104 _{abcde}	1,150	TCTATATATACCCTGTAGATCCGGATTIGTGTAAACAGACGCA 77 CAGTCACAAATTCGTATCTAGGGGAGTATGTAGT GTGATTTAGGAGGCTTTGTAACCTGAATTAGTTGATGAATTTTC
DreBA _{GH} 48	1,591	311	ATTTATTTATTTATTTATTTATTTATTTATTTA	DreBA _{KL} 105 _{abc}	635	77 TATCGATCTTAAACAAGCCTAGATTCATCTCTG
				DreBA _{KL} 106	457	13 TTTTCATGAACAC
			TAACAGCTTTTTTGATGCACTACGTCAACAACAACAGTAGGGG	DreBA _{KL} 107	1,440	36 TITCTGATTGTAGGAAAATTATGTTTCAGAGCCACA
			CGITTATTGCATTTATAGTTGTTAAACCATTTACAACCACATT TACCATTACAACCAGGCCAGG	DreBA _{KL} 108	60	AAACGAGTAAAGGGATACATATAAATTTTAGTATATTTTGTGT 59 GCAATTCAAAGAAATT
D. D. 50			TICTGTAAATACATTAATAGAATATTGTTGTCAAAGAATTGAAT ACGACTCGGCCTACCTCGCTTATTTTTGACGCCGCGGGCCACAG	DreBA _{LM} 110 _{abc}	22,379	CAGATTTGGTGAAGATGGATCCGCGTTTCATCTTTAATCACGCC 71 AAACTCGGCCCCATTTGTCATGTTTAC
DreBA _{GH} 50 _{bcf}	1,068	331	TCTCATTAACTTACCCGCTTGAACATATTAATGTGCATATTCTC			CTOTECA ACATEA CTOCOTECTOTOTOTOTO A TELATATOCOTO
DreBA _{GH} 51 _{bcd}	550	50	CCCTCC			CATTGCGAGTAATCCTGGTACATTACGCCTTGTAATCTTATTCT
			GTCCGTGTGGGGATGCGAGAAACCATAGTGGAACGAGGATCA GACAGAAGATGCAAAATGATCATCAAAACACACCCCCCAAAATAT			AAATCACAAAAACCCTTTCTTTCTGTCTCGCCTCTTTTTTAATTTAA
			GAAACTACTCATTTGCAGCCGAGTAAATCATAGAAAACTGATC			CGGIGCACAAACCCICIGTICAACGACGCCGIGAAIGCGCCIA AAATATGGATCCATAGTAGAAAAAAGCTGAAGTTAAATAGTTT
DreBA _{GH} 52 _{acd}	368	139	GGGAACTGGCAC	DreBA _{LM} 113 _{bc}	21,228	557 CTCGGCTCGTGGGCTTTTAATGCTTTAATGAGTGTA
DreBA _{HI} 55	1,971	27	AGTGTTTGTGTGTGTGTGTCAGTCAATCAAA			
DreBA _{HI} 56	1,598	31	TAGTTTTTAAGTTAAATGGTGCACTTTTAAC	DreBA114	20 131	75 TGTGAGAATTATACAGAAAAATCATTAATCAC
DreBA _{HI} 60 _{ab}	1,520	24	CAACATGAAACTGCCTATTTATGC	L	20,101	
DreBA _{HI} 62 _b	1,219	32	ACAATAAAGTTTACAAGCGAGAATCCGTGACA			GGTCATAGTAATCCCGCGAGCGTGCAAGCCGTGGTGCCCCCCA
			ACATTAGACAAGGCTCTTGGAAGCTGTATACTCATTGGAGGAT	DroBA 118	15 208	TCCCCTCCTGGTCACCGTGATTCATTAAATAATTAATGACGG TTGCAGAATAGATATGTATTCGTCAGGAATATCGCAGACATGG 474 TCTCCTAGTGTCTGACCGTGAATTCAAACA
			GGGTGATTTTTGGTGTAAATCTAGACTGTAATTCTGTAATATAT	DroBA 110	13,290	
D. D.4. 00			CATTGGACCTCGTAAAACCGACACTAAAACTTCTTAGCATATA	DreDA_LM119	11,000	
DrebA _{HI} 03 _b	189	189	AAICACHCICAAAH	DIEBALMIZU	6,750	
			AGATGGCGACGGCAGAGCTACTGCTGTTAAAACAGTCATGAA GAAATGCAATAAATTCCTTGTTGTTTTTTGAAAAATTTACAACTT			CTCGTGCCCCTCTTATTATGCCTCTTATAACCTTTCAGGTCA GCTTCCAAGAGGCCATTGGAAAGAGACCGTCACGTGACAACT
			TGTGATAGAACTITATGAGTGCCTGGGTCCTGGGATTGGCCGA	DreBA _{LM} 127	192	147 GGTGCCAATGTTCTTCC
DreBA 65.	5 885	208	GATTTCCCAAGTGGTTATATTGCAGCATTCTTTTGG	DreBA _{LM} 129	9,435	27 TAATITAATIGATITTATCATAAATCA
- · · · · · · · · · · · · · · · · · · ·	0,000	200	TIGAATTAACATIGIGITAACACATTAAGGCAGGAGTIIGIIGA	DreBA _{LM} 132	4,465	36 TGCAGACACCTACATTTTTGCCTTGTGCCTTCCTCC
DreBA _{IJ} 67	2,278	51	TTACCCC			CTCGTCAGAGGCTAAGGTAAGCTGGTCTGAAATAGGCTATCAG
DreBA _{IJ} 68	1,387	22	TATTTTGAGTTACGCTCAAAAA			TITGIGAATGGCGGTATGTGIGTCCTAGTGATTTATGACCGTAT GACTCCAAACGCGGTTCAAGAAGAGTTCACAATGCTTTAAGCT
DreBA _{IJ} 69	141	26	CCCGCACTGGCACATAGCCACCCAGA	DreBA _{LM} 134 _{abcd}	2,969	133 TCC
DreBA _{LI} 70 _{ab}	89	61	CCAATCTCCGATAAACTACTAATAGCTAAACCACTTGGACTAT AAAACACAAACAAATCATA	DreBA139	3 459	41 TTAACGTGGATACAGGGTATATTTGAACAAAATGCATGTCC
DroPA 77	000	50	TCAACAAACCATATATCTTTTTGGAACATAAATCATGATCTCA	DTOD/ MN TOODCOB	0,400	
DICDAJKI	303	50	TCGTCATCATTTGTAACCATAGAGCATGAATTACCTCTTGAAGT CATCAGTGAGAATTTACCACTGGTCAACAAAAGCACGTGATTC			TCTGGGCATCATTGTTGCACTTAGAGTTTACATTAAATGGGTGA GGAAGAAAAGTAAATCTTATTTTGAATCGGAAGACTTCAATC AGCGTCTTTCGCTAAGTGTGTTCAAGTGAACATTCATAAATATA TATTTATTTGTTATAGCCAGTTTAAATACTTTCTTTTTTGTATTAT
			IUAAAUGCACCCCCACCCCATATTTGGCCGCATACATAGCAA AAACGAAGTACAGTGCATTGCTATAATTCATTAATACATCATA	D. DA 110		TTATCCCCATGTATTTATATCGATAAAAATGTACTTTTTTAGTAT
DreBA _{JK} 79 _{bc}	236	215	AATCGTGAAGCACAGCGTTATAACGACCAAGATCTACAAATC	DreBA _{MN} 140 _{abc}	3,366	229 CTACCTG
DroBA 93	40 505		AACATTACCTACAGAGTACTGTACATCGCGGCACCTTTCGGCA	DreBA _{MN} 141	2,895	17 ΑΑCΑΑΤΙΟΙΤΙΑΑΤΑΑΑ
DreBA _{KL} 83	12,508	64	IGHAIGGAIGIIHAGGCAI	DreBAnn 144	1.213	41 GGCTGCTGTCAAGCGCTTTGCCGGCGAAAAGATTGATCACC
			GTTGTTCTTGTTACAAATATTGTTTATGTGTCAAGTGCTATGTTA	DreBA 145	791	17 ATAAAACATATAAACAA
D. D.4. 05			ATGCTTTCTTGAGAGTTAGCATGTGAGCTCTTAAATGTTATAAC	MIN		
DIGRAKT 82	12,316	131				CCAGGCCCCGAATTTCAATTGGCTGAGATGAGTCACGTGACCA GGAATTGGCTGCAATTTCGCCCATAGTCTTCAGTTTAGTAGACC
			TTACTGGATCATGTTTATGTTCCAAAAAAGGTTGTATATATTGA			CIGGTCCCCATACGCTAGTAATATCACCAATATACACAATTAT TAAAGCCCCGCAAATGCCGCCATAGCAGGAGCGCAAAATAAAT
			ACATTITITATIGIGATCAGITGGCTATITIGIAGIGGGCAGAATA	DreBA _{MN} 146	242	194 CATAGCTTTTTGGATGTTATTT
DreBA86	11 959	217	AACGGCAATGTGGAAAAAAGTCATGTCAATCTGCCTGTTAGCA TTTTGCCAAAATGCTTTTTGTATTTGTTTGTAGTTTAACTTG			TTTAGACCTAGTTTATTTATTGAGATCCTTTAATAGTAAATTTCA
	11,000	211		DreBA 147	14 240	AATITATTTATTGTACGTTATTTTCATAGTTGAAATAATAAAAA 94 TAAAA
			AAAAGTAGCTATGACATTTACATGTCAAACGGATGAGCGTTTT	DICDANO 14/	14,210	CTGCTCTCGCCCTGATGCAAAATGGCGCTCGAAACACAAAGAA
			ATCTTGAAGTTAGATCGTAAAAATCGCCCAGGCCACAGACAG	DreBA _{NO} 148	13,453	72 GGATATGAACAATAAAGCGGCAGCCATTA
			TTAGTTTTATGGTTTTGGGGAGTTGACAATGTACTATATATTTCA	DreBA _{NO} 149	13.066	20 ΑΤΤΤΑΤΑΤΑΤΑΑΑΑΑΑΤΤΑΑ
DreBA _{KL} 87 _{abcdef}	11,215	201	CATTCTAGAATGCAAGTGACGGTTTAAC	DreBANC 154	14 161	34 TATTTATTGTACGTTATTTTCATAGTTGAAATAA
DroBA 00	0.500	~~	TIGCATATIGATAGGAGCAATCTCCCACCATATCTCATC	DreBA _{ve} 155	6 600	33 AGGTITGTTAATTGTTTGGCAATAAAAATTATG
DreBA 01	8,533	39		DreBA 157	0,099 E 111	20 TAAATAAATAAATAAATAAA
DIEBAKEAI	7,654	19	CAGAGEEEGEIIIAGAEEA	DIEDANO 137	5,114	AGCCATATTCGACAGTTTTAAAAAAATAAACTACTGATAATAA
DreBA _{KL} 94	5,716	42	AAGTTTAATGCTGCCAGTCTCTTTTTTCAAAATTTAATTATT			ACATAAGACTGAGTTTCAGTATTTTTATTGTATTTTTGTCAAGA
				DreBA _{NO} 158	2,044	106 GACGTITGATTTTTTTTTTTTTT
DreBA _k 98	8 534	83	111GCA1ATIGATAGGAGCAATCTGCGAGCATATCTCATCCAT AATGCATAGGGACAGGATCATCCAAGGGTCAGCAGACGGG	DreBANO161	281	ICAGATIGATGGGCIGGTTIGATTGAAGTGGCTTTGTCATGCAA 63 ATGTCAAGCGCGTGATGGA
	0,004	00		apc	201	

Danio rerio zebrafish Hox Ba

Oryzias latipes	medaka Hox Ba Dist to 3' gene	l enath	Sequence			
OlaBA _{AC} 3	4,855	21	AATTAAATATTTTTCAGTGCT			
OlaBA _{CG} 5 OlaBA _{CG} 6	25,610 19,300	37 16	AACCAGTAACTGAACTATATATAAGTCATAATAAATT AGAATAGTATTTAACA			
			ААААСАТТІТСАGГІТІGАТІGСАААGААТІТІТІGСАААТААААТІ ТІТСТАТАСТІТІТІТІGССТСТААСССАААGТАТІGТААТАААТА АЛАААААТААААААТТІТІGСТІСАСТІGGATITIAGCATITITIG Гадасалгаассиготісасасасастостінгістігі стігібадос			
OlaBA _{CG} 7	9,969	199	TTATTGTTGTGCTCCTTGCCTG			
OlaBA _{CG} 12	8,237	23	GTTAGTTAGACCTCTGCATTCAG			
OlaBA 13	1 565	82	AATTAACGCGCTCTCTGGTTAGCAGCGAACCCAGCAGGCGGA GGCCCCGAAAAATTAAAATTCCCCCGAGCTTTGCGGTCTG			
OlaBA 14	1,303	26	AAAGCGGGTTTTTTTTTTTTTTTTT			
Clab, CG	1,200	20	AGCAAAGCAGAAGAAAAGAAGAAAAGAGTGACGTAAATCTCA			
			TAATGTCCCTCTTCTTCTGCTTTAACAAACTCGCGGCTGCACGC			
OlaBA _{CG} 15	101	101	GGATAATGICCGAGA			
OlaBA 18	4,219	23	TTETEACATHIGHTHOT			
OlaBA 21	10,345	21	TGATCTCTTCATATT			
OlabA _{CG} 21	3,382	15	CIGTTFICCCCTTIGTIGATGTICTCGCTTATTATGCATTGGATAA			
OlaBA _{CG} 30	19,382	47	A			
OlaBAcu39	9.226	63	AGAAAGAAACAGCATTICCITTICITTICITATIGAAGCACTIC			
OlaBA _{cu} 40	5,500	29	TGTAATAGCCTATAAATATAGAGAGAAAA			
OlaBA _{GH} 42	7.066	26	ATGAAAGAGGATTCCAAACATGCAGA			
OlaBA _{GH} 43	8,371	15	TCTTCCGTTTCTCAC			
0-04	0.077		GCAATAAAAGAATATGACGGCAATAAAAGTTTATAGCGTATAA			CCGTTCATGCCGCAGGGAGTCCGGCGCGCGCCCGGTCTGC TGCTGCTGCGGCTCCAGGAGGGTGGTGCTGCTGCTGCTGCTGCTGCTGC
OlabA _{GH} 45	3,377	83	АПТЕГОЛАООТТАЛОЛАСТАЛАСООСТОТАЛАОСЛАЛСА	OlaBA _{LM} 124	2,850	107 TGGTCGCCAGCAGCCGTGCT
			AACATGCAGTCGGATTATTTTGATTTTTCAAATTCAAGATACTTC	OlaBA _{LM} 125	2,564	24 CCACCGGTGCTGAGGAAGGTAAGG
			CAATTCTCCAAAATACCAGATTTTCTTTGTTTTGCGTGCG			TITAATGGCTITTCTCTGTCTCCTCCACCTGCAAAGCTCCTCATG
0.04			ACTTAAACAATTGCCCTGCAGTAGACCAAATTCTCCAGGCCAT AATCTGGAACGGAAC			GCAGGCGCCATTTGTAATTTTATATCCCGGGATAAATCGCAGAG TGGACACCAAGGCCGAGCTCGTCCCCCCCCCC
OlabA _{GH} 48	1,753	318	AIGOICCCAICCAIGIIIAHGGAIGAGAAACAAAA			GTGTGAGTCGATTATTCAGGGAGGCGTCTAGTAAAGTTGGTGAT
			CGCTGTGGTTTGCTCTGGCTGCTCACCGTCGCTCTTAGCAGCCG	OlaBA _{LM} 126	2,068	442 TGTATTAAGCTGTAGTCCTACATGCAAGGGGCA
			GCAGCCGCGCGCCIGTIGIGGCIGIGAGGGGAAACACCACAAC GACGGTCACCGACACCGGCGGTAGACCTGCATTGCCTGCC			CTATICATGTCACGGAGCCTTICAGGGGAGGAAGATGGATITAA CTCTGTCATTTCTTTATICTGTCTCTCTAACCTTTAAGGTCAGATI
01.04.50			CCCCCACCCGCCTTGGTCTCTGTGTGTTATTAGGTCTGCCACAA			GCAGGGGACCGTTGGAAAGACACCGTCACGTGACCTCCGGTAC
OlaBA _{GH} 53	235	212		OlaBA _{LM} 127	203	146 CAAATGGTCTTCC
OlaBA _{HJ} 54	9,435	31		OlaBA _{LM} 128	12,880	22 TCCTCCTGCCTACCTGCAGCCT
OlaBA _{HJ} 57	24,265	37	CAACATGAAACTGCCTATTTATGC	OlaBA _{I M} 135	204	41 CCTATTCATGTCACGGAGCCTTTCAGGGGAGGAAGATGGAT
OlabA _{HJ} OU _{ab}	28,111	24	ATGAAGAAATGTAATAAATTCCTTGTTGTTTTATGAAAATTTAC	OlaBA _{MN} 136	9,069	20 AATCAAGAGCTATCTTTTCT
			AACTTTGTGATACAAGTTTATGAGTGGCCGCGCGTGGGGATTGG			
OlaBAu 65to	6.481	146	ACGAGGGGTIGGICAIGIGGACGCGCTIAACGIGAACAIGAAC			AGCTCTCCTGCCTGGTAGATGAAATAGTTGAGATTTAATGGGC AGTTAAGGAGGTCGTTGTATTTATTATGCCGGGGTTTTCTCCCCCCT
Harrie	-,		CCAATCTGCGATAAACTAAGTGATAGCAGCAGTCGGACTGTCG			GCAGGCAACACATGTTGTTGTCAGCAGAGCTGAGCTGTGTGCTG
OlaBA _{HJ} 70 _{ab}	256	66	ACTATAAAGCACAACAAATCATA			GGCTCAGGCCCTCCATCAGCTGGAGAGCGACAGAGAAAAGCA ACGCTGCTCCACAAAAGCACAGAGAAAAACCACTGGACGGCC
OlaBA _{JK} 75	1,118	45	GC	OlaBA _{MN} 137	8,843	270 TCCCACTCGCTGTCTACTCTTTTTTGCTTCCTGCAGTA
	676	71	TITATGGCTTCTGGTCTCGGGCTTCTAATTTCCAGCCTCAGCAAA GGTCAATTAACAGGCCTGAGTGATGA			
OlabAjki U	0/0	11	of children and the second s			CATTAAGCTCACTTCCTTTCACAAGCAGAGTTGCCAGCTGTTGA
			TGACATTTACATGTCAAACAGATGAGGGGTTTTATCTCCGCGTC			CGTGTTCAAACAAACCTGTGAGAGGACATGCAAGGCGCATTTT
			GGATCGTAAAGACCAGGCCGAGCCTCAGACTGACACATCTCAC TGGCTCTCCTCTGGTCACGTGTGGTCCATAAAGTTAGTTTTATGG	OlaBA _{nn} 138	8,486	199 AAGAGTTGAGAGAACTATTTATTTA
			TITTGGGGAGTIGACATIGTACTATATATITCACATICTAGAAA	IVIN -		TCTTGACTTTTAATGTGGAAACAGGGTATATATATTTGAACAAA
OlaBA _{KL} 87 _{bcdef}	10,515	193	GCAAGTGACGGTTTAAC	OlaBA _{MN} 139 _{acde}	8,186	54 ATGCATGTCC
OlaBA _{KL} 96	8,524	14				
OlaBA _{KL} 91	6,950	19	CAGAGECEGETTCAGACEA			TCTGGGCATCATTGTTGCACTTAGAGTTTACATTTTGATGGTTAA
			GGTGAACTGGAGGTCAGCGCGTCTCACCGACATTAAAATGTGC			AGGTTAAAAAAATAATAATGAAATCTTATTTTGAAGACGGAAG GCCTTCCAATCAAAGCGTCTTTCACCAATGCGTGTTCAAGGGAA
OlaBA 102	4 567	110	ACAGGGGAACGCGGGGTGACACGCCTCGCCTGTTAAACAAAG			CATTCATATATAAATATTTATTTGTTATAGCCAGTCTAAAAGGA
OlaBA _{KL} 102 _b	4,567	10	AACATTTGGGCATTTATTG	OlaBA 140	7.051	CTITCTGTTTTATATTAATATTATTATTATCCTTCATGTATTTATATT 260 GAGGAAAAAAAATACTGTACTTTTTAGTATTT
CIGD: IKL 100	1,000	15	TCTATATCTACCCTGTAGATCCGGATTTGTGTGACGGTCGATGA	OlaBA 140 abc	7,901	17 AACAATTCTTTAATAAA
OlaBA _{KL} 104 _{abcd}	1,310	71	AACAATCACAAATTCGCTTCTAGGGGA	CIGBRANNIT	7,001	GCTGCTGTCAGCTCTCTCCAAGAGAAAGATTGATCACCGCATTT
			GTGATTTAGGAGGCCGTGCGCCCAGAATCACTTGATGAATTTTC	OlaBAm 142	5.129	CTITITCTCCCACTCGGGGGCTCCTGTGGCCCTCCTCAAAACTTCC 104 CTGTTAAACTCCCAAA
OlaBA _{KL} 105 _{ac}	682	76	TATEGATECTAAACAAGCCAGATICATCTCIG	NUN	-,	
			ACACAAAGAAGTGGGTTTTTTGCGGCTTTTGCACACAGAATGCG			CATATTGTAAACGGTACTGGCCAGCTCCTCTCGCCTGATGTTAC
			CTCTGGCGCACAGGCAGGAGGGCGCGATGATGCGTCCGTC			TTTGCGCCTGTCATCGGCTGGGATGCGCGGACTTGCCGCCCACA
			AATCACAAGCCTTCCCCCGTTTCACTCCCGTTCTCCCGTTAAT			CGGCGCACATGGCGACCGGTCGCCTTCTCCCTTTCTTGCCCCTC
OlaBA _{LM} 109	26,025	190	TTAACGGCAGCTCAG	OlaBA _{MN} 143	4,504	619 TCTTTGCCTCCATATTTGGTGGAAAAAAATAATAATC
			AATGGCTTCTTTTGTGCAGCGCGGCTCCCGTATTAATCCAAGACG			TTTAGACCTTAGTTTATTTATTGAGATTCTTTAATAGTGAAAATC
$OlaBA_{LM}113_{bc}$	256,339	104	TCTTTTCTGAGAGCAGG	OlaBA 147	8 175	CAAATTATTTATTGTACATATATTTTCATAGTGGAATAATAATA O5 ATAAAA
$OlaBA_{LM}118_{b}$	18,643	26	CTGACGTGGAAAATTCAACTGTCCTT	Olabrino	0,175	TATTTATTGAGATTCTTTAATAGTGAAAATCCAAATTATTTAT
OlaBA _{LM} 119	11,949	29	TTATTTAAATATAAACAAAACGTAAATAT	OlaBA _{NO} 154 _{ab}	8,161	62 TACATATATTTTCATAG
OlaBA _{LM} 120	7,000	24	TGTAATGTTCATTAAATTTAAATG	OlaBA _{No} 148	7 478	CTGCTCCCCTCCAGAGTCAAAATGGCGCTGGAGACAAAGGAGG 72 ATGTGAACAATGAGCAGTGGCAGCCATTA
			GATGTGTAAGATGAGAACCAGAATCAATAAGAGCTCATATCGC	OlaBAuo149	7,96	17 ATTTATCTCTGCATTAA
			TCCCACTCAGCCTCCATCCTCTCTGCTGCTTTTGCTTTTATTCC	OlaBAno 155	961	30 AGGTTTCTCTGTTAAACTGGCAGAATTATG
			GGGAATAATTCCAGGTCAGCAGTACCTGTCAGCGGCTGCTCCT GTCCCACAACCTTCGATTAGACTACAAGAGGTTGGTGCTCCCTA	S.abrino 100	301	
			TCTGATTTTTCAGCCCCTGCATCTTTCTTCCCCTTTCTTT			GCTCCTCTTTTATTCCACACCGCTCTGCGCTCTGACACATCCGC
UIABA _{LM} 121	5,846	227				GCTGATATCAGATTGATGGGCCGGTTTGATTGAAGTCTCTTTGTC GCGCTGATGTCACTGCGAGTGATGGATGAGGCGCGCGCCAC
UIABA _{LM} 122	5,232	14	ACICOIOIAAIOIA			TATTGACGCGCGCGCGCACCAACTTCACTCCTGAGCCGAAAAC
			GGAGAACCGCGGGGACGATCAGGAGGAGGACGGCTGATCACA	OlaBA _{NO} 156	740	288 TGCCGTGACCAGCTGACAACTTCTGGCCCGGTCACCA
			GAAAATGCGATGGGGTAACGGTTCCGTCTGGATCTTTGTCTGAG ATTCTCGGCCCGGATGGCTGCCGGCAGAGCCGCTCAAGCCAGA			TCAGATTGATGGGCCGGTTTGATTGAAGTCTCTTTGTCGCGCTG
0.04			GAAATTCGAGGCCATTGTTATCAGCCAGCAGCGGCGCGCAGCCA	UlaBA _{NO} 161 _{abc}	687	64 AIGTCACTGCGAGTGATGGA
OlabA _{LM} 123	3,199	207	040610010100000000000000000000000000000	UIADA _{NO} 160	812	Z1 CETCHCACGEACGHCCHT

Tetraodon nigro	viridis spotted gree	en pufferfish Hox Ba			
PFC	Dist to 3' gene L	ength Sequence			
TniBA _{AC} 1	3,439	36 AAACAATATGGTGTTAATGCTCAAATGGTATTCCAG			
TniBA _{AC} 2	13,381	26 AAACAAAGGCAGCTTTTTTGAGAAAT			
TniBA _{AC} 4	908	23 TITAATAATACATAATAATACAT			
TniBA _{CG} 5	30,138	38 AACCAGTAATCAACATGTAGCGCAACAACTAATAAATT			
TniBA _{CG} 7	11,747	19 ТТӨТТӨТССТӨССТӨССТӨ			
TniBA _{CG} 8	15,031	19 ATTAATACCTGTGTATCAC			
TniBA _{CG} 9	12,637	18 TCACAGTTCCCGTGAGAC			
TniBA _{CG} 10	6,064	25 CTTACAGATTGGGAGACATATTTAA			
TniBA _{CG} 11	5,598	12 CATGAATTCACA			
		AATTAAGGCGCTGTTTGGTTGGCTGCTCGGCTGCAGGGTGGAC	i		
TniBA _{CG} 13	2,578	81 GCCCTCCATAGATTAAAATTCCCACAGCCTGCGGTCTG			
TniBA _{CG} 14	2,238	26 AAAGCGATCTTGTTTTTGTCTTTTTC			
		AGCAA AGGGCAGA AGAGAGA AGGAGA AATAGACAGAGGG			
		AAGAGTAAAAATCTCGTAATGTCTCTCTGCTTGTTCTCTGTCTAC	i		
TniBA _{CG} 15	686	118 TAAAATCGCGGTGCGTCGCAGATAATGTCCGAGA			
TniBA _{CG} 27	4,461	37 TAGATAAAAACTAATATTTTACAATAATTAACATTAT			
TniBA _{CG} 28	22,698	22 CATAAAGATTTCAACTTGGGCC			
TIDA	0.004	AGAAAGAAAACCGCAGCTGTGCGCTGGACAGAAATGCAGAA			
ThiBA _{GH} 39	9,294				
ThibA _{GH} 44	10,338	20 10411411004404444410			
		GCAATAAAAGAATATGACGGCAATAAAAGTTTATAGCGTATA			
IniBA _{GH} 45	4,408	83 AATTICIGAAGGITAAGAACIAAACGGCIGIAAAGCAAACA			
IniBA _{GH} 47	9,023	13 CAGICGICCHCA			
		CGCTGTCGGTGTGCTGGTGTTTGTGGTCGTTACTCTTGCCGGCA			TTTAATGCATTCTGGGTGCTTCCCTGCCCGCATTGCTCCTTATG GCAGGCGCCATTTGTAATTTTATATCCCAGGATAAAACAGACA
		GCCGTCACCTTTACGCGCCCCGCTCCTCTGTTGTGGCCGCGGG GCGAAACACCACACACCCCGCTCCTCCTCCACCTGCCCCTGCTCCACCTGCTCCACCTGCCCCTGCTCCACCTGCCCCTGCTCCACCTGCTCCACCTGCTCCACCTGCTCCACCTGCCCCCTGCTCCCACCTGCTCCACCTGCCCCCTGCTCCACCTGCCCCCCCTGCTCCCACCTGCCCCCCTTCCCACCTGCCCCCCCTGCTCCCACCTGCCCCCCCC			CTGGACACCAAGGCCGACCCCTCTCTCTCTTTCTGTGTCTTT
		CTTTCTCCCTCCCTCCGTCTCCCTCTTTTCGTGCCCGAGTCTC	r		CTCTCTCTCCCTCCTTCCCTGTTGTTTTGTTTGGGTGGCTGTTT CTCGGTTGGTGTAAGTAGATTATTCCCGGGAGGCGTCACAGTGA
TniBA _{GH} 53	260	214 CCGCTTCCAACAGCCTCTTCCTTCACTTCTACTCTGACTC	TniBA _{LM} 126	2,236	435 AGTTGGTGATTGTATTAAGATGTGGCCCTACAAGCA
TniBA _{HJ} 54	9,170	28 AAAAGAAATAGTGCGTTACCGCCATCAG			
TniBA _{HJ} 55	17,063	28 AGTGTTTACGATCTCTTGCTGTATCAAA			CIATICATGICAIGGIGCCITICAGIGCIGGAAGAIGGAITTAT CTCTCTCATTTCTTTATTCTGCGTCTCCTAACCTTTCAGGTCAG
TniBA _{HJ} 56	16,665	31 TAGITICTICTITIGITGGAAGCATTTITAA		204	ATTGCAGGGGACCGTTGGAGAGATACAGTCACGTGACACCCG
TniBA _{HJ} 58	6,599	27 TIGGIGICICAAATATGTCACCGAAGGAAGACGTAATTA TTGAATTCAAATATGTCACTGTATCCCGAGGAAGACGTAATTA	IIIBA _{LM} 127	204	147 GIACCAAAIGGICIICC
TniBA _{HJ} 67	2,551	47 CCCC			CAGTTTGTTAGCGGCGGAGTGGCTGGCTCAGTGATTTATGGCC
TniBA _{HJ} 68	1,652	27 TATTTTGAAGGCCTATTTTCTCAAAAA	TniBA _{LM} 134 _{bc}	2,766	78 CGTATGACTCCAATCCCGGTTCAAGAAGAGTTCAC
TniBA _{HJ} 69	373	26 CCCGCACTGGCACTCAGCCACCCAGA	TniBA _{MN} 136	5,567	20 AATCAATGATGGGCTTTTCT
					AGCTCTCCTGCCTGGTAAATGAAATAGTTGAGCTTTTAATGGG
TniBA _{H I} 70 _{ab}	257	76 GCGGACTGTCGGCTATAAAACACAACAAATCATA	r		CAGTTAACGAGGTGCTTAGATTTATGACACCGAGCTCGCTC
110 40		CTGAAATGCATCTCATCCAGGGAATCAACAAATCATAAATCA			CCTCCAGGCAACACATGTTGTTGTCAGCCTAGCTAAGCTATGT GGCGGCTCTTGCTCTCCATCAGCCAAAGAGAGCAAGGGAGAG
TniBA _{JK} 75	1,161	44 GC			CAGAAATGGATGTGTGGAGCTGCGGCTAACACTTGTCTTTCTC
TniBA _{JK} 76	694	69 GTTAATTAACAGCTCTGAGTGATGA	Iniba _{mn} 137	5,354	299 ICTICAAAAAACCACIGGGCGCICTTICGCIGCGCCGIGIC
		TCAACAAATCATAAATCAGCAGATTTCCGTGCACGGATCAGG			
TniBA _{JK} 77	1,137	54 TITAACATTCCT			AACAGGGTTTAAGAAGCTACGAGCTAAGCTAGCTCCAGTAGA
		TGACATTTACATGTCAAACGGAAGAGGGTTTTTATCTCCAAGT			ACATGCATAGGCAGTGTGAGCTAGCCACTGCTTTATACACACA TTCAATGCTAAGCTAGCCTTCCTTTTGGTTGACACACAACTAT
		TGGCTCGTAAAGATCAGGCAAGGCCTCAAAATGATACCTCTC			AGCCAGGTTGCTCTGGCTGTTGACTTGTTGACTTGTTCAAATAA
		ACTGGCTCTCCGCTTGTCACGTGGGGTCCATAAAGTTAGTT	TniBA138	4 889	ACACATAAAAGGACATGGAAAAGACATTTTTATGTTGTTATTT 268 TAGCACATCATCGACACAGGGTAATAAGAAGAGGCAGAGAA
TniBA _{KL} 87 _{bcdef}	14,162	193 AAAGCAAGTGACGGTTTAAC	MIN	1,000	TCTTGACTTTTAATATGGATACAGGGTATATATTTGAACAAAA
TniBA _{KL} 91	8,415	19 CAGAGCCCGCTTCAGACCA	TniBA _{MN} 139 _{acde}	4,482	53 ATGCATGTCC
TniBA _{KL} 95	4,712	20 ATTTTTTAGCAGTCTGTTCA			
		GGTGAAAGAGAGGTCAGCGCGTCTCACCAATATTAAAATGTG			TCTGGGCATCATTGTTGCACTTAGAGTTTACATTTTGATGGTTA
		TACCGGGGACGCGGGGGGGGGGACACGCCTCGCCCGTTAAACAA			AAGTTAAGAAAATAATAATAATGAAATCTTATTTTGAAGACG GGAGACCCTCCAATCAAAGCGTCTTTCGCCAATGTGTGTTCAC
TniBA _{KL} 102 _b	6,232	118 GAGTATGCCAAACTGGCAGATTAATTTGAAAACT			GTGAACATTCATATATAAATATTTATTTGTTATAGCCAGTTTAA
TniBA _{ki} 104 _{abod}	2.012	71 AGCAATCACAAATTCGCTTCTAGGGGA	ΤοiΒΔ140	3 765	AAAGACTTTCTGTTTTGTATTATTATTATCCTCCATGTATTTAT 255 ATATAGAAAAAAAAATGTACTTTTTTAGCATTTACCTG
		GAATTAGTTGATGAATTTTCTATCGATCCTAAACAAGGCAGAT	ThiBA 140 abc	3,705	17 AACAATTCTTTAATAAA
TniBA _{KL} 105 _{bc}	840	52 TTATCTCTG	THE MN I T	3,205	17
TniBA _{KL} 110 _{bc}	29,183	44 CATCTTTAATCACGCCAAACTCGGCTCCCATTCGTCATGTTTA	2		GCTGCTGTCAGGCTCTTTGGAGGGAGAGAAAGATTGATCACCG
			TniBA _{MN} 142	1,393	128 TAGGCTATCCTCTGCTAAACTACTTTAGATCTTTTCCCAAA
		ACACAAATATTTTCATTAAATTTCAATGTTGGTTTTGTCTATAG CCTGTCTTGAGAAATCAGCAGCCTGCGATGATTAATCTGTGCC			
		GGCCTTGAGTGATCTTGGTACATTACGTCCAGTAATCTCGTTT			CATATTGTAAACGGTGCTGGCTAGCTTCGTTCACCTAATGTTA
TniBA109	27 710	AAATCACAGACCGTCCCTTCGTTTCACTCTCGTTCTCCCGTTA/ 101 TTTAACGGCTGCTCAG	1		AAGATCCAGAGATGCTCTTTTGTTGTGCGTAACACTGGACCA
THEALWIGE	27,710	ATAGCTCAAACCCTGACAACCAAATAGATAATCAACAAGAC	3		GGATGCGCCAGCCCGCCGCCCACACGCGCACATGGCGACCG
T.:DA 440		AATGGCTTCTTTTGTAAGGAGCGGCTCCTGTATTAATTTTCATT	TniBA _{MN} 143	661	639 AGACAAAACAAAAGTAAGTACCCCTGTGATGGAGCCTCTT
THIBA _{LM} TT3 _{bc}	27,288	104 HEITHEITAGAGEAGG			
		TCACGTGATTCATTAAATAATTAATGTGGAGGTGGCAGAATG	, IniBA _{MN} 144	1,394	43 GGCTGCTGTCAGGCTCTTTGGAGGGAGAGAAAGATTGATCACC
ToiBA 118	19 470	ATGTGTATCGTCAGAAATATAACGGTAAGACATGCGGCTGCT 100 CAGCGGGTCTGACGTCGAAAATCCAACTGTCCTT	r Iniba _{mn} 145	929	16 ATAAAAAGCAAAACAA
THIDALMTTO	18,479	120 сабеоблетоженевааа сонести			CCAGGCCCGGACCCCGCGATTGGTGAGTTTGAATCACGTGAC
		GAATCAATAACATCTGAGATCACTTTAACCCCGGCCTTCATCC	2		CAGGAATTGGCTGCAATTTCGCCCCATAGTTCTTCATTTTAGCC
		TICTTCCTTICCTATTAGCCTACTITTACTCCGAGATTTGGCCT GGAATATAACCATCAGCATTACCTCTCACTGGTCGCCCCCTCTC			TACUCAGGICUCA FACGUTATATUACCAATATACACAATTAT TATATAGTCACCGCATTACGCCATTGCGGTCGGGAGACAGGC
		TCGTGCGTTCGATCGGACTACCAGAGGTCTGCGCTCTTTATCG	TniBA _{MN} 146	341	196 GCTCGTGCGTGTATTTATTTATTTATTT
TniBA121	6 383	GATTITTACCGAGACCITTCTGATTGTATATCTTCTTTCCCTCT 235 TCTGCCCCTCTTTATC	TniBA _{No} 154	10 101	TATITATTCAGATTCTTTAATAGTGCAAAATCCAAATTATTTAT
TniBA122	5,673	15 ACTCGTGCTAATGTA		10,101	
	5,075				GCTCCTCTTTTCTTCTCTGCTCTCTTTGCTCTGACAGATCCGCG
		GGAGAATGGGACCGTGAGCGCGGACGATTCACCGCCAAATA/	1		CTGATATCAGATTGATGGCCCCGTTTGATTGAAGTCTCTTTGTC GTGCTAATGTCACGGCGATTGATGGATGAGGCGCGTGCGT
		A LAAGA IGGGG LAA LA LI FIGFIGGAG FFFFFFFFFTTTTTTTTTCC TCCACAAACGCACGCCGGCCTCTGTCGTGTGGCCGCGGTGGAC			GGCAGCCGCGCGCGCACACACCCAACTTTAAAAACCGAATAGG
		ATTITAAGGCCATTGTTGTCGGTAAGCAGCGGTGCAGGCAGCC	TniBA _{NO} 156	838	1UUCCTCCCTTAATGCACACACACACACACACTCCCCCCGTCCC 293 TGTGACCGGCTGACAAACTTGTGGCCTCCCGGTCACCAG
I NIDA _{LM} 123	2,833	204 CIGUTCATGCCCCACGGTGTCCGGCCCGCCGCTGCCCCCCCC	TniBA _{NO} 157	4.128	20 ТАААТАААСАААСАААТААА
		CGCCGCCGCTGGCTCCCGGAGGTGTCGTTGTGGTGGCGGTGCC	TniBA _{NO} 158	1,185	33 TIGTATTITITAAATGGATATTAACTTITTATT
TniBA _{LM} 124	3,117	96 TCGCCGTGCT		,	
TniBA _{LM} 125	2,837	24 CCACCGGTGCTAGAGAAGGTAAGG	TniBA _{NO} 161 _{ab}	787	38 TCAGATTGATGGCCCCGTTTGATTGAAGTCTCTTTGTC

			Oryzias latipes	medaka Hox Bb	
			PFC	Dist to 3' gene	Length Sequence
			OlaBB _{IJ} 70 _b	57	22 CTATAAAAGACAACAAATCATA
					CATGTTAGAAGCGTGGTCTTTATTTCTGTTTCTGCACGGCAACACTGT
			OlePP 72	4.040	CCGCATAATCAGAGCCTCCTCTGTCTGTCTTTGTGCTTGTGTATTTATT
			UIABB _{JK} /2	1,048	113 IAGGGACIAIGCAAA
			Old PR 73	000	TIGICCTICCICGIGAACCIGCICCGIGACTCIGIGCTIGIAGICIGI AGGCICGICGITIACACCIGICGCATAAACGITICCATTIGIACAGAT GAGATATGITICATIGATIATITATIGITITATATIGIGIGITICAATGAC AACIGGATIACIGIGIGCAATATITIGITIAAAGGGAATIGTAAATATG CAAAATAAGGUTTITATIATI
			Olabbjk73	022	
			OlaBB _{JK} 74	523	28 CAATAAATIGACATAAACTCIGCGTAAA
			OlaBB _{JK} 78	738	24 CATTIGTACAGATGAGATATGTTT
Danio rerio zebratish Ho	ox Bb	anthe Oceanies			
PFC Dist to 3	gene Le	ngin Sequence			CCTAACGACCATTATTTCGTCATCATTTGTAACCATGGAGCATGAATT ACCTCTTGAAGTCATCAGTGAGGATTTACGACTGGTCAACAAAGGCA
DIEDDHJ39	5,541				CGTGATTCCCGAACGCTCTCCCATATTTGGCCGCATACCTGGCAAAG
DreBB _{HJ} 61	5,332	20 AAAICATATAGGATATITI			TACAGTAGGGCTTCATTGCTTATAATTCATGATTGCATCCATAAATCG
DreBB _{HJ} 64	7,249	27 TTAAATAAAAGTCTGAAGTTCAAAAAC	OlaBB _{JK} 79 _{abc}	252	230 TGCAAGCACACAGGATTATAGCGACAAAGATCTACAAATC
DreBB _{HJ} 65 _{cd} DreBB _{HJ} 70 _b	3,061 50	ТПАТGААААТПАСААСТПІGТGATAGAACTПАТGIGGGTICIGCC АGTGGATGGCTGACGGAGGACGACGTGACGACACTCTGTGGAACAG 142 ААСПТПТАГАТПССААСАПОБОСТАТААТОСАGCATICTПТЮG 22 СТАТААЛАСАСААААТСАТА	OlaRR 91	10 164	GACAATAAACTGAAAAGCATGAGTCTTGTAACGGGAGGGCAGCGCCT TCCACAACTGAACAACTTTTTGGGGAGAGTAAATTAGGGAACGGAG AAAAACAATTACGATACTGTAAGCACTATTTAAAAAGCCACGCCACGCAC TTTCAGCATGCCATTGTGAATGAAGAAGAAGTATTCTGTGCTCTTAAA 20C CATCCCATTUTGACTGTG
			Olabb _{KM} o I	10,164	205 CARCEATTINATION
DreBB _{JK} 79 _{bc}	230	тсбтслтсятиблассьтвоатся стольтисстствоателст сабабаям титасая стойсталеся анализато стетессилатибоссоссятае способолаласся абагаса гисстатаятистя титагася талалибо соссоссос состобатита 209 асбассалабатетасалала то			ТСТСТСТГЛАААГГӨГГГГСГСТАТТGГАТААСТТСТГGАСGGTСТА АСАбGAГЛААЛТСАТТGГЛТАGTГАСАААААААGAA ТАААААТАСАААGСААGGCACTTITTAAACCTATIGCTGCTTГ САТГGААТGТААТGТААСТGССGGGTCATTGAAAGCGCTTAGTGGTGAC ТГТТАСТСАТТГГГААТGГАСТGТСТGGCCAAGACTATAACTT
DreBB _{KO} 87 _{df}	9,352	GTCACGTGAGGTCCATAAAGTTAGTTTTATGGTTTTAGGGGGGGTTGAA 94 AATGCGCTACATAATTCACATTCTTGAATGTAACTGACTG	OlaBB _{KM} 82	9,967	471 CATAAACAAGCCAATG
DreBB _{KO} 88	9,782	42 CCAACTITGATCCACGCAAAACATATGCAACTAGTTTCCTTT	$OlaBB_{KM}87_{de}$	9,057	85 ATGTACTATATICCATATAGGGTTATICGTTTGGAGGGGGGGGGG
		ATAATGCGTTTTGCATATTGATAGGGTAATCTGGGCGCTGTTCTCATC	OlaBB _{KM} 90 _{abc}	8.280	73 TGCATAATTCATGGTGGCGGGGATCA
DreBB _{KO} 90 _{abcd}	8,468	82 AATTATTCATTGGGAAGGGATCACTCGGAGGTCA	OlaBB-u92	637	17 AGAATTCAATTTTACTT
DreBB _{K0} 92	724	18 AGAATTTAGCGTTTACTT	CIGBERMOL	001	TTIGTCATGTAAATGCAAGCAGTTTGATGGACGAGCCTGCAGACTTG
		TTTGTCATGTAAATACGAATCGTTTGATGGACACCTGCAACGCCCAG AGTGCTACCGCAGGTCGCACACTATTGGCCGCAAAATTAGTCACATGA			ACAGGCCGCTTTAGGTCATCAGCTATTGGAGTTTATCGGGTCACGTGG TGTGTCAGGAAGGTGATATGAGGGTGGAAGGCAGTTTTACAGCTTTG
DreBB _{wo} 93	229	143 C	Olabb ^{MO} 83	233	144 AC
DIODDROOD	225	TCTATATATACCCTGTAGATCCGAATTTGTGTGAATATACAGTCGCAA	OlaBB _{KM} 99	6,922	22 CGCTGCACTGAATAGAGGCAGA
DreBB _{KO} 104 _{abce}	6,652	73 ATTCGTGTCTTGGGGAATATGTAGT	OlaBB _{KM} 117	8,349	26 TIGGTITITCAAAGCTGAAAATGTTIC
DreBB _{KO} 115	8,249	17 CACAACATTGAGAAACA	OlaBB _{MO} 159	743	16 CCTTCAGTTAGAAAAT
DreBB _{K0} 161 _{bc}	229	31 TTTGTCATGTAAATACGAATCGTTTGATGGA	OlaBB _{MO} 161 _{bc}	233	31 TITGTCATGTAAATGCAAGCAGTTTGATGGA
Tetraodon nigroviridis s	potted gre	en pufferfish Hox Bb	110 10		
TniBB70.	57 57	22 CTATAAAAGACAACAAATCATA			
TniBB _{JK} 72	1,093	сладтиаваасосатиалосостиалостеститовосссссос асобесобобагатестстве Асселавается и полного соссавается с 123 агостеатол и полного соссавается с составается с составается с с с с с с с с с с с с с с с с с с			
TniBB _{JK} 73	848	типесттесстоятся и типеститизи типестелитизит спасаетсовотитизов состатося и тиле и сососности садатадаала то так состати и типести сособят апосалатизовалитизовалитити стибаланитот 216 аспланияти ализана соститизитата			
TniBB _{JK} 74	532	29 CAATAACCCAGCAAAGAAATGCGCGTAAA			
ToiRB 70	252	CCTAACGACCATTATTICGTCATCATTIGTAACCATGGAGCATGA ATTACCTCTTGAAGTCATCAGTGAGGATTTACGACTGGTCAACAA AGGCACGTGATTCCCGAAGCCTTCCCATATTTGGCCCCATACCT GGCAAAGTACCATGAGGCTTCATTGCTTATATTCATGATTGGAA CCATAAATCGTCCAAGCACCACAGGATTATAGCGACAAAGATCTA 220 CAAAT			
JK' Sabc	202	200			

GAAAAAGACAGGAGTCCATGAGTACTGTAAAGCTATTGAAAGC CAGCACCTTCCAGCATGCCATTGTGGTAGAAGTAAAGTCATCTGT 114 GGTCTCAAAACGCTGTTTTAGTTGA

ТСГСТСТПТААСЛІДТІСААСТІДАССІСТТАПТІДГІДАСТІСІСІ АССІДТІХАСАЮДАГІЛААЛТІСАСТІДІАСЛІТАЛАЛДІ ТАЛААДБАЛАСІЛАЛАЛТІСАСТІДІАСЛІТІССТІ ТСАСТІДАЛТІДТАЛІТІССССІЛАСВІССАЛІТАСТІСТІСТІ ТАЛАПТІПИСТІСІСТІТІТІЛІСАСТІПТІДСІССАВАСССІЛТІСАТ 469 GAACGAGCCCATGITGTAGCTGTAGGAGAT

GTCACGTGAGGTCCATAAAGTTGCTTTTATGGTTTTGGGGAGTAG 85 ACAATGTACAATATAATTCACAACCTTGAATGAAAGTGAC

85 ACANGUACANTANAN TEALANCE TIRANGARANGAC TICCATATEGATAGGAGGAACTETAGCCGATTECATGCATA 46 TICATACCGGCGGGGATCA TITGTCATATATACCAGGGCGTTGATGGACGACCCCCCACCC TGACAGACCCCCCCGGGTCCTCCCCCCATTGGCGTGCACCGGGC ACGTGGTTGTGTCAGGAGGGGGCATATGAGGGGGGGGAAGGCAGTTT 145 TACAGCTTTGAC

22 ACCCTGTAGATCCGAATTIGTGT

31 TTTGTCATGTAAATACGAGGCGTTTGATGGA

20 TGCAGCGCTGGTCCCTCTGC

TniBB_{KM}81

TniBB_{KM}82

TniBB_{KM}87_{de}

TniBB_{KM}90_{bc}

TniBB_{MO}93

TniBB_{MO}104_b

TniBB_{KM}131

TniBB_{MO}161_{bc}

7,329

7,088

6,247

5,319

236

3,420

3,542

236

PFC	Coelacanth C	Frog C	Human C	Zebrafish Ca	Medaka C	Tetraodon C	Zebrafish Cb
1					OlaC _{CD} 1	TniC _{CD} 1	
2				DreCA _{CD} 2	OlaC _{CD} 2	TniC _{CD} 2	
3					OlaC _{CD} 3	TniC _{CD} 3	
4				DreCA _{CD} 4	OlaC _{CD} 4	CD	
5				DreCA _{CD} 5	OlaC _{CD} 5	TniC _{CD} 5	
6				CD-	OlaC _{CD} 6	TniCcp6	
7				DreCA _{cp} 7	ошесре	TniC _{cp} 7	
, 8	I meC 8 .	XtrC8.	HsaC 8	DreCA8	OlaC8 · · ·	TniC8	
0	LmcC_0	Auccood	HeaC 0	DiccarCDoabcde	OldCDOabcde	TheeDoabede	
10	LineC _{CD}		HsaC 10				
10	LineC _{CD} 10		HeaC 11				
11	$L_{\rm meC}$ 12		HsaC _{DE} 11				
12	LineC _{DE} 12		IISaC _{DE} 12		OleC 12	TriC 12	+
15					OlaC _{DE} 13	$TmC_{DE}13$	
14					OlaC _{DE} 14	TniC _{DE} 14	
15					OlaC _{DE} 15	TriC _{DE} 15	
16					OlaC _{DE} 16	TniC _{DE} 16	-
17					OlaC _{DE} 17	TniC _{DE} 17	_
18					OlaC _{DE} 18	TniC _{DE} 18	
19					OlaC _{DE} 19	TniC _{DE} 19	
20					OlaC _{DE} 20	TniC _{DE} 20	
21					OlaC _{DE} 21	TniC _{DE} 21	
22				DreCA _{DE} 22	OlaC _{DE} 22		
23			HsaC _{DE} 23				DreCB _{DE} 23
24	LmeC _{DE} 24		HsaC _{DE} 24				
25		XtrC _{DE} 25	HsaC _{DE} 25				
26	LmeC _E 26 _{abc}	XtrC _{DE} 26 _{abcde}	HsaC _{DE} 26 _{abcde}	DreCA _{DE} 26 _{bcde}	OlaC _{DE} 26 _{bcd}	$TniC_{DE}26_{bcd}$	DreCB _{DE} 26 _b
27					OlaC _{EF} 27	TniC _{EF} 27	
28				DreCA _{EF} 28	OlaC _{EF} 28	TniC _{EF} 28	
29				DreCA _{EF} 29	OlaC _{EF} 29	TniC _{EF} 29	
30				DreCA _{EF} 30	OlaC _{EF} 30	TniC _{EF} 30	
31				DreCA _{EF} 31		TniC _{EF} 31	
32			HsaC _{EF} 32				DreCB _{EJ} 32
33		XtrC _{EF} 33	HsaC _{EF} 33				
34		XtrC _{FF} 34	HsaC _{FF} 34				
35	LmeC _{EF} 35 _{abc}	XtrC _{EF} 35 _{ab}	HsaC _{EF} 35 _{ab}	DreCA _{EF} 35 _{abc}	OlaC _{EF} 35 _{ac}	TniC _{EF} 35 _{ac}	
36	LmeC _{FG} 36	XtrC _{FG} 36	HsaC _{FG} 36				
37					OlaC _{FG} 37	TniC _{FG} 37	
38	LmeC _{EG} 38 _{ab}	XtrC _{EG} 38 ₂	HsaC _{EG} 38 _{ab}	DreCA _{EG} 38 _{ab}	OlaC _{EG} 38 _{ab}	TniC _{EG} 38 _{ab}	
39	10 10	10 a	10 40	10 10	OlaC _{FC} 39	TniC _{EG} 39	
40	LmeC _{EC} 40 _{aba}	XtrCrc40aba	HsaC _{EC} 40	DreCA _{EC} 40 _{bad}	OlaCrc40had	TniC _{EC} 40had	DreCB _{EC} 40 _{aba}
41	- I'd - abc	- I'd - abc	in it it it	i i i i i i i i i i i i i i i i i i i	OlaC _{EC} 41	TniC _{EC} 41	10 auc
42					OlaC _{FG} 42	$TniC_{FG}42$	
43	1	1	HsaC _{r=} 43	DreCA43	Smc _{FG} 12	True _{FG} 12	1
44	1	1	OFG . 5	DreCA _{rc} 44	1	TniCrc44	1
45				DreCA _{re} 45		TniC _{ro} 45	1
47		1	HsaC47	2.00.4G 10	1	T more is	DreCB-47
48		XtrCrc48	HsaC _{FG} +7			1	DICCDEJT/
40		XtrC 40	Hear 40	+			+
49 50	I meC 50	XtrC 50	Hear 50	DreCA 50		TniC 50	1
51	LineC _{FG} JU _{ab}	$X_{FG} U_a$	Hear 51	DICCAFGJUab		T Inc _{FG} JU _{ab}	+
51	I moC 52	XuC _{FG} J1	Heac 52	DroCA = 52	Old C = 52	TpiC 52	+
52	LINEC _{FG} 32 _{abc}	Auc _{FG} J2 _{bc}	TISAC _{FG} JZ _{abc}	DICCA _{FG} 32 _c	$OlaC_{FG}SZ_{abc}$	$T_{\rm HC} = 52$	+
55			Head 54		OlaC _{GH} 33	T IIIC _{GH} 33	DroCD 54
54	I.m. C 55	V4=C 55	HsaC _{GH} 54				DIECB _{EJ} 34
	LineC _{GH} 55	Atrugh 33	HsaC _{GH} 55	Durch 71	01-0 55	T.:0.51	
56	1 0 77			DreCA _{GH} 56	OlaC _{GH} 56	1 mC _{GH} 56	
57	LmeC _{GH} 57		HsaC _{GH} 57			+	+
58	LmeC _{GH} 58		HsaC _{HJ} 58		01.0.52	TT : C . T .	
59					OlaC _{GH} 59	1 mC _{GH} 59	

60					OlaC _{GH} 60	TniC _{GH} 60	
61					OlaC _{GH} 61	TniC _{GH} 61	
62					OlaC _{GH} 62	TniC _{GH} 62	
63					OlaC _{GH} 63	TniC _{GH} 63	
64					OlaC _{GH} 64	TniC _{GH} 64	
65				DreCA _{HJ} 65	OlaC _{HJ} 65		
66					OlaC _{HJ} 66	TniC _{HJ} 66	
67 Lr	meC _{HJ} 67 _b	XtrC _{HJ} 67 _b	HsaC _{HJ} 67 _b	DreCA _{HJ} 67 _{abc}	OlaC _{HJ} 67 _{abc}	TniC _{HJ} 67 _{abc}	DreCB _{EJ} 67 _b
68					OlaC _{HJ} 68	TniC _{HJ} 68	
69					OlaC _{HJ} 69	TniC _{HJ} 69	
70					OlaC _{HJ} 70	TniC _{HJ} 70	
71					OlaC _{HJ} 71	TniC _{HJ} 71	
72					OlaC _{HJ} 72	TniC _{HJ} 72	
73					OlaC _{HJ} 73	TniC _{HJ} 73	
74			HsaC _{HJ} 74	DreCA _{HJ} 74			
75 Lr	meC _{HJ} 75		HsaC _{HJ} 75				
76			HsaC _{HJ} 76				DreCB _{EJ} 76
77 Lr	meC _{HJ} 77		HsaC _{HJ} 77				
78 Lr	meC _{HJ} 78	XtrC _{HJ} 78	HsaC _{HJ} 78				
79 Lr	meC _{HJ} 79		HsaC _{HJ} 79				
80 Lr	meC _{HJ} 80		HsaC _{HJ} 80				
81 Lr	meC _{HJ} 81		HsaC _{HJ} 81				
82					OlaC _{JK} 82	TniC _{JK} 82	
83				DreCA _{JK} 83	OlaC _{JK} 83	TniC _{JK} 83	
84					OlaC _{KL} 84	TniC _{KL} 84	
85					OlaC _{KL} 85	TniC _{KL} 85	
86					OlaC _{KL} 86	TniC _{KL} 86	
87 Lr	meC _{KL} 87 _{abcd}	XtrC _{KL} 87 _{abcd}	HsaC _{KL} 87 _{abcd}	DreCA _{KL} 87 _{bc}	OlaC _{KL} 87 _{ac}	TniC _{KL} 87 _{ac}	
88 Lr	meC _{KL} 88		HsaC _{KL} 88				
89 Lr	meC _{KL} 89		HsaC _{KL} 89				
90 Lr	meC _{KL} 90		HsaC _{KL} 90				
91 Lr	meC _{KL} 91		HsaC _{KL} 91				
92					OlaC _{KL} 92	TniC _{KL} 92	
93				DreCA _{KL} 93		TniC _{KL} 93	
94					OlaC _{KL} 94	TniC _{KL} 94	
95					OlaC _{KL} 95	TniC _{KL} 95	
96				DreCA _{KL} 96	OlaC _{KL} 96		
97					OlaC _{KL} 97	TniC _{KL} 97	
98				DreCA _{KL} 98		TniC _{KL} 98	
99		XtrC _{KL} 99 _{ab}	HsaC _{KL} 99 _{ab}	DreCA _{KL} 99 _b	OlaC _{KL} 99 _{ab}	TniC _{KL} 99 _{ab}	
100		XtrC _{KL} 100	HsaC _{KL} 100				
101		XtrC _{KL} 101	HsaC _{KL} 101				
102 Lr	meC _{KL} 102	XtrC _{KL} 102	HsaC _{KL} 102	DreCA _{KL} 102	OlaC _{KL} 102	TniC _{KL} 102	
103				DreCA _{LM} 103	OlaC _{LM} 103		
104				DreCA _{LM} 104	OlaC _{LM} 104		
105				DreCA _{LM} 105	OlaC _{LM} 105		

<i>Latimeria men</i> PFC	<i>adoensi</i> s coelaca Dist. To 3' gene	nth Hox C Length Sequence			
LmeC _{CD} 9	5,426	23 TICTTICCCTTICAAGCTCCATG			
LmeC _{CD} 10	3,444	22 ACTAGACAGTGACCTTGAACTG			
LmeCcp8cde	99	CACGTGATTCACTATGGACCAATGGTGCAGACCCTTAGGTTTA ACTATGTTTAATGTCAGATAGCAATAAAGTAGAAGCTCTTGGT 99 CAGGCCCGCGGAA			
LmeC _{DE} 11	6,857	14 GTAATTACTTAAAT			
I meC12	4 280	A2 AAACGTTACAAGGAACATATTTTCTTGTACTTTCACAGTCTGA			
LmeC _{DE} 24	2,544	12 AAATCTGAATCT			
LmeC _F 26 _{abc}	in 11	AAATCIGCAATIGATITTICATAATGITCCTGCGGGTITTIGAAA CCAATCATIGAACCCAGGAGCTTACCTAAGGAGACCACTC CTACGTATCTAAGTGCTCCAAATIGATATATGGCAATATCTAC TIGGATCACGTGTTCTAGGGAGACTTAGACGGGTAGCGCGTC 194 ATCTGCCTTCCCAAATTIT	ſ		
2 400					
		CITIGATCAACTICCAGCTICCTIGTITITITITITATCCCCCGAAA ATGTGGTAGAATGCCCGTGTGCACCACGGTCATTCCCACATCI GAACAACTIGACCCCCTGTGACGTCATTGGTGTCTGAATCATCA AGTCCATTTICAGTTGTGAATGGTTTGAAAGTCACGTGGGAGG CCAATGCGTTGATAATTATGTGCGAATTTITTCCTAAAAAA	Xenopus trop PFC 3 XtrC _{CD} 8 _d	<i>bicalis</i> western claw Dist to 3' gene L 47	eed frog Hox C ength Sequence 28 AATGTCAGATGGCAATAAACTAGAAGCT TITTTATGGTGGTCAGGAAATTGACATTGGTCAAATTCAAGTGCTCT
$LmeC_{EF}35_{abc}$	269	230 AGATGTCAGC	XtrC _{DE} 25	2,849	63 GACTCTCCAGCTGTCTC
LmeC _{FG} 36	8,999	29 TITGCATGTATCCTATTTGTAAAGAAAAA			
LmeC _{FG} 38 _{ab}	8,839	ATAACGTIGATTTAAATAITATCCAGGTGACCACAATAAGTCA AGGTCATAAAACAGTAATGTCAGGACAGTCCTGGTAAGCGCT GAGGTGGATTTTATGATCTGCAAATATAATGTGCTGCAGCAGCAG 163 AAAAGATECATTTAAAGGTGACTGTGGAGGAGGG	3 XtrCp=26abodo	257	AAAICIGCAATIBAATTICATAAIGTICIGCGGGTIGAAAACC AAAICGTTTIGAACCICICCAGATTAAGCTAAGGAACCCTCCT ACGCATCTAAGTGCTCCGGACTGATATATGGCAATATCTACTGGG GCATACCGTGTCCTCGGGACGGACAAGCAAGACGGACAGCCGGTCA TCCAGCCATCCCAAATTITTCCCCCCTCTCAGATGGCCGCCAAAA 255 CATCATTCATAGAGCCGAGAAGGAA
I meCro40	7 965	CAGCTGATCTGTGGTTTAGGTAGTTTCATGTTGTGGGATTGGC 71 TTTTAACTCGGCAACAAGAAACTGCCT			CATTCTGCTCTTACCTAATTTTGTTTGGCCCAAAGAATGCTACTGT
LmeC _{FG} 50 _{ab}	750	18 TITATGAACAATCAAATG	XtrC _{EF} 33	9,061	59 ACTITIGTATCCTC
ab			XtrC _{EF} 34	8,882	21 GIGCACAATIATATAAGITTA
$\rm LmeC_{FG}52_{abc}$	172	ССССАТГСАТСССС-ССТСТАТТТГГСАСТАААТАТАСССССГС АСТАСАТССАСАТССАСТСАТАТТТГСАСТААСААТАТАТА ТТАССТСССССТСАТТСТАТСАССАСАТАААААСТААА ТТАССТССССТСАТТСТТАСАСТСААА (СТГССТСАТССАТАСАТАТСТТАТСААТСТААА СПТСТССАТССТИСАТАТСТТАТСААТСТААА СПТСТССАТССТИТИТСТСАТСААТСААСАА	i VitrC 35	267	CTITIGTICAACITTAAGGTCCTTGGGTCTATACCTCACAAAGTCAG ATAGATGGCGCTCTTACTCCACGTTCATTTCCTCCTCTGACAAC TTGACCCCTGTGACGTCACCTGCGTCGAATACACCAAGGCCATT TCAATCCTCATTGCCTTGGGGAGTCACGTGGTGGGGCCCATTGCGTG QG GATAATAGTCTCTCA
		AAACCTCAGTTCTGGCTAGACGTCTGGCTTTAATTGTTTTATGG	XtrCro36	9,236	30 TTTGCATGTATTTTCCTTTGTGGAGAAAAA
LmeC _{GH} 55	3.457	138 AATGTTT	; morgoo	0,200	ATAACGTTGATTTAAATATTATCCAGGTGACCACAATAAGTCAAG
		GCCTGTCTTTGGCTGCTGAATTGATTAATAGAAATCGCGTGTGA AAGCCTTACCACCGGGATTTTGGAGAATTTGCCTGTGGTGTTA/	\ XtrC _{FG} 38 _a	8,986	GTCATAAAACAGTAATGTCAGGACAGTCTTGGTAAGCGCTGGAG GTGGATTTTATGATCTGCAAATATAATGTGCCGCAGCAGTAAAAG 149 ATGCATTTAAAGGTG
LmeC _{GH} 57	286	129 AGGAAGAAGCAGTGAGGAAAACTGAGATAGAGCTCTACCTA	VtrC 40	7 724	CAGCTGATCTGTGGTTTAGGTAGTTTCATGTTGTGGGATTGCTTTT 74 TCTTAACCCCCCCAACAAGAAACTGCCT
		TCA A CITYOCOTITITA TCCATCATCATA A A ATCA A ATCITITA CCA	XIIC _{FG} 40 _{abc}	1,734	27 ATTEGETCATTA A A A CA A A A A GGAGGTA A A A GCCGT
LmeC _{HJ} 58	16,211	86 CCTTCACTTACTTTTCTAGTGAACACAATGGAGAGACTCACA	XtrCro49	4,300	29 GGGGAAAGAAGCATGGATCAGCTGCTGAA
$LmeC_{HJ}67_{b}$	10,485	27 AATTTACAGCTGAGTAATAAAAGTTTA	XtrCro50-	826	12 TITATGAACAAT
LmeC _{HJ} 75	5,922	17 AGATATTGTATGTCATT	XtrC _{E0} 51	294	26 ATGGGTGCACAGGCAGAGCCCAGATG
LmeC _{HJ} 77	1,578	AATAAACTGGTCACTTICTICTTTTATGCCTTTTATAGCTTTATT 87 GTCACCATTAACTCGCTTACATTCTTTCACAGGAAAAAGATC	XtrCro52	154	TITITIGGTAAATACAATCACGTGGGACCCGAGAGCCAATGACA AGCGTGAAAGGCTGAAAAAAATAATTACCTGCCCTGATTGTTCTAT GAGCAGATAAAAAGTACACATACAGTTCATACAATAATCTTATG 141 AATGTAA
		GGGAATCAACACAAGCAAAACCATTTTTTCCTTTCTTGTCATCT AGCTTGCTATTGGTCCAAATCAAGTCATCTGACTTTGTCATTTT GTCTGTCCTGGAGTGGAG	+pg+=bc		GTTTGTCTCACTCATGTGTGTGTCTTTGAATGGATGTGAACAAAAC AAGACCATAGGACTGGCTAGACGTCTGGCTTTAATTGTTTTATGG TTTAAATAAGGTGCATACTCTGCTCTTTGAAACGGAATTATTGGA
LmeC _{HJ} 78	193	170 AGTACAAACCGGAGCTCAGAAATAAATATTAAAGAAATC TCCCACAAATTITTATTTTTTTTTTTTTTTTTTAAATAATTAAT	XtrC _{GH} 55	3,420	142 ATGTTT
LmeC _{HJ} 79	2,483	52 AAGTGGAC	XtrC _{HJ} 67 _b	9,009	27 AATTTACAGCTGGGCAATAAAAGTTTA
LmeC _{HJ} 80	2,026	IGIGIGAATCATIGIAGTIGIAATIGIGACATCIGIATATATX TITAIGITIGGTATIGIACTGATAAACAGCIAAAAGIGACTGAI TICAIGAAGTIGGAAAATIGIGITITGCITIJAAATGCACAGC 168 AACCATATIGITAAGATAAACTGATAT	XtrC _{HJ} 78	194	GGGAATCAACACAAAGCAAAACCAATTTTTCCCTTTCTTGACATCT CCCCTCTATTGGCTCCAAGTGGGTCACTGACTTTGTCATTTTGT CTGTCCTGGATTGGACCGCTCCCTATACAATTCAAGAAATCAGTCAG
		ACATATCAGGCACGTTTTGCAGACCTCCATCAATAACCTCCTG GGGTCATCAAGCCAAATTTATGACTGGCCAACAAATCACGT ATTCTATTTAAACATCCCATATTTGGGCAGCGACGTAGAATA AAGAAAAGAA	3 ^A XtrC _{KL} 87 _{abod}	36,678	AGGTTATTTATGTGAATGGCCCTAAGGAAAGGCCCTGAATGGCTC TCACGGAGCACGTGATGTCATTAAAGTAAGTTTATGGTTTGGGG GAGCTGACAAAGCTACAATGTATTTACATCATATATAATCTTAAC TGTCCACACATGCCAGCTGCCGGGTCTCTTTAATGCTGGGACAGTG 205 GGACAAGGCACTTAGTGTGGATTAC
LmeC _{HJ} 81	238	229 AAAGGTGTAAATTTT AGGTTAATTATGAGGATGGCCCTTAGCAAAGGCCCTGAATGGC	2		ACATTATAACTAGTTATTGAACTAGCTCTGAGATCTAAAGGCCAT TIGTGCTGAGACAGATTTCAATGGAGTTIGCCCATCAATAATCTTT GGCAGTGACCTATIGGTGGAAGTCAAGCAACCGAGGTGAAATTC
		TCAAAAGGAACACGTGATGTCATTAAAGTTAGTTTTATGGTTT GGGGAGCTGACAAACCCACAATATATTTACATCATATATAAACC	XtrC _{KL} 99 _{ab}	4,718	163 AGGTCACGCTGTCTAACCGGTATTAAAA
LmeC _{KI} 87 _{abod}	21,028	TTAACTGTCCACCATCGCAGCTGCTAGGGCTTTTTAATGCTGGC 205 ACTGTGGGACAAGACATTTAGTGCGGATTAC	, XtrC _{KL} 100	2,806	TGALAGGACLAACTGACATAGTGGGGTAACUCATAGTTATAGGA 56 TTGTTTGGGAGA
LmeC _{KL} 88	17,002	36 CAAAAGCATTGGAGCTGCCTTCTAAGTAGTGATTGG			
LmeC _{KL} 89	16,659	31 GGATTTGCATGTCTATTGGGCTTGTTGGATT			GCAGCCACCGCAACGAGCAGGTCCCAACCAGTGCAAAGACTCT AAACCATTCCTCCTGCTTGATTTATGGCTTTTTACTGCCCTATAAA
LmeC _{KL} 90	13,346	20 TTCTGGGAAGATATTCAAAC			AGCTGTTACAAGGAACCTAAGCCTGCAACACCGCTGGCACATTT
LmeC _{KL} 91	10,496	18 TAGGGAGGAGTAATATIT			TATTGTTATCAAATAAAAATATTGCATTGCCCCTGCAAGCTATGAT
		GGTTCCTTATCCGGGGACTAGCTCCTTTTGTCTCATTGGATAAC	XtrC _{KL} 101	1,805	25/ TCCGTGCTATAATTGTTATCAAGCAGAACAAG GGTTCCTTATCCGGGGACCTGAGCGCACGTTGTGATTGGCTGGAG GACTCACATTGGTGAAAGTTACCGCGGTCGCCACGTACTAC
1		AGGAGGGCTTTATGGAGCAGAAAACGACAAAGCGAGAAAA	X1-0 100	. –	GAGGGCTTTATGGAGCAGAAAAACGACAAAGCGAGAAAAATTA
LmeC _{KL} 102	157	151 ATTATTTTCCACTCCAGAAATTA	XtrC _{KL} 102	156	151 TTTTCCACTCCAGAAATTA

Homo sapiens human Ho	x C				
PFC Dist to 3	gene L	ength Sequence			
HsaC _{CD} 9	5,643	23 HETHECOCAGATCCCTCCATG			
HsaC _{CD} 10	3,635	22 ACTAGACAGTGACCTTGAACTG			
		GAAGTTAGAGTGCGGGATGGGATGGTGGGGGGGGGGGGG	т		
		TGTCCCCACCCCTCCCCTGGCGGCCGTGCCCACGTGAGTGGG	iG		
	170	CGGCCAATGGGTGACTGGTGCAGATTTAACTATGTTTAATGTC/ 172 GATAGCAATAAAGTAGAAGCTGCCGGTCGGGCCCCCGCGGAA	4		
HsaC 11	0.094	12 GTAATTCTTAAAT			
I ISAO _{DE} I I	9,904	13 0111101111			
HsaC _{DE} 12	6,843	42 AAACGTCATAAAGAAAAGTTCATTTACAGCTTAAATGTCTGA			
HsaC _{DE} 23	6,264	22 AGAAAGAAGGAGGAGGAGAAAATAA			
HsaC _{DF} 24	4,786	17 AAATCTCTGGCGAATCT			
		TTTTATGGTGGCCCAGGAATAAACTTTGGTGGTCAAATTCAAG	Г		
HsaC _{DE} 25*	2,505	65 GCTCAGTCCAGCAGCTGTCTC			
		AAATCTGCAATTGATTTTCATAATGTTTCTGCGGTGTTTGCAAA	с		
		CAATCGCCTGAACGTCCCCGATCTTACCTAAGAGAGAACCCC	r		
		CCTACGTCTGCGAAGTGCTCCGAACTGATATATGACAATATCT. CTTTGCATCACGTGCTCAGAGAGAGAGAGACTAAGACGGATA	A		
		CGCGTCATCTCGCCTTCCCAAATTTTCCCCCCTCGCTAGACCGC	3		
HsaC _{DE} 26 _{abcde} *	259	257 GTCCAAAACCTCCATCCGGAGCCGGCAGGAGAGGAG			
HsaC _{EF} 32	9,811	20 GGAAAATTATTTTATTTTAT			
110 00	0.050	CATTCTGTTCAATATTATGATTTTATTTGACCCTTTTATTAACCC	.C		
HsaC _{EF} 33	8,852				
HSaC _{EF} 34	6,692	17 GIGCACGIGGGAGIIIA			
		CTTTGTTCGCGGGGAAGGGCTCCGGTGCCCCTACCCCGAGGCA	٨G		
		CTGCTAGATGGCGCTGTTACTCCACTCTGCGCGCTCCGCCTGCC	- -		
		GACAACTTGACCCCGCTGACGTCACGGCCGTCTGAATCATCAA GGCCATTTTCAAATCCCATTGGTCTAGCCGTCACATCCTGAGA	۱ A		
HsaC _{EF} 35 _{ab} *	330	204 CCGAATGCGCGGGATAATTACGGAGCTGAT	-		
HsaC _{FG} 36	9.975	30 TTTGCATGTAGCTTCCTTAATGGAGAAAAA			
	2,510				
		ATAACGTIGATITAAATATTATCCAGGTGACCACAATAAGTCA	A		
		GGTCATAAAACAGTAATGTCAGGACGGTCTTGGTGCGCGCGGA AGGTGGATTTTATGATCTGCAAAATATAATGTCGTGCTCCACTA	3 A		
HsaC _{FG} 38 _{ab} *	9,764	161 AAGATGCATTTAAAGGTGACTGGAGGAGGG	•		
		CAGCTGATCTGTGGCTTAGGTAGTTTCATGTTGTTGGGATTGAG	Т		
HsaC _{FG} 40 _{ac}	8,443	72 TTTGAACTCGGCAACAAGAAACTGCCT			
HsaC _{FG} 43	7,032	30 TGTTTTGACTCCCAAGGAAGCTGGAGGAGA			
HsaC _{FG} 47	6,650	18 TCTCTGTGCCCCCATTTC			
			c		
		GCTGGAAAAAAATCGGGAAAAACGGCGGAATTTGCACTTC	A		
HsaC _{FG} 48	5,053	129 TTCATTGGGTTATCTGCAACTGAGAGGGGGCTGGTTAAGGCGT			
HsaC _{FG} 49	2,076	29 GGGGAAGACAGTGGCGCCAAGGAGCTGAA			
HsaC _{FG} 50 _{ab} *	1,183	18 TTTATGAACAATCAAATG			
HsaC _{FG} 51	347	34 ATGGGTGGACATGGGCACAGGGGCTTCTCAGATG			
		GCGCATTGATCCGCGCCGTATTTTTGGGTAAATACGATCACGT	3		
		GGGGCCGGGGAGCCAATGAGCTGTGGGGGAAAAGGCTGGAAAA ATAATTACCTGACTTGATTGTTCTGTGAGCAGATAAAAAGTAC	A		
HsaC _{FG} 52 _{abc} *	175	164 TATACAGTTCATACAATAATCTTATGTATGTAAA	-		
HsaC _{GH} 54	5,999	42 TGITATGGTAGAACAGCCCTGTGTTAATATATTGAAGTCACT			
		GTTTGTCTCCCTGTTCTGGGTTCTCAATGGGGCCGAACAAAAC/ GCAGCGCGGAGCTGGCTAGACGTCTGGGCTTAATTGTTTTATG	A G		
		TTTAAATAAGGTGGACACTTTCCTTTGAAATCGGATTATAGGA/	A		
HsaC _{GH} 55*	3,848	137 TGTTT			
		GCCTGTCTTCATGTCGTGGATTGATGAACGCGAATCGCGTGTA	Δ		
		GCGCCGCCACCGCCGGGAGTCTGAGGAATCGCCTGGGCTGT	TA.		
HsaC _{GH} 57	400	126 GAGGAAAGAGCTAAGTGAGAGAGCGCGAGCTCTACCTA			
		TCA A CTUTCCTUTTATCCT A CCA CATA A ATTCA CA A CTUTA CC			
HsaC58	17 102	83 CTGTCATTTGCTTTTATAGAGAATAGAATGACACTCACA			
HsaC67.*	11 757	27 AATTTACAGCTGAGTAATAAAAGTTTA			
OHJO'D	11,737	TICTCTAAGGTCCCCCAAATACCCAGATCTGGTTACTGGATGA	A		
HsaC _{HJ} 74	7,266	54 CTGCGTTTTA			
HsaC _{HJ} 75	6,257	17 AGATATAGCATGTCATT			
HsaC _{HJ} 76	6,080	27 TATTAAATTTAAAAGAGTATCATTGAA			
		AATAAACGAGTTTTTTCTCAGCATAGTCCCGTTTATGGCTTTAT	T		
HsaC77	1 717	GCTACCCATTGATTACTCCGCTTTGTTACACAGAAGGAAAAGA 90 C	.1		
I I GUOHJI I	1,111	50 -			
		GGGAATCAACAGAAGCAGAAGCGATTTTTTTCCCCCTTCCTGA	.c		
		ATCTGGCTTGCGATTGGCTGGGAGGGGGTCAGCTGACTTTGTC/	4		
HsaC78*	200	1111GIUIGICUIGGATIGGAGCCGTCCCTATAACCATCTAGTR 173 CGAGTACAAACTGGAGACAGAAATAAATATTAAAGAAATC	2		
	200	TGGCACAATTGATGTGTTTTGATTCCCTAAAACAAAATTAGGG	A		
HsaC _{HJ} 79	3,075	57 GTCAAACGTGGAC			
		IGIGTGAAGATTTTTAGCTGTATTTGTGGTCTCTGTATTTATATT ATGTTTAGCACCGTCAGTGTTCCTATCCAATTTCAAAAAAGGA	I A		
		AAAAAAGAGGGAAAATTACAAAAAGAGAGAAAAAAAAGTGAA	AT		
		GACGTTTGTTTAGCCAGTAGGAGAAAATAAATAAATAAAT	A HsaC _{KL} 91	8,173	18 TAGGGAACAAATATATTT
HsaC _H 80	2,561	247 TCTCGAATATTTAATAAAACTGATATT	-		ACATTATAACTAGTTATTGAACTCGCTGGAAGATCTAAACCCCA
	2,001				TTTGCGAAGAGACAAATTTCAATGGAGTTTCCCCATCAATAACC
		ACATATCGAGATGCTTTTCGCCGGCTTCCATCACTAACCTCCC	3 U0 00 *		CCATGGCAGTGAACTATTGGAACAAGTCAAACACCCGAGGTGA
		GAGGTCATCAAGCCAAATTTATGAGTGGCCGCTCGAGTCACGT	.G HSaU _{KL} 99 _{ab} *	4,717	164 AATOCAGGTCACCTTTCCAGGTGAGGCAGCCGCATCCAGCTACA TCACAGCTCACCTTTCCAGGTGAGGCAGCCGCATCCAGCTACA
		ACTUTATITAAGGUTUUTTATTTGGGAAGAGUGUATAGGATA AGAAAGAGATATCTCCACCTATAAATTGTCCACTTTGGAGAAG	A HsaC _{kl} 100	2.751	58 GGCCTAGAAGGGAGA
		AAAAACCCCTCAACTTCAAAGAGTCACAAATCACCCTTAATCA	A	-,	
HsaC _{HJ} 81	255	238 AAAAGGGTGCAGAAATTTT			GCAGCCAGCGGCCGCCAGCCCTGCGCCGCCGACACAAAG
		ACCITATITATICA ATACCITCA ACCOA ACCOCTO ACTOC	T		AGTGCGGGCGATTCCGCGAGACTGATTTATGACGTTTTACAGCC
		CTTGGGGGACCACGTGATATCATTAAACCAAGCCCGTGAGTGG	A		GGCAGATTTAGTCTAATAAATAAAACATAAACAGTTAACTTTAT
		GGGAGAGCTGACAAACCCACAATATATTTACATCATATATAAA	r		GTGTCACTTTTATTGTTATCAAGTAAAATATAGCTGAGCCCTGGC
HsaC., 87 *	16 174	CITAACIGIUUAGCCACGCAGCTGCTGGTGAGGTTAATGCTA 206 GACAGAGGGCCTGGCAGTTAGAGGGGATTAC	J HsaC _{KL} 101	1,720	262 AAGCTATGATTTTAAACTATAATTGTTATCAAGTACA
HsaC _{in} 88	13.050	33 CAAAAGTGGAGATTTTTTGAAAGTTCTGATTGG			GGTTCCTTATCCGGGGACTGGGTTGCTCCGTGTGATTGGCCGG∆
HsaC 80	10,000	20 GGATTTCAGTGTTTGAGTTTACATGGATT			GGAGTCACATGGTGAAAGTAACTTTACAGGGTCGCTAGCTA
HaaC 00	12,787		HaaC 102*	454	GGAGGGCTTTATGGAGCAGAAAAACGACAAAGCGAGAAAAAT
1340KL30	10,282	11	1340KL 102	101	101

<i>Danio reri</i> o zebra PFC	afish Hox Ca Dist to 3' gene	Length	Sequence			
			TACCCTTGACCATGACTATGCAGTCGCTTTGACCTTGACATCAC			
			AGAGTCTTGTGAATAATAAACAGAGGGGGCTGGACACCACTGCC GTGGTTTGTTTTCAGGCAAACAAGGTGTTATTTCCCTGTCTAGA			
DreCA _{CD} 2	4,973	167	CGGCGAGAGTTAATGACATACCATAAATGCATAAAA			
DreCA _{CD} 4	3,046	23	AAAATATICIAAGCICGAAAAAT CTITGTTTACGCTATGGCCCTGTCTGGACGGAAAAGGATTCCAA			
DreCA5	2 4 2 2	03	GACAGCAATCTTACAGCGGCGCAGACAGTGCACTAGACACTG			
Diconco	2,422	. 55				
DreCA _{CD} 7	1,302	43	AATCCAAATTTAAAATTATAAAATATATTTTACATAATATATTT			
DreCA _{CD} 8 _{abcde}	775	775	CCTCTGCCAGCTTGTAAAATTCAAATAAAAGAATTGCGAGATG TGTAACAATCTACCATGAGTTGACTGCGAGTATTTATAGGATG TATCGTTAAAGTGTTCACTGTGAGGTGTACTAGAGCATATTAT CTAAAATATAGGCTAGCGCTCTTAAACATTTCTTATGGAATATCA TCATCTTTACGGAGCCAATGGTTCAACCGCGGCGACCACTA CAGTAAATATGAGTGGAGTCACCACTGGGGACTCAG			
			GTIAGATATTIGICTICCTIAGGCCTTITIAATTATTIAACTITTA TITGITITICIGIAGAACAAGAGATICTIGCTITICCGCCGTICG GACTITIAIGGCGCCTGCAGTGAGAATTITAGTGGTCAAATICA AGTGCCTGGTCGGCCACTGTCGCTICTITIGTACTIGGTGA			
DreCA _{DE} 22	1,975	206	AGGCATATTGCACACCAACCTTTTGT			
			CTCCTACGCATCCATGTGTTCCAAATTGATATATGACAATATCT			
			ACTITICGATCACGIGITIGCGGGGCGACTTAGACGGATTIGCGCGF CATCTCGCCTTCCCAAATTTTCTCCTTCTGCAGCTCGAATCCAA			
DreCA _{DE} 26 _{bcde}	167	165	AACATCATATCTGTAGTACGGACTACAGGAGAA			
DreCA _{EF} 28	5,968	286	ТПТСАССАПТАGААСТGГGAСTIGГACAATCTGTAAAAATGT ATTCCTIGFACAGAGATTATGCATTGTGCATCGTGAATGTAAT TATAATGTATTTTGAGTATCCTCAACTTATCCCTGCGGCTATAT TCTTTACATUGCCTIGGACCTCGTGGACTTGTGTGCATT CTTTAAATTATTGCTGTACGCCCAAATGCGTCGCTTTTTTT TCTTAAGGGAGGTCGGCGCGATTG CTTTAGTACCTCTCTAAATGGATCGCCAACTGCTCTAGTCAGG CAGTGCAATAAGGTAGGCCCTAATTGCCTTTTTTTGTGACTA			
DreCA_29	5 234	145	ATTGCACCGTCTGTTCTAGGGGAATGGTGTTCACTTCCGCAGTA			
DICONEF20	3,234	· 143				
D. 01 00			ТАТААТТААААGTTGICTITGAACTICAATAATGICAAGGCCT САССТТТАССТАТГGCATAAGGCAATCAAGGCCCCT ТГБГСАGGAAGAACGTGGTGAACAGACAGATCCAATCAGCCA АGTGGGAAGAACCAAGGAATGICTAAGAACTAACACTITGA ССТСГСССАТТАААСТАСАGCAGGTAACTITTCCAGTITTAGCA			
DreCA _{EF} 30	4,757	253	CAAGGCTGGAAGGCTTGTCTTTTTGTCACACCCACCAACCTTGG			
DreCA _{EF} 31	4,091	71	CCCTGGCTCAGTGACGTAGTTAATTTG			
DreCA _{EF} 35 _{abc}	297	223	СТПОТІСТОСТОТІВОСТІССТІОТІСТСАЛІАСАСОВСТАВАТ ОБОССАЛІГОСІСТСАТАЛАЛІТСАЛЕААСТІВ АССССАЛІВСАГІСАДАСЯГІСТОБОСАТІСАЛАЛАСТІ САЛААССТІАЛІВОГІОДАЛАГСАСЛІВАСАЛАСОССІТІВА АПССАЛАЛІТАЛІВІТОСТОВАЛАГСАСЛІВАСАЛАСОССІТІВА АПСАЛАЛІТАЛІВІТОСТОВАЛАГІЛІГОВОСССССССАЛАЛАВІВ ТСАБС			
			ATAACGTIGATITAAATATTATCCAGGTGACCACAGTAAGTCA			
			AGGTCATAAAATTGTAATGTCATGACGGTCCTGGAAAGCGCTG GGGGTGGATTTTATGATCTGCAAATATAATGTGCTGCTGCAGTA			
DreCA _{FG} 38 _{ab}	8,336	160	AAGATGCATTAAAAGGTGAGTGGAGGAGGGG			
DreCA _{FG} 40 _{bcd}	7,264	157	GTGGTTTAGGTAGTITCATGTTGTTGGGATTGGCTTCCTGGCTCG ACAACAAGAAACTGCCTTGATTACGTCAGTTCGTCTTCATCAA GGGCGACAATGCCCTTAAATTACACCCCTGTGCAATGAAGTTT CCCCAAATGGCATTGTAATGAACTG			
DreCA _{FG} 43	5,670	20	TGTTTTGCGACGGGAGGAGA			
DreCA _{FG} 44	824	64	TTATTAACGACACGTTTATGAACAATCAAATGGTCCTCGTAAA AATTTATTGAAGGACATAAAA			
DreCA _{FG} 45	409	29	GACAGAGATTGATTACACCAACAAATAGT			
DreCA _{FG} 50 _{ab}	810	18	TTTATGAACAATCAAATG			
$\rm DreCA_{FG}52_{c}$	100	82	AAATAATTACCTGTCTTGATTGTTCTACGGTCAGATAAAAAAGT ACACATACACTCCATATAATAATCGGATGCATGTAAA			
			AAATICAAAGCCTGATCGACCACGTTCCCCCCTAGAACTAAA ATGCCAGTTTACAGCCCGTTGGGGCTTGGTGTTGTTTGTCTC GATGCAGACGAACAAAGCCAACCTGGCTAACTGGCTAGACGT			
DreCA _{GH} 56	2,723	206	; CTGGGCTAAATTACTTTATGGTTTAATGGACG	DreCA _{KL} 98	2,893	32 ATTAAATATCATATAGGAGTAAAATGTCATTC CATCAATAACTCCTTGGCAGTGAAACTATTGGAACGAGTCGAAC
			TAAACACTTATGATTATCGAGCATTTTGTCGTCTTCGGAAGACA	DreCA _{KL} 99 _b	2,503	GUGAGGGGTGAAATGCGGGTCAGGCTGTCTAACTAATATTAAA 87 A
			CGAATAGCTCGAAGCCAATCTTAACTATTTTAAAAGATTGTATC ACGGCACTACCTAAAACAAAGTTTTGCTAGAAAGAATGAAT			GGTTCCTTATCCGGGAACTACATCGCCCCATGCCATTGGGCCAT
			ATTTATTCTACGTGCTGCTTTGTTAAAAATAATTATACATTTTCC CCCAACAACTTAAACTGCCTATAGAAAATGCACATTTATGTGT			CGAATCACGTGGTAAAAGTAACTTTACAGGGTTGCTCGCTAGT
DreCA _{HJ} 65	11,180	391	AGTTGAACAAACACGCTGATTACTACCCTACCTTAC	DreCA _{KL} 102	151	151 TTATTTTCCACTCCAGAAAAAACGACAAAGCTAGAAAAAA
			ACATTCCTAGTTGTTTAGAGGGGGAATTTACAGCTAAGTAATAA			
DreCAu 67-	6 174	130	AAGTTTACGACTGAATACACGCGGTCATTGGTTGCGTCAGACC ACGTGGTGTTCACTCTATGAACATGAACTTTGTGCTGTTGTCT			TTATTTATAAAAATATAAATATATATTTTGTTTTCGTAGGTATCTTGTG
	0,114	.50	TICTCTCCAGTCACATCAACATACCAACTGCAGACTGAGTGTG			CGTAAAGGGGGTTCCTTTAAGTCCACAGTTATATAAAATGCAT GTTATATAGCATGGATTATTGCGAATACCTATGGATTATTTTTTA
DIECA _{HJ} /4	2,864	53	GIGIGITITA			CGCGACACAGGGTTTAATTTATCTAAAACTGAATCAATATGAT GTTTGTTTTGT
			TGACGCTCTTGTCTAACGGTCTCGCCCTTTTAGCCAAGACCCT TGCATGATTTCCATACCGAGAAGTTATCGGACACGTTCCCTGT CTATCAATAACCTCCTGGGGATCAAGCCAATTTATGACTGGCC AGGAGCTGCACCGGATCTATTTAAACATTCCATATTTGGGCGA	DreCA _{LM} 103	12,836	310 AGCAGGTTATGGACATTTTATTCAAATGTTATTC GTTGTGTTTAGGCTATTAACAGCAGATTGTTGTGAGATGCAATA AAACCAGTTAGTGTATTTGTGCTAATTATTGGTCAATAAAA
DreCA _{IK} 83	482	226	TACACGTCGTACCAAGAAAAAAAGAAAATGATTTCCTCCACCT ; ATAAATCC	DreCA _{LM} 104	12,328	132 CGTAAGTGTCTATTAGTTTAACCTAGACTTGGGTGACTTTTATT
	102	0	TCATTAAAGTGGGTTTTATGGCCTGCAAGACCTGACAAACCCTC			TTATGTGACTGAACAGCAGAGAGAGAAATGAATGTGCACGCCTAA
DreCA _{KL} 87 _{bc}	8,555	91	AATATATTIACATCATATATAATGITAACIGICCGIAATCGCAG CTG			ATCATAGCATCCCGGCAGTCTCTTTCGAGACGCTGTCGCCTCCA TGTCGCGAGGCTGAAAAGATACTTTATTCAACGTTGCCGCCCCA
DreCA _{KL} 93	4,817	' 19	AAAGAATTTATTTATTTTT			AGAAAAGTCGAGTTCAATTGAGGACACATTTTCTGTCCCATT
DreCA _{KL} 96	3,001	50	TATATTICAGAATAGCTTAGGTCACTTAAACTACAATTCACTCG ATTTTT	DreCA _{LM} 105	10,733	AGTITICATTICAGCCGGGTCGGCCGACCTTCACACCCCTTGAC 402 CCCACTGGCTCTCCAACGTGTACCTTCTGTGTGCA

PFC	Dist to 3' gene	e Length	Sequence			CCTIGTTTTCTCAGCTCCCTCATTATGGCTTTAGTACCGCTGGAAG
			TCCATCAACTEECTCGACCACGTCAACAAGACCCCTGCTCCCAGT			ACAGTCTAGAATCCAAAGTCACTTTCATTCAGGCCCCTGAATGAG TGTCTCCCTTGGAATGCATCACTCACAAAGACTTTACAGCGCTGG
			TTAGAGAAAATGCTCTAAAAAACTGTGAAAATGTTCAAATCGCTTC			AAACAGGCTGTAAGAGCAGCACAGCTTTCACCCTAAAAACCATATG
01-0 4	0.5		ACAATTTTGTTTTATAAGAATGTACATATATAAAATATATAATATTT	01-0 44	4.050	CACATAAAGTCATTTATTTCACTTTGTTGTGGCGCACAGGAACTGA
OlaCCDI	6,53	32 172	AAACOAIAICIOIAITICAGACAAGIIAITGCOIG	OlaC _{FG} 41	4,650	TATTAACGGCACGTTTTTGAATAATCAAATGATCCTCGTTAAAATT
			TACCCTTGACCATGACTATGCCGTCACTTTGACCTTGACATCACAG			TATTGTTGGGTATAAAAAACATGAATGGAGAGCTGTCGAATATAG
			TAGATTGTGAATAATAAATAGGGGGCTGGACATCAAGGCTTTCGG GTTGTTTGTAGGCAAACAAGGTGTTTCCTCCTGTCTAGACAGCCG	OlaC _{FG} 42	824	112 TGCGCTGTAGTGGAGCTGCTT
OlaC _{CD} 2	4,58	53 167	GGCTTAATGGCATGCCATAAATTAATAAAA			GCGCATIGATCCACIGTACAATTETGIGGGGGTAAATATAATCAC
						GTGTCAGCGAGGCAGCCAATAGGAGCCCGGGAAGCTCTGAGAAA
			GGCTGATAACCTCTGGTGGTGACCAGAGGAAAATATCAGGAAGT GCTGCAACTGTTGCTAATTTATGGATCTTTTGGCTCCCCCAATTTG	0100 52	100	TAATTACCTGCCTTGATTGTTCTATGGCCAGATAAAAAAGTACAC
			ATTTATTTAATGTAAGCAAATTTGGCTTTTATTGCTGGAAAACAT	OlaC 52	2 202	12 TIGETTCATTIGT
0100 3	2.20		TTTAAAATATTTTTTTTACATTTTATTTATGTTTATGCAATTCCTTAC	UIAC _{GH} 53	3,283	13 Horneamor
OlaC _{CD} 5	3,30	208				AAATTGCCTTTTTGTGGTGGCAAACAATACAAGCAGGATGCCGTA
OlaCCD4	2,12	20 22	CTTIGTTTAGACTATIGCCTIGTCTGGACGGGGCACAGGATTCCAG			ATTTCAAAGCCCAATCCCGTGCATTTCCGCTCATCCCGGACAAAA
0.0 -			ACGGCTGATTTCAATACTGCGCAGACGGTGGACTAGACAGTGACC			TGCAGACGAACAAAGCAAACTCGACTAACTGGCTAGACGTCTGG
OlaC _{CD} 5	2,16	59 95	TIGA	OlaC _{GH} 56	2,467	209 GCTAAATTACTITATGGTTTTAATGGACG
			GAGAGAGCTGCGGTGTCTTTGCTCAGGATACTTGGTCACAAGTGA			OT A CATCA CONTENTION CONTENTION ACCORA A CONTENT
			CAGATACGGCTCTCAAATATCGTCTGTGTTGCAAACCGTTCTCAA GTCTGTGTTTAAATGAATCCTAATGTCTCACATAACACCTTCATG			GCGGACTTTTTTTAACTGCTTTGTGGCTTGGCTGAAGAATGAAAAGT
OlaC _{CD} 6	1,65	59 190	GCACATTT		1 902	AACCTATCGATGACAAAGTGAAGGATTTGGTCAAGCATCCCATTT 155 TGTGTAATCGGCCACAGA
				OlaC 60	1,092	25 ACATETTACACCETA ACCCCCCETCTCATEGA AAT
			CCTCTGATATCTTGTAAAATTCATATAAAAGAAGTGTGAGAGGGTA TAACTAGCCCACCAGAGTTTGGCTCCGACCGTTATTCGAGTTATC	OlaC _{GH} OU	1,505	35 ACATTIACACCTIAACCCCOUTCICATIOAAAT
			TGTTAAAGTTGCTCGTGTGAGGTGTACAAGAGAATATTGTGTGAA			CTATGTTTTATAAAAATGCGTAAAAAAACGCAGGGAACCCCAGA
			ATACACCCTCTTAAAGTAACCTTGTAGAATATCGTCTTCTTTACA GAGCCAGTGGTTTCAACCTCCTGACCTCCTTACTGTAAATACGAGT			AAAACCACGCAAGCCACCGCTTTTGCATGTCAGGAGCAAAGTTGT
OlaC _{CD} 8 _{abcde}	74	41 741	GGTGTGCGGCAATGAGCATCAGTCTTT			CATTTTATGAACTCCCGTGTGGGGAGATTTACTGCGTCTCCTCGCCG
OlaC _{DE} 13	9,45	55 14	AATGCATGCACTCA	OlaC _{GH} 61	1,134	224 GTTTTACGGGGTCAGTTAGTGGCACACGGTATTCATAGGTCGTG
OlaC _{DE} 14	8,90	09 19	GTTCACGGTCACGGGCAGG			
OlaC _{DE} 15	8,68	85 16	AAAACGGGTTTGAGCT			TTATGATTAGTGAAGCTTTGCTCAAGGTGGTAATACGCAGGGCCC GCGTCTGACCGGTCATGGAAAGATGAAGGGGTGGGGAAGGTGGA
			AGCATGTICTTGATGTGAAGTAGATATGACTCATTTTCTGTTTTGCG			TGAGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
OlaCor16	8.40	15 110	GGCCACTTTTTATGCAGGTGACCCTTTTTCTACTTTTTTTCACTTA AGTAAAATATAAAAGC			GAAAGAAAAGAGCAGCGTCCGTGACTGTGCCGGTGGGACAATCC AGCTGTAATCGCAGCTTACGTACATGCAAACTCTCACGCCATGAG
GIGODETO	0,40	55 110		OlaC _{GH} 62	459	451 CTGCTTTTGAGACTGCAAAGCCCGAAGAAGAAC
			GTATAACCTIGTAAAATAAAATCACACAAATTAGTATTIGCATCC			
OlaCos 17	8.16	62 119	ATCGTCTCGTACAATATGGCATTCCATA			TTTTATIGTCCTTTTTATGGTTATATGGCTGAAAAGAGAAAAAGAA GGCTCCCATAAACAGAGCAAGAGTCACAAGGAGGCAGTGAGCGT
DE	-,					CAACTITATGACCACCCTTCCATTITGTCAAGAGGAATCCCCCCTC
012018	7.00	no 79	TITGCGCTTGTAAGACTGCTACGTTGTCTGTAAAAGTAATAACGA TATGAATGTATATGCGTTATGTGTTCAATAAA	OlaC _{GH} 63	9,080	170 CAAAAAAATAAATAAATAAATCCTGCTTCATAAA
OldODETO	7,50	50 70				TCAGACATCAGAATTTTTTTTTTTTTCTAGGATTACCAGGGAAACGCAACA GTTTGAAATCCTTTGATGCTACCTAAACCTGGGGAAATTGCAATA
			TTATTTTATGGGTACATCATCAACCTTTTAACTACATTTCTTTTCAA			GAGATTTCTGAATATAGAGATTTCATATGGTTTAAAAACATTTTTTA
			CAACAACCCCCCTTTGCTGTTGTTGTTCTTTAACCTTTTTTTCCTTTTAA ACCCTTGAAGTTCGACCTAATCAATGTCACCACTGTGCTACAAGC	OlaC _{GH} 64	8,469	149 GIGTICTATATCA
			CTTTAACGCTGCAGCCAAACAAGCAAAACAGCTCTGTAAAGCAG			TAAACACTEGTEGAAGACAATETTEEGAGECTEGGGAGGACAAG
OlaC _{DE} 19	7,49	93 195	TAATAGGGTTAC			TAGCTGAAAGCCAAGCGAACAATTGAGAGAGTTTTACCACGGCACT
OlaC _{DE} 20	7,09	92 32	CCTGCTGGCAATGAAGTGTAAAGCCACGCAGC			ACCTAATCTCAGAGCTTTGCCTTTGCGGAGTTTACCTTCCGCACAA GTGCGGCATCGCTCCGACGTGATTGCAAGCTATATTTCCCCAACA
			AGCTCATACGGCCATGCTTAACTGCCCGACTTACATCCAATTAAA			ACTAAAACTGCCTATGACGCACACACTTATTGCGTACCTGCTACAAT
			CTTATCTAGGCCAATAGGGGACAGTAATATGATTAGACCGGCTTC	OlaC _{HJ} 65	8,272	370 TACAACGTCTTTAAAGTGAGGTCAATTTA
			CCGCATICAGCICAGACICCAGTITACIGGGCAGCAGIGICICCGF GCCCATIGTCAGTGTTTGGTGTGTGGGGGAGAGTTTGTATCGTTTGG			GIGIGIATATACTITITACTAGIGAGITAACATTACCAATAAAGITT
0.0.04			AGCAGGATTTATCACCACAGAAGCAAAACACCATGATTTTCAAA			AGTGTACCTGCAGTAAACTTTATTGGGGTGTAAAGACATGGGTCA
OlaC _{DE} 21	3,56	56 279	GITTICATCICIGITIAAAAGACGAIGA	OlaC66	6 174	CATGGCTCTGCGTCTTTTGTCTCCTTGTGGCTCTGCTGTTTGCGGGA 174 AAAACGGCCTGCGAGGATTCCCCGCATTTCTAGTGT
			GTTAGAATCGAAATTCCTCCCATTCTCAATGTTTATGGTTTTCTCTG	OldoHjoo	0,174	
			GAAGAAAGGGATTTAGCGTTACTACAGCCATTCGGGCTTTTATGA			ACATTCCTGGTTGTTAAAGGAGAGAAATTTACAGCTGAGTAATAA
			GGACAGCTGTCTGCTTTCTTTGTACTTGGGTGCAGGATGCATCTTG	OlaCu 67aba	5.250	131 GTGGCGCACGCTCTGTGAACATGAACTTATGCTGTTGTCT
OlaC _{DE} 22	2,02	29 199	GGAGACAACCTTTTGT	abc	-,	
			CTCCTACACATCCAACTCTTCCAAATTGATATATGACAATATCTAC TTTCGATCACGTGTCTGCGGGGGGGGCCCTAGACGGATTGCGCGTCA			TGACCTAACCTGTAGCCTGTATATAGATATGCTGATGCTGGGAGC
			TCTCGCCTTCCCAAATTTTTCCCTTCTGCAGCAGCTCGAATCCAAA			GGTIGICATGGTICCICATIGITIGGAGCACCIGCGIGCGGCIGGC ATCGTGGGGAAAACATTTCACAAGAGCTGTGCTAATCTGTTGTAG
OlaC _{DE} 26 _{bcd}	17	74 139	AC			TAAACTGCACTCTAATCGTGAACTTTCTCATCACTCATAGGCCCTT
OlaC _{FF} 27	6.38	83 56	ATAACACCAA	OlaC _{HJ} 68	4,606	206 GIGACCAGGCAGIGACGAATIACA
2.				OlaC _{HJ} 69	3,833	33 TITATIGGAAATGTAAAACAACGCGACCGTITT
			TITITCACCITITGAAAACTGTGATGTACAACTTGTGAAAGTATATAC			TAAATCTCCTTTTAAGATTAAGAAGGGAAAATCGCGGGCCATTGT
			ATGTAAATAGCGTATGTTGACCCCCCCCCCCCCCCCCCC			TGAGCTCTTTAGGATTTTAAAAAGCAGAGTTAAGCTGACATCAAA
			CCCGCTGCTATATTCATCACACCGCCCATGTAACTCCAATAGCTTT			CTCCATGAAAGTCGTGAAGCTGTCTGCGTCACCACATTTAGAAAC TCACTTACAAACCCCGACAGGACAAAAATTTTCCCCCAAACTAATG
OlaC _{FF} 28	5,98	87 286	GGATTTCAGAGAGGATGGGCAGATC			GTCATAATTTATGACGTGCGGATCAACATGTGCTCATTGGGCAGC
	.,		CTTTTACTGGCCACTAAATGGAATCGCCACTCTTAGTCTAGACACT	UlaC _{HJ} 70	3,146	349 AGCTICCTGAGTGCITAACGAGCATGAAGT
			GCCATAAAGACACAGGCACTAAATGGCTATTTTTTCCTCTTAATTG CACCGTCTGTTCTGGGGAAACAGCATTCACTTCCGCAGTAAACAG			ATA A A ACACTA A A ACTCTGGGGA A AGA ATGACCTTTCTGATGCTG
OlaC _{EF} 29	5,31	16 145	TAAACAAG			CACACGGACACAGCCTCTGCTGCATTCCAGTCCACACATTGGCTT
						CACTGTTCAGCTTTTATTTACAGCCTCCACTTTGAGGACGAGCGGG TTTTCGTCCCTCTCTTTGAGAGAGAAACCACCAGCCTGAAAAACA
			TATAATTAGTCTTTGAACTTCAATAATGTCAAGGCCCCCACCTTTA ACCTGCTGCAATAAAGTGAAATCAGGGAGCCCCGGAAATGTGCTG			AAACACACATATTTGCTTTCAGTTTTCACACTTTTGATTGTATTATT
			AGAGGCAGAAGGAGCCAATGAGAGTGGGCGGGAGGATCGTGGAA	OlaC _{HJ} 71	2,186	236 TGTTTTAT
			TGTGTACGACACCAACTTTGACCCTTTGCCTTAAACTGCGGCAGGT AACTTTACCAGTTTTAGCACACCCAGTAAATACACTTTATTGTCCT			GCTTTCATCTGTGCGTCCGGATGATAGCCTTGAGCTGCTCCGCTGC AGAGATAGCTCTTGGTGAGCTGTGGAACGTTACTTGTTTTATTGCC
OlaC _{EF} 30	4,92	22 237	TGTAAAATGTA			CTCGCAGAAAAGAGACTATAAACGCATTCTTAACCCCCCCC
				OlaC72	030	GCCCCCAAAAAGCTGTGCTCACTTGACAGATAAATCATACACAA
			CATTAGGTGGCGCTCTTGCTCCACGGAAAAGCCTTCGGTTTTTCCA	OldoH)/2	565	100
			ACTTGACCGCGCTGACGTCACTTCAGTCTGGAGCTTCAAGGCCAC			GTTAACAGCTCCGTGTCTTCCTCTAAAACAAATGCTTCTAAACTTG
			CATCCATAATTATGTTACTGATATTTTTTGCACCCCCCTCTAAAAGA			AAGICCAAACTTCCCATTGCGTTTAGCTGGACGGTGCGCCTCTCC AAATCCACGTTGTGTTTATCGGCATTTAGCACTAATGTTCAAGCTG
$OlaC_{EF}35_{ac}$	32	22 235	TGTCAGC			TGAGCTAAAAGCTACAGTTTCGCCTCAACTCCTGCGCCTCAATTG
OlaC _{EC} 37	6 04	55 66	ACAAAACATAGCAAACTGCAC ACAAAACATAGCAAACTGCAC	OlaC73	469	GCTGAGAAGGGTCAGCTGACACTGTCATATTGTCTCTCACCGAGC
	0,50			- 100HJ, 0	400	TAACTACCTAAAAAAACTACCTAAAAAATGTATGGACTTGAGTGCG
			ATAACGTIGATITTAAATATTATCCAGGTGACCACAGTAAGTCAAG GICATAAAATTCTAATGTCACGTCGCCCCCCAAACCCCTCCCCC			ACTTCACTGCATGATGGCTTCCCCGCTGCTCTTTATCTCTTGTTGAC
			TGGATITTATGATCTGCAAATATAATGTGCTGCAGCAGTAAAGAT	OlaC _w 82	1.607	150 CTTGTGACATTTG
OlaC _{FG} 38 _{ab}	6,52	21 162	GCGTTTAAAGGTGTGTGTGGGAGGAGGG	JV	.,	
OlaC _{FG} 39	6,14	43 21	AGGTAGGACTAATGCTTTTAT			TGACGCTCTTGTCTAACTGTCCTGCCCTATTTGCGCCAAAGAACCC
			GIGGTITAGGIAGITICATGITGTIGGGGTTGGCTCCTGGCTCCGC			IGCUIGGUUUTAACAACTAACAGCTCAAAGTTTACCGGACACGT TTCTCCTATTCATCAATATCCCCCATTGAGCATCAAGCCAATTTATG
			AACAAGAAACTGCCTTGATTACGTCAGTCGTCTTCATCAAGGGC			ACTGGCCAACACGTGCACGTGATCACATACAAATACTCCATATTT
OlaCer 40	5.60	93 162	AUAATTTCCGCTGAATTACCGCTTACAGTCAGTCACCCAAGTCCC CGTAAATGGCATTGTAAATGAACTG	OlaC _{1K} 83	410	255 GATAACAAAGCTCACTCCACCTATAAATCC
	0,00			wike the		

		CCTTGTTTTCTCAGCTCCCTCATTATGGCTTTAGTACCGCTGGAAG ACAGTCTAGAATCCAAAGTCACTTTCATTCAGGCCCCTGAATGAG
		TGTCTCCCTTGGAATGCATCACTCACAAAGACTTTACAGCGCTGG
50	398	AAACAGCAGCACAGACAGACAGACAGACAGACAGACAGA
24	112	TATTAACGGCACGTITTTGAATAATCAAATGATCCTCGTTAAAATT TATTGTTGGGTATAAAAAACATGAATGGAGGGGGGCTGTCGAATATAG TGCGCTGTAGTGGAGCTGCTT
	112	
	100	GCGCATTGATCCACTGTACAATTTTTTGTGGGGGGAAATATAATCAC GTGTCAGCGAGGCAGCCAATAGGAGCCCGGGAAGCTCTGAGAAA TAATTACCTGCCTTGATTGTTCTATGGCCAGATAAAAAAGTACAC
33	100	TIGTTICATTIGT
		AAATTGCCTTTTTGTGGTGGCAAACAATACAAGCAGGATGCCGTA
		ATTTCAAAGCCCAATCCCGTGCATTTCCGCTCATCCCGGACAAAA ATGCCAGTTTTACGGCCCCTGTTGGAGCTCGGCTGTTGGTCTCAAA TGCAGACGAACAAAGCAAACTCGACTAACTGGCTAGACGTCTGG
57	209	GCTAAA ITACTITAIGGITTIAAIGGACG
		CTAGATGACGCTGTIGGTCCGTGTTTTGAGCGAAGCCTGACTGTTG GCGGACTTTTTTAACTGCTTTGTGGCTTGGCCTGAAGAATGAAAAGT AACCTATCGATGACAAAGTGAAGGATTTGGTCAAGCATCCCATTT
92 15	155	TGTGTAATCGGCCACAGA ACATTTTACACCTTAACCCCGGTTCTCATTGAAAT
	00	
34	224	CTATGITTIATAAAATGCGTAAAAAAAGCAGGGAACCCCGG AAAACCACGCAAGCATTIGCATGTAGGAGCAAATGTG GCTGAGCAGGGAGCTCCCCCCGAGACTGCACCTAAACATCCAATGTTA CATTITATGAGACTCCCGTGTGGGGAGATTTACTGCGTCCCTGCCG GTTTTACGGGGTCAGTTAGTGGGCACACGGTATTCATAGGTCGTG
		TTATGATTAGTGAAGCTTTGCTCAAGGTGGTAATACGCAGGGCCC GCGTCTGACCGGTCATGGAAAGATGAAGGGGGGGGGAAGGTGGA TGACGCTGGCGCCCTTTGCTCGCGAAGCTAAAAAAAGGGAAAA
59	451	GAAAGAAAAGAACAGCGTCCGTGACTGTGCCGGTGGGACAATCC AGCTGTAATCGCAGCTTACGTACATGCAAACTCTCACGCCATGAG CTGCTTTTGAGACTGCAAAGCCCGAAGAAGAAC
		TTTTATIGTCCTTTTTATGGTTATATGGCTGAAAAGAGAAAAAGAA
30	170	GGCTCCCATAAACAGAGCAAGAGTCACAAGGAGGCAGTGAGCGT CAACTITATGACCACCCTTCCATTTTGTCAAGAGGAATCCCCCCCTC CAAAAAAATAAATAAATAAATCAGCTGCTTCATAAA
		TCAGACATCAGAATTTTTTTCTAGGATTACCAGGGAAACGCAACA GTTTGAAATCCTTTGATGCTACCTAAACCTGGGGAAATTGCAATA GAGATTTCTGAATATAGAGATTTCATATGGTTTAAAACATTTTTTA CTCTTTCT+ATCA
59	149	GIGHCIAIAICA
		TAAACACTTGTTGAAGACAATTTTTTGGAGTCTTGGGAGGACAAG TAGCTGAAAGCCAAGCGAACAATTGAGAGATTTAACCACGGCACT ACCTAAATCTCAGAGCTTTGCCTTTGCGGAGGTTTACCTCCGCACAA GTGCGCCGCATCGCTCTGACGTGATTGCAAGCTATATTTCCCCAACA
72	370	ACTAAAACTGCCTATGACGCACACTTATTGCGTACCTGCTACAAT TACAACGTCTTTAAAGTGAGGTCAATTTA
		GTGTGTATATACTTTTACTAGTGAGTTAACATTACCAATAAAGTTT AGTGTACCTGCAGTAAACTTTATTGGGGTGTAAAGACATGGGTCA
74	174	CATGGCTCTGCGGCTTTGTGCTCCTGTGGCTCTGCGGGGGGG
		ACATTCCTGGTTGTTAAAGGAGAGAAATTTACAGCTGAGTAATAA AAGTTTACGACTGAATCCTTCCTACGATTGGCTGCGGCGAGCCAC
50	131	GTGGCGCACGCTCTGTGAACATGAACTTTATGCTGTTGTCT
		IGACCIAACCIGIAGCEIGIAIAIAGAIAIOCIGAIGEIGGGGGC GGTIGTCATGGTICCTCATIGTITGGAGCACCTGCGTGGGGCGGGG ATCGTGGGGAAAACATITCACAAGAGCIGTGCTAATCTGTIGTAG TAAACTGCACTCTAATCGTGAACTITCTCATCACCACTATAGGCCCTT
06	206	GTGACCAGGCAGTGACGAATTACA
33	33	TTIATIGGAAAIGIAAAACAACGCGACCGITIT
		TAAATCTCCTITTAAGATTAAGAAGGGAAAATCGCGGGCCATIGT TGAGCTCTTTAGGATTTAAAAAGCAGGGTAAGCTGACATCAAA CTCCATGAAAGTCGGAAGCTGTCGCCTCCACCACATTAGGAAC TCACTTACAAACCCCGGACGGCAAAAATTTTCCCCAAACTAATG
46	349	AGCTTCCTGAGTGCTTAACGAGCATGAAGT
		ATAAAACACTAAAACTCTGGGGAAAGAATGACCTTTCTGATGCTG CACACGGACACAGCCTCTGCTGCATICCAGTCCACACATIGGCTT CACTGTCAGCTTTATTTACAGCCCTCCACTTGAGACAGAGCGG TTTTTCGTCGTCTTTTTTGACAGCAGAAACCAGCCTCAAAACCA
36	236	AAACACACATATTTGCTTTCAGTTTTCACACTTTTGATTGTATTATT TGTTTTAT
		GGAGATAGCTCTTGGTGAGCTGTGGAACGTTACTCTTTTTTTT
39	193	AGGACACATTAA
		GTTAACAGCTCCGTGTCTTCCCCTAAAACAAATGCTTCTAAACTTG AAGTCCAAACTTCCCATTGCGTTTAGCTGGACGGTGCGCCTCTCC AAATCCACGTTGTGTTTATCGGCATTTAGCACTAATGTTCAAGCTG
		TGAGCTAAAAGCTACAGTTTCGCCTCAACTCCTGCGCCTCAATTG GCTGAGAAAGGGTCAGCTGACACTGTCATATTGTCTCTCACCGAGC CAACCCCCCCTATAAAGACTCCCCCCCCCC
58	466	CAACCICGGCIAIAAAACICGGGTTIG TAACTACCTAAAAAAACTACCTAAAAATGTATGGACTIGAGIGCG ACTICACTGCATGATGGCTTCCCCGCGCTCCTCTTATCTCTIGTIGAC
07	150	CACATGAGTGTGGAGCCACATATCCAAATAATCTACAGTTTTGTC CTTGTGACATTTG

OlaC _{KL} 84	8,578	ССАСБАСТСССССССССССССССССССАССААССААСС АСАТСАТБАСАССССССТСЯТСССТСАТСАССААТТАЛСЯТСКС ТГОСТССАСТТОБОАСССТААТСАТСААТТАЛСАТТСАСТСАТТ СААТССССТТААСТТССААТТААТТАА
OlaC _{KL} 85	8,134	АЛБИБИВИСАСТСААССИСТАТАЛОГОВАЛТСТССОГСТ GREETERCATTCCCCCCGAAGGAAGTAATCATTCCGTAACTGTATT GACUGTATGTTAAAATATTGTAACGTGCAATGAAGTCGTTTCCTC CTGACGGTGCCTGCCTAAACATCACGGCCTCAAAAATTCACTGAAAG 215 ATAGCCTGTTGTTGTCGTCCTGATTAATAAAGTT
OlaC _{KI} 86	7,734	GACAAACGCGCTGAGAAGTTTAAAGCCCCCCCATAAAACTTTATT GCCCCTTTTTCCATTACTCCGCAGGCACACTGCGCTTCCTGTTTTG CCAGGGAAGGAAGGAAGCCACCAATCCTGTAATAACAACACACAC
OlaC 87	7 192	AGGTTACATATGCCAATTGCCCCAAGCAGGGCCTGTGAATGGTGC ATGGGGAGCACGTGGTGTCATTAAGTGGGTTTATGGCCTGGAA GAGCTGACAAACCTTCGATATATACACATCATATATAATCTTAAC 152 TGTCCGAATCGCAGCTG
OlaC _{KL} 07 _{ac}	7,105	ATAGGGGGCACTGTGTGACGCGCTCCATGTGCGGGTCGGCAACGT GTTCTTGTCACAGCCTCTTCTGATTTTCAGACCTGCAAAATGTTTGT
OlaC _{KL} 92	5,615	ТПТСССОПТИТААЛАТСИСТИССКАЛТИАСНОСААЛАЛИТ СПСТАТСЯСТСЯТИААСНОСТИТИССТССАСССОСААЛАЛИТ ТАПТССИТИССТАААСААТААЛАСССТСССОСОСОСТИААЛАЛИТ 602 ССТСТАСТСИТАТСАСАНТСАЛАА
		CCACAGCTCTGCACTAAAACACAGTCAGTGGTTTATGTGGCGAAT GCAGTTTTAAAACCTCTGCTCCCCTAACTGCAGCTTCCAGAGAG CATTCAAACCCTACGAGTCCCAGTCTGTGCACACTTCATTAAA AACTTTTTTTTTT
OlaC _{KL} 94	4,195	646 ATTAAAAGCGCATCGTTACCATTTTTA
		TGTGCATCTCTACTCTTATCAATICCATCGATTCACAATCTGAGCA TGTTGCTGGCTTTAATAACTTCCAAACAGGTTGCAIGTCGATAT TACATTTTCATCGAGGCTTTCTCATTAGGTCGAGGGCAG GAAAAAGGTTACGGCGCGGGTCATATGGTAATGGCAGTCAGGA GAAAAAAGGTTACGGCGCGGGTCATATGGTAATGGCAGTCAGGA
OlaC _{KL} 95	3,256	TATATTTTAAAAACTATCAGTTTGGGTTTAAACGCGAATCTTGTGA
OlaC _{KL} 96	2,857	51 TITTT
		TTAGTIGCCTATATGTACCCTGTAGAACCGAATTIGTGTGGAGTAC AAGCATTCGCAAATACGTCTCTACAGGAATACATGGGGACTGA AATACCACGCCAACAAGGATGGCTCGATTGTTTCTCTACAGCC CCTCCTACTCGCCCTCTAGCGGTGGTTCGTCGCCCCCCTCCTCCTC GCATACAACGCTACATACGATGGCTGCAGCCCAGCC
OlaC _{KL} 97	2,769	551 CCAGCAGTGCTATCTCTTTCCCCTGCAAA
OlaC _{KL} 99 _{ab}	3,711	АСАТТАТААСТАСЯТАТІСААСТАССТАСССАТСТСАААСССАТ ТІСПСОССАААДСААТІСАТІССТІСССТСАТААТССТІС ССАСПСААСТАТІССАЯСССЯГСААССССССССССССССССССССССССССС
OlaC _{KL} 102	151	GGTTCCTTATCCGGGAACTACCTCTTTCTGCTATTGGGCCATTG GGTCACGTGGTTAAAGTAACTTTACAGGGCTGCTCCCAAGTAGGA GGGCTTATGAAGCAGAAAAACGACAAAGCTAGAAAAATTATTT 151 CCACTCCAGAAATTA
		TIAITTATAGGACAATICTACATTTIGTITTCGTAGCTATCTIGTGC GGTITCCTITTAGTICCAAGTIATATAAAATGCATGTIATATGGCA TGGATTACTGCGAATACCGATGAATATTITTTACGGCACACGGGT TIAATTTATTGAAGTICCAATTAGATGTITTITTTATAAAACGT
OlaC _{LM} 103	7,707	TITGAATGAAGGTGGAAAAAACAGTAAAAAAAAAAAAAAA
OlaC _{LM} 104	7,229	GTIGTGTTTAGACCGTCAAAAGCGGATTATTGTGAAATGCAATAA ACGGACTTTAGTGTATTTGTGCTAATCATATTGGTCAATAAAACAG 133 TGAGTGTCTACTAGTTTTAAACACGTTTTGTCGGAGTTTATT
		TTATGTTGCTGGACAGATGGAAAAATTAATGTGCTCGCCACAGT CGCAGCATCCCTTTAGCCCCCCTTCTAGGGACGTGCGCCTCCATGT CGCGCAGCTGAAAAGGTGTCATTGAAGTAGTTGGGGCGCAAATG GAGAGGCCGAGTTCACTCGGGGACCACTTTCTGTGCCATAG GTCATTTCACTTGAGTCGCACCTTCTCACTGCACCTTCCCTTCCCATAG
OlaC _{LM} 105	5,763	398 CTCACTCTCTTATTCGTGTACCCTCTGTG

					TGGAATGO
		TCCATCAACTCCATAGACGCTGACACGCCGCCTATCGTTCCCAGTT CAGAGATGATGCTCTAAAAACTGTGAAAAAACAATAAAAAAAA			CGAGAAC
		CCTGTCACATTTGTTTTATATAAATGTACATATATAAAATATATA	TniCeo41	4 035	TATGTCCA 343 CACTGACA
TniC _{CD} 1	6,217	177 TATTTAAAACTGTCCGTATTTCATTGACAAGCATTGCGTG	THIOFG T	4,000	TATTAACO
		TACCUTTGACCATGACTATGCTGTCGCTTTGACCTTGACATCACAG	T.: 0 40		TATTGACG
		CAGATTGTGAATAATAAATAGGGGGGCTGGACCCCAACACCGACGG	IniC _{FG} 42	842	111 GCICCAIC
TniC2	4 204	TTIGTTIGCAGGCAAACAAGGTGCTATTTCCCTGTCTAGACAGTTA 167 GGCTTAATGGCACGCCATAAATACATAAAA			GCGCATTO
THIC CD2	4,204	167 OCTIANOCACOCCATAAATACATAAAA			GTGTCACA
		GGCTGATAACCTCTGCTGGTGACCAGAGGAAAATATCAGAAGGGC	TniCro52.	192	AATTACCI 172 CACATAC/
		TACCAGTTGGTTATTGTAAGGGATTGGCTTTTGTTCATTCA	-re-abc		TTATTAAC
TniC _{CD} 3	3,035	166 TITITAAATGATTCTCTGGTCAGAC	TniC _{FG} 44	843	64 TTATTGAC
		CTTTGTTTGGCCGATTGCCCTGTCTGGACTGGACCGCCTGAATCCA	TniC _{FG} 45	433	29 GACAGAG
TniC5	2.051	GCGGGGTCATTTCAATATGTCTCAGACGTCGGACTCGGCAGTGACC	TniC _{FG} 50 _{ab}	829	18 TTTATGAA
THIOCDO	2,001	GCTTCTCCAGTTAAGCATTTGATATTTGTTCTGTCTATTTAAAGCT	TniC _{GH} 53	3,322	13 TIGTTITA
		GAAGGGAACCCCTGTGTCTTTGGGTTAAGTAGGATGGTCGCTTTAA			
		GTGACAGATACGCCTCTCAAATATCGACTGGGTAGCAAAATCTTTAC			TTTAGAAG
TniC _{cp} 6	1.593	191 ACATTT			GCCAGTTI
00	,		TniCou56	2 480	AATGACG/ 211 TAAATGAG
TniC _{CD} 7	1,163	41 AATCCATCTTTTCTTCTACAGGGATGACTACACAAATATTT	1110 _{GH} oo	2,400	CTAGATGA
					TGCTGCTG
		GTAAAAGTCCCACCAGAGTTTGGCACAAAAGAACTGTAAGAAGT GTAAAAGTCCCACCAGAGTTTGGCACAAAATGTTTATGGGAGATA	ToiC 50	4 024	ATCGATGA
		TCTGTTATAGTTGTTAATGTAAGGTGAACTGAAGATTATACGTGAA	ThiC _{GH} 59	1,634	149 AACAGOC
		ATAGGCTCTCTTAAAGTCACCTTGTAGAATATCTCGGGCTTTTACA GACCTGGCGGTTTCAACCTGCTGACCCTGATATTGTAACTATGAAG	I NIC _{GH} OU	1,485	27 ACATITI
TniC _{CD} 8 _{abcd}	le 681	681 GGAGCTCGGCAATGAGCATCATTCCTT			CTATGTGT
TniC _{DF} 13	10,463	14 AATGCATGCACTCA			AAAACCT
TniC _{DE} 14	9.924	19 GTTCACGGTCACGGGCAGG			CGAACTCC
TniCor15	9 707	16 AAAACGGGTATGAGCT	TniC _{GH} 61	1,138	224 CGGGGTCA
DE	0,101	AGCATGTTACTAATGTGAAATACAGTAGCAACATATGTTTTGCTGG			
		CCACTTTCCTGTAAGTTTTTTTTTTTTTTTTTTTTAACTTATGCGTAAAAAGAC			TTATGAAT
TniC _{DE} 16	9,450	106 GAATTCAAAAAGC			TACGTCTG
		GTATAACCTCGTCAAATGAACTTCTGTATGCTACTATGTGCATCCC			AAGGAAA
		ATTIGAGGATATGTTATCACTATGTAATAGTGTTTTATCTGTTCACC	ThiC 62	474	GAGCAAG
TniC _{DE} 17	9,206	119 GTCTTGTAAGTCATTATCATTCCATA	ThiC _{GH} 62	471	463 AUCCOU
		TTECCCTECTA ACCATECTCTCTCTCTCTCTA A A ACTA A A A A A			TTTTATGG
TniC _{DF} 18	8,947	78 AATGAATGTATATGCGTAAGGTCTTCAATAAA			AGAGTGGG
		TTATITATAACACTGTGTAACCTGTAGGGGGCAGTTAAATAGTATTTT	TniCou63	9 638	GCGTTAAC
		TATAATGGAACAACACTGTCGCAGTTTCTTTTCTTGAGTTTTGTGG	1110 _{GH} 00	3,030	TCAGACCO
		GTICICITIGAAGTICAACCIAATCATIGICACCAGTTIGITACAAGT CTATAGCGTGGAAGCTAAACAGCTCTGTAAAGTATTAATAGGGTTA			GTTGAAAT
TniC _{DE} 19	8,563	188 ^C	ThiC 64	0.007	GATTCCTG
TniC _{DE} 20	8,170	31 CCTGCTAGAGAGGAAGTGTAAAGCACGCAGC	THIC _{GH} 04	9,027	146 CIAIAICA
					GTGTGTCT
		AGCTCATTCAGTCAAGTTTAACTGGCCGACATCCATCCAATTAAAC			AAGTACC
		AGCTCATTCAGTCAAGTTTAACTGGCCGACATCCATCCAATTAAAC TTATCTGGGCCACGAGGGGCCAGTAACGTGATTACAGGCGCCCCA CATTTAGCTTTGATTCCAGCAAATCGCGAAGCCTGATCCTGTTGAA	TniC66	6 305	AAGTACCT TTGGTCCC 174 CAAAGCA
		AGCTCATTCAGTCAAGTTTAACTGGCCGACATCCATTCAATTAAAC TTATCTGGCCCACGAGGGCCCAGTAACGTGATTACAGCGCCCCCA CATTAGCTTTGATCCAGCAATCAGCGAGCCTGATCAA CGGCGTCCATTGTGTGTCATGAGTGTTGTATAATTTTGAGCAGAT	TniC _{HJ} 66	6,305	AAGTACCT TTGGTCCC 174 CAAAGCA
TniC21	4 66 1	AGCTCATTCAGTCAAGTTFAACTGGCCGACATCCATCCAATTAAAC TTATCTGGCC2CGGGGGGCGATAACGGGCCGTAACAGGGCCCCCA CATTTAGCTTTGATTCCAGCAAATCGCCAAGCCTGATCCTGTTGA CGGCGTCCATTGGTGTGCTAGGGTGTGTTATATTTTGACGAGAT TTATTTTCCAGGACAAAGCCACTAAGCAATAGTTAGAAGAGTCG 241 GTGAGTCATCTTAGCAGTGGGCG	TniC _{HJ} 66	6,305	AAGTACCT TTGGTCCC 174 CAAAGCA ACATTCCT
TniC _{DE} 21	4,661	АGCTCATTCAGTCAAGTTTAACTGGCCGACATCCATCCAATCAAAC TTATCTGGCCCGGGAGGGCGATAACGGGCCGTAACAGGCCCCCA CATTTAGCTTTGGTTGGCAGCAAATCGCGAAGCCGGATCCTGGTGAA CGGCGTCCATTGGTGTGCACTGAGGTTGTATAATTTTGACCAGAT TTATTTTCCAGAGCAAAAGCACTAAGCAATAGTTGAAGAATGGTCG 281 GTTAGAGTCAACTGCTACAATGATCAATAGTAGACAATAGT CTTCTCAACATCGACTGCTCTCCAAATGATTATATAGACAATATCTAC	TniC _{HJ} 66	6,305	AAGTACCI TTGGTCCC 174 CAAAGCA ACATTCCI GTTTACGA
TniC _{DE} 21	4,661	AGCTCATTCAGTCAAGTTTAACTGGCCGACATCCATCCAATTAAAC TTATCTGGCCACGAGGGCCAGTAACGGAATCACGGCCCCCCA CATTAGCTTGGTTCCAGCAAATCGCGAAGCCTGATCCTGTTGAA CGGCGTCCATTGGTGGTGCATGAGTGTTGTATAATTTTGACGAGT TTATTTTCCAGGACAAAAGCCTAAGCACATAGTTAGAAGAGTCG 281 GTTAGGGTCATCTTCACAAGGGAT CTCCTACACATGCAACTCTTCCAAATTGATATGACAATATCAC TTTCGATCACGTGTTTGCGTGGCGACTTAGACGGATTGCCGGTCAT	TniC _{HJ} 66 TniC _{HJ} 67 _{abc}	6,305 5,360	AAGTACCT TTGGTCCC 174 CAAAGCAT ACATTCCT GTTTACGA 129 GCGCACGT
TniC _{DE} 21	4,661	AGCTCATTCAGTCAAGTTTAACTGGCCGACATCCATCCAATTAAAC TTATCTGGGCCACGAGGGCCAGTAACGTGATTACAGGCGCCCCA CATTTAGCTTGGTTCCAGCAAATCGCGAAGCCTGATCCTGTTGAA CGGCGTCCATTGGTGGTGCATGAGTGGTGATAATTTTGACGAGT TTATTTTCCAGGACACAAAGCCTAAGCCATAGTTAGAAGAGTCG 281 GTTAGAGTTCATCTTAGCACGAGGGAT CTCCTACACATGCAACTCTTCCGAAATGATAATGACAATACTAAC TTTCGATCACGTGCTCCTCCGGGCGCATTCAACGAGTACGGGTCA CTCCGCCGTCCCAAATTTTCCCTTCTGCAGCAGCTCGGAATCCAAAA 200	TniC _{HJ} 66 TniC _{HJ} 67 _{abc}	6,305 5,360	AAGTACCT TTGGTCCC 174 CAAAGCA ACATTCCT GTTTACGA 129 GCGCACG TGACCTGA
TniC _{DE} 21 TniC _{DE} 26 _{bcr}	4,661	ΑGCΤΕΛΤΤΕΛΟΤΕΛΑΓΙΤΤΑΛΟΤΟΘΕΟ CACATOCATECΛΑΤΤΑΛΑΕ ΤΤΑΤΕΤΟΘΕΟ CACAGEGGGC CATAΛCIGGTCATECAGEGCCCCCA CATITAGCTITGGTCCAGEGGGCGTATAACGEGCCCCCA CATOLAGCTITGGTCATEGGTGTTGTTATATTITGACGAGAT TTATTITCCAGEGACAAAGCCACTAACCAATAGTTAGAAGAGTCG 281 GTTAGAGTCATCTTAGCACGAGGAT CTCCTACACATEGCAACTCATCCAAATGATAATAGACAATATCTAC TTTCGATCACTEGTGTTGCCGGCGCACTTAGACGGAATTCCACA TTCGATCACTGTGTTGCCGGCGCACTTAGACGGAATTCCAAA 139 C CTCACTCAAGTCTAATCTTGCGGCGTTTTTCCAAAGGAGTCCACATA	TniC _{HJ} 66 TniC _{HJ} 67 _{abc}	6,305 5,360	AAGTACCT TTGGTCCC 174 CAAAGCAU ACATTCCT GTTTACGA 129 GCGCACGE TGACCTGA
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27	4,661 169 6,343	АGCTEATTEAGTEAAGTTFAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCACGAGGGGCGATAACGGGCCGTAACACGGCCCCCA CATTTAGCTTTGGTCGTCATGAGGGTGTGTATAATTTGGACGAGA TTATTTTCCAGAGACAAAAGCACTAAGCAATAGTAGAAGAGTGG 281 GTTAGAGTCATCTTAGCACGAGGAT CTCCACACACATGCACAAAGCACTAAGCAATAGTAGAGAATAGTCA CTCCACACACATGCAATCGTCCCAATGATAGACGAGTAGCGGGCAT CTCGCCGCCCAAATTTTTCCCTGCGGCGCTTTCCAAAGGAGCCCCAAATA 139 C CTCACTCAAGTCAATCCTGGGCGTTTTCCAAAGGAGCCCCACATCA 50 CCAA	TniC _{HJ} 66 TniC _{HJ} 67 _{abc}	6,305 5,360	AAGTACCT TTGGTCCC 174 CAAAGCA ACATTCCT GTTTACGA 129 GCGCACG TGACCTGA TTCTGCAC GCTCCAG CGGTTGCA
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27	4,661 169 6,343	AGCTCATTCAGTCAAGTTTAACTGGCCGACATCCATCCAATTAAAC TTATCTGGCCCGGAGGGGCGATAACGGGAGCCTGATCAGGGCCCGA CATTTAGCTTTGGTCGTGCATGAGGGCGGAGCCTGGATCCCGGTGAT CGGCGTCCATTGGTGGTGCATGAGGGTGTGTATAATTTGACGAGTA TTATTTTCCAGGACAAAGCACTAAGCAATAGTCGAGAGGATGCGGGT 281 GTLAGGGTCATCTTAGCACGAGGAT CTCCTCACACGTGCATCTCTCCAATGGTATATGACAATAGTCAC TTCCGATCACGTGGTGGGGGACCTAGGACGGATTGCGCGTCAT CTCCCCCAAATTTTTCCCTTCCC	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68	6,305 5,360 4,704	AAGTACCI TTGGTCCC 174 CAAAGCA ACATTCCT GTTTACGA 129 GCGCACG TGACCTGA TCGGCAC GCTCCAG CGGTTGCA 215 CAGGCCT
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27	4,661 169 6,343	AGCTCATTCAGTCAAGTTTAACTGGCCGACATCCATCCAATTAAAC TTATCTGGCCACGAGGGCCAGTAACGGGATACCAGCCCCA CATTAGCTTGGTTCCAGCAAATCGCGAAGCCTGATCCAGTGGA CGGCGTCCATTGGTGGTGCATGAGGGATCCCTGTGAA CGGCGTCCATGGTGGTGGTCAAAGCACTAAGCACAATAGTAGAAGAGTCG 281 GTTAGAGTTCATCTAGCACGAGGAT CTCCTACACATGCAACTCTTCCAAATGGATATATGAACAATATCTAC TTTCGATCACGTGCTTCCCAAATGGATATATGAACAATATCTAC TTTCGATCACGTGCTTTCCCTGCGGGCGTTTGCCGGGACTCCAAAA 139 C CTCACTCAAGTCTAATCCTGGGCGGTTTTCCAAAGGAGCCCACAATA 50 CCAA	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 68	6,305 5,360 4,704 3,956	AAGTACCT TTGGTCCC 174 CAAAGCA ACATCCT GTTTACGA 129 GCGCACG TGACCTGA TICTCCAC GCGCTCCAC 215 CAGGCCT 34 TTTATTGG
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27	4,661 169 6,343	AGCTEATTEAGTEAAGTTFAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCACGAGGGGCGATAACGGGCCGTAACACGGCCCCA CATTTAGCTTTGGATTCCAGGGACATAGTGGAAGCCCCTATCCTGTTGAA CGGCGTCCATTGGTGGTCATGATGTGTGTTATAATTGACGAAAT TTATTTTCCAGGACAAAGCCACTAACCAATAGTTAGAAGAGTCG 281 GTTAGAGTCATCTTAGCACGAGGACT CTCCTACACATGCAACTCTTCCAAATGATAATAGACAATAGTCAA CTCCCACACATGCAACTCTTCCAAATGATAATAGACAATAGTCAA TTTCGATCACTGTGTGTCCGGGCGCATTAGACGGAGTCGCAGTCCAAAT CTCCCCCCGTCCAAATTGTTCCTTCCGCAGCAGCTCGAATCCAAAA 393 C CTCACTCAAGTCTAATCCTGGGGGCTTTCCAAAGGAGCCCACATCA 50 CCAA TTTTCACCACTACAAAATGTGACGTCCAATCGTGGAAGTACTCTC CCCCCCTGTACAGAGCAGAG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69	6,305 5,360 4,704 3,956	AAGTACC TIGGTCCC 174 CAAAGCA ACATTCCT GTTTACCA 129 GCGCACG TIGGCCC GCTCCAG CGGTTGCA 215 CAGGCCTC 34 TITATTG.
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27	4,661 169 6,343	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCACGAGGGGCGATAACGGGCACTAACACGGCCCCCA CATTTAGCTTTGGTGTGTGTCATGAGTGTTGTATAATTTTGGAGGAGT TTATTTTCCAGAGACAAAAGCACTAAGCAATAGTTAGAGAGAG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69	6,305 5,360 4,704 3,956	AAGTACC TIGGTCCC 174 CAAAGCA ACATTCCI GTTTACGA 129 GCGCACG TICTGCAC GCTCCAG CGGTTGCA 215 CAGGCCTC 34 TTTATTTG
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27	4,661 4 169 6,343	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAAC TTATECTGGCCCGGAGGGGCGATAACGGGGACTAACGGCCCCA CATTTAGCTTTGGTTGGTGCATGGGGGCGGTAACGGGGCCCCA CGGCGTCCATTGGTGGTGCATGGGGGGCAATAGTTGAGAGGGG TTATTTTTCCGAGGCAAAAGCCCTAAGCAATAGTTGAGAATAGTTG CTCCTACACATGCAATGCTTGCCAATGGTTGACAATAGTTGACAATAGTCA CTCGCCGGTCCCAATTTTTCCCTTCTGCAGGGGCTATGGCGGGGCAA TTGGGTCAGGTGTAGCCGGGGCTTAGACGGACTGGGGGGCAA CCCA CCC	TniC _{HJ} 66 TniC _{HJ} 67 _{abc}	6,305 5,360 4,704 3,956	Албтаст: твоятесс 174 саласса адттаса 129 оссаласт тастаса остаса сабитаса 215 слабоста 34 пттатия. Талатска талатся талатаса талатаса
TniC _{DE} 21 TniC _{DE} 26 _{bc} TniC _{EF} 27 TniC _{EF} 28	4,661 169 6,343 6,030	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCC2CGG2GGGCGTAAACGGGCCGTAACGGCGCCCCA CATTTAGCTTTGGCATGGGTGGCAGTAGCGGGCCGCACA CGGCGTCCATTGGTGGTCATGGGTGTGTTATATTTGACGAGAT TTATTTTCCAGGACAAAGCACTAAGCAATAGTTAGAAAGAGTCG 281 GTTAGAGTCATCTGCGCGGCACTTAGACGGAATTAGCAGATAGTCAA CTCCCCACACATGCGAACTCCGCGGACTTAGACGGAATTACGACATAGTCAA TTGGATCACGTGTTGCCGGGGCGCTTAGACGGAATTACGACATAGTCAAA 139 C CTCACTCAAGTCTAATCCTGGGGGCTTTCCAAAGGAGCCCACATCA 50 CCAA TTTTCACCACTACCAAAGTGGGCGTCTCCGAAGGAGCCCACATCA 50 CCAA	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69	6,305 5,360 4,704 3,956	Албтаст тгодгосо 174 САЛАССА АСАТТССТ GTTACCA 129 GCCCACG TGCCCACG GCTCCACG CCCCACG CCCCACG CCCCCACG ACTIVATICC TAAATCCC CAAATCCC CAAATCCC CAAATCCC
TniC _{DE} 21 TniC _{DE} 26 _{bol} TniC _{EF} 27 TniC _{EF} 28	4,661 4 169 6,343 6,030	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCCGGGGGGGCGATACAGGGCCGTAACAGGCCCCCA CATTTAGCTTTGGATTCCAGGGCACGTAAGTGGGAATGCTGATCCTGTGGA CGGCGTCCATGGTGGTGTCATGGTGTGTTTATATTGACGAGAT TTATTTTCCAGGACACGAGGAT CTCCTACACATGCAACGCAGGACTAGGCAGATGCGGGAT CTCCTACACATGCGAACTCATCCAGAGGGAATTAGGCGAATAGTCA CTCCCCCCGTCCAAATGTTCCCTAGGCGGACTTAGGCGGAATTCCCGGGCCT CTCCCCCCGTCCAAATTGTTCCCTTGCGGAGCGCGAATCCCGGACTCAG S0 CCA TTTTCACCACTGCAAATGTGACGGCGTTTTCCAAAGGAGCCCACATCA 50 CCA TTTTCACCACTGCAAATGGGCGTGCATTCGTGGAAGTACTCTC CCCCCCTGTACAGGACGCAGGCGGACTTGCGGAAGTCCGGGGCCT CCCCCCTGTACAGGCCGACTGCGGTGCGTCATGGGGAGTCCAGGGGGCT ACTACCACTACGAGACGGCGTGCGGTGCG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69	6,305 5,360 4,704 3,956	Албтаст тгодтссс 174 САЛАССА АСАТССС GTTTACCA 129 GCCACG TGACCTGA TGACCTGA TGACCTGA 215 CAGGCCT 34 TTTATTGA ТААТССС САЛТСС САЛТСС САЛТСС САЛТСС САЛТССС САЛТСС
TniC _{DE} 21 TniC _{DE} 26 _{bo0} TniC _{EF} 27 TniC _{EF} 28	4,661 169 6,343 6,030	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCACGAGGGGCGAGTAACGGGCACTAACAT CATTTAGCTTGGCTCGAGGGGCAGTAACGGGGACTTAGGCGCCCCA CATTTAGCTTGGATCCAGGGGCACTTAGTGTGATAATTTGGAGGAGT TTATTTCCAGAGCAAAAGCACTAAGCAATAGTTAGAGGAGTG 281 GTTAGGGTCAATCTTAGCAGGAGGAC CTCCACTACACATGCAAAAGCACTAAGCAATAGTTAGAGAATAGTCA CTCCACACACTGCAAATGCTCCCAATGATAGAGGAGTAGCAGAATAGTCA CTCCACCGCCCAAATTGTCCCTGCGGCGTTTTCCAAAGGAGCACCAATAGT CCCCCCGCCCAAATTGTCCCTGCGGCGTTTTCCAAAGGAGCCCCACATCG 50 CCA TTTTCACCACTGCAAATGGGAGCTGGCAGTGGGGGGCATCAGGGGGCA CCCCCCGGTGGAAATGGGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69 TniC _{HJ} 70	6,305 5,360 4,704 3,956 3,335	Албтасст тгодоссо 174 САЛАССА АСАТСССТ дТТАССА 129 GCCACG ТСАССТСА СССТТСАСА СССТТССАС СССТТССАС 215 САССССТ 34 ТТТАТТГС ТАЛАТССТ ТСАЛАТССС САЛАТССС АЛАТСССТ 402 ТАЛАТССТ 402 ТАЛАТССТ
TniC _{DE} 21 TniC _{DE} 26 ₆₀₀ TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29	4,661 6,343 6,030 5,390	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATETGGCCACGAGGGGCGATAACAGGGCACTAACATGGGAAGCACGATCATTATG CGGCGTCCATGGGCACGAAGGGCACTAACGGAATGCCGAAGCCTGATCCTGGGCACA CATTAGCTTIGGTGGTGCATGAGGTTATAATGACAATATTGGACAAAT CTGTCACACATGCAACTCTTCCCAATGATTAATGACAATATTAA CACACATGCAACTCCTCCCAATTGATAATGACAATATCAC TTTCGACACGCAAATGCTTCCCAATGATTAATGACAATACTCAC TCCGCCGTGCTCAAGTCTTCCCAATGATTAATGACAATACTCAC CCCCCCCAAATGCTCAAGTCTGCCAGCAGCCCGAATCCAAAA 139 c CTCACTCAAGTCTAATCCTGGGGGCTTTCCAAAGGAGCCCCACATCA 50 CCAA TTTTCACCACTACAAAAAGTGTGACGTCCAATCGTGGAAAGTACTCCT CCCCCCTGTACGAGCAGCGTATGCCAGTGTGGGTTAATGAGGATGAAGTAATCTC CCCCCCTGTACGAGCAGCGTATGCCAGTGTGGGTTAATGAGGTTAAAGGATTGCTGGC CCCCCTGTACGAGCCGGATTCCCAGTGTGGGTTAATGAGGTTAAAGGATTGCTGGC 265 CTGTGTATTCGAGCTTCCAGGGGGAACAACTGTTGGC 265 CTGTGTATTCGTAGGATCCCAAGGGAGGAACAAGATTGTTGGC CCCCCTGTAAGGCCACAAATGGAATCGCCACTCTGTGGCGTCAGGAC CTTTCACGCCACTAATGGAATGG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69 TniC _{HJ} 70	6,305 5,360 4,704 3,956 3,335	Албтаст: тподгосо 174 САЛАСАЧ АСАТССТ детитасаа 129 соселост тастосаа состоса состостоса состоса состоса состостоса состоса состоса состостоса состоса состоса состостоса состоса состостоса состоса состоса состоса состостоса состоса состоса состоса состостоса состоса состоса состоса состостостостостостостостоса состостостостосто состо
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29	4,661 169 6,343 6,030 5,390	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCCAGGAGGGCCGTAACGCGGCCCTACCATCAATTAAG CGGCGTCCATTGGTGGTCATGAGTGTTGTTATATTTGACGAGAT TTATTTTCCAGGACCAAGCCTAAGCAATAGTTAGAAGAGTCG 281 GTTAGATTCATCTTAGCACGAGGACT CTCCTACACATGCAACTCTTCCAAATGATAGAGAGACCACATAGTCA TTTCGATCACTGGCGACCTGGCGACTTAGACGGAATTAGCAGATAGTCAA TTTCGATCACTGTAATCCTGGGGGCGTTTCCAAAGGAGCCCACATCA 50 CCAC TTTCCACCACTACCAAATGTGCGGTGCGTCATGAGGGGCCACATCA 50 CCAC TTTCCACCACTACCAAATGTGCGGTGCGTCATGAGGGGCCCACATCA 50 CCAC TTTCCACCACTACAAAATGTGGCGGCCACATCGTGGAAGGACCCACATCA 50 CCAC TTTCCACCACTACAAAATGTGGCGGTCATGGGGGGTCATGGGGGGCCACATCC CCCCCCTTTACAGGCCGCGGTATGCCAGTGGGGGTCATGGGGGTATGTGCAGTTGCGGCCACATCG CCCCCCTTACAGGACGCGGTATGCCAGTGGGGGTCATGGGGGTAGTGCGC CCCCCTTTACAGGCCGCACTCGGGGGGGGAGGACGACGGTATGTGGC CCCCCCTTACCAGGACTTCCGGGGGAGGACGACGACGTATTGTGC CCCCCCTTACCAGGACTTCCGGGGGAGGACGACGACGTATGTGCG CCCCCTTACCAGGACTAGGCACTCCGTGGGGGTTAGGGCGTCATGGGC 265 CTGTGTATCATGGAATATGCGAATGCCCACTCTTGTCAAGGACATCGCCACTACTGGCCACTCTGTGCGCCACTCTGTGCGCGAGGACGACGACGATGTGGCCATCTTGTGCAGGACGACGACGACGACGACGACGACGACGACGACGAC	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69 TniC _{HJ} 70	6,305 5,360 4,704 3,956 3,335	Албтаст тгодоссо 174 САЛАДСА АСАПТССТ GTTACGA 129 GCCCACG TGACCTGA TCTGCAC GCTGCA 215 САВСССТ 34 ТПАТПСС ТААЛССС АЛАТССС АЛТСССС АЛТССС АЛТССС АЛТССС АЛТССС АЛТССС АЛТССС АЛТССС АЛТСССС АЛТССС АЛТСССС АЛТСССС АЛТСССС АЛТСССС АЛТСССС АЛТСССС АЛТССССС АЛТСССС АЛТСССС АЛТССССС АЛТСССССС АЛТСССС АЛТСССССС АЛТСССССССС АЛТСССССС АЛТССССС
TniC _{DE} 21 TniC _{DE} 26 _{bol} TniC _{EP} 27 TniC _{EP} 28 TniC _{EP} 29	4,661 4 169 6,343 6,030 5,390	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCCGGAGGGGCGTAATCAGGGCCCTAATCATCA CGGCGTCCATTGGTGTGTCATGGTGTGTGTATAATTGACGACAT TTATTTTCCAGGACAAAAGCGCGACTAGCAAGACGAAGACGG 281 GTTAGGTTCATCTTGCCAGCGGACTTAGACGGAATAGTTAGAAGAGTCG CTCCTCACACAGTGCTACCGGGGGACTTAGACGGAATAGTCAAA TTTCGACCACTGCGAACTCCTCCGAATGATAGTAGACAATAGTCAA CCCCCCGTCCCAAATTGTTCCCTTGCGGACGACGCCGAATCCCAAA 393 C CTCACCAAGTCTAATCCTGGGGGCTTTCCAAAGGAGCCCACATCA 50 CCA TTTCACCACTGCAAATGTGACGGCGTCTTCCAAAGGAGCCCACATCA 50 CCA TTTCACCACTGCAAATGTGCGGTGCGTCATGGGAAGTCCGGGCCT CCCCCCTGTACAGGCCGACTGCGAGTCGGAAGTCCGGACTCC CCCCCCTGTACAGGCCGACTGCGAGTCGGAGTCCAGGGGGCT ACTACCACTACTGCAGGCGGTTTCCCAAGGGGGGCTCAGGGGGCT CCCCCCTGTACAGGGCGGCGTGCGGTGCG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69	6,305 5,360 4,704 3,956 3,335	Албтаст тгодоссо 174 САЛАСА АСАГТССТ GTTTACGA 129 GCGCACG TGCCTGA TGCTGCA CGGTGCA 215 САGGCCT 34 ТТТАТТG ТААТССС САЛТСС САЛТССА СССТА 402 ТСАСССТА АЛТССТ САЛТССА СССТА СССТА АЛТССТ САЛТССА СССТА АЛТССТ САЛТССА САЛТССА СССТА САЛТССА СССТА АЛТССТ САЛТССА САЛТССА САЛТССА САЛТССА СССТА АЛТССТ САЛТССА САЛСССА АЛТССА САЛТССА АЛТССА САЛТССА АЛТССА САЛССА САЛТСА САЛТСАЛТСА СА
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29	4,661 169 6,343 6,030 5,390	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCCGGAGGGGCGGTAAGCGGGACTAAGGGCCCCCA CATTTAGCTTTGGTCATGGGTGTGTATAATTGAGGCCCCGA CATTTAGCTTTGATTCCAGGGGCAGTAGGCAGGAGGCGCCGA TTATTTTCCAGAGGACTAAGCACTAAGCAATAGTTAGAGGGTGG [28] GTAGAGTICATCTTAGCAGGGGACT CTCCACTACACATGCAATGCTTGCGGGCATTAGACGGACTAGACGGGCGCCCAAATGTTCCGTGGGGGACTAGACGGGGACTAGACGGGGCACTAGACGGGGCACTAGACGGGCCACAATG CTCCACCGCCCAAATTTTTCCCTTCTGCAGGCGGTTTCCAAAGGAGCCCACATCA 50 CCA TTTTCACCACTACAAAAGTGGCACTGGGGAGCTGGGAGGCGCACAATG CCCCCCCGTGCAAATGTGGAGGGCGTCATGAGGGGACTAGGGGGACTAGGGGGACTAGGGGGGACTAGGGGGGACTAGGGGGCCACATCCAAG 50 CCA TTTTCACCACTACAAAATGTGGACGTCCAATGGTGGGGTAATGATG CCCCCCCGTGTACGAGGCGGTATGCAGGGGGCGTCATGAGGGGAAATG CCCCCCCGGTGGAGGGCGGACGGGGAGGAGGACGACGACGGTATG CCCCCCCCGGTGGAGGGCGCGCACGGCGGCTGTGGGGGAGGAGGACGACGACGGCTTGGGGGGGATGGCCGTCCTGAGGGCACGAATGGTCCAGGGCACGAATGGTCCAGGGCACGAAGGGCAGGAGGACGAACGA	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69 TniC _{HJ} 70	6,305 5,360 4,704 3,956 3,335	Албтаст: тгодоссо 174 САЛАССА АСАТССС доттасса 129 СССССБА тстосас ссстосас ссстосас таластсс 215 САССССБА таластсс САЛАТССС таластсс саботоса 402 ТАЛАССС аттата 402 ТАЛАССС САЛТССС САЛТССС САЛТССС САЛТССС САЛТССС САЛТССС САЛТССС САЛТССС САЛТССС СССТСА 402 ТАЛААСС СССТСА ТСАЛАССС СССТСА ТСАЛАССС СССТСА ТСАЛАССС СССТСА ТСАЛАССС СССТСА ТСАЛАССС СССТСА ТСАЛАССС ТССАССС САЛТССС СССТСА ТСАЛАССС СССТСА ТСАЛАССС СССТСА ТСАЛАССС СССТСА ТСАЛАССС СССТСА ТСАЛАССС СССТСА СССССТСА ТСАЛАССС СССТСА СССССТСА
TniC _{DE} 21 TniC _{DE} 26 ₆₀₀ TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29	4,661 6,343 6,030 5,390	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCCAGGAGGGCAGTAACGAGGCCCATCAGCCCCCC CATTTAGCTTGGCCAGGGGGGCAGTAACGAGGCCCCCCGACCCCTGATCCTGGTAGCGGGGCCCCATGGGGGCCATGGCGCCCCCCGAGGCGCCCCCGAGGGCCTTGCGAGGGGGGGCGGCGGGGGGGG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 68 TniC _{HJ} 70 TniC _{HJ} 71	6,305 5,360 4,704 3,956 3,335	Албтаст: тгобтесс 174 САЛАССА АСАПТССТ GTTTACCA 129 GECCACG 215 САБССТСА 215 САБССТСА 241 ТПАТТСА 241 ТПАТТСА САССТСА 144 ТПАТТСА САССТСА 144 ТПАТТСА 1444 СССТСА 1444 СССТ
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30	4,661 169 6,343 6,030 5,390 4,654	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCCAGGAGGGCCGTAACAGGGCCCTCAC CATTTAGCTTTGGCTCAGGGTGGTGTTATAATTTGAGCAGAT TTATTTTCCAGGACCAGGGCCGTAACGGCGACTGAGCGGCCCC 281 GTTAGGTTCATCTTGGCAGCGGACTTAGACGGATTGCGCGGCGC TTTCGATCACTGTGCGGGGGCGTTGCGAGTGGGATTGCGGGGGCGCCAATTGTCGGGGGGCGCGAATTGGTGCGGGGGGCGGAGTGGGGGGCGGAATGGCAGTGGGAGTGCGGAGTGGGGGCGCACATCA 393 c ctCaCCCAAGTCTAATCCTGGGGGGTTTCCAAAGGGGCCCCACATCA 50 CCAC TTTCGACCACTGCGAAATTGCTGGGGGGTTGCGGAGTGGGGGCCCCACATCA 50 CCAC TTTCGACGACGGGGGGGGGGGGGGGGGGGGGGGGG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69 TniC _{HJ} 70 TniC _{HJ} 71	6,305 5,360 4,704 3,956 3,335 2,393	Албтаст тгодоссо 174 САЛАДСА АСАПТССТ GTTACGA 129 GCCCACG 129 GCCCACG 215 САGGCCT 34 ТПАТПССА СССТАС СССТАС ТААЛССС АЛТТАТТАС ТААЛССС АЛТТАТАС 402 ГОАЛСССТА 402 ГОАЛСССТА АЛААЛССС АЛТАТАТАС СССТАС АЛТАТАСА 402 ГОАЛСССТА 402 ГОАЛСССТА СССТАС АЛТАТАСА 402 ГОАЛСССТА СССТАС СССТАС СССТАС АЛТАСССТА 402 ГОАЛСССТА СССТАС СССССТАС СССТАС СССТАС ССССТАС СССТАС
TniC _{DE} 21 TniC _{DE} 26 _{bol} TniC _E 27 TniC _E 28 TniC _E 29 TniC _E 30 TniC _E 30	4,661 4 169 6,343 6,030 5,390 4,654	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCCGGAGGGGCGATAACGGGCCTCAATCAATC	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69 TniC _{HJ} 70	6,305 5,360 4,704 3,956 3,335 2,393	Албтаст тгодоссо 174 САЛАСАМ АСАГТССТ GTTTACGA 129 GCGCACG 129 GCGCACG 215 САGGCCT 215 САGGCCT 215 САGGCCT 34 ТГТАГТССА САЛТССС САЛТСС ССССА САЛТССС САЛТСС ССССА САЛТССС САЛТССС САЛТССС САЛТССС ССССА САЛТССС САЛТССС ССССА СССА ССССА ССССА ССССА ССССА ССССА ССССА СССА СССА ССССА СССА СССА СССА СССА СССА СССА ССССА СССА СССА ССССА С
TniC _{DE} 21 TniC _{DE} 26 _{bo0} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31	4,661 169 6,343 6,030 5,390 4,654 4,002	AGCTEATTEAGTEAAGTTTAACTGGCCGACATCCATECAATTAAG TTATETGGCCACGAGGGGCGGTAAGACGGGACTAAGGCGCCCCA CATTAGCTTTGGTCATGGTGTGTGTGTATAATTGAAGAGTGG TATTTTTCCAGAGACAAAAGGACTAAGCAATAGTTAGAGAGTGG 281 GTTAGGTTCATCTTAGCACGAGGAC TTATTTTCCAGAGCAATAGTCAGGGACT CTCCACACACACGACAAAGGCACTTAGACGGACTTAGACGGGTCAT CTCGCCGCCGAAATTGTTCCCATGTGGAAGGCCCCCGAATCCAAAA 139 C CTCACCACGTCCAAATTGTCCCTGCGGCGTTTTCCAAAGGAGCCCACAATC 50 CCA 50 CCA TTTTCACCACTACAAAAGGTGGCGTCATGGGAAGGAGCACCACATCA 50 CCA CTCACTGAAGGCAGGGTATGCAGTGGGGTCATGAGGGGACTACGAGG CCCCCCGTGACGAGGCGGACTGGCGGTCATGAGGGGACTACGAAG TTTTCGCCGCCCAAATTGTGGACGTCCAAGGGGGCCACATCA 50 CCA CCCCCTGTACGAGGCAGGGTATGCAGTGTGGGTTCATGAGTGCAA TAGGCATATGGCAGCGTGAGCGTGCGGTGCG	TniC _{HU} 66 TniC _{HU} 67 _{abc} TniC _{HU} 68 TniC _{HU} 69 TniC _{HU} 70 TniC _{HU} 71	6,305 5,360 4,704 3,956 3,335 2,393	Албтаст: тгодотсс: 174 САААДСА АСАТГССТ доттасса 129 СССССА 129 ССССССА 129 ССССССА 215 САСССТСА 215 САСССТСА 174 СААДССС 215 САСССТСА 174 СААДССС 407 ТГААДССС АТТГАТСА 402 ТСАСССТСА 402 ТСАСССТСА 174 СААДСС 2017 СССССТСА 174 ССССТСА 174 СССССТСА 174 ССССТСА 174 СССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 СССССТСА 174 СССССТСА 174 СССССТСА 174 СССССТСА 174 СССССТСА 174 СССССТСА 174 ССССТСА 174 ССССТСА 174 СССССТСА 174 СССССТСА 174 СССССТСА 174 СССССТСА 174 СССССТСА 174 СССССТСА 174 ССССТСА 174 СССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 СССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСА 174 ССССТСТСА 174 ССССТСА 174 СССССТСА 174 ССССТСТСА 174 ССССТСА 174 ССССТСТСА 174 ССССТСА 174 ССССТСТСА 174 ССССТСА 174 ССССТСТСА 174 ССССТСТССТССТСТСА 174 ССССТСТСТСТСТСТСТСТСТСТСТСТСТСТСТСТСТС
TniC _{DE} 21 TniC _{DE} 26 _{bo0} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31	4,661 169 6,343 6,030 5,390 4,654 4,002	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCACGAGGGGCAGTAACGGGCACTAAGGCCCCCA CATTTAGCTTGGCATCGAGGGCCGTAACGGGCCCCCA CATTTAGCTTGGATCCAGGGGCACTTAGGCAATGGCAGGCGCCCA CGCCGCCAATGGTGGCGCGGACTTAGACGGAATGCCGGCGC 281 GTAGAGTCATCTTGCGGGGCACTTAGACGGAATGCCGGCGC TTTCGACCACTGCGACGCGGCGCTGGCAGCGGAGTGCGGGACTGCGGGGCCACATGC CCCCCCACACTGCGAACTGCGCGGCGCTGGCGGAGCGGA	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 68 TniC _{HJ} 70 TniC _{HJ} 71	6,305 5,360 4,704 3,956 3,335 2,393	Албтасст тгобтесс 174 САЛАССА АСАПТССТ GTTTACCA 129 GECCACG 215 САБССТБА СССТСАG 215 САБССТБА 241 ТПАПТСБА 241 САБССТБА ТАЛАТССТ ТСССССБА ТАЛАТССТ ССЛАТСССТБА 402 ТБАСТССА 402 ТБАСТСА 402 ТБАСТСА
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31	4,661 169 6,343 6,030 5,390 4,654 4,002	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCCAGGAGGGCCGTAACAGGGCCCCACA CATTTAGCTTTGGCTCAGGGTGGTGTATAATTGAGCAGAT TTATTTTCCAGGCCAGG	TniC _H ,66 TniC _H ,67 _{abc} TniC _H ,68 TniC _H ,69 TniC _H ,70 TniC _H ,71 TniC _H ,72	6,305 5,360 4,704 3,956 3,335 2,393 975	Албтаст тюбятсс 174 САЛАСА АСАТТССТ GTTACGA 129 GCCCACG 129 GCCCACG 215 САССТЕР 11СТОСАС 215 САССТЕР 215 САСССТСА 215 САСССТСА 14 ТТАТТСС САЛАТССС АЛТТАТАС 102 GCCCCCAC 102 GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
TniC _{DE} 21 TniC _{DE} 26 _{bol} TniC _{EP} 27 TniC _{EP} 28 TniC _{EP} 29 TniC _{EP} 30 TniC _{EP} 31	4,661 4 169 6,343 6,030 5,390 4,654 4,002	AGCTEATTEAGTCAAGTTTAACTGGGCCGACATCCATCEAATTAAG TTATCTGGCCCGGAGGGGCGGTAACAGGGCGCCTAA CATTTAGCTTTGGTCAGGGGGGCGTAAAGCGGCCCCCA CATTTAGCTTTGATTCCAGGACATAGTCAGAAGAGGCCC TTATTTTCCAGGACAAAGCACCTAGCAAGCGAATAGTTAGAAGAGTCG 281 GTTAGGTTCATCTTGGCGGGCACTTAGACGGAATAGCTAGC	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69 TniC _{HJ} 70 TniC _{HJ} 71 TniC _{HJ} 72	6,305 5,360 4,704 3,956 3,335 2,393 975	Албтаст тюбятсс 174 САЛАСА АСАТТССТ GTTTACGA 129 GCCACG 129 GCCACGA 129 GCCACGA 129 GCCACGA 129 GCCACGA 129 GCCCAC 215 CAGGCCT 34 TTTATTGA 215 CAGGCCT 100 CCCCAC 100 CCCC
TniC _{DE} 21 TniC _{DE} 26 _{b00} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31	4,661 4 169 6,343 6,030 5,390 4,654 4,002	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCCGGAGGGGCGGTAAGCGGGACTAAGGCGCCCCA CATTTAGCTTTGGTCAAGGGGGCGGAAGCAGGGACGGACG	TniC _H 66 TniC _H 67 _{abc} TniC _H 68 TniC _H 69 TniC _H 70 TniC _H 71 TniC _H 72	6,305 5,360 4,704 3,956 3,335 2,393 975	Албтаст: тгодстос 174 САЛАДСА АСАТГССТ GTTTACGA 129 GCGCACG 129 GCGCACG 4129 GCGCACGA TTCTGCAC GCGTGCA 215 CAGGCCTC 34 TTTATTG 402 TGAGTGCT CAARICC CAARICC 402 TGAGTGCT 402 TGAGTGCT CCCCAGA 262 GCTTTCAT 262 GCTTTCAT 262 GCTTTCAT CCCCAGA CCCCCCAGA CCCCCAGA CCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCAGA CCCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCCCCCAGA CCC
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 35 _{ac}	4,661 169 6,343 6,030 5,390 4,654 4,002	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCACGAGGGGCCGTAACGGGCCCTCACGCGCCCCC CATTAGCTTGGCACGAGGGGCCGTAACGGGACTCAGCGCCCCCC CATTAGCTTGGATCCAGGGCACTTAGTTAGACGATAGTCAGCGGCCCC TATTAGCTTGGATCCTGGCGGCACTTAGCAGGATTGGCAGTGGCGC 281 GTAGAGTCATCTTGCGCGGCGCTTGCAAGCGGATTGGCAGTGCGGCGCATTGCGGGGGCGCATTGGCAGGGGGGCGCGGACTTGGCAGGGGGATTGGCAGTGGGGCCCAAAT TTCGTCACCACTGCAAATTGCCTGGGGGCGTTGCGAAGGGCCCACATCA 50 CCAC CTCACTCAAGTCTAATCCTGGGGCGTTTCCAAAGGAGCCCACATCA 50 CCAA TTTCCACCACTACAAATGGGCGGCACTGGGGGGTCATGGGGGCCCACATCA 50 CCAA TTTCCACCACTGCAAATTGTGCCGGCGCCTCGGGAGGCCGCACATCA 50 CCAA TTTCCACCACTGCAAATTGTGCCGGCGCTCTGGGAGGCCCCACATCA 50 CCAA TTTCCACCACTGCAAATGGGCGCGCACTGGGGGGTCATGGGGGGGCCCCCACTCA 50 CCAA TTTCCACCACTGCAAATGGGCCGCCACTGGGGGGGCCCCCACTCA 50 CCAA TTTCCACCACTGCAGGCGTGGCGTTCCGAAGGGGGGGGGG	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 68 TniC _{HJ} 70 TniC _{HJ} 71 TniC _{HJ} 72	6,305 5,360 4,704 3,956 3,335 2,393 975	Албтасст тгобтесс 174 САЛАССА АСАПТССТ GTTTACCA 129 GECCACG 215 САБССТБА СССТСАG 215 САБССТСА 215 САБССТСА 215 САБССТСА 215 САБССТСА 34 ТПАТТПСА САЛАТССС АТТАТТАС САЛАТССС АТТАТАС СССТАА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА СССТАА 402 ТБАСТСА СССТАА 402 ТБАСТСА СССТАА 402 ТБАСТСА 402 ТБАСТСА СССТАА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА 402 ТБАСТСА 402 ТСАСССА 402 ТБАСТСА 402 ТБАСТСА 402 ТСАССА 402 ТСАССА 402 ТСАССА 402 ТСАССА 402 ТСАСТСА 402 ТСАССТСА 402 ТСАССА 402 ТСАССА 402 ТСАССА 402 ТСАССА 402 ТСАССА 402 ТСАССТСА 402 ТСАССА 402 ТСАСА 402 ТСАСА 402 ТСАССА 402 ТСАССА 402 ТСАСА 402 ТСА
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31 TniC _{EF} 35 _{cc}	4,661 169 6,343 6,030 5,390 4,654 4,002 324 6,182	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAA TTATCTGGCCACGAGGGGCCGTAACGGGCCCTACCTGGTCATCCAGGCCCCC CATTTAGCTTTGATTCCAGCAAATGCCGAAGCCGAGCCCCACCTGGTCCATTGGTGATTGGTGGCGCGCCCGAATGGCTATGGTGTGACGGGGGCCCGAATGGCAGGCGGCCCGAATGGCATGGGCGGCGCGCATTAGACGGGACTTAGCGGGGGGCGCCCGAATGCTAGCGGGACTTAGACGGGACTTAGCGGGGGCCCCAATGCT CTCCCCCCGCCAAATGTTCCCTGCGGCGGCGCACTGGGGGGCCCCCAATCA 139 C CTCACTCAAGTCTAATCCTGGGGGGTTTCCAAAGGGGCCCCACTCA 50 CCAC TTTCCACCACGCGAATGCCGGGGGGTTGCCGGAGTCGGGGGCCCCACTCA 50 CCAC TTTCCACCACGGGCGGATGGCGGTCCGGAGTGGGGGCCCCCACTCA 50 CCAC TTTCCACCACGGGCGGATGGCGGTCCGGAGGCGGAGGGGGGCCCCCACTCA 50 CCAC CCCCCTGTACAGGCCGGAGGGGGGGGGGGGGGGCGCGGAGGGGGGGCCCCCTTCCACGGGGGGGG	TniC _H ,66 TniC _H ,67 _{abc} TniC _H ,68 TniC _H ,69 TniC _H ,70 TniC _H ,71 TniC _H ,72	6,305 5,360 4,704 3,956 3,335 2,393 975	Албтасст тгодоссо 174 САЛАДСА АСАПТССТ GTTACGA 129 GCCCACG 129 GCCCACG 215 САGGCCTC 34 ТПАТПССАС СОДИТСА 126 СССССТА 127 САGGCCTC 126 ССССТА 126 ССССТА 127 САGGCCTC 126 ССССТА 127 САGGCCTC 126 ССССТА 126 ССССТА 127 ССССТА 128 СССТА 128 СС
TniC _{DE} 21 TniC _{DE} 26 _{bol} TniC _{EP} 27 TniC _{EP} 28 TniC _{EP} 29 TniC _{EP} 30 TniC _{EP} 31 TniC _{EP} 35 _{bol} TniC _{EP} 35 _{bol}	4,661 4 169 6,343 6,030 5,390 4,654 4,002 324 6,183	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCCGGAGGGGCGGAAAAGCGAAGCCTGATCCATGGCGCCCC CATTAGCTTTGGTCCAGGGGCGCAAAAGCCGAAGCCTGATCCTGTGGA TTATTTTCCAAGGCGTGCTGTCCGAATGGTATAATGACAATATCAC TTTCGTACACATGCAACTCTTCCCAATGGTATAATGACAATATCAC TTTCGATCACTGCTAATCCTGCGGCGCACTTAGACGGGATTGCGGGGCC CCCCCGTCCCAAATTGCTTGCGAGGCGCACTAGGCGGAATGCCGGGCC TTCCACCAAGTCTAATCCTGGGGCGTTTTCCAAAGGAGCCCACATCA 50 CCC TTCCACCAAGTCTAATCCTGGGGCGTTTTCCAAAGGAGCCCACATCA 50 CCC TTTCCACCACTGCAAATTGTGCCGTGCGTCCGAATCCTGG CCCCCCTGTACAAGGCGGATTGCCGAGCCGA	TniC _{HJ} 66 TniC _{HJ} 67 _{abc} TniC _{HJ} 68 TniC _{HJ} 69 TniC _{HJ} 70 TniC _{HJ} 71 TniC _{HJ} 72 TniC _{HJ} 73	6,305 5,360 4,704 3,956 3,335 2,393 975 473	Албтаст тюбятсс 174 САЛАСА АСАТТССТ GTTTACCA 129 GCCACG2 129 GCCACG2 129 GCCACG2 129 GCCACG2 215 CAGGCCT 34 TTTATTG 215 CAGGCCT 126 CCAGCCT 126 CAGGCCT 126 CAG
TniC _{DE} 21 TniC _{DE} 26 _{bo0} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31 TniC _{EF} 35 _{ac} TniC _{EF} 35 _{ac}	4,661 4 169 6,343 6,030 5,390 4,654 4,002 324 6,183	AGCTEATTEAGTCAAGTTFAACTGGCCGACATCCATCEAATTAAAC TTATCTGGCCACGAGGGGCCGTAACTGGGCACTACCATGATCAAGGCCCCCA CATTTAGCTTGGCACGAGGGCCGAAACCCCACGCATGATCCTGGCGCCCCCATGGTGGCTGCATGGGTGGTGTGATGAGTTGGACGGCGCCCCC CATTTAGCTTGCATGGGGGCACTTAGCAGAATAGTCACAGGCCCCCCCC	TniC _H 066 TniC _H 067 _{abc} TniC _H 068 TniC _H 068 TniC _H 069 TniC _H 070 TniC _H 070	6,305 5,360 4,704 3,956 3,335 2,393 975 473	Албтаст: тгобсос 174 САЛАССА баттаста 129 СССССС састеса са
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31 TniC _{EF} 35 _{ac} TniC _{FF} 35 _{ac}	4,661 169 6,343 6,030 5,390 4,654 4,002 324 6,183	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCATGGGGGGCGGTAATCAGGGCCCCATCATTAGGTGGCCATGGGGGCCCTAGGGGGGCCCTGGAGGGCGCCATGGGGGCCCCAATGGTAGCAGGGCCCCGGGGGGGG	TniC _H 66 TniC _H 67 _{abc} TniC _H 68 TniC _H 68 TniC _H 69 TniC _H 70 TniC _H 71 TniC _H 72 TniC _H 73	6,305 5,360 4,704 3,956 3,335 2,393 975 473	Албтаст тюбятсс 174 САЛАСА АСАТТССТ GTTACCA 129 GCCCACG 215 САСССТА 129 GCCCACG 215 САСССТА 215 САСССТА 24 ТПАТТСА 34 ТПАТТСА 34 ТПАТТСА 402 ТАСАТСС САЛАТССС АЛТААТСС САЛАТССС АЛТААТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА СССААА ССССАА 402 ТАСАТТСА СССААССТТ ССТААТССС АЛТААТСА СССААССТТ ССТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТАСАТТСА 402 ТССААССТТ 402 ТАСАТТСА 402 ТАСАТАСС ТАСАССТС 402 ТАСАТСА 402 ТАСАТАСС 402 ТАСАТАСС 402 ТАСАТАС 402 ТАСАТАС
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31 TniC _{EF} 35 _{ac} TniC _{FG} 37	4,661 4 169 6,343 6,030 5,390 4,654 4,002 324 6,183 5,772	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCACGAGGGGCCGTAACGGGGCCTCACTCGATCCATGGCCCCC CATTTAGCTTTGGTCAGGGTGTGTGTGTGATAATTGAGCAATATCTAC TTATTTTCCAGGACAAAGCCCTAGCAAAGCACTAGGCGCCCCC 281 GTTAGGTTCATCTTGGCGGGCACTTAGACGGAATTAGGCGATCACGGGCC CCCCACACTGTGCGCGGCGCCTGGCACGAGCGAATAGTTAGACAGATACTCAC TTCGCACCCGTCCCAAATTGCTGCGGGCGCGCACTAGACGGGATTGCGGGCCCCAATCA 399 C CTCACTCAAGTCTAATCCTGGGGGGTTTCCAAAGGAGCCCACATCA 50 CCAC TTTTCACCACTACCAAATGTGCCGTGCGTTCCGAAGGCGCACATCA 50 CCAC TTTTCACCACTACCAAATGTGCCGTGCGTTCCTGGGAGGCCCACATCA 50 CCAC TTTTCACCACTACCAAATGTGGCGTCCCGCAGTCGGAGTCCGGAGTCCCAA TTTTCACCACTACTAATCCTGGGGGTTTTCCAAAGGAGCCCACATCA 50 CCAC TTTTCACCACTACCAAATGTGCCGTGCGTTCATGAGGGCCCACATCA 50 CCAC TTTTCACCACTACCAAATGTGCCGTGCGTTCATGAGGGCCTCATGTC ACTACCACTACTTCCAAGGCTTAACGCCACACTTGTGTAAATGAGT TCCTTGAGCCACTGCAGTCCGGGGAGGAGACACAGGTTGTGGC 265 CTGTGTATCATGGAGTTCCGAGGGAGAGACACAGGTTGTGCC CCCCCTGTACAGGCTTCCGGGGGAATGGCCACTTTGTGCGTCAAATGTGCA CTTTTAGTGCGCCACTAATGGCACTGATGCGCTTTCCGAGGGCCTCAAT CTTTTAGTGCGCCACTAATGGCATGAATGCCACTCTGGTGCGTCAAATGGC CCGGAAATGGCGGCACTAAAGGCCTGACTGCGGGTGCGTCAG CCGGGAATGTGCGGCGCCACAACGGCCACTTGCGCGGGCACGAATGGCCTTTAG CCGGGAATGTGCGGCGCCACAACGGCCACTGGGCGCCACTA 255 ATAACGACTGGGGGCCCCCGGCCACTGCGGCGCGCCACTA 255 ATACGGGGGGCGCCCTGGCACCAACGGCCCACTGGGCCGCGGGGGCCCCCGGGGGCCGCCGCGGCCCCCGGCCCC	ТпіС _н ,66 TпіС _н ,67 _{асс} TпіС _н ,68 TпіС _н ,69 TпіС _н ,70 TпіС _н ,71 TпіС _н ,72 TпіС _н ,73 TпіС _к ,82	6,305 5,360 4,704 3,956 3,335 2,393 975 473 1,693	Албтаст тюбятсс 174 САЛАСАА АСАПТССТ GTTACCA GTTACCA GCCCACG 215 САССССА 215 САССССА 215 САССССА 34 ТПАЛТСС ТААЛССС АЛТАТАССТА 402 ТСАССССА 402 ТСАССССА 402 ТСАССССА 402 ТСАССССА 402 ТСАССССА 402 ТСАССССА 402 ТСАССССА 402 ТСАССССА 402 ТСАСССА 402 ТСАСССА 402 ТСАСССА 402 ТСАСССА 402 ТСАССА 402 ТСАССАС 402 ТСАССАС 403 ТСАСА 404 ТСАСА 405 ССТТСА 405 ССТСА 405 СССА 405 ССС
TniC _{pE} 21 TniC _{pE} 26 _{b0} TniC _{EP} 27 TniC _{EP} 28 TniC _{EP} 28 TniC _{EP} 29 TniC _{EP} 30 TniC _{EP} 31 TniC _{EP} 35 _{ac} TniC _{FQ} 37 TniC _{FQ} 38 _{ab} TniC _{FQ} 38 _{ab}	4,661 4 169 6,343 6,030 5,390 4,654 4,002 324 6,183 5,772 5,381	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCCGGAGGGGCGGTAAAGGGGCCCTAACGCGCCCCA CATTTAGCTTTGATTCCACGAGCAAATGCCGAAGCCTGATCCTGTGGA CGGCGTCCATTGGTGGTGTCATGGTGTGTTATAATTGACAATATCAC TTATTTTCCAAGGCACTAAGCAAAGCA	ТпіС _н ,66 ТпіС _н ,67 _{аbc} ТпіС _н ,68 ТпіС _н ,69 ТпіС _н ,69 ТпіС _н ,70 ТпіС _н ,71 ТпіС _н ,72 ТпіС _н ,72 ТпіС _н ,73 ТпіС _н ,82	6,305 5,360 4,704 3,956 3,335 2,393 975 473 1,693	Албтаст тюбятсс 174 САЛАСА АСАПТССТ GTTTACGA 129 GCCACGG 129 GCCACGG 215 САGGCCT 215 САGGCCT 215 САGGCCT 34 ТПАЛТТG СССТА 402 ТБАЛТСС САЛАТСС АЛТАТА 402 ТБАЛТСС СССТА 402 ТБАЛТСС СССТА 402 ТБАЛТСС СССТА 402 ТБАЛТСС СССТА 402 ТБАЛТСС СССТА 402 ТБАЛТСС СССТА 402 ТБАЛТСС СССТА 402 ТБАЛТСС СССАА 402 ТБАЛТСС СССАА СССССА ССССАА СССССА ССССАА ССССАА СССССА ССССАА СССАА ССССАА ССССАА ССССАА ССССАА ССССАА ССССАА ССССАА СССАА ССССАА СС
TniC _{pE} 21 TniC _{pE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 30 TniC _{EF} 31 TniC _{EF} 35 _{ac} TniC _{FG} 38 _{ab}	4,661 (169 6,343 6,030 5,390 4,654 4,002 324 6,183 5,772 5,381	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCACGAGGGGCCGTAACTGGGCACTAGGCGCCCCA CATTAGCTTGGCCAGGGGGCCGTAACTGGGCACTGAGGCGCCCCA CGCGCGCATTGGGGGGCCGCAGCTGAGCGGGCGCCCCACTAG CGCGCGCATGGGGGGCGGCGGGGGGGGGG	TniC _H 66 TniC _H 67 _{abc} TniC _H 68 TniC _H 68 TniC _H 70 TniC _H 70 TniC _H 71 TniC _H 72 TniC _H 73 TniC _H 73	6,305 5,360 4,704 3,956 3,335 2,393 975 473 1,693	Албтасст тгобтесс 174 САЛАССА САЛАССКА 129 ССССССА ССССССА 215 СЛОСССТА 215 СЛОСССТА 24 ТПАТПСЕ 34 ТПАТПСЕ САЛАССССТА 1402 ТСЛОССТА 402 ТСЛОССТ
TniC _{pE} 21 TniC _{pE} 26 _{bo} TniC _{EF} 27 TniC _{EF} 28 TniC _{EF} 29 TniC _{EF} 30 TniC _{EF} 31 TniC _{EF} 35 _{ac} TniC _{FG} 37 TniC _{FG} 38 _{ab}	4,661 169 6,343 6,030 5,390 4,654 4,002 324 6,183 5,772 5,381	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCCAGGAGGGCCGTAACACGGCCCCCATCATTAGCTTGGCATCGGGGCCCCAA CATTTAGCTTTGGTCAGGGGGGCCGTAACGGGCCCCCAGGCGCCCC CATTTAGCTTGGTCAGGGGGGCGGACTTAGGCAGGGGACTTAGGCGGCGCCAATGTTGCGGGGGGCGCGAATGTGCGGGGGGGG	TniC _H ,66 TniC _H ,67 _{abc} TniC _H ,68 TniC _H ,69 TniC _H ,70 TniC _H ,71 TniC _H ,72 TniC _H ,72 TniC _H ,73 TniC _H ,82	6,305 5,360 4,704 3,956 3,335 2,393 975 473 1,693	AAGTACC TTGGTCCC 174 CAAAGCA ACATTCCT GTTACGA 129 GCCCACG 129 GCCCACG 215 CAGCCTC 241 CAGCCTC 34 TTTATTG 34 TTTATTCC CAAATCCC AATTATCC CAAATCCC AATTATCC CCCCAC 210 AATTATCC CCCCAC 210 AATTATCC CCCCAC 210 CACTTCC CCCCAC 210 CACTTCC CCCCAC 210 CCCCCC 210 CCCCCC 210 CCCCCC 210 CCCCCC 210 CCCCCC 210 CCCCCC 210 CCCCCCC 210 CCCCCCC 210 CCCCCC 210 CCCCCCC 210 CCCCCCC 210 CCCCCCC 210 CCCCCCC 210 CCCCCC 210 CCCCCCC 210 CCCCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCCC 210 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
TniC _{DE} 21 TniC _{DE} 26 _{bo} TniC _{EP} 27 TniC _{EP} 28 TniC _{EP} 29 TniC _{EP} 30 TniC _{EP} 31 TniC _{EP} 35 _{ac} TniC _{FO} 37 TniC _{FO} 38 _{ab}	4,661 4 169 6,343 6,030 5,390 4,654 4,002 324 6,183 5,772 5,381	AGCTEATTEAGTCAAGTTTAACTGGCCGACATCCATCEAATTAAG TTATCTGGCCCGGAGGGCCGTAAACGGGCCCTCATCCGATCAGGCCCCC CATTTAGCTTTGGTCAGGGTGTGTGTGTGTGTGTGTGATGATGAGGCCCCATGGGGGCCCTATGGTGTGGCGGGGGGCCGAAGTGGCGGGGGCCCTGATGGGGGGGG	TniC _H ,66 TniC _H ,67 _{abc} TniC _H ,68 TniC _H ,69 TniC _H ,70 TniC _H ,71 TniC _H ,72 TniC _H ,73 TniC _H ,82	6,305 5,360 4,704 3,956 3,335 2,393 975 473 1,693	Албтасст тюбятсс 174 САЛАСАА АСАПТССТ GTTACCA GTTACCA GCTCCAG 215 САССССТА 215 САССССТА 215 САССССТА 34 ТПАЛТСС САЛАТСС САЛАТСС САЛАТСС АЛТАТАСА 402 ГОЛОВО 202 ССТТСА СССССТА 402 ГОЛОВО 402 ГОЛОВО ССССАС СССССССАС СССАС ССССАС ССССАС ССССАС ССССАС СССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС СССАС СССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС ССССАС СССАС ССССАС ССССАС ССССАС ССС

	CCTTGTCTCCCCCACCCAGCCACACACTGGCAGAGACAGTCTG
	GAATCCAAAGTCACTTTCATTCAGCTGGGTGAAAGAACGTTTTCCG
	TATGTCCAGGAACTGGATCTTCATCGTGGGGGGGGGCTGCGTTAGTGC
343	CACTGACAGGATGAGACACGAACCAAAAT
	TATTAACGGCACATTTATGAACAATCAAATGGCCCTCGTTAAAATT
	TATTGACGGGCATAAAATCACGAAGGCCCACAAGCTGAAAAAAA
111	GCTCCATGATTTGGGCTGCTT
	GCGCATTGATCCACTGTACAGTTTTTTGCAGGAGTAAATATAATCAC
	A ATTACCTGCCTGATTGTTCCATGGCTAGATAAACTCCTAGAAAT
172	CACATACAGCCCATATAATAATCCGATGCATGTAAA
	TTATTAACGGCACATTTATGAACAATCAAATGGCCCTCGTTAAAAT
64	TTATTGACGGGCATAAAA
29	GACAGAGATGGATTACACCATCAAATAGT
10	TTTATGAACAATCAAATG
10	
13	TIGITITATTIGI
	AAATTGCCTTTTTGTGGTGCCAAACAATACGGACAGGATGCTGTGA
	GCCAGTTTTACAGCCCCTCTTGGAGTTCGGCTGTTTGTCTCAAATGC
	AATGACGAACAAAGCAAACTAGACTAACTGGCTAGACGTCTGGGC
211	TAAATGACTTTATGGTTTTAATGGACG
	CTAGATGACGCTGTTGCTCCACGTTTTGAGGCGAGTTACCCAAGGG
	TGCTGCTGCAGCTCTGTGGCTTGGCTGAAAAATGAAGAACAACAT
1/0	AACAGGCCACAGA
143	
27	ACATTITITIAATTOTAAATTOAAAT
	CTATOTOTAAAAACGCTAGCAGCAGAAAAAAAAAAAA
	AAAACCTTACTGTGTATTTTCTGCAGCCTTGGAGCTGCGTGAGTGT
	ATAGTGCGCGATGTCATTGCAGCAAACCATCAGATGTTAAATTTTA
	CGAACTCCTGCGTCTCTGAGATTTACTGCGTTTCCACATCGGTTTTA
224	CGGGGICACTATAAATGGGAACCCTGTATTCACACGTCGTG
	I I A IGAA IAATACAGUUUUUUGAGGTGCACATGCGTAGGCCCCA TACGTCTGAGCGCTCTCTGAAAGGATGAGGGCTATGGCTAGCCCCT
	GGGGGCGCCCCTGGCGGGGGGGGGGGGGGGGGGGGGGGG
	AAGGAAAAAGAAAGAAAAGAGCAGCGTCTGTGACTGTGCCGGTC
	GAGCAAGCCCAGCTAACGCGCAAAAAAAAAAAAAGCACATGCCATG
463	AGCCGGGTTTGAGCCTGCACAAAGCTCGGGG
	AGAGTGGCCCCATAAACAGATGAAGAGTCACAGGGAGTCAGAGC
	GCGTTAACTTTATGACCATCCTTTCATTTTTTTTTGTCAAGAGGGAAC
167	CCAAAATCCCTCCAATTTTGCTGTCATAAA
	TCAGACCCTGTTTTTTTTTTTTTTTTATAGGATGACCAGGGAAATGCAATC
	GTTGAAATCCTTTGATGCTACCTAAACCTGGGGAAATTGCAATAGA
	GATTCCTGAGCGAGGAGATTTCAGATGTTTTAAATTTTAAAGTGTC
4 4 6	(TATA II A
146	CIATAICA
146	
146	GTGTGTCTGTATTTTTACCACACGGTTGCTATTACCAATAAAGTTGA AAGTACCTGCTGTAAAACTTTATTGGCGGGTGTTGTATATAACCAGCA
146	CTATATICA GIGIGICTIGTATTITTACCACACGGTIGCTATTACCAATAAAGTIGA AAGTACCTGCTGTAAACTITATTGGCCGGTGTIGTATATAACCAGCA TIGGTCCCATCCGGCATCITTIGTIGTGGATGCCAGCGCGCGCGCGCGCGCGCGCG
146	CTATALCA GTGTGTCTGTATTTTACCACACGGTTGCTATTACCAATAAAGTTGA AAGTACCTGCTGTAACTTTATTGGCCGTGTGTGTATATAAACCAGCA TTGGTCCCATCCCCCACTTTTGGGCCGCGCAGCCCGCCAGG CAAAGCACCTCTCCCCCCAGCCCTAAAACTAGTGT
146 174	CTATALCA GTGTGTCTGTATTTTTACCACACGGTTGCTATTACCAATAAAGTTGA AAGTACCTGCTGTAAACTTTATTGCCGGTGTGTGTATATAAACCAGCA TTGGTCCCATCCGCACTTTGTTCTGGGATCCCAGCCTGCCCCAGG CAAAGCACCTCTCCCCCCAGCCTAAAACTAGTGT
146 174	CIATALCA GIGIGICIGITATITIACCACACGGITIGCTATTACCAATAAAGTIGA AAGTACCIGCIGITAAACTITATIGGCGGIGITIGTATATAACCAGCA IIGGICCCCAICCCCAICTITIGTICIGGATCCCAGCCIGCCCAGG CAAGCACCICICCCCCAGCCCTAAAACTAGTGI ACATICCIGGITIGTICAAGGAGAAATTIACAGCIGAGTAATAAAA GUTTAGGCCCGAGTCCTUTGGCGATCGAGTGACTAGTGG
146 174 129	CIATALCA GIGIGICIGTATITITACCACACGGTIGCTATTACCAATAAAGTIGA AAGTACCTGCTGTAAACTITATIGGCGGTIGTIGTATATAAACCAGCA TIGGICCCATCCCCCCACCTTIGGGCGCGCAGCCCAGG CAAAGCACCTCCCCCCCAGCCTAAAAACTAGTGT ACATTCCTGGTIGTTAAAGGAGAAATTTACAGCTGAGTAATAAAA GTTTACGACTAGATCCTCTCCGCCATTGGCCTGACTAACACGTG GCCACGTCTTAGAACTGAACTTAGACCTGAGT
146 174 129	СТАТАТСА GTGTGTCGTGTATTTACCACACGGTTGCTATTACCAATAAAGTTGA AAGTACCTCGCTGTAAACTTTATTGCCGGTGTGTGTATATAACCAGCA TTGGTCCCATCGCCATTTTTGTTCTGGGATCCCAGCCGCCAGG CAAAGCACCTCTCCCCCAGCCGCAATAAACTTACCAGCTGAGTAATAAAA GTTTACGACTGGTTGTTAAAGGAGAAATTTACAGCTGAGCTAACAACGT GCCCACGTTCTATGAACATGAACTTTATGCTGTTGTCT
146 174 129	CIATALCA GIGIGICIGITATITTACCACACGGITIGCIATTACCAATAAAGTIGA AGATACCTECGIGTAAACTITATIGGCGGIGITIGTATATAACCAGCA TIGGICCCATCCGCAACCITATIGTCGGGATCCCAGCCAGG CAAACCACCTCCCCCCAACCCTAAAAACTAGTGT ACATCCCTGGITIGTAAAGGAGAAATTACAGCIGAGTAATAAA GITTACGACTGACCTCCCCCCCACGCCTGCCTCACGAGCAACCACGGG GCGCACGITCTATGAACATGAACTITATGCTGTIGTCT TGACCTGACCTACAGCCCATAGCCACATTIGTIGCGCAGGCCATGGT
146 174 129	GIGIGICIGTATITITACCACACGGTIGCTATTACCAATAAAGTIGA AAGTACCTGCIGTAATTACCACACGGTIGCTATTAACACCAGA TIGGICCCATCCGCACITTATGGCCGIGTIGTATATAACCAGCA TIGGICCCATCCGCCACITICIGGGCTCCACGCCGCGCAGG CAAAGCACCTCCCCCCCAGCCTAAAACTAGTGT ACATTCCTGGTIGTIGTAAAGGAGAAATTTACAGCTGAGGTAATAAAA GTTTACGACTAGATCCTCCCGCCATGGCCTCCACGCGAGCAAGGG GCCCACGTTCTAGAACATGAACTTATCCTGTIGTCCCACGCCACG
146 174 129	GIGIGICIGIAITITIACCACACGGITIGCIAITIACCAATAAAGTIGA AGATACCTECIGITAACTTAATGGCGGIGITIGATATAACAGCA TIGGICCCATCCGCATCTITIGTICTGGGATCCCAGCCIGCCAGG CAAAGCACCTCTCCCCCAGCCGACATAAAACTAGTG ACATICCTGGTIGITIAAAGGAGAAATTIACAGCTGAGTAATAAAA GITIACGACTGGATGTIAAAGGAGAAATTIACAGCTGAGCTG
146 174 129	CIATALCA GIGTIGCIGTATITTACCACACGGITIGCIATTACCAATAAAGTIGA AAGTACCTGCIGTAAACTTATTGGCGGIGTIGTATATAACCAGCA IGGICCCAICCGCAICTITTGTCIGGGATCCCAGCCIGCGCAGG CAAAGCACCTCICCCCCAGCCTAAAAACTAGTGT ACATCCCTGGITGTTAAAGAGAGAAATTACAGCTGAGTAATAAA GITTACGGCTGAGACCTCTCGGCCCACHTGGTGCAGCAGCGAGG GCGCACGTTCTATGAACATGAACTTATGCTGTIGTCT TGACCTGACCTTACGGAGCGCAGCACTTGGTGCCCCACTGCG GCCCCAGCACTTACGCACCATTGGTGCCGCCACCACTGGT GCCCCAGCCACTTAGCGCACACTTGGTGCCCCACGCG GCCCCAGCACCATTAGCGCACACTTGGTGCCCCACGCG GCCCCAGCACCATTAGCGCACACTTGGTGCCCCACGCG GCCCCAGCACCATTAGCGCACACTTGGTGCCCCACGCGC GCCCCAGCCCTTACGCACCATTGGGAGCCACTGGTGCCCCACGCG GCCCCAGCCCTTACGCACCATTGGGAGCCACTGGCTGCCCACGCCG GCCCCGGCCCTACGCCCTGCCCCCACTTGGGGCGCCCCCGCTGCCCAC GGCCCGGCCCGCACTTGCGGCCCCAATTGGTGCCCCCACGCC GCCCCGGCCCGCCCGCCGCCGCCCCCCCCCC
146 174 129 215	CIATALCA GIGIGICIGIATITITACCAACACGGITIGCATTACCAATAAAGTIGA AAGTACCIGCIGTAAACTITIATIGGCGGIGIGITATATAACCAGCA GIGGICCCAATCCGCAICTITIATIGGGATCCCAACCAGG CAAGCACUTCCCCCCAGCCTAAAACTAGTGT ACATCCIGGITIGITAAAGGAGAAATTIACAGCTGAGGAACACGG GCCACGTICTCCGCCATIGGCCGCAGTGAGCTGAGCACCGG GCCACGTICTATGAACATGAACTTATGCIGTIGIGCCCAGCGCAGG GCCACGTICTATGAACATGGAGGGAGGCACCTGGTGCCCCACTGG GCCCACGTICTAGAACTGAACTTATGCIGGGCGCGCCCACTGG TICIGACCTGACCAGCCACATTIGTICCGCAGCCACTGG GCTCCAGACAGCCACTAGCCCACATTIGTICCGCAGCCACTGG GCTCCAGACAAATTACCACTGATTGGAGCCGCCTGCGCCCCACTGCA GCTCCAGACGCCCCGGCGCCGCCGCCGCCGCCGCCCCCCCC
146 174 129 215 34	CIATALCA GIGIGICIGTATITTACCACACGGITGCTATTACCAATAAAGTIGA AGTACCTCRCGTGTAAACTITATGGCGGIGTIGATATAACCAGCA TIGGICCCATCGCGTGTITTIGTICTGGGATCCCAGCCIGCCAAGG CAAAGCACCTCTCCCCCAGCCCTAAAAACTAGTGT ACATTCCTGGTIGTIAAAGGAGAAATTACAGCTGAGTAATAAA GITTACGACTAGATCCTCTCGGCCATTGCTCCCACCTGACCACGG GCCCACGTTCTACAGCCCATAGCCCACATTGCTGCCCACCGACCACGG GCCCACGTTCTACAGCCCATAGCCACCTTGGTGCCCCACTGC TCCGGACCTACAGCCCATAGCCACCCTTGGTGCCCCACTGC GCCCACGCACTGAGCCCATAGCCCACCTTGGTGCCCCACTGC GCCCACGCACTGACGCCATAGCCCACCTTGGTGCCCCACTGC GCCCCGCCCACACTTAGCCCACATTCGGACCGCCTGCCCCACTGC GCCCGACGCACTGAGCCCATGCCCCCCCCCCCCCCCCCC
146 174 129 215 34	CIATALCA GIGIGICIGITATITTACCACACGGITIGCIATTACCAATAAAGTIGA AGATACCTECIGITAAACTIATIGACGGIGITIGIATATAACCAGCA TIGGICCCATCCGCAACCITATIGACGGIGITIGIATATAACCAGCA GGICCCATCCCCCCAACCCAACAACTAGTGI ACATICCCTGGITIGITAAAGGAGAAATTACAGCTGAGTAATAAA GTITACGACTGACACTCCTCCGCCCATIGGICCCCAGGCACCACIGGI GCGCACGTICTATGAACATGAACTITATGCTGTIGICT TGACCTGACCTACAGCCCATAGGCACACTITGITGCCCACGCCACTGGI GCCCCAGACGACTACCCACGCACATTICGAGCCCACTGGI GCCCCAGACGACTACCACGCACATTICGAGCCCCCTGCGCCACGCAC CGCCCGACGCACTAGCCCACATTICGGACGCCCCCCCGCCCCCACGCA CGCCCGACGCACTAGCCCACGACTTICGGACCCACGCCCCCCCCCC
146 174 129 215 34	CIATALCA GIGIGICIGTATITITACCACACGGITIGCATTACCAATAAAGTIGA AAGTACCIGCIGTAAACTIATIGGCGGIGGITGTATATAACCAGCA TIGGICCCACACCGCCATATIGGCGGCGGIGCAGCACGG CAAGCACCICICCCCCCACCCTAAAACTAGTGT ACATICCIGGTIGTAAAGGAGAAATTIACAGCIGAGTAATAAA GITTACGACTGATCCTCCCGCCATTIGGCGCCGAGCGACCACGG GCCCACGTICATGACCTGGACCTATIGTIGCGCAGCCATTIGT TICGGCCCACGTICAGCCACACTTIGGGGCGCGCCATGGT TICGGCACCTTITIGGATGGGGGGCGCACGCACGGGCCCAGGC GCTCCAGCACATTAGCCCAGCATTIGGGGGCCGCCAGGCCATGGT CIGCGCACGTITAGGACGGAGCAATTACCA GGTGCCAATAAATTACACTGGAGCAGCACGTCGGCCCCACGCA GCTCCAGCCCAGCAGCAGCAATTACCA CIGGTGCCAATAAATTACCACGGAGCAGCATGGT TICATIGTAAGCAAAAAAAAACGGCTTT TAAATCCTGGTTTTAAACGCAGGAAAACCGCGGGCACTATGGTT TAAATCCCTGGTTTTTAAACGCAGGAGAAAACCGCGGGCGCATTGGTTT TAAATCCTGGTTTTAAACGCAGGAGAAACCGCGGGCGCTCTTGGTTT TAAATCCTGGTTTTTAAACGCAGGAGAAACCCGCGGGCGCATTGGTTT TAAATCCTGGTTTTTAAACGCAGGAGAAACCGCGGGCGCGCTCTTGGTT
146 174 129 215 34	CIAIAICA GIGIGICIGTAITITACCACACGGITIGCIATIACCAATAAAGTIGA AGTACCTECIGTIAACTITATGGCGGIGITIGATATAACCAGCA TIGGIECCAICCGCAITITIGITICIGGGAITCCAGCCIGCCAGG CAAAGCACCTCICCCCCAGCCIAAAACTIAGGT ACATICCIGGITITIAAAGGAGAAAATTACACGCIGGGTAATAAA GITTACGACTAGAICCICTICGGCCATIGGCIGCACCAGGG GCCACGTICTAGAACATGAACCTITATGCIGTIGCCI CAGCCIGACCTACAGCCCATAGCCACACTIGGITIGCGCCACCGCG GCCCACGACGACTAGCCCCATAGCCACCCGCGICGCCCACTGG GCCCACGACCATAGCCCACATIGGIGCGCCACCGCCGCCCCACTGG GCCCACGACGACTAGCACGCACATIGGIGCGCCCACCGCGCCGCCACT GGCTCGAACAACATTAGCACACTICGGACCGCGCCCCACTGG GCCCAGCACTAGCCCACATIGGCGCCACCACCGCGCCCCCACT CGGTIGCAATAACTICACCACTTICGACCGCGCCCCCACT CGGTCGCACGACTAGCCCACAATTGCA CAGGCCCTGGACGCACACATTAGCA TITATITIGAATIGTAAGCAAAAAAAAAACGTITT TAAATCCTIGTITTAAATGCGAGGAGAAAACCGCGGGCTCATIGTTT TGCCCTGAAGTGTITTAAAAGCGAGGAGAAAACCGCGGGCTCATIGTTT TGCCCTGAAGTGTITTAAAAGGCAGGAGAAAACCGCGGGTCATTGTTT TGCCCTGAAGTGTTTAAAAGCGAGGAGAAAACCGCGGGGCTCATTGTTT TGCCCTGAAGTGTTTAAAAGCGAGGAGAAAACCGCCGGGTCATTGTTT
146 174 129 215 34	CIATALCA GIGIGICIGTATITTACCACACGGIGIGCATTACCAATAAAGTIGA AGTACCTECGIGAAACTTATAGCGGIGITGATATAACCAGCA TIGGICCCATCCGCAACCATATIGGCGGIGITGATATAACCAGCA CAATCCCTGGITGITAAAGGAGAAATTACAGCTGAGTAATAAA GITTACGACTAGACCCTCCGCCACATGGCTCACAGCCACCGG GCGCACGTICTATGAACATGAACTITATGCTGTIGTCT TGACCTGACCTACAGCCCATAGCCACACTIGGICTCCACTGCA GCCCCAGACGACTAGCCGCCGCACACTIGGICTCCACTGCA GCCCCGACGCACTAGCGCGCACATTGGTGCCCCACGCG GCCCCAGACGACTAGCCACGCACTTGGTGCCCCACGCG GCCCCGACGCACTAGCCGCGCCACTTGGTGCCCCACGCG GCCCCGACGCACTAGCCGCGCGCCTGCCATCGC CGCCGGCCGCACGACGTAGCGCGCGCTGCACTGCA CGGTGCGAACAAATTGCCCGGGGGCAAAACCGCGGCGTCTATGGTT TAATTGGATGTGTTTAAAGGCGAGAAAACCGCGGCGCTCTATGGTT TAATGCCTTGTTTTAAAGGCGAGGAGAAACCGCGGCGCTCTATGGTT TAAATCCTTGTTTTAAAAGGCGAGAAAACCGCGGCGCTCTATGGTT TAAATCCGTGTTTTAAAAGGCGAGGAGAAACCGCGGCGCTCTATGGTT TAAATCCCTGGACGAGGACAAACCGCCGCGCCTCCATTGGATCGCA CAAATCCGCGCCCAAAAAAAAAAAATTGGCCCCACTAAGACCCCA
146 174 129 215 34	CIATALCA GIGIGICIGTATITITACCACACGGITIGCATTACCAATAAAGTIGA AAGTACCIGCIGTAAACTIATIGGCGGGIGIGITATATAACCAGCA IIGGICCCAACICCGACCITAATACIAGGIGI CAAGCACCICICCCCCAGCCCTAAAAACTAGIGI ACATICCIGGITIGTAAAGAGAAAATTACAGCIGAGTAATAAA GITTACGACTAGACICCICCGCCACHIGGICICCAGCGCAGGIG GGCACGITICTAGAACATGAACTITATGCIGITIGICCI IIGACCIGACCITAGGACAATGGAACCITIGTICCGCAGCCACIGGI GCCCAGCITAGGACATGGGACGCACCIGIGIGCICCACIGCA GCCCAGCCIACAGCCCATAGCCACACIGIGIGCICCACIGCA GCCCAGCCIACAGCCCATAGCCACACIGIGIGCICCACIGCA GCCCGACGACITAGCCACGCACHIGGIGICCCCACIGCA GCCCGACGCICIGACCIAGGACAAAAAAAGAGCITIGI TAAATCCIGIGITITAAAAGGAGAAAAACCGCGGGICCATIGGIT TAAATCCIGIGITITAAAAGGCAGAAAACCGCGGGICCATIGGIT TAAATCCIGGITITAAAAGGCAGAAAACCGCGGGICCATIGGIT TAAATCCCIGAGTITIAGAAGGAGAAAAACCGCGGGICCATIGGIT TAAATCCCIGAGTITITAAAAGGCAGAAAACCCCCGGGICCATIGGIT TAAATCCCIGAGTITITAAAAGGCAGAAAACCCCCGGGICCATIGGIT TAAATCCCIGAGTITITAAAAGGCAGAAAACCCCCGGGICCATIGGIT TAAATCCCIGAGACAAAAAAATTIGCCCCACACACACIGCCAAATGAGACCCCCA TAAAGCAGGACAAAAATTIGCCCCATAGGCACACACIGCICICICTA AJTITAGACGGAGCAAAAAAAAAATTIGCCCCATAGGCAGCACACGCCICICCTA AJTITAGCGGGACCAAAAAAAATTIGCCCCATAGGCAGCACACGCCICICCTA AJTITAGACGGACAAAAAAATTIGCCCCATAGGCAGACACGCCCCCATAGGCCCAAAAATTIGACCGCCAAAAAATTIGCCCCAAAAAATTIGACGCCAAAAAATTIGACGCCAAAAAATTIGCCCCAAAAATTIGACCCCAATAGGACAAAAATTIGACGCCAAAAAATTIGCCCCAAAAATCCCCAATAGGACAAAAATTIGACCCCAAAAAACCCCCGCCTCCCCATAGGCACAAAATTIGCCCCAAAAAAATTIGACGCCCAAAATCCCCAATAGGACAAAAATTIGCCCCAAAAAAAATTIGACGCCAAAAAAAATTIGCACCAAAATTIGCACCAAATGCCCAAAATTIGACCACAAATTIGCCCAAAAATTIGCCCCAAAAAATTIGACGCCAAAAAAATTIGCACGACAAAATTIGCCCCAAAAATTIGCCCCAAAAAATTIGCCCCAAAAAAAAAA
146 174 129 215 34 402	GIGIGICIGTATITTACCACACGGITGCTATIACCAATAAAGTIGA AGTACCTCGIGTAACTITATGGCGGGITGCTGATATAACCACGCA TIGGICCCATCGCACTITTIGTICTGGGGATCGAACCACGCG CAAAGCACCTCTCCCCCAGCCCTAAAACTAGTGT ACATICCTGGTIGTIAAAGGAGAAAATTIACACGCTGAGCAACGGG GCCACGTCTACAGCCCATAGCCCCCACTGCCTCCACCCAC
146 174 129 215 34 402	GIGIGICIGIATITTACCACACGGIGIGCATIACCAATAAAGTIGA AGTACCTEGIGAAACTITATIGGCGGIGITGATATAACCAGCA TIGGICCCATCCGCAACCTIATIGGCGGIGITGATATAACCAGCA TIGGICCCATCCGCCAGCCTAAAAACTAGTGT ACATICCTGGITGITAAAGGAGAAATTIACAGCTGAGTAATAAA GITTACGACTGAGACCTICTGGCCCCATIGGCTCCACGGG GCCCACGGICCTACGGCCCACATIGGITGCGCCACGCGGCGCCACGGG GCCCACGACGATCGGGGCGCACGCGGCGCCACGGG GCCCAGCACGATTAGGCACGACTITGGIGCCCCACGCG GCCCCGACGACGATTAGGACGACTITGGIGCCCCACGCG GCCCCGACGACGATTAGGACGACTITGGIGCCCCACGCG GCCCCGACGACTAGCCGCGCATIGGGGCCCCACGGCGCCCACGCG GCCCCGACGACGATTAGGACGACATITGGACGCGCGCGCCCACGCA GGTCCGACGACGATTAGGACGACATITGGACGCGCGCTCCCACTGC CGGCCGGCCGACGACGACGGGGAAAACCGGCGGCTCACTGC AGGCCCTGGACCATIAGCGCAGGAGAAACCGCGGCGCTCACTGCA TITATITGGAATGGAAGCAAAAAAAAAAAACACGTTT TAATGCCTGGTTTAAAGCGAGGAGAAACCGCGCGCTCTATAGTT TAAATGCCTGGTTTAAAAGCGAGAAAACCCACATTAGGACCCCATAGCGC TAAAGTCCTGGTTTAAAAGCCAGGAGAAACCCGCGGCTCATTGGAT TAAATGCCTGGTTTAAAAGCCAGGAGAAACCCGCGGCGCTCATTGGAT AAAGTCCTGGTTTAAAAGCCAGGAGAAACCCGCGGCTCCATTGGA TAAAGTCATGGAATCGAGCCAAAAAAAAAA
146 174 129 215 34 402	СТАТАКСА GTGTGTCTGTATTTTACCACACGGTTGCTATTACCAATAAAGTTGA AGTACCTCGTGTATTTTACCACACGGGTTGTGATATAACCAGCA TTGGTCCATCGGCATTTTTGTTCGGGGATCCCAGCTGCGCAGG CAAAGCACCTCTCCCCCAGCGCAGACACGCTGACCACGTG ACATTCCTGGTTGTTAAAGGAGAAATTTACAGCTGAGTAATAAA GTTTACGACTTTTGTGCGCAGCCCACATGCCTCCAGCTGACCACGTG GCCCCGACCACACGCCATAGCCCCACATTGTCGCCAGCCGACCACGTG GCCCCGACCACACGCCATAGCCCCACATTGTTCGCCAGCCGACCACGTG GCCCCGACCAGCACGACTGAGTCGAGCCGCCTGCCACCGC GCTCCGACCTAGACCCCATGGCCCCCCAGTGGCCCCACTGCA GCTCGACCTTGGACGAGCACATTGTGGCGCAGCCCCTGGC GCCCCGACCAGCAGTAGCCCACATTGGGAGCCGCCTGCCAGT GGTGCGATAAATTACACTGATATAAAGTTTT TAATTGGAATTGTTAGCCAGGAGGAGAAACGCCGGTCTATTGTTT TGCCCCTTGTACAGGCCACAATTGCCCCCGGTCTATTGTTT TGCCCCTGTTTTAAATGCCAGGAGGAAAAACGCCGGCTCTTGACTCCA TTAGTGCACTTTTTAAAGCCAGGAGGAAAAACGCCGGCTCTTGATGCCA TTAGTGCACTTTTTAAAGCCAGGAGGAAAACGCCGGCTCTTGAACCCCC TGGTCCGATAGAATCGGAGCGACCCACCTTGGACCCCGGTCTTTGGATCCCCTTGAAGCCACAAGAAAAAAAA
146 174 129 215 34 402	GIGIGICIGTAITITIACCACAGGGIGCATTACCAATAAAGTIGA AGTACCTEGIGAACTTATAGTGGCGGGITIGATATAACCAGCA TIGGICCCATCGCACTTITIGTICGGGGGITIGATATAACCAGCA GCAAGCACCTCTCCCCCAGCCCTAAAACTAGTGT ACATTCCTGGTIGTIAAAGGAGAAAATTACAGCTGCGGCACCAGCGG GCCACGTTCAGACCTGCCGCCATGGCTGCCGCACCAGG GCCACGTTCAGACCAGCATGGCCGCACCCGCGCCACCAGG GCCACGTTCAGACCATGGCCGCACTGGCTGCCCCACCG GCCCACGACTAGCGCGCATGGCCGCCACCCGCGCCCCACTG GCCCGACGACTAGCGCGCATGGCCGCCGCCCCCGCC GCCCGGCCACGATTAGCCACATTGGTGCCCCACCG GCCCGGCCACGATTAGCGCGCACCACCTGGTGCCTCCACCGAC GCCCGGCCGACGATTGGGGCGCACCACCTGGCTGCCCCACCA GGTCCGGACGACTTAGCGCGCATTGGGTGCGCCCCCCCCAC GCCCGGCCGCCTGCCTGCCCCCCCTG GCCCGGCCGGC
146 174 129 215 34 402	GIGIGICIGIAITITIACCACACGGIGIGCIAITACCAATAAAGTIGA AGTACCTEGIGAAACTITAATGGCGGIGIGIGATATAACCAGCA TIGGICCCATCCGCAACCATATGGCGGGIGIGAATATAACCAGCA TIGGICCCATCCGCCAGCCTAAAAACTAGTGI ACATICCTGGITGITAAAGGAGAAATTIACAGCTGAGTAATAAA GITTACGACTAGACCCTCGCCACATGGCTGCAGGCAGCCAGG GCGCACGTICTATGAACATGAACTITATGCIGTIGICT TGACCTGACCTACAGCCCATGGCCACACTGGGTGCCCCACTGG GCCCAGCGTCTACGGGGGGGCACACCCIGIGGCTCCACTGCA GGCCCGACGATTAGCGACGCACATTGGTGCCCCACGCG GCCCAGCGCCATTAGCCACATTIGGTGCGCCCACGCG GCCCCAGCACTTAGCCACGACTTICGGACGCGCGCCCACTGC GGCCCGACGACTTGGGACGCACACCGGGGCCCACTGC GGCCCGACGACTTAGCGCAGCACTTGGGACGCCGCGCTCCCATGC CGGCCGGCCGACGACTGGGACGACACTGGACGCGCGCCTCCCACTGC CGGCCGGCCGACGACTGGGACGACACCGGCGGCCCACTGCA GGGCCCGGCCGATGGCGCGCACTGGGACGCCGCGCCCCCACTGC CGGCCGGCCGAAGATGGGACAAACACCGCGGCGCCTCCACTGC CGGCCGGCCGAAGATGGGCCCACACTGGACGCCGCCCCCCACTGCA CAGGCCCTGGACGAAAAAAAAAA
146 174 129 215 34 402	CIATALCA GIGIGICIGITATITTACCACACGGITIGCTATTACCAATAAAGTIGA AGTACCTCGIGAACCTTATATGCCGGITIGCTATTACCAATAAAGTIGA AGTACCTCGIGAACCTTATATGCCGGGITIGATATAACCAGCA TIGGICCCATCGCCACGCCCTAATACCAGCIGACGACGCAGG CAAAGCACCTCTCCCCCCAGCCGCCAGCIGACCACGIG GCCCACGTICATGAACATGACCTTATGTICGCAGCIGACCACGIG GCCCACGTICATGAACATGACCTATGTICGCAGCIGACCACGIG GCCCACGTICATGACCCCCATGCCCCCAGCIGACCACGIG GCCCACGTICATGACCCCCATGCCCCCAGCIGACCACGIG GCCCACGTICATGACCCCATGGCCCCCAGCIGACCACGIG GCCCCGGCCCGACCACGACGIGACGACCCCCCTGGCCCAC GGTICGAACTAATGCCCACGCATGGCCCCCCGCGCCAGC GGTICGAACTGGCAGGAGAAAAGGTIGTCCATCAGGC GGTICGAATAATTACTCACGCGAGCACCCCCTGGCCCACTGC GGTICGAATGTIGACGAGGAGAAAACGCCGCCGCGCGCCGCCGCC GGTICGAATGGTITTAAAGGCGAGGAGAAAACGCCGCGCGCGCGCCTGCACAC GGGTICGAATGGTITTAAAGGCGAGGAGAAAACGCCGCGCGCGCGCCTCTGA CAGGCCCCTGGACCAGTCAGCCAATGACCCCCATTATGTTT TAAGGCCGGAGGTGACAAAAAAAAACGCCGCGCGCGCGCG
146 174 129 215 34 402 262	GIGIGICIGIAITITIACCACAGGGIGCATIACCAATAAAGTIGA AGTACCTEGIGAACTITAGGGGGGIGCIGATATAACAGCA TIGGICCCATCGGAACTITAGTGGGGGGIGCIGAACTAAAAGTIGA AAGTACCTEGIGAACTITAGTGGGGGGGTCCAAGGCACAGGG CAAAGCACCTCICCCCCAGCCCAAAAACTAGTGT ACATICCIGGITITAAAGGAGAAATITACAGCTGAGTAATAAA GITTACGACTAGAICCICTCGGCCATIGGCICCCACCTGACCACGTG GCCCACGTICTAGAACATGAACTITATGCIGTIGCT TGACCGACTAGAGCCATAGGCACACATIGGIGCCCCACCGACGCCATIGG GCCCACGACTAGGCCACTAGCACCACCTGIGGCICCACCGACG GCCCACGACGACTAGGCCGCATIGGCICCACCGCGCCGCCACCA GGCCGGACGACTAGCCCACATIGGACGCAGCCACTIGG GCCCGACGACTTAGGCAGCACATICGGACCGCGCCTGCCACT CGGTGCGAACAAATITACTACTGATAATAAAGTITT TAAAGCCCTGAAGTAGCACAATAGCACCTGGACGACGCCTGCCACT AGGCCCTGGAGGACAAAAAAAAAA
146 174 129 215 34 402 262	GIGIGICIGIAITITIACCACACGGIGIGCIAITACCAATAAAGTIGA AGTACCTEGIGIAACTITAIGCGGGIGIGIGAIATAACCAGCA TIGGICCATCOCCACTITIGITICIGGGGIGIGIGAIATAACCAGCA TIGGICCATCOCCACGCCITIGIGICIGGGGIGAICCAAGCCIGCCCAGG CAAGCACCTCICCCCCAGCCIAAAAACTAGIGT ACATICCIGGITGITAAAGGAGAAATTACAGCIGAGTAATAAA GITTACGACTAGACCCATGGCCACATIGGICGCCCAGCCATGG GCCCACGTICIAIGAACATGAACCITIAIGCIGIGIGCICCACCACIGG GCCCACGTICIAIGAACATGAACTITAIGCIGIGIGCICCACCACIGG GCCCACGACGACTACGCCACATIGGICGCCCCACGCG GCCCACGCCCACAGCCCATAGCCACACTIGGIGCICCACCACG GCCCGACGACGACATACGCACATIGGIGCCCCACCACG GCCCGACGACGATTAGCCAGCACTICGGACGCGCCCCACGCA GGCCCGGACGACGATGCGCGCCACACTIGGI CGCCGGACGACGATGGGCGCACAATIGCA CAGGCCCIGACGACGACGAGCACAAATGCA CGGCCGGCCGAGACCAGTGGGGCACAATGCA AAGGCCIGAGAGACGAAAGCGCGGGGCCATIGGI TCGCCGGACGAGCGAAAAACGGCGGGCCATIGCT AAAGCCCGGAGGACCAAAAACGGCGGGCCATIGCT AAAGCCCGGACGAGCGAAAAACGGCGGGCCATIGCT AAAGCCCGGACGAGCAAAAACGGCCGCGCCCCTCCAA AAGGCCGGGCCAGGCCA
146 174 129 215 34 402 262	CIAIAICA GIGIGICIGTAITITTACCACACGGITIGCIAITACCAATAAAGTIGA AGTACCTEGTGAACTTAATGCGGGITIGGTAATAACCAGC TIGGICCCATCGGCACTTITTATGCGGGGGTCGAACGCCAGG CAAAGCACCTCTCCCCCAGCCGCAGGCAGACCGGCGCAGG CAAAGCACCTCTCCCCCCAGCCGCAAAAACTTACCGCGAGCGA
146 174 129 215 34 402 262	GIGIGICIGTAITITIACCACAGGITIGCTATIACCAATAAAGTIGA AGTACCTEGTGAAACTITAITGGCGGGITIGTATATAACAGCA AGTACCTEGTGAAACTITAITGGCGGGGITIGATATAACAGCA AGTACCTEGTGAACTITAITGGCGGGGTTCAAGGITAATAACAGG CAAAGCACCTCICCCCCAGCCCAAAAACTAGTGT ACATICCIGGTITIAAAGGAGAAAATTIACAGCTGAGTAATAAA GITTACGACTAGATCATGGACCAGCAGTGGCTGCCACCGAGCCACGG GCCACGTTEATGAACATGAACTITATGCTGTIGTCT TGACCTGACTTAGGAGGAGAACTITATGCTGTIGTCT CGGCCAGCACTTAGGCAGCAATTGGACCGCGCTGCCACGG GCCCACGACGATTAGCCAGCACATTGGAGCGCCGCCGCCGCCACT GGCCGAGCACTTAGGCAGCACATTGGAGCGCGCGCCGCCACT GGCCGGACGACTTAGGCAGCACATTGGAGCGCCGCGCC
146 174 129 215 34 402 262	GIGIGICIGTAITITIACCACACGGIGGCATTACCAATAAAGTIGA AGTACCTEGIGAACTTATAGGEGGGIGGIGATATAACCAGCA TIGGICCCATCCCCACACCACAGCGIGGGGAGCACAGCIGGCAGGCAA TIGGICCCATCCCCACCCCTAAAACTAGTGT ACATICCTGGTIGTIAAAGGAGAAATTACAGCTGAGTAATAAA GITTACGACTAGACCCATGGCCACATTGGTCACGCGGCGCCACGGG GCCACGTICTATGAACAGCACATGGACCACGGCGCACCACGG GCCCACGACGACGACGCACCACGGCGCCACGGCGCCACGGG GCCCACGACGACGACGGGGGCACACGTIGGGCCCCACGCG GCCCAGCGCCACGACGGGGGCACACGGCGCCCCCCCC
146 174 129 215 34 402 262 210	GIGIGICIGIAITITIACCACACGGITIGCIAITACCAATAAAGTIGA AGTACCTCGIGAACTTIATATGCGGGIGITIGATATAACCAGC TIGGICCCATCGGAACTTIAITGCGGGIGITIGATATAACCAGC GAAGCACCTCTCCCCCAGCCCAAAAACTAGTGT ACATTCCTGGTIGTAAAAGGAGAAAATTIACAGCIGAGCAACAGTG GCCCACGTICATAGACCAGCAATTIGTICGCAGCIGACCACGTG GCCCACGTICATAGACCATGCGCCACTIGCTCCACGCGACCACGTG GCCCACGTICATAGACCATGCCCACTIGGCCCCACTGCCCCACGG GCCCACGTICATAGACCATGCCCCACTGCCCCCACGCGCCATGC TICGCACTITIGGATGGTGGCCACATTIGGACCCCCTGCA GCTCCAGACAGCATTAGCCCACGCCCCTGGCCCCACTGCC GGTGCCATAAATTIACCCATGCGCACACTGCGCCCCTGCCA GCTCCGACATGAGCCCATGCCCCCCCTGCCCCCCC GGTGCCATGACTGCCCCAGTGCCCCCCCTGCCCCAC GCTCCGACAGCATTGGCGCACATTIGCGACCCCCCTTGCCCA CGGTGCCAGCAGTGCGGCGACAAATACCC GGTGCCAGCAGTGCGGCCCCCCCCCC
146 174 129 215 34 402 262 210	CIAIAICA GIGIGICIGTAITITTACCACACGGTIGCTATTACCAATAAAGTIGA AGTACCTECIGTAACTTATAGTGGGGGTIGCTATTACCAAGAG TIGGICCCATCGGAACTTATAGTGGGGGGTIGCTATATAACCAGG CAAAGCACCTCICCCCCAGCCCTAAAACTAGTGT ACATTCCIGGTIGTIAAAGGAGAAATTACAGCTGAGTAATAAA GTTACGACTGACTACAGCCACATGGCCCCCACCTGACCACGTG GCCCACGTICTATGAACATGAACTTTATGCTGTIGCT TGACCTGACTTACGAGCCACATGGACCCACTGGCTCCCACCGA GCCCACGACCACTAGCCCCACATTGGTGCCCCACCGACCACGTG GCCCACGACGACTTAGCCACACTTIGGTGCCCCACCGACCACGTG GCCCAGCACTTAGCCACACTTIGGTGCCGCCGCCCCCCACT CGGTGCGACACATTAGCCAGCACACTTIGGTGCCCCACCGAC GCCCGGACGACTTAGCCACACTTICGGACCGCCTGCCCAC CGGTGCGACACATTAGCCAGCACACTTICGACCGCGCTCGCCTG CGCCGGGCCACGACTTAGCGAGGAGAAAACCGCGGCTCACTGCA CGGTGCGGACGACTAGCCCACTGGCCTCCCACTGA CGGTGCGGCAGAAATTGGCAGGGAAAAACCGCGGGTCACTGGTT TAAATCCTTIGTITTAAATGCGAGGGAAAAACCGCGGGTCATTGTT TGCCCTGAAGTGTTTTAAATGCGAGGGAAAACCGCGGGCCACACGCTTCC TAAGGCCTTGCGAGTCACACATGCCCACTATGGACCCTTCT AAAGTCCTGGAGTCGCGCGGCGCGCTCCCCCTATGGTTC TGCGCTTAGGTCGGCGGCGCCACCACAGGCCCCCCTCCTGCTCT ATTATAGCGTGGGGCGACAAATGCCGCGGCCCCCCTCCTGCTCCT CGCGTGACGTGCGGCGGCGCGCTCCATTGCCCCCTATGGCCCTCCT GCCGCGGCTTAGCGCGGCGGCGCCACACAGCCTTCCTAATTCT GCCCTGAAGTTATTATTCTTATCGCCCCACACTGGCCCTCCTGCCTT GCCTCCAAATTTATTCTGTGGTGCGGTGCACTGCCACCTGCCTG
146 174 129 215 34 402 262 210	GIGIGICIGTAITITIACCACACGGIGGCATTACCAATAAAGTIGA AGTACCTEGIGAACTTATAGGEGGGIGGIGAATAAAGTIGA AGTACCTEGIGGAACTTATAGGEGGGIGGIGAATAAAGTIGA AGTACCTEGIGAACTTATGGIGGGGGAAACTAGGGCAGCCAGCCAGC AGGCCCGCACTCCCCCCAGCCCTAAAAACTAGTGT ACATICCTGGTIGTAAAGAGAAAATTACAGCTGAGTAATAAA GITIACGCAGACTTCAGACCCACTGGCTCACACGTGG CCCACGCCTACAGCCCATAGCCCACAGTGGCTCACACGTGG CCCCACGCCTACAGCCCATAGCCCACACTGGCTCACCACTGG GCCCACGCCTACAGCCCATAGCCACACTGGGCTCCACGCC GCCCACGCCTACAGCCCATAGCCACACTGGGCTCCACGCC GCCCACGCCTACAGCCCATAGCCACACTGGGCTCCACGCCA GCCCGGCCCG
146 174 129 215 34 402 262 210	CIAIAICA GIGIGICIGTAITITIACCACACGGITIGCIAITACCAATAAAGTIGA AGTACCTEGTGIAACTTAATGGCGGGITIGATATAACCAGCA TIGGICCCATCGGAACTTAATGGCGGGGTIGATATAACCAGG CAAAGCACCICTECCCCAGCCGCAGTGCCTGCAGCGCAGG CAAAGCACCICTECCCCCAGCCGCAAAAACTAGTGT ACATTCCTGGTIGTIAAAGGAAAATTAACACTGGGT GCCCCCGTECTATGAACAGGAGAATTACCGCGAGCGACCACGTG GCCCCCGTECTATGAACAGGAGAACTTATGCTGCAGCTGACCACGTG GCCCCGGCTAGCGGCCCATGGCCGCCGCCTGGCCGCCATGC TICTGCACTTITIGGATGGTGGGAGGACACCTTIGTGCCCCAGCCGCCATGC GCCCCGGCTGACCAGCACGACGACCTGGGTGGCGCCCATGC GCCCCGGCCTGGCGGCGGCGGCCGCTGCGCAGC GCCCCGGCTGACGAGCAGCAGCACTTICGGAGCGGCTCGCCAT CGGTGCGAGAGACGAGCAGCAGCACTTGGGGCGCGCTCGCCAT CGGTGCGAGAGAGCAGAAAAAAAAAAAACGTTIT TAAATCCTTGTTITAAATGCGAGGAGAAAACCGCGGGCCATTGTT TCCCCGTGTTTTAAATGCGAGGGGAAAACCGCGGGCCATTGTT TCCCCTGGAGTGTTTAAAAGGCAGGAGGAAAACCGCGGGGCTAATGTT TCCCCTGGAGTGTTTAAAAGGCAGGAGAAACCGCGGGCCATTCTTA CAAGTCCCTGGAGTGTTTAAAAGGCAGTAGCCCCTCATAAACTCCA ATTATAGCGTGGGGCGCAAAATGACGCGCGGCCGCTCTCTA CAAGTCCTGGGGGCGCGCGCGCCATGCCCCATAAACTCCA CATTGCCGTGAGGGCGAAAACCAACTGACCCTTCTAGACCTCTCT CGCGTGAAGTGTTAGCGCGGGGGCAAACAATGACCCTCCTATGCTC TGGGCTTGGGGTGGCGGCGCGCTGCATGCACCCTATGACGCCTCTC GCGGCCGGCTAACGGCGGCGCGCTGCATGCCACCACTATGCTCT CGCGCGGCTAACGGCGGCGGCGCACAAATGGCG CTTTCGAATTATGCGGGAAACCACGCGGGCGCCGCCCCCCCC
146 174 129 215 34 402 262 210	GIGIGICIGIAITITIACCACAGGGIGCATIACAATAAAGTIGA AGTACCTECIGIAACTITATGCGGGGIGTIGCAATAAAAGTIGA AGTACCTECIGIAACTITATGGGGGGIGTIGCAATAAAAGTIGA AGTACCTECIGGIGAACTITATGGGGGGIGTIGCAGCAGCCGCCAGG CAAAGCACCTCICCCCCAGCCCTAAAAACTAGTGT ACATICCIGGITIGIAAAGGAGAAATTACAGCTGAGTAATAAA GTITACGACTAGACCTCIGGGCGCAGTGACCCACGTG GCCCAGCGTCAAGACCATGAGCCACATTGGIGCGCCACCGGG GCCACGTICTATGAACATGAACCTITATGCTGTGCT TGGCCGACGACTTACGGCGCATGGCTGCCCCCCCGCGCCCACTGG GCCCAGCCCTACAGCCCATAGCCACATTGGIGCGCCCACCGCG GCCCAGCGCCTACAGCCCATAGCCACCTGIGGCTCCACCCAC GGTCCGACACATTAGCCACATTICGGACGCCCCCCGCCGCCCAC CGCCGGCCGGCCACTTGGGGCGCCACCCGCGCCCCCCCG GCCCGGCCGGCCATTGCGGACGCACCCGCGCCCCCCGC GCCCGGCCGGCCGCTGCCCACTCG AGGCCCTGGACGCACTAGCCGCGCGCCCCCCCCCC
146 174 129 215 34 402 262 210	CIATALCA GIGIGICIGTATITITACCACACGGTIGCTATIACCAATAAAGTIGA AGTACCTEGTGTAACTTATAGGCGGGTIGTATATAACCACA TIGGICCCATCCGCACCACACCGCAGCCTIGGTAATATAACCACA TIGGICCCATCCGCCACCCCACCCCTAAAAACTAGTGT ACATICCTGGTIGTIAAAGGAGAAATTACAGCTGAGTAATAAA GTITACGCACGACCCCCCCACGCCCAATACCACACGGCGACCACGG GCCCACGACGACACACACACACACGCACGCGCCCCCCGG GCCCACGACGATAGCCACCACGCCACGCGCCCCCCCCCC
146 174 129 215 34 402 262 210 471	CIAIAICA GIGIGICIGTAITITIACCACACGGTIGCTATIACCAATAAAGTIGA AGTACCTCGTGTAACTTAATGGCGGGTIGGTAATAACACGCA TIGGICCATCGGAACTTAATGGCGGGGTIGGATATAACCAGG CAAGCACCTCTCCCCCAGCCGAAAAACTAGTGT ACATTCCTGGTIGTIAAAGGAGAAATTACAGCTGAGTAATAAA GTTIACGACTGCCCCAGCCCATAGCCTGCAGCGACCACGTG GCCCACGTICTAGAGCCCCATGGCCGCAGTGCCTGCACCGCCGTG GCCCACGTICTAGAGCCCATGGCCGCATTGGTGCCCACGCGCCATGC TIGGCCCTTTIGGATGGTIGGCGACGCTGTGGCTGCCACTGCA GCTCCAGCGACGACGACGCCGCATGGCCGCCGCTGGCCACTGCA GCGCCGGCTTIGGAGGAGAAAAACAAAAAAAAACGTTT TAAATCCTTGTTITIAAATGGCAGGAGAAAACCGCGGGTCATGGTT TGCCCGTGAGTGTTAAAAGGCAGGAGGAAAACCGCGGGTCATGGTT TGCCGCCTGGAGGTGTTAAAAGGCAGGAGGAAAACCGCGGGTCATGGTT TGCCGCCTGGAGGTGTTAAAAGGCAGAGGGGAAAACCGCGGGGCTATGGTT TGCCGCTGGAGGTGTTAAAAGGCAGGAGGAAAACCGCGGGGCTATGTTT TGCCGCCTGGAGGTGTTAAAAGGCAGAGGGGAAAACCGCGGGGCTATGTTT TGCCGCTGGAGGTGTTAAAAGGCAGGAGGAAAACCGCGGGGCTATGTTT TGCCGCTGGAGGTGTTAAAAGGCAGAGGGGAAAACCGCGGGCTCATGGTC TGGGCTGGGGGGGGGCGAACAATGACCTCTTA CAAGTCCTGGTTGCGGGCGCATGCCCCATTAGGCCTTCTGAGACCTCTCT AAAGTCCTGGTGGGGGGGGGGCAAACAATGAGCCTTCCTATG ATTAAGGCCTGGGGGGGGGGCGAAACAATGGCGCTTGCCATGAAGCCTCCT TGGGCTTGGGTTGGCGGCGGCGCTGCATGGCGCTGCCTCT GGGTGCGGGTTAACGGGGGGGAAACAATGGCGGACGCCGCTGCCTCT GGGTGGGTTAACGTGGGGGGGGGAAACAATGGCGGACGCCGCTCCTCT GGGTGGGTTAGGGTGGGGGGGGGAAACAATGGCGGACGCCGCCTCCTGCGC CCCAAATATTGTGGGGAACAATGGCGGACGCGCGCGCCGCCCCCCCC
146 174 129 215 34 402 262 210 471	GIGIGICIGIAITITIACCACACGGITGCTATIACCAATAAAGTIGA AGTACCTECIGIAACTTATAGGGGGITGCTATIACCAATAAAGTIGA AGTACCTECIGIAACTTATAGGGGGGITGCTATATAACCAGCA TIGGICCCAICCGGAACTTATIGGGGGGITGCAGACAGCCIGGCCAGG CAAAGCACCTCICCCCCACGCCTAAAAACTAGTGT ACATICCIGGITGTAAAGGAGAAATTACACGCTGAGTAATAAA GTITACGACTGGACTACAGCCGACATIGGTGCCGCACCGAGCCACGG GCCACGTTCATGAACATGAACCTTATGCTGTGCT TGCGCACGACTACAGCCCATAGCCCCCACTGGCTGCCCACCGAC GCCCACGACCTACAGCCCATAGCCCCCACTGGCTGCCCCACCGAC GCCCAGCACGACTGGGGGGCAGCACCCGGTGCCTGCCCACCGAC GCCCGACGACGATTAGCCAGCACTTICGGACCGCGCTGCCCAC CAGGCCTGGACGACTTAGCGACGACACTTICGGACCGCGCTGCCCAC AGGCCCTGGACGACTAGCCGACGACACTGGCTGCCCACTG GGTCCGAATAAATTACTACTGATAATAAAGTTTGTCATCAGTCA CAGGCCTGGACGACTGGGGCGACAAATTACA CAGGCCTGGACGACTGGCGCGCGCGCTGCATTGTT TCCCCGGAAGTGTTTAAAAGGCGAGGAGAAACCGCGGGTCATTGTT TCCCCGGAAGTGTTTAAAAGCGGGGGAAACCGCGGGCCATTCCT AAAGTCCTGGATGGTGTGCGCCGCGCGCGCCTCCTGTGCTC CAGGGCCGGCTAGCGCGGGGCGAACCAAGGCCTCCCTTA CAATTCCCGTGAGGGCGAAACGACGCGGGCCAACTGCCCCTTAGGCCCCCTATGGTCCTCTA CAATTCCCGTGAGGGCGGCGCGCGCCTCCCGCGCGCCTCCCTGCGCCGCCTCCCGCGCCTCCCCGCCG
146 174 129 215 34 402 262 210 471	GIGIGICIGIATITTACCACAGGIGGIGATTACCAATAAAGTIGA AGTACCTEGIGAACTTATAGGEGGIGTIGATATAACCAGCA TIGGICCATCOGCAATTITTGGEGGGIGTIGATATAACCAGCA AGTACCTEGIGAACTTATAGGEGGGIGTIGATATAACCAGCA TIGGICCCATCOGCAATTITTAGGEGGGIGTIGATATAACCAGCA GITTACGACTAGACCTTITTGGTCGGGGAAACTATAAA GITTACGACTAGACCACTAGCACAATTICGACGCGCCACCGG GCCAACGTICTATGAACATGAACTITATGCIGTIGICT TGACCTGACCTACAGCCCATAGCCACACTIGGIGCCCCACCCAC GCCCAGCCTACAGCCCATAGCCACACTIGGIGCCCCACCCAC GCCCAGCCTACAGCCCATAGCCACACTIGGIGCCCCACCCAC GGTICCGACACATTACGACCACTITCGACCGCGCTCCCACTGC GCCCCGACCACTAGCCCACATTICGACGCCGCGCTCCACTGC GCCCGGACCGACTAGCCCACAATTACA CAGCCCTGGACCACACTACGCACACTICGACGCCGCGCTCCACTGC CGCCGGCCGGACGACTAGCCACACTTICGACCCACTGC GGTICCGAAAAATTACTACTGATAATAAAGTTTGTCATCAGTCA CAGGCCTGGACGCACTAGCCACAATTACA CAGGCCTGGACGACTGCGACGCACATTCGA CAGGCCCTGGACGACCACATGCACACTGGACCACTTG CAGGCCTGAAGAATTGACCACATTGCACCACTATGGTT TCGCCTGAAGGIGTITTAAATGCCAGGGGAAACACGCGCGGCTCATTGTT TGCCCGGAAGTGTTCGGCGCATCACCACTATGGAACCGCCTTC AAATCCCGGAGACCAAAAGTCGCG CATAAACACTAAAAATCCAAGGGGGAAACAAGCCCTCCCT
146 174 129 215 34 402 262 210 471 141	GIGIGICIGTATITTACCACACGGITGCTATIACCAATAAAGTIGA AGTACCTCGIGAACTTATAGCGGGGITGGATATAACCAGCA TIGGICCCATCGGAACTTATAGCGGGGATGGATATAACCAGG CAAAGCACCTCTCCCCCAGCCGCAGCGGCGCCAGG CAAAGCACCTCTCCCCCCGCCATGCCTCCCAGCTGACCACGIG GCCCCCGTCTATGAACGCCATAGCTGCCCCAGCTGACCACGIG GCCCCCGTCTATGAACGCCATAGCCGCCAGTGCCTCCCAGCTGACCACGIG GCCCCGTCTATGAACGCCATAGCCGCATTGGCCCCCCTGCCA GCCCCGGCTTAGCGCCCATGGCCGCCGCGCCTGGCCAG GCCCCGGCTTAGCGCCCATGGCCGCGCGCCGCCCCGCA GCCCCGGCTGACGAGCCATGGCCGCCGCGCGCCCTGGCA GCCCCGGCTGGCGGCGCATGGCGCGCCGCTGGCCAAT GCGCCCGGGCGGGGGGAAAACCGCGCGGCGCTGGCCAAT GCGCCGGGGGGGGGG
146 174 129 215 34 402 262 210 471 141	GIGIGICIGIAITITIACCACAGGGIGCTATIACCAATAAAGTIGA GIGIGICIGIAITITIACCACAGGGIGCTATIACCAATAAAGTIGA AGTACCTEGIGIAACTITIATIGGGGGIGTIGGAATATAAACAGTGA TIGGICCAICGGAACTITITIGGGGGGGIGCGCAGCCAGGCGAGG CAAAGCACCTCICCCCCAGCCCAAAAACTAGTGT ACATICCIGGTIGIAAACTAGGAGAAATTACAGCTGAGTAATAAA GITTACGACTACAGCCCATAGCCCCACATIGGICGCCACCGGG GCCACGTICIAGAGCCATGGACCCACTIGGICGCCCACCGG GCCCACGTICIAGGGIGGGGAGCACCCGIGGCCCCACGG GCCCACGTICIAGGGIGGGGAGCACCCGIGGCCCCACGCA GGTCCGACACATTAGCCAGCACTICGGACCGCGCCCCACT GGTCCGACACATTAGCCAGCACTICGGACCGCGCCCCACT GGTCCGACGACATTAGCCAGCACTTICGGACCGCGCTCGCCAC GGTCCGACGACTAGCCCACATTGGACGCCGCGCTCCCAT GGTCCGACGACTAGCCCACATTGGACGCCGCGCTCCCTGC GCCCGGACGACTAGCCCACACTGGACGCCGCGCCCCCCAC GGTCCGACGACGACTAGCCCACTGGACGCCGCTCCCTTG GCCCGGACGATTGGCCAGCACATGCAC GGTCCGGACGACTAGCCCCCCCCCC
146 174 129 215 34 402 262 210 471 141	CIATALCA GIGIGICIGIATITTIACCACACGGITIGCIATTACCAATAAAGTIGA AGTACCTEGIGIAACTITATGGEGGIGITIGATATAACACGA TIGGICCATCOGCAATTITIGGEGGGIGITIGATATAACACGA AGTACCTEGIGAACTITATGCIGGGGGATICGAATATAAAGTIGA ACATICCIGGITIGITAAAAGGAGAAATTIACAGCIGAGTAATAAA GITIACGACTAGACCCATGGCCACATIGGCGCAGCCACGG GCCACGITICIAGAGACCATGAGACACGCGCCACGGG GCCACGITICIAGGAGCACATGGACCACGCGCCACCGG GCCCACGACGACGACGGGGGGACAACTIGGICGCCACCACTGG GCCCAGCCCACAGCCATAGCCACACTIGGIGCCCCACCACG GCCCAGCCTACAGCCCATAGCCACACTIGGIGCCCCACCACG GCCCAGCACGACGACGACACTICGAGCCCCGCGCCCACGCA GGTCGGACCACGACTAGCCGCGCACTICGGACCCACGCGC GCCCGGACGACGACGACGACAATGCA CGGTCGGCACGACGACGACGACAATGCA CGGTCGGCACGACGACGACGACAATGCA CGGTCGGCACGACGACGACAAATGCACCGCGCGCCTCCACGCA GGTCGGACGACGACGACAAATACACGCCGCGCCCCACTGCA GGTCGGACGACGACGACAAATGCACCACTAGGACCACTTG CGCCGGACGGGGTGCGCATGCCACCACTAGGACCACGCCC ATAAGCCCTGAGGAGCGCAAAAAGCGCGCGCGCCACCACAGCCCC ATAAGCCCTGAGGAGCGCAAAAGCGCGCGCCTCCCTGATGAACCGCC ATAAGCCCTGAGGAGCGCAAAAAGCGGG ATAAAACACTAAAACTCAAGGGGGAAACAGCCCTCCCTGCATGAACGCCCCC CCCCAAAGACGCAAAAAGCCGGGGACAAATGACCCTCCCT
146 174 129 215 34 402 262 210 471 141	CIAIAICA GIGIGICIGTAITITIACCACAGGITIGCTATIACCAATAAAGTIGA AGTACCTEGTGIAACTTATAGTGGGGGITIGGATATAACAGGA TIGGICCATCGGAACTTATAGTGGGGGGTIGGATATAACAGGA GCACAGCCCTCCCCCAGCCCTAGCCTGCAGCGCAGCGAGG CAAAGCACCTCCCCCCAGCCCTAAAACTAGTGT ACATCCTGGTIGTIAAAGGAGAAATTACAGCTGAGTAATAAA GTTIACGCATAGACCCCTGGCGCCATGCCTGCGCCGCACTGACCACGTG GCCCCGGCTGACGACACCATGGCCCCCATGCCTGCGCGCCCATGC TICGCACTTITIGGATGGTIGGGAGGACACTTIGTIGCCCAGCCCA
146 174 129 215 34 402 262 210 471 141	CIAIAICA GIGIGICIGTAITITIACCACACGGTIGCTATIACCAATAAAGTIGA AGTACCTECIGIAACTTATAGGGGGGTIGGCAATAAAAGTIGA AGTACCTEGIGAACTTATAGGGGGGTIGGCAATAAAAGTIGA AGTACCTEGIGAACTTATAGGGGGGTIGGCGGCAGCCAGGC CAAAGCACCTCICCCCCACACCCCAAAAACTAGTGT ACATICCIGGTIGTIAAAGGAGAAATTACACGCTGAGTAATAAA GTITACGACTACAGCCCATAGCCCCACATIGGTIGCGCCACGGGCACAGTG GCCCACGTICATGAACATGAACATTATGCIGTIGCCT CAGCCTGACACTACAGCCCATAGCCACACTIGGTIGCGCCACGCCA

TniC _{KL} 84	7,689	GCAGGAGIGE IGC TGACETEC GOATGAACCACUMACAGCAATG ACATECATGACACCCCTCTGGGGGTETCACCCACATTAGTGTCAC TCTTGCAGTTGGAACCTAATGATTGAATATCACTCACTTGATC TATTGGTTACATTCTAATGAATGACTGCCGCGTGGCAGAGATATCC 217 TIACTTTGCGACGTGCAGAGGACACGAGGTTG
TniC _{KL} 85	7,250	ААТGГGITAAATGTITAGIGAAGTAATACTITTAIGTTIGTAGITGT САПТПСТGGTAAATCCICTGACTGTATATGGTATATGTAATGCG САААТААСТСАТТССАССТГССАGAAATGACTIGATIGTIGATT 154 GAAAGAATAAAGTT
TniC _{KL} 86	7,031	GACAAACGCTITCTGGAGTITAAGACCCTCATAAAACTITATIGCC CCGTITCCACAGCCCCGCTAGTITCCTGTITGGTCTGGGAAGGAAGC 126 GACCCAACCTGTGACAACGCTCACCCACCAAAAC
TniC _{KL} 87 _{ac}	6,559	AGGTTACATATGCCAATTGCCCTAAGCAGGGCCTGTGAATGGTGC ATAGGAAGCACGTGGTGTCATTTAAGTGGGTTTTATGGCCTGGAAG AGCTGACAACCTTCGGTATATACACATCATATATAATCTTAACTG 153 TCCGGAATCGCAGCTG
ToiC92	5 286	ATAGGGGGCGGTGTGTGACACACTGTTGGTTGGGGAAAACTAAAG CAAAATGTGTTTATTTTAAGTATTGATGGAGTATGGTTCTTT TACATATATATACATTTTATTCACTGCTATTACTGCGTAAATTGCTG GAGAGCTCCTGAAAGATGCAATGGTTGGTTTGGT
TniC _{kl} 93	2,948	16 AAAGAAACTTATTTTT
TniC _{KL} 94	4,022	CCACAGCATCGTTAAGACCAACTTGGTCTTTGCATGACAGCAAGTT TGCTAAAACCGAGTCCTTGTCTCCCCTGCTGCTTTAAACTGTCCAT GCCCAATTAGTCTCCAGTTGTGCAGCTTTGTTATAACCGTCCAT TTTTCTACGGACGTTATCCACCTTAACTTAA
TniC _{KL} 95	3,149	AAGAAATGGCTGGGAACAAAAGAAACTTATTTTTCATCAGTGCTG 312 TCACGCCATCCCTTTGTACCCTGTGTG TTAGTTGTCTATATGTACCCTGTAGAACCGAATTTGTGTGGAGTTCAG
TniC _{KL} 97	2,679	Аслотс-Асалатасотстрасловодатасловодскастована тоса-соведоссастоводскастостостстрессовскасс титсетсетитисастосаладокастостостретстрессовскасс титселеститисастована и полнати и полнатисатора посостаталосталастика и полнатистика и полнатисаторато 492 слада-саятесоводскатовата и полнатися 493 слада и полнати и полнати и полнатися 494 слада и полнати и полнатися и полнатися 494 слада и полнати и полнатися и полнатися 495 слада и полнати и полнатися 495 слада и полнатися и полнатися и полнатися 495 слада и полнатися и полнатися и полнатися и полнатися 495 слада и полнатися и по
TniC _{KL} 98	1,114	31 ATTAAAACCCTGTTAAGATCCCATTTCATTC
TniC _{KL} 99 _{ab}	3,522	АСАТТАТААСТАGTTATTGAACTAGGTGCGCGATCTGAAAGCCATT ТGTGTGGATAAGGAATTCATTGCTGTCCCTCCATCAATAACCCTTG GCAGTGAACTATTGGAACCAGTCAAACGCGGGGGGGAAACCGCG 163 GGTCAGCCTGTCTAACTAATATTAAA
TniC _{KL} 102	151	GGTTCCTTATCCGGGAACTACCTCTAAGCCCACTATTGGCCCATTG TGTCACGTGGTAAAAGTAACATTACAGGGCTGCTCGCAAGTAGGA GGGCTTTATGGACCAGAAAAAACGACAAAGCTAGAAAAATTATTT 151 CCACTCCAGAAATTA
Danio rerio zebrafia	sh Hox Cb	anath Saquanaa

Danio reno zebransi i nox ob							
PFC	Dist to 3' gene	Length	Sequence				
DreCB _{DE} 23	1,295	21	AGAAAGCAGTTTTAAAAATAA				
			CTCCTACGTTTGCAACCGTTCCAAATTGATATATGAGAATATCTACT				
DreCB _{DE} 26 _b	168	59	TTCGATCACGTG				
DreCB _{EJ} 32	14,468	20	GGAAAATTAAGCCTTTTTAT				
DreCB _{EJ} 47	12,556	17	TCTCTGGAGCTCATTTC				
DreCB _{EJ} 54	12,259	43	TGTTATGATTATGTACACCATGGGGATATGTGGTGACGTCACT				
			CAGCTGATGCGTGGTTTAGGTAGTTTGATGTTGTTGGGGGTTGACTTC				
DreCB _{FG} 40 _{abc}	11,859	72	CTGGCTCGACAACAAGAAACTGCCT				
DreCB _{EJ} 76	7,169	32	TATTAAATCTACAGTCCATTGAGGGCATTGAA				
DreCB _{EJ} 67 _b	3,950	30	GAAAATTTACAGCTATGTAATAAAAGTTTA				

PFC	Hornshark D	Frog D	Coelacanth D	Human D	Bichir D	Zebrafish D	Medaka Da	Tetraodon Da	Medaka Db	Tetradodon Db
1	HfrD ₁ c1	XtrD.cl ·	LmeDust	HsaDacl		DreDacl	OlaDA .r.1.	TniDA1.		
	AC ¹ ab	ACTab	AD1ab	ACTab		DraD 2	OlaDA 2	AD b		
2						DreD _{CD} 2	OIADA _{AD} 2			
3				HsaD _{AC} 3			OlaDA _{AD} 3			
4						DreD _{CD} 4		TniDA _{AD} 4		
5		XtrD _{CE} 5		HsaD _{CD} 5						
6		XtrD		HsaD						
7		Mubleo		TISUD (DO		Dep 7		TriDA 7		
/						DIED _{DE} /	01 P. J. 0	TIIDA _{DE} /		
8				HsaD _{DE} 8			OlaDA _{DE} 8			
9	HfrD _{DE} 9 _{abcd}		LmeD _{DE} 9 _{bcd}			DreD _{DE} 9 _{abcde}	OlaDA _{DE} 9 _{abce}	TniDA _{DE} 9 _{abe}		
10	HfrD _{DE} 10 _{bcde}	XtrD _{CE} 10 _{abcde}	LmeD _{DE} 10 _{bcde}	HsaD _{DE} 10 _{abcde}		DreD _{DE} 10 _{cd}	OlaDA _{DE} 10 _d	TniDA _{DE} 10 _{cd}		
11	HfrDre 11.	XtrDrr 11ab	LmeDre11.	HsaDer 11ab		DreDgg11	OlaDArr11.h	TniDAFF11ab		
12	HfrD_12		1.1 10	HeaD_12				Li ub		
12	IIIID _{EF} 12			H-D 12		DD 12				
15				HsaD _{EF} 15		DreD _{EF} 15				
14		XtrD _{EF} 14		HsaD _{EF} 14						
15		XtrD _{EF} 15		HsaD _{EF} 15						
16				HsaD _{FF} 16		DreD _{FF} 16				
17				HsaDer 17			OlaDArr17			
18		VtrD 18		UcaD 18			S IIII I EFT			
10	UCD 10	XuD _{EF} 10	L D 10	IISaD _{EF} 10		D D 10	01 D 4 10	77 TD 4 10		
19	HIrD _{EF} 19 _{ac}	AtrD _{EF} 19 _{bc}	LmeD _{EF} 19 _{abc}	HsaD _{EF} 19 _{abc}		DreD _{EF} 19 _{abc}	OlaDA _{EF} 19 _{ac}	IniDA _{EF} 19 _{ac}		
20				HsaD _{FG} 20			OlaDA _{FG} 20			
21	HfrD _{FG} 21 _{abc}	XtrD _{FG} 21 _b	LmeD _{FG} 21 _{ab}	HsaD _{FG} 21 _{ab}		DreD _{FG} 21 _{abc}		TniDA _{FG} 21 _{abc}		
22						DreD _{FG} 22	OlaDA _{FG} 22	TniDA _{FG} 22		
23	HfrD _{rc} 23	XtrD _{rc} 23	LmeD _{rc} 23	HsaD _{pc} 23		DreD _{EC} 23	OlaDA _{EC} 23	TniDA _{rc} 23		
20	ru abce	ro-vabce	ruabce	HsaDow24		ru-bcd	- TO bed	-ru-bod		TniDB _{cr} 24
24			LmoD 25	HooD 25			ł	1	1	
25			LineD _{GH} 25	nsaD _{GH} 25						
26				HsaD _{GH} 26				ļ		TniDB _{GL} 26
27				HsaD _{GH} 27	//////////////////////////////////////		OlaDA _{GL} 27	L		
28			LmeD _{GH} 28	HsaD _{GH} 28						
29						DreD _{er} 29	OlaDA _{ct} 29			
20				Head 30		DraD 30				
21				HsaD _{HL} 30		DieD _{GL} 30				
51				HsaD _{HL} 31		DreD _{GL} 31				
32							OlaDA _{GL} 32	TniDA _{GL} 32		
33		XtrD _{HL} 33		HsaD _{HL} 33						
34	HfrD _{HK} 34			HsaD _{HI} 34						
35	HfrD35	XtrD., 35.	LmeD.,, 35 .	HsaDer 35		DreD ar 35.	OlaDA 35.	TniDA ar 35.		
26	HKJJabe	Http://http://abc	Enter HL 35 ab	HoaD 26		DroD 26	GLUDI GLUDDed	THE TGLOOBE		
30			x x 40	HsaD _{HL} 30		DIED _{GL} 30	01 D 1 48	m m .		
57	HIrD _{KL} 3/ _{bc}	AtrD _{HL} 3/ _{bc}	LmeD _{HL} 37 _b	HsaD _{HL} 3/ _{bc}		DreD _{GL} 3/ _{abcd}	OlaDA _{GL} 37 _{abed}	IniDA _{GL} 3/ _{abcd}		
38						DreD _{GL} 38	OlaDA _{GL} 38	TniDA _{GL} 38		
- 39				HsaD _{HL} 39						TniDB _{GL} 39
40		XtrD _{HI} 40,		HsaD _{HI} 40 _{ab}		DreD _{GI} 40 _{ab}	OlaDA _{CI} 40 _{ab}	TniDA _{GI} 40 _{ab}		
41		1112 11		HsaD., 41		012 110	01. 10	GE ab		TniDB _{er} 41
42				HeaD 42					OleDB 42	THE DGL IT
42				HSaD _{HL} 42					OlaDB _{GL} 42	T TDD 42
45									OlaDB _{GL} 43	IniDB _{GL} 43
44									OlaDB _{GL} 44	TniDB _{GL} 44
45									OlaDB _{GL} 45	TniDB _{GL} 45
46		XtrD _{HI} 46 _{abod}	LmeD _{HI} 46 _{absda}	HsaD _{HI} 46 _{abode}		DreD _{GI} 46 _{brd}	OlaDA _{CI} 46 _{cde}	TniDA _{GI} 46 _b		
47		XtrDru 47.	LmeDur 47.	HsaDur 47.		DreDer 47				
18		VtrD 48	LmaD 48	UcaD 48		DraD 48	010DA 48	TriDA 48	OlaDB 48	ThiDR 48
40		AuD _{HL} 40 _{abcde}	LineD _{HL} +o _{abcde}	HSaD _{HL} 40 _{abcde}		DICDGL48abcde	OlaDA _{GL} 40 _{abcde}	THDAGL40abed	OlaDD _{GL} 40 _{bc}	ThiDD _{GL} 40 _{ab}
49		AtrD _{HL} 49 _{abc}	LmeD _{HL} 49 _{abc}	HsaD _{HL} 49 _{abc}		DreD _{GL} 49 _b	OlaDA _{GL} 49 _{bc}	IniDA _{GL} 49 _b		
50					PseD _{LM} 50	DreD _{LM} 50				
51	<u>/////////////////////////////////////</u>				PseD _{LM} 51	DreD _{LM} 51				
52							OlaDA _{LM} 52	TniDA _{LM} 52		
53							OlaDA _{LM} 53	TniDA ₁₃₄ 53		
54			İ		PseD ₁₁ 54		OlaDA	Laft -		
55			1		LM-		OleDA 55	ThiDA., 55		
		V. D. 57		U.D. CT		D D 57	GIADALM33	THIDALM33		
56		AtrD _{LM} 56 _{abcde}	LmeD _{LM} 56 _{abcde}	HsaD _{LM} 56 _{abcde}	PseD _{LM} 56 _{bcd}	DreD _{LM} 56 _c				
57	//////////////////////////////////////	XtrD _{LM} 57		HsaD _{LM} 57						
58	<u>/////////////////////////////////////</u>	XtrD _{LM} 58 _{bc}	LmeD _{LM} 58 _{bcd}	HsaD _{LM} 58 _{bd}	PseD _{LM} 58 _{bcd}	DreD _{LM} 58 _{abcd}	OlaDA _{LM} 58 _{abcd}	TniDA _{LM} 58 _{abcd}		
59						DreD _{1M} 59	OlaDA _{LM} 59			
60			1			DreD60	OlaDA, 60	TniDA. 60		
60		VteD 61	LmoD (1	HeeD 61	BaaD 61	DroD C	LMOO	TwiDA (1		
61		AITULM01ab	LINED _{LM} 01 _{ab}	nsaD _{LM} 01 _{abc}	rseD _{LM} 01 _{ab}	DreD _{LM} 01 _{abcd}	0	1 filDA _{LM} 61 _{acd}		
62		$\Lambda trD_{LM}62_a$	LmeD _{LM} 62 _{ab}	HsaD _{LM} 62 _{ab}	PseD _{LM} 62 _{ab}	DreD _{LM} 62 _{ab}	UIaDA _{LM} 62 _a			
63	<u>/////////////////////////////////////</u>				PseD _{LM} 63		OlaDA _{LM} 63			
64			LmeD _{LM} 64	HsaD _{LM} 64						
65			LmeD _{1 M} 65	HsaD _{1M} 65						
66		1	1.041	HeaDaree		1	1	TniDA. 66		
00		Vt-D (7	L	H-D (7	DD (7	D-D (7	Ob DA 77	TaiDA (7		
67		AtrD _{LM} 0/ _{ab}	LmeD _{LM} 67 _{abc}	HsaD _{LM} 67 _{abc}	rseD _{LM} 6/ _{bc}	DreD _{LM} 6/ _{bc}	UIADA _{LM} 67	1 niDA _{LM} 67		
68			LmeD _{LM} 68	HsaD _{LM} 68						
69	<u>/////////////////////////////////////</u>	<u> </u>	LmeD _{LM} 69 _{abcd}	HsaD _{LM} 69 _{abd}	PseD _{LM} 69 _{abcd}	DreD _{LM} 69 _{abcd}	OlaDA _{LM} 69 _{bc}	TniDA _{LM} 69 _{bc}		
70			LmeD _{LM} 70 _{ab}	HsaD _{LM} 70 _a	PseD _{LM} 70 _{ab}	DreD _{LM} 70 _{ab}	OlaDA _{LM} 70 _{ab}	TniDA _{LM} 70 _{ab}		
71			LmeD _{M0} 71	HsaD _{M0} 71		HU		/A 1467		
72		1	I meDuo72	HeaD. to 72		1	1	1		
12			LuncD _{MO} /2	113aD _{M0} /2						
73			LmeD _{MO} 73	HsaD _{MO} 73						
74		1		HsaD _{MO} 74	PseD _{NO} 74		1	1		

Xenopus tropicalis western clawed frog Hox D PFC Dist to 3' gene Length Sequence

			XtrD _{AC} 1 _{ab}	7,140	CTGGTCAAAATGACCCATACATCCTCCCAGGCAGCAGTGTCATTC ATCAAAACTGGGGCTCGTCATTAAGGTCTGAATGACCCTGTTTG AATAATCATTTATTGTAACGATTTAATGACGAATAAATGAGGC CCTGTCAGTGGCTAATGAAGGCGGATTCCTGGCAGACAAATAGGG CCAGGTAGGGAGAGACACAACGAATGGACTGGCCGGCCCTCTCTCCC 336 CCTCCAGCTACATCTCAGCTCAGTCCCA
			XtrD _{CF} 5	3,800	27 TTGAGGTAGGGTAACAAATGGCAGAGA
			XtrD _{CE} 6	1.551	39 TTGGCCAAAAGCCTCTTGAGGGAGATTGCAGTTCCCTGG
			XtrD10	3 403	CTIGCAGAACTGTGGTGGCAATAAATGAAATGAAATGACTCACAATCTCT TCCCCAGTCACGTTTTACGAGAGCTGCCAGACAGCGTCTGTTCCC GTTCCCCAGATACTACGGGCCCCCATAACAAAGTTAAGGTCAAGTT 142 aGTGTT
			VtrD 14	5,455	24 GGAACAAGGACTTGAATTTGATGTCTCAAAAGCA
			XIID _{EF} 14 XtrD 11	5,242	
			XUD _{EF} TI _{ab}	5,033	
			XtrD _{EF} 15	4,801	26 TGAGAACAAAGGGTGGGGGGGGAGAAAA
			XtrD _{EF} 18	1,098	АТТІĞТĞІТААААСАААААĞСААААААААААĞAĞAĞĞĞĞ ТІТІТІĞÜĞĞCAĞTAAAĞIĞTAAAATCAATĞĞĞĞĞATITICAA TAATICATATIĞCAAATĞCCATTATĞCAAĞTITIACCTATTAATC TICCCCCTITACTAĞITICGATIĞCATÇĞCICĞTGAAAĞARTEĞC CCGTĞIĞIĞĞĞAACAĞAĞCĞITATAACTCTITAAAAATCATCAĞA 408 AĞĞTAĞAAATIĞACCAAĞTATITCAAĞA
					CACGTGACCCACAGGGAGGCAGCAGCAGCTCAAGGCCATTTTCAAATC TCATTGGCTCGCTTGTCATGTGGTTGTGCAGAGGCCTTCACAATTAC
			XtrD _{EF} 19 _{bc}	162	132 ACAGGGAATGTTTTGCTAGAGATGTCAGCCTACAAAGGACA
			XtrD _{FG} 21 _b	679	22 TAATCAAATGCACCTCATAAAA
			XtrD _{FG} 23 _{abce}	158	AGCGGATTGATTTACTCAGTATTGGTAAATATGATCACGTGGACTC CGCAACCAATGGACGGAGGTTGCAGTCTGCAAAATACTATGATTG 128 TTCTCAGGGAGGGTATTGCATACAGTTAAGAGTGTAA
	for a start of the				AAATCCGCAAGGAATTGCAGTAAATTCCTTTTTTGTTTGAAGAAAA TTTACAACTTGGTAATAGACCTTTTTATGACCTCTGCGGGGCTGTG ATTGGCTCCTTCTGGTCACATGCAGGCTGGGATATTCTTCATGGCC
PEC	Dist to 3' gene 1	Irk Hox D ength Sequence	XtrD _{HL} 35 _{abc}	21,956	154 TTTTGCCTGATTTCCC
FIC	Dist to 5 gene L	engar bequence	XtrD., 40	10.262	GAACAAAGAAAGTATTTCAGGCTATTTGGCAGACAGCTGGGAGAG 53 GTATTTAC
		CTGGTCAAAATGACCCGTGCTTCCTTTCTCCCGATGTGTCATTCAT	VtrD 22	15,202	
		ACTAGTGCTCGTCATTAAGGTACGAATGACGCTGTTCGAATAATCATT	Aud _{HL} 33	16,579	CACCETGATTCCA ATA A ACTITCETETTATCCCCTGAGACTTGACA AG
		TGATGAAGGCGGCCTAGCGACAGGCGAATACATCCAGGTAGAGAAGA	XtrD _{HI} 37 _{bc}	4,957	61 СТААААТАТААТТС
		ATCAGAGGACAGCCCCTGTCCTCAGCCGATGATTGTATGCCCGGATGC			AATAACCGTGTGGCTTTGACCTGTCTGAGCGAGTCGTGCGATAAG
HfrD _{AC} 1 _{ab}	13,773	317 ICIGGGCTIGGCCT	XtrD _{HL} 46 _{abcd}	2,790	74 GTGAAATTCAGGTCACTCAGTCTAACAAA
$HfrD_{\rm DE}10_{\rm bcde}$	3,033	77 ATAACAAAGTTAAGGTCAAGTTAGTGTCT	XtrD., 47	2 212	TGAACTTITTGTACTGCACTGTGTGACTGTCGGCCACGTAAAAATAA 86 TGGAACTTITTGCATATGTTTGCAAATGATTTCCAATGACC
		TAATGACCAAAACTGATATATGGTAATTTCTACATTGGATCACATGAC	All DHL47 abc	2,212	0 100 100 101 101 101 101 100 101 100 1
HfrD _{DE} 9 _{abcd}	250	88 TCGTTTACCCTTAGAATCAATCAAGATGAATTGCACGTCA			GTCTATATGTACCCTGTAGAACCGAATTTGTGTGGGTTCGTACAGTC
HfrD _{EF} 11 _{ab}	7,328	28 TGTTTACAAAACCTTGAACTGTCTAGAC	XtrD _{HL} 48 _{abcde}	1,232	80 ACAGATTCGATTCTAGGGGGGATATATGGTCGATG
HfrD _{EF} 12	6,741	31 CCCAAAGTCTCTTTGCACAGCATAAATAAAC			TGATAAACTTTCTGCTCTGTGATGGCTGCAGCGGTCACATGGCCA CCTAACTTTATTCAGTTGACAGCAAGTAGGAGGGCTTTATGGAGG GAGAAAAAAGACAACACGAGAAAAATTAGTATTTTCTATCCTCA
		TGATGTGCGGGGGGTATGCCTCAAGCCAATTCAAATTCAATTGG TGATGTGCGGGGGGTGTGGCTCAAGGCCATTTCCAAATTCATTGG CTCAGTAGTCATGTGGTTGTACAGAGGCATCCACAATTACAAAGGGA	XtrD _{HL} 49 _{abc}	143	143 GAAATTA ATTGTTTCTATGGCCAAAAGCTCATAGTTCCTAAAGAGCAGAGGG
HfrD _{EF} 19 _{ac}	218	178 AIGHTIGHAGAGAIGICAGCHACAAAGGACA TITTATTAAAGGACACATTAATGTGTAATCAAATGCACCTCATAAAAAT			TTCTTTTTCTAGAAGCTTTCACGTTGAGCAGTTGAAAAGGTATTTTA CTGCAGAAACAGGTTCAACCGAGGGCAAATTTTCTCTCTC
I III D _{FG} Z I abc	807	57 ······1041	XtrD _{LM} 56 _{abode}	11.397	187 GGAC
		AGCGGATTGATTTACTCGCTGTATTGGTAAATACAATCACGTGAGCCC	XtrD 57	10 334	12 TATTATTTATAC
HfrD 22	450	CGCAACCAATAGCTGCAACTGTAGTCGGCAAAATACTATGATTGTTCT	EW	. 5,00 1	CACGTGATCCACCAAATAATTAATTCAGCTCGTCCCTTAAGAAAC
HfrD	158 6 259	27 AGCTGTCGGATGCACAACTGGTACATT	YtrD	8 600	ACAGCGTCGTCATTAATTTGCCAAGCAAAGGACTCTATCAGACTT 105 GAAAACTTGAAGAGAT
nKo .	0,200		Ma D LWOOPC	0,090	TGACAATGGCCCAAGTTGTTGGTATAAATCATTGTAAGTAA
11/ D 05		GACTITIGGTCATGTGAATCTAGTAACTACGTTCATGGCCTTTTCATGAT	XtrD _{LM} 67 _{ab}	7,419	103 CCCAGTITTATT
mifD _{HK} 35 _{abc}	5,928	151 LICC CACGEGATGICATEAAACTEIGETETATGGETAGGGCACETGACAAGCC	XtrD _{LM} 61 _{ab}	37,166	42 GTCATAAATTTACCTCCCAAGCAAAATGACAGGTGC
$HfrD_{KL}37_{bc}$	-1,572	61 AAAATATAATTC	$XtrD_{LM}62_a$	35,469	36 GTCATAAATTTACCTCCCAAGCAAAATGACAGGTGC

		CTGGTCAAAATGACCCATGCATCCTTTCTAGCCCGAAATGTCAT TCATCAAAAAGTTGTCCCGTCATTAAGGTAGGAATGACCCTGT TGGAATAATATTATTATTGTAACGGTATAAGGAATAAATA
LmeD _{AD} 1 _{ab}	59,957	331 CTIGTCCTAAGCTIGATCACTGCTIGGCTGGATIGTT CTIGCAACACTGGCGGTAATAAATGGAATGACTCAAGACACTC TICTCTIGCCTGCCATTTITTTACGGAGCGGTCAGACAGTGTCTG TTCTCTTGCCTGCCATTTITTTACGGAGCGCGTCAGACAGTGTCTG TTCTCTTGCCCTGCCATTTITTTACGGAGCCGCGCAGACAGTGTCTG
$LmeD_{DE}10_{bode}$	2,950	145 CAAGTTAGTTACTOCCAGATACTGGGGGGGGGGGGGGGGG
LmeD _{DE} 9 _{bcd}	191	TATGGTAATTICTACATTGAGACACGTGACGCAATTACTCCTAG 70 AATCGATCAAGATGCATTACACGTCA
LmeD _{EF} 11 _{ab}	5,450	28 TGTTTATAAAACCTTGAACTGTCTAGAC
		GTCGCTGTTCACCATATTTGAGGTGAAAGTCAACCATCAACAAC CACGTGACTCCTAACGAGGTAGTGTCTCAAGGCCATTTTCAAAT TTCATTGGCTTCTCTGTCATGTGGGTCTGFAGAGACACTCACAAT TATACAGAGAATATTTTCCTAGAGATGTCAGCCTACAAAGGAC
LmeD _{EF} 19 _{abc}	207	177 A TTTTATTAGGGAGGCATTATAGTATAATCAAATGCACCTCATAA
$LmeD_{FG}21_{ab}$	726	46 AA AGCGGATTGGTTTACTCCTCATATCGGTAAATATAACCACGTGA
$\rm LmeD_{FG}23_{abce}$	160	GCTCCGTAACCAATGGTTGAAGTCGCTATCTGCAAAATACTATG 130 ATTGTTGAGAGTGGAACGTATCTTTTACTCTTAACAGTGTAA
		GAAGGTGTIGGTGCGTGTACCTATTTCACCGCGTTTACCTATAA TGCATTAAAGCAGGAAGTAACGGGTACAATAACCCCATAGA ATTGGCTAGACGTCGGGAGCTAATGAGTTTATGAGTTGTGTACCTT GGAATTGCACGGCGCGAGCAAGGAACCGATCTTATTGGAGTGTTGTGT CTGCTGGCGGACAGCAACGATCCAAACAATATTGGAAGG
LmeD _{GH} 25	5,468 3,362	235 AAATCTAGACAATAAA 33 AAAATCCATTGGTCTTCCATTAAGGTACAAACA
Line D. as	10.051	AAATCCACAAGGAATTGCAGTAAATTCCTTTTTTGTTTGAAGAA
LmeD _{HL} 35 _{ab}	19,854	52 AATTTACA CACGTGATCGCAATAAAACTTGTTTTATGACAAGGGAGTTGACA
LmeD _{HL} 37 _b	6,869	46 AG
$\rm LmeD_{\rm HL}46_{\rm abcde}$	2,687	ААТААСТСТСБССТТГБАССТБТСТБАССААБТСССАСААТААGG 81 ТБАААТТСАББТСАСААСБТСТААСАААТТТБААААТ
$\rm LmeD_{HL}47_{abc}$	2,053	TGAACTITIGIACTICTITGCGIGGTIGICGGCAAAGTAAAAATA 86 ATGAAACITIGIGATATGTITGTAAATGAITTAGTATGACC
LmeD _{HL} 48 _{abcde}	1,286	GICTATATATACCCIGTAGAACCGAATITGIGTGAIGITATCAG 82 AATCACAGATTCAATICTAGGGGAGTATATGGTCGATG
LmeD _{HL} 49 _{abc}	153	тоаталастестиболтитилитобстатестсибсаслобог лесталаситилитесяритовслосаядия подобородитило обоабабалалалалабасластесбабалалалитабиятит 147 спасетисабалата
LmeD _{LM} 56 _{abcde}	12,504	АПТОТИТОТАТСАСАЛАЛАССАСАСАЛАТГСАСССАТАССАЛАС АССАСТИСТИТИТСАССССИТСАССИТСАССИТСАСАЛАССТАЛАСАЛАС ПИТАСТСАЛАГИССССИТСАССИТСАССИТСАССИССАСАЛАССАСС GGACAATITUCTATICCATICATITATITCACCCCGGGACACC 203 TGACCICTAAACCCTIGACCTITIGGAC
$LmeD_{LM}58_{bod}$	10,151	САССИБАТІТАСТАААТААТТААТІСАСІТАССИСССТААБААА САССОССИСИТАТІАТССАССААССААДСАТСТАТСАБА СПІБАЛАЛСТБАЛСВАГІСССАЛБАТАТАТАТАСААЛАССЫТ ССАСІТАЛСТААТИСТАСІСПІБААССІСТІТІССТААСАТІБСС 198 АСАЛАТССАЛАКСТІССТАСАТАТА
LmeD _{LM} 64	9,650	GAACAATGECGACTGTCAGTGCATCTGCTCCTATTCTTAAAGAC GGTGAGAAAAGGGCCTGGGTCAGTACATGCAGGGTAGTAA ATTTTTCTTTGCGTCATTAGAGAAAGGCTATAAAACTGAGTGCGA 149 ATGTTTCCCAAGGCAGGT AAAGTTCCCAAGGCCAGT AAAGTTCCTTTTTAGGCTACTATGGGATAATAAACCATTAA TTAGGAGTTCCAAGATGACCATTAGGATAATAAACCATTAA TTGGGGAAATAATCATTGTGGTCGTCTATTGGTGGTGTTTGTT
LmeD _{LM} 65	9,074	143 GACCAGAATC
LmeD ₁₁₆ 7	8.770	AAACAGTGCGAGGCTGTTGGGGGCCCGGGCGAAGATTGTAAATC 116 TTTCAGTTTTATTGCCCCGTGAACATATG
LmeD _{LM} 68	8,090	21 ATATTTTACIGTAAAATATAA
LmeD _{LM} 69 _{abcd}	7,246	СТСААТСАGААСААТСТGGTATACAGATCACGTGAACAAATAT GCTTGTATTTTAAGGCAGCGCCTATATTTGTGATTATAAAAGGTT 92 TCCG
		TITATIGGTAGITGAGCCIGAGACTGTTICCATICIATCGGGAAT ACIGICIGCACTGGTATATGGAATGTCIGTAAAACTGCAGAGA CAGGTTAGGACGTATIGTCGCGAGACAAAGGGTGAAGGGTA TACACAAGCAACCGCCGGCGAGAAACTGAGCTAIGCATGAC CAGGTTATGATAAATGTATACAGGTAAAGCTAGCA
LmeD _{LM} 70 _{ab}	7,026	233 AAATGGAACCTTTAA
$LmeD_{LM}61_{ab}$	4,621	42 GTTCATTAAGGGGTGAGTTATTGCTGTATAAGCCAAAGGTCA GTCATAAATTTTGTTGCAAACCCCAATGACAGGTGCATTGATAT
$LmeD_{LM}62_{ab}$	2,302	45 G
LmeD _{MO} 71 LmeD _{wo} 72	19,338 9 621	ТГААТІТАТGТАСТІТІТІСААТААТGГССGAATIGCAITAAACTC GATAIGTATTIATITTATITTAAATAAGAGCAITTIGTATCACITAT TIATCCITIGICITAAIGTAITTAIGIGAACAITTGTAGAACTICCI ACAGCATAGCGIGGACGGGGGGTGATTCAGAITCAIGGAACTICA ATTITICCICITITAGTAAACTIGGITTGGAAATAGTICCGAAAGTA 474 GITCIGAAATGGATAGGACGGGGGGGGGGGGGGGGGGGGG
LmeD _{M0} 73	7,631	27 АЛАЛАЛАЛАЛАДАЛАЛАЛАЛАЛАЛАЛАЛАТТ

			CTGGTCAAAATGACCCATACATCCTTCCGATCCCGAGATGTCA			
			TTCATCAAAAAGTAGCGCCCGCTCGTCATTAAGGTACGAATGA			
			AAATACACCCTCCTGTCAGTGGGTAATGAAGGCAGCTTCAGAG			
			CAGACAAATAGATCCAGGTAGGAGGCGAGAAGAGACAAGTG			
Hsal	D _{AC} 1 _{ab} *	8,977	339 AGGAGGAAGGCTCCGGTCCTTTGCCCGCTCCGAGCCAGTTC			
			TAATGCACCCACACACAAAACACAAAGGCTTGGTCTGTGTTCCTG			
Hsai	D _{AC} 3	3,006	55 GCCACCTAAAGA			
Hsal	D _{CD} 5	2,973	26 TTGAGGGGGGGGGGGGGACAGAGACAGAGA			
Line		700	O TROCCA CONTROCTOR ATCCA COTO A TOCOTTOR			
nsai	D _{CD} 6	783	39 11000040041100100410040010410001100011			
Hsal	D _{DE} 8	4,835	25 ATGTTTTGGATTCCACCTTAATGTT			
			CTTGCAGAACTGTAGTGGCAATAAATGAAATGACTCAGAATCC			
			CITUCUCAGUAGUTITIACGAGAGCIGUCAGACAGIGUUGIT CACGTTCTCCAGATACCAGGGGGCGCCCTGACAAAGTTAAGGTC			
Hsal	DDE10abode*	3.031	142 AAGTTAGTGTCT			
Heal	D 11 *	6 554	28 TGTTTACAAAACCTIGAACTGTCTAGAC			
11541	D _{EF} II _{ab}	0,554	28 1011111111111111111111111111111111111			
Hsai	D _{EF} 12	6,463	32 CUCAAAAGAGATTICCGCAATGIGCAATAAAC			
Hsal	D==13	6 226				
	- 56	0,220	10			
Hsal	D _{EF} 14	5,739	39 GGAACAAAAGGAAATATAGTTATAATGCTTTTAAAAGCA			
Hsal	Dee15	5.278	25 TGAGAAGTTGTATAGAGACAGAAAA			
	Er -	-,	TGCAAAAGAATACCTTGGTATAACCAGATGGTGTGGAGCAGA			
Hsal	D _{EF} 16	5,360	43 G			
Hsal	D _{EE} 17	3.266	29 TITATTCCATTIGTCTCACCTCAGCCTTA			
	Er.	-,				
			ATTTGTATTAAAAACAAAAATGACCTTCTTGGTTAGCAGCGAAG			
			GGAAAAAAATCAATAGTATAATTTTCAATAATTCATAAAGCGA			
			ACGCCATTATGGTAAATTTAACTATTAATCTTATCCTTTACAAA			
			CAGCGGGCATAACTCTTTAAAAAACCTTCAGAAGCAAGAAAAT			
Hsal	D _{FF} 18	1.464	387 TACCAAGTAGCCCAAGAATGTAGATGAGAATTTTATTGA			
	Er ·	.,	GTCGCTGTTGTCCGTGCTTACCCGGCCGGCCAGGCTCTG			
			GAGCACGTGACCCGAGAGGAGGCTGCGGCTCAAGGCCATTTT			
			CAAATCTCATTGGCTTGGTTGTCATGTGGTCGGCAGAGGCATCC			
			ACAATTACACGGGGAATGTTTTCCTAGAGATGTCAGCCTACAA			
Hsal	D _{EF} 19 _{abc} *	208	178 AGGACA			
Hsal	D _{FG} 20*	2,906	33 TGCATGTTCTGGTCGCATGTATAATGCAATAAA			
	D 04 *		TTTTATTAGGGACACATTAATCTATAATCAAATACACCTCATA			
Hsai	D _{FG} 21 _{ab} ⁻	691	46 AAA			
			AGCGGACTGATTTACTCCCGGTATTGGTAAATATGATCACGTG			
			CGGTGGCTCGGGCGCCGGCGGGGGAGCTGCTCGGCGGCGGACA			
Hsal	D _{EG} 23 _{aba} *	162	133 GTGTAA			
Hsal	Dau24	6 120	23 TTTGGTGCTTGATTTCCAGAAAC			
	GH- ·	0,120	20			
			CAACCTCCTCCCACCCCCCCCCCCCCCCCCCCCCCCCC			
			AGGGCTCTTTGAAAACAGGAAGAGCCGAGGTGTCATAAAGCC			
			ATCTAGCGGGCCAGACGTCTGGAGGTAATGAGTTTACGACAGG			
			CCCAGTGCTTTGCTTTGAAACCATCTCATTTTGATGTTTGTGTTT			
Line			OTOCOLOLI LI LOCI I LI LTOCI CI CI LI LOTOCOTOTTI LI LI			
- ESAI	D 05	4 504	GIGGGAGAAAAGGAAAAAIGCAGACAAAACIGGGICIIAAAA			
- ioui	D _{GH} 25	4,591	228 TCTAGACAATAAA			
Hsal	D _{GH} 25 D _{GH} 26	4,591 4,157	228 TCTAGACAATAAA 17 TAGAAACAAACAAACAA			
Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27	4,591 4,157 3,022	0100040AAAA00AAAA10CAGACAAAAC10001C11AAAA 228 TCTAGGACAATAA 17 TAGAAACAAACAAACAA 19 CTATTAATTICTGTGTTTG			
Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28	4,591 4,157 3,022 2,631	219 TCTAGACAATAAA 228 TCTAGACAATAAA 17 TAGAAACAAACAA 19 CTATTAATTCTGTGTTG 31 AAAATCCACTCATTATCCAGGGTTCAAACA			
Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D 30	4,591 4,157 3,022 2,631 17,402	опосодаладоваладосаладосалад (сабасалад Госогс I галаа 228 ТСТАбасалтала 17 ТАбаласаласаласал 19 СТАТТАТТГСТВИТТГ 31 Алалтссастсалттатсслобобтсаласа 29 активителасатссаластатбабосалс			CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA
Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30	4,591 4,157 3,022 2,631 17,402	28 TCTAGAACAATAA 17 TAGAACAATAA 19 CTATTAATTICIGIGITIG 31 AAAATCCACTCATTATCCAGGGTTCAAACA 29 AIGIGTCAACATCCAGCATTGAGGCAAC 20 TATGTGCAACATCCAGCATGAGGCAAC			CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCTCTCCG
Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31	4,591 4,157 3,022 2,631 17,402 16,788	онисколаладоваладоваланислика настолого палаа 228 тетабасаладаа 17 табаласаласаласал 19 станталтегениятия 31 алалтегениятия 29 агону састеанталесаводителаласа 29 агону састеанталесаводителаласа 29 агону састеанталеские састеана 29 агону састеана састабована састаба 24 тапталалаталиятиятиански састаба			CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGCTCTCTCCG ACTTGGAAAGTCCAGGATTCCAAGAATATCACCCGTCCAGG
Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31 D _{HL} 33	4,591 4,157 3,022 2,631 17,402 16,788 15,895	29 TCTAGACAATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICUGUGUTU 31 AAAATCCACCTCATTTATCCAGGGTCAAACA 29 ATGTGCAACATCCAAGCATTGAGGCAAC 34 TAATTAAAATATUGTITTATCCGTAACACAGA 31 GTATTICCGAGAGGTGACAAGTACCTAAAA	HsaD58. *	11 855	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCCTCCG ACTTGGAAAGTGCAGGGTTCCCAAGAATTCACCCGTCCAG GGGGCGGCGGCGGCCCCCGGCCCCCGCCCCCG 108 CGGCCCGCGGCGCCCCCGCCCCCGG
Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31 D _{HL} 33	4,591 4,157 3,022 2,631 17,402 16,788 15,895	28 TCTAGACAATAAA 17 TAGAAACAAACAAACAA 19 CTATTAATTTCTGTGTTTG 31 AAAATCCACTCATTATCCAGGGTTCAAACA 29 ATGTGTCAACATCAAGCAATGAGGCAAC 34 TAATTTAAAATATTGTTTATTCTGTAACACAGA 31 GTATTTCGGGGAGGGTGGCAAGTACCTAAAA	HsaD _{LM} 58 ₆₄ *	11,855	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCTCTCCG ACTTGGAAAGTGCAGGGTCCCCAAGAATATCACCCCGTCCAGG GGGCCGCGGGGGGCCCCCAGGGTAAA CGGGCCCGGGAGCGCCGCCGGCGGTAA
Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31 D _{HL} 33 D _{HL} 34	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588	опосололлационалациалания посого посололлания посого палал 17 тадаласаласаласал 19 стапталтистовитите 31 алалатескатисалесятите 31 алаласкасисатитатесководителаласа 29 автивисалетисаласалитадоссалас 34 талтиталалатативититатистегаласасада 31 егаптисодадаерителегосталала 40 авсивитеодостиссосладоссидаесациалати	HsaD _{LM} 58 ₆₃ * HsaD61*	11,855	CACGIGATIGGCGAAATAATTAATICAGCACGICCCTTAAGAA ACACGGAGTCGITCATTAATCTGCCACGCAAAGGGCTCCTCCG ACTIGGAAGTGCAGGGTGCCCACGATATCACCCGITCCAGG GGGGCCGGGGGGGGGCCCCCGGCGCTCAACCCCCGGCCCCGG 198 CGGGCCGGGGGGGGGGGTATTGCGGGGCGCAGGTAA GTTCATTAAGGGGTGAGTTATTGCGGTGCGAGCCAAAGGTCAC 57 TTCAAAGGGCTTAG
Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31 D _{HL} 33 D _{HL} 34	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588	29 ТСТАБАСАЛААС 17 ТАБАААСАААСАА 17 ТАБАААСАААСАА 19 СТАТТАЛТТІСТВІТТІ 21 ААААТССАСТСАЛТТАГСАĞĞĞĪTCAAACA 29 АТБГӨГСААСАТССАГТАЛТБАĞĞCAAC 34 ТААТТТААААТАТТӨГТТТАТСТБІААСАСАĞA 31 БТАТТТАСĞĞAĞĞĞTGACAAĞIACCTAAAA 40 АĞCTĞIĞĞĞĞATCĞCTTCCCAĞBAĞCĞIĞAĞCAĞIACATT ААЛССĞCAAĞĞAATГССАĞIAAATICCTTITIĞITĞAAĞAA	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} *	11,855 5,973	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCCTCGA GGGGCGGGGGGGGCCCCGGCGCTCCACGCATTCACCGTCCAG GGGGCGGGGGGGGCGCCCCGCCGCAGGTAA GTTCATTAGGGGTGGCGCGCGCGCGGGGCCACGCAAAGGTCAC 57 TTCAAAGGCTTATG
Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31 D _{HL} 33 D _{HL} 34	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588	29 TETAGACAATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICEGGETTEG 31 AAAATCCACTCATEGETTEG 31 AAAATCCACTCATEGETTEG 32 TAATTTAAATATEGETTGATGAGGCAAC 34 TAATTTAAATATEGTTTATTCEGTAACACAGA 31 GIATTICEGGAGGGGTEGACAAGTACCTAAAA 40 AGCTGGTGGGGGATEGCTTCCCCAGAGCGTGAGCAGTACATT AATTCGCCAAGGAATTCCAGTAAATTCCTTITTGTTGAGGAA AATTTACAACTEGGTAATGCACTTATTGGCGCCCGTCACCTCCCCCAGGCGCCGTCACCCAGGAATTCCAGTAATTCGCTTATTGGCGCCCGTCACCCCAGGCGCCCGTCACCCAGGCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCG	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _o *	11,855 5,973 3,899	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCAAGGATATCACCCGTCCAG GGGCCCGGCGGGGTCCCCAAGAATATCACCCGTCCAG GGGCCCGGCGGGGTCCCCCGGCCCTCACCCCCCGGC 198 CGGCCCGGCGGCGCCCCAGGTAAA GTTCATAAGGGTGAGTTATTGCGGTGCGAGCCAAAGGTCAC 57 TTCAAAGGCTTATG GTCATAAATTTTGCTACAAACCACAATGACAGGTGCATTGATA 45 TG
Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31 D _{HL} 33 D _{HL} 34	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588	29 TETAGACAATAAA 17 TAGAAACAAACAAACAAACAAACAAACAAACAAACAAACA	HsaD _{LM} 59 _{cd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} *	11,855 5,973 3,899	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATCTGCCACGCAAAGGGCTCTCTCCG ACTTGGAAAGTGCAGGGTGCCCACGAATTCACCGTCCCAG GGGGCCGGGGGGGGGCCCCCGGCGCCCCCCCCCC
Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{GH} 30 D _H 31 D _H 33 D _H 34	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588	29 ТСТАGАЛАТАА 17 ТАGAAACAAACAAACAA 19 СТАПТААТПССИЯНТИЯ 31 ААААТССАСТСАТГАТГАССАGGGTCAAACA 29 АГСГСГСАСТСАТГАТГАССАGGGTCAAACA 29 АГСГСГСАСТСАТГАТГАССАGGGTCAAACA 34 ТААТТСААСАТССАGCATGACCAACA 34 ТААТТСАGAAGAGGTGACAAGTACCTAAAA 40 АGCTGTGGGGATCGCTCCCCAGAGCGTGAGCAGTACATT АААТССGCAAGGAATGCAGTAAATCCTTITTGTAGACA 41 ТААТТСАGCTGGGTCGCTGCCAGGCAGGCGCCCCCCCCCCTC 40 CGCCTTITTCCGATTCCCCCCCGGAATTCCCCCCCCCCCC	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} *	11,855 5,973 3,899	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCCTCCG ACTTGGAAAGTCAGGGTGCCCCGGCACCTCCACG GGGGCGCGGGGGGCCCCCGGCCCTCCACCCCGGGGGGGGG
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G1} ,27 D _{G1} ,28 D _{H2} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{mbol} * D _{H2} ,35 _{mbol} * D _{H2} ,35 _{mbol} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588	228 TCTAGGAATAAA 17 TAGAAACAAACAAACAA 19 CTATTAATTICTGTGTTTG 31 AAAATCCACTCAATGATGAGGGTCAAACA 29 ATGTGTCAACATCCAAGGATTGAGGCAAC 34 TAATTTAAAATATGTTTTATCCTGAACACAGA 34 TAATTTAAAATATGTTTTATCTGTAACACAGA 34 GACTGTGGGGGGGTGCACGTGAGGCGTGAGCATACATT AAATCCGCAAGGAATGCAGTAAAGACCTTTTGTGAAGAA AATTTACAACTTGGTAATGACCTTTTGTGAGGCAGCCTCCCTTC CGTCATTGCCTCCCCGGGCAGTGCAGCCTTCCCTTC ACGCCCTTTTTCCGATTGCAGGCGTGCAGCCTCCCTTC ACGCCCTTTTTCCGATTGCAGGCGTGCAGCCTCCCTTC ACGCCCTTTTTCCGAGTGATTGCCTGCCAGCCCCCCCCTCCCT	HsaD _{LM} 58 _{6d} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} *	11,855 5,973 3,899	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATCTGCCACGCAAAGGGCTCCTCCG GGGGCCCGCGGGGCCCCCAGGCATCCACGCGCCCCCGG GGGGCCCGCGGGGCCCCCCGGCCCCCACCCCCGG GTGCCTTAGGGGTGGAGTTATGCGGTGCGAGCCAAAGGTCAC GTTCATAAGGCTTATG GTCATAAATTTGCTACAAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCCGTCACGGCATCGCCGCCTATTCTTAAAC CGGTGGAAAAGGCCTGGCCCCTCTTTCAAGCGAGGGTGCTA
Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _H 30 D _H 31 D _H 33 D _H 33 D _H 34	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588	29 TCTAGACAATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICTGTGTTTG 31 AAAATCCACTCATTTATCCAGGGTTCAAACA 29 ATGTGTCACATCCATGAGCATGAGGCAACA 34 TAATTTAAAATATTGTTTATTCTGTAACACAGA 31 GTATTTCCGAGGGGTGGCAGGTCAAACA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCCGTTCCCCGGGCGTGAGCAGTACATT AAATCCGCCAGGAATGCCGTCACGTGAGCAGTACATT AAATCCGCCAGGAATGCCGTCCGCGGCGAGTACAGT ACGTCGTCGCCGCCGGCGGTCATGCCGGCCGCCGCCCTCC 177 TG 33 AATAAGAAACTTGAGTGATTGTTATTTATTGGCCTGTGGAGGTGACA	HsaD _{LM} 58 _{cd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} *	11,855 5,973 3,899	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATGTGCCACGCAAAGGGCTCTCTCCG ACTTGGAAAGTGCAGGGTGCCCACGAGTTCAACGATTCACCGTCCCAG GGGGCCGGGGGGGGGG
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G2} ,27 D _{G2} ,28 D _{F4} ,30 D _{F4} ,30 D _{F4} ,31 D _{F4} ,33 D _{F4} ,34	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380	29 TCTAGACATAAA 17 TAGAAACAAACAAACAAACAAACAAACAAACAAACAAACA	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64	11,855 5,973 3,899 11,225	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCTCCCG ACTTGGAAAGTCCAGGATTCCAAGAATTACACCGTCCAG GGGGCGGGGGGCGCCCCGGCGCCGCCGCAGGTAA GTTCATTAAGGGGTGGCGCGCGCGCGGGGGCGCCCCGG GTCATTAAGGGGTGGCGCCGCAGGTGCATGGAAGGTCAC 57 TTCAAAGGCTTATG GCATAAATTTTGCTACAAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCTGTCACGGCATCTGCCGCCTATTCTTAAAC CGGTGGAGAAAGGCCCTGGCCCTCTTTTCAAGGAGGGTCGTA AATTTTTCTTTGCGTCAATAATGAAGGCCTATAAAATCGAGTTGA 149 AATTTTACCCCAGGCAGGT
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G2} ,26 D _{G2} ,27 D _{G1} ,28 D _{H2} ,30 D _{H2} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{mbol} * D _{H2} ,35 _{mbol} * D _{H2} ,37 _{bc} * D _{H2} 39 D _{H2} 37 _{bc} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554	20 TERGAGAATAAA 20 TETAGAAATAAA 17 TAGAAACAAACAA 19 CTATTAATTICTGTGTTTG 31 AAAATCCACTCATTATCCAGGGTCAAACA 29 ATGTGTCAACATCCAAGCATTGAGGCAAC 34 TAATTTAAAATATTGTTTTATCTGTAACACAGA 31 GTATTTCGGAGGGGTGACAGTTGAGGCAAC 34 GAATTGCGAAGGGAATGCAGTAAACACAGA 40 AGCTGTGGGGATGCCAGGTGAAGCGTGAGCAGTACATT AAATCCGCAAGGAATTGCAGTAATACCTTATTGTTGAGAA AATTTGCAACTGGTAATGGCTGGCAGGGGCGCGCCCCCCTCC CGTCATTGCCTCCCGGTGAATGGCAGTGGAGCGGCCCGCCTCC 177 TG 33 AATAAGAAACTTGGATGATTGTTATTTTATTTG CACGTGATTCCAATAAACTTGTTTTATGGCTGGAGGGGGCGGCTGGACT 60 AGCCAAAATATAATTC 27 GGGAAGGCGAACCTGGAATTGATAAA	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64	11,855 5,973 3,899 11,225	CACGTGATTGGGGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATCTGCCACGCAAAGGGCTCCTCCG GGGGCCCGCGGGGCCCCCAGGATACGCCCCCGG GGGGCCCGCGGGGCCCCCAGGGTAA GTTCATAAGGGTGAGTTATTGCGGTGCGAGCCAAAGGTCAC 57 TTCAAAGGCTTATG GTCATAAATTTTGCTACAAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCCGTCTCACGGCATCTGCAGCGAGCTATTGAAC CGGTGGAAAAGGCCTGGCCCCTCTTTCAAGCGAGGTGCA AATTTTTCTTTGCGGCAGCTGACAAAAGGCTATAAAATCGAGTTGA 149 AATTTTACTCCGGCGCGT
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,26 D _{G1} ,27 D _{G1} ,28 D _{H2} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abco} * D _{H2} ,36 D _{H2} ,37 _{bc} * D _{H2} ,39	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554	29 TCTAGACAATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICTGUGUTUG 31 AAAATCCACTCATTTATCCAGGGTTCAAACA 29 ATGUTGCACACTCATGAGCATGAGGCAAC 34 TAATTTAAAATATTGTTTATTCTGTAACACAGA 31 GTATTTCCGGAGGGTGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCCGTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAAGGAATGCGCTTCCCCGGGCGGTAGCCGTACCATT AAATCCGCCAAGGAATGCGCTTCCCCGGGCGGAGCAGTACATT AAATCCGCCAAGGAATTAGACTTTTTTGAGCCTATTGGCGT CGTCATGGCTGCGGGCGGTGAGCGGAATTCCCCCGCCGCTCC 177 TG 33 AATAAGAAACTIGGATTGTTATTTATTGG CACGTGATCCAATAAACTTGGTTATTTATTGG CACGTGATCCAATAAATTCCATTGTTATTGACGTGAGGGGGGGG	HsaD _{LM} 58 _{cd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64	11,855 5,973 3,899 11,225	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCTCTCCG ACTTGGAAAGTCCAGGGATTCCAAGAATATCACCCGTCCAGG GGGGCCGCGGGGGGCCCCCGGGCTCCACCCCCGGCCCCGG 198 CCGGCCGCGGGGGCCCCCGGGTAA GTCATTAAGGGTGGGTGACTCATGCGGTGCGAGCCAAAGGTCAC 57 TTCAAAGGCTTATATG GTCATAAATTTTGCTACAAACCACAATGACAGGTGCAATGATA 45 TG GAACAATGGTCGCTGTCACGGCATCTGCCGCCCTATTCTTAAAC CGGTGGAGAAAGGCCTGGCCGCCTCTTTCTGAGGGAGGTCAT AATTTTTCTTGCGTCAATATGAAGGCCTATAAAATCGAGTTGA 149 AATTTACCCCAGGCAGT
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G1} ,27 D _{G1} ,28 D _{H1} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abc0} * D _{H2} ,35 _{abc0} * D _{H2} ,37 _{bc} * D _{H2} ,39 D _{H2} ,40 _b *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419	29 TCTAGACATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICUGUGUTTIG 31 AAAATCCACTCATTTATCCAGGGTCAAACA 29 ATGTGCAACATCCAAGCATGAGGCAACA 29 ATGTGCAACATCCAAGCATGAGGCAACA 34 TAATTAAAATATATGTTTTATCGTAACACAGA 31 GTATTICGGAGGGGTGACAAGTACCTAAAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCAGTAAATTCCTTTTGTGTGAGAGA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAAGGAATGCAGTAAATTCCTTTTGTGAGAGA 40 AGCTGTGGGGGATCGCTTCCCCGGGAGCGGGAGCGGTGACATT 40 AGCTGTGGGGGATCGCTTCCCCGGGGAGCGGGAGCGGTGACATT 40 AGCTGTGGGGGATGCGCTGCCCGGGAAGCTGGAGGTTGACA 40 AGCTAATAAATTACTTTCTTTTATGCCTGGGAGGTGACA 40 AGCCAAATATAATTC 27 GAGAAAGACGAAGCTCGAATTATAAA 6 AACAAAGACAGATTTTCCCCCGGGCTGGCCAGGCAGCAGCTGTTA 73 GAGCTTTTACGGCCTGGCAGGCGCGCGCGCAGCTGTTA	HsaD _{LM} 58 ₆₀ * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64	11,855 5,973 3,899 11,225	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCTCCCG ACTTGGAAAGTCCAGGATTCCAAGAATTACACCGTCCAG GGGGCGGGGGGGCGCCCGGCGCGCGGGGGGCAGCCCCGG GTGCATTAAGGGGTGGCGCGCGCGGGGGGGCGCCCCGGG GTCATAAAGGCTTATG GCATAAATTTTGCTACAAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCTGTCACGGCATCTCTTTCAAGGGGGGGCGAG AATTTTTCTTGCGTCGACGGCATCTCTTTCAAGGAGGGTGA AATTTTTCTTTGCGGCGAAGGCTATAAAATCGAGTTGA 149 AATTTTACCCCATTATGAAGTGACAAATGTTACAGGATGAATAAACACA TAATTCACATTATTCAAGATGACAAAATGTTAGAATAAAACACA TAATTCACATTATTCAAGATGACAAAATGTTAGAGTGCTTGCT
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G1} ,27 D _{G1} ,28 D _{H2} ,30 D _{H2} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,39 D _{H2} ,40 _{ab} * D _{H2} ,41	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512	20 ПОКОЛОАЛАЛОКАЛОК	HsaD _{LM} 58 ₅₀ * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65	11.855 5,973 3,899 11,225	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAAGGGCTCTCCCG ACTTGGAAAGTGCAGGGATTCCAAGAATATCACCCGTCCCAG GGGGCCGGGGGGGGCCCCGGGGTAAA GTTCATTAAGGGGTGACGCCGAGGTAAA GTTCATTAAGGGGTGACGCCGAGGTAAA GTTCATAAGGGCTATG GTCATAAATTTTGCTACAAACCACAATGACAGGTGCATTGATA 45 16 GAACAATGGTCGCTGTCACGGCATCTGCCGCCTATTGCTAAAGTGACGGGGGCGCGAGGTAA AATTTTCCTTGCGGCAGGCATTGAAAGGCTATAAAATCAGGTGGA 149 AATTTACCCCCGTTATTGAAAGTCATAAAATGAACGAGTGGA AAAGTTTCCCCCCATTATTGAAAGTCATAAAAATGAAGTGG TATATACAATTATTCAAAGTATTATACATTCAAACAATAACACA TTAATTCAATTATTCAAGAGTACTAAAGATCAAATGAACGAGTTGC GAGGACTCGGGGCGCGAGTCCAAGGCGCTTCTCTGGAGCGCGCTTTGCCG AGTGACTCGGGGCGCAATTCAAGAATCATCAAGCAATGACCCT
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31 D _{HL} 33 D _{HL} 33 D _{HL} 35 _{abco} * D _{HL} 36 D _{HL} 37 _{bo} * D _{HL} 39 D _{HL} 40 _{ab} * D _{HL} 41 D _{HL} 41 D _{HL} 41	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 5,510	29 TCTAGACATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICUGUGUTU 31 AAAATCCACTCATTTATCCAGGGTCAAACA 29 AUGTGTCACATCCAACATCAGGGCTAAACA 29 AUGTGTCACACTCATTTATCCAGGGGTCAAACA 20 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAGTGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAAGGAGTGCACGCTCCCCGGAGCGGAGCAGTACATT AAATCCGCCAAGGAGTGCACGCTCCCCGGAGCGGAGCAGTACATT AAATCCGCCAAGGAGTGCACGCTGCCAGGCGGAGCAGTACATT AAATCCGCCAAGGAGTGCAGTCCAGTAAATTCCTTTTTGTTGAGCAA 40 AGCTGTGGGGGATCGCTTCCCCGGCGGCAGAGCGTGCGCCTCCCCCGCAGTCCATTCCCTGCCGCCGGCGGAAATTCCCTTTTGGTGCAGGCCTTGCCGGCCTGCCGCCTCGCCGCCTCGCTGCGCGCGCC 17 TG 17 TG 10 AGCAAAATATAATTC 27 GAGAAAGACGAGCTGAAATTCCATTATAA 10 AGCCAAAATATAATTCC 27 GAGAAGCAGACGTCGAAATTATAA 10 AGCCCAAAGCAGCTGCAAATTATAA 10 AAAGCACCCTGGTCCCC 12 AAAAGCCCCTGGTCCCC 13 AAAAGCCCCTGGTCCCC	HsaD _{LM} 59 ₆₄ * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 65	11,855 5,973 3,899 11,225 10,461	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCTCTCTCCG ACTTGGAAAGTCCAGGATTCCAGGATTATCACCCGTCCAG GGGGCCGCGGGGGCGCCCCGGCGTCATACCCCCCGGCCCCGG 198 CCGGCCGCGGGGGCCCCCGGGTAA GTTCATTAAGGGTTGATTGCGGTGCGG
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	$\begin{split} D_{G_1,25} \\ D_{G_1,26} \\ D_{G_1,27} \\ D_{G_1,28} \\ D_{H_1,30} \\ D_{H_2,33} \\ D_{H_2,33} \\ D_{H_2,33} \\ D_{H_2,33} \\ D_{H_2,34} \\ D_{H_2,35} \\ D_{H_2,36} \\ D_{H_2,39} \\ D_{H_2,39} \\ D_{H_2,39} \\ D_{H_2,40} \\ D_{H_2,42} \\ \end{split}$	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519	29 TCTAGACATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICUGUGUTTIG 31 AAAATCCACTCATTTATCCAGGGTCAAACA 29 ATGTGCAACATCCAAGCATGAGGCAACA 34 TAATTAAAATATTGTTTTATCGTAACACAGA 34 TAATTAAAATATATGTTTTATCGTAACACAGA 31 GTATTICGGAAGGAGTGACAAGTACCTAAAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCAGTAAATTCCTTTTGTGGAGT CGTCAATGGCTGGGGGATGGTACAGTACATTCAATGCCTATTGGGGT CGTCAATGGCTCGCGCGCGCGCGCAGCGCGGCAGCAGTGACATT 17 TG 33 AATAAGAAACTTGAGTAGAACTTTTTTTATGGCTGAGAGTTGACA 60 AGCCAAAATATAATTC 27 GAGAAAGAACGAAGCTCGAAATTATAAA GAACAAAGACAGTATTACACCTGGGCTGGCAGGCAGCAGCTGTTA 73 GAGGTATTTCCGCCCTGGCAGTGCGGC 18 AAAAGACCCCTGGTTCAC 22 CGTTTTACACCTGTTGGGGGC	HsaD _{LM} 58 _{cd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66	11,855 5,973 3,899 11,225 10,461 10,176	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACCCAAGGGCTCTCCCG GGGGCGCGGGGGGCCCCCGCCCCCCCCC
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G2} ,28 D _{H2} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{mbol} * D _{H3} ,36 D _{H3} ,35 _{mbol} * D _{H4} ,37 _{bc} * D _{H4} ,37 _{bc} * D _{H4} ,40 _{mb} * D _{H4} ,42	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519	228 TCTAGGAATAAA 17 TAGAAACAAACAAACAA 19 CTATTAATTICTGTGTTTG 31 AAAATCCACTCATTTATCCAGGGTCAAACA 29 ATGTGTCAACATCAAGCATGAGGCAAC 34 TAATTTAAAATATTGTTTTATTCTGTAACACAGA 31 GTATTTCGGAGGGGTGGACAAGTACCTAAAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAGGGAGTGGCAGGACTGTAGCAGGCAGTACATT AAATCCGCGAGGGATGCGCTGCCGGGAGCGGGAGCAGTACATT AAATCCGCGAGGGATGCGCTGCCCGGGAGCGGGAGCGGACACTT AAATCCGCGAGGGATGGCATGGCAGTACATTCATTGGCCTTTGGGTGCGCCTGCCGCCGGCGGCAGGCGGCAGGCGCGCCGCCTGCCT	$HsaD_{LM}58_{bd}^*$ $HsaD_{LM}61_{abc}^*$ $HsaD_{LM}62_{ab}^*$ $HsaD_{LM}64$ $HsaD_{LM}65$ $HsaD_{LM}66$	11,855 5,973 3,899 11,225 10,461 10,176	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATTCAGCACGCCCAAGGGCTCTCTCCG ACTTGGAAAGTGCAGGGATTCCAAGGATTCACCGTCCCCG GGGGCCGCGGGGGGCCCCCGGCGCCCAGGTAA 198 CCGGCGCGGGGGGCCCCCGGGGTAAA 198 CCGGCGGGGGGGGGCGCCGGAGGTAAA 198 CCGGCGGGGGGGGGGGGGCGCAGGTAAA 198 CCGGCGGGGCCGCGGGGTAAA 198 CCATTAATTTGCCTACAAACCACAATGACAGGGCCATTGATA 45 T0 GGCATAAATTTGCCTGCACGGCCACTTCAAGGAGGGCGTGTA AAGTTTCCTTGCGTGCAGGCCACTTCAAGGAGGTCGTA AAGTTTCCCCCGGTTGATGAATTATACATCAAGGAGGTCGTA AAGTTTCCCCCCATTATGAATTATACATCAAGGAGGTGGTA AAAGTTTCCCCCCATTATGAATTATACATCAAACAATAAACCAGTGCG GGGCGGCGGCGGCGGGGGTGGTA 199 AATTTACCCCCGGCCCGGG TGACAATCGTCGGGCGCCGGGCTCCTTCTCGGAGCTGCTT 24 CGCTTGGCGGGCACTGGCCCCGGG TGACAATCGTCGGGCGCGCGTGGGGTGGG
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{GH} 25 D _{GH} 26 D _{GH} 27 D _{GH} 28 D _{HL} 30 D _{HL} 31 D _{HL} 33 D _{HL} 33 D _{HL} 34 D _{HL} 35 _{bbc0} * D _{HL} 39 D _{HL} 40 _{ab} * D _{HL} 41 D _{HL} 42 D _{HL} 46 _{brob} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614	29 TCTAGACAATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICUGUGUTTA 31 AAAATCCACTUGUTTTG 31 AAAATCCACTUCATTIATCCAGGGTTCAAACA 29 ATGTGTCAACATTCAACCATGAGGCAACA 34 TAATTICAGAGAGGTGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAGTGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAGGAATTCCGTTCCCCGGAGCGTGAGCAGTACATT AAATCCGCCAGGAATTCCGTTCCCCGGAGCGTGAGCAGTACATT AAATCCGCCAGGAATTCCGTTCCCCGGCGGAGCAGTACATT AAATCCGCCAGGAATTCCGGTGCAGCGGCAGTGACATTC AAATCCGCCAGGAATTCCCGGTCGAGCGGCGCCCCCCCCC	HsaD _{LM} 58 ₆₄ * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66	11,855 5,973 3,899 11,225 10,461 10,176	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCTCTCCCG ACTTGGAAAGTGCAGGGTGCCCAGGATTCACCAGTGCCCAG GGGGCCGCGGGGGCGCCCCGGCGTCCACCCCCCGGCCCCGG 198 CCGGCCCGGGGCGCCCGCGGTAA GTTCATTAAGGGTTGATTGCGGTGCGAGCCAAGGTCAC 57 TTCAAAGGCTTATG GGCATAAATTTTGCTACAAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCTGTCACGGCATCTGCCGCCTATTCTTAAAC CCGTGAGAAAAGGCCCTGGCCGCCTCTTTCTAAGGCGAGGTCAT AATTTTTCTTGCGTCATAATGAAGCCACAATGACAGGTGCA TAATGCTCCCCCGGCGCGCCTCTTCTCAAGCGAGGTCGT AAAGTTTCCCCCGGCGCGCCTCTTTCTAAAATCGAGGTGGT AAAGTTTCCCCCGGCGCGCCCTCTTTCTAAAATCGAGGTGGT 149 AATTTTACCCCAGGCAGGT AAAGTTTCCCCCGGCGCGCCGGCGCCCTTCTTCAAGCAGAGGTCGT 151 GCATTTTCCGGGCCAGGTCCAAGCAAATGTTTATGTGCTTTGCGT 151 GCATTTTCCGGGCGCAGTCCCGCGGG CGCCTGGGGGGCGACTGGCCCGGGGGGGGGCCGGGCC
Hsali Hsali Hsali Hsali Hsali Hsali Hsali Hsali Hsali Hsali Hsali Hsali Hsali Hsali	D _{G1} ,25 D _{G1} ,27 D _{G2} ,27 D _{G1} ,28 D _{H1} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 D _{H2} ,39 D _{H2} ,39 D _{H2} ,41 D _{H2} ,40 _{ab} * D _{H2} ,41 D _{H2} ,42 D _{H2} ,46 _{abcob} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,588 13,285 5,380 12,554 12,419 9,512 6,519 2,614	228 TCTAGGAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTATTAATTICTGTGTTTG 31 AAAATACCATCCAAGGATTGAGGCAACA 29 ATGTGTCAACATCCAAGGATTGAGGCAACA 34 TAATTTAAAATATTGTTTTATCCGGGGGCAACA 34 TAATTTAAAATATTGTTTTATCCGGGGGCAACA 34 TAATTCGCAGGGGTCGCACCCGGGCGGGCGCGTACATT AAATCCGCAAGGAATTGCATTAGACCTTATTGTGAGAA 40 AGCTGTGGGGATCGCATCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCAATGACCTTTTGTTGAGAAA AATTTGCACAGGGATTGCCAGTGCAGGCGTGAGCAGTACATT AAATCCGCAAGGAATGCCGTCACTGCAGGCGCGCGCCGCCCTCC 177 TG 33 AATAAGAACCTGGGTGATGGATTGTTATTTGTGCCGCGCGCCCCCCCC	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66 HsaD _{LM} 67 _{abc} *	11,855 5,973 3,899 11,225 10,461 10,176 10,138	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACCCAAGGGCTCTCCCG ACTTGGAAAGTCCAGGGATTCCAGAATATTCACCCGTCCCGG GGGGCGCGGGGGGCCCCCGGCCGCCGGGAGGCACCGG GTCATTAAGGGGTGGCGCCGCAGGTAA GTCATTAAGGGGTGGCGCCGCAGGTGCATGCATTGATA 45 TG GAACAATGTCGCGGCGCCGCCTCTTTCTCAAGGAGGTCGA CGGTGGAGAAAGGCCCGGCCC
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,26 D _{G1} ,27 D _{G1} ,28 D _{H2} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{mbol} * D _{H2} ,36 D _{H2} ,35 _{mbol} * D _{H2} ,37 _{bc} * D _{H2} ,37 _{bc} * D _{H2} ,40 _{mb} * D _{H2} ,42 D _{H2} ,46 _{mbom} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,523 13,285 5,380 12,554 12,419 9,512 6,519 2,614	228 TCTAGGAATAAA 17 TAGAACAATAA 17 TAGAACAATAA 19 CTATTAATTICTGTGTTTG 31 AAAATCCACTCATTTATCCAGGGTTCAAACA 29 ATGTGTCACACTCATTTATCCAGGGTTCAAACA 29 ATGTGTCACACTCAGGCATGAGCAACA 31 GTATTICGGAGGGTGGACAAGTACCTAAAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGGCAGGGATGCGCTGCCGGGAGCAGGACGTACATT AAATCCGGCAGGGATGCGGTCAGTACCTAAAA 40 AGCTGTGGGGGGATCGCTTCCCCGAGGCGTGAGCAGTACATT AAATCCGGCAGGGATGCGCTGCCGGGAGTGAGCAGTACATT AAATCCGGCAGGGATGCGGTGGCAGGCGGGCGCGCGCGCCTCC 177 TG 33 AATAAGAAACTTGGATTGTCCCCGGCGGATTGCGGCCGCCGCCGCCTCC 177 TG 33 AATAAGAAACTTGGATTGTCCCCGGCGGAATTCCCCCGCGCATC 27 GAGAAAGAACGTGGAATTGTTATTGGCTGGAGGGCGCCAGGCAGC 28 AAAAGAACGGAGCTCGAAATTATAAA GAACAAGAAGACGATTTCCCCCGGGCTGGCAGGCCAGCCGGCTGTA 73 GAGGTATTACCGGCTGGCCAGGCCGGCCAGGCAGCTGTA 73 GAGGTATTACCGGTGGCCGC 18 AAAAGACCCCTGGTCACC 22 CGTTTTACACTGTTGGTCGCC AATAACTCGTTGGCTGGCCGGACAGTCGGACAATA 83 AGGTGAAATGCAGGTCGACAGGCGCCCAAAGTCGAGCAAAT 83 AGGTGAAATGCAGGTCGACAGGCGCTGAACAAGTCGAGCAATA 83 AGGTGAAATGCAGGTCGCACAGGCGCTGAACAAGTCGAGCAAAA	$HsaD_{LM}58_{bd}^*$ $HsaD_{LM}61_{abc}^*$ $HsaD_{LM}62_{ab}^*$ $HsaD_{LM}64$ $HsaD_{LM}65$ $HsaD_{LM}67_{abc}^*$ $HsaD_{LM}67_{abc}^*$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,388	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATCTGCCACGCAAGGGCTCTCTCCG ACTTGGAAAGTGCAGGGTGCCCACGACTAAGGGCTCCACGA GGGGCCGCGGGGGGGCCCCCGGCGCCAGTAA GTCATTAAGGGGTGGCCCCCGGCGCGAGGTAA GTCATTAAGGGGTGGCCCCCGGCGAGGTAA GTCATTAAGGGTGGCGGCGCCGAGTAA GTCATTAAGGGCGGCGGCGCGGGGGGCCCAGGGAA GGCATAGTTGCCGCGCGCCTTTTCAAGCGAGGGCGTGA AAGTTTTCCTGGCCCCTTTTCAAGCGAGGGCGGA AAGTTTCCCCCCATTAGAATCAACACAACA
Hsala Hsala Hsala Hsala Hsala Hsala Hsala Hsala Hsala Hsala Hsala Hsala Hsala	D _{G11} 25 D _{G12} 25 D _{G12} 27 D _{G12} 28 D _{H2} 30 D _{H2} 31 D _{H2} 33 D _{H2} 33 D _{H2} 34 D _{H2} 35 _{abc0} * D _{H2} 35 _{abc0} * D _{H2} 37 _{bc} * D _{H2} 39 D _{H2} 40 _{ab} * D _{H2} 40 _{ab} * D _{H2} 46 _{abc0} * D _{H2} 46 _{abc0} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005	228 TCTAGACATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICUGUGUTU 31 AAAATCCACTUGUTUTU 29 ATGTGCAACATTAACAACAA 29 ATGTGCAACATCAAGCATTGAGGCAACA 34 TAATTTAAAATATTGTTTTATTCTGTAACACAGA 31 GTATTICOGAGGGGTGGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AATTCCGCAAGGATTGCAGTAAATTCCTTTTTGTTGAGCAA 40 AGCTGTGGGGACGCTGCCCCGAGAGCGTGAGCAGTACATT AATTCCGCCAGGAATTGCCTTCCCCGGAGCGTGAGCAGTACATT AATTCCGCCAGGAATTGCCGTTCCCCGGAGCGTGAGCAGTACATT AATTCCGCCAGGAATTGCCGTTGCCGGCGGAGTTGACAGT CGCGTATTGCCTGCGGCGGCGGAGGTGAGCAGTGCAG 40 AGCTAAAATTGTATTATGCCTTTTTGTTGAGCAA 40 AGCTAAAATTGGATTGTAATTTTATTTG CCCGGTGATTCCCTGAATTGCCCGGCGGCAGGCGGCGCCTGCCT	$HsaD_{LM}59_{ca}^{*}$ $HsaD_{LM}61_{abc}^{*}$ $HsaD_{LM}62_{ab}^{*}$ $HsaD_{LM}64$ $HsaD_{LM}66$ $HsaD_{LM}66$ $HsaD_{LM}67_{abc}^{*}$ $HsaD_{LM}68$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398	CACGIGATIGGCGAAATAATIAATICAGCACGICCCTIAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCCTCTCCCG ACTIGGAAAGTGCAGGGATCCCAGAATATCACCCGTCCAG GGGGCCGCGCGGGGGCCCCCGGCCTCCACCCCCGGCCCCGG 198 CCGCCCGCGGGGCGCCCCGCGGTAA GTICATAAGGGTGAGTTATIGCGGTOCGAGCCAAGGTCAC 57 TICAAAGGCTTATG GGCATAATITIGCTACAAACCACAATGACAGGTGCATIGATA 45 TG GAACAATGGTCGCGCGCGCGCCTCTTCTCAAGGAGGGTCAT AATITTICTTGGGCGCAATATAGAAGGCTATAAAATCGAGGTGA 149 AATITTACCCCAGGCAGCTCTTTCAAGGAGGGTGAT 149 AATITTACCCCCAGGCAGGT AAAGTTICCCCCAGGCAGGT AAAGTTICCCCCCATTATGAAGGCAATAAAATCGAGGTGCA TAATGCGGGCGCAGGTATCCAGGCGCTTTCTGGAGGGGCGTTG 151 GCATTTTCCAAGGAGATC 24 CGCCTGGGCGGCACTGGCCGGGGGGGGC TGACAATGGCCCGGGCACTGGCCGGG TGACAATGGCCCGGGCACTGGCCGGGG TGACAATGCCCCGGGTGGGTGGAAATCATCGTAAGTAATAC CCTGAACGTTCCCGGGCTGAGTTGACGGCCGCCGGGAGCTGT 119 AAATCTTCCCGGTTTATGCTTAGCGCGGGCCGCGCGGGAGCTGT 17 AATTTCCAATATAA
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G1} ,27 D _{G1} ,28 D _{HL} ,30 D _{HL} ,30 D _{HL} ,33 D _{HL} ,33 D _{HL} ,35 _{abcd} * D _{HL} ,41 D _{HL} ,42 D _{HL} ,46 _{abcod} * D _{HL} ,47 _{abc} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,523 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005	20 TELGAGAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTATTAATTICTGTGTTTG 31 AAAATCCACTCATTAATCCAGGGTTCAAACA 29 ATGTTGTCAACATCAAGCATTGAGGCAAC 34 TAATTTGAACATCCAGGCTTGAGGCAACA 31 GTATTTCGGGGGGTGGCAGGCTGGACAGGTGAGAGTTGAGAA 40 AGCTGTGGGGATGCGCTTCCCCAGAGCGTGGAGCAGTACATT AAATCCGCAAGGAATTGCAGTAATAGTCCTTHTGTTGAGAA AAATCCGCAAGGAATGCAGTAATAGTCCTTHTGTTGAGAA AAATCCGCAAGGAATGCAGTGAATAGTCCTTHTGTTGAGAA AAATCCGCTHTGCTGCGGCGGCGCGCCGCCCCCCTCC 177 TG 33 AATAAGAAACTTGGTGATGGATGGATGGTGGCGGCGCCGCCGCCTGC 177 TG 33 AATAAGAAACTTGGAGTGATTGTTATTTATGGCTTGAGGAG 40 AGCCAAATAATATTC 27 GGGAAGGCGAAGTCGGAATTGTTATTTATGGCTTGAGGAGGTGGAG 40 AGCCAAATAAAATTC 27 GGGAAGGCGAAGTCGGAATTGTTATTAAA GAACAAAGACCCTGGTTCAC 28 AAAAGACCCTGGTTCAC 22 CGTTTTACGGCTTGGCGCGGGGCGCC AATAACTCGTTGGCTTGACCGGCTGCGAACAAGTCGAGCAATA 33 AGTGAAATCCAGGTCACAGGTCGAACAAGTCGAACAATTGGAAAT 16 AATGAAAGTCGGGCTTGGCCGCGCTGCCAGGCGAGCAATA 33 AGTGAAATGCAGGTCCTGGCCGCGCCTGCCCGAAGTCGAGCAATA 34 GGTGAAATGCAGGTCCTGGCTGCCGCAGTCGAACAAGTCGAGCAATA 35 AGTGAAATGCAGGTCCTGGCTGCCGCCTGCCCGCAAGTCGAGCAATA 36 AATGAAAGTCGGGTTTGCCCGCGCGCCTGCCGCAGTCGAGCAATA 36 AATGAAAGTCGGGCTTGGCCGCGCCTGCCGCAAGTCGAACAAGTCGAGCAATA 37 GAGGTGAATGCAGGTCCTGGCCGCGCCTGCCCGAAGTCGAACAAGTCGAGCAATA 38 AGTGAAAGCCAGGTCCTGGCCGCCTGCCCGCAGTCGAACAAGTCGAAGCAAAAT 36 AATGAAAGTCCGTGGTTGCCCGCGCGCCGCCGCCGCCAGGCGACGCGGCC AATAACTCGTGGCCTTGCCCGGCGCCGCCGCCGCAAGTCGAACAAGTCGAGCAAAT 36 AATGAAAGTCCGGTTGCCCGCGCGCGCCGCCGCCGCCAAGTCGAACAAGTCGAGGCAATA 36 AATGAAAGTCCGTGGTTGCCCGCGCGCGCGCGCGCAAGTCGAACAAAGTTGGAAATGCAGGTCGCCGCGCGCG	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66 HsaD _{LM} 66	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACCCAAAGGGCTCTCCCG ACTTGGAAAGTCAGGGGTGCCCCACCCACCAAAGGGCTCCCCGG GGGGCCGCGGGGGCCCCCGCCCCCCCCC
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,26 D _{G1} ,27 D _{G2} ,28 D _{H2} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{mcd} * D _{H2} ,35 D _{H2} ,35 ^{mcd} * D _{H2} ,37 ^{mc} * D _{H2} ,40 _{mb} * D _{H2} ,40 _{mb} * D _{H2} ,42 _{mbcd} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005	228 TCTAGACAATAAA 17 TAGAAACAAACAAACAA 19 CTATTAATTICTGTGTGTTTG 31 AAAATCCACTCATTTATCCAGGGTTCAAACA 29 ATGTGTCACATCCAGGCTTGAGGCAACA 34 TAATTTAAAATATTGTTTTATTCTGTAACACAGA 31 GTATTTCCGGAGGGTGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCAGTAAATTCCTTTTTGTTGAGCAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAAGGAATGCAGTAAATTCCTTTTTGTTGAGCAA 40 AGCTGTGGGCGGATCGCTTCCCCGGGCGAATTGCAGTACATT AAATCCGCCAAGGAATGCAGTAAATTCCTTTTTGTTGAGCAA 40 AGCTGATGCCGCGGGCGGCGGGCAGGCGGCGCCCCCCCCTCC 177 TG 33 AATAAGAAACTTGGATTGTCAGTGAAATTCTTTTTGCC 177 TG 33 AATAAGAAACTTGGATTGCCCGGCGGCAGGCCGGCAGGCGGC 18 AAAGAACGAAGCTGGAAATTCCTTGGGTGCAGGCCGGCCG	$HsaD_{LM}58_{bd}^*$ $HsaD_{LM}61_{abc}^*$ $HsaD_{LM}62_{ab}^*$ $HsaD_{LM}64$ $HsaD_{LM}65$ $HsaD_{LM}66$ $HsaD_{LM}67_{abc}^*$ $HsaD_{LM}68$ $HsaD_{LM}69_{abd}$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATGTGCCACGCAAGGGCTCTCTCCG ACTTGGAAAGTGCAGGGGTGCCCACGACGACGACGGCCTCCACG GGGGCCGGGGGGGCCCCCGGGTAAA GTTCATTAAGGGGTGGCCCCCGGGTAAA GTTCATAAGCGGTGACGCCCCAGGTAAA GTTCATAAGCGGTGGCCGCCGCAGTAAA 45 TG GAACAATGGTCGCTGTCACGGCATCGCCGCCCTATTCTTAAAC CGGTGGAAAAAGGCCTGGCCACTCTCTTCAAGGAGGTCAT AATTTTTCTTGCGTCATAATAGAAGCTATAAAATCGAGGTGGA AATTTTCCCCCCATTAGAATCATCAAAACAATAAAATCGAGTTGA 149 AATTTTACCCCAGGCAGTCCAGGCGCTTCTTCGGAGGTCGT AAAGTTTCCCCCATTAGAATCATCAAAATCAACGATAAGAATG 151 GCATTTTTCTGGGCAATCCAGGGCG TGACAATGGCCGGGCCACGGCCGGG TGACAATGGCCGGGCACTGGCCGGG TGACAATGGCCGGGCACTGGCCGGG TGACAATGGCCGGGCACTGGCCGGG TGACAATGGCCGGGCACTGGCCGGG TGACAATGGCCGGGCACTGGCCGGG TGACAATGGCCGGGCACTGGCCGGG TGACAATGGCCGGGCACTGGCCGGGC TGACAATGCCCGGGTTGTGGTGGTGAAAATCATCGTAAGTAA
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G1} ,27 D _{G1} ,28 D _{H1} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abco} * D _{H2} ,35 _{abco} * D _{H2} ,37 _{bc} * D _{H2} ,37 _{bc} * D _{H2} ,40 _{ab} * D _{H2} ,41 D _{H2} ,46 _{abcob} * D _{H2} ,47 _{abc} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314	228 TCTAGACATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICUGUGUTTA 31 AAAATCCACTGUGUTTA 29 ATGTGCAACATTAACAACAA 29 ATGTGCAACATCAAGCATTGAGGCAACA 34 TAATTICAGACATCCAAGCATTGAGGCAACA 34 TAATTICAGAAGAGTGGCACATGAGCCAGTACATT AATTCCGCAAGGAGTGGCACAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AATTCCGCCAGGAGTGCACTCCCGAGAGCGTGAGCAGTACATT AATTCCGCCAGGAGTGCACGCTCCCCGAGAGCGTGAGCAGTACATT AATTCCGCCAGGAGTGCCGCTCCCCCGAGAGCGTGAGCAGTACATT AATTCCGCCAGGAGTGCCGCTCCCCGGAGCGTGAGCAGTACATT AATTCCGCCAGGAGTGCCGCTCCCCGGGCGGCGAGCAGTACATT AATTCCGCCAGGAATTGCCGTGCCAGGCGGCAGTGCGCCCCGCCTCC 177 TG 33 AATAAGAAACTTGGATTGTATTTTATTTG 27 GAGAAGACGATTCCAGTAAATTGCTTTGTGGCGCCGCCGCCGCC 18 AAAAGACGCATTGTCTGCCGGCCGCCGCCCGGCCGCC 18 AAAAGACCCCTGGTCGCC 22 CGTTTTACCGCTGGCGCCAGGCCGGCCCGGCCAGAAATTGGAACT 33 AGTGGAAATGTCCGTGGGCGCCGCAGACGAGCAGCAATA 34 GGTGGAAAGCCGTGTGGGCGCCGCAGACGAGCAGCAATATGGAAAT 35 AATGACAGTTGTGTATGTGTGGAGCAATATGGAAAAT 36 AATGAAGTTGTGGATTGTGTGGCGCGCCAAAGGCCAAAAT 37 GGGGAAAGCCGGTCCTGGGCGCAATATGGAAATTGGAAAAT 38 AATGGCGAATGTCCTGGGGCGCCGAATGTGGGAACAATGGCAAAAT 39 AGTGAAAGTTGTGGATTGTGGAGCGAATATGGAACATAGCCAAAAT 30 AGTGAAAGTTGTGGATTGTGGAGCGAATATGGAACATAGCCAAAAT 30 AGTGAAAGTTGTGGATTGTGGGCGCGCGCCGAATGACGCGAAAATTGGAACATTGGAACATTGGAACATTGGAACCCTGTGGGCGAATATGGAAATTGGAACATTGGAATGACCCTGGGGCGAATGACGGACG	HsaD _{LM} 59 _{ca} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66 HsaD _{LM} 67 _{abc} * HsaD _{LM} 69 _{abd}	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCTCTCTCG ACTTGGAAAGTGCAGGGTGCCCACGAGTCCACGAAGGGCTCCCCGG GGGGCCGCGCGGGGGCGCCCGCGCCTCAACCCCCCGGGCCCCGG T198 CCGCCCGCGGGGCGCCCGCGGTAAA GTTCATTAAGGGTGAGTTATTGCCGTCCGGGGCCCAGGGAA GTTCATAAATTTTGCTACAAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCTGTCACGGCATCTGCCGCCCTATTCTTAAAC CGGTGAGAAAAGGCCTGGCCCCTCTTTCTCAAGGAGGGTGTA AATTTTTCTTTGCGGCATATATGAAGGCTATAAAATGAGGTGCA TAATTCAATTATTCAAGGAGGCATTGAAAATCGAGGTGCA TAATTCACCCCAGGCAGGT AAAGTTTCCCCCAGGCAGGCCCTTTCTCTGAAGCAGGGTGCT 151 GCATTTTCCAGGAGGCATTCCAGGCGCTTTCTTGGGCGCAGGTGCT 151 GCATTTTCCGGGCGCAGTTCCAGGGCCTTCTCTGAGCTGCTGC 4CGGCTGGGCGCGCACTGGCCGGG TGACAATGCCCGGGTGGTGTGTGTAAATCATCGTAAGTAA
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G1} ,28 D _{H1} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abc0} * D _{H2} ,35 _{abc0} * D _{H2} ,35 _{abc0} * D _{H2} ,35 _{abc0} * D _{H2} ,37 _{bc} * D _{H2} ,39 D _{H2} ,41 D _{H2} ,42 D _{H2} ,46 _{abc00} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,523 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314	228 TCTAGGAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTATTAATTICTGTGTTTG 31 AAAATCCACTCATTAATCCAGGGTTCAAACA 29 ATGTGTCAACATCAAGCATTGAGGCAAC 34 TAATTTAAAATATTGTTTTATTCTGTAACACAGA 31 GTATTTCGGAGGGTGGCAGCGTGACACAGAC 40 AGCTGTGGGGATGCGCTCCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATTGCAGTAATACCTTAAAA 40 AGCTGTGGGGATGCGCTCCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCGCTACCTAAAA 40 AGCTGTGGGGATGCGCTCCCCCGGGAGCGGGAGCAGTACATT AAATCCGCAAGGAATGCGGTGAATAGCCTTTTTGTTGAGAA AATTTGCAACTTGGTAATAGACCTTTTTGTTGGGGT CGTCATGGCTCCCGGCTGGCAGGGGAGCGGCCCCGCCTCC 177 TG 33 AATAAGAACCTGGATAAAACTTGGTTTTATGGCTTGAGGAGGTGACA 60 AGCCAAATATAATTC 27 GGGAAGGCGAAGTCGCAATTGTTATTATG 27 GGGAAGGCGAAGTCGGAATTGTTATTAAA 30 AGCCAAATATAAATTC 27 GGGAAGGCGAGCTGGCCGGCGGGCGC 18 AAAGGACCCAGGTTCAC 22 CGTTTTTACGGCTTGGCCGCGGGCGGCGCGGGGGGGCGCGGCGGC 18 AAAGGACCCTGGTTCAC 22 CGTTTTTACGGCTTGGCCGCGGGCGGCGGGGGGGCGAGCGGCTGCC AATACCTCGTTGGCTTGGCCGCGGGTCGCAAGGCGAGCCAATA 83 AGGTGAAATGCAGGTCGAACGGTCTAACAAGTCGGAGCAATA 84 AGGAAAGTCGGGTTGGAACGGGCTTACCAAATATGGAAAGCCAAAAT 15 AACTTTGTTGGTTGGGAACCGGAATTAGGTGGGGGCC GTCTATATACCCCCTGGTTGGGCAACTAGGTGGGGGCC 16 ATAACGTCGTTGGGAACCGGAATTGGTGGTGGGCACTGGCGGGC 17 TGGCCAAGAATTCCCCTGGTTGGCGCAATTAGGAACGAAGCAAAAT 17 AGCGTTGTTGGGTTTGGAACGGGCTTACCAAATTGGAAGCCGAATA 18 AAAGGAACCCCGGGTTGACCGGGGCGCGGCGGGGGCC 17 TGGCCGAATTGCGGGGCTTGCCGGGGGGGCC 17 ATAACGACGTCGGCTTGGCCGGGGGGCGCC 17 ATAACGACGTCGGCTGGCGGGGCGCGCGGGGGGCGCC 17 AGCCGAATTCGGGGCTGGCGGGGGCGCGCGGGGGGGGGG	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66 HsaD _{LM} 67 _{abc} * HsaD _{LM} 68 HsaD _{LM} 69 _{abd}	11.855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCACAAGGGCTCTCTCCG ACTTGGAAAGTGCAGGGGTGCCACGAGTAATCACCGTCCCCG GGGGCCGGGGGGGGCCCCCGGGCAAGGAA GTTCATTAAGGGGTGACGCCGCAGGTAA GTTCATTAAGGGGTGACGCCGCAGGTAA GTTCATAAGGTTAG GTCATAAATTTTGCTACAAACCACAATGACAGGGCCATTGATA 45 10 GACAATGGTCGCTGTCACGGCATCTCCCCGCCTATTCTTAAC CCGGTGAGAAAGGCCCTGGCCTCGTCACGGCAATGAAAATGACGATGA AATTTTCCTTGCGGCAGGCAATTAAAGGGCATAAAATCAACGAGTGA AATTTTCCCCCGGTATTAATAGAAGGCATAAAAATGAGTGA 149 AATTTACCCCAGGCAGGT AAAGTTTCCCCCCATTATAGAAGTACAAAAAATCAACGAGTGA TAAAGTTCCCCCCGTTATGCAGGCACGTCCTTCTCGGAGGCGCTTT 151 CCATTTGCCAGGCAGGT 162 CATTTTTCCCAAGGCAGGT 163 CAATTTTTCCCAGGGCGCCTGTTCCTGGGGCCGGCGAGGACGT 164 AAATCTCCCCGGGTGGTGGTGATAAATCATCGTAAGTAAT 174 AATCTTCCCCGGGTTGGTGTGATAAATCATCGTAAGTAAT 194 AATCTTCCCCGGGTTGGTGTGATAAATCATCGTAAGTAAT 194 AATCTTCCCCGGGTTGGTGTGATAAATCATCGTAAGTAAT 194 AATCTTCCCCGGGTTGTGTGTGATAAATCATCGTAAGTAA
Hsai Hsai Hsai Hsai Hsai Hsai Hsai Hsai	D _{G1} ,25 D _{G1} ,26 D _{G2} ,27 D _{G4} ,28 D _{H4} ,30 D _{H4} ,30 D _{H4} ,33 D _{H4} ,33 D _{H4} ,34 D _{H4} ,35 _{mbod} * D _{H4} ,35 _{mbod} * D _{H4} ,37 _{bc} * D _{H4} ,37 _{bc} * D _{H4} ,40 _{mb} * D _{H4} ,46 _{mbod} * D _{H4} ,46 _{mbod} * D _{H4} ,48 _{mbod} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314	228 TCTAGACAATAAA 17 TAGAAACAAACAAACAA 19 CTATTAATTICTGTGTGTTTG 31 AAAATCCACTCATTTATCCAGGGTTCAAACA 29 ATGTGTCACATCTAATCAGGGTTCAAACA 29 ATGTGTCACATCCAAGCATTGAGGCAAC 31 GTATTTCCGGAGGGTTGACAAGTACCTAAAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCGAAGGAATGCGGTCAAATACCTTTTTGTTGAGCAA 40 AGCTGTGGGGGATCGCTTCCCCGAGGCGTGAGCAGTACATT AAATCCGCGAAGGAATGCCGTTAAAATTCCTTTTTGTTGAGCAA 40 AGCTGGTGGCGGATCGCTGCCGGGCAGTGAGCAGTACATT AAATCCGCGAAGGAATGCCGTGACAGGCGCCGCCGCCCTCC 177 TG 33 AATAAGAAACTTGGATTGTCAGTAAATTCTTTTTGTGC 27 GAGAAAGAACGTGGAAATTCCCTGGCGCGCGCGCGCGGCAGGCA	$\label{eq:limbolic} \begin{split} & \text{HsaD}_{\text{LM}} \text{S8}_{\text{bd}}^{*} \\ & \text{HsaD}_{\text{LM}} \text{61}_{abc}^{*} \\ & \text{HsaD}_{\text{LM}} \text{62}_{ab}^{*} \\ & \text{HsaD}_{\text{LM}} \text{64} \\ & \text{HsaD}_{\text{LM}} \text{65} \\ & \text{HsaD}_{\text{LM}} \text{66} \\ & \text{HsaD}_{\text{LM}} \text{67}_{abc}^{*} \\ & \text{HsaD}_{\text{LM}} \text{69}_{abd} \\ \end{split}$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGCTCATTAATCTGCCACGCAAGGGCTCTCTCCG GGGGCCGGCGGGGGCCCCCGGCCACGCCCAGGCCCCGG 198 CCGGCCGGGGGGCCCCCGGCTAA 198 CCGGCCGGGGGGCCCCCGGTAA GTTCATTAGGGGGGGGGCCCCCGGGTAA 57 TTCAAAGGCTTATG GTCATTAAGGGCGTGCCACGCCAGGTAA 45 TG GAACAATGGTCGCTGTCACGCCATCGCCGCCCATTGATA 45 TG GAACAATGGTCGCTGTCACGCCATCGCCGCCCATTGATA 45 TG GAACAATGGTCGCTGTCACGCCATCGCCGCCTATTCTTAAAC CGGTGGAAAAGGCCTGGCCCCCCTTCTTCAAGGAGGTCAT AATTTTTCTTGCGTCATATGAAGGCATTCAAAATCGAGTTGA 149 AATTTTACCCCGGCAGGT TTAATGGTCGCCGGCATCCAGGCGCTTCTTCGGAGGTCGT TAATGTTCCCCCATTATGAATCATCCAAACAATAAACGCTGCCCGGC AGGACTCGGGGCGCAGGTCCCGGGCGGG CGGCTTGGCGGGCACTGGCCGGGG TGACAATGGCCGGGCACTGTCCGGGG CGGCTTGCCCGGTTTGTGGTGGTGATAAATCATCGTAAGTAA
Hsai Hsai Hsai Hsai Hsai Hsai Hsai Hsai	DG1+25 DG1+25 DG1+26 DG1+28 DG1+23 DH1/30 DH1/33 DH1/33 DH1/35/sto0* DH1/35/sto0* DH1/35/sto0* DH1/35/sto0* DH1/35/sto0* DH1/40/sto0* DH1/46/sto0* DH1/46/sto0*	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314	29 ICTAGACAATAAA 17 TAGAAACAAACAAACAA 19 CLAITIAATTICUGUGUTIG 31 AAAATCCACTCAITIATCCAGGGITCAAACA 29 AUGUGUAAATAATATTIATCCAGGGITCAAACA 29 AUGUGUAATAATATTIGTITTIATICUGTAACACAGA 31 GIATITICOGAGGAGIGGCACAGGACACAT AAATCCGCAAGGAGTGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAGGAATGCCTTCCCCGGAGGCGTGAGCAGTACATT AAATCCGCCAGGAATGCCGCTTCCCCGGAGGCGTGAGCAGTACATT AAATCCGCCAGGAATGCCGCTTCCCCGGAGGCGTGAGCAGTACATT AAATCCGCCAGGAATGCCGCTTCCCCGGGCGGAGCAGTACATT AAATCCGCCAGGAATGCCGGTCCGCGGCAGGCGGCGCGCGC	$HsaD_{LM}59_{ca}^{*}$ $HsaD_{LM}61_{abc}^{*}$ $HsaD_{LM}62_{ab}^{*}$ $HsaD_{LM}64$ $HsaD_{LM}66$ $HsaD_{LM}66$ $HsaD_{LM}67_{abc}^{*}$ $HsaD_{LM}69_{abd}$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541	CACGIGATIGGCGAAATAATIAATICAGCACGICCCTIAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCTCTCTCG ACTIGGAAAGTGCAGGGATCCCAGGATATCACCCGTCCAGG GGGGCCGCGCGGGGGCCCCCGGCCTCCACCCCCGGGCCCCGG I98 CGGCCCGCGGGGGCCCCCGGCGAAA GTICATAAGGGTGAGTGATGCCGGGCCCGAGGTAA GTICATAAGGGTGGCGCCGCGGGAAA GTICATAAGGGTGGCGCCGCGGGAGAA GGCATAAATTTGCTACAAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCGGCGCCGCTCTTCTCAAGCGAGGGTCGT AAAGTTTCCCCCAGGCGCCCCTCTTCTCAAGCGAGGGTCGT AAAGTTTCCCCCAGGCGCCCCTCTTCTCAAGCGAGGGTCGT AAAGTTTCCCCCAGGCGGCCCCTTTCTCTAAACACGAGGTCGT 149 AATTTTACCCCGGCGCGCCCCCTTTCTCGAGGGGGGCGT GGCATAATGCGGCGCGGGCCCGGGGCCCTCGCCCCTT 151 GCATTTTCCGGGCGAGTTCCAGGGCGTTTCTTGGGCGGCGGCGCGGG GGCCTGGGGGCGGGC
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G1} ,27 D _{G1} ,28 D _{H1} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,37 _{bc} * D _{H2} ,40 _{ab} * D _{H2} ,41 D _{H2} ,42 D _{H2} ,47 _{abc} * D _{H2} ,48 _{abcda} D _{H2} ,49 _{abc} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,523 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314	228 TCTAGGAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTATTAATTICTGGTGTGT 29 ATGTGTCAACATCAAACAA 29 ATGTGTCAACATCAAGCATTGAGGCAACA 29 ATGTGTGCACATCTATTATCCGGGGTCAAACA 20 AGCTGTGGGGATGCAGCTGGACAGGTCAAACA 20 AGCTGTGGGGATGCGCTCCCCCGGGCAGGCGGAGCAGTACATT AAATCCGCAAGGAATGCAGTAATACCTTATAA 40 AGCTGTGGGGATGCCGTCCCCCGGGAGCGGGAGCAGTACATT AAATCCGCAAGGAATGCAGTAATAGCCTTATTGTGGAGCAGTTGAGAA AATTTGCACTTGGTAATAGACCTTATTGTGGCGTCGCGCGCCTCCCCTCC ACGGCCTTTTCCCGATGGGATGGCAGGCGGAGCGGGAGCGGTCGCC 20 GGCAAGGAATGCAGTGATATAGCCTTATTGTGGCGT 217 TG 23 AATAAGAAACTTGGGTGATGGTATTGGCTTGGGGCGGCGCCGCCCTCC 27 GGCAAGGACGAGCTGGAATTGTTATTGGC 27 GGCAAGGACGAGCTGGAATTGTTATTGGC 20 GGCAAGGACGAGCTGGAATTATAAA 30 AGCCAAGACAGTATTCACCTGGGCTGGCAGGCAGCTGTA 20 AGCCAAAATATAATTC 21 GGCAAGGCCAGGCTGCACGGCGCGC 22 CGTTTTACACTGTTGGGCGCGCGGCGGCGGGGCGGACGGCGATA 23 AGGTGAATGCAGGTTGGCTGGCCGCGGTCGCACAGGCGAATA 23 AGGTGAATGCCGGGTTGCCGCGGGTCGACAAGTCGGGCCAGCCA	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66 HsaD _{LM} 67 _{abc} * HsaD _{LM} 69 _{abd} HsaD _{LM} 69 _{abd}	11.855 5.973 3.899 11.225 10,461 10,176 10,138 9.398 8,541 8,233	CACGIGATIGGCGAAATAATTAATICAGCACGICCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCACAAGGGCTCTCTCCG ACTIGGAAAGTGCAGGGGTGCCCACGCACGACAAGGGCTCTCTCCG GGGGCCGCGGGGGGCCCCCGGCTCAATCACCCCCCGGCCCCCGG GGGGCCGGGGGGGCCCCCGGGTAAA GTTCATTAAGGGGTGACGCCCAGTGAAA GTTCATAAGTTTTCCTACAAACCACAATGACAGGGCCAATGATA 45 10 GGACAATGGTCGCTGTCACGGCATCTACAGCGAGGTCGAT AATTTTCCTTCGGTGACGGCACTTTAAGGGGGGTCGTA AATTTTCCTCCCCCATTAATAGAAGGCTATAAAATCAATGAGTTGA 149 AATTTTACCCCAGGCAGT AAGTTTCCCCCCATTATGAATTATACATCAAGCAAGTGACA 149 AATTTTACCCCCGGGCAGTGTAAAACCAATAAACAA TAAGTTCCCCCCATTATGAATTATACATCAAACAATAAACCA TAAATTCCCCCCCATTATGAATTATACATCAAACAATAAACCA TAATTCCCCCCGGGTGGTGTGGT
Hsai Hsai Hsai Hsai Hsai Hsai Hsai Hsai	D _{G1} ,25 D _{G1} ,26 D _{G2} ,27 D _{G4} ,28 D _{H4} ,30 D _{H4} ,30 D _{H4} ,33 D _{H4} ,33 D _{H4} ,34 D _{H4} ,35 _{mbod} * D _{H4} ,35 _{mbod} * D _{H4} ,35 _{mbod} * D _{H4} ,37 _{bc} * D _{H4} ,40 _{mb} * D _{H4} ,40 _{mb} * D _{H4} ,46 _{mbode} * D _{H4} ,46 _{mbode} * D _{H4} ,48 _{mbode} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314	228 TCTAGACATAAA 17 TAGAAACAAACAAACAA 19 CTATTAATTICTGTGTGTTTG 31 AAAATCACACTCATTTATCCAGGGTCAAACA 29 ATGTGTCACATCTAATTATCCAGGGTCAAACA 29 ATGTGTCACATCTAATTATCCAGGGTCAAACA 20 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGGCAGGGATGGCTGCCCCCAGAGCGTGAGCAGTACATT AAATCCGGCAGGGATGCGCTTCCCCCAGAGCGTGAGCAGTACATT AAATCCGGCAGGGATGCGCTTCCCCCAGAGCGTGAGCAGTACATT AAATCCGGCAGGGATGCGCTGCCGGGCAGTGAGCAGTACATT AAATCCGGCAGGGATGCGCTGCCGGGCAGTGAGCAGTCCTTC 177 TG 33 AATAAGAAACTTGGATTATGGCTTGTTATTGGCCTTTTGGTGC 27 GAGAAAGACGAAGCTCGAAATTATTTATTGC 27 GAGAAAGACGAAGCTCGAAATTATTATGGC 27 GAGAAAGCGAAGCTCGAAATTATTATAG 38 AAGGACCAAAATTCCCCTGGGCTGGCCAGGCCAGCTGTA 73 GAGGTATTACCGGCTGCCCGGGCGGCCGGCCAGGCAGCTGTA 73 GAGGTATTACGGCCTTGCCCGGGCGCGCCCAGGCAGCTGTA 73 GAGGTATTACGGGCTGGCCGC 18 AAAGACCGCCTGGGTCACCGGCCCGAAATATAGAAAT 17 GACCTTTGTACCCTGGGCGCC 18 AAAGACCGCGTGGCCGC 18 AAAGACCGCGGTGGCCGCC 18 AAAGGCGAAATGCAGGGCCCTGGCCCAAATATAGAAAT 17 GACCTTTGTGTGGGCGC 18 AAAGGCGAAATGCAGGTCGACAGGCGCCAAATAT 20 GGTGAAAGCGAGCCTGGACCAGGCCGCCCAAGCGACAATA 20 GGTGAAAGCGAGGCCTGGACCAGGCCGCCCAAGCGACAATA 20 GGTGAAAGCGAAGCTGGACGCCGCGCCGGCCCAAGCGACAATA 20 GGGTGAATGCGGCCTTGCCCCGGGCCGCCGGCCCAGCCGGCCCAGCCGGCCCCGGGCCCCCGGGTGCCCCCGGGCCCAAGCCGGCCCTGGCCCCCGGGCCCAAGCCGGCCCTGGTCCCCCCGGCCCCGGCCCCGGCCCCCGGCCCCGGGCCCAAGCCGCC	$HsaD_{LM}58_{bd}^*$ $HsaD_{LM}61_{abc}^*$ $HsaD_{LM}62_{ab}^*$ $HsaD_{LM}64$ $HsaD_{LM}66$ $HsaD_{LM}66$ $HsaD_{LM}67_{abc}^*$ $HsaD_{LM}69_{abd}$ $HsaD_{LM}70_{a}^*$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541 8,233	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATGTGCCACGCACGAAGGGCTCTCTCCG GGGGCCGGGGGGGCCCCGGGTTCCACGACGACGCCCCGG 198 CCGGCCGGGGGGGCCCCCGGGTAA GTTCATTAGGGGGGGGGCGCCGCGGTAA GTTCATAAGCGGTGCCACGCCCCGGGTGCACGGGCCAAGGTCAC 57 TTCAAAGGCTGTCACAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCTGTCACGGCATCTGCCGGCCTATTCTTAAAC CGGTGGAAAAAGGCCTGGCCCCCTCTTCTCAAGGAGGTCAT AATTTTTCTTGGTGGCGTGTCACGGCATCGACGGCCATTGATA 45 TG GAACAATGGTCGCTGTCACGGCATCTGACGGCCATTGATA 44 JAATTTTCCTCAGGAGGCGT AAATTTTCCCCCCATTATGAATCATCCAAACAATAAACGAGGTGCT AAATTTTCTTGGGCGAATTCAAGGAGGTCATTAAAATCGAGTTGG 35 GCACTTGTCCCCCATTATGAATCATCCAAACAATAACACT 151 GCATTTTCTCAGGCAGCTGGTCGGGG CGGCCTGGCCGGGCACTGGTCGGGG CGGCTTGCCGGGGCACTGGCCGGGG 17 ATATTTCCAAAGGAACTGCCCGGG 17 ATATTTCCAAAGGAACTTCCCTCGGGGCCACGGACAGTTC 19 AAATCTTCCCGTTTGTGGGGCCCGGGCCGGGACAGGACTGT 17 ATATTTCTAAAGGAACTCCCCGGGGTCACGGACAGACTGT 17 ATATTTCTAAAGGCACGCCTGGTGTGTGTGTAATTGCCCTATGGGGCCGGGCCGGGACAGT 17 ATATTTCTAAAGGCACCCCAGGCCGGGTCCGGGACAATAT CCCTGCATTTGAAAGGCACCCCAGGCCGGGGCCAGGACAGT 17 ATATTTCTGAAAAGGACCCCAGGCCGGGCCGGGACAATAT CCCTGCATTGGAAGGCACGCCCGGGTGGTGTGTGTGTGCGGTCACGGAACAAATAT CCCTGCGTTGCCCCCAGGTGTGTGTGGTGCTACGGCACGGCGAGGACGGG 94 GTTTCGG CTTGCCTCCCCCCCTGGCTCCCGGGTTCCGGTCACGGAACAAATAT CCCGGGTTGGGGCACATGTTGTCGCGGCCCCGCGCGAGGACGG CTAGCTTGCCCCCCCGGCTCGGGTGTGTGTGTGGGGCCACGGACAAAATAT
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	DG125 DG126 DG127 DG128 DG128 DH130 DH131 DH133 DH133 DH135	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314	228 TCTAGACATAAA 17 TAGAAACAAACAAACAA 19 CLATTAATTICUGUTTG 31 AAAATCCACTCATTATCCAGGGTTCAAACA 29 ATGTGCAACATCAAACAA 20 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGCA 31 GTATTICCGCAGGGTGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAGGAGTGCACAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAGGAATTGCGCTTCCCCGGAGCGTGAGCAGTACATT AAATCCGCCAGGAATTGCGCTTCCCCGGGCGGAGCAGTACATT AAATCCGCCAGGAATTGCCGTGCCAGGCGGCAGCAGTACATT AAATCCGCCAGGAATTGCCGGTCGCGGCAGTACATT AAATCCGCCAGGAATTGCCGGTGCAGGCGCGCGCCGCCCTCCCT	HsaD _{LM} 58 _{6d} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 66 HsaD _{LM} 66 HsaD _{LM} 67 _{abc} * HsaD _{LM} 68 HsaD _{LM} 69 _{abd}	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541 8,233	CACGIGATIGGCGAAATAATTAATTCAGCACGICCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCTCTCCCGG ACTIGGAAAGTGCAGGGTGCCCACGACGACGCCCCCGGCCCCGG GGGGCCGCGCGGGGGCCCCCGGCCCCCC
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G1} ,25 D _{G1} ,27 D _{G1} ,28 D _{H1} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 D _{H2} ,35 D _{H2} ,35 D _{H2} ,42 D _{H2} ,40 _{ab} * D _{H2} ,42 D _{H2} ,47 _{abc} * D _{H2} ,48 _{abcob} D _{H2} ,49 _{abc} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,523 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314	228 TCTAGGAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTATTAATTICTGTGTTTG 31 AAAATCCACTCATTTATCCAGGGTTCAAACA 29 ATGTGTCAACATCAAGCATTGAGGCAAC 34 TAATTTAAAATATTGTTTTATCCGTGAACACAGA 31 GTATTTCGGAGGGTTGCACGGGTGACAGGTCACATG 40 AGCTGTGGGGATGCCGTCCCCCGGGAGCGTGACCAGTACATT AAATCCGCAAGGAATGCAGTGAATGCCTTAAAA 40 AGCTGTGGGGATGCCGTCCCCCGGGAGCGTGACCAGTACATT AAATCCGCAAGGAATGCAGTGAATGCCTTATTGTTGAGAA AATTTGCACTTGGTAATGACCTTTTTGTTGAGCAA AATTTGCACTTGGTGACGGCGGGCAGGCGGGCGGCCGGCC	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66 HsaD _{LM} 67 _{abc} * HsaD _{LM} 69 _{abd} HsaD _{LM} 70 _a *	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541 8,233	CACGIGATIGGCGAAATAATTAATICAGCACGICCCTTAAGAA ACACGGAGTGGTCATTAATGCGCACGACGAAGGGCTCTCCCG ACTIGGAAAGGCGGGGGCCCCAGGCAAA GIGGCCGGGGGGGGCCCCGGGGCAAGGAAA GITCATTAAGGGGIGGCTCCACGAATGACCACGGGCCCAGG GGGCCGGGGGGCGCCGGGGGAAA GITCATTAAGGGGGGGGGCGCCGGGGGAAA GITCATTAAGGGGGGGCGCCGGGGGAGGAAA GITCATTAAGGGGGGCGGCGGGGGGGCCCAGIGAAA GGGCGAGAAAGGCCGGGCGCGGGGCAGGGAAAAGGCCATIGATA 45 10 GGCATAAATTTICCTGCGGGCACGTCAAAGGACGATGAAAAAGGGGGAAAGGCCGCGGGGCGCGGGGGGGG
Hsai Hsai Hsai Hsai Hsai Hsai Hsai Hsai	D _{G1} ,25 D _{G1} ,26 D _{G2} ,27 D _{G4} ,28 D _{H4} ,30 D _{H4} ,30 D _{H4} ,33 D _{H4} ,33 D _{H4} ,34 D _{H4} ,35 _{bbcd} * D _{H4} ,35 _{bbcd} * D _{H4} ,35 _{bbcd} * D _{H4} ,37 _{bc} * D _{H4} ,40 _{bb} * D _{H4} ,46 _{bbcd} * D _{H4} ,46 _{bbcd} * D _{H4} ,46 _{bbcd} * D _{H4} ,46 _{bbcd} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314 143	228 TCTAGACATAAA 17 TAGAAACAAACAAACAA 19 CTATTAATTICTGTGTGTTTG 31 AAAATCACACTGGTTTATCCAGGGTTCAAACA 29 ATGTGTCACATCGAGGGTTGACAGGCAACA 34 TAATTTAAAATATIGTTTTATTCTGTAACACAGA 31 GTATTTCGGAGGGGTGACAAGTACCTAAAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAGTGACAAGTACCTAAAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCCAAGGAATTGCGTTCCCCGGGGCAGTGAGCAGTACATT AAATCCGCCAAGGAATTGCGGTCAGTGACAGCGCCCCCGCCTCC 177 TG 33 AATAAGAAACTTGGATTATGGCTTATTGGCCTGTTGCGGC 177 TG 33 AATAAGAAACTTGGATTGGTATTTTATTGGCCTGTTGGCGGC 177 TG 34 AATAAGAAACTTGGATTGGATTGGTATTTATTGGCTGGCAGGCA	$HsaD_{LM}58_{bd}^{*}$ $HsaD_{LM}61_{abc}^{*}$ $HsaD_{LM}62_{ab}^{*}$ $HsaD_{LM}64$ $HsaD_{LM}66$ $HsaD_{LM}66$ $HsaD_{LM}67_{abc}^{*}$ $HsaD_{LM}69_{abd}$ $HsaD_{LM}70_{a}^{*}$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541 8,233	CACGIGATIGGCGAAATAATTAATTCAGCACGICCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCACAAGGGCTCTCTCCG ACTTIGAAAGTCATGGGTGCCCCAGCTCACCCCCGGCCCCGG GGGGCCGCGGGGGGCCCCCGGTCAA GITCATTAAGGGGTGGCTCCCGGCCCCGGTCAA GTTCATTAAGGGGTGGCTGTCACACAATGACAGGTGCATTGATA 45 TG GAACAATGTCGCTGTCACGCCACTCACCGCCCCTTTCTTAAAC CGGTGAGAAAAGGCCCGGCGCACTTAAAAATCGGTGCAATGATA 45 TG GAACAATGTCGCTGTCACGCCACTCACGCCCCCTTTCTTAAAC CGGTGAGAAAAGGCCCGGCCTCTCTCTCAAGCAGGGTGTA AATTTTCTTTCGTCACAAACAATGACAGGTGCAATGACA 149 AATTTACCCCCGGCAGTTAATGCAGGCTATTAAAAATCGAGTTGA 149 AATTTACCCCCGGCAGTCACGGCCGGG TGACAATGGCCGGGCCACGGCCGGG CGCGTTGGCGGCGCACTGTCCGGGG TGACAATGGCCGGGCACTGTCCGGGG CGCGTTGGCGGGCACTGGCCGGGG TGACAATGCCCGGGGTTGGTGGTGAAAATCATCGTAAGTAA
Hsal Hsal Hsal Hsal Hsal Hsal Hsal Hsal	D _{G11} 25 D _{G12} 25 D _{G12} 27 D _{G12} 28 D _{H1} 30 D _{H1} 33 D _{H1} 33 D _{H1} 33 D _{H1} 35 _{abcd} * D _{H1} 35 _{abcd} * D _{H1} 35 _{abcd} * D _{H1} 36 D _{H1} 37 _{bc} * D _{H1} 40 _{ab} * D _{H1} 46 _{abcde} * D _{H1} 46 _{abcde} * D _{H1} 47 _{abc} * D _{H1} 47 _{abc} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314 143	228 TCTAGACAATAAC 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTATTAATTICTGTGTTTG 11 AAAATCCATCCAAGCATTAACCAGGGTTCAAACA 29 ATGTGTCAACATCCAAGCATTGGGGCAACA 29 ATGTGTCAACATCCAAGCATTGGGGCAACA 29 ATGTGTCAACATCCAAGCATTGGGCAACA 29 ATGTGTCAACATCGAAGGGTTGACAGGCAACA 31 GTATTICCGAGGGGTTGCCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATTGCGTTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATTGCGTTAATCCTTTTTGTGAAGAA AATTTGCAACGGGGTTGCATGGCAGCGGGAGCAGTACATT AAATCCGCAAGGAATTGCGTTAGGCAGCGGCGCGCCGCCTCCCTTC ACGGCCAATTGACTGCGGCTGGCAGTGCAGCGGCGCCGCCCGC	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 66 HsaD _{LM} 66 HsaD _{LM} 67 _{abc} * HsaD _{LM} 68 HsaD _{LM} 68 HsaD _{LM} 70 _a *	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541 8,233	CACGIGATIGGCGAAATAATTAATTCAGCACGICCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCTCTCTCCG ACTIGGAAAGTGCAGGGTGCCCACGACGACGGCCCCCGG GGGGCCGCGCGGGGGCCCCCGGCCCCCCC
Hsai Hsai Hsai Hsai Hsai Hsai Hsai Hsai	D _{G1} ,25 D _{G2} ,26 D _{G2} ,27 D _{G1} ,27 D _{G1} ,23 D _{H2} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,40 _{ab} * D _{H2} ,41 D _{H2} ,42 D _{H2} ,46 _{abcob} * D _{H2} ,47 _{abc} * D _{H2} ,48 _{abcob} * D _{H2} ,49 _{abc} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,523 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314 143	228 TCTAGGAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTAITAATTICTGIGITTG 11 AAAATCCACTCATTAATCCAGGGTCAAACA 29 ATGTGTCAACATCAAGCATGAGGCAAC 31 TAATTTAAAATATIGTITTATICTGTAACACAGA 31 GATTICGGAGGGTGACAAGTACCTAAAA 40 AGCTGTGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCAGTAATACCTTHTIGTTGTGAAAA 40 AGCTGTGGGGGATGCGCTGCCCGGAGCGTGAGCAGTACATT AAATCCGCCAGGGATGCCGTGACAAGGCGTGAGCAGTACATT AAATCCGCCAGGGATGCCGTGACAAGGCGTGAGCAGTACATT AAATCCGCGCAGGGATGCGGTGATAGACCTTHTTGTTGGCGT 177 TG 13 AATAAGAAACTTGGATAGACCTTTTATGGCCTTGGGGGCGCCCCGCCTCC 177 TG 13 AATAAGAAACTTGGATGGGTGTGTTATTTGGCCTGGGGGGGG	$HsaD_{LM}58_{bd}^*$ $HsaD_{LM}61_{abc}^*$ $HsaD_{LM}62_{ab}^*$ $HsaD_{LM}64$ $HsaD_{LM}65$ $HsaD_{LM}66$ $HsaD_{LM}67_{abc}^*$ $HsaD_{LM}69_{abd}$ $HsaD_{LM}70_a^*$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541 8,233	CACGTGATTGGCGAAATAATTAATTCAGCACGTCCCTTAAGAA ACACGGAGTGGTCATTAATCTGCCACGCAAGGGCTCTCTCCG ACTTGGAAAGTGCAGGGTGCCCACGCACGCACGAAGGGCTCTCTCCG GGGGCCGCGGGGGGCCCCCGCGCCCACGCAA TTGTATAAGGGGTGGCTGACGCGCCGCGGTGAA GTCATTAAGGGGGGGGGG
Hsai Hsai Hsai Hsai Hsai Hsai Hsai Hsai	D _{G1} ,25 D _{G2} ,27 D _{G2} ,27 D _{G2} ,28 D _{G4} ,30 D _{H4} ,30 D _{H4} ,30 D _{H4} ,33 D _{H4} ,34 D _{H4} ,35 _{abc0} * D _{H4} ,37 _{bc} * D _{H4} ,40 _{ab} * D _{H4} ,40 _{abc0} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,223 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,614 2,005 1,314 143	228 TCTAGACAATAA 17 TAGAAACAAACAAACAA 19 CTATTAATTICTGTGTGTTG 31 AAAATCCACTCATTTATCCAGGGTTCAAACA 29 ATGHTGCACATCGAGGTTGACGGGCCAACA 34 TAATTTAAAATATGTTTTATTCTGTAACACAGA 31 GTATTTCCGGAGGGTGGCAGGACTTGAGCAGCAGTACATT AAATCCGCGAGGGATGGCTTCCCCAGGGCGTGAGCAGTACATT AAATCCGCGAGGGATGGCTTCCCCAGGGCGTGAGCAGTACATT AAATCCGCGAGGGATGGCTTCCCCAGGGCGTGAGCAGTACATT AAATCCGCGAGGGATGGCTTCCCCAGGGCGTGAGCAGTACATT AAATCCGCGAGGGATGCGCTTCCCCGGGGCAGTGAGCAGTACATT AAATCCGCGAGGGATGGCTGCCGGGCGAGTGCGCGCCGCCGCCTCC 177 TG 33 AATAAGAAACTTGGATTATGGCTTGTGTGGCGGCGGCGCGCGC	$HsaD_{LM}58_{bd}^{*}$ $HsaD_{LM}61_{abc}^{*}$ $HsaD_{LM}62_{ab}^{*}$ $HsaD_{LM}64$ $HsaD_{LM}65$ $HsaD_{LM}66$ $HsaD_{LM}67_{abc}^{*}$ $HsaD_{LM}69_{abd}$ $HsaD_{LM}70_{a}^{*}$ $HsaD_{LM}71$	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541 8,233	CACGIGATIGGCGAAATAATTAATTCAGCACGICCCTTAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCTCTCTCCG ACTTGGAAAGTCCAGGGATCCCAGGATATCACCCCTCCAGG GGGGCCGCGCGGGGGCCCCCGGGTAA GTTCATTAAGGGGTGGGTGCACCCGGGCCCCAGGAA GTTCATTAAGGGGTGGCTCACGGCCCCAGGTAA GTCATTAAATTTGCTCCTCACAACCACAATGACAGGTGCATTGATA 45 TG GAACAATGGTCGCTGTCACGGCATCTGCCGCCCTATTCTTAAAC CGGTGGAGAAAGGCCTGGCCCCTCTTCTCAAGGAGGGTCAT AATTTTTCTTGCGTCATAATGAAGGCTATAAAATCGAGTGCA AATGTTTCCCCCCATTATGACGGCATCTAAAAATCGAGTGCA TAATTCATTATTCAGGCAGGCCGCCGGTTAAAAATCGAGTGCA TAATTCATTCATTCTGCCCCATTATGACGGCTGCACGCGCTT 151 GCATTTTCTCCCCATTATGAAGGAGCCTGGCCCCGGG TGACAATGGCCGGGCACTGGCCCGGGG TGACAATGGCCGGGCACTGGCCCGGGG TGACAATGCCCGGGGTGGTGGTAAAATCGTAAGTAATA CCCGCTTGCCCCGGTTGTTGGGGCCGGGCC
Hsai Hsai Hsai Hsai Hsai Hsai Hsai Hsai	D _{G11} 25 D _{G12} 25 D _{G12} 27 D _{G12} 28 D _{H1} 30 D _{H1} 31 D _{H1} 35 _{abcd} * D _{H1} 45 _{abcd} * D _{H1} 46 _{abcde} * D _{H1} 46 _{abcde} * D _{H1} 46 _{abcde} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,523 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314 143	228 TCTAGGAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTATTAATTICTGTGTTTG 31 AAAATCCACTCATTATCCAGGGTCAAACA 29 ATGTGTCAACATCAAGCATTACCAGGGTCAAACA 20 AGCTGTGGGGATGCGCTCCCCCAGGCGGAGCAGTACATT AAATCCGCAAGGAATGCAGTAACACAGA 40 AGCTGTGGGGATGCGCTCCCCCAGAGCGTGAGCAGTACATT AAATCCGCAAGGAATGCAGTAATACCCTTATGTTGAGAA 40 AGCTGTGGGGATGCGCTCCCCCGAGCGGGAGCAGTACATT AAATCCGCAAGGAATGCAGTAATACCCTTATGTGAGCAA 40 AGCTGTGGGGATGCGCTGCCCGGGAGCGGTGACAGTCCTTC AAATCCGCAAGGAATGCAGTAATAGCCTTTTGTTGGGGT GGTCATGGCTGCGGCGGGCGGGCAGGCGGCCGCCCCCTC 177 TG 33 AATAAGAAACTTGGATGGATGGATGGTTGTTATGGCTGGAGGAGGTGGAC 40 AGCCAAATAAATTC 27 GGGAAGGCAAGCTGGAATTGTTATTTATGGCTGGGGGGCGC 18 AAAAGAACCTGGATTCACCGGGCGGCGCGGCGGGCGGCCGGC	HsaD _{LM} 58 _{bcl} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 66 HsaD _{LM} 66 HsaD _{LM} 68 HsaD _{LM} 69 _{abcl} HsaD _{LM} 70 _a *	11.855 5,973 3,899 11,225 10,461 10,176 9,398 8,541 8,233 8,233	CACGIGATIGGCGAAATAATIAATICAGCACGICCCTIAAGAA ACACGGAGTCGTCATTAATCTGCCACGCAAGGGCTCTCCCG GGGGCCGCGGGGGGCCCCCGCCCACCCACGGGCCCCAGG GGGGCCGCGGGGGGCCCCCGGGCCCCCGGCCCCAGG GGGCCGCGGGGGGGG
Hsai Hsai Hsai Hsai Hsai Hsai Hsai Hsai	D _{G1} ,25 D _{G1} ,26 D _{G1} ,27 D _{G1} ,28 D _{H1} ,30 D _{H2} ,31 D _{H2} ,33 D _{H2} ,34 D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,35 _{abcd} * D _{H2} ,40 _{ab} * D _{H2} ,41 D _{H2} ,40 _{ab} * D _{H2} ,41 D _{H2} ,47 _{abc} * D _{H2} ,48 _{abcob} D _{H2} ,49 _{abc} *	4,591 4,157 3,022 2,631 17,402 16,788 15,895 15,588 15,588 15,523 13,285 5,380 12,554 12,419 9,512 6,519 2,614 2,005 1,314 143	228 TCTAGGAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 17 TAGAACAATAAA 19 CTATTAATTICTGGTGTTG 11 AAAATCCACTCATTTATCCAGGGTCAAACA 29 ATGTGTCACATCAAGCATTGAGGCAAC 24 TAATTTAAAATATTGTTTTATCCGGGGTCAAACA 29 ATGTGTCACATCCAQCATTGAGGCAAC 31 GATTTCCGGAGGGTGACAAGTACCTAAAA 40 AGCTGTGGGGGATCGCTTCCCCAGAGCGTGAGCAGTACATT AAATCCGGCAGGGATTGCGTTCCCCAGAGCGTGAGCAGTACATT AAATCCGGCAGGGATTGCGGTCATGACACGGGCCCTGGCCGCCTCCCCCC 17 TG 13 AATAAGAAACTTGGTAATAGACCTTTTTGTTGAGCAA AATTACACTTGGTAATAGACCTTTTTGTTGAGCAA 10 AGCCAAATATAAACTTGGTTATGGCTTGGCGGCAGGCCGCGCCCCCCCTC 17 TG 13 AATAAGAAACTTGGATGGGATTGTTATTTGGCCTGGAGGAGTTGACA 60 AGCCAAATATAAATTC 27 GGAAAGGCGAACTCGGAATTGCCGGCGGCCAGGCGGCCAGCTGTTA 73 GAGGTATTTCCGCCGGCGTGGCCGGCCGGCCAGGCGGCCAGCTGTTA 74 GAACAAGACAGTATTTCACCCCGGGCTGGCCAGGCAGCCAGTGTA 75 GAGGTATTTCCGCCTGGCGGCCGGCCAGGCGGCCAGCTGTTA 76 AATAACTCGTTGGCCTTGACCAGGCGCCCAGGCGAGCCAGT 84 AAAGGCCCCTGGTTGACCGGCCTGGCCGGCCAAGCCAAAAT 85 AATGAAAGTTGCTCTGTGGGCGCCTGACAAGTCGAACAAGT 84 AATGAAAGTTGCTCTGTGGGCGCGCTGGCCGAAAGCAAAAAT 86 AATGAAAGTTGCTCTGTGGGCGCCTGGCCGGAAAGCAAAAAT 86 AATGAAAGTTGCTCTGTGGGGCGAATTAGGTGGATC 82 AGTCAAAAGATTGCTCTGTGGGGGCAATTAGGTGGATC 82 AGTCAAAAGTTGCTCTGTGGGGGCAATTAGGTGGATC 82 AGTCAAAGTTGCTCTGTGGCGCCTAGCTGGCCGGCAAAGCAAAAAT 86 AATGAAAGTTGCTCTGTGGCGCCTAGGTGGGCCGGGAAATAGCTAAAATTAGCTGTGTT 143 ACCTTCTGAAATTA 143 ACCTTCTGGACAAGCGAAAAGCAACGAGGAAAAATGGTGTATCC 143 ACCTTCTGGACAGGGAAAAAGCAACGAGGAAAAATGGTGTATCCAA 143 ACCTTCTGGACAGGGAAAAGCCACGAGGAAAAATGGTGTATCCAA 143 ACCTTCTGGACAGGGAAAAGCCACGAGGAAAAATGGTCAATCC 143 ACCTTCTGGACGGGAAATTACGAAAAGCCAAGGGAAAAATTGGTTCATCC 143 ACCTTCTGGACAGGGAAAGCCACGAGGAAAAATGGTTATCCAAGCGGGAAAATTACTATCCGAAGTCGGACTCCAACGCGGGAAGCCAAAGCGGGAAAATTACGAAAGCCGGGAAAGCGGAAAAAGCCGGGAAAATTACGAAAGCTGAAATTACTATTCCGACGTTCCAACGGGGAAAGCGGAAAAAGCCGGGAAAATTACGAAACCGAGGGCCTAAGCTGAAAAGCCGAAAAGCCGGGAAAATTCGCAAGCCGAAAACCGGGGAAAATTACGAAACCGAGGGCCCAAGGTCCAACGCGGAAACCGGGAAAATTGCCAAGCCGGAAAGCGGAAAAACCGGGTTACCAAGCCGAAAACCGAGGGCCCAAGGGGGCCCGAAGGTCCCAAGCCCCGAGGCCCGAGGTTCCAACCCCAACGCCGAAACCGGGGTAACGTGCAAAACCAAAAACCAAAACCAAAAA	HsaD _{LM} 58 _{bd} * HsaD _{LM} 61 _{abc} * HsaD _{LM} 62 _{ab} * HsaD _{LM} 64 HsaD _{LM} 65 HsaD _{LM} 66 HsaD _{LM} 67 _{abc} * HsaD _{LM} 69 _{abd} HsaD _{LM} 70 _a *	11,855 5,973 3,899 11,225 10,461 10,176 10,138 9,398 8,541 8,233 8,541 8,233	CACGIGATIGGCGAAATAATTAATTCAGCACGICCCTTAAGAA ACACGGAGTGGTCATTAATGCGCCACGCACAAGGGCTCTCTCCG ACTIGGAAAGGCGGGGGGCCCCCGCCCACGCAAGGGCTCTCTCCGG GGGGCCGCGGGGGGCCCCCGGGTCCACCCCCGGCCCCCGG 198 CCGGCCGGGGGGGCCCCCGGGTGAA GTCATTAAGGGGGGGGGG

			Danio rerio z	ebrafish Hox Da	1	Sociasion
			PFC	Dist to 3' gene	Length	Sequence
						ATTCATCAAAAAGTGGTTTGCGCCTTCGTCGTTAAAGGTGCGCGTGA CGCGGCTCGAATGATCATTTATTGTAACAGGTTTATAAGGAAATAAA TAGGAAGAGAGACGTGCATCGGTTGATAGGTGGCCCTTGATCGGCC AGACGCTTATATCCAGGTGGAGAGAGAGAGAGAGAGAGAG
			DreD _{AC} 1 _b	12,618	296	CTGGGGTGAAATTGACAGTCT
			DreD _{cp} 2	2,475	27	ATTTTAGACTCGGTGTCTGAATAAGTT
						TACTTTGCATATCACGTGATGGTGCATTAACAAATCAACAATTACCTT
			DreD _{CD} 4	111	75	GCTCGTATTCTTTAGGGGTAACTAAAA
			DreDn=7	3.509	53	GAGAAGA
			Drop 0	0.40	450	TAATGACTGATATTGATATATGGTAATTTTTTTTACCGGATCACATGAC ACAATTACCTCAAGAATCGATCAAGATGAATTGCACGTCAGCGTACG TTTCCGGATTTTTTCTTCCTCGCGAGTCCTATCCGCACGCA
			DreD 40	249	152	
			DreD _{DE} 10 _{cd}	2,061	28	
			DIEDEFIL	5,617	20	TTIGAACTICIGTAATGTCAAGGTCGTCACCCTTAACCTTTTIGAATA
			DreD _{EF} 13	5,259	49	A
			DreD _{EF} 16	4,948	46	TGCAAAACAAACAAAGCCGTAATATGCTTATAGTGATCGAGCAGAG
			D D 40		470	GTCGCTGTTGACCACGTCTGAAACTTCAAATCATGTGTCAATCCGCC CACGTGACGGGGAAGAGCCTGCGGTCTCAAGGCCATTTTCAAATTTCA TTGGTGAGAGTGTCATGTGGTTGCAGAGAGACTCCCCTGGGTATACA CCCATCGTTTCCTACGTTGTCACCTGCGCGAGAGACTCCCCTGGGTATACA
			DreD _{EF} 19 _{abc}	226	179	
			DreD _{FG} 21 _{abc}	713	58	GTTTATIGAT
			DreD _{EG} 22	476	33	TTTACAGCATGTTATTACATTTATTTTACGAGG
			- 10			GTAAATATGATCACGTGATTCATGTAACCAATCACTGAAGGTGAAGG
			DreD _{FG} 23 _{bcd}	127	111	CAGCAAAAATACTACGATTGTTCGGAGGCAAGGTTTCGGAAACAGA GTACCGTTTTATATGAGT
			DreD _{er} 29	12 865	81	CAGGAAGAAACGGGGTCCAATAAAGCTATAGAAAGAGCTAGACGTC TGGACTAAATGAGTTTATGGTACACGACTGTAATT
			DreD., 30	11 317	20	ATGTGTGTGTTTTAAAACAGCGAGGCAAC
			DreD., 31	10,317	23	TAATETTATCTGEETGGGAAATCTGCGGCACAGA
			DICDGLUI	10,723	54	AATTTACAGCTTCGTAATAGATCTTTTTATGAGCCTATTTCGTCTGTCA
			D D 05			TTGGATGCCACTGGTCATGTGCAGCACGCCAAACGTCTTCATGACCCC
			DreD _{GL} 35 _{bcd}	8,951	135	
			DIED _{GL} 36	7,359	31	
			DreD _{GL} 37 _{abcd}	5,107	136	TCATGAATGACTGCGGGAAGCACGTGATACCATTAAACTTTGTTTTA TGGCCAGGGAGTTGACAAGCCAAAATATAATTCACATTGT
						TTATTGATTGGCACGGCGCATTGATGGCGAACCAGGGCGCCCCTATAC AGCGAGCTGAAAGGATGAGAAGCGCTGGAACGATGAGACTCCAGTA ACTTCTGGTGCACCTCTACATGACAAAGACGGCGCTTCATCATTGGTT
			DreD _{GL} 38	615	191	GAAGCATTTATGCGCTCTTTTTGTGCCCCTGGACCGTTTTTATCTTTTGT GAACAAAGACAGTATTTCACAGTCAGCTGACAGGCCGCTGCAGAGG
			$\mathrm{DreD}_{\mathrm{GL}}40_{\mathrm{ab}}$	7,758	72	TATTTACAACCTCTCTGCAATGCGGC GGCTTTGACCCGCCTGAACAAGTCGCAATTCAAGGTGAAACACAGGT
			DreD _{GL} 46 _{bcd}	3,372	63	CACGCTGTCTAACAAA
			DreD _{GL} 47 _b	2,771	39	AAAAATAATGAAACATTGTGATGTGTGTGTGTAAATGATT
Polypterus senegalus b	ichir Hox D					GTCT AT AT A TA C C TGT A G A A C C G A A TT TGTGTG A A A A A A A A A A A C A TT
PFC Dist to 3	'gene Le	ngth Sequence	DreD _{GL} 48 _{abcde}	a 2,257	82	CACAGATICGATTCTAGGGGAGTATATGGTCGATG ATTGGCCAAGCTGGTCACATGGTAGGCTAACTTTATTCAGTTGACAG
PseD _{LM} 56 _{bord}	21,864	GAAAGGAACAGAAACGGACAAATTTTTACIGAAGITCGGCCCT GAAACGAAACAGGTCACTCCAGAGGACAAATTTTCTATTCGATT 128 AGCTGTATTTCAGCCGGGAGGACTGACCTATAAACCC	DreD _{GL} 49 _b	63	60	CAAGTAGGAGGGC
			DroD 50	o /		CAGGTTCATCCAGAGGACACAGTTTCTGTTGCATTACAGACGCTTTTC
PseD50	21 809	CAGGTTCATCCAGAGGACAAATTTTCTATTCGATTAGCTGTATTTC 87 AGCCGGGAGGACTGACCTATAAACCCCTTGACCTGATGGACC	Drop 54	9,100	89	TATA ATA A A A A A ATA
PseD 51	20,240	15 TATAATTGCAAAATA	DIEDLMST	9,979	15	CAGGTTCATCCAGAGGACACAGTTTCTGTTGCATTACAGACGCTTTTC
PseD _{LM} 54	18,323	17 TITITIATTAGTIGTAT	$\text{DreD}_{\text{LM}}56_{\text{c}}$	9,100	65	AGCCGCGAGCACTGACC
		САСБІБСІТТАСТАЛАТАЛТІЛІГСАБСАСБІССССТАБАЛАСА СБАСЛІСБІСЛІТЛАГІСВССАЛАСАЛАББАСІТТІЛІСЛІССІГ АЛАЛСТІБЛАБАБАТЕССАЛБАЛТАТАЛАТАТАСТАЛССБІССБІТА ТССТАСБСТАСАТІЛІССАБСІСІТТІБІЛАБСАЛІСТІБЛААСАЛІ				TGACCTGGATGTCTGAACAGAATAAATGGGAGCCATACGCAGTTCCA TTTGCAATGACACTGCACCGGATACCACCGCCGCTCTCACAATGCCT CTCAAACGCCATTTTGGTTTCG CCCATCGGACACCAGCCGTTAAGATAATCAACTGCGCTGTGGACAT CCCGAGACACGATTCGTTATGGTATAGTGTCGTTCTTATTTTTTT
rseD _{LM} 58 _{bcd}	17,931	199 OGAOULTIOLAODIAAA	DreD _{LM} 58 _{abort}	6,965	432	GACCACGTGATTGTCTA
		CCGGGCGAAGACTGTAAATCTTTCAGTTTTATTGCCCTATGACCAT	DreD _{LM} 59	5,325	19	GTCATTGCCTAAACCATAA
PseD _{LM} 67 _{bc}	16,624	95 ATG	DreD _{LM} 60	3,333	29	CAAACTTACCGTGGGAGTGCGTAGGCGAA
PseD _{LM} 61 _{ab}	12,717	GTICATTAAACGGTGAGTTATTGCCTAACATGCCAAAGGTCATGTA 70 AAAGGCTTATGACTGCTAAATATT	DreD _{LM} 61 _{abcd}	2,922	70	GTICATTAATCAGTGAGTTATTGGAGAGCAAGCCAAAGGTCACCCAA AAGGCTTATGAGTGCTAAATATT
PseD 62	10.006	45 GTCATAAATTTTACCGCAGCCCACAATGACAGGTGCATTGATATG	DD 00			CTCATA & ATTITICTCCCCCTTCACA ATCA CACTOCATINA A TTTTC
PseD _{LM} 63	13,811	22 CATTITIGIGATCAATACATATA	DreD _{LM} 62 _{ab}	1,724	45	
PseD _{LM} 69 _{abcd}	15,091	CTCAATCAGTACAATCTGGTACACCGATCACGTGAACAAATATGC 91 TTGTTTCTGAGGCATCGCCTTTATTTGTCATTATAAAAGGTTTCCG	$\rm DreD_{LM}67_{bc}$	5,816	95	TARAA ICA IOL ICAUAA I ICU IOAAAGGIGAGAGAGGIGAGAGCIGI IGUGGGGC CGGGCGTGGACTGTAAATCTTTCACTTTTATTAGCCCGTGAACATATG
		TTIATIGGIAGTIGAGTGGAGTAGGITICCATICTATCGGGAATAC TGICTCCATTGGIACATGGAAATGCICTGIGAAACCGCAAGATCAGG TTIAGGACGTTATIGTCTCAGACAAAGGGTAAGGATATATTCTA GAGACTACAGCCGAAGAAATTGAGACCGAGGACCAACGGTCAT GATAATTGATACGCAGTGAAGCAATTGCATGCCAAATGCAACC	DreD _{LM} 69 _{abcd}	4,802	90	
PseD _{LM} 70 _{ab}	14,873	233 TTTAA				GACACIACIGICIAIAGACAAAGGGIGAAGGATATATUUGAGCAGC TGAACTGAGAGATATTGAGACTAAGAAGCACGGCTATATAATAAATT
PseD _{NO} 74	2,645	19 ААААСАСАСАТААААСААА	$\mathrm{DreD_{LM}70_{ab}}$	4,600	231	GACATCACAGGTAAGCAATTGCATTGCAAAAACGTAACCTTTAA

Oryzias latipes PFC	medaka Hox Da Dist to 3' gene	Length	Sequence			
			ATTCATCAAAAGTGCCGGCGCTTCGCTGGTAAAACGCAGGCTG ACGTTGCTCCAATGATCATTTATTGTAACAGGTTTATAGCAAA TAAATAGGAGGGGCGTGCACTTGATGATGAGGGGGGCGCCTCG GTCGACCGAATATTATCCAAGTGGAGAGGAGA			
	9 694	200	GGAGCGCGCTCGTCCCTGAGTTGATATCTGAGTCTGTTTTA GATTGCTCTTGGGTTTGGCCTCATGGGCGAAATTGACAG			
OlaDA _{AD} 2	4,918	200	ATTITAAGTICATTAAGTICATAAGTT			
CIGBRADZ	4,010	21	TAATGCATTACACAAACAAGTCACATTGGTTTAAATATAATGA	Totroodon nigrou	iridia apottad graa	n nufferfich Hex Do
OlaDA _{AD} 3	3,333	57	TTATCAATTAAAGA	PFC D	ist to 3' aene Le	enoth Sequence
OlaDA _{DE} 8	3,353	24	ATGTTTGCATGTTTATTAAATGTT			
OlaDA _{DE} 10 _d	1,910	16	CAAAGTTAAGGTCAAG TAATGACTGATATTGATGTATGGTAATTCCTTAGCTCGATCACA			ATTCATCAGAAGTGCTCGCCGCTCGTTGTTAAAATGCTCGCTGAC GTCGCTCCAATGATCATTTATTGTAACAGGTTTATCAGCAAATAA ATAGGAGAGGGCTGTCACTTGATGATGGAGGCGGCCTTCGGTCA
			TGACACAATTACCTCAAGAATCGATCAAGATGTATTGCAGGTC TGCCTGCGTTTCCTAATTTTTTTCTCCCTCGCTGGGTCTTTCCACA			GACGAATAATATCCAGGAGGAGAGGAGGAGAGGAGGAGGAGGAG AGATGCTCGTCCTGGGTTGATCTCTCCGTCTGCTCCACATTGCT
OlaDA _{DE} 9 _{abce}	218	153	CGCGCGCCGTGCTATAGATGG	TniDA _{AD} 1 _b	5,394	297 CTTGGGTTTGGCCTCTTGGGTGAAATTGACAGTC
OlaDA _{EF} 11 _{ab}	2,657	28	TGTTTACTAAACCTTGAACCGTCTAGAC			TACTIFIC AT ATC ACCTICACCTCTATTA AC A AATC AAC AATTA
OlaDA _{EF} 17	1,738	30	TITATIGICITCTAAATIGCAATAGCCTTA	TniDA _{AD} 4	111	75 CCTACCCTCGATTCTTCAGGAGTTGCTAAAA
			CTCCCTCTTCA CCA CCTCTCCA TCCCCA CTCCCA A CCCCTCCC		0.454	ATTAATTCTCCTAAATAAGACAATTATACTGTTTTTAAAAAAAA
			TGGCGAGGAGGCTGCGTCTCAAGGCCATTTTCAAATCTCATTG	ThiDA 40	3,451	
0.04	100	100	GTGGGTTTGTCATGTGGGTCTGGAGGCATCCTGACTTACAGATTG	INDA _{DE} 10 _{cd}	2,186	28 GGGGCGCCAAAGCAAAGTTAAGGTCAAG
OlaDA _{EF} 19 _{ac}	193	162				TAATGACCGATATTGATGTATGGTAATTTCTTGGCCGGATCACAT
OlaDA _{FG} 20	1,409	33	TTACAGCATGTTATTACATCTCATTTACGAGG			GACGCGATCACCTCCAGAATCGATCCGGTTGTGCTGCAGGTCTG
UIADA _{FG} 22	434	- 33	macadealonamacaleleannacdadd	TniDADE9aba	241	155 CGCTTGCGCGGCTACAGATGG
			GTAAATATGATCACGTGATCCACGTAACCAATCCCTGTAGATG		2.387	28 TGTTTAGCAAACCTTGAACCGTCTAGAC
	100	110	CAGGCCAGCAAAAATACTATGATTGTTCACAGAGGGAAGCTTC CCGTACGAGTGCCTGTATTTTATGAGT	er ab	2,001	GTCGCTGTTGACCACGTCTGTATCCGCAGTGCGCGGACGCAGAC
OlaDA _{FG} 20 _{bcd}	120	113	GAACAAAGACAGTATTTCACTGGTGCCTGACAGGCAGCTGCG			GTGGGAGGGGGGAGAGAAAAGGCTGCGTCTCAAGGCCATTTTCA
$OlaDA_{GL}40_{ab}$	5,098	71	AAAGTATTTACAGCCAACTGCAATGCGGC			GATCCGTAGATIGTTTTTCCCAGATATGTCGGCGTACAAAGGAC
OlaDA _{GL} 27	4,754	16	CTATTAATTTIGTTIG	$TniDA_{EF}19_{ac}$	214	177 ^A
			CAGGAAGGAGCGTGGTCCAATAAAGCTAAAGAAATGGCCAGA	TniDA21	646	TITITATIGACAGCACGTATAATCACACGCACCTAATAAAACATT 51 TATIGAT
OlaDA _{GI} 29	11,025	80	CGTCTGGTCTAAATTAGTTTATGACTCTTTCAGTAATT	ThiDA _{FG} 21 _{abc}	427	22 TTACACCATATCATTACAGCATTITACGAGG
OlaDA _{GI} 32	3,631	24	GGATTGGCCTAAAAGAAGGAATGA	THIDA _{FG} 22	437	32 IIIACACCATATCATIACAGCATTIACGAGG
			AATTTACAACTTGGCAATAGAGGTTTTTATGTGCCTCCATCGCC			GTAAATATGACCACGTGATCTATGCAACCAATCCCTGTAGATGC
			TGTCATTGGATGCCACTGGTCATGTGTGAGAGGCAAACGTCTT CATGGCCCTTTTCCTGATTTCCCAGGCGATTTCCCCCCACTGCA		407	AGGCCACCAGAAAAGGAAATACTATGATTGTTCATAGAGGGAA
OlaDA _{GI} 35 _{bcd}	7,177	136	TICIG	ThiDA _{FG} 23 _{bcd}	137	
			TATTGAATAAGTGCAACTTCGGGGGATTATTTATGGGCCAGTGC	ThiDA _{GL} 32	3,309	A ATTEL CAACTELAGEA ATA AACCETTELETATGECCTCCATCGCC
			GGGGTTGTGAATGGCTGCGAGGAAACACGTGACGCCATTAAA GTTGTTTTATGGCTTGGGACTTGACAAGCCAAAATATAATTCT			TGTCATTGGATGCCACTGGTCATGTGTGAGAGGGAAACGTCTTC
OlaDA _{GL} 37 _{abcd}	3,308	135	CATTGT	TniDA _{GL} 35 _{bc}	5,149	111 ATGGCTTTTCTCCTGATTTCCC
						TATTGAGTAAGTGCAAGTTTGCGGATTATTTATGGTCTTTCGCGG TGTTGTGAGTGGCTGTGAGGAAACACGTGACACCATTAAAGTTT
			TTATTGATTCCCAGAAGCTGTTGCCACTGACCAATGGGCTCCC GAAACACTTTTCTTCTCCTTTTTTCAAAGGGACAGGGGCAGAT			GTTTTATGACCCGGGAGTTGACAAGGCAAAAATATAATTCTCAT
			GAAGAGATGAGAGTCATGTAACTTTTTGGATGACCCCATCTTGA	TniDA _{GL} 37 _{abcd}	2,995	136 TGT
	644	205	CAAAGACAGTGTCCATCACTTGTCCTCAGTCATTCTTCCCTGCT TTTATGCCAAAGGCCTTTTTGTGTCTTTTGT	TniDA _{GL} 46 _b	1,941	18 AAGGTGAAAGACAGGTCA
OlaDA _{GL} 38	641	205	паюссааобоспппоюсппо			TTATTGATTCCCAGAGGCGGCTGCTGCCGACCAATAGGCTCCCG
OlaDA _{GL} 46 _{cde}	2,326	41	AAGGTGAAAGACAGGTCAGGGCGTCTAACAAATATCAAAAT			TCGTGTAACTTTTGGATGACCCCTCCTTGACAAAGACAGTCTTCA
				T. DA OG		TCAATTGTCCCCAGTCATTCTTCGCTGCTTTTATGTGATGGGGGGCT
OlaDAo 48	980	82	CAATCACAGATTCGATTCTAGGGGGAGTATATGGTCGATG	I NIDA _{GL} 38	575	184 TEIGE GAACAAAGACAGTATTTCACTGCGGCCTGACAAGCAGCTGCGA
GL abude				TniDA _{GL} 40 _{ab}	4,229	72 AAGTATTTACAGCCTTGCTGCAATGCGGC
			ATTGGCCGATCTGGTCACATGGTTCGCTAACTTTATTCAGTTGA CACCAAGTAGGAGGGCCTTTATGGAGGGGAGG			
OlaDA _{GL} 49 _{bc}	123	123	CTCGAGAAAAATTAGTATTTTCTACCTTCAGAAATTA	TniDAci 48abad	930	GICTATATATACCCCIGTAGAACCGAATTIGIGIGATCAAGTCAC 76 AGTCACAGATTCGATTCTAGGGGAGTATATGG
				GL GL GL		ATTGGCCGATCTGGTCACATGGTTCGCTAACTTTATTCAGTTGAC
			TOTATE A COTTA TRUTCE A CA A A A TA A CEA COTTOCCA A A TOTO	TniDA _{GL} 49 _b	63	60 ACCAAGTAGGAGGGC
			CTTAACCCAAATTTCTATTCCCACACGGAAGACATTCCTGCGC			
			GCATTCTGGTCTGAGCGCCCTTATAAATCTCCTCTGACATCTCT			TAAATATTATTCCCAACAGCAAGACCTTCCTGCGTTCAAACTCTT
			ACTCACATGAATGATCATTCGATCCTGCATGGCTCAAATTGAT			CCGAGTGCCCTAATAAATCTTTGCTGACATCTATCTAAACAGTGT
OlaDA _{LM} 52	7,599	307	TTGGCCGTTTTTACCCCCATCGGACATAATCGAATA			ACATITICAGAGGGICITITIGIGCCATTIGAAAATTAAAIGAAAG ATCGTTTCTTCCTGCATGGCATTAAATAATTGATGGTCCTTTTTGG
				TniDA _{LM} 52	10,660	305 TCAGAAATAATCAAAGCCAGATTATTTA
			CCAGAAGCTTTTTTAGTACAAGGAGGGTCTCTACTCTAAAGTGA			
			TGAGAGGGTTGAAAAGGTATTTCATCCGAAGGTCGACAAAGG			ATATTTCTTGTTTGATACCGTCATTGTCCTGAAACAAAAAAGCAC AGAATCTCTCGCAGTCCAAGGAGGTCCTCTTTCTGAAGTCTTCAC
			GACTGACCCCAGCACCCTGACCCGCCGGACAGGCAGCATTTT			CATGCCGAGCCTGAAAAGGTATTTCAGCCGAAGTCCGACAGAA
OlaDA _{LM} 53	7,101	336	CTCTCCCAGGCGCTACTCGCTTTGGTTTGGAAGACTGTTG			CAGCGGAGGCAGGTTCATCCAGGGGACACGTTTCAGCCGCAAG GAGCTGACCCCAGCACCCATGACCCGCTGGACGAGCGCCATTTT
OlaDA _{LM} 54	6,678	15	TTTTTTATCTIGTAT	TniDA _{LM} 53	10,159	347 CTCTCCCAGGCGCTTTTGTCTTTCAGTTTGGACCC
OlaDA	5 731	60	AGACAAAGTGATGCTTCCAGTTCAGCGTCCTGTCAAAAGTGAT CCGGATATTGATGCTGA	T. DA SS		AGACAAAGTGATGCTATTTTCACCATGCTGCCAGAAATGATCTG
OIGENLWOO	5,751	00		I NIDA _{LM} 55	9,047	56 CACATAIGCIGA
			TGACCTACATGTCTGAACAGCAATAAATGAGAGCCAAAGGCA GTGCCATTTTCAATGACACTGCACCAGTGCATGAACACAACA GCCTTGCTCTCCAATGACACTGCATGCATGCAGCGCTTTTTTC			TGACCTACATGTCTGAACAGCCATAAATGGGAAGCAAAGGCGC TGCCATITTCAATGACACTGCACCCGGTGCAGGAATACGGCGTC
			GCAGAAACCTCTCCGAGCCAGACAACCCCCTAAGATATATTA			GIEGEIEICEAICEGGECAIATTIGATTICCAGEIGIGTTCGCAG AAGCTGCTGCGCGCCAGACAGCCCCCCAAAGATACATGAGAG
OlaDA58	5 /13	425	AAGIGCGCTGTCTGCATTCAGAGAATATAATCCAGAGACTATGC CACTCCGCTCTCTATTCTCGACCACGTGATTGTCTAAATA	T. D		CGCGCTGTCTGCATTCAGAGATATAATACTGAGACTATACCACT
OlaDA50	3,413	420	GTCATTTTCCCCATAA	IniDA _{LM} 58 _{abcd}	8,782	423 CCGCTCTCTATTCTGGACCACGTGATTGTCTAAATA
OlaDA,60	4,040	20	CAAACTTACCGTAACAGCGCGTAGGCGAA	i nida _{lm} 60	5,798	29 CAAACITACUGIAACAGCGCGTAGGCGAA GTTCATTAAACTTCGGCTTAACGCAAAATGACCCCGGCCTCACT
OlaDA,62	2,310	28	GTCATAAATTITTGCCACGGTCCACACTGACAGGTGC	TniDA _{LM} 61 _{acd}	5,434	70 AAAAAAGCTTATGACTGCTAAATATT
OlaDA63	310 2 400		CATTITITGGACAAAAGCATATA	TniDA _{I M} 66	5,421	24 CGGCTTAACGCAAAATGACCCGGG
SIGENEMOD	2,423	22	TAAATCAGTGTAAGTAATCCTTAAGTGTGCGAGGCTGTTGGGG	Littl	- , -= -	TAAATCACTCTCGGTAATTCCTAAAAGGGTGCAAGGCTGTTGGG
0.04			GCCGGGCGAAAACTGTAAATCTTTCACTTTTATTACCCTCCGA		7 704	GGCCGGGCGAAAACTGTAAATCTTTCACTTTTATTGCCCTCCTGA
UIADA _{LM} 67 _{bc}	4,439	93	ACATATG TCACGTGAACAAATATGCTTGTATCTAAAGGCAGCGCCTTTAT	MDALMO1 pc	7,791	30 ACATAIN
OlaDA _{LM} 69 _{bc}	3,614	47	TIGT	TniDA _{LM} 69 _{bc}	7,004	41 TCACGTGAACAAATATCTTATAACGCTGCGCCATTATTTGT
			TITATIGGTAGTIGAATGCAAGTCCTTCCATTCTTTCGGGAATA CTGTCTCCACTGGTGTATGGAAATGTCTGAAAAACAGCAAGAT			TITATTGGTAGCTGAACGCGAGTCCTTCCATTCTTCGGGAATAC TGTCTCCGTTGGTTTATGGAAATGTCTGAAAAAACAGCAAGATCA
			CAGGTTTAGGACAACTCTGTCTGCAGACAAAGGGTGAAGGATT			GGTTTAGGACAGCACTGTCTGCAGACAAAGGGTGAAGGATTTAT
			TATICTAGAGACTGCGTGGAAAGGAACCCATGCTCAGAGGAA ACTTGCTTTATATGATGAATGATTCCCAGGTAAGAAACTGCA			CCCCGTGCACTGCGTTTAAGGGAGCTGAGGCTGAGGAGGGAG
OlaDA _{LM} 70 _{ab}	3,430	235	CGGCGGAAAGCAACCTITAA	TniDA _{LM} 70 _{ab}	6,797	225 CTITAA

Oryzias latipes PFC I OlaDB _{GL} 42	: medaka Hox Db Dist to 3' gene 6,176	Length Sequence 22 CGTITIACGACCACTAGGIGGC	Tetraodon n PFC TniDB _{GL} 24 TniDB _{GL} 26 TniDB _{GL} 39 Troc TniDB _{GL} 41	igroviridis spotted Dist to 3' gene 6,494 4,430 11,470 8,478	I green pufferfish Hox Db Length Sequence 2 23 TITGGTCATCGTGGTGTACAAAC 3 17 TAGAAATCGGTGAACAA 3 24 GAGAAAACGGCGCGAATTATAAAA 3 18 AAAAGAAAGATCGTGTCAC
OlaDB _{GL} 43	5,693	CCATGTACGGAACAGGGGGGGGGGGGGGGGGGGGGGGGG	TniDB _{GL} 43	5,598	GACGCGCGGTATGTTTTCACAGACTTGGTTTATGGTTTTATGGCTCC CCTTTTACGGAAATCAAAGCAGGAAACAAATGCTTCAAACAGCA 3 107 TCCTGAAACATCCGG
OlaDB _{GL} 44	5,351	AGAACACGTGACAGTAATAAAGCGTATITTATIGCCGCCGTT AAGCCCCAAAATATAACTCAGACAGAAAAGCCGACAGGCAGG	GAC CCA TniDB _{GL} 44	5,178	CCTAATAATTTATGAACCCGGGTGGGAGCAGAGAGGGGGGAAAA TGAGCACGTGACTGTAATAAAGTGTGTTTTATTGCCGGCGGTTGA AAGCCCCCAAAATTAACTCAGAGGAAAAGCGGACAGGCGGCCC/ 3 160 GATAGGATTGGTAGCCGATATTTG
OlaDB _{GL} 45	218	АТGAACATTITITGTCCTCCAAATTATCCCATTACATCTGACAT CAGCCCAACGTGCTGCTCCTCATTGCTGCCCGCCAGGGTCACA CCCACACGACCGTCCCGTC	TAAA ATGA GATG AAA GATT TNIDB _{GL} 45	224	ATGAACACTITITICTCGCTTTAAACGATCCCATTACCTTTGCACAT AACAAACCCCCAAAAGTGCCGGCTCTIATTGGTCGGCCGCGGGG ACGTGACCCGCGGTGCCGTCCGTCTATTGACAGCCGACGAGGAG TTGATCCCCAGAGGGGAAAAGGACAGAGGAGGAGAA 224 AAAATTAGTATTCTCCTACCAGTCTCGCTATAAATCAATC
$OIaDB_{GL}48_{bc}$	1,498	58 GGGTICTAGGGG	TniDB _{GL} 48 _{at}	, 1,921	27 GTCTATACATACCCTGTAGAACCGAAT

Table S2-Conserved PFC Data Supplement to Figure 9

Data in this table corresponds to Fig. 9. For each hox cluster the order in this file corresponds to the order in the figure from left to right. Each PFC is also color coordinated with the lines representing them in Fig. 9. The groups are coded as such 1) horn shark, 2) >2 lobe-finned fish, 3) bichir, 4) >2 teleost fish. In this analysis the PFC was color coded according to the following code: Red lines represent PFCs that are found within untranslated regions (UTRs) of Hox gene mRNAs. Blue lines represent PFCs that are found within 500 nucleotides of a Hox gene proper region but have not been identified as UTRs. Green lines represent PFCs that have high or identical sequence identity to sequences in the EST library. Yellow lines represent PFCs that are not found in any databases or published papers. Black lines are sequences with known function and labeled accordingly. If a PFC fits into more than one category then colors are used in this decreasing order: Black, Red, Blue, Green, then Yellow. In the description block Fantom3 refers to a non-coding database of Mus musculus that was submitted to the RNAdb (Pang et al. 2005). RNAz refers to non-coding RNA predicted to have function as assessed by Washietl et al. 2005. Evofold also refers to non-coding RNA predicted to have function as assessed by Pedersen et al. 2006.

			Hox A Clu	ster							
PFC A30 _{BC}	Group 1.2.3.4	Color Yellow	Identity unknown function	Accession #	Brief description						
A31 _{AC}	1,3,4	Red	DreAa 88/89-103	#CK142034.1	Dre whole body cDNA						
A43cs	123	Green	DreAa 91/91-103 HsaA 101/101-101	#XM_693696.2 #BG259921.1	Dre HoxA13a mRNA Hsa cancer cell line						
	.,=,=		HsaA 69/74-101	#AK020562	Fantom3						
A57 _{CE}	2,3,4	Green	HsaA 175/175-175 HsaA 70/70-175	#BM742665.1 #AF071165.1	Hsa stomach cDNA Hsa A11 antisense						
A60 _{CE}	1,2,3,4	Red	HsaA 169/169-169	#DB289082.1	Hsa uterus cDNA						
			HsaA 70/70-169 HsaA 94/94-169	#BC033706 #U20366	Hox A11 mRNA Hox A11 antisense						
A62 _{EF}	1,2,3	Yellow	unknown function		TISK TT CHROCHOO						
A75 _{EF}	1,2,3,4	Red	HsaA 106/106-106	#BQ215499.1	Hsa cancer cell cDNA						
A78 _{FG}	1,2,3	Green	HsaA 164/167-170	#NM_018951 #CO601426.1	Cfa testis cDNA						
470	4004	Disali	HsaA 70/70-170	#16273071	RNAz						
Ar 9 _{FG}	1,2,3,4	DIACK	HsaA 54/54-54 HsaA 54/54-54	#BQ923616.1 #15105502	mir-196b ⁶						
A92 _{FG}	1,2,3	Red	HsaA 198/209-209	#CF957153	rice leaf mRNA, also rat						
A98 _{GI}	1.4	Yellow	HsaA 155/162-209 unknown function	#NM_010456	Mmu HoxA9 mRNA						
A103 _{GI}	1,2,3,4	Green	XtrA 94/94-129	#CR440650.1	Xtr tailbud cDNA						
A111 _{GI}	1,2,4	Red	HsaA 169/169-169	#BP263590.1	Hsa intenstine cDNA						
			HsaA 64/64-169	#16628248	Evofold						
A119 _{IJ}	1,2,3,4	Green	HsaA 160/172-192 HsaA 187/192-192	#BY737288.1 #AK146012	Mmu placenta cDNA Fantom3						
A130 _{IJ}	1,2,3	Blue	unknown function								
А132 _{JK}	1,2,3,4	Red	HsaA 285/292-292	#DN125225.1	Screarly devo cDNA						
А136 _{кі.}	1,2,3,4	Black	HsaA 201/201-201	#DB026292.1	Hsa testis cDNA						
			HsaA 52/52-201	#AK028207 #16628248	Fantom3						
			HSaA 40/40-201	#10028246	A5 mesoderm enhancer ¹						
A140 _{KL}	1,2,3,4	Yellow	unknown function								
A143 _{KL} A149 _M	1,2,3,4 1,2,3,4	Yellow Black	unknown function HsaA 132/138-152	#BU205782.1	Gga embryo cDNA						
					A4 RARE ⁷						
A157 _{KL}	1,2,3,4	Blue	HsaA 49/49-71	#DT837650.1	Bta liver cDNA				Here C Clur	tor	
A181 _{LM}	1,2,3,4	Yellow	unknown function			PFC	Group	Color	Identity	Accession #	Brief description
A193 _{LM}	1,2,3,4	Yellow	unknown function			C8 _{CD}	2,4	Red	HsaC 91/97-172	#BC120847.1	Mmu HoxC12 mRNA
A194 _{LM}	1,2,3,4	Green	HsaA 28/28-151 DreAa 67/67-151	#DB001242.1 #CO923716.1	Hsa tumor cDNA Dre larvae cDNA	020 _{DE}	2,7		HsaC 95/95-257	#BC001543.1	Hsa HoxC11 mRNA
A198 _{LM}	1,2,3	Green	HsaA 114/117,28/28-166	#BB660130	Mmu embryo cDNA	C35cc	2.4	Blue	HsaC 28/28-257 HsaC 123/123-204	#16628248 #AI830498.1	Evofold Hsa kidnev cDNA
A199	1.2.3.4	Red	HsaA 114/117-166 HsaA 197/199-197	#AK142386 #DA631881	Fantom3 Hsa kidney cDNA	C38 _{FG}	2,4	Green	HsaC 146/161-161	#CK024405.1	Dre whole cDNA
	.,.,.,.,.		92/92-197	#NM_153631	Hsa HoxA3 mRNA	C40 _{FG}	2,4	Black	underson for sting		mir196-2 ³
A204 _{MN}	2,3,4	Black	HsaA 76/82-84	#BY717422.1	Mmu embryo cDNA	C52 _{FG}	2,4	Red	HsaC 159/164-164	#BU514229.1	Mmu limb cDNA
A210 _{MN}	1,2,3	Green	HsaA 155/162-162	#AI046800.1	Mmu stem cell cDNA				HsaC 159/164-164	#NM_008272.3	Mmu HoxC9 mRNA
A211 _{MN}	1,2,3,4	Red	HsaA 207/207-207 HsaA 131/131-207	#CR452916.1 #NM_006735	Bta extraembryonic cDNA Hsa HoxA2 mRNA				HsaC 33/33-164	#16628248	Evofold
PEC	Group	Color	Hox B Clus	ster	Brief description	C55 _{GH} C56 _{GH}	2 4	Black			C8 early enhancer
B50 _{GH}	2,3	Red	HsaB 203/221-342	#BU450737.1	Gga ovary cDNA	C67 _{HJ}	2,4	Green	DreC 130/130-130	#CT615268.1	Dre myoblast cDNA
851	2.2	Red	HsaB 163/165-342	#NM_010461.2	Mmu HoxB8 mRNA	C87 _{KL}	2,4	Green	HsaC 101/101-206	#BP872195.1	Hsa kidney cDNA
GH			HsaB 69/71-71	#NM_010461.2	Mmu HoxB8 mRNA	Caakr	2,4	Green	HsaC 108/108-164	#16628248	Evofold
В52 _{GH}	2,3	Red	HsaB 153/153-153	#DA691980.1	Hsa NT2 cDNA	C102 _{KL}	2,4	Red	HsaC 149/151-151	#AA792111.1	Mmu myotubes cDNA
B60 _{HI}		Yellow	unknown function						Hox D Clus	ster	wind H0x04 mKNA
B63н	2,3	Red	HsaB 154/161-238	#CB805852.1	Rno prostate cDNA	PFC D1 _{vc}	Group	Color Green	Identity HsaD 266/280-339	Accession # #CA327595 1	Brief description Mmu brain cDNA
			HsaB 54/54-238	#16628248	Evofold				HsaD 46/46-339	#16628248	Evofold
B65 _{IJ}	2,4	Yellow	unknown function	#DA680465.4	Hea NT2 cDNA				HsaD 65/65-339	#16628248	Evofold
B79 _K	2,4	Red	HsaB 110/110, 107/107-246	#DA669465.1 #DN996030.1	Hsa cancer cDNA	D10 _{DE}	1,2,4	Green	HsaD 142/142-142	#AW785383.1	Ssc cDNA
			HsaB 108/110, 107/107-246	#BC040755.1	Mmu HoxB5 mRNA	D19 _{EF}	1,2,4 1,2,4	Red	HsaD 175/178-178	#CV397708.1	Hsa kidney cDNA
B87 _{KL}	2,3,4	Green	HsaB 75/75-204	#AA373970.1	Hsa stem cells cDNA				HsaD 40/40-178	#NM_002148.3	Hsa D10 mRNA
ROC	0.0.1	Mall.	HsaB 87/87-204	#16628248	Evofold	D21 _{FG}	1,2,4	Yellow	unknown function	#NM 014212-2	
B102ki	2,3,4 2.3,4	Green	HsaB 188/200-200	#CR522341.1	Mmu cDNA clone	D35 _{HL}	1,2,4	Green	HsaD 177/178-177	#DA384584.1	Hsa thalamus cDNA
B104 _{KL}	3,4	Yellow	unknown function			D37	124	Vollar	HsaD 28/28-177	#1628248	Evofold
B108 _{KL}	2,3	Blue	unknown function	HOTOMOTO	December 1 - Ditt	D46 _{HL}	1, <u>2,4</u> 2,4	Black	unknown function		D4 RARE⁵
BTTO _{LM}	2,4	Red	XtrB 71/71-71	#C1631859.2 #BC090114	Xtr HoxB4 mRNA	D48 _{HL}	2,4	Black	HsaD 79/82-82	#CJ057604.1	Mmu spinal cord cDNA
В113 _{LM}	2,4	Green	HsaB 152/156-156	#BG835561	Ssc pooled cDNA				HsaD 82/82-82	#X17360.1	Hsa Hox 5.1 mRNA mir-10b ³
B118, "	2,4	Green	HsaB 122/122-156 HsaB 184/184,81/82-393	#16628248 #BF996393.1	evotold Hsa placenta	D49 _{HL}	2,4	Red	HsaD 143/143-143	#DR006918.1	Hsa spleen cDNA
			HsaB 82/82-393	#16273071	RNAz	D58	2.3.4	Green	HsaD 143/143-143 DreD 243/255-432	#NM_014621.2	Hsa HoxD4 mRNA Ppr(fish) brain cDNA
B139 ₁₀₁	2,4	Yellow	unknown function		DNIA	D61 _{LM}	2,3,4	Yellow	unknown function		
B140.	24	Red		#BG114205.4			_				
B140 _{MN}	2,4	Red	HsaB 104/104,28/28,24/24-232 HsaB 104/104,28/28,24/24-232	#BG114205.1 #NM_002146.4	Hsa HoxB3 mRNA	D62 _{LM}	2,3,4	Yellow	unknown function		
B140 _{MN}	2,4	Red	HsaB 104/104,20/28,24/24-232 HsaB 104/104,28/28,24/24-232 HsaB 81/81-232 HsaB 33/33-232	#BG114205.1 #NM_002146.4 #16628248 #16273071	Hsa HoxB3 mRNA Evofold RNAz	D62 _{LM} D67 _{LM} D69 _{LM}	2,3,4 2,3,4 2,3,4	Yellow Yellow Yellow	unknown function unknown function unknown function		

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Curriculum Vitae

Jeremy Don Raincrow

Education:

2010 Ph.D. in Cell and Developmental Biology-Rutgers, The State University of New Jersey and University of Medicine and Dentistry of New Jersey 2004 B.S. in Biology-University of Central Oklahoma

Publications:

Zhang YQ, Guo N, Peng G, Han M, Raincrow J, Chiu CH, Coolen LM, Wenthold RJ, Zhao ZQ, Jing N and Yu L. 2009. Role of SIP30 in the development and maintenance of peripheral nerve injury-induced neuropathic pain. Pain. 146(1-2): 130-40.

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