



**HAL**  
open science

## Revisiting the evolution of the somatostatin family: already five genes in the gnathostome ancestor

Hervé Tostivint, Anne-Laure Gaillard, Sylvie Mazan, Guillaume Pézeron

### ► To cite this version:

Hervé Tostivint, Anne-Laure Gaillard, Sylvie Mazan, Guillaume Pézeron. Revisiting the evolution of the somatostatin family: already five genes in the gnathostome ancestor. *General and Comparative Endocrinology*, 2019, 279, pp.139-147. 10.1016/j.ygcen.2019.02.022 . mnhn-02276574

**HAL Id: mnhn-02276574**

**<https://mnhn.hal.science/mnhn-02276574>**

Submitted on 2 Sep 2019

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0  
International License

## **Revisiting the evolution of the somatostatin family: already five genes in the gnathostome ancestor**

Hervé Tostivint<sup>a</sup>, Anne-Laure Gaillard<sup>a</sup>, Sylvie Mazan<sup>b</sup>, Guillaume Pézeron<sup>a</sup>

<sup>a</sup> Physiologie moléculaire et adaptation UMR 7221 CNRS and Muséum National d'Histoire Naturelle, Paris, France

<sup>b</sup> Biologie intégrative des organismes marins, UMR 7232 CNRS, Observatoire Océanologique, Sorbonne Université, Banyuls-sur-Mer, France

(Correspondence should be addressed to H. Tostivint; E-mail: [htostivi@mnhn.fr](mailto:htostivi@mnhn.fr))

*Keywords:* somatostatin, neuropeptides, evolution, multigenic family, cartilaginous fish, chondrichthyes, elasmobranchii, holocephali, vertebrates

## Abstract

The somatostatin (SST) family members are a group of neuropeptides that are best known for their role in the regulation of growth, development and metabolism. The occurrence of six paralogous SST genes named *SST1*, *SST2*, *SST3*, *SST4*, *SST5* and *SST6* has been reported in vertebrates. It has been proposed that *SST1*, *SST2* and *SST5* arose in 2R from a common ancestral gene. *SST3* and *SST6* would have been subsequently generated by tandem duplications of the *SST1* and *SST2* genes respectively, at the base of the actinopterygian lineage. *SST4* is thought to have appeared more recently from *SST1*, in teleost-specific 3R.

In order to gain more insights into the *SST* gene family in vertebrates, we sought to identify which paralogs of this family are present in cartilaginous fish. For this purpose, we first searched the recently available genome and transcriptome databases from the catshark *Scyliorhinus canicula*. In a previous study, three *S. canicula* *SST* genes, called at that time *SSTa*, *SSTb* and *SSTc*, were identified and proposed to correspond to *SST1*, *SST5* and *SST2* respectively. In the present work, two additional *SST* genes, called *SSTd* and *SSTe*, were found in *S. canicula* plus two other chondrichthyan species, elephant shark (*Callorhynchus milii*) and whale shark (*Rhincodon typus*). Phylogeny and synteny analyses were then carried out in order to reveal the evolutionary relationships of *SSTd* and *SSTe* with other vertebrate *SSTs*. We showed that *SSTd* and *SSTe* correspond to *SST2* and *SST3* respectively, while *SSTc* corresponds to *SST6* and not to *SST2* as initially proposed. Our investigations in other vertebrate species also led us to find that the so-called *SST2* gene in chicken, lungfish, sturgeons and teleosts actually corresponds to *SST6*. Conversely, the so-called *SST6* gene in actinopterygians corresponds to *SST2*.

Taken together, our results suggest that: *i*) *SST3* and *SST6* were already present in the gnathostome ancestor, much earlier than previously thought; *ii*) *SST6* was also present in the tetrapod ancestor and still occurs in living birds; with this respect, it is likely that *SST6* was independently lost several times during evolution: in euteleosts, amphibians, squamates and mammals; *iii*) *SST2*, *SST3* and *SST5* were probably lost in euteleosts, sarcopterygians and tetrapods, respectively.

## Introduction

Somatostatin (currently known as somatostatin 1 or SST1) was originally isolated from ovine hypothalamus and found to inhibit the release of growth hormone from the rat pituitary (Brazeau *et al.* 1973). It has been subsequently shown that SST1 is widely distributed in the central nervous system and in various peripheral organs where it plays important roles in the regulation of growth, development and metabolism (Günther *et al.* 2018). The occurrence of SST1 was reported in all vertebrate species investigated so far. Moreover, most species were shown to possess additional SST forms. In gnathostomes (jawed vertebrates), it was demonstrated that all these SST variants are the products of at least six paralogous genes named *SST1*, *SST2* (also known as *Cortistatin* in mammals) *SST3*, *SST4*, *SST5* and *SST6* (de Lecea *et al.* 1996, Liu *et al.* 2010, Tostivint *et al.* 1996, 2008, 2013, 2014). SST-related peptides are thought to act through at least six SST receptor subtypes (Ocampo Daza *et al.* 2012). In lampreys, three *SST* genes have characterized but their phylogenetic status is still unclear (Tostivint *et al.*, 2016), while in the hagfish *Myxine glutinosa*, the occurrence of only one *SST* gene, encoding a SST1-like peptide, is attested to date (Conlon *et al.*, 1988).

It is currently well accepted that the evolution of the *SST* gene family, as that of many other neuropeptides (Elphick *et al.* 2018), was strongly shaped by the different rounds of whole-genome duplications that took place in the vertebrate history, especially the two basal rounds of vertebrate genome doubling (2R) and the teleost fish-specific genome doubling (3R) (Dehal & Boore 2005, Putnam *et al.* 2008, Sacerdot *et al.* 2018). Thus, *SST1*, *SST2* and *SST5* seem to have been generated during 2R from a common ancestral gene, while *SST4* is likely to have appeared during 3R from *SST1*. Impact of 2R on the early evolution of *SST* gene family is notably supported by synteny analysis showing that *SST* genes are located on a same tetraparalogon that contains paralogous genes of at least ten other families (Liu *et al.* 2010, Tostivint *et al.*, 2013, 2014). For their part, *SST3* and *SST6* would have been independently generated by tandem duplications of *SST1* and *SST2* respectively, at the base of the actinopterygian lineage (Liu *et al.* 2010, Tostivint *et al.* 2004, 2008). Some of these genes could have been subsequently lost explaining their absence in some lineages. For example, *SST5* is believed to have been lost in tetrapods.

Cartilaginous fish (chondrichthyans) are of particular interest in evolutionary studies because of their key phylogenetic position at the base of the gnathostome lineage. They consist of two major groups: elasmobranchii (sharks and skates/rays) and holocephali (chimaeras). Until 2013, SST-related peptides were characterized in only a very few species of cartilaginous fish: SST1 from the ray *Torpedo marmorata* (Conlon *et al.* 1985), a SST1-like peptide exhibiting a serine residue at position 5 from the ratfish *Hydrolagus colliei* (Conlon 1990), a SST2-like sequence from the elephant shark *Callorhinchus milii* (Tostivint *et al.* 2008) and finally a totally atypical SST-related sequence from both the little skate *Leucoraja erinacea* and *C. milii* (Liu *et al.* 2010). In 2013, three *SST* genes, called *SSTa*, *SSTb* and *SSTc*, were identified in the common dogfish (today referred to as small-spotted catshark, *Scyliorhinus canicula*) and proposed to correspond to *SST1*, *SST5* and *SST2*, respectively (Quan *et al.* 2013). Surprisingly, none of these genes appeared as the apparent ortholog of the atypical SST-like gene found in *C. milii* and *L. erinacea*. Nevertheless, these findings were regarded as in good agreement with the model described above since they support the existence of these three *SST* genes in the gnathostome ancestor (Liu *et al.* 2010, Tostivint *et al.* 2013, 2014). However, due to the lack of a fully sequenced and assembled *S. canicula* genome, this view could not be confirmed (Quan *et al.* 2013).

The first goal of the present study was to determine the complete repertoire of the *SST* gene family in cartilaginous fish. For this purpose, we searched the newly available *S. canicula* genome and transcriptome databases (unpublished data). We also took the opportunity to explore or reexplore the genome and transcriptome databases from two additional species, the



whale shark, *Rhincodon typus* (Read *et al.* 2017) and the elephant shark, *C. milii* (Venkatesh *et al.* 2014). We found two novel *S. canicula* SST genes that we propose to provisionally call *SSTd* and *SSTe* (according to the nomenclature initially proposed in Quan *et al.* 2013). *S. canicula* *SSTd* was shown to be the ortholog of the *L. erinacea* and *C. milii* atypical SST-like gene above-mentioned, while *S. canicula* *SSTe* appeared as a totally new SST gene. In both *R. typus* and *C. milii*, four SST genes were found that correspond *SSTa*, *SSTc*, *SSTd* and *SSTe*.

Taking advantage of the genome assembly of various representative species from other vertebrate groups, we then carried out phylogeny and synteny analyses in order to reveal the evolutionary relationships of chondrichthyan *SSTd* and *SSTe* with other vertebrates SSTs. From our investigations, it appeared that *SSTd* and *SSTe* correspond to *SST2* and *SST3*, respectively, while *SSTc* corresponds to *SST6* but not to *SST2* as initially proposed (Quan *et al.* 2013).

The major implication of these results is that the repertoire of the SST gene family in the gnathostome ancestor was already composed of five paralogs namely *SST1*, *SST2*, *SST3*, *SST5* and *SST6*. Our observations also led us to revisit the phylogenetic status of *SST2* and *SST6*. As a result, the nomenclature of these genes had to be corrected in some species.

## Material and methods

### Nomenclature

In this article, *S. canicula* SSTs, as well as their counterparts from other chondrichthyans, will be first described as *SSTa-SSTe*, according to the provisionnal nomenclature proposed by Quan *et al.* (2013), without prejudice to their evolutionary relationships with other vertebrates SSTs. Thereafter, in the light of the phylogeny and synteny data, they will be renamed according to the phylogenetic nomenclature, *SST1-SST6*, initially introduced by Tostivint *et al.* (2008) then extended by Liu *et al.* (2010). Nevertheless, the correspondence between the two nomenclatures will be regularly reminded throughout the article as follows: *SSTa* = *SST1*; *SSTb* = *SST5*; *SSTc* = *SST6*; *SSTd* = *SST2* and *SSTe* = *SST3*. Note that in Quan *et al.* (2013) *SSTc* was initially but mistakenly referred to as *SST2*.

### Identification of *SSTd* and *SSTe* sequences from cartilaginous fish

*S. canicula* *SSTd* and *SSTe* genes were sought by TBLASTN (Altschul *et al.* 1990) using the *C. milii* and *L. erinacea* SST2-like sequences (AGCKLFFWKTFSHC and APCKLFFWKTFSHC) as queries against the *S. canicula* genome draft assembly (version 1, unpublished). *S. canicula* full-length *SSTd* cDNA (but not *SSTe* cDNA) was also retrieved from *S. canicula* Illumina transcriptome (version 1, unpublished).

The SST repertoire of SST genes in *R. typus* and *C. milii* was sought by TBLASTN using the *S. canicula* SST cDNA sequences as queries against the *R. typus* and *C. milii* genome assembly databases (Read *et al.* 2017; Venkatesh *et al.* 2014).

Protein sequences were predicted by using consensus splice donor and acceptor site and by sequence identity comparison with related SST genes. The signal peptide cleavage site was determined using SignalP (<http://www.cbs.dtu.dk/services/SignalP/>) (Petersen *et al.* 2011).

### Molecular cloning of the coding sequence of *S. canicula* *SSTe* cDNA

5'RACE-ready cDNAs used for this procedure were constructed as previously described (Gaillard *et al.* 2018). The coding sequence of the *S. canicula* *SSTe* cDNA was amplified by nested PCR using the Advantage 2 PCR kit (Clontech). Nested PCR was carried out in a MyCycler thermal cycler (Bio-Rad, Marne la Coquette, France) with the following primers, csSSTe Rev x Universal Primer A Mix (UPM) then csSSTe Rev Nest x Nested Universal Primer A Mix (NUP) (see **Table S1**) using the manufacturer's procedure. PCR amplifications were carried out for 35 cycles (denaturation 94°C, 30 sec; annealing between 57 and 60°C depending on the T<sub>m</sub> of the primers, 30 sec; and extension 72°C, 30 sec) and a final extension

of 72°C for 7 min. The product of the nested PCR was subcloned into the pGEM-T vector (Promega, Charbonnières-les-Bains, France) and sequenced (Value Read Sequencing at MWG Biotech, Ebersberg, Germany).

### **Synteny analysis**

To generate synteny maps, genes flanking *C. milii* and *R. typus* *SST* genes were obtained from the NCBI database. Non-protein coding genes and genes coding unknown proteins were excluded from further analysis. Note that *SSTb* was not included in the study since it is absent in both *C. milii* and *R. typus*, while in *S. canicula*, it is located on a very short scaffold that did not contain any other genes. Genes flanking the *SST* genes in eight additional osteichthyan species, namely human, chicken (*G. gallus*), green anole lizard (*A. carolinensis*), Western clawed frog (*X. tropicalis*), coelacanth (*L. chalumnae*), spotted gar (*L. oculatus*), zebrafish (*Danio rerio*) and medaka (*Oryzias latipes*), were obtained from Genomicus (version 92.01) (Muffato *et al.* 2010).

### **Phylogeny analysis**

A set of 147 vertebrate *SST* precursor sequences was primarily collected from Yun *et al.* (2015) and Tostivint *et al.* (2016) and supplemented by the chondrichthyan sequences characterized in the present study. All these sequences were aligned using the Muscle algorithm (Edgar 2004) then manually adjusted. The phylogeny of *SST* precursors was inferred by Maximum Likelihood using PhyML (Guindon & Gascuel 2003) with the LG model of substitution combined to the neighbor-joining interchange (NNI) method on Seaview browser (Gouy *et al.* 2010). The robustness of the tree was assessed by the approximate likelihood test (aLRT) SH-like branch support and by bootstrapping procedure from 500 data set replicates. The Genbank accession numbers for all sequences used in the analysis are listed in **Figure S1**. The alignment is presented in **Figure S2**.

### **Tissue expression of *S. canicula* *SSTd* and *SSTe* genes by reverse transcriptase-polymerase chain reaction (RT-PCR) amplification**

The expression profiles of *S. canicula* *SSTd* and *SSTe* genes were examined by RT-PCR, as previously described (Quan *et al.* 2013, Gaillard *et al.* 2018). Total RNA was extracted from various tissues, including telencephalon, diencephalon, mesencephalon, cerebellum, brain stem, spinal cord, skeletal muscles, heart, spleen, gills, stomach, duodenum, valvular intestine, pancreas, liver, kidney, ovary and testis and purified by using RNAeasy Plus Mini kit (Qiagen, Courtabœuf, France). For each tissue, ~330 ng of total RNA were reverse transcribed using ImProm-II Reverse Transcription System (Promega, Charbonnières, France). Gene-specific primers of *S. canicula* *SSTd* and *SSTe* were designed according to the predicted sequences (**Table S1**). PCR amplifications were carried out for 35 cycles (denaturation 94°C, 30 sec; annealing between 57 and 60°C depending on the T<sub>m</sub> of the primers, 30 sec; and extension 72°C, 30 sec) and a final extension of 72°C for 7 min. The *S. canicula* *Egfl* gene was amplified in parallel with specific primers (**Table S1**) to verify the quality and quantity of all cDNAs samples. Negative controls were performed without cDNA template. All PCR products were electrophoresed through 2.0% agarose gel and stained with ethidium bromide and then detected under UV light with the ChemiDoc Touch Imaging System (BioRad). Three independent PCR amplifications were performed to check the consistency of amplification.

## **Results**

### **Structure of *S. canicula* *SSTd* (*SST2*) and *SSTe* (*SST3*) precursor cDNAs and genes**

The nucleotide and deduced amino acid sequences of *S. canicula* SSTs including *SSTd* and *SSTe* are shown in **Figure S3**. The coding region of the *SSTd* cDNA consists of 315 nucleotides (nt) that encode a 105-amino acid (aa) protein (PSSTd) including a 20-residue potential signal sequence (Petersen *et al.* 2011). The primary structure of PSSTd contains a monobasic processing site at position 91 (Lys) potentially yielding the mature 14-aa peptide SSTd (SST2), TPCKLFFWKTFSHC, plus one dibasic and one monobasic processing sites at positions 87-88 (Arg-Arg) and 79 (Arg) respectively, potentially yielding 17- and 26-aa NH<sub>2</sub>-extended forms of SSTd.

The coding region of the *SSTe* cDNA consists of 321 nt that encode a 106-aa protein with a 18-residue potential signal sequence. The *SSTe* sequence is flanked by a pair of basic residues (Arg-Lys) at position 92-93 potentially yielding the mature 14-aa peptide *SSTe* (SST3), NCKNFFWKTYTLC, plus two monobasic processing sites at positions 85 (Arg) and 90 (Arg) respectively, potentially yielding 17- and 22-aa NH<sub>2</sub>-extended forms of *SSTe*.

Comparison of the cDNAs with genomic sequences revealed that *SSTd* and *SSTe* genes are each composed of two exons and one intron (**Figure S4**). For each gene, exon 1 encodes the 5' UTR, the signal peptide and the N-terminus of the prepro-peptide while exon 2 encodes the C-terminus of the precursor, including the putative mature peptide.

### **Repertoire of SST cDNAs and/or genes in cartilaginous fish**

The entire repertoire of *SST* cDNAs and/or genes found from *S. canicula*, *R. typus* and *C. milii* databases is shown in **Figures S3-S8**. *S. canicula* SST family appears as the richest with no less than five *SST* genes: the three genes previously reported in Quan *et al.* (2013), namely *SSTa*, *SSTb* and *SSTc*, plus two additional genes characterized in the present study, *SSTd* and *SSTe*. All these genes, with the exception of *SSTb*, were retrieved from *R. typus* and *C. milii*. Only a partial sequence of the *SSTd* gene could be detected from *L. erinacea* (already reported in Liu *et al.* 2010).

### **General organization of the chondrichthyan SST genes and SST precursors**

The molecular organization of the *SST* precursors is the same in all species examined, with a signal peptide followed by a long central segment, a conserved pair of basic residues and, finally, the *SST* sequence at their C-terminus (**Figure 1**). All putative *SST* possess a cyclic conformation ensured by the presence of two Cys residues, and their cyclic region encompasses the Phe-Trp-Lys motif. The structure of the corresponding genes is also very well conserved with two exons and one intron (**Figures S4, S5, S7**). Note that the first exon of *S. canicula* *SSTd* and that of *S. canicula* *SSTa* (*SST1*) exhibit almost the same nucleotide sequence (**Figure S4**). This sequence identity was also found in the corresponding cDNA identified by RT-PCR ruling out an artefact of genome assembly (**Figure S3**).

### **Structural features of the chondrichthyan putative SST tetradecapeptides**

#### **- SSTa (SST1)**

The primary structure of *SSTa* is AGCKNFFWKTFSTC both in *S. canicula* and *R. typus*. In *C. milii*, it exhibits one substitution, Ser vs Asn, at position 5, as previously reported in the ratfish *H. colliei* (Conlon 1990) (**Table S2**). It is to note that the genomic *SSTa* sequence encodes for a Leu in place of Phe at position 6 that was not retrieved in the cDNAs (**Figures S3 and S4**). Chondrichthyan prepro-*SSTa* exhibit high sequence identity (ranging from 66.3 to 74.1% between one another) (**Table S3**).

#### **- SSTb (SST5)**

As mentioned above, the *SSTb* sequence could only be found in *S. canicula* (see Quan 2013 for a complete description of the precursor). Just as a reminder, *S. canicula* *SSTb* exhibits the same primary structure as *SSTa* (*SST1*) (**Table S2**).

- SSTc (SST6)

SSTc exhibits two substitutions at positions 1 and 2 when compared to SSTa (**Table S2**). The residue at position 2 is a Pro, except in *R. typus*. The residue at position 1 is more variable. Chondrichthyan prepro-SSTc exhibit high sequence identity (ranging from 53.8 to 86.7% between one another) (**Table S3**).

- SSTd (SST2)

When compared to that of SSTa, the primary structure of SSTd can be distinguished by the Ser-His-Cys (SHC) motif at its C-terminus (**Table S2**). Variable residues are present at position 1 and 2. However, the residue at position 2 is generally a Pro, except in *C. milii*. Chondrichthyan prepro-SSTd exhibit high sequence identity (ranging from 51.9 to 76% between one another) (**Table S3**).

- SSTe (SST3)

In all species examined, the primary structure of SSTe exhibits the unique Tyr-Thr-Leu-Cys (YTLC) motif at its C-terminus (**Table S2**). Only the residue at position 1 is different depending on the species. *S. canicula* and *C. milii* prepro-SSTe exhibit only 38.1% identity (**Table S3**).

### Synteny analysis of SST genomic regions

In both *R. typus* and *C. milii*, SSTe (SST3) and SSTa (SST1) are tandemly arranged on the same scaffold (**Figure 2, Table S4**). However, this scaffold is very short and does not contain any other genes. On the basis of our previous results suggesting that SSTa probably corresponds to SST1 (Quan *et al.* 2013), we aligned the chondrichthyan SSTa-SSTe scaffold with the SST1 locus from the other species analyzed. In teleosts, SST3 is localized in tandem with SST1, as SSTe and SSTa in cartilaginous fish.

In spotted gar, the SST1-SST3 locus bears a third SST gene, here called SST4, surrounded by *Nyap2* and *Irs1* (**Figure 2, Table S4**). In teleosts, the SST known as SST4 is located on a different chromosome than that bearing SST1 and SST3. Its closest neighbors are *Nyap2b* and *Fgf12a* (**Figure 2, Table S4**). The co-orthologs of these two latter genes, *Nyap2a* and *Fgf12b*, are present in the vicinity of both SST1 and SST3. Thus, the teleost SST4 can be viewed as either an ortholog to gar SST4 (as this is what its name implies) or a 3R duplicate of either SST1 or SST3. These three possibilities are illustrated in **Figure 2**.

*R. typus* and *C. milii* SSTd (named SST2 in **Figure 3**) were found in a genomic region containing several genes, *Kif1b*, *Pgb*, *Cenps* and *Dffa*, that are also present in the vicinity of the human SST2 gene (**Figure 3, Table S4**). It is to note that the gar and zebrafish SST genes present in the syntenic region correspond to genes previously known as SST6.

The neighborhood of the *R. typus* and *C. milii* SSTc (named SST6 in **Figure 3**) is composed of several genes, *Tardbp*, *Masp2* and *Srm*, that, in the other species examined, were present in the vicinity of SST genes previously known as SST2, notably in chicken, spotted gar, zebrafish and medaka (**Figure 3, Table S4**).

### Phylogeny analysis of SST precursors

**Figure 4** displays an unrooted tree constructed from 147 selected vertebrates SST precursor sequences using maximum likelihood phylogeny analysis. In the resulting tree, osteichthyan SST sequences cluster into six main clades, SST1-SST6. Bootstrap support values for these six groups were 53, 10, 94, 29, 68 and 75%, respectively. The only discrepancy of this patterning is the presence of the gar SST4 sequence into the SST3 clade. It is to note that the actinopterygian SST sequences belonging to the SST2 clade were previously known as SST6. Likewise, chicken, lungfish, sturgeon and teleost SST sequences included in the SST6 clade were previously known as SST2.

Chondrichthyan SSTb, SSTc and SSTd branch at the base of the SST5, SST6 and SST2 clades, respectively. Gnathostome SST2-SSTd and SST6-SSTc appeared as two sister groups as well

as osteichthyan SST1 and SST3. For their part, chondrichthyan SSTa and SSTe formed a monophyletic group that branch at the base of the osteichthyan SST1-SST3 clade. As previously reported (Tostivint *et al.* 2016), lamprey SST sequences did not group to any of the gnathostome SST clades.

### **Tissue-specific expression of *S. canicula* SSTd (SST2) and SSTe (SST3) genes**

The distribution of *S. canicula* SSTd and SSTe mRNAs in various tissues was examined by RT-PCR. **Figure 5** shows the results of one representative experiment out of three performed with identical results. SSTd mRNA was detected primarily in the brain (notably in the diencephalon, mesencephalon and brainstem) and spinal cord. In contrast, SSTe mRNA appeared particularly abundant in the central nervous system (in all subdivisions examined except in the cerebellum) as well as in the intestinal tract and pancreas. Note that traces of SSTd mRNA were also seen in the spleen, gills, pancreas and gonads.

## **Discussion**

The main aim of the present study was to determine the repertoire of the SST gene family in cartilaginous fish. For this purpose, the genome and/or transcriptome databases from three representative chondrichthyan species were examined, namely the small-spotted catshark *S. canicula* (unpublished, see Gaillard *et al.* 2018 for more details), the whale shark, *R. typus* (Read *et al.* 2017) and the elephant shark *C. milii* (Venkatesh *et al.* 2014). In *S. canicula*, two new SST genes, named SSTd and SSTe were found, in addition to the three SST genes, SSTa, SSTb and SSTc, previously identified (Quan *et al.* 2013). All these genes, with the exception of SSTb, were retrieved from *R. typus* and *C. milii*. It is noteworthy that the occurrence of partial sequences of the SSTc (Tostivint *et al.* 2008) and SSTd genes (Liu *et al.* 2010) were already reported in both *L. erinacea* and/or *C. milii*. In contrast, SSTe appeared as a totally novel gene. The nomenclature used above (SSTa-SSTe) was initially (and provisionally) proposed to designate the *S. canicula* SSTs without prejudice to their evolutionary relationships with other vertebrate SSTs (Quan *et al.* 2013). Synteny comparisons and phylogeny analysis were subsequently carried out in order to reveal the phylogenetic status of all these genes.

Synteny comparisons suggest that SSTd is the chondrichthyan counterpart of SST2 since both *S. canicula* and *C. milii* SSTd reside in the same chromosomal environment as that of human SST2. For the same reasons, SSTc can be legitimately viewed as the chondrichthyan counterpart of SST6. These conclusions are quite consistent with our phylogeny analysis because SSTd and SSTc precursor sequences branch at the base of the SST2 and SST6 clades, respectively, although the bootstrap support values of the new clades are extremely weak (4% and 37% respectively).

Our investigations on the chondrichthyan SSTc and SSTe also led us to redefine the relationships between SST2 and SST6. The SST2 gene was first characterized in frog (Tostivint *et al.* 1996) and mammals (de Lecea *et al.* 1996, 1997a), then in most other vertebrates, including chicken (Trabucchi *et al.* 2003), lungfish (Trabucchi *et al.* 1999) and sturgeons (Trabucchi *et al.* 2002, Li *et al.* 2009) (see Tostivint *et al.* 2008 for review). All peptides encoded by SST2 possessed a Pro residue at position 2 and most of them exhibited the APCKNNFWKTFTSC sequence (Quan *et al.* 2013), except in mammals and some other species such as frog (Vaudry *et al.* 1992; Tostivint *et al.* 2008 for review) (**Table S2**). As for, the SST6 gene was initially characterized in only one teleost species, the zebrafish (Liu 2010), then in spotted gar (Tostivint *et al.* 2013) and coelacanth (Yun *et al.* 2015) (**Table S2**). In the present study, we found an ortholog of this gene in several other teleost species belonging to various groups (particularly from otocephala) but not from euteleosts. Peptides encoded by SST6 also shared a Pro at position 2, suggesting a common origin with SST2. In support of this latter view, in both zebrafish and gar, SST2 and SST6 are closely linked on the same chromosome, indicating that

they most likely arose by tandem duplication. Our phylogeny and synteny analyses showed that most of the non-mammalian *SST* sequences previously referred as to *SST2* are not orthologous to *cortistatin* (the other name of the mammalian *SST2*) but actually correspond to *SST6*. Such is notably the case for birds (chicken) and fish (lungfish, sturgeons, bony and cartilaginous fish), but not for reptiles (lizard) and amphibians (marsh frog). Conversely, all *SST* sequences previously referred to as *SST6* appeared to correspond to *SST2*. As a result, all the *SST* genes concerned with these observations were renamed accordingly. It is to note that the nomenclature adopted in the present article was already proposed in Yun *et al.* (2015) but without explicit justification.

In *R. typus* and *C. milii*, *SSTe* and *SSTa* are tandemly arranged suggesting that both genes arose by local duplication of a common ancestral gene. Synteny analysis of the *SSTa-SSTe* locus was inhibited by the fact that *SSTa* and *SSTe* were the only genes present on their scaffold. However, based on previous results showing that *SSTa* probably corresponds to *SST1* (Quan *et al.* 2013), the most credible assumption is that *SSTe* corresponds to *SST3* because in all species possessing both *SST1* and *SST3*, these genes are systematically localized in tandem (Tostivint *et al.* 2004, 2008, 2013, 2014). Phylogeny analysis is in agreement with close evolutionary relationships between *SSTa* and *SSTe*, on the one hand, and *SST1* and *SST3*, on the other hand. However, it does not fully support the orthology between *SST1* and *SSTa*, on one hand, and *SST3* and *SSTe*, on the other hand, since chondrichthyan *SSTa* and *SSTe* sequences did not strictly group with osteichthyan *SST1* and *SST3*, respectively. One explanation to reconcile these contradictory results would be that *SST1/SSTa* and *SST3/SSTe* genes were subjected to concerted evolution, a genetic process that leads to homogenize repetitive DNA sequences over time (Liao 1999). Indeed, the major hallmark of concerted evolution is that paralogous genes within species are more similar to one another than they are to their orthologous counterparts in closely related species (Liao 1999). DNA recombination mechanisms, especially unequal crossover and gene conversion, are responsible for concerted evolution (Liao 1999). Interestingly, we have shown that nucleotide sequences of the first exon of *S. canicula SSTa* and *S. canicula SSTe* are almost identical (93.5% of identity), while those of the second exon are much more divergent (only 61% of identity). Such level of similarity may be a good indicator of a recent recombination event occurring between the two genes.

The phylogenetic status of the *S. canicula SSTd* and *SSTe* genes suggested by synteny and phylogeny analyses is consistent with their tissue expression pattern since *SSTd*, as *SST2*, is primarily expressed in the central nervous system (SNC) (de Lecea *et al.* 1997b, Lin *et al.* 1999, Trabucchi *et al.* 1999, 2003), while *SSTe*, as *SST3*, is expressed both in the SNC and the gastrointestinal tract (Moore *et al.* 1995, Xing *et al.* 2005). Further studies at the cellular level will be needed to speculate about the functions of the corresponding peptides.

In contrast to the other *SST* genes found in cartilaginous fish, *SSTb* was detected only in *S. canicula* and not in *R. typus* and *C. milii*. Phylogeny analysis showed that *SSTb* grouped into the *SST5* clade, as previously reported (Quan *et al.* 2013). However, the orthology relationships between *SSTb* and osteichthyan *SST5* could not be confirmed by synteny analysis since the *S. canicula SSTb*-bearing scaffold was too short.

Among the six *SST* paralogs characterized so far in gnathostomes, *SST4* is the only one not to exist in cartilaginous fish. Up to now, the *SST4* gene was considered as a *SST1* paralog generated by 3R (Liu *et al.* 2010), in agreement with the fact that it was found only in teleosts (**Figure S9A**). Recently, however, Yun *et al.* (2015) reported the occurrence of a so-called *SST4* ortholog in spotted gar. This finding is clearly in conflict with the Liu's view since the gar lineage is known to have diverged from teleosts before the 3R (**Figure S9B**) (Braasch *et al.* 2016). In the present study, synteny analysis showed that teleost *SST4* can be equally viewed as orthologous to the gar *SST4*, or co-orthologous to either teleost *SST1* or teleost *SST3*, without

the possibility to decide between these three conceptions. Indeed, in both zebrafish and medaka, the *SST4*-bearing chromosome block contains only very few paralogs of the neighboring genes of *SST1* and *SST3* (such as *Fgf12* and *Nyap2*), making it impossible to precisely place the teleost *SST4* in relation to gar *SSTs*. Examination of other teleost species whose genome is available in Ensembl failed to resolve the problem (data not shown). What is clear, however, is that phylogeny analysis absolutely does not support the orthology of gar *SST4* and teleost *SST4* since gar *SST4* groups within the gnathostome *SST3* clade, thus without any obvious relationships with the teleost *SST4* clade. Rather, the very high level of sequence similarity between gar *SST3* and gar *SST4* (91 % nucleotide identity) strongly suggests that gar *SST4* arose very recently by tandem duplication of *SST3*. It therefore appears unlikely that gar *SST4* and teleost *SST4* are orthologous unless gar *SST4* and *SST3* were subjected to concerted evolution, as shown above for *S. canicula* *SST1/SSTa* and *SST3/SSTe*.

### Concluding remarks

Over the past few years, significant advances have been made in the understanding of the evolution of the *SST* family. One of the most important results has been the demonstration that the current diversity of the family was initially caused by 2R (Liu *et al.* 2010, Tostivint *et al.* 2013, 2014). According to this view, the last common ancestor of vertebrates possessed four *SST* genes, three of which, *SST1*, *SST2* and *SST5*, are still present in all extant vertebrate species. A fourth *SST* gene (referred to as *SST?* in **Figure 6**) is likely to have been generated by 2R but since this gene has never been found in extant vertebrate species, it is assumed to have been lost very early after 2R. Conversely, the rest of the diversity of the family, represented by *SST3*, *SST4* and *SST6*, was considered restricted to only some groups of bony fish (Tostivint *et al.* 2013, 2014): actinopterygians for *SST3* and *SST6* and teleosts for *SST4*.

The principal result of the present study is the demonstration of an unexpected diversity of *SST* genes in cartilaginous fish. Thus, in *S. canicula*, not less than five *SST* genes, *SST1*, *SST2*, *SST3*, *SST5* and *SST6*, have been identified, while only three of them were characterized so far (Quan *et al.* 2013). Therefore, contrary to what was previously thought, it is likely that all these five genes were already present in the gnathostome ancestor (**Figure 6**).

It is to note that our study did not provide any new data supporting the impact of 2R in the evolution of the *SST* gene family due to the small size of the scaffolds from the three chondrichthyan species examined. Thus, within the regions containing *SST* genes, *Masp 1* and *Masp 2* were the only genes indicating that *SST1* and *SST3*, on the one hand and *SST2* and *SST6*, on the other hand, belong to the same paralogon. In contrast, our study confirm the idea that *SST3* and *SST6* likely arose by tandem duplications from *SST1* and *SST2*, respectively (**Figure 6**). In strict logic, however, we must admit that it is currently impossible to know which of *SST1* and *SST3*, on the one hand and *SST2* and *SST6*, on the other hand are the ancestral genes. The uncertainty on this matter will remain as long as the phylogenetic status of lamprey *SSTs* is unsolved (Tostivint *et al.* 2016) because the lamprey *SST* sequences are the only ones that could be currently used as outgroups. Thus, in **Figure 6**, *SST1* and *SST2* are displayed as ancestral genes in a totally arbitrary manner.

Another important result of the present study was the finding that *SST6* was not totally lost in sarcopterygians, as previously thought, because it is still present in coelacanth and birds (**Figure 6**). In this context, it is noteworthy that chicken *SST6* was initially but mistakenly reported as *SST2* (Trabucchi *et al.* 2002), now refuted by synteny and phylogeny analysis. In a general way and for the same reasons, all teleost genes previously known as *SST6* had to be renamed *SST2*, and *vice versa*. Notably, the true *SST2* is also present in amphibians (but not in *Xenopus*), sauropsids (but not in birds) and mammals (**Figure 6**). Taken together, our result show that *SST2* and *SST6* have been lost independently and repeatedly during evolution: in euteleosts, birds and some amphibians for *SST2* and amphibians and mammals for *SST6* (**Figure 6**). After

their appearance, *SST3* and *SST5* were also secondarily lost in sarcopterygians and tetrapods, respectively.

Finally, the present work was unable to precisely determine the phylogenetic status of teleost *SST4*. In particular, whether teleost *SST4* and gar *SST4* are truly orthologous or not remains to be investigated. Further studies in other species than those examined here will be needed to address this issue.



## **Acknowledgements**

This work has been supported by the Centre National de la Recherche Scientifique (CNRS), the Muséum National d'Histoire Naturelle (MNHN) and the Agence Nationale de la Recherche (ANR) grant NEMO (n° ANR-14-CE02-0020-01 HT). The authors thank Hélène Mayeur (Observatoire Océanologique de Banyuls, France), and Patrick Wincker, Jean-Marc Aury and the Genoscope staff (Evry, France) for catshark genome sequencing and assembly. They also thank Dr Nicolas Buisine for helpful discussions. Finally, they are very grateful to Mitchell Fleming and Stephan Couderq (Museum National d'Histoire Naturelle) for the English corrections.

## Legends to figures

**Figure 1.** Alignment of the amino acid sequences of prepro-SST1 (PSSTa), -SST2 (PSSTd), -SST3 (PSSTd) and -SST6 (PSSTc) characterized from cartilaginous fish. (\*) denotes conserved residues. SST peptide sequences are in red. Potential cleavage sites are in bold. Signal peptides are in grey. (p), partial sequences. Sequences of *S. canicula* SST2 (SSTd) and SST3 (SSTe) cDNAs have been deposited in the GenBank database under the accession numbers MK491629 and MK491630, respectively.

**Figure 2.** Synteny of genes in the *SST1-SST3* locus in *R. typus* and *C. milii* plus eight selected bony vertebrate species (human, chicken, anole lizard, western clawed frog, coelacanth, spotted gar, zebrafish and medaka). Genes are represented by block arrows. Genes with conserved synteny are coloured. For the teleost *SST4* gene, three possible positions are proposed with respect to the gar SSTs (see the text for more details). Position of the genes (in megabases -Mb) is displayed below each box, according to the Ensembl database. Empty circles indicate the end of scaffolds. Letters inside the boxes refer to the specific and provisional nomenclature of *S. canicula* SSTs initially proposed in Quan (2013). The detailed chromosomal locations of genes displayed in this map are included in **Table S4**.

**Figure 3.** Synteny of genes in the *SST2-SST6* locus in *R. typus* and *C. milii* plus eight selected bony vertebrate species (human, chicken, anole lizard, western clawed frog, coelacanth, spotted gar, zebrafish and medaka). Letters inside the boxes refer to the nomenclature of *S. canicula* SSTs proposed in Quan (2013), while numerals refer to the previous nomenclature of vertebrate SST genes (Tostivint 2013, 2014). Legends are the same as in the **Figure 3**.

**Figure 4.** Phylogenetic tree of vertebrate SST precursor sequences. Phylogenetic analysis of 147 vertebrate SST amino acid sequences was performed using Maximal Likelihood, with 500 bootstrap replicates. The number shown at each branch node indicates in percentage the bootstrap value. Sequence references and alignment are given in **Figure S1** and **Figure S2**, respectively

**Figure 5.** Tissue distribution of *S. canicula* SST2 (SSTd) and SST3 (SSTe) mRNAs using RT-PCR. Parallel amplification of dogfish *Egf1* mRNA served as internal control. NC, non-template control.

**Figure 6.** A proposed evolutionary scheme for the evolution of the *SST* gene family in gnathostomes with special emphasis on chondrichthyan species (in red). The names of the different paralogous genes are given in the boxes. Note the unresolved status of the teleost *SST4*. Gar *SST4* is shown here to have arisen independently of teleost *SST4*. Boxes connected by a vertical line represent linked genes. Crossed-out boxes represent lost genes. Double-headed arrows represent local duplications. R, rounds of whole genome duplication.

## Supplementary data

**Table S1.** Sequences of the oligonucleotides used for PCR amplifications.

**Table S2.** Primary structure of SST-related peptides from different vertebrate species. Peptides from chondrichthyan species are in red. Conserved residues are in bold.

**Table S3.** Pair-wise comparison of full-length SST protein sequences from *S. canicula*, *R. typus*, *L. erinacea* and *C. milii*. Values represent percentage of amino acid identity.

**Table S4.** Chromosomal locations of gene orthologs in the synteny analysis of the *SST* loci. All human gene names in the table are approved HGNC symbols and the genes from other species have been given the name of their human orthologs. Chromosomal locations of genes are expressed in bp. Blanks represent genes that have not been found in the current genome databases. Non-syntenic genes are in grey.

**Figure S1.** Protein sequences of prepro-SSTs used for phylogenetic analysis and their accession numbers. Chondrichthyan sequences are in red.

**Figure S2.** Amino acid sequence alignment of the SST family used for the phylogenetic analysis. The alignment was made using Muscle and then manually optimized. Conserved residues between all orthologs are in black bold. Characteristic residues of each ortholog are colored.

**Figure S3.** Nucleotide sequence and deduced amino acid sequence of *S. canicula* cDNAs. Nucleotides are numbered 5' to 3' and amino acids N-terminal to C-terminal from the putative starting methionine. Signal peptides are in grey. SST peptide sequences are in red. Potential cleavage sites are in bold. Polyadenylation signals, when detected, are underlined. Nucleotide sequence (almost) identical between *SST1* and *SST3* is in red.

**Figure S4.** Sequence of *S. canicula* *SST* genes, inferred from the cDNA sequences given in **Figure S3**. Exons are indicated by colored boxed. The exon/intron boundary consensus sequences (GT/AG) are highlighted in red. Initiation (ATG) and stop codons are boxed. Polyadenylation signals are underlined. The identity of the scaffolds containing the sequences is indicated. Nucleotide sequence (almost) identical between *SST1* and *SST3* is in red.

**Figure S5.** Predicted sequence of *R. typus* *SST* genes, inferred from the *SST* cDNA sequences given in **Figure S6**. Legends are the same as in the **Figure S4**.

**Figure S6.** Nucleotide and deduced amino acid sequences of *R. typus* *SST* cDNAs. Legends are the same as in the **Figure S3**.

**Figure S7.** Predicted sequence of *C. milii* *SST* genes, inferred from the *SST* cDNA sequences given in **Figure S8**. Legends are the same as in the **Figure S4**.

**Figure S8.** Nucleotide and deduced amino acid sequences of *C. milii* *SST* cDNAs. Legends are the same as in the **Figure S3**.

**Figure S9.** Two alternative conceptions regarding the phylogenetic status of the teleost *SST4* gene. **A.** Conception from Liu *et al.*, (2010). **B.** Conception from Yun *et al.* (2015).

## References

- Altschul, S.F., Gish, W., Miller, W., Myers, E.W., Lipman, D.J., 1990. Basic local alignment search tool. *J. Mol. Biol.* 215, 403–410.
- Brazeau, P., Vale, W., Burgus, R., Ling, N., Butcher, M., Rivier, J., Guillemin, R., 1973. Hypothalamic polypeptide that inhibits the secretion of immunoreactive pituitary growth hormone. *Science* 179, 77–79.
- Conlon, J.M., Agoston, D.V., Thim, L., 1985. An elasmobranchian somatostatin: primary structure and tissue distribution in *Torpedo marmorata*. *Gen. Comp. Endocrinol.* 60, 406–413.
- Conlon, J.M., Askensten, U., Falkmer, S., Thim, L., 1988. Primary structures of somatostatins from the islet organ of the hagfish suggest an anomalous pathway of posttranslational processing of prosomatostatin-1. *Endocrinology.* 122:1855-9.
- Conlon, J.M., 1990. [Ser<sup>5</sup>]-somatostatin-14: isolation from the pancreas of a holocephalan fish, the Pacific ratfish (*Hydrolagus colliei*). *Gen. Comp. Endocrinol.* 80, 314–320.
- Dehal, P., Boore, J.L., 2005. Two rounds of whole genome duplication in the ancestral vertebrate, *PLoS Biol.* 3, e314.
- de Lecea, L., Criado, J.R., Prospero-Garcia, O., Gautvik, K.M., Schweitzer, P., Danielson, P.E., Dunlop, C.L., Siggins, G.R., Henriksen, S.J., Sutcliffe, J.G., 1996. A cortical neuropeptide with neuronal depressant and sleep-modulating properties. *Nature* 381, 242–245.
- de Lecea, L., Ruiz-Lozano, P., Danielson, P.E., Peelle-Kirley, J., Foye, P.E., Frankel, W.N., Sutcliffe, J.G. 1997a. Cloning, mRNA expression, and chromosomal mapping of mouse and human preprocortistatin. *Genomics* 42, 499–506.
- de Lecea, L., del Rio, J.A., Criado, J.R., Alcántara, S., Morales, M., Danielson, P.E., Henriksen, S.J., Soriano, E., Sutcliffe, J.G., 1997b. Cortistatin is expressed in a distinct subset of cortical interneurons. *J. Neurosci.* 17, 5868–5880.
- Edgar, R.C., 2004. MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics* 5, 113.
- Elphick, M.R., Mirabeau, O., Larhammar, D., 2018. Evolution of neuropeptide signalling systems. *J. Exp. Biol.* 221, jeb151092.
- Gaillard, A.L., Tay, B.H., Perez Sirkin, D.I., Lafont, A.G., De Flori, C., Vissio, P.G., Mazan, S., Dufour, S., Venkatesh, B., Tostivint, H., 2018. Characterization of gonadotropin-releasing hormone (GnRH) genes from cartilaginous fish: evolutionary perspectives. *Front Neurosci.* 12, 607.
- Gouy, M., Guindon, S., Gascuel, O., 2010. SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building. *Mol. Biol. Evol.* 27, 221–224.
- Guindon, S., Gascuel, O., 2003. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst. Biol.* 52, 696–704.
- Günther, T., Tulipano, G., Dournaud, P., Bousquet, C., Csaba, Z., Kreienkamp, H.J., Lupp, A., Korbonits, M., Castaño, J.P., Wester, H.J., Culler, M., Melmed, S., Schulz, S., 2018. International Union of Basic and Clinical Pharmacology. CV. Somatostatin Receptors: Structure, Function, Ligands, and New Nomenclature. *Pharmacol. Rev.* 70, 763–835.
- Li, C.J., Wei, Q.W., Zhou, L., Cao, H., Zhang, Y., Gui, J.F., 2009. Molecular and expression characterization of two somatostatin genes in the Chinese sturgeon, *Acipenser sinensis*. *Comp. Biochem. Physiol. A Mol. Integr. Physiol.* 154, 127–134.
- Liao, D., 1999. Concerted evolution: molecular mechanism and biological implications. *Am. J. Hum. Genet.* 64, 24–30.
- Lin, X., Otto, C.J., Peter, R.E., 1999. Expression of three distinct somatostatin messenger ribonucleic acids (mRNAs) in goldfish brain: characterization of the complementary

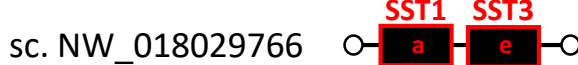
- deoxyribonucleic acids, distribution and seasonal variation of the mRNAs, and action of a somatostatin-14 variant. *Endocrinology* 140, 2089–2099.
- Liu, Y., Lu, D., Zhang, Y., Li, S., Liu, X., Lin, H., 2010. The evolution of somatostatin in vertebrates. *Gene* 463, 21–28.
- Moore, C.A., Kittilson, J.D., Dahl, S.K., Sheridan, M.A., 1995. Isolation and characterization of a cDNA encoding for preprosomatostatin containing [Tyr<sup>7</sup>, Gly<sup>10</sup>]-somatostatin-14 from the endocrine pancreas of rainbow trout, *Oncorhynchus mykiss*. *Gen. Comp. Endocrinol.* 98, 253–261.
- Muffato, M., Louis, A., Poinsel, C.E, Roest Crolius, H., 2010. Genomicus: a database and a browser to study gene synteny in modern and ancestral genomes. *Bioinformatics* 26, 1119–1121.
- Ocampo Daza, D., Sundström, G., Bergqvist, C.A., Larhammar, D., 2012. The evolution of vertebrate somatostatin receptors and their gene regions involves extensive chromosomal rearrangements. *BMC Evol. Biol.* 12, 231.
- Petersen, T.N., Brunak, S., von Heijne, G., Nielsen, H., 2011. SignalP 4.0: discriminating signal peptides from transmembrane regions. *Nat. Methods* 8, 785–786.
- Putnam, N.H., Butts, T., Ferrier, D.E., Furlong, R.F., Hellsten, U., Kawashima, T., Robinson-Rechavi, M., Shoguchi, E., Terry, A., Yu, J.K., Benito-Gutiérrez, E.L., Dubchak, I., Garcia-Fernández, J., Gibson-Brown, J.J., Grigoriev, I.V., Horton, A.C., de Jong, P.J., Jurka, J., Kapitonov, V.V., Kohara, Y., Kuroki, Y., Lindquist, E., Lucas, S., Osoegawa, K., Pennacchio, L.A., Salamov, A.A., Satou, Y., Sauka-Spengler, T., Schmutz, J., Shin-I, T., Toyoda, A., Bronner-Fraser, M., Fujiyama, A., Holland, L.Z., Holland, P.W., Satoh, N., Rokhsar, D.S., 2008. The amphioxus genome and the evolution of the chordate karyotype. *Nature* 453, 1064–1071.
- Quan, F.B., Kenigfest, N.B., Mazan, S., Tostivint, H., 2013. Molecular cloning of the cDNAs encoding three somatostatin variants in the dogfish (*Scylorhinus canicula*). *Gen. Comp. Endocrinol.* 180, 1–6.
- Read, T.D., Petit, R.A. 3<sup>rd</sup>, Joseph, S.J., Alam, M.T., Weil, M.R., Ahmad, M., Bhimani, R., Vuong, J.S., Haase, C.P., Webb, D.H., Tan, M., Dove, A.D.M., 2017. Draft sequencing and assembly of the genome of the world's largest fish, the whale shark: *Rhincodon typus* Smith 1828. *BMC Genomics* 18, 532.
- Sacerdot, C., Louis, A., Bon, C., Roest Crolius, H., 2018 Chromosome evolution at the origin of the ancestral vertebrate genome. *Genome Biol.* 19, 166.
- Tostivint, H., Lihmann, I., Bucharles, C., Vieau, D., Coulouarn, Y., Fournier, A., Conlon, J.M., Vaudry, H., 1996. Occurrence of two somatostatin variants in the frog brain: characterization of the cDNAs, distribution of the mRNAs, and receptor-binding affinities of the peptides. *Proc. Natl. Acad. Sci.* 93, 12605–12610.
- Tostivint, H., Joly, L., Lihmann, I., Ekker, M., Vaudry, H., 2004. Chromosomal localization of three somatostatin genes in zebrafish. Evidence that the [Pro<sup>2</sup>]-somatostatin-14 isoform and cortistatin are encoded by orthologous genes. *J. Mol. Endocrinol.* 33, R1–R8.
- Tostivint, H., Lihmann, I., Vaudry, H., 2008. New insight into the molecular evolution of the somatostatin family. *Mol Cell. Endocrinol.* 286, 5–17.
- Tostivint, H., Quan, F.B., Bougerol, M., Kenigfest, N.B., Lihmann, I., 2013. Impact of gene/genome duplications on the evolution of the urotensin II and somatostatin families. *Gen. Comp. Endocrinol.* 188, 110–117.
- Tostivint H., Ocampo Daza, D., Bergqvist, C.A., Quan, F.B., Bougerol, M., Lihmann, I., Larhammar, D., 2014. Molecular evolution of GPCRs: Somatostatin/urotensin II receptors. *J. Mol. Endocrinol.* 52, T61–86

- Tostivint, H., Dettaï, A., Quan, F.B., Ravi, V., Tay, B.H., Rodicio, M.C., Mazan, S., Venkatesh, B., Kenigfest, N.B., 2016. Identification of three somatostatin genes in lampreys. *Gen. Comp. Endocrinol.* 237, 89–97.
- Trabucchi, M., Tostivint, H., Lihrmann, I., Jégou, S., Vallarino, M., Vaudry, H., 1999. Molecular cloning of the cDNAs and distribution of the mRNAs encoding two somatostatin precursors in the African lungfish *Protopterus annectens*. *J. Comp. Neurol.* 410, 643–652.
- Trabucchi, M., Tostivint, H., Lihrmann, I., Sollars, C., Vallarino, M., Dores, R.M., Vaudry, H., 2002. Polygenic expression of somatostatin in the sturgeon *Acipenser transmontanus*: Molecular cloning and distribution of the mRNAs encoding two somatostatin precursors. *J. Comp. Neurol.* 443, 332–345.
- Trabucchi, M., Tostivint, H., Lihrmann, I., Blähser, S., Vallarino, M., Vaudry, H., 2003. Characterization of the cDNA encoding a somatostatin variant in the chicken brain: Comparison of the distribution of the two somatostatin precursor mRNAs. *J. Comp. Neurol.* 461, 441–451.
- Vaudry, H., Chartrel, N., Conlon, J.M., 1992. Isolation of [Pro<sup>2</sup>, Met<sup>13</sup>]somatostatin-14 and somatostatin-14 from the frog brain reveals the existence of a somatostatin gene family in a tetrapod. *Biochem. Biophys. Res. Commun.* 188, 477–482.
- Venkatesh, B., Lee, A.P., Ravi, V., Maurya, A.K., Lian, M.M., Swann, J.B., Ohta, Y., Flajnik, M.F., Sutoh, Y., Kasahara, M., Hoon, S., Gangu, V., Roy, S.W., Irimia, M., Korzh, V., Kondrychyn, I., Lim, Z.W., Tay, B.H., Tohari, S., Kong, K.W., Ho, S., Lorente-Galdos, B., Quilez, J., Marques-Bonet, T., Raney, B.J., Ingham, P.W., Tay, A., Hillier, L.W., Minx, P., Boehm, T., Wilson, R.K., Brenner, S., Warren, W.C., 2014. Elephant shark genome provides unique insights into gnathostome evolution. *Nature* 505, 174–179.
- Yun, S., Furlong, M., Sim, M., Cho, M., Park, S., Cho, E.B., Reyes-Alcaraz, A., Hwang, J.I., Kim, J., Seong, J.Y., 2015. Prevertebrate Local Gene Duplication Facilitated Expansion of the Neuropeptide GPCR Superfamily. *Mol. Biol. Evol.* 32, 2803–2817.
- Xing, Y., Wensheng, L., Haoran, L., 2005. Polygenic expression of somatostatin in orange-spotted grouper (*Epinephelus coioides*): molecular cloning and distribution of the mRNAs encoding three somatostatin precursors. *Mol. Cell. Endocrinol.* 241, 62–72.

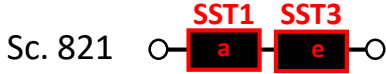


Figure 2

Whale shark (*R. typus*)



Elephant shark (*C. milii*)



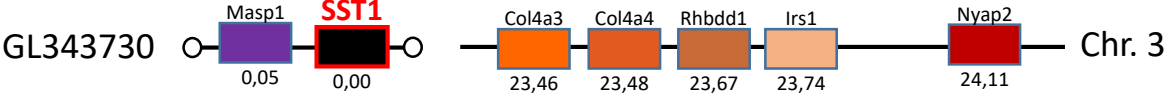
Human (*H. sapiens*)



Chicken (*G. gallus*)



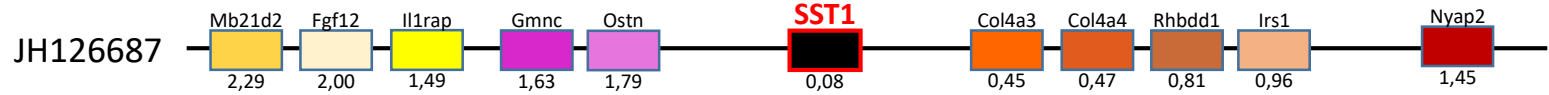
Anolis (*A. carolinensis*)



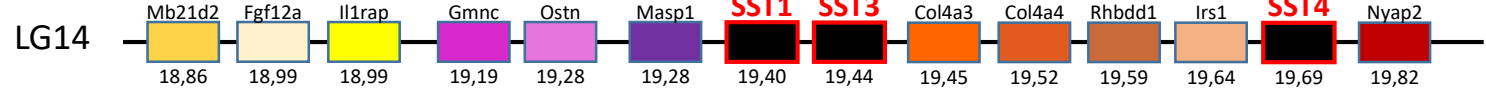
Xenopus (*X. laevis*)



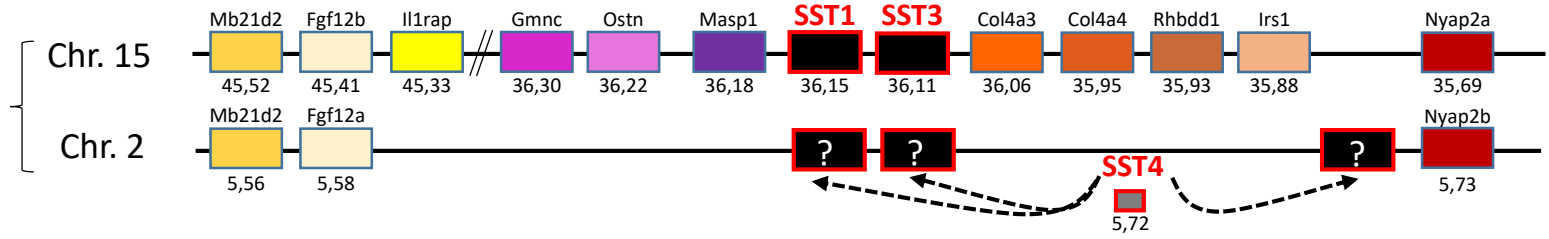
Coelacanth (*L. chalumnae*)



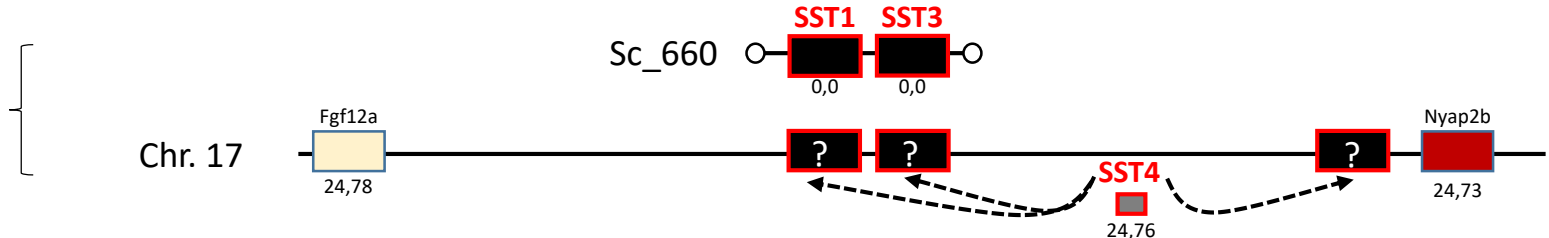
Spotted gar (*L. occulatus*)



Zebrafish (*D. rerio*)



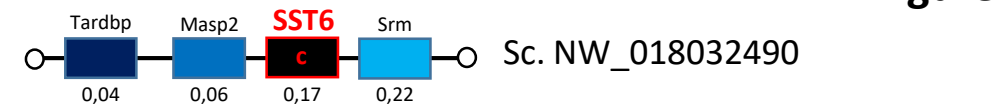
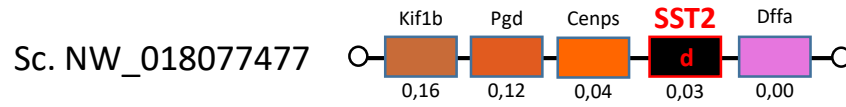
Medaka (*O. latipes*)



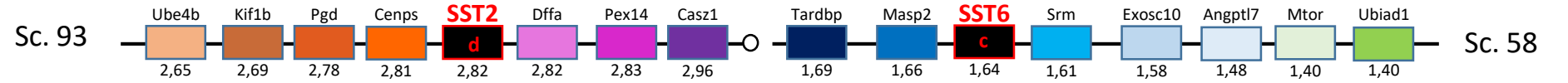


**Figure 3**

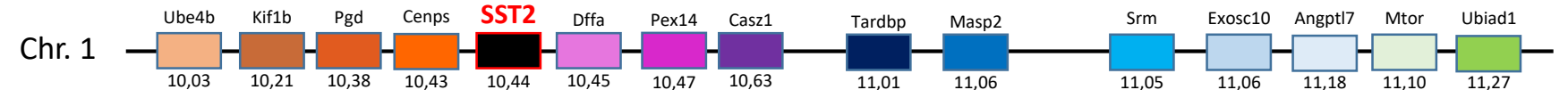
Whale shark (*R. typus*)



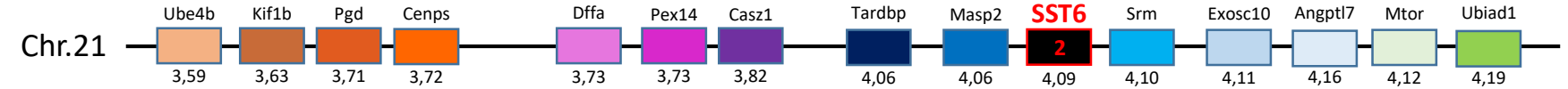
Elephant shark (*C. milii*)



Human (*H. sapiens*)



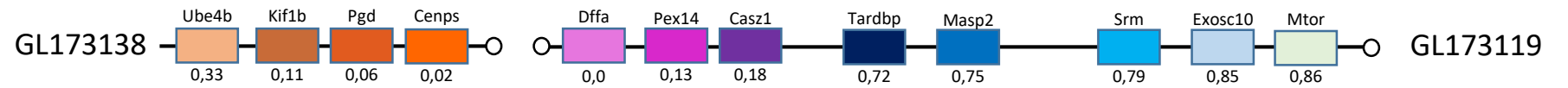
Chicken (*G. gallus*)



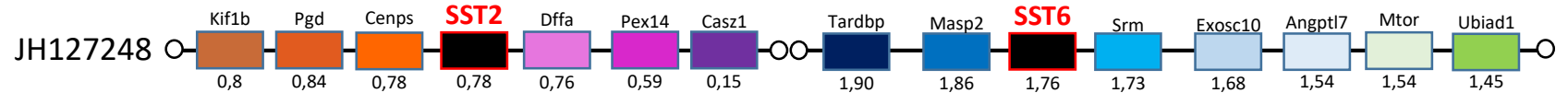
Anolis (*A. carolinensis*)



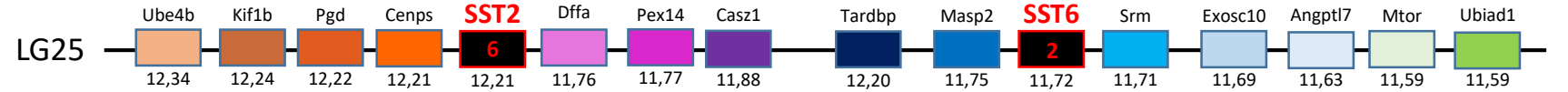
Xenopus (*X. tropicalis*)



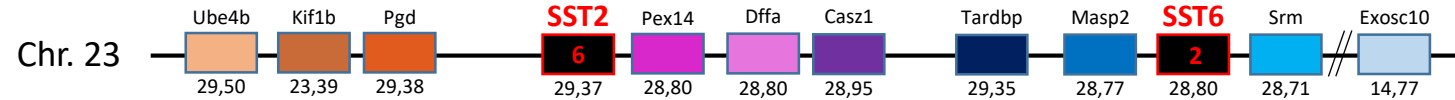
Coelacanth (*L. chalumnae*)



Spotted gar (*L. occulatus*)



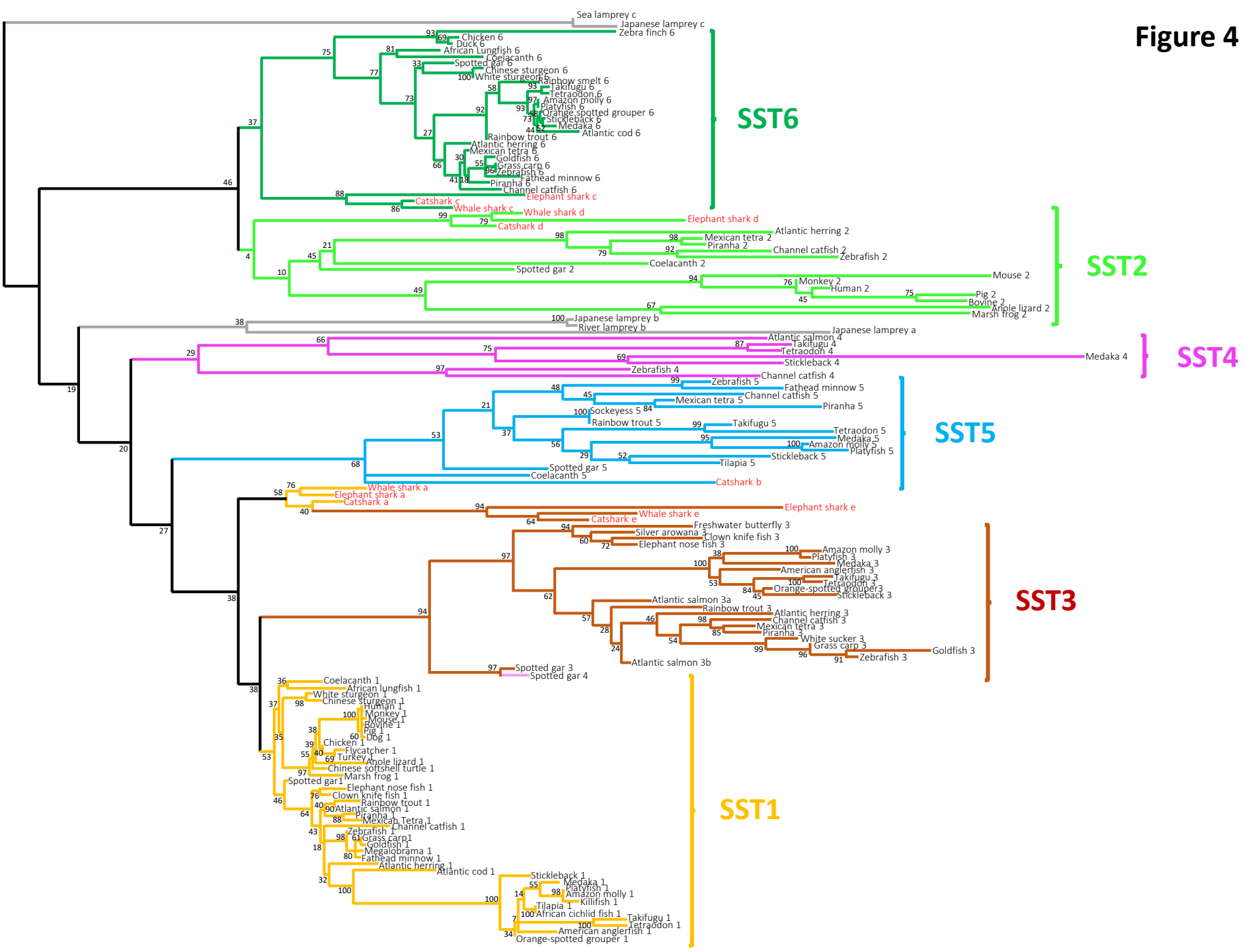
Zebrafish (*D. rerio*)



Medaka (*O. latipes*)



Figure 4







## Figure S1

### Somatostatin 1

#### Primates

>Human (*Homo sapiens*) SST1 (BC032625)

MLSCRLQCALAALSIVLALGCVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN  
QTENDALEPEDLSQAAEQDEMRLLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC

>Monkey (*Macaca fascicularis*) SST1 (XP\_005545499)

MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN  
QTENDALEPEDLSQAAEQDEMRLLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC

#### Other mammals

>Bovine (*Bos taurus*) SST1 (NP\_776385.1)

MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN  
QTEIDALEPEDLSQAAEQDEMRLLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC

>Dog (*Canis lupus familiaris*) SST1 (NP\_001003307.1)

MLSCRLQCALAALSIVLALGGVTCAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN  
QTENDALEPEDLSQAAEQDEMRLLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC

>Mouse (*Mus musculus*) SST1 (NP\_033241.1)

MLSCRLQCALAALCIVLALGGVTGAPSDPRLRQFLQKSLAAATGKQELAKYFLAELLSEPN  
QTENDALEPEDLPQAAEQDEMRLLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC

>Pig SS1 (*Sus scrofa*) SST1 (AAT02532.1)

MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN  
QTENDALEPEDLSQAAEQDEMRLLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC

#### Birds

>Flycatcher (*Ficedula albicollis*) SST1 (ENSFALT00000007767.1)

MLSCRLQCALALLSIALALGTVSAAPSDPRLRQFLQKSLGGGGGGGELAKYFLAELLSEPSQ  
TENEAESEDLRGAEQDEVRLLELERSANSNPALAPRERKAGCKNFFWKTFTSC

>Chicken (*Gallus gallus*) SST1 (CN210817.1)

MLSCRLQCALALLSIALAVGTVSAAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPSQ  
TENEAESEDLRGAEQDEVRLLELERSANSNPALAPRERKAGCKNFFWKTFTSC

>Turkey (*Meleagris gallopavo*) SST1 (ENSMGAT00000008507.2)

KELAKYFLAELLSEPSQTENEAESEDLRGAEQDEVRLLELERSANSNPALAPRERKAGCKN  
FFWKTFTSC

#### Reptiles

>Anole lizard (*Anolis carolinensis*) SST1 (XP\_003228868)

MLPCRLPCALALLSLALALGSGAAAPADPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN  
GQAENEALEPEELSRGGGAEQDEVRLLELERSASLNPALAPRERKAGCKNFFWKTFTSC

>Chinese softshell turtle (*Pelodiscus sinensis*) SST1 (ENSPSIT00000016437.1)

MLSCRLQCALALLSLALAVSSVSGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLAEPS  
QPENEALEPEDLSRGPEQDEVRLLELERSANPNPALAPRERKAGCKNFFWKTFTSC

#### Amphibians

>Marsh frog (*Pelophylax ridibundus*) SST1 (P87384.1)

MQSCRVCALTLALLSLALAINSISAAPTDPRRLRQFLQKSLASAGKQELAKYFLAELLSEPSQTD  
NEALESDDLPRGAEQDEVRLLELERSANSNPALAPRERKAGCKNFFWKTFTSC

#### Lobe-finned fish

>Coelacanth (*Latimeria chalumnae*) SST1 (XP\_005992512.1)

MLSSRLQCAFAFLSLALVVSNIASAAPSDLRLRQLLQKSLAAAAGKQEVSKYSLAELLAELAQ  
AENEAELESDDFSKTSQDEVRLLELERSANGNPALAPRERKAGCKNFFWKTFTSC

>African lungfish (*Protopterus annectens*) SST1 (AAD39138.1)

MLSCRFQCALVLLSLAVVFSKVSAAPSDLRLRQLLQRSLAAAAGKQELTKYSLAELLSELA  
QSENDALDSSDLRGADQDEVRLLEDRSANSSPLAARERKAGCKNFFWKTFTSC

### Euteleosts

>Orange-spotted grouper (*Epinephelus coioides*) SST1 (AAU93565.1)  
MKMVSSRLRCLLLLLSLTASISCSAAQRDSKLRLLLLHRTPLLGSKQDMSRASLAELLSD  
LLQVENEALEEENFPLAEGEPEDVHVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC  
>Killifish (*Fundulus heteroclitus*) SST1 (EV461374.1)  
MKMFSSLSLRCLLLLLCLASISCSAAQRDSKLRLLLLHRTPLLSSQQDVSRSSLAELLSD  
LLQMENEALEEDGFTLPEGEPEDIRVDLERAASSGPLLAPRERKAGCKNFFWKTFTSC  
>Atlantic cod (*Gadus morhua*) SST1 (AAZ85702.1)  
MMSVRSTLLLLSCAAMLSGSSAAPSDTKLRQLLQRSLAPMPGQEETVRYTLAQLLSELAQ  
AENEALGTTDDQDDERMDLERAAGPMMAPRERKAGCKNFFWKTFTSC  
>Stickleback (*Gasterosteus aculeatus*) SST1 (KT235748)  
MVSSRLRCLLLLLSLTASISCSSTAQRDGKHLHLLHRTPLLSSKQDMSRASLVELLLSDLLQ  
VQNEALEEENLAPAGGEPEEVHLDLERAADAGPLLGPRLERKAGCKNFFWKTFTSC  
>African cichlidfish (*Haplochromis burtoni*) SST1 (AAS97964.1)  
MNSSRLRCLLLLLVSLTASISCTSAQRDSKLRLLLLHRTPLLGSKQDMSRSSLAEALLSDLL  
QVENEALEEENFPLADGEPEDIRVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC  
>American anglerfish (*Lophius americanus*) SST1 (P01169.1)  
MKMVSSRLRCLLVLVSLTASISCSFAGQRDSKLRLLLLHRYPLQGSKQDMTRSALAEALLS  
DLLQGENEALEEENFPLAEGPEDAHADLERAASSGPLLAPRERKAGCKNFFWKTFTSC  
>Rainbow trout (*Oncorhynchus mykiss*) SST1 (CA364601.1)  
MLSTRVQCALALLSLALAISSVSAAPSDAKLRQLLQRSLMAPAGKQELARNTLVELLSELAH  
VENEAIELDDMSHGVEQEDVDLELERAPGPVLAPRERKAGCKNFFWKTFTSC  
>Tilapia (*Oreochromis niloticus*) SST1 (ENSONIT0000001338.1)  
MNSSRLRCLLLLLVSLTASISCTSAQRDSKLRLLLLHRTPLLGSKQDMSRSSLAEALLSDLL  
QVENEALEEENFPLADGEPEDIRVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC  
>Medaka (*Oryzias latipes*) SST1 (XP\_004084505.1)  
MMSSSSRLLLLLSLTASISCSAAQRDSKLRLLLLQRTPLLGSKQDMSRSSLAEALLSDLLQM  
ENEVLEEDGFPLSDGEPEDVRVDLERAASSGPLLAPRDRKAGCKNFFWKTFTSC  
>Amazon molly (*Poecilia formosa*) SST1 (ENSPFOT00000005658.1)  
MKMLSSLSLRCLLLLLLSLSASISCSAAQRDSKLRLLLLHRTPLLSSKQDASRSSLAEALLSDL  
LQMENEALEEDGFGLPEGEPEDIRVDLERAASSGPLLAPRERKAGCKNFFWKTFTSC  
>Atlantic salmon (*Salmo salar*) SST1 (CB509644.1)  
MLSTRVQCALALLSLALAISSVSAAPSDAKLRQLLQRSLMAPAGKQELARYTLAELLSELAQ  
AENEAIESDDLDRGVEQEDVRLELERAAGPVLAPRERKAGCKNFFWKTFTSC  
>Takifugu (*Takifugu rubripes*) SST1 (ENSTRUG00000010048)  
MFSSNSMCLLMLLLSLSASFSCSSAAHRDFKLPLLQSNALMGNKQEMTRSSLANLLSDLL  
QVGNLAEENLALAEGEPEEVHIDMERAAGIGPFLTPRERKAGCKNFFWKTFTSC  
>Tetraodon (*Tetraodon nigroviridis*) SST1 (KT235747)  
MKMFSNSCCLLMLLLSLSASFSCSSAAHRDSKLRLLMLPPNPLLGHRQEMSRSSLADLLSDL  
LQVENQALDENFPLVEGEPEEVHVDMERAADAGIGPFLTPRERKAGCKNFFWKTFTSC  
>Platyfish (*Xiphophorus maculatus*) SST1 (ENSXMAT00000014478.1)  
MKMLSSLSLRCLLLLLLSLSASISCSAAQRDSKLRLLLLHRTPLLSSKQDASRSSLAEALLSDL  
LQMENEALEEDGFPEGEPEDIRVDLERAASSGPLLPRERKASCKNFFWKTFTSC

### Other teleosts

>Mexican tetra (*Astyanax mexicanus*) SST1 (ENSAMXT00000006698.1)  
MLSTRVQCALALLSIALAVGSVSGAPSDAKLRQFLQRSLIGSAGKQELARYTLAELLSELAQ  
AENEALEDDVPRGAEQEDVRMELERAAGPVLAPRERKAGCKNFFWKTFTSC

>Goldfish (*Carassius auratus*) SST1 (Q9YGH5.1)  
 MLSTRIQCALALLSLALAVCSVSAAPTDALRQLLQRSLLNPAGKQELARYTLADLLSELVQ  
 AENEALEPEDLSRAVEKDEVRLERELERAAGPMLAPRERKAGCKNFFWKTFTSC

>Clown knife fish (*Chitala chitala*) SST1 (AAK97070.2)  
 MLSTRIQCALALLSLALAVSSVYAAPSDLKLRQLLQRSIIAPASKQELARYTLAELLSELAQV  
 ENEALESDDLARGADQEEVRLERELERAAGPPLAPRERKAGCKNFFWKTFTSC

>Atlantic herring (*Clupea harengus*) SST1 (XP\_012673158.1)  
 MLSLRLQCALALLSIVLAISCISAAPTDVQLRQLLQRSFLFAPGGKQELARLTAEELLSELAQA  
 ENEALESEDMSRGAEGEDVRYELERSAGSMLAPRERKAGCKNFFWKTFTSC

>Grass carp (*Ctenopharyngodon idella*) SST1 (ACB69423.1)  
 MLSTRIQCALALLSLALAVCSVSAAPTDALRQLLQRSLLNPAGKQELARYTLADLLSDLV  
 QAENEALEPEDLSRAVEKDDVRLERELERAAGPMLAPRERKAGCKNFFWKTFTSC

>Zebrafish (*Danio rerio*) SST1 (AAH76254.1)  
 MLSTRIQCALALLSLALAVSSVSAAPSDAKLRQLLQRSLLSPAGKQELARYTLADLLSDLVQ  
 AENEALEPEDLSRGAEKDDVRLERELERAAGPMLAPRERKAGCKNFFWKTFTSC

>Elephant nose fish (*Gnathonemus petersii*) SST1 (AF292652)  
 MLSSRIQCALALLSLALAVSSVSAAPSDLKLRQLLQRSLLAPASKQDLARNPLEELLSEMVR  
 VENEALEPDDLARGADQEEVRLERELERAAGPALAPRERKAGCKNFFWKTFTSC

>Channel catfish (*Ictalurus punctatus*) SST1 (CAA23877.1)  
 MPSTRIQCALALLAVALSVCSVSGAPSDAKLRQFLQRSILAPSVKQELTRYTLAELLAELAQ  
 AENEVLDSDEVSRAAESEGARLEMERAAGPMLAPRERKAGCKNFFWKTFTSC

>Megalobrama (*Megalobrama pellegrini*) SST1 (AAO92644.1)  
 MLSTRIQCALALLSLALAVSSVSAAPSDAKLRQLLQRSLLNPAGKQELARYTLTDLLSDLVQ  
 AENEVLEPEDLSRAVEKDEVRLERELERAAGPMLAPRERKAGCKNFFWKTFTSC

>Fathead minnow (*Pimephales promelas*) SST1 (DT100930)  
 MLSTRIQCALALLSLALAISSVSAAPSDAKLRQLLQRSLLNPAGKQELARYTLADLLSELVQ  
 AENEALEPEDLSRAVEKDDVRLERELERAAGPMLAPRERKAGCKNFFWKTFTSC

>Red-bellied piranha (*Pygocentrus nattereri*) SST1 (XP\_017539070.1)  
 MLSTRVQCALALLSLALALSSVSGAPSDAKLRQFLQRSILIGPSGKQELARYTLAELLSELAQ  
 AENEALEAEDMPRGAEQEDVRMELERAAGPVLAPRERKAGCKNFFWKTFTSC

**Other ray-finned fish**

>White sturgeon (*Acipenser transmontanus*) SST1 (AAL13248.1)  
 MLSSRLQCALAFSLALAVSSVSAAPSDPRLRQLLQRTLAASAGKQELLKYSLAELLSELAQS  
 ENDALASDELSRAAEQNDVRLERELERSANGNPAMAPRERKAGCKNFFWKTFTSC

>Chinese sturgeon (*Acipenser sinensis*) SST1 (FJ792687.1)  
 MLSSRLQCALALLSLALAVSSVSAATSEPRIRQLLQRALVASAGKQDLLKYSLAELLSELAQ  
 SENDALASDELSRAAEQNDVRLERELERSANGNPAMAPRERKAGCKNFFWKTFTSC

>Spotted gar (*Lepisosteus oculatus*) SST1 (XP\_006637937.1)  
 MLSSRVQCALALLCLALAVSSVSAAPSDLRQLLQRSLLAASAGKQELARYTLAELLSELA  
 QSENEALESDDLRAAEQDEVRLERELERSANPALAPRERKAGCKNFFWKTFTSC

**Cartilagonous fish**

>Elephant shark (*Callorhynchus milii*) SSTa (XP\_007910586.1)  
 MSCGRVQCALALLSIALTVLSVTSAPAHDRYREILQRSLLAAGARSKPELTKYSLAQLLAEL  
 ANAENEALEAEDMARATAQDEVRLERELERSANPNLAQRERKAGCKSFFWKTFTSC

>Whale shark (*Rhincodon typus*) SSTa (XP\_020365362.1)  
 MWCSRVCALALLSIALAVLSAGAAPTADRYRELLQTSMAGAEPRSKAELIKYNLVQLLAE  
 LANAENEVLGDGDLPRMAKQDEVRLERELERSANPNPQRERKAGCKNFFWKTFTSC

>Catshark (*Scylorhinus canicula*) SSTa (JX964750)  
 MWCSRQLSLALLSIALAVLSVSSAPTNDRYREILQRAMAATGSGGKAELTKYSLAQLLSEL  
 ENAENEALETDAMGGRNEVRLERELERSINPNLANRERKAGCKNFFWKTFTSC



## Somatostatin 2

### Primates

>Human (*H. sapiens*) SST2 (AAB66895.1)

MPLSPGLLLLLLSGATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWF EWTSQAS  
AGPLIGEEAREVARRQEGAPPQQSARRDRMPCRNFFWKTFFSSCK

> Monkey (*M. fascicularis*) SST2 (XP\_015298230)

MPLPPGLLLLLLSGATATAALPLEGSPTGPDSEHMQEAAAGIRKSSLLTFLAWWF EWTSQASA  
GPLIGEEAREVARRQEGAPPQQSARRDRTPCKNFFWKTFFSSCK

### Other mammals

> Bovine (*B. taurus*) SST2 (NP\_001191825)

MLPLCLLLPLLLPSGATTALSPEGGLAGHESGHMQEVAEIKTNSLLTFLAWWYEWASQAR  
AVPFVGGEAREVSKRQEGAPLHQSTRQDKTPCKNFFWKTFFSSCK

> Mouse (*M. musculus*) SST2 (AAD51127.1)

MMGGRGTGGKWPSAFGLLLWGVAAASALPLESGPTGQDSVQEATEGRSGLLTFLAWWHE  
WASQASSSTPVGGGTPGLSKSQERPPPQPPHLDKKPCKNFFWKTFFSSCK

> Pig (*S. scrofa*) SST2 (NP\_001191865)

MLPPLCLLLLLLPLGATTALPLEGGLTSHDRDSGHMQEVAEIKKNSLLTFLAWWHEWMS  
QAREVPFVGGETREMPKKQEGLPRQQASRGDRTPCGNFFWKTFFSSCK

### Reptiles

> Anole lizard (*A. carolinensis*) SST2 (XP\_008119733.1)

MAFLVHPPPSAPFLALLSFSRLMGAAPAAVLPPIPGGLAWKHNEGSADLGRDELLAFLSGLV  
DRASRRHGMPLSKQEKVVRSPREERVPFFRHPVREKAPCKNFFWKTFFSSC

### Amphibians

> Marsh Frog (*P. ridibundus*) SST2 (AAC60094.1)

MLGSAGTLLLLLLAWGARALSQPDDNRITTGRNQDLNAIQDLLLLKLLSGWTDRESNLVE  
VERNVPDPPEPKIPPSVKFPRLSLRERKAPCKNFFWKTFTMC

### Lobe-finned fish

> Coelacanth (*L. chalumnae*) SST2 (NW\_005819697)

MQPLILLVPLVLMAWN LGVAAVPKEERLMLYDKVNRETTGFGEERKQFLSNMLDALIGLN  
TLENDTPLLGTKEQEEHNSERSAFKYSSLKKAPCRNFFWKTFFSSC

### Teleosts

> Mexican tetra (*A. mexicanum*) SST2 (ENSAMXT00000013558.1)

MALSGGGDTCGAADGGMFIMRMLLSLVPLLLIAWSGTNTDALPIDNKLPQSKEVLTKEQKD  
LLIKIMSDLAELNMTLKD LGALDLEQLLNGKLGERSVEKSPCTNFFWKTFSAC

> Atlantic herring (*C. harengus*) SST2 (XP\_012681486.1)

MGVLARVDPCSVAQSARITMRVLTSLVPLILIVWSGSQTGALPVREKPLRNE SLADEERILL  
KILAGLTEKNLTEENLTGHDLEGLLNGTLKGGSVPTPQERSPCKNFFWKTFFSSC

> Zebrafish (*D. rerio*) SST2 (ENSDART00000146411.2)

MFLMRVLLSLFPLVFVIWNGEALPIQDKQSQTNEILSKEEDGLKMITYVAELNLTSKELADL  
DAELNGKLWEKSDKPSKDKSPCKLFFWKTFFSSC

> Channel catfish (*I. punctatus*) SST2 (XP\_017341959.1)

MALGGRINLYQAVDSPMFTMRVLLSLIPLLFVAWSANNADALPVQDKLPNSNEVLTKEQK  
DFMTQFLANLAELNMTIKDLETMDHEQLSKLSERAAFGLPAREKSQC NFFWKTFFSSC

> Red-bellied piranha (*P. nattereri*) SST2 (XM\_017706353.1)

MALAVGGTSCGGADGGMFIMRMLLSLVPLLLIAWSGTSTDALPVENKLPQSNEVLTKEQK  
DLLIKIMSDLAELNMTVKDLGALDLEQLLSGKLGERSVFGLPAQEKSPCKNFFWKTFSACQ

H



### Other ray-finned fish

>Spotted gar (*L. oculatus*) SST2 (NC\_023203.1)

MHLLSSLVPLALLVWSLKCAAAPSEERRALQSNGLAKERKDVLLKVLGGLVSNLLRKE  
QSAVDSEQLKSSLMGERSVFGPSVSRERTPCKNFFWKTFS

### Cartilaginous fish

>Elephant shark (*C. milii*) SSTd (XP\_007900347.1)

MQWQAFASVVCLLFIVTVQGVPEPQEERMGLQLNREMVKDKKRLIAKLLAGLLDVDDNLE  
SVIAPLGLSKEEGTDFEERSAAGEIPPRKPKAGCKLFFWKTFSHC

>Whale shark (*R. typus*) SSTd (XP\_020390988.1)

MTVCLMSLLLLLSVEAADPLEERMKLQVNREVTKSRYLMLKLLSGLLDPDDNLENDFTS  
LSPGEESSLEERSVNAGIPRRPQKAPCKLFFWKTFSHC

>Catshark (*S. canicula*) SSTd (MK491629)

MKWLMTVSLMSLLYLLRVEGTDLLEERMKLQVNREMTKSRLNIVKLLAGLLETDDNLE  
NGFAPLKPEEAEGTLFEERSVNAGIPRREQKTPCKLFFWKTFSHC

### Somatostatin 3

#### Euteleosts

>Orange-spotted grouper (*E. coioides*) SST3 (AAU93566.1)

MQCIRCPTILVLVALVLCSPGVFSQPDRDQDQYQNQDLDELRRHRLRARSAGLLSQEW  
SKRAVEDLLAQMSLPEADTQREAEVVS MATGGRMNRLERSVDPPNNLPPRERKAGCKNFY  
WGFTSC

>Stickleback (*G. aculeatus*) SST3 (KT235756)

MQYTRCPAILVLVGLVLCGPGVSSQRNRDQDQDQYQNQDLDPHLLRARGAGLLSQD  
WSKRAVEDLLAQMSLPEADSQLGAEVVS AATGGRLHLERSVDPPNNLPARERKAGCKNFY  
WKGFTSC

>American anglerfish (*L. Americanus*) SST3 (P01170.2)

MQCIRCPTILALLALVLCGPSVSSQLDREQSDNQDLDELRRHRLRARSAGLLSQEWSK  
RAVEELLAQMSLPEADVQREAE DASMATGGRMNRLERSVDSTNNLPPRERKAGCKNFYWK  
GFTSC

>Rainbow trout (*O. mykiss*) SST3 (Q91194.1)

MKVCRICHALALLGLALAICSQGAASQPDLRLSRRLRARAAAWPHRSGVSRWRFTFYP  
NCPCLRPRKVKCPAGAKEDLRVELERSVGNPNNLPPRERKAGCKNFYWKGFTSC

>Medaka (*O. latipes*) SST3 (AU168379.1)

MQHARGPAFVLAALALSSLGVSSQSDRDQDQFQNHDLDELRRHRLRARSAGLLSQD  
WSKRAIENMLARMPDPEAEAEAEVGRNNMERSVDANVPPRNRKDGCKNFYWKGFTSC

>Amazon molly (*P. formosa*) SST3 (ENSPFOT00000005672.2)

MHHARCPTILVLAALAALSGLVSSQADRDQDPYQNQNLDELRRHRLRARSAGLLS  
QDWSKRAVEDLLAQMSRSAVEAQDDPEAASKGTDSRLNRLERSVETTARERKAGCKNFY  
WKGLTSC

>Atlantic salmon (*S. salar*) SST3a (DW531645.1)

MKFSQIHCALALLGLALAICSQGAASQPDLRLSRRLRARAAASIAATQEW SKRVMEDVLS  
KLSLPDVEAQKSVGSTADAKEDLERSVDNSNNLPPRERKAGCKNFYWKGFTSC

>Atlantic salmon (*S. salar*) SST3b (CB505007.1)

MKVCRHICALALLGLALAICSQGAASQPDLDLRSRLLQRARAAGIATQEWSKRAVEDILS  
 QLSWPEAQESEVSPAGAKEDLRVELERSVGNPNLPPRERKAGCKNFYWKGFSTC  
 >Takifugu (*T. rubripes*) SST3 (ENSTRUT00000025350.1)  
 MQRIHSSSTILMLTTLVLCIQGVSSQPDRDLNQNQDLEMEVRHHRLQLHVHGAGLLSQEWSK  
 RAVEDLIAQMSMPEGTGQRDTEVVSMATGGRMNLERSVDTTNNLSPPERKAGCKNFYWK  
 GPTSC  
 >Tetraodon (*T. nigroviridis*) SST3 (ENSTNIT00000001563.1)  
 MPGVRSSSTILVLTALVLSIQAVSSQPDRDLNQNQDLDQEVRRHRLQLRAHGAGLLSQDWSK  
 RAVEDLIAQMSLPEGTGQRDTEVVSMATGGRMNLERSVDTTNNLPPRERKAGCKNFYWKGF  
 SC  
 >Platyfish (*X. maculatus*) SST3  
 MHHARYPAILVLAALAALSGLVSSQADRQDPYQNQNLDLDLELRHHRLQLRARSAGLLS  
 QDWSKRAVEDLLAQMSRSEVEAQDQGPAAASRGTSRLNERSVETTARERKAGCKNFY  
 WKGLTSC  
**Other teleosts**  
 >Mexican tetra (*A. mexicanum*) SST3 (ENSAMXT00000006711.1)  
 MKVCVLQCGLVLLGLALVLCSSGASSQPDLDLDLVDLDRHRLLQRARALGIAAQEWKKR  
 EMEDLLSQLTLPESEFQESEISTLGSKQDVRVEMDRSAENPNLPPRERKAGCKNFYWKGF  
 SC  
 >Goldfish (*C. auratus*) SST3 (AAF15306.1)  
 MRLCELHCYLALLGLSLVLCGRANSQLEPDLDFRHHRLQLRASATGQATRWDFTKRDVE  
 KLLSLLSIPEMEMREKGLSMAGESEDLRLEQERSAESSNQLPTRVRKEGCKNFYWKGFSTC  
 >White sucker (*Catostomus commersonii*) SST3 (AAK97071.2)  
 MRLCELHCYLALLGLSLVLCDRGADSQLEPDMDFRHHRLQLRARAIGLATQDWTKKDIEEL  
 LSQSLPEIEARENGVSTTGGNDDLHLELERSAENTNQLYPRERKAGCKNFYWKGFSTC  
 >Clown knife fish (*C. chitala*) SST3 (AAV48555.1)  
 MKNCQAQCILALMGLFLGLCWPSDASQPDLRYRSLQLRAHSAPASPDWTRRTVEDLLAR  
 LPPPEGEFTPVEDVPAADEGEEVRVELERSVDPNNLPPRERKAGCKNFYWKGFSTC  
 >Atlantic herring (*C. harengus*) SST3 (XP\_012693360.1)  
 MMRFSGIHCSLALLGLSLVLCSHSASSQPDLDLDLRHHRLQLRARAAGMSTQEWSKRAV  
 EDLLSQLSLPEEETQDREVSTVGAAKDDLHMERSAETNNIPPKDRKSGCKNFFWKGRSTC  
 >Grass carp (*C. idella*) SST3 (ACB69424.1)  
 MRLCELQCYLALLGLSLVLCGRSANSQLEPDLDFRHHRLQLRARAIGQATQDWTKKDVEEL  
 LSLLSMPMEMRENDISTVDENEDLRVELERSAESSNHIPARERKAGCKNFYWKGFSTC  
 >Zebrafish (*D. rerio*) SST3 (XP\_694143.1)  
 MRLCELQCYLALLGLSLVLCGRSANSQLEPEMDFRHHRLQLRARAIGQAQEWTKKDVEEL  
 LSLLSMPMEMQRESDLSTTDENEDLRVELERSAESSNHIPARERKAGCKNFYWKGFSTC  
 >Channel catfish (*I. punctatus*) SST3 (CK424149.1)  
 MRTCVLQCCLTLLGLSLVLCNGVSSQPDLDRHRLLQRVQALGVAAQEWTKNDLKAIL  
 AQLTMPSEFQESDVSTLGTKQDLTVELERSAEDPNLPPRERKAGCKNFYWKGFSTC  
 >Elephant nose fish (*G. petersii*) SST3 (AAV48556.1)  
 MKTCQVHCVLVLLGLVLGLCYPSAASQPDLRYRSFMQRAHTAAMSPQDWSRRVVEDLLSR  
 LAPPEDDTPQSEMSTAEEGEETRVELERSVEPNLPPRERKAGCKNFYWKGFSTC  
 >Silver arowana (*Osteoglossum bicirrhosum*) SST3 (AAK97067.1)  
 MKICQIHCTLVLLGLVLGLYCPSAASQPDLRYRSFLQRAHAAAMSPQDWSKQAVEELLSRL  
 APAQGEVPQGAVSAADEEEDVRVDLERSLELNNLPPRERKAGCKNFYWKGFSTC  
 >Freshwater butterfly fish (*Pantodon buchholzi*) SST3 (AAK97068.2)  
 MKLCQVHCILALLGLVLGMCGSSSATQLDSRYRSLVQRARAASMGPQQDWGKLSVEDLSL  
 LAATEADMPFGDMSAAEESEGAHLDLERSVEPGNVPPRERKAGCKNFYWKGFSTC

> Red-bellied piranha (*P. nattereri*) SST3 (XP\_017539071.1)  
MRVCVLQCCLALLGLSLVLCGNGASSQPDLMDVDVLDLDPYHRLLRARALGMAAQD  
WRKREMEDLLSQLTLPESEFKESEITSLGAKHDVRELSAENPNLPPRERKAGCKNFY  
WKGFTSC

#### Other ray-finned fish

>Spotted gar (*L. oculatus*) SST3 (ENSLOCT00000011545.1)  
MLSYRVHCTLALFGLVLAFCVSAVSHSDLRFRRFLQKAKAAGLNKQDSSKYAIEDLISQL  
VQSDSEALENEMSVLDENSDARLELERSTEIGKEIPPRERKAGCRNFYWKTFSTC

#### Cartilaginous fish

>Elephant shark (*C. milii*) SSTe (XP\_007910587.1)  
MQARCTLTLALLSLAALGLSALPHLRDQLVLQGGSPAMELRDGVVRELIQAVADAESKPQS  
EAAEDFAPDEKAELRLALAPRWRKDCKNFFWKTYTLC

>Whale shark (partial) (*R. typus*) SSTe (XP\_020365363.1)  
DFLKDTIQLLHVADADKDAVEVNASQVETPPXNKIPMKFQQRQLGTRMRKNCKNFFWK  
TYTLC

>Catshark (*S. canicula*) SSTe (MK491630)  
MWCSRLQLSLALLSIALAVLSVSSAPTNRHREILQRALDQELLKDTMMKLLPLVTDVDE  
AGTLDVSNAAETSEENTTPMKFQHRQLGMRMRKNCKNFFWKTYTLC

### Somatostatin 4

#### Euteleosts

>Stickleback (*G. aculeatus*) SST4 (KT235754)  
MAHILCVFALLCFAFCAAQDGETQRGFKDNRLQRDSLPLWLDKLQDEQDSTKKNLIEWLYS  
FYKFDNGNIVKGPTDAEPEKNRRGLGKTTRRFVGRVFFWKSWSWPC

>Medaka (*O. latipes*) SST4 (KT235752)  
MANVLCVLAFLCFAVCVVQNTAIMVESEDLPAGQGLLSSFDRISSDFQQSVETGILMNLLYKL  
SRPDSAITLQQVRDSEKQEKNRGVEIATQRPCRQVFFWKSWSWAKC

>Atlantic salmon (*S. salar*) SST4 (CA039604.1)  
MALTGIWCAFVLVCVTLCQMGKVDSFVNEDKPTWLETLQDKQVSAADDKYNLVWLLYKL  
SQSHHDNTFKINFPHPGPEVSGKPESSRETIPQDSRVRKEGCKVFFWKSWSWAC

>Takifugu (*T. rubripes*) SST4 (NC\_018911.1)  
MARALCILVLLCFAPCCAENSKTEHRFNDLQVQEDLLSWLKPQEKWEPSKRQTLEDLLYKL  
TNYKSENRIPLQQPGDTENQEKNRDLNLRVQQRQFGCRMFFWKSWSWTC

>Tetraodon (*T. nigroviridis*) SST4 (KT235753)  
MARALCFLVLLCFASRCAGNSKTEHRLKDLQVEEDVLPWLNSQEKWEPSKQNLLEDLLYK  
LTNYRSENRIVSQQPSDTNQEKNRRGLDNLKVQQRQAGCRIFFWKSWSWTC

#### Other teleosts

>Zebrafish (*D. rerio*) SST4 (NP\_571802.1)  
MASSQLHLTATLLCLAMMAGIICGRSHMLLNSALQASRGTSADDEEIPERYSLSELEWLLSNS  
DPAVFQPDSSSLGSLHSGLELMRRDTKEERKTGCKNYFWKSRTAC

>Channel catfish (*I. punctatus*) SST4 (P01172.1)  
MSSSPLRLALALMCLVSAVGVISCGRPHVVLNSALEEARNVPPFGEEVPERLTLPELQWMLS  
NNELTPVQVEEAPRSRLELVRRDNTVTSKPLNLCMNYFWKSRTAC

#### Other ray-finned fish

>Spotted gar (*L. oculatus*) SST4 (ENSLOCT00000011651.1)  
MLSYRVHCTLALFGLVFAFCVSAVSNSDLRFRRFLQKAKAASLSTRDSSKYALEDLISQIA  
QSDNEALENEMSVLDENSDARLELERSADMVKVIPPRERKAGCRNYYYWKTTTSC

### Somatostatin 5

### Lobe-finned fish

>Coelacanth (*L. chalumnae*) SST5 (XP\_005999859.1)  
MMCSHVQSLLA VLSASLLL VGVGGLPKGEVLTDLFQGGQAEKGEDFSRMLMLKMOVSNLL  
KSENDVLVPSAEDTASQDELTRRLAPSRRERKAGCKNFFWKTFTSC

### Euteleosts

>Stickleback (*G. aculeatus*) SST5 (ALD51533.1)  
MQVLLVALFSSVLLVQVSGAPRGDMPTQRGDPADNKDLAYSMLLKVFVSELTAARGGETLL  
VPEQEEEEAEGRQEVMMRRHLPLTQRERKAGCRNFFWKTFTSC

>Rainbow trout (*O. mykiss*) SST5 (BX909872.3)  
MLCSQLQVLLVALSASVFLARVSAAPHRDMLAELLRADSTKGNEDLSRTLLLKMMSDLMS  
AAVGENEVLPDLEEALGVREEVVRQLPLSHRERKAGCRNFFWKTFTSC

>Sockeyess (*Oncorhynchus nerka*) SST5 (EV380196.1)  
MLCSQLQVLLVALSASVFLARVSAAPHRDMLAELLRADTTKGNEDLSRTLLLKMMSDLMS  
TAVGENEVLPDLEEALGVREEVVRQLPLSHRERKAGCRNFFWKTFTSC

>Tilapia (*O. niloticus*) SST5 (XP\_005464163.1)  
MLRSQVLLVALGLSVLLVRVSTAPYSDMLTETLRADLTNDKDLTHWLLLKFMAELMAARG  
DETRRGREEVTRRHL SLSQRERKAGCRNFFWKTFTSC

>Medaka (*O. latipes*) SST5 (XP\_020567335.1)  
MLLAALGLSLLMACVSGAPQRNPLTHTKQLQLLKSEVDPTRLLMLKLVLELVALRRQEML  
QELEEEELGGRERLMKRHIRFTQRERKAGCRNFFWKTFTSC

>Amazon molly (*P. formosa*) SST5 (XP\_007551472.1)  
MLCSQMKVLFVALCSSLALHVSSAPQMDDEL TETLQAE LISDKDLTGLLLLLRFMSELMASR  
GEEMLRKQEEEEELGGRQRLMRRHIRF SHRERKAGCRNFFWKTFTSC

>Takifugu (*T. rubripes*) SST5 (N.D.)  
MLSQVQLLLVTSFSSMLLMEVSSAPRKHMPSELLPADPLKDKDLAILILLRIISEVMAAEREM  
LLLPQEGEEEAGVREGEVMMRRQVPFSQRDRKAGCRNFFWKTFTSC

>Tetraodon (*T. nigroviridis*) SST5 (ALD51532.1)  
MTRSQLLLAASF SLLLMEAGGTPRKHKFLPADSVKDKDLALVTSLKFAFEGTAAQREMLL  
LLQEDEEDAGVREMMMMMRRQIPFSQRERKAGCRNFFWKSYSYTC

>Platyfish (*X. maculatus*) SST5 (XP\_005804860.3)  
MLCSQMKVLVVALCSSLALHVSSAPQMDDEL TETLQAE LISDKDLTGLLLLLRLMSELTASR  
GEEMLRQEEEEDELGGRQRLMRRHIRFTHRERKAGCRNFFWKTFTSC

### Other teleosts

> Mexican tetra (*A. mexicanum*) SST5 (XP\_007243346.1)  
MCSQLQVVLLVALSVLVLVSRVSAAPRGDVLTQLLQNEADTKENEDISRMLMLKLLSELEVA  
GENEVLSGADV RNDVVRQLPFSQRERKTGCRNFFWKTFTSC

>Zebrafish (*D. rerio*) SST5 (XP\_001333082.1)  
MFSRLQVVVVTLWV SLLL CRVSSAPRGDLLFQLLRSQVDPKENELQDLSRLLLLKQLSESVT  
PEEKDALDSIDELDVRNEVVRQIPVSQRERKAGCRNFYWKTFTSC

> Channel catfish (*I. punctatus*) SST5 (XP\_017327476.1)  
MSSQMQUIVVLAVSLLVLVSRVRTAPRTDLLAHMLQNEADGKEDLSRILLKLISELKIPDEN  
DTLSDDDMELNRILRHLPLTTREKAGCRNFFWKTFTSC

>Fathead minnow (*P. promelas*) SST5 (DT105503.1)  
MFSPLQMVAATLSLSLLLCSVSSAPGGDMLIQLLRSEVEPKEIELQDFFRLLLLKQLSESAAP  
EEKQPRESIDDDPEVHNEVVRQIPLSHRERKTGCRNFYWKTFTSC

> Red-bellied piranha (*P. nattereri*) SST5 (XP\_017578562.1)  
MNFVKSLLSRAAGRSASTPVIQTFFEEFEYFKSICLLNHLITRVSAAPRGDILAQLQADPKG  
NEELSRMLILKLLSDLEIPGDNEVLSGTDVRS DMVRQLPFPQRERKTGCRNFFWKTFTSC

### Other ray-finned fish

>Spotted gar (*L. oculatus*) SST5 (XP\_006627411.2)

MSTGQPSLPPAPAPNQGFFQHKLQVLLVALSVSVLLARVSGVPQRDRDLADLLRAEVPEGKE  
DLRMLLLKIFSDLLRAENEIPPGSAEDAGIRSDVPRQLPLAQRERKAGCRNFFWKTFTSC

### Cartilaginous fish

>Catshark (*S. canicula*) SSTb (JX964751)

MPRSQTQVLLTLVTVALLLRGSSTARVQGLPDILQERNDEGTEELSRTMVLNLLSELLHAG  
DKGLPSTERRGLPQAEIVRRWNSPRDRKAGCKNFFWKTFTSC

### Somatostatin 6

#### Birds

>Duck (*Anas platyrhynchos*) SST6

MQLVASLVSVLLLWVSVRATALPGEERLALQNSREQTKLRKDAILKMLAGLLESVDVASPD  
LEEEGKLEERATLGRLAQLSQRDRKAPCKNFFWKTFTSC

>Chicken (*G. gallus*) SST6 (DQ279789)

MQLVASLVSVLLLWVSVRATALPGEERLALQNSREQTKLRDALLKMLAGLLESSDVASP  
DLEEEGKLEEERAALGRLAQLSQRDRKAPCKNFFWKTFTSC

>Zebra finch (*Taeniopygia guttata*) SST6

MQLVASLASVLLLWVSVRATALPGQEGQLSTREQSTARKDVILKMLAGLLGSVDAGAEVA  
FPAGQEKARLEEDQAALGRLAQLSQRDRKAPCKNFFWKTFTSC

#### Lobe-finned fish

>Coelacanth (*L. chalumnae*) SST6 (XP\_005994063.1)

MQLTSLVSFLLVVWSVRATALPIEEKLMSHNNVELTKERKELMLKMIAGLLEGIDSPPMG  
GEVGSMDLEEPVEPKLEERAAFNRPLPQLPQRDRKAPCKNFFWKTFTSC

>African lungfish (*P. annectens*) SST6 (Q9W7E9.1)

MQFLASLVSFLLVVWSVKATALPVEDRLSVHSNRDLTREREEMILKMISGLLDGSDNSLFG  
GEVTSMDIEEPLNLEERAAYNALPQLPQRDRKAPCKNFFWKTFTSC

#### Euteleosts

>Orange-spotted grouper (*E. coioides*) SST6 (AAU93567.1)

MQLLVVLAALMGVLFVRAAAVLPVEDRSSIHVNRELSKERKELILKLVSGLLDGALDTNM  
LPGEAAPVDLEEPLESRLERAAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Atlantic cod (*G. morhua*) SST6

MQLMVVLAALMGVLFVRAAALLPVEDRSNFHSSRELSKERKELILKLVSGLLEGSPDSNM  
LPGELSPVELEEPLESRLERAAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Stickleback (*G. aculeatus*) SST6 (ENSGACG00000007077)

MQLLVVLAALMGVLFVRAAAVLPVEDRSSINVNRELSKERKELILKLVSGLLDGAADAN  
MLPGEAAPVDLEEPLESRLERAAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Rainbow trout (*O. mykiss*) SST6 (CX153272.1)

MQLLVILASLMGVLYSVRAAAVLPVEERSPLLNRELSKERKELILKLVSGLLDGATDTNMLP  
GEGVSPVDLEEPLESRLERAAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Medaka (*O. latipes*) SST6 (BJ885293.1)

MQLLVVLAALMGVLFVRAAAVLPVEDRSSIHVNRELSKERKELILKLVSGLLDGSGLDTNM  
LPGEAAPVDLEEPLESRLERAAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Rainbow smelt (*Osmerus mordax*) SST6 (EL519905.1)

MQLLVVLAALMGVLYSARAAVLPVEERSPIQANRELSTERKQLILKLVSGLLDGASDSNM  
LPGDVSPLDLEEPLESRLERAAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Amazon molly (*P. formosa*) SST6

MQLLVVLAALMGVLFVRAAAVLPVEDRSPIHANRELSKERKELILKLVSGLLDGALDTNM  
LPGEAAPVDLEEPLESRLERAAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Takifugu (*T. rubripes*) SST6 (ENSTRUG00000012370)

MQLLVVLAALMGVLLSIRAAVLPVEERSPVHLNRELSKERKELILKLVSGLLDGALDTNML  
PMETVDLEEPLESRLERAAVYNRLSLPQRDRKAPCKNFFWKTFTSC



>Tetraodon (*T. nigroviridis*) SST6 (ENSTNIG00000015178)  
MQLLVVLAALTGVLLSVRAAAVLPVEERIPLHLNRELSKERKELMLKLVSGLLDGALDTNM  
LPMEAVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Platyfish (*X. maculatus*) SST6

MQLLVVLAALMGVLFVRAAAVLPLEDRSPIHANRELSKERKELILKLVSGLLDGALDTNM  
LPGEAAPVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

#### Other teleosts

> Mexican tetra (*Astyanax mexicanus*) SST6 (ENSAMXT00000013526.1)

MQILASLVSLLLVLYSVRAAAVLPVEERSPAHTRELSKERKELILKLVSGLLDGVDNSVLGG  
DLVPMEAEPELESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Goldfish (*C. auratus*) SST6 (AAD09631.1)

MQLLSSLVSLLLVLYSVRAAAVLPVEERNPAQSRELSKERKELILKLISGLLDGVDNSVLDG  
EIAPVPFDAEPELESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

> Atlantic herring (*Clupea harengus*) SST6 (XP\_012681579.1)

MQLLASLVSLMLVLYSIRAAAVLPVDERSPAARELSKERKELILKLVSGLLDGVESNMLPG  
DEAPLDLEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Grass carp (*C. idella*) SST6 (ACB69425.1)

MQLLASLVSLLLVLYSVRAAAVLPVEERNLAQSRELSKERKELILKLISGLLDGVDNNVLAG  
EIAPVPLDVEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

>Zebrafish (*D. rerio*) SST6 (BG307388)

MQLLASLVSLLLVLYSVRAAAVLPLEERNPAQSRELSKERKELILKLISGLLDGVDNSVLAG  
EIAPVPLDVEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

> Channel catfish (*I. punctatus*) SST6

MQLLASLVSLLLVLYSVRAAAVLPAAERSPAHTREPSKERKEMILKMVSSLLDGVDNNMLA  
GDLLPLEEEEPIDSRLEERAVYNRLAQLPQRDRKAPCKNFFWKTFTSC

>Fathead minnow (*P. promelas*) SST6 (DT250237.1)

MQLLASLVSLMLVLYSVRAAALLPVEERNLAQSRELSKDRKELILKLISGLLDGVDNSVLAG  
EIAQVPMDAEPELESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

#### Other ray-finned fish

>White sturgeon (*A. transmontanus*) SST6 (AAL13249.1)

MQLRARLVSLMLVVYSLRVVAVLPGEERLSVHSNRELSKERKEGFLKLLSGLLDRVDSSVV  
LGEDVSPMDLEEPDLSRLEERAIYNRLSQLPLRARKAPCKNFFWKTFTSC

>Chinese sturgeon (*A. sinensis*) SST6 (FJ792688.1)

MQLRASLVSLMLVVYSLRVVAVLPGEERLSVHSNRELSKERKEGFLKLLSGLLDGVDSSVV  
LGEDVSPMDLEEPDLSRLEERAVYNRLSQLPQRARKAPCKN

>Spotted gar (*L. oculatus*) SST6 (XP\_006642047.1)

MQLLASLAVSLMLVVYSVRAAAVLPGEERATLHTKELSKDRKELILKLISGLLDGADSAMLA  
GDVASVDLEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC

#### Cartilaginous fish

>Elephant shark (*C. milii*) SSTc (XP\_007895974.1)

MQILVALISTLFLVSGVSTTTASLDDRFNLQSSREMNRKEMILKLLSGLLDNAAVSGQTG  
SEAGYPEPADGGPVMLEERSRYSQLPQRSRKVPCKNFFWKTFTSC

>Whale shark (*R. typus*) SSTc (XP\_020368528.1)

MQLLGSASXVSILLIVSSVKATAPLEDRLSLRANQELNKERKEVVLKLLSALLDSSSNQMGIE  
NTFPDQEDMEEMKVEDRSRFSQLPQRERKTSCNFFWKTFTSC

> Catshark (*S. canicula*) SSTc (JX964752) = SST6

MQLLGTASLLSMLLIVSSVRATAPLEDRLSLRANQELNKERKEVILKLLSGLLDSSSNQIAIE  
NTFPDPEDVEEMKVEERSRFSQLPQRERKAPCKNFFWKTFTSC

#### Other somatostatins

## Lampreys

>Japanese lamprey (*Lethenteron japonicum*) SSTa (KU522234)

MPAMPTTCVLLLFSLGVTALLPRPLGASPFRRPAEGSSLAGLGAWALGPGAGXGGAGLIDD  
RLQQRVEAVLTQELSREERALVGRLLAELAAGGAGLGGALPPLGWGPGSSSDEEGGEEGEG  
AGGDGGRGERALSARVRKAGCKNFFWKTFTSC

>River lamprey (*Lampetra fluviatilis*) SSTb (KX345282)

MKISRATTTTTSTFSSTLSTSSTSSCRAVRLLFVLPMLSVVVLGSVTADVRPLHVRMALERVM  
DGPGMENLDQDQKQFLVRLLAIDSSADETNELNHSEDGSLPEVLVARALRAAAAPGAAG  
GAQLPLGNRERKAGCKNFFWKTFFSSC

>Japanese lamprey (*Lethenteron japonicum*) SSTb (KU522235)

MKISRATTSTTTSTFSSTLSTSSTTSSCRAVRLLFLLSVLSVVVLGSVTADVRPLHARMALERVM  
DGLGMENLDQDQKFLVRLLAIDSSADETNELNHSEDGSLPEALVARALRAAAAPGAAG  
GAQLPLGNRERKAGCKNFFWKTFFSSC

>Japanese lamprey (*Lethenteron japonicum*) SSTc (KU522236)

MKATAAICCSLALVLVATGGRRGGGLHAASIGRSAILRAPASYRQLEAHPDLQMGDQDDSQ  
MLLNMIVEAMRMRDAGPETDGPGEAARVVDGLPEFPREEVREALGPNERPFVVPVLSPRD  
RKANCRMFYWKTMAAC

>Sea lamprey (*Petromyzon marinus*) SSTc (KU529940)

MKATAAICCSLALVLVASGGRRSGLHAASIGRSAILRAPASFRQLEAHPDLQMGDQDDSQIL  
LNMIVEAMRMRDAGPETDGPGEAATRVVDGLPEFPREEARALVPNERPFVPGALSPRDRK  
ANCRMFYWKTMAAC

	1									
2Human						MPLSPGL			LLLLL	
2Mouse				MM		GGRGTGGKWP			SAFGL	
2Pig						MLPPL			CLLLL	
2Bovine						MLPL			CLLLP	
2Monkey						MPLP			PGLLL	
2Lizard						MAFLVHPPP			SAPFLLA	
2Frog						ML		G	SAGTLLL	
2Coelacanth									ILLVP	
2Lepisosteus									SSLVP	
2Astyanax		MAL	SGGGDT	CGAA		DGGMFIMRML			LSLVP	
2Pygocentrus		MAL	AVGGTSCGGA			DGGMFIMRML			LSLVP	
2Clupea		MGV	LARVDP	PCSV		QSARITMRVL			TSLVP	
2Ictalurus		MAL	GGRINLYQAV			DSPMFTMRVL			LSLIP	
2Zebrafish		M				FLMRVL			LSLFP	
Catshark2						MKWL			MTVSL	
Whale_shark2									MTVCL	
Elephant_shark2									AFASV	
Skate2									MEDRTTL	
aLethenteron						MPAMPITCVL			LLFSLGVI	ALLPRPLGAS
bLethenteron	MKISRATTST	TSTFSSTLST				SSTTSSCR			RLFL	
bLampetra	MKISRATTTT	TSTFSSTLST				SSTSS-CR			RLFLV	
cPetromyzon						MKATAAI			CCSLA	
cLethenteron						MKATAAI			CCSLA	
3Lepisosteus						MLSYRVH			CTLAL	
3Astyanax						MKVCVLQ			CGLVL	
3Clupea						MMRFSGIH			CSLAL	
3Ictalurus						MRTCVLQ			CCLTL	
3Pygocentrus						MRVCVLQ			CCLAL	
3Amazon_molly						MHHARCP			TILVL	
3Platyfish						MHHARYP			AILVL	
3Rainbow_trout						MKVCRH			CALAL	
3Freshwater_butterfly						MKLCQVH			CILAL	
3Grass_carp						MRLCELQ			CYLAL	
3Goldfish						MRLCELH			CYLAL	
3Clown_knifefish						MKNCQAC			CILAL	
3Orange-spotted						MQCIRCP			TILVL	
3American_anglerfish						MQCIRCP			AILAL	
3Silver_aronana						MKICQIH			CTLVL	
3White_sucker						MRLCELH			CYLAL	
3Elephant_nose_fish						MKTCQVH			CVLVL	
3Zebrafish						MRLCELQ			CYLAL	
3Stickleback						MOYTRCP			AILVL	
3Takifugu						MQRHSS			TILML	
3Tetraodon						MPGVRSS			TILVL	
3Medaka						MQHARGP			AFVVLAA	
3aAtlantic_salmon						MKFSQIH			CALAL	
3bAtlantic_salmon						MKVCRH			CALAL	
Elephant_shark3						MQ-ARCT			LTLAL	
Whale_shark3										
catshark3						MWCSRLQ			LSLAL	
Catshark1						MWCSRLQ			LSLAL	
Whale_shark1						MWCSRVQ			CALAL	
Elephant_shark1						MSCGRVQ			CALAL	
1Human						MLSC-RL	Q		CALAA	
1Mouse						MLSC-RL	Q		CALAA	
1Monkey						MLSC-RL	Q		CALAA	
1Bovine						MLSC-RL	Q		CALAA	
1Pig						MLSC-RL	Q		CALAA	
1Dog						MLSC-RL	Q		CALAA	
1Chicken						MLSC-RL	Q		CALAL	
1Flycatcher						MLSC-RL	Q		CALAL	
1Turkey						MLSC-RL	Q		CALAL	
1Anole_lizard						MLPC-RL	P		CALAL	
1Chinese_softshell_turtle						MLSC-RL	Q		CALAL	
1Frog						MQSC-RV	Q		CALTL	
1Lungfish						MLSC-RF	Q		CALVL	
1Coelacanth						MLSS-RL	Q		CAFAL	
1Lepisosteus						MLSS-RV	Q		CALAL	
1White_sturgeon						MLSS-RL	Q		CALAF	
1Chinese_sturgeon						MLSS-RL	Q		CALAL	
1Platyfish						MKMLSSLSL	R		CLLLL	
1Tilapia						MNSSSRL	R		CLLLL	
1Elephant_nose_fish						MLSS-RI	Q		CALAL	
1Carp						MLST-RI	Q		CALAL	
1Goldfish						MLST-RI	Q		CALAL	



1Clown_knife_fish	---	---	---	MLST-RI	Q	CALAL	---	---		
1Orange-spotted_grouper	---	---	---	MKMOVSSSR	R	CLLLL	---	---		
1Anglerfish	---	---	---	MKMOVSSSR	R	CLLVL	---	---		
1Megalobrama	---	---	---	MLST-RI	Q	CALAL	---	---		
1African_cichlid_fish	---	---	---	MNSSSR	R	CLLLL	---	---		
1Cod	---	---	---	MMSV-R	-	STLLL	---	---		
1Zebrafish	---	---	---	MLST-RI	Q	CALAL	---	---		
1Medaka	---	---	---	MMSSSR	R	LLLLL	---	---		
1Stickleback	---	---	---	MVSS-RL	R	CLLLL	---	---		
1Takifugu	---	---	---	MFSSNSM	-	CLLML	---	---		
1Tetraodon	---	---	---	MKMFNSC	-	CLLML	---	---		
1Trout	---	---	---	MLST-RV	Q	CALAL	---	---		
1Fathead_minnow	---	---	---	MLST-RI	Q	CALAL	---	---		
1Killifish	---	---	---	MKMFSSLSL	R	CLLLL	---	---		
1Salmon	---	---	---	MLST-RV	Q	CALAL	---	---		
1Pygocentrus	---	---	---	MLST-RV	Q	CALAL	---	---		
1Ictalurus	---	---	---	MPST-RI	Q	CALAL	---	---		
1Astyanax	---	---	---	MLST-RV	Q	CALAL	---	---		
1Clupea	---	---	---	MLST-RL	Q	CALAL	---	---		
1Amazon_molly	---	---	---	MKMLSSL	R	CLLLL	---	---		
5Coelacanth	---	---	---	MMC	SHVQ	-	SLLAV	---		
5Zebrafish	---	---	---	MFS	R	LQ	-	VVVVT		
5Stickleback	---	---	---	---	---	---	---	MQVLL		
5Takifugu	---	---	---	MLS	Q	VQ	-	LLLVT		
5Tetraodon	---	---	---	MTR	S	Q	-	LLLAA		
5Medaka	---	---	---	---	---	---	---	MLLAA		
5Sockeyess	---	---	---	MLC	S	Q	LQ	-	VLLVA	
5Trout	---	---	---	MLC	S	Q	LQ	-	VLLVA	
5Fathead_minnow	---	---	---	MFS	P	LQ	-	MVVAT		
5Amazon_molly	---	---	---	MLC	S	Q	MK	-	VLFVA	
5Platyfish	---	---	---	MLC	S	Q	MK	-	VLVVA	
5Tilapia	---	---	---	MLR	S	Q	V	L	-	LVAL
5Lepisosteus	MSTG	QPSLPPAPAP	NQGFQCHKLQ	---	---	---	---	---	---	VLLVA
5Astyanax	---	---	---	MCS	Q	LQ	-	VLLVA	---	---
5Ictalurus	---	---	---	MSS	Q	MQ	-	IVVLA	---	---
5Pygocentrus	---	---	MNFE	VKSSLLSRAA	GRSASTP	---	---	---	---	VIC
Catshark5	---	---	---	MPR	S	Q	TQ	-	---	VLLTL
6Chicken	---	---	---	---	---	---	---	---	---	ASLVS
6Zebra_finch	---	---	---	---	---	---	---	---	---	ASLAS
6Duck	---	---	---	---	---	---	---	---	---	ASLVS
6Lungfish	---	---	---	---	---	---	---	---	---	ASLVS
6Coelacanth	---	---	---	MLN	M	Q	L	L	-	TSLVS
6White_sturgeon	---	---	---	MQL	R	-	-	-	-	ARLVS
6Chinese_sturgeon	---	---	---	MQL	R	-	-	-	-	ASLVS
6Lepisosteus	---	---	---	MQL	L	-	-	-	-	ASLAS
6Carp	---	---	---	MQL	L	-	-	-	-	ASLVS
6Goldfish	---	---	---	MQL	L	-	-	-	-	SSLVS
6Orange-spotted_grouper	---	---	---	MQL	L	-	-	-	-	VVLAA
6Zebrafish	---	---	---	MQL	L	-	-	-	-	ASLVS
6Stickleback	---	---	---	MQL	L	-	-	-	-	VVLAT
6Takifugu	---	---	---	MQL	L	-	-	-	-	VVLAA
6Tetraodon	---	---	---	MQL	L	-	-	-	-	VVLAA
6Rainbow_smelt	---	---	---	MQL	L	-	-	-	-	VVLAA
6Trout	---	---	---	MQL	L	-	-	-	-	VILAS
6Medaka	---	---	---	MQL	L	-	-	-	-	VVLAA
6Fathead_minnow	---	---	---	MQL	L	-	-	-	-	ASLVS
6Astyanax	---	---	---	MQL	L	-	-	-	-	ASLVS
6Pygocentrus	---	---	---	MQL	L	-	-	-	-	ASLVS
6Clupea	---	---	---	MQL	L	-	-	-	-	ASLVS
6Ictalurus	---	---	---	MQL	L	-	-	-	-	ASLVS
6Amazon_molly	---	---	---	MQL	L	-	-	-	-	VVLAA
6Cod	---	---	---	MQL	M	-	-	-	-	VVLAA
6Platyfish	---	---	---	MQL	L	-	-	-	-	VVLAA
Catshark6	---	---	---	MQL	L	-	-	-	-	GTASL
Elephant_shark6	---	---	---	MQL	V	A	L	I	-	STLFL
whale_shark6	---	---	---	MQL	G	S	A	S	X	VSILL
4Lepisosteus	---	---	---	MLS	Y	R	V	H	-	CTLAL
4Zebrafish	---	---	---	MASS	Q	L	H	-	-	LTATL
4Takifugu	---	---	---	MAR	A	L	-	-	-	CILVL
4Medaka	---	---	---	MAN	V	L	-	-	-	CVLAF
4Tetraodon	---	---	---	MAR	A	L	-	-	-	CFLVL
4Channel_catfish	---	---	---	MSS	S	P	L	R	-	LALAL
4Stickleback	---	---	---	MAH	I	L	-	-	-	CVFAL
4Atlantic	---	---	---	MAL	T	G	I	W	-	CAFVL

2Human	---	---	SGAT	ATAALPL	---	---	EG	---
2Mouse	---	---	LLL-WGVA	ASALP	---	---	---	---
2Pig	---	---	LLL-PPLG	ATTALPL	---	---	EG	GL
2Bovine	---	---	LLL-LPSG	ATTALSP	---	---	EG	GLA
2Monkey	---	---	LLL-SGAT	ATAALPL	---	---	EG	---
2Lizard	---	---	LLSFS-RLMG	AAPAAVL	---	---	PI	PGGLA
2Frog	---	---	LL---	LAW	GARALSO	---	PD	DNRIT
2Coelacanth	---	---	LVLMAWNLG	-VAAVPK	---	---	EE	RLMLYD
2Lepisosteus	---	---	LALLVWSLK	CAAAVPS	---	---	EE	RRALQ
2Astyanax	---	---	LLLIAWSGT	NTDALPI	---	---	DN	KLPQ
2Pygocentrus	---	---	LLLIAWSGT	STDALPV	---	---	EN	KLPQ
2Clupea	---	---	LILIV-WSGS	QTGALPV	---	---	---	REKPL
2Ictalurus	---	---	LLFVA-WSAN	NADALPV	---	---	QD	KL-PN
2Zebrafish	---	---	LVFVI-WNGE	---ALPI	---	---	QD	KQ-SQ
Catshark2	---	---	MSLL-YLLR	VEGTDLL	---	---	EE	RMKLO
Whale_shark2	---	---	MSLL-LLLS	VEAADPL	---	---	EE	RMKLO
Elephant_shark2	---	---	VCLL-FIVT	VQGVPEQ	---	---	EE	RMGLQ
Skate2	---	---	---	---	---	---	QE	---
aLethenteron	PFRP	PAEGSS	LAGI	GAWAIG	PGAGXGG	---	AG	LIDDR
bLethenteron	---	---	LSVLS	VVLG	SVTADVR	---	PL	HARMA
bLampetra	---	---	LPMLS	VVLG	SVTADVR	---	PL	HVRMA
cPetromyzon	---	---	LVLV-ASGG	RRSGLHA	---	ASIGR	SA	ILRAPA
cLethenteron	---	---	LVLVA-TGGR	RGGGLHA	---	ASIGR	SA	ILRAPA
3Lepisosteus	---	---	FGLV-LAFC	CVSAVSH	---	---	DL	RFRRF
3Astyanax	---	---	LGLA-LVLC	SSGASSQ	---	PDLDDL	DV	DLRHRRL
3Clupea	---	---	LGLS-LVLC	SHSASSQ	---	---	PDL	DLDLRHRRL
3Ictalurus	---	---	LGLS-LVLC	SNGVSSQ	---	---	P	DLDLRHRRL
3Pygocentrus	---	---	LGLS-LVLC	GNGASSQ	-P	DLDMDVDVDL	DP	RYHRL
3Amazon_molly	---	---	AALAALSLG	VSSQADR	-DQ	DPYQNQNLDL	DL	ELRHRRL
3Platyfish	---	---	AALAALSIG	VSSQADR	---	DQDPYQNQN	DL	DLRHRRL
3Rainbow_trout	---	---	LGLA-LAIC	SQGAASQ	---	---	P	DLDLRSRRL
3Freshwater_butterfly	---	---	LGLV-LGMC	GSSSATQ	---	---	L	DS--RYRSL
3Grass_carp	---	---	LGLS-LVLC	GRSANSQ	---	---	LEP	DLDFRHRRL
3Goldfish	---	---	LGLS-LVLC	GRCANSQ	---	---	L	EPDLFRHRRL
3Clown_knifefish	---	---	MGLF-LGLC	WPSDASQ	---	---	P	DL--RYRSL
3Orange-spotted	---	---	VALV-LCSP	GVFSQPD	---	RDQDQYQNO	DL	DLRHRRL
3American_anglerfish	---	---	LALVL-CGPS	VSSQLDR	---	EQSDNQDL	DL	ELRQHW
3Silver_aronana	---	---	LGLV-LGLY	CPSAASQ	---	---	P	DL--RYRSF
3White_sucker	---	---	LGLS-LVLC	DRGADSQ	---	---	LEP	DMDFRHRRL
3Elephant_nose_fish	---	---	LGLV-LGIC	YPSAASQ	---	---	P	DL--RYRSF
3Zebrafish	---	---	LGLS-LVLC	GRSANSQ	---	---	L	EPDMFRHRRL
3Stickleback	---	---	VGLV-LCGP	GVSSQRNRDQ	---	DQDQYQNO	DP	RPPLL
3Takifugu	---	---	TTLV-LCIO	GVSSQPD	---	RDLNQNO	DL	EMEVRHRRL
3Tetraodon	---	---	TALV-LSIQ	AVSSQPD	---	RDLNQNO	DL	QEVRRHRRL
3Medaka	---	---	LALSSIGVS	SQSDRDQ	---	DQFQNH	DL	DLRHRRL
3aAtlantic_salmon	---	---	LGLA-LAIC	SQGAASQ	---	---	P	DLDLRSRRL
3bAtlantic_salmon	---	---	LGLA-LAIC	SQGAASQ	---	---	P	DLDLRSRRL
Elephant_shark3	---	---	LS---	LAAL	GLSALPT	---	---	HLRDQLV
Whale_shark3	---	---	---	---	---	---	---	---
catshark3	---	---	LSIA-LAVL	SVSSAPT	---	---	DN	RHREI
Catshark1	---	---	LSIA-LAVL	SVSSAPT	---	---	DN	RYREI
Whale_shark1	---	---	LSIA-LAVL	SAGAAPT	---	---	AD	RYREI
Elephant_shark1	---	---	LSIA-LTVL	SVTSAPA	---	---	HD	RYREI
1Human	---	---	LSIV-LALG	CVTGAPS	---	---	DP	RLRQF
1Mouse	---	---	LCIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Monkey	---	---	LSIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Bovine	---	---	LSIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Pig	---	---	LSIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Dog	---	---	LSIV-LALG	GVTGAPS	---	---	DP	RLRQF
1Chicken	---	---	LSIA-LAVG	TVSAAPS	---	---	DP	RLRQF
1Flycatcher	---	---	LSIA-LALG	TVSAAPS	---	---	DP	RLRQF
1Turkey	---	---	---	---	---	---	---	---
1Anole_lizard	---	---	LSLA-LALG	SGAAAPA	---	---	DP	RLRQF
1Chinese_softshell_turtle	---	---	LSLA-LAVS	SVSGAPS	---	---	DP	RLRQF
1Frog	---	---	LSLA-LAIN	SISAAPT	---	---	DP	RLRQF
1Lungfish	---	---	LSLA-VVFS	KVSAAPS	---	---	DL	RLRQL
1Coelacanth	---	---	LSLA-LVVS	NISAAPS	---	---	DL	RLRQL
1Lepisosteus	---	---	LCLA-LAVS	SVSAAPS	---	---	DL	RLRQL
1White_sturgeon	---	---	LSLA-LAVS	SVSAAPS	---	---	DP	RLRQL
1Chinese_sturgeon	---	---	LSLA-LAVS	SVSAATS	---	---	EP	RIRQL
1Platyfish	---	---	LLSL-ASIS	CSSAAQR	---	---	DS	KLRL
1Tilapia	---	---	LVSLT-ASIS	CTSAAQR	---	---	DS	KLRL
1Elephant_nose_fish	---	---	LSLA-LAVS	SVSAAPS	---	---	DL	KLRQL
1Carp	---	---	LSLA-LAVC	SVSAAPT	---	---	DA	KLRQL
1Goldfish	---	---	LSLA-LAVC	SVSAAPT	---	---	DA	KLRQL
1Clown_knife_fish	---	---	LSLA-LAVS	SVYAAPS	---	---	DL	KLRQL
1Orange-spotted_grouper	---	---	LLSLT-ASIS	CSSAAQR	---	---	DS	KLRL
1Anglerfish	---	---	LLSLT-ASIS	CSFAGQR	---	---	DS	KLRL

1Megalobrama	-----	-LSLA-LAVS	SVSAAPS	-----	DA	-KLRQL
1African_cichlid_fish	-----	LVSLT-ASIS	CTSAAQR	-----	DS	-KLRLL
1Cod	-----	-LSCA-AMLS	GSSAAPS	-----	DT	-KLRQL
1Zebrafish	-----	-LSLA-LAVS	SVSAAPS	-----	DA	-KLRQL
1Medaka	-----	-LSLT-ASIS	CSSAAQR	-----	DS	-KLRLL
1Stickleback	-----	LLSLT-ASIS	CSSTAQR	-----	DG	-KLHLL
1Takifugu	-----	LLSLS-ASFS	CSSAAHR	-----	DF	-KLPLL
1Tetraodon	-----	LLSLS-ASFS	CSSAAHR	-----	DS	-KLALM
1Trout	-----	-LSLA-LAIS	SVSAAPS	-----	DA	-KLRQL
1Fathead_minnow	-----	-LSLA-LAIS	SVSAAPS	-----	DA	-KLRQL
1Killifish	-----	LLCLS-ASIS	CSSAAQR	-----	DS	-KLRLL
1Salmon	-----	-LSLA-LAIS	SVSAAPS	-----	DA	-KLRQL
1Pygocentrus	-----	-LSLA-LALS	SVSGAPS	-----	DA	-KLRQF
1Ictalurus	-----	-LAVA-LSVC	SVSGAPS	-----	DA	-KLRQF
1Astyanax	-----	-LSIA-LAVG	SVSGAPS	-----	DA	-KLRQF
1Clupea	-----	-LSIV-LAIS	CISAAPT	-----	DV	-KLRQL
1Amazon_molly	-----	LLSLS-ASIS	CSSAAQR	-----	DS	-KLRLL
5Coelacanth	-----	-LSAS-LLLV	GVGGLPK	-----	GE	-VLTDL
5Zebrafish	-----	-LWVS-LLLC	RVSSAPR	-----	GD	-LLF
5Stickleback	-----	VALFSSVLLV	QVSGAPR	-----	GD	
5Takifugu	-----	-SFSSMLLM	EVSSAPR	-----	KH	
5Tetraodon	-----	-SFSFLLLM	EAGGTPR	-----	KH	
5Medaka	-----	-IGLS-LLMA	CVSGAPQ	-----	R	NP
5Sockeyess	-----	-LSAS-VFLA	RVSAAPH	-----	RD	-MLAEL
5Trout	-----	-LSAS-VFLA	RVSAAPH	-----	RD	-MLAEL
5Fathead_minnow	-----	-LSLS-LLLC	SVSSAPG	-----	GD	-MLIQ
5Amazon_molly	-----	-LCSSMLALH	VSSAPQM	-----	DE	
5Platyfish	-----	ICSSM-LALH	VSSAPQM	-----	DE	
5Tilapia	-----	-GLS-VLLV	RVSTAPY	-----	SD	-MLTET
5Lepisosteus	-----	-LSVS-VLLA	RVSGVPO	-----	RD	-RLADL
5Astyanax	-----	-LSVL-VLVS	RVSAAPR	-----	GD	-VLTQL
5Ictalurus	-----	-VSLL-VLVS	RVRTAPR	-----	TD	
5Pygocentrus	IFEEFEYFKS	ICLLN-HLIT	RVSAAPR	-----	GD	-ILAQL
Catshark5		V-TVA-LLLL	RGSSTAR	-----	VO	-GLPDI
6Chicken	-----	VLLLV-WSVR	A-TALPG	-----	EE	-RLALQ
6Zebra_finch	-----	VLLLL-WSVR	ATALPGQ	-----	EG	
6Duck	-----	VLLLV-WSVR	A-TALPG	-----	EE	-RLALQ
6Lungfish	-----	FLLVV-WSVK	A-TALPV	-----	ED	-RLSVH
6Coelacanth	-----	FLLVV-WSVR	A-TALPI	-----	EE	-KLM
6White_sturgeon	-----	LMLVV-YSLR	VVAVLPG	-----	EE	-RLSVH
6Chinese_sturgeon	-----	LMLVV-YSLR	VVAVLPG	-----	EE	-RLSVH
6Lepisosteus	-----	LMLVV-YSVR	AAAVLPG	-----	EE	-RATLH
6Carp	-----	-LLLVLVSVR	AAAVLPV	-----	EE	-RNLAQ
6Goldfish	-----	LLLVL-YSVR	AAAVLPV	-----	EE	-RNPAQ
6Orange-spotted_grouper	-----	LMGVL-FSVR	AAAVLPV	-----	ED	-RSSIH
6Zebrafish	-----	-LLLVLVSVR	AAAVLPL	-----	EE	-RNPAQ
6Stickleback	-----	LMGVL-FSVR	AAAVLPM	-----	ED	-RSSIN
6Takifugu	-----	LTGVL-LSIR	AAAVLPV	-----	EE	-RSPVH
6Tetraodon	-----	LTGVL-LSVR	AAAVLPV	-----	EE	-RIPLH
6Rainbow_smelt	-----	LMGVL-YSAR	AAAVLPV	-----	EE	-RSPIQ
6Trout	-----	LMGVL-YSVR	AAAVLPV	-----	EE	-RSPL
6Medaka	-----	LMGVL-FSVR	AAAVLPV	-----	ED	-RSSIH
6Fathead_minnow	-----	LMLVL-YSVR	AAALLPV	-----	EE	-RN
6Astyanax	-----	LLLVL-YSVR	AAAVLPV	-----	EE	-RSPAH
6Pygocentrus	-----	-LLLVLVSVR	AAAVLPV	-----	EE	-RSPTH
6Clupea	-----	LMLVL-YSIR	AAAVLPV	-----	DE	-RSPAH
6Ictalurus	-----	LLLVL-YSVR	AAAVLPA	-----	EE	-RSPAH
6Amazon_molly	-----	LMGVL-FSVR	AAAVLPL	-----	ED	-RSPIH
6Cod	-----	LMGVL-FSVR	AAALLPV	-----	ED	-RSNFH
6Platyfish	-----	LMGVL-FSVR	AAAVLPL	-----	ED	-RSPIH
Catshark6	-----	-LSMLLIVSS	VRATAPL	-----	ED	-RLSLR
Elephant_shark6	-----		VSGV	STTTASL	DD	-RFNLQ
whale_shark6	-----		IVSS	VKATAPL	ED	-RLSLR
4Lepisosteus	-----	-FGLV-FAFC	CVSAVSN	S	DL	-RFRRF
4Zebrafish	-----	-LCLA-MMAG	IICG	-----		-RSHML
4Takifugu	-----	-LC-FAFC	CAENSKI	-----	EH	-RFNDL
4Medaka	-----	-LCFAVCVVO	NTEIMVE	-----	SE	-DLPAGQ
4Tetraodon	-----	-LC-FASR	CAGNSKI	-----	EH	-RLKDL
4Channel_catfish	-----	-MCLV-SAVG	VISCGRP	-----		-HVVLNS
4Stickleback	-----	-LCFA-FCAA	QDGETQR	-----		-GFKDNR
4Atlantic	-----	V-CVILCOMG	KVDSFVN	-----	ED	-KPTWLE

2Human	-GPTGRDSEH	MQEAAGI	---	RKSSLLT	-FL	AWWFEWTS	--	QASAGPLI	--
2Mouse	-LESGPTIGQD	SVQEATE	---	GRSGLLT	-FL	AWWHEWAS	--	QASSSTPV	--
2Pig	-TSHDRDSDGH	MQEVAEI	---	KKNSLLT	-FL	AWWHEWMS	--	QAREVPFV	--
2Bovine	---GHESGH	MQEVAEI	---	KTNSLLT	-FL	AWWYEWAS	--	QARAVPFV	--
2Monkey	-SPTGPDSEH	MQEAAGI	---	RKSSLLT	-FL	AWWFEWTS	--	QASAGPLI	--
2Lizard	-WKHNEGSA	---	DL	GRDELLA	-FL	SGLVDRASRR	---	HGMPLSK	---
2Frog	-TGRNQDLN	---	AI	QQDLLLK	-LL	SGWTD	-SRE	SN	-LVE
2Coelacanth	KVNRETTGF	---	GEE	RKQFLSN	-ML	DALIGL	---	NTLENDTP	---
2Lepisosteus	-SMGGLAKE	---	---	RKDVLK	-VL	SGLLV	---	NLLRKEQS	---
2Astyanax	-SKEVLTKE	---	---	QKDLLIK	-IM	SDLAELNMTI	---	KDLGALDL	---
2Pygocentrus	-SNEVLTKE	---	---	QKDLLIK	-IM	SDLAELNMTV	---	KDLGALDL	---
2Clupea	-RNESLADE	---	---	ERILLK	-IL	AGLTEKNLTE	---	ENLTGHDL	---
2Ictalurus	---SNEVLTKE	---	---	QKDFMTQ	-FL	ANLAE LNMTI	---	KDLETMDH	---
2Zebrafish	---TNEILSKE	---	---	EDGL	-K	MI	TYVAELNLTS	KELADLDA	---
Catshark2	-VNREMTKS	---	---	RKNLIVK	-LL	AGLLETDD	---	NLLENGFA	---
Whale_shark2	-VNREMTKS	---	---	RKYLMLK	-LL	SGLLPDD	---	NLLENDFT	---
Elephant_shark2	-LNREMKVD	---	---	KKRLIAK	-LL	AGLLDVDD	---	NLLESVIA	---
Skate2	-LTKN	---	---	RKSLILK	-LL	AGLLDVDD	---	HLGESGYT	---
aLethenteron	-LQORVEAVL	TQELSRE	---	ERALVGR	-LL	AELAAGGAGL	---	GGALPPLGWG	---
bLethenteron	-LERVMDGLG	MENLDQD	---	QKLFVLR	-LL	AAIDSSADET	---	NELNHSDE	-G
bLampetra	-LERVMDGPG	MENLDQD	---	QKQFLVR	-LL	AAIDSSADET	---	NELNHSDE	-G
cPetromyzon	SFRQLEAHPD	LQMGDQD	---	DSQILLN	-MI	VEAMRMRDAG	---	PETDGPGE	---
cLethenteron	SYRQLEAHPD	LQMGDQD	---	DSQMLLN	-MI	VEAMRMRDAG	---	PETDGPGE	---
3Lepisosteus	-LQKAKAAG	-LNKQDS	---	SKYAIED	-LI	SQVQSDS	---	EALNEMS	---
3Astyanax	-LQRARALG	-IAAQEW	---	KKREMED	-LL	SQTLPESEF	---	QESEISTL	---
3Clupea	LLQRARAAG	-MSTQEW	---	SKRAVED	-LL	SQSLPEEET	---	QDREVSTV	---
3Ictalurus	-LQRVQALG	-VAAQEW	---	TKNDLKA	-IL	AQLTMPSEF	---	QENDVSTL	---
3Pygocentrus	-LQRARALG	-MAAQEW	---	RKREMED	-LL	SQTLPESEF	---	KESEISTL	---
3Amazon_molly	LLQRARSAG	-LLSQDW	---	SKRAVED	-LL	AQMSRSV	---	EAQQDDPE	---
3Platyfish	LLQRARSAG	-LLSQDW	---	SKRAVED	-LL	AQMSRSEV	---	EAQQDGPE	---
3Rainbow_trout	-LQRARAAA	P	---	HRSGVSE	---	-RWRTFYPNC	---	PCLRPRKV	---
3Freshwater_butterfly	-VQRARAAS	MGPQQDW	---	GKLSVED	-L	SLLAATEA	---	DMPFGDMS	---
3Grass_carp	-LQRARAIG	-QATQDW	---	TKKDVEE	-LL	SLLSMPEM	---	EMRENDIS	---
3Clownfish	LLQRASATG	QATRQDF	---	TKRDVEK	-LL	SLLSIPEM	---	EMREKGLS	---
3Clown_knifefish	-LQRAHSAP	-ASPQDW	---	TRRTVED	-LL	ARLPPPEG	---	EFTPVEDV	---
3Orange-spotted	LLQRARSAG	-LLSQEW	---	SKRAVED	-LL	AQMSLPEA	---	DTQREAEV	---
3American_anglerfish	LLERARSAG	-LLSQEW	---	SKRAVEE	-LL	AQMSLPEA	---	DVQREAEV	---
3Silver_aronana	-LQRAHAAA	-MSPQDW	---	SKQAVEE	-LL	SRLAPAQG	---	EVPQGAVS	---
3White_sucker	-LQRARAIG	-LATQDW	---	TKKDIEE	-LL	SQSLPEI	---	EARENGVS	---
3Elephant_nose_fish	-MQRHTAA	-MSPQDW	---	SRVVED	-LL	SRLAPPED	---	DTQSEMS	---
3Zebrafish	LLQRARAIG	-QAEW	---	TKKDVEE	-LL	SLLSMPEM	---	QMRESDLS	---
3Stickleback	-LQRARGAG	-LLSQDW	---	SKRAVED	-LL	AQMSLPEA	---	DSQLGAEV	---
3Takifugu	LLQHVHGAG	-LLSQEW	---	SKRAVED	-LI	AQMSMPEG	---	TGQRDTEV	---
3Tetraodon	LLQRAGHAG	-LLSQDW	---	SKRAVED	-LI	AQMSLPEG	---	TGQRDTEV	---
3Medaka	LLQRARSAG	-LLSQDW	---	SKRAIEN	-ML	ARMPDPEA	---	EAERAEV	---
3aAtlantic_salmon	-LQRARAAS	-IATQEW	---	SKRMED	-VL	SKLSLPDV	---	EAQKS	---
3bAtlantic_salmon	-LQRARAAG	-IATQEW	---	SKRAVED	-IL	SQSLWPEA	---	QESEVSPA	---
Elephant_shark3	-LQGSQA	---	MEL	RDGVRE	-LI	QAVADAESKP	---	QSEAAE	---
Whale_shark3	---	---	DF	LKDTIIC	-LL	HVVADADKDA	---	VEVNASQV	---
catshark3	-LQR	-ALD	---	QEL	---	LKDTMMK	-LL	PLVTDVDTA	---
Catshark1	-LQRAMAATG	SGGKAEI	---	TKYSLAQ	-LL	SELENAEN	---	EALETDAM	---
Whale_shark1	-LQTSMAGAE	PRSKAEL	---	IKYNLVC	-LL	AELANAEN	---	EVLDGEDL	---
Elephant_shark1	-LQRSLAAAG	ARSKPEL	---	TKYSLAQ	-LL	AELANAEN	---	EALAEADM	---
1Human	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Mouse	-LQKSLAAA	-TGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Monkey	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Bovine	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEI	---	DALEPEDL	---
1Pig	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Dog	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPNQTEN	---	DALEPEDL	---
1Chicken	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	SEPSQTEN	---	EALASEDL	---
1Flycatcher	-LQKSLGGG	-GGGEL	---	AKYFLAE	-LL	SEPSQTEN	---	EALASEDL	---
1Turkey	---	---	KEL	AKYFLAE	-LL	SEPSQTEN	---	EALASEDL	---
1Anole_lizard	-LQKSLAAA	-AAGKQEL	---	AKYFLAE	-LL	SEPGQEN	---	EALPEEL	---
1Chinese_softshell_turtle	-LQKSLAAA	-AGKQEL	---	AKYFLAE	-LL	AEPSQEN	---	EALPEEDL	---
1Frog	-LQKSLASA	-GKQEL	---	AKYFLAE	-LL	SEPSQTDN	---	EALASDDL	---
1Lungfish	-LQRSLAAA	-AGKQEL	---	TKYSLAE	-LL	SELAQSEN	---	DALDSSDL	---
1Coelacanth	-LQKSLAAA	-AGKQEV	---	SKYSLAE	-LL	AELAQEN	---	EALASDDL	---
1Lepisosteus	-LQRSLAAS	-AGKQEL	---	ARYTLAE	-LL	SELAQSEN	---	EALASDDL	---
1White_sturgeon	-LQRTLAAS	-AGKQEL	---	LKYSIAE	-LL	SELAQSEN	---	DALASDEL	---
1Chinese_sturgeon	-LQRSLVAS	-AGKQDL	---	LKYSIAE	-LL	SELAQSEN	---	DALASDEL	---
1Platyfish	-LHRTPLLS	---	SKQDA	SRSSLAE	-LLL	SDLLQEN	---	EALAEEDGF	---
1Tilapia	-LHRTPLLG	---	SKQDM	SRSSLAE	-LLL	SDLLQEN	---	EALAEENF	---
1Elephant_nose_fish	-LQRSLLAP	-ASKQDL	---	ARNPLEE	-LL	SEMVRVEN	---	EALPEDDL	---
1Carp	-LQRSLLNP	-AGKQEL	---	ARYTLAD	-LL	SDLVQEN	---	EALPEEDL	---
1Goldfish	-LQRSLLNP	-AGKQEL	---	ARYTLAD	-LL	SELVQEN	---	EALPEEDL	---
1Clown_knife_fish	-LQRSLIAP	-ASKQEL	---	ARYTLAE	-LL	SELAQEN	---	EALASDDL	---
1Orange-spotted_grouper	-LHRTPLLG	---	SKQDM	SRSSLAE	-LLL	SDLLQEN	---	EALAEENF	---
1Anglerfish	-LHRYPLQG	---	SKQDM	TRSLAE	-LLL	SDLLQEN	---	EALAEENF	---

1Megalobrama	-LQ <sup>R</sup> SL <sup>L</sup> LN <sup>P</sup> -	-AG <sup>K</sup> Q <sup>E</sup> L---	ARY <sup>T</sup> LT <sup>L</sup> D-LL	SDL <sup>V</sup> QA <sup>E</sup> N--	EV <sup>L</sup> EP <sup>E</sup> DL--
1African_cichlid_fish	-LH <sup>R</sup> TPL <sup>L</sup> LG-	--SK <sup>Q</sup> DM---	SR <sup>S</sup> SLA <sup>E</sup> LLL	SDL <sup>L</sup> Q <sup>V</sup> EN--	EAL <sup>E</sup> EE <sup>N</sup> F--
1Cod	-LQ <sup>R</sup> SL <sup>L</sup> AP-	MP <sup>G</sup> Q <sup>E</sup> ET---	VRY <sup>T</sup> LA <sup>Q</sup> -LL	SE <sup>L</sup> AQA <sup>E</sup> N--	EAL <sup>G</sup> T <sup>D</sup> DD <sup>Q</sup> --
1Zebrafish	-LQ <sup>R</sup> SL <sup>L</sup> SP-	-AG <sup>K</sup> Q <sup>E</sup> L---	ARY <sup>T</sup> LA <sup>D</sup> -LL	SDL <sup>V</sup> QA <sup>E</sup> N--	EAL <sup>E</sup> PE <sup>D</sup> L--
1Medaka	-LQ <sup>R</sup> TPL <sup>L</sup> LG-	--SK <sup>Q</sup> DM---	SR <sup>S</sup> SLA <sup>E</sup> LLL	SDL <sup>L</sup> Q <sup>M</sup> EN--	EV <sup>L</sup> ED <sup>G</sup> F--
1Stickleback	-LH <sup>R</sup> TPL <sup>L</sup> LS-	--SK <sup>Q</sup> DM---	SR <sup>S</sup> SLV <sup>E</sup> LLL	SDL <sup>L</sup> Q <sup>V</sup> QN--	EAL <sup>E</sup> EE <sup>N</sup> L--
1Takifugu	-LQ <sup>S</sup> NAL <sup>M</sup> G-	--NK <sup>Q</sup> EM---	TR <sup>S</sup> SLAN <sup>L</sup> LLL	SDL <sup>L</sup> Q <sup>V</sup> GN--	EAL <sup>E</sup> EN <sup>L</sup> A--
1Tetraodon	-LPP <sup>N</sup> NPL <sup>L</sup> LG-	--HR <sup>Q</sup> EM---	SR <sup>S</sup> SLAD <sup>L</sup> LLL	SDL <sup>L</sup> Q <sup>V</sup> EN--	QAL <sup>D</sup> EN <sup>F</sup> P--
1Trout	-LQ <sup>R</sup> SLMAP-	-AG <sup>K</sup> Q <sup>E</sup> L---	AR <sup>N</sup> TLV <sup>E</sup> -LL	SEL <sup>A</sup> HV <sup>E</sup> N--	EAL <sup>I</sup> EL <sup>D</sup> DM--
1Fathead_minnow	-LQ <sup>R</sup> SL <sup>L</sup> NP-	-AG <sup>K</sup> Q <sup>E</sup> L---	ARY <sup>T</sup> LA <sup>D</sup> -LL	SEL <sup>V</sup> QA <sup>E</sup> N--	EAL <sup>E</sup> PE <sup>D</sup> L--
1Killifish	-LH <sup>R</sup> TPL <sup>L</sup> LS-	--SQ <sup>D</sup> DV---	SR <sup>S</sup> SLA <sup>E</sup> LLL	SDL <sup>L</sup> Q <sup>M</sup> EN--	EAL <sup>E</sup> ED <sup>G</sup> F--
1Salmon	-LQ <sup>R</sup> SLMAP-	-AG <sup>K</sup> Q <sup>E</sup> L---	ARY <sup>T</sup> LA <sup>E</sup> -LL	SE <sup>L</sup> AQA <sup>E</sup> N--	EAL <sup>E</sup> S <sup>D</sup> DL--
1Pygocentrus	-LQ <sup>R</sup> SLIG <sup>P</sup> -	-SG <sup>K</sup> Q <sup>E</sup> L---	ARY <sup>T</sup> LA <sup>E</sup> -LL	SE <sup>L</sup> AQA <sup>E</sup> N--	EAL <sup>E</sup> A <sup>E</sup> DM--
1Ictalurus	-LQ <sup>R</sup> SILAP-	-SV <sup>K</sup> Q <sup>E</sup> L---	TRY <sup>T</sup> LA <sup>E</sup> -LL	AEL <sup>A</sup> QA <sup>E</sup> N--	EV <sup>L</sup> DS <sup>E</sup> DEV--
1Astyanax	-LQ <sup>R</sup> SLIG <sup>S</sup> -	-AG <sup>K</sup> Q <sup>E</sup> L---	ARY <sup>T</sup> LA <sup>E</sup> -LL	SE <sup>L</sup> AQA <sup>E</sup> N--	EAL <sup>E</sup> ED <sup>D</sup> VP--
1Clupea	-LQ <sup>R</sup> SLFAP-	-GG <sup>K</sup> Q <sup>E</sup> L---	AR <sup>L</sup> TLA <sup>E</sup> -LL	SE <sup>L</sup> AQA <sup>E</sup> N--	EAL <sup>E</sup> SE <sup>D</sup> M--
1Amazon_molly	-LH <sup>R</sup> TPL <sup>L</sup> LS-	--SK <sup>Q</sup> DA---	SR <sup>S</sup> SLA <sup>E</sup> LLL	SDL <sup>L</sup> Q <sup>M</sup> EN--	EAL <sup>E</sup> ED <sup>G</sup> F--
5Coelacanth	-FQ <sup>G</sup> GA <sup>E</sup> G-	---KED <sup>F</sup> ---	SR <sup>M</sup> LM <sup>L</sup> K-MV	SN <sup>L</sup> LK <sup>S</sup> EN--	DV <sup>L</sup> VP <sup>S</sup> AE--
5Zebrafish	QL <sup>L</sup> RS <sup>Q</sup> VDP <sup>K</sup>	ENE <sup>L</sup> Q <sup>D</sup> L---	SR <sup>L</sup> LLL <sup>L</sup> K-QL	SE <sup>S</sup> VT <sup>P</sup> E <sup>E</sup> K	DAL <sup>D</sup> SI <sup>D</sup> E--
5Stickleback	-MPT <sup>Q</sup> RG <sup>D</sup> P-	-AD <sup>N</sup> K <sup>D</sup> L---	AYS <sup>M</sup> LL <sup>K</sup> -FV	SEL <sup>T</sup> AARG <sup>G</sup> E	TLL <sup>V</sup> PE <sup>Q</sup> E--
5Takifugu	-MP <sup>S</sup> ELL <sup>P</sup> AD-	PL <sup>K</sup> DK <sup>D</sup> L---	AIL <sup>L</sup> LR- <sup>I</sup> I	SE <sup>V</sup> MAA <sup>E</sup> R--	EML <sup>L</sup> L <sup>L</sup> P <sup>Q</sup> E--
5Tetraodon	---K <sup>F</sup> L <sup>P</sup> AD-	SV <sup>K</sup> DK <sup>D</sup> L---	AL <sup>V</sup> TS <sup>L</sup> K-FA	FEG <sup>T</sup> AA <sup>Q</sup> R--	EML <sup>L</sup> LL <sup>L</sup> Q <sup>E</sup> --
5Medaka	-LTH <sup>T</sup> K <sup>Q</sup> L <sup>Q</sup> L-	LK <sup>S</sup> EV <sup>D</sup> P-	TR <sup>L</sup> LL <sup>L</sup> MK-LV	LE <sup>L</sup> VAL <sup>R</sup> --	QEM <sup>L</sup> Q <sup>E</sup> LE--
5Sockeye	-LRAD <sup>T</sup> TKG-	---NED <sup>L</sup> ---	SRT <sup>L</sup> LL <sup>L</sup> K-MM	SDL <sup>M</sup> STAV <sup>G</sup> E	NE <sup>V</sup> L <sup>P</sup> DL <sup>E</sup> --
5Trout	-LRAD <sup>S</sup> TKG-	---NED <sup>L</sup> ---	SRT <sup>L</sup> LL <sup>L</sup> K-MM	SDL <sup>M</sup> SAAV <sup>G</sup> E	NE <sup>V</sup> L <sup>P</sup> DL <sup>E</sup> --
5Fathead_minnow	-LLR <sup>S</sup> EVE <sup>P</sup> K-	EIE <sup>L</sup> Q <sup>D</sup> F-	FR <sup>L</sup> LL <sup>L</sup> K-QL	SE <sup>S</sup> AA <sup>P</sup> E---	EK <sup>Q</sup> PRE <sup>S</sup> I--
5Amazon_molly	-LTET <sup>L</sup> QAE-	LIS <sup>D</sup> K <sup>D</sup> L---	TGL <sup>L</sup> LL <sup>L</sup> R-FM	SEL <sup>M</sup> AS <sup>R</sup> G--	EEM <sup>L</sup> RE <sup>K</sup> Q--
5Platyfish	-LTET <sup>L</sup> QAE-	LIS <sup>D</sup> K <sup>D</sup> L---	TGL <sup>L</sup> LL <sup>L</sup> R-LM	SEL <sup>T</sup> AS <sup>R</sup> GEE	ML <sup>R</sup> E <sup>Q</sup> EEE--
5Tilapia	-LRAD <sup>L</sup> TND-	---KDL---	TH <sup>W</sup> LL <sup>L</sup> K-FM	AEL <sup>M</sup> AA <sup>R</sup> --	-----
5Lepisosteus	-LRAE <sup>V</sup> PEG-	---KED <sup>L</sup> ---	SR <sup>M</sup> LL <sup>L</sup> K-IF	SDL <sup>L</sup> RA <sup>E</sup> N--	---E <sup>I</sup> PP <sup>G</sup> ---
5Astyanax	-LQNEAD <sup>T</sup> K-	---ENED <sup>I</sup> ---	SR <sup>M</sup> LM <sup>L</sup> K-LL	SE <sup>L</sup> EVAG <sup>E</sup> N--	EV <sup>L</sup> SGAD <sup>V</sup> --
5Ictalurus	-LLAH <sup>M</sup> LQNE	AD <sup>G</sup> KED <sup>L</sup> ---	SR <sup>I</sup> LL <sup>L</sup> K-LI	SEL <sup>K</sup> IP <sup>D</sup> EN--	DT <sup>L</sup> SDD <sup>D</sup> M--
5Pygocentrus	-----QAD	PK <sup>G</sup> NEEL	SR <sup>M</sup> LIL <sup>K</sup> -LL	SD <sup>L</sup> EIP <sup>G</sup> D-N	EV <sup>L</sup> SGT <sup>D</sup> V--
Catshark5	-LQER <sup>N</sup> DEG-	---TEEL---	SRT <sup>M</sup> VL <sup>N</sup> -LL	SEL <sup>L</sup> HAG <sup>D</sup> --	-----
6Chicken	-NSRE <sup>Q</sup> TKL-	-----	RRD <sup>A</sup> LK-ML	AG <sup>L</sup> ESS <sup>D</sup> --	---VAS <sup>P</sup> DL--
6Zebra_finch	-LQST <sup>R</sup> EQS-	---IA---	RKD <sup>V</sup> ILK-ML	AG <sup>L</sup> LGS <sup>V</sup> D--	AGA <sup>E</sup> VAF <sup>P</sup> --
6Duck	-NSRE <sup>Q</sup> TKL-	-----	RKD <sup>A</sup> ILK-ML	AG <sup>L</sup> LES <sup>V</sup> D--	---VAS <sup>P</sup> DL--
6Lungfish	-SNRD <sup>L</sup> TRE-	-----	REEM <sup>I</sup> LK-MI	SGL <sup>L</sup> DGS <sup>D</sup> --	NS <sup>L</sup> FGGE <sup>V</sup> --
6Coelacanth	-SHNN <sup>V</sup> EIT-	---KE---	RKEL <sup>M</sup> LK-MI	AG <sup>L</sup> LEG <sup>I</sup> D--	SPP <sup>M</sup> GGE <sup>V</sup> --
6White_sturgeon	-SNRE <sup>L</sup> SKE-	-----	RKEG <sup>F</sup> LK-LL	SGL <sup>L</sup> DRV <sup>S</sup> --	SV <sup>V</sup> LGED <sup>V</sup> --
6Chinese_sturgeon	-SNRE <sup>L</sup> SKE-	-----	RKEG <sup>F</sup> LK-LL	SGL <sup>L</sup> DGV <sup>S</sup> --	SV <sup>V</sup> LGED <sup>V</sup> --
6Lepisosteus	--TKEL <sup>S</sup> KD-	-----	RKEL <sup>I</sup> LK-LI	SGL <sup>L</sup> DGAD--	SAM <sup>L</sup> AGD <sup>V</sup> --
6Carp	--SRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LI	SGL <sup>L</sup> DGVD--	NN <sup>V</sup> LAGE <sup>I</sup> AP
6Goldfish	--SRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LI	SGL <sup>L</sup> DGVD--	NS <sup>V</sup> LGE <sup>I</sup> AP
6Orange-spotted_grouper	-VNRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGAL <sup>D</sup> I	NML <sup>P</sup> GEAA--
6Zebrafish	--SRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LI	SGL <sup>L</sup> DGVD--	NS <sup>V</sup> LAGE <sup>I</sup> AP
6Stickleback	-VNRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGAAD <sup>A</sup>	NML <sup>P</sup> GEAA--
6Takifugu	-LNRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGAL <sup>D</sup> I	NML <sup>P</sup> ME <sup>T</sup> V--
6Tetraodon	-LNRE <sup>L</sup> SKE-	-----	RKEL <sup>M</sup> LK-LV	SGL <sup>L</sup> DGAL <sup>D</sup> I	NML <sup>P</sup> MEAV--
6Rainbow_smelt	-ANRE <sup>L</sup> STE-	-----	RK <sup>Q</sup> LIL <sup>K</sup> -LV	SGL <sup>L</sup> DGAS <sup>D</sup> S	NML <sup>P</sup> GD <sup>V</sup> S--
6Trout	-LNRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGAT <sup>D</sup> I	NML <sup>P</sup> GGE <sup>V</sup> --
6Medaka	-VNRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGSL <sup>D</sup> I	NML <sup>P</sup> GEAA--
6Fathead_minnow	-LAQS <sup>R</sup> ELS-	---KD---	RKEL <sup>I</sup> LK-LI	SGL <sup>L</sup> DGVD--	NS <sup>V</sup> LAGE <sup>I</sup> AQ
6Astyanax	--TRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGVD--	NS <sup>V</sup> LGG <sup>D</sup> L--
6Pygocentrus	--TRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LI	TGL <sup>L</sup> DGVD--	SS <sup>V</sup> LAG <sup>D</sup> L--
6Clupea	--ARE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGVE--	SN <sup>M</sup> LPG <sup>D</sup> E--
6Ictalurus	--TRE <sup>P</sup> SKE-	-----	RKEM <sup>I</sup> LK-MV	SS <sup>L</sup> LDGVD--	NN <sup>M</sup> LAG <sup>D</sup> L--
6Amazon_molly	-ANRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGAL <sup>D</sup> I	NML <sup>P</sup> GEAA--
6Cod	-SSRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> EGSP <sup>D</sup> S	NML <sup>P</sup> GE <sup>L</sup> S--
6Platyfish	-ANRE <sup>L</sup> SKE-	-----	RKEL <sup>I</sup> LK-LV	SGL <sup>L</sup> DGAL <sup>D</sup> I	NML <sup>P</sup> GEAA--
Catshark6	-ANQEL <sup>N</sup> KE-	-----	RKEV <sup>I</sup> LK-LL	SGL <sup>L</sup> DSSS--	NQ <sup>I</sup> AIEN <sup>T</sup> --
Elephant_shark6	-SSRE <sup>M</sup> NQE-	-----	RKEM <sup>I</sup> LK-LL	SGL <sup>L</sup> DNA <sup>A</sup> VS	QOT <sup>G</sup> SEAG--
whale_shark6	-ANQEL <sup>N</sup> KE-	-----	RKEV <sup>V</sup> LK-LL	SAL <sup>L</sup> DSSS--	NQM <sup>G</sup> IENT--
4Lepisosteus	-LQKAKA <sup>A</sup> S-	-LSTR <sup>D</sup> S-	SKYA <sup>L</sup> ED-LI	SQIA <sup>Q</sup> SDN--	EAL <sup>E</sup> NEMS--
4Zebrafish	-LNSAL <sup>Q</sup> ASR	GTSAD <sup>E</sup> EIP-	ERY <sup>S</sup> LSE--L	FW <sup>L</sup> LSNS <sup>D</sup> --	PA <sup>V</sup> FQPD <sup>S</sup> SS
4Takifugu	-QVQED <sup>L</sup> LSW	LK <sup>P</sup> QEK <sup>W</sup> EPS	KRQ <sup>T</sup> LED-LL	YK <sup>L</sup> TNY <sup>K</sup> SEN	RIL <sup>P</sup> QQ <sup>P</sup> G--
4Medaka	GL <sup>L</sup> SSF <sup>D</sup> R <sup>I</sup> -	SDFQ <sup>Q</sup> SV-	ETG <sup>I</sup> LMN-LL	YK <sup>L</sup> SRP <sup>D</sup> SAI	TL <sup>Q</sup> QVR <sup>D</sup> S--
4Tetraodon	-QVEED <sup>V</sup> L <sup>P</sup> W	LNSQ <sup>E</sup> K <sup>W</sup> EPS	KGON <sup>L</sup> ED-LL	YK <sup>L</sup> TNY <sup>R</sup> SEN	RIV <sup>S</sup> QQ <sup>P</sup> S--
4Channel_catfish	-ALEEARN <sup>V</sup> P-	-FGEE <sup>V</sup> P-	ERL <sup>T</sup> LPE--L	QW <sup>M</sup> LSN----	NEL <sup>T</sup> PV <sup>Q</sup> V--
4Stickleback	-LQ <sup>R</sup> DSL <sup>P</sup> WL-	DK <sup>L</sup> QDE <sup>Q</sup> DST	KKL <sup>N</sup> LIE-WL	YS <sup>F</sup> YK <sup>F</sup> D <sup>N</sup> G-	NIV <sup>K</sup> GPT <sup>D</sup> --
4Atlantic	-TLQ <sup>D</sup> KQ <sup>V</sup> SA-	---AD---	DKYN <sup>L</sup> VW-LL	YK <sup>L</sup> SQ <sup>S</sup> SH <sup>D</sup> -	NT <sup>F</sup> KIN <sup>F</sup> PPH

2Human	---	GEEARE	VARR	QEG	---	APPOQS	---	ARRDRM	PCRNFFWKTF
2Mouse	---	GGGTPG	LSKS	QER	---	PPPQQP	---	PHLDKK	PCKNFFWKTF
2Pig	---	GGETRE	MPKK	QEG	---	LPRQQA	---	SRGDRT	PCGNFFWKTF
2Bovine	---	GGEARE	VSKR	QEG	---	APLHQS	---	TRQDKT	PCKNFFWKTF
2Monkey	---	GEEARE	VARR	QEG	---	APPOQS	---	ARRDRT	PCKNFFWKTF
2Lizard	QEKVVRSPRE	ERVP	FFR	---	---	H	---	PVREKA	PCKNFFWKTF
2Frog	VERNVPDPPE	PKIPP	SVK	---	FPRL	S	---	LRERKA	PCKNFFWKTF
2Coelacanth	LLGTKEQEE	HNLS	ER	---	SAFKY	---	SSLKKA	PCRNFFWKTF	
2Lepisosteus	AVDSEQ	LKSSLMGER	---	SVFGPSVS	---	---	RERT	PCKNFFWKTF	
2Astyanax	EQLLN	GKLG	ER	---	---	---	SVEKS	PCTNFFWKTF	
2Pygocentrus	EQLLN	GKLG	ER	---	SVFGL	---	PAQEKs	PCKNFFWKTF	
2Clupea	EGLLN	GTLK	---	GGSV	---	TPQERS	---	PCKNFFWKTF	
2Ictalurus	EQLS	KLS	ER	---	AAFGLP	---	PAREKS	QCNFFWKTF	
2Zebrafish	ELLN	GKLW	EK	---	SDK	---	PSKDKS	PCKLFFWKTF	
Catshark2	PLKPEEAE	TLFE	ER	---	SVNAGIP	---	RREQKT	PCKLFFWKTF	
Whale_shark2	SLSPGEE	SLE	ER	---	SVNAGIP	---	RRPQKA	PCKLFFWKTF	
Elephant_shark2	PLGLSKEEG	TDFE	ER	---	SAAGEIP	---	PRKPKA	GCKLFFWKTF	
Skate2	YSNTEEAGE	RSLE	ER	---	AVVAVIP	---	RREQKA	PCKLFFWKTF	
aLethenteron	PGSSSDEEGG	EEGE	GAGG	DGGRGERALS	---	ARVRKA	GCKNFFWKTF		
bLethenteron	SLPEALVARA	LRAA	AAPG	AAGGAQLPLG	---	NRERKA	GCKNFFWKTF		
bLampetra	SLPEVLVARA	LRAA	AAPG	AAGGAQLPLG	---	NRERKA	GCKNFFWKTF		
cPetromyzon	ATRVDGLPE	FPRE	EARA	LVPNERPFVP	GALS	SPDRKA	NCRMFFWKTM		
cLethenteron	AARVVDGLPE	FPRE	EVRA	LGPNERPFVP	VVLS	SPDRKA	NCRMFFWKTM		
3Lepisosteus	VLDENS	ARLE	LER	STEIGKEIP	---	PRERKA	GCRNFYWKTF		
3Astyanax	GSKQD	VRVE	MDR	SAENPNSLP	---	PRERKA	GCKNFYWKGF		
3Clupea	GAAKDD	LHME	---	RSAETNNIP	---	PKDRKS	GCKNFFWKGR		
3Ictalurus	GTKQD	LTVE	LER	SAEDPNTLP	---	PRERKA	GCKNFYWKGF		
3Pygocentrus	GAKHD	VRVE	LER	SAENPNLNP	---	PRERKA	GCKNFYWKGF		
3Amazon_molly	AASKGTD	SRLN	LER	SVETT	---	ARERKA	GCKNFYWKGL		
3Platyfish	AASRGTG	SRLN	LER	SVETT	---	ARERKA	GCKNFYWKGL		
3Rainbow_trout	KCPAGAKED	LRVE	LER	SVGNPNLNP	---	PRERKA	GCKNFYWKGF		
3Freshwater_butterfly	AAESEG	AHLD	LER	SVEPGNVP	---	PRERKA	GCKNFYWKGF		
3Grass_carp	TVDENED	LRVE	LER	SAESSNHIP	---	ARERKA	GCKNFYWKGF		
3Goldfish	MAGESED	LRLE	QER	SAESSNQLP	---	TRVRKE	GCKNFYWKGF		
3Clown_knifefish	PAADEGEE	VRVE	LER	SVDPNLNP	---	PRERKA	GCKNFYWKGF		
3Orange-spotted	VSMATG	GRMN	LER	SVDPPNLP	---	PRERKA	GCKNFYWKGF		
3American_anglerfish	ASMATG	GRMN	LER	SVDSTNLP	---	PRERKA	GCKNFYWKGF		
3Silver_aronana	AADEEED	VRVD	LER	SLELNNLP	---	PRERKA	GCKNFYWKGF		
3White_sucker	TTGGNDD	LHLE	LER	SAENTNQLY	---	PRERKA	GCKNFYWKGF		
3Elephant_nose_fish	TAEEGEE	TRVE	LER	SVEPNLNP	---	PRERKA	GCKNFYWKGF		
3Zebrafish	TTDENED	LRVE	LER	SAESSNHIP	---	ARERKA	GCKNFYWKGF		
3Stickleback	VSAATG	GRLH	LER	SVDPPNLP	---	ARERKA	GCKNFYWKGF		
3Takifugu	VSMATG	GRMN	LER	SVDTTNLS	---	PPERKA	GCKNFYWKGP		
3Tetraodon	VSMATG	GRMN	LER	SVDTTNLP	---	PRKA	GCKNFYWKGF		
3Medaka	---	GRNN	MER	SVDANVP	---	PRNRKD	GCKNFYWKGF		
3aAtlantic_salmon	VGSTAD	AKED	LER	SVDNSNLP	---	PRERKA	GCKNFYWKGF		
3bAtlantic_salmon	GAKED	LRVE	LER	SVGNPNLNP	---	PRERKA	GCKNFYWKGF		
Elephant_shark3	DFAPD	EKAE	LRL	A	LA	PRWRK	DCKNFFWKTY		
Whale_shark3	ETPPX	NKIP	MKF	C	QOLG	TRMRK	NCKNFFWKTY		
catshark3	ETSEE	NTTP	MKF	QH	RQLG	MRMRK	NCKNFFWKTY		
Catshark1	GGRNE	VRLE	LER	SINPNLA	---	NRERKA	GCKNFFWKTF		
Whale_shark1	PRMAKQDE	VRVD	LER	SANPNP	---	QRERKA	GCKNFFWKTF		
Elephant_shark1	ARATAQDE	VRVE	LER	SANPNLA	---	QRERKA	GCKSFFWKTF		
1Human	SQAAEQDE	MRLE	LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Mouse	PQAAEQDE	MRLE	LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Monkey	SQAAEQDE	MRLE	LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Bovine	SQAAEQDE	MRLE	LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Pig	SQAAEQDE	MRLE	LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Dog	SQAAEQDE	MRLE	LQR	SANSNPAMA	---	PRERKA	GCKNFFWKTF		
1Chicken	SRGAEQDE	VRLE	LER	SANSNPALA	---	PRERKA	GCKNFFWKTF		
1Flycatcher	SRGAEQDE	VRLE	LER	SANSNPALA	---	PRERKA	GCKNFFWKTF		
1Turkey	SRGAEQDE	VRLE	LER	SANSNPALA	---	PRERKA	GCKNFFWKTF		
1Anole_lizard	SRGGAEQDE	VRLE	LER	SASLNPAL	---	PRVRKA	GCKNFFWKTF		
1Chinese_softshell_turtle	SRGPEQDE	VRLE	LER	SANPNPALA	---	PRERKA	GCKNFFWKTF		
1Frog	PRGAEQDE	VRLE	LER	SANSSPALA	---	PRERKA	GCKNFFWKTF		
1Lungfish	SRGADQDE	VRLE	LDR	SANSSPLA	---	ARERKA	GCKNFFWKTF		
1Coelacanth	SKTSDQDE	VRLE	LER	SANGNPALA	---	PRERKA	GCKNFFWKTF		
1Lepisosteus	SRAAEQDE	VRLE	LER	SANPALA	---	PRERKA	GCKNFFWKTF		
1White_sturgeon	SRAAEQND	VRLE	LER	SANGNPAMA	---	PRERKA	GCKNFFWKTF		
1Chinese_sturgeon	SRAAEQND	VRLE	LER	SANGNPAMA	---	PRERKA	GCKNFFWKTF		
1Platyfish	PEGEPED	IRVD	LER	AASSGPLL	---	PRERKA	GCKNFFWKTF		
1Tilapia	PLADGEPED	IRVD	LER	AAGSPLLA	---	PRERKA	GCKNFFWKTF		
1Elephant_nose_fish	SRGADQEE	VRLE	LER	AAGPALA	---	PRERKA	GCKNFFWKTF		
1Carp	SRAVEKDD	VRLE	LER	AAGPMLA	---	PRERKA	GCKNFFWKTF		
1Goldfish	SRAVEKDE	VRLE	LER	AAGPMLA	---	PRERKA	GCKNFFWKTF		
1Clown_knife_fish	SRGADQEE	VRLE	LER	AAGPPLA	---	PRERKA	GCKNFFWKTF		
1Orange-spotted_grouper	PLAEGEPED	VHVD	LER	AAAGSPLLA	---	PRERKA	GCKNFFWKTF		
1Anglerfish	PLAEGGPED	AHAD	LER	AASGPLLA	---	PRERKA	GCKNFFWKTF		



1Megalobrama	--SRAVEKDE	VRLE	--LER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF	
1African_cichlid_fish	-PLADGEPED	IRVD	--LER	---	AAGSGPLLA	----	PRERKA	GCKNFFWKTF	
1Cod	-----	DD	ERMD	--LER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF
1Zebrafish	--SRGAEKDD	VRLE	--LER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF	
1Medaka	-PLSDGEPED	VRVD	--LER	---	AAASGPLLA	----	PRDRKA	GCKNFFWKTF	
1Stickleback	-APAGEPEE	VHLD	--LER	---	AADAGPLLG	----	PRERKA	GCKNFFWKTF	
1Takifugu	--LAEGEPEE	VHID	--MERA	AAAGIGPFLT	----	PRERKA	GCKNFFWKTF		
1Tetraodon	--LVEGEPEE	VHVD	--MERA	ADAGIGPFLT	----	PRERKA	GCKNFFWKTF		
1Trout	--SHGVEQED	VDLE	--LER	---	APGPVLA	----	PRERKA	GCKNFFWKTF	
1Fathead_minnow	--SRAVEKDD	VRLE	--LER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF	
1Killifish	-TLPEGEPED	IRVD	--LER	---	AASSGPLLA	----	PRERKA	GCKNFFWKTF	
1Salmon	--SRGVEQED	VRLE	--LER	---	AAGPVLA	----	PRERKA	GCKNFFWKTF	
1Pygocentrus	--PRGAEQED	VRME	--LER	---	AAGPVLA	----	PRERKA	GCKNFFWKTF	
1Ictalurus	--SRAAESEG	ARLE	--MER	---	AAGPMLA	----	PRERKA	GCKNFFWKTF	
1Astyanax	--RGAEQED	VRME	--LER	---	AAGPVLA	----	PRERKA	GCKNFFWKTF	
1Clupea	--SRGAEGED	VRVE	--LER	---	SAGSMLA	----	PRERKA	GCKNFFWKTF	
1Amazon_molly	-GLPEGEPED	IRVD	--LER	---	AASSGPLLA	----	PRERKA	GCKNFFWKTF	
5Coelacanth	---DTASQDE	LTRR	--LAP	-----	-----	-----	SRRERKA	GCKNFFWKTF	
5Zebrafish	-----	LD	VRNE	--VVR	-----	QIPVS	-----	QERKA	GCRNFFWKTF
5Stickleback	---EEEAEAG	GRQE	--VMR	---	RHLPLT	-----	QERKA	GCRNFFWKTF	
5Takifugu	---GEEEAG	VREGEVMMR	---	---	ROVPFS	-----	QRDRKA	GCRNFFWKTF	
5Tetraodon	---DEEDAG	VREMMMMR	---	---	ROIPFS	-----	QERKA	GCRNFFWKS	
5Medaka	---EEELG	GRER	--LMK	---	RHIRFT	-----	HRERKA	GCRNFFWKTF	
5Soockeyess	---EALG	VREE	--VVR	---	QLPLS	-----	HRERKA	GCRNFFWKTF	
5Trout	---EALG	VREE	---	---	VRQLPLS	-----	HRERKA	GCRNFFWKTF	
5Fathead_minnow	---DDDPE	VHNE	--VVR	---	QIPLS	-----	HRERKA	GCRNFFWKTF	
5Amazon_molly	---EEEEELG	GRQR	--LMR	---	RHIRFS	-----	HRERKA	GCRNFFWKTF	
5Platyfish	---EEDELG	GRQR	--LMR	---	RHIRFT	-----	HRERKA	GCRNFFWKTF	
5Tilapia	---GDETRR	GRE	--VTR	---	RHLSLS	-----	QRERKA	GCRNFFWKTF	
5Lepisosteus	---SAEDAG	IRSD	--VPR	---	QLPLA	-----	QERKA	GCRNFFWKTF	
5Astyanax	-----	RND	--VVR	---	QLPFS	-----	QERK	GCRNFFWKTF	
5Ictalurus	-----	E	--LNR	---	ILRHLPLT	-----	TREK	GCRNFFWKTF	
5Pygocentrus	-----	RSD	--MVR	---	QLPFP	-----	QERK	GCRNFFWKTF	
Catshark5	---KGLPST	ERRG	--LPC	---	AEIVRRWNS	-----	PRDRKA	GCKNFFWKTF	
6Chicken	---EEE	GKLE	--EER	---	AALGRLAQLS	-----	QRDRKA	PCKNFFWKTF	
6Zebra_finch	---AGQEK	ARLE	--EDQ	---	AALGRLAQLS	-----	QRDRKA	PCKNFFWKTF	
6Duck	---EEE	GKLE	--EER	---	ATLGRLAQLS	-----	QRDRKA	PCKNFFWKTF	
6Lungfish	TSMDIEEPE	NKLE	--ER	---	AAYNALPQLP	-----	QRDRKA	PCKNFFWKTF	
6Coelacanth	GSMDLIEEPE	PKLE	--ER	---	AAFNRLPQLP	-----	QRDRKA	PCKNFFWKTF	
6White_sturgeon	SPMDLIEEPLD	SRLE	--ER	---	AIYNRLSQLP	-----	LRAR	PCKNFFWKTF	
6Chinese_sturgeon	SPMDLIEEPLD	SRLE	--ER	---	AVYNRLSQLP	-----	QRAR	PCKNFFWKTF	
6Lepisosteus	ASVDLIEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Carp	VPLDVEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Goldfish	VPFDVEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Orange-spotted_grouper	-PVDLIEEPE	SRLE	--ER	---	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF	
6Zebrafish	VPLDVEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Stickleback	-PVDLIEEPE	SRLE	--ER	---	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF	
6Takifugu	---DLIEEPE	SRLE	--ER	---	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF	
6Tetraodon	---DLIEEPE	SRLE	--ER	---	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF	
6Rainbow_smelt	-PLDLIEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Trout	SPVDLIEEPE	SRLE	--ER	---	AAYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Medaka	-PVDLIEEPE	SRLE	--ER	---	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF	
6Fathead_minnow	VPMDAEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Astyanax	VPMDAEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Pygocentrus	VNMEVEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Clupea	APLDLIEEPE	SRLE	--ER	---	AVYNRLSQLP	-----	QRDRKA	PCKNFFWKTF	
6Ictalurus	LPLEEEEPID	SRLE	--ER	---	AVYNRLAQLP	-----	QRDRKA	PCKNFFWKTF	
6Amazon_molly	-PVDLIEEPE	SRLE	--ER	---	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF	
6Cod	-PVELEEPE	SRLE	--ER	---	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF	
6Platyfish	-PVDLIEEPE	SRLE	--ER	---	AVYNRLSLP	-----	QRDRKA	PCKNFFWKTF	
Catshark6	-FPDPEDVEE	MKVE	--ER	---	SRFSQLP	-----	QERKA	PCKNFFWKTF	
Elephant_shark6	-YPEPADGGP	VMLE	--ER	---	SRYSQLP	-----	QRSRKV	PCKNFFWKTF	
whale_shark6	-FPDQEDMEE	MKVE	--DR	---	SRFSQLP	-----	QERK	PCKNFFWKTF	
4Lepisosteus	---VLDENSD	ARLE	--LER	---	SADMGKVIP	-----	PRERKA	GCRNFFWKTF	
4Zebrafish	LGSLSGLEL	MRRD	---	---	I	-----	KEERK	GCRNFFWKS	
4Takifugu	---DTENQEK	NRRD	--LDN	---	---	---	VQQRQF	GCRNFFWKS	
4Medaka	---EKQEK	NRRG	--VEI	---	---	---	ATQR	PCRVFFWKS	
4Tetraodon	---DTNQEK	NRRG	--LDN	---	---	---	VQQRQA	GCRNFFWKS	
4Channel_catfish	---EEAPR	SRLE	--LVRR	DNTVTSKPLN	-----	---	---	CMNFFWKS	
4Stickleback	---AEEPEK	NRRG	---	---	---	---	KTTRRF	GCRVFFWKS	
4Atlantic	GPESVGPES	RRET	--IPC	---	---	---	SRVRKE	GCKVFFWKS	

2Human	SSCK-
2Mouse	SSCK-
2Pig	SSCK-
2Bovine	SSCK-
2Monkey	SSCK-
2Lizard	SSC--
2Frog	TMC--
2Coelacanth	SSC--
2Lepisosteus	SSC--
2Astyanax	SAC--
2Pygocentrus	SACQH
2Clupea	SSC--
2Ictalurus	SSC--
2Zebrafish	SSC--
Catshark2	SHC--
Whale_shark2	SHC--
Elephant_shark2	SHC--
Skate2	SHC--
aLethenteron	TSC--
bLethenteron	SSC--
bLampetra	SSCX-
cPetromyzon	AAC--
cLethenteron	AAC--
3Lepisosteus	TSC--
3Astyanax	TSC--
3Clupea	TSC--
3Ictalurus	TSC--
3Pygocentrus	TSC--
3Amazon_molly	TSC--
3Platyfish	TSC--
3Rainbow_trout	TSC--
3Freshwater_butterfly	TSC--
3Grass_carp	TSC--
3Goldfish	TSC--
3Clown_knifefish	TSC--
3Orange-spotted	TSC--
3American_anglerfish	TSC--
3Silver_aronana	TSC--
3White_sucker	TSC--
3Elephant_nose_fish	TSC--
3Zebrafish	TSC--
3Stickleback	TSC--
3Takifugu	TSC--
3Tetraodon	TSC--
3Medaka	TSC--
3aAtlantic_salmon	TSC--
3bAtlantic_salmon	TSC--
Elephant_shark3	TLC--
Whale_shark3	TLC--
catshark3	TLC--
Catshark1	TSC--
Whale_shark1	TSC--
Elephant_shark1	TSC--
1Human	TSC--
1Mouse	TSC--
1Monkey	TSC--
1Bovine	TSC--
1Pig	TSC--
1Dog	TSC--
1Chicken	TSC--
1Flycatcher	TSC--
1Turkey	TSC--
1Anole_lizard	TSC--
1Chinese_softshell_turtle	TSC--
1Frog	TSC--
1Lungfish	TSC--
1Coelacanth	TSC--
1Lepisosteus	TSC--
1White_sturgeon	TSC--
1Chinese_sturgeon	TSC--
1Platyfish	TSC--
1Tilapia	TSC--
1Elephant_nose_fish	TSC--
1Carp	TSC--
1Goldfish	TSC--
1Clown_knife_fish	TSC--
1Orange-spotted_grouper	TSC--
1Anglerfish	TSC--



1Megalobrama	TSC	--
1African_cichlid_fish	TSC	--
1Cod	TSC	--
1Zebrafish	TSC	--
1Medaka	TSC	--
1Stickleback	TSC	--
1Takifugu	TSC	--
1Tetraodon	TSC	--
1Trout	TSC	--
1Fathead_minnow	TSC	--
1Killifish	TSC	--
1Salmon	TSC	--
1Pygocentrus	TSC	--
1Ictalurus	TSC	--
1Astyanax	TSC	--
1Clupea	TSC	--
1Amazon_molly	TSC	--
5Coelacanth	TSC	--
5Zebrafish	TSC	--
5Stickleback	TSC	--
5Takifugu	TSC	--
5Tetraodon	TSC	--
5Medaka	TSC	--
5Sockeyess	TSC	--
5Trout	TSC	--
5Fathead_minnow	TSC	--
5Amazon_molly	TSC	--
5Platyfish	TSC	--
5Tilapia	TSC	--
5Lepisosteus	TSC	--
5Astyanax	TSC	--
5Ictalurus	TSC	--
5Pygocentrus	TSC	--
Catshark5	TSC	--
6Chicken	TSC	--
6Zebra_finch	TSC	--
6Duck	TSC	--
6Lungfish	TSC	--
6Coelacanth	TSC	--
6White_sturgeon	TSC	--
6Chinese_sturgeon	TSC	--
6Lepisosteus	TSC	--
6Carp	TSC	--
6Goldfish	TSC	--
6Orange-spotted_grouper	TSC	--
6Zebrafish	TSC	--
6Stickleback	TSC	--
6Takifugu	TSC	--
6Tetraodon	TSC	--
6Rainbow_smelt	TSC	--
6Trout	TSC	--
6Medaka	TSC	--
6Fathead_minnow	TSC	--
6Astyanax	TSC	--
6Pygocentrus	TSC	--
6Clupea	TSC	--
6Ictalurus	TSC	--
6Amazon_molly	TSC	--
6Cod	TSC	--
6Platyfish	TSC	--
Catshark6	TSC	--
Elephant_shark6	TSC	--
whale_shark6	TSC	--
4Lepisosteus	TSC	--
4Zebrafish	TAC	--
4Takifugu	TYC	--
4Medaka	AKC	--
4Tetraodon	TSC	--
4Channel_catfish	TAC	--
4Stickleback	SPC	--
4Atlantic	TAC	--

## Figure S3

### A. Catshark SST1 (SSTa)

gctgtccacagagccagtgctgaaaccaccgccaatttcaaagcgtttgtaa  
atgtggtgcagccgcttcagttgagcctggctctcctctccatcgccctggcagtagt  
M W C S R L Q L S L A L L S I A L A V L  
agtgtcagctcagcaccacagacaacaggtatcgcgaaatcctgcagagagccatggca  
S V S S A P T D N R Y R E I L Q R A M A  
gccacaggaagcggaggaaagcggagttgacgaaatattccctcgcccaactgctctcc  
A T G S G G K A E L T K Y S L A Q L L S  
gaactggaaaacgcgagagaatgaagctctggaaacggatgcaatggcggagcgaacgag  
E L E N A E N E A L E T D A M G G R N E  
gtgcggctcgaactggagatcgataaatcccaacctggcgaacagggagcgaanaagcg  
V R L E L E R S I N P N L A N R E R K A  
ggatgtaagaacttcttttggaaaaccttcacatcctgttaactctccgaattctccata  
G C K N F F W K T F T S C -  
gcaaccacacactcagaatgtggcattcagataactaaataaatcatgtggtgaatgat  
tctatttgaattatgtaagagaagacaattggtttgaattgtccaatagcaggccagttt  
gaatggtgactggatagagtcgctatcttttccattaatctgttgcaataaaatctctgtt  
gaaattg

### B. Catshark SST2 (SSTd)

tttagcattttgtccaggagtgctcgaagattcagc  
atgaagtggctaatacagctgagcctgatgtctctgctgtaccttctgagagtcgagggg  
M K W L M T V S L M S L L Y L L R V E G  
actgacctactggaagaaagaatgaaacttcaggtaaacagagaaatgacaaaaagcagg  
T D L L E E R M K L Q V N R E M T K S R  
aagaatctgattgtaaagctactggctggcttggttggagactgatgataatctcttgag  
K N L I V K L L A G L L E T D D N L L E  
aatggctttgcacctttgaaaccagaagaggcagaagggactttgttcgaagagaggtcg  
N G F A P L K P E E A E G T L F E E R S  
gttaacgctggaattccacgcagggagcaaaaaaccccatgcaaactgttctcttgaaa  
V N A G I P R R E Q K T P C K L F F W K  
accttttccactgttaataaccgtgtagcggatcttctaaagcagtgaggatgataaaa  
T F S H C -  
gaaaaatgggtgtaaaggcttaacttttaaaactatcgaaaatacactgcaatcatgtttt  
tctctatcccaaatattttaattcaaatttacaggaaatgcttgcaataaagttaacctga  
aagttacaccttttaagacatgtgaaattattgtgttttaaatgagatagcaatccagtt  
aaactttctcagtttggttctatcatgcctgttatttccctgttttccagcattgtttt  
ctctctcagttcctcgctttcctttggcatgttagccccctctctccacagaatgct  
cctgggattccgtaactctccccctcgctttacctttccctctttcgctagacgaatgttt  
ctgaaagattgcacctgccccctgacacagccggctgggacttctggaagcacttgaattt  
tgccagacacaatttgggatattttctgagttaaagcctatatatatgttgacagtgacc  
tttctcttgatcgtagatctgagcatattgtaatggtgttaattgttttgaccagtct  
atctgcatacaatgtacatacttctcgaatatcctgtgagtaatgctaacaataaa  
agaca

### C. Catshark SST3 (SSTe)

acatgg  
ggagagacagtgctgaaacgcctctccactttccgctcggttctctcgcttgtgcagag  
atgtggtgcagccgcttcagttgagcctggctctcctctccatcgccctggcagtagt  
M W C S R L Q L S L A L L S I A L A V L  
agtgtcagctcagccccacagacaacagggcatcgcgaaatcctgcagagagccctggat  
S V S S A P T D N R H R E I L Q R A L D  
caggaacttctgaaggacacaatgatgaaactgttgccctttggttactgatgtagact  
Q E L L K D T M M K L L P L V T D V D T  
gaggccggaacactggatgtttccaatgctgagacttcagaagaaaacacaacaccgatg  
E A G T L D V S N A E T S E E N T T P M  
aaattccagcatcgtagttgggaatgagaatgcggaaaaactgcaagaacttcttttgg  
K F Q H R Q L G M R M R K N C K N F F W

aaaacctacactttatgctaatccactgtacccagtgagcccttctcactggaccctgct  
K T Y T L C -  
gtacccac

**D. Catshark SST5 (SSTb)**

tcgaccctcgcgctccggagcagttacacagagaagctcgccctcgcccactgcccga  
cgagacagtttgccaatcgttcccatctcccactccgcagtaagaaaatcagagctcgag  
atgccgagatcgagactcaagtcctcctcactctgggcactgctcgctctgctgttactg  
M P R S Q T Q V L L T L V T V A L L L L  
cggggatcgagtacagccagagtgaggggctgcccgatattcttacaggagaggaacgac  
R G S S T A R V Q G L P D I L Q E R N D  
gaggggactgaggagctgtccaggaccatgggtgctgaacctcctctccgagctgctccat  
E G T E E L S R T M V L N L L S E L L H  
gctggggacaaggggttgcccagcaccgagagagcgggagcttcccaggctgagatcgtc  
A G D K G L P S T E R R E L P Q A E I V  
cgccgggtggaactcaccgcccggaccgcaaagcaggctgcaagaacttcttttgaaaacc  
R R W N S P R D R K A G C K N F F W K T  
ttcacctcttgtaacgtgcccggagagagagaggggaaagagaaagtgagccggcgggggga  
F T S C -  
gagatataaagagaattcctccctctcccaaaaccatcttcagctcctgaagggaggca  
aaaaaaaaatcaattgcctctaactttagattttaagattcaciaatcccaaccacctcc  
gtccctcgaaagattgcctccccctttgggctgctctccgctgaggatttctctgtgtc  
tttatccaaggtgtttgtaaattgattgacttgtttgctttgttctctgagcatggacttg  
ctctcacatcataaaatatctttattttctcagcaaaaaaaaaaaaaa

**E. Catshark SST6 (SSTc)**

tcgaccctcgcgctccgccaaggtcgaggcaca  
ttgagaagatctcgccaggctccgcttcattccaacttcacaagatcgagagtgctcagc  
atgcagttgctgggaacggcgagcctcctgtccatgctgctcatcggtgctccagtggtgagg  
M Q L L G T A S L L S M L L I V S S V R  
gccacggcacctttggaagatcggctgagctctgcccggcaaatcaggagctgaacaaagaa  
A T A P L E D R L S L R A N Q E L N K E  
aggaaagaggtcattttgaaagctgttatccggactgcttgactccagcagcaatcaatc  
R K E V I L K L L S G L L D S S S N Q I  
gcgattgagaacactttcccggatccagaggatgtggaggagatgaaagtggaggagagg  
A I E N T F P D P E D V E E M K V E E R  
tcccgttccagccagttaccgagagagagcgcaaggctccctgcaaaaacttcttttgg  
S R F S Q L P Q R E R K A P C K N F F W  
aaaaccttcacctcctgctgacgacagacaatgccacctggctgccaactaaagccgccc  
K T F T S C -  
agaaaggaactgatttagcactgtacataagctgctttttattttatttcatctgtgaggg  
gtgggtggaggtggggggggggttaatattttctgctcgtgcacaagaaaaataaaaagagc  
atgattgtgtgatttcaccgcaacctgtatgtattttattttctttccagtaatgtgtgc  
cgctcaacctgcccagagcaataaagtggatccgagataaaaaaaaaaaaa

# Figure S4

## A. Catshark SST1 = SSa (scaffold122178)

AACAGAAGTAAAATGATACCTGGTCCCAGTGTGTAATCTGTAACAGCCCCATTTCTGTGGCATTTC AAT  
GAAAAGCTAGTTTAAACCTGACGAATACAGTGGAGTTATTGAGATGAACACATTGCAGATTGGCACATGT  
GGGCCACAAAGAGAACACGCTGTAAAATCACAACTACACACAATTATTAGATGGCAGCGAGTCTTTC  
CCCAGGAAACATTCCCTTATTCTGTCTCACTCAGTCTCTAACTTTGTACATTAGTTCAGTTCAGTGGGATTACC  
CAACCCATTCCCCACTGATCCAGTGTGTTCAATGCTCAAGGAAGATTGAGATTTATGGATGAGGGTGT  
ACTGGGGATTGATGTTCACTTTTTCCACGGATTTTCTAGTTGAAGACTTGGCTGCATTTCATTTGTGATC  
GACACGAACCAATAACAATCGTAGGGCCAGCTGCCAACACGCGATAGGGTGTCCACATTGAGACTCCATGG  
ATCTATCTCAATCTTCCCTCATGGGTAATGGGTTGGTTGAGGATGTGACTGGGTTGTGCGTAAATACTCGT  
CATCTCCTGGGACCCTCCTCCCAACGTGTGAGCTGGTGTGAAGGCGGCTTTAAAAGGAGCTTCCCCGATT  
GCAGGGACAGAAGGAGCGGAGCTGTCCACAGAGCCAGTGTGAAACCACCGCCAATTTCAAAGCGTTTGG  
AAACTGCTCTCCTTCTCGCTGTCTCTCCCGTTGATCTTCGCTTGTGCAGAGATGTTGGTGCAGCCGCTT  
M W C S R L  
CAGTTGAGCCTGGCTCTCCTCTCCATCGCCCTGGCAGTACTGAGTGTGAGCTCAGCACCACAGACAACA  
Q L S L A L L S I A L A V L S V S S A P T D N  
GGTATCGCGAAATCCTGCAGAGAGCCATGGCAGCCACAGGAAGCGGAGGGAAAGCGCTAAGGACCAGCA  
R Y R E I L Q R A M A A T G S G G K A  
AAAAGTCACATTCAATAGAAATGGTAGTTTGTGTTTCATCCCGTTCACCTCGAATAGAAACAGGGACTGGG  
AAATAACTGGTTCAATTCTGATCTAGTGAGAAGACCCACTTTAACAGGACTATAATATTGAGAGTGAAT  
TGGCTTTGTTTAGTGTGGGGATCATTTCATTGGTTTAGAAAGGTTTCTGAGCGCGTTGATCCAAAATTAC  
TGGATTTCTCGTGCATCGAGTAAAATCTCGTCTCTCCAATCCATAGCCACTCTGCACAAAAGAGTAACAG  
ACAAGAAGTAGACATCGTTCCACAATCCCAGAGAACTTACTGCTCTTCTCTCTTCCCAAACCTGCTCTCC  
CATCTTAACCCCAACCCCTCCTCTCTCCCCAAATCCCGTCTCCCATCCCAACCCCAACCCCTCCTCTCTCC  
CAAATCCCCTCTCCTGTCCCAACCCCAACCCCTCCTCTCTCCCAAGCTCCCAACCCCCCTCTCCCATCC  
CAACCCCAATCCCCTTTCTCCCAACCCCTCTCCCAACCCCAACCCCTCTCTCTCCCAACCCCTCTCTCC  
CCTCTCTCCCAACCCCAACCCCTCTCTCTCCCAACCCCTCTCTCTCCCAACCCCTCTCTCTCCCAACCC  
TTGGTCTGTTTATCATTTGAAGACGAGCACCTGAGTCTCTCTCAGTCACCTCCAATAACCATCTAGAAT  
GGGGCAGCTGAATCAAATCTTGCAACCAAGTCATTTCAGTTTGAAGAAATATTTCATTACAATTATGTTTT  
CAATTGCCTTCATGTTGAAAAGAACTCCGAGCACGGGGATTGGTTCCCTTCCAGAGATTTTCTCGCTCTT  
TCCAATGTCCACCTCCCTTTGAAGGGTTCAGAATTGTGGTGGATGGAATGGAGTTCCGGGGTGGAGTGGGA  
GGGGGTTTGGGCAGTTCAGGTCTCTATTTGCGAATTGGGATCTTCCCGCCGGTTGCAATGGAGAAATAT  
GAAGATAAATGAAGATAATTTACAAAGTTGAATTTAATTCATTGTAGATTTATTTCGGGGAGTTTGCAA  
CTTTTCGTTTGCAAAACAAACGTAATATAGCGTCAATTGGCGGAAATTTCTCCCTAATCTATTTCCTGT  
TGTTCTCAGGAGTTGACGAAATATTCCTCGCCCAACTGCTCTCCGAACTGGAAAACCGGGAGAATGAAG  
E L T K Y S L A Q L L S E L E N A E N  
CTCTGGAACGGATGCAATGGGCGGACGCAACGAGGTGCGGCTCGAACC GGAGAGATCGAGAAATCCCAA  
E A L E T D A M G G R N E V R L E P E R S N P N  
CCTGCCGAACAGGGAGCGAAAAGCGGGATGTAAGAACTTATTTTGGAAAACCTTCACATCCTGTAACTC  
L P N R E R K A G C K N L F W K T F T S C -  
TCCGAATTCTCCATAGCAACCCACACACTCAGAATGTGGCATTTCAGATAACTAAATAAATCATGTGGTGA  
ATGATTCTATTTGAATTATGTAAGAGAAGACAATTGGTTTGAATTGTCCAATAGCAGGCCAGTTTGAATG  
GTGACTGGATAGAGTGCCTATTTTTTCAATTAATCTGTTGCAATAAAATCTCTGTTTGAAGTGGACCATT  
GTTGGATTTGTTCTCTGGGAGATGGGGCAATATAACAAGGGACAGAATTAACCTCGGCTAGTTTCAACA  
CCAGTCTGTGTCCAAAGGTACAGAGCGAGGGGAGTCATTTTCCACAGTTGTGACTTTGTAATCAGTCT  
GGGTGGAATCGCTCTGGGTCAGTCTCTGATCTGGGAAATGTGTTGCTGGAAGTTCCCTCCGCTATTCA  
AACTCAGAGGAGACAATGAATGGACGGATATTAAGGGGGTTCTGCTCTGTCCAATGCAACCGTGTCTG  
TGAGTGTGTAATCTGCAGGAGAGCAAATATTACCTGCATCACACTGGTAAAAGTCTAACCCCTGGTCA  
ATGAAAGCATCAATCCACAAATCACAAACCTGCTTCCAGCCTTCCCTTGTAAAAGCCGGTTTCCATTCTAA  
CCTAGCGGCACGGTAGCACAGTGGTTAGCACTGCTACTTCACAGCGGCAGGGTCCGGGGTTTCGATTCCCA  
CTTGGGTCACTGTCCATGCGGAGTCTGCACGTTCTCCCGTGTCTGCGTGGGTTTCCCTCCGGGTGCTCCG  
GTTTCCCTCCCAAGTCCCGAAAGACGTGCTGTTGGGTAATTTGGACATTTCGGAATTCCTCTCTGTT  
CCCGGACAGGCACCAGAATGTGGCGACTAGGGGCTTTTACAGTGGAAATGTCAGTGGAGGTTCTGTACA  
ATACCAATGTTCCGTACAGGTGTTGAATTGTGTTCTACACAGGAAATTCCTTCCATCATCCCTATTAT  
GTCTAGAAACATAGAAAATAGGTGCAGGAGGAGGTCATTTGGCCCTTTGAGCCTGTTCTGCCATTCAATTA  
TGATCATGGCTGATCATCCAGCTCAATAGCCTTCTCCAGCGTTCCCCCATATCCTTTGATCTCCTTCACC  
ATAAGTGTATATCTAACTGCTTCTTGAATAATATTGAGAGGGATTCTCCATCCTGCCACACCAGGAGC  
TGGATTCTCTGCCGTGCGGATTCTCTATTTTGGCAGAAGCACGGGGTTTCCCAACAGCGTAGGGTGGCC  
CCACAAGGAGAAACCCCGTTGACCAGCTGGCGAAACGGAGAATCCCGATGGCATATGGTGGGACAGAGAA

ACCCGCCCCAGATTTCTGATGCGGCATGTCTGTCGGGATTCTCCATTTTCGCCGACTGGTCAATGGGGTTTC  
CCATCATGGGGCAGCCCCATGTCTGTCGGAAAACCCCTTGGGCTGGGGGTAAAATGGAAAATCATGATGCC...

**B. Catshark SST2**  
(scaffold 83887)

...CACTCTTTCTCAAAAAGCAGTGGACGCAGTCTTAAATATGTTCAAGACAGAGGTAGATAGATTCTTGAA  
AGGTAATGGGGTGAAGGTTGTTGGGGGTAGGCGGGAGATTACAGTCCGATGGGCCATGATCTTATTGAA  
TGGCAGATCAGGCTCGAAGGGCCGAGTGGCCTACACGTCTTAGTTCTATGTCTGTAACATCCGACA  
CTTTGGAGAAGAATATTTTTGATTGTGTGTCAGGAATCCAGCCCTCCAGAATTTTCCAGGGTGCTAATAAT  
CAGTTTTTACTTAGATTTCTAGTCAACCTACAGGTTTTAGATTTTGTATTTTCTTATACTGCATTGGAGGG  
TCAGTTGTTGAACAGCATCCATCCAATTCACCTTTTATAAATTCTAAAAATATAATTTTGTTTAAATGGC  
TGGAACATTCTTGGATTGGAGGCTATAAAGCTCTTTAATGGCTGCTTCATTCAAATTGAACTGCAATTTT  
AACTGTCCACATTACAGATCCTTCATCTACTTGGCCATAAATTTACAGAACGTAAAAGTGTAATATAATC  
AGTCAGGTATGTTCTTCTGAATTAATATTCCTCCATTTACGATAACGCAAACCTGTTACTCCTTATATA  
CATATTGTTTTTCCAGGCCTGTATTGGGTTAATGATGCACACTGGCTATTAGGCTTTGATTGTATCATTAAT  
TTTGTGCGTCAGAGTTGCTTCTGCTGTGCTATAAAGAGCTGGAAACACTTTTCGGAAAAATAGATTGAGG  
AGTTCACAATACATTTAGCATTTTGTCCAGGAGTGTCTGAAGATTGAGC

ATG AAGTGGCTAATGACAGTG  
M K W L M T V

AGCCTGATGTCTCTGCTGTACCTTCTGAGAGTTCGAGGGTACTGACCTACTGGAAGAAAAGAAATGAAACTTC

S L M S L L Y L L R V E G T D L L E E R M K L  
AGGTAAACAGAGT GAGTAGAAAGATCATTACTAAATGCACAGAGGTGGCGGCAGTGTGGTGAAGGGGTG  
Q V N R

GGAGGGACGAAATCCACAGCCATAAGGAGAGAATTGACGTAAAAATATTGGGAAAATTATGTAGAGAGAT  
GAGAGACAATGGGATTGTTCTCTAATGCTAGGAGATTAAGGGAAGACTTAATAGAGGTGTTCAAAAATA  
ATGAGAAAGCGTTTTCCACAGGCAGATGGGCCGGTACCACGAGGAGAACATTTTAAACTAATTGATAAAA  
GAGCAAGAGGGAGCGATGAGGAAAATTGTTTTTTACATCGTCAATCATTATAATCTGAAACGTGTTGCCT  
GAAAGTTGATGGAAGCAGATTCAATAGTAACTTTTCAAAGGACTTAGATATATACTTGAAGGTTGGAAA  
CTTGCAGAATATCAGGAAGAGGGGAGGGAGCACTATAAATTCTGCACTGTAAATCTATGATTACGTTA  
AGGCAGGAAAATGGAAGTAATTGAGTAGCTCTTTACAAAGGGCTGGTATAGATGTGATGGGATGAATGCC  
CTTTTTTGCTGTAAAGTTCCATGAAAGCCAACATCAGCAATAATCAGACTTTCAGATTTCCAGCATCCAC  
ACTATTTTGCTTTAATCAGCATTAAATATATCATCAAGGGATCTGGTAGTGGGTAGTTGTCTTACTGGACA  
AGATTAATAATCACGAGAATTTGAGTTCAAAAACCACCATGGCAGTTTGAAGAACTCGAATTTGGTTTTGAA  
AATAAATCTGGAAACAAGAACTGGTTTTAGTCAAAGACGTAAACTGTCCGATTGTCAAAAACCCCTCAA  
CTGGTTCGTCAATACCTTTTTTTAATATAAGTTTAGAGTTCCAATTAATTTTTTTTCCAATTAAGGGGCA  
ATTTAGCGTGGCCAATCCACCAACCCTGCACATCTTTTGGGTTGTGGGGGTGAGACCCACGCAGACACGG  
GGAGAATGTGCAACTCCACACGGACAGTGACCCGGGGCTGGGATCGAACCTGGGGCCTTGGCGCTGTGA  
GCCAGCAGTGTAAACCCACTGCGCCACCCTGCTGCCCTGGCCAATACCTTCTAAGGAAGAAAATGATCT  
GGCAGGTATCCTGGGCCATAGCAATCTGTTTTGGCTGTTAACAGATTTCTTAGTGACCTAACAGCCACAC  
AGGTTTAAACCAGGATGGCAATAATGTGCCAGTCCGACTTGAATTTCTGTGAAAAGATCAGAAAACCCGGC  
GCAGACTGTTCTTCGGGAAAATTGCTGATTAAAGTTTGGTGGATTTACTTTAAACTAGTGGAAACATTAT  
TGAAAGGACCTGTGGACCTGAACAAGCTCGACACTCATTTTTTGCCTTTAATCTAATGTCTTTCAGGGAAT  
GAAATCTGCCGTCTTACCTGGTCTGGCCTACATGTGACTCCAGATCCACAGCAATGTGGTTGGACTCTT  
AACTGCCCCCTCAAGGGCAATTAGATATGGGCAATAAATGCTGCCAGCCTGCGACGCCCATGTCCCTTG  
AGCGAATAAAAATAAATCAGGCCAAGTACAAAAATATATTGAGGGAACAGAAAGATTTAGGCTTAGGGAT  
GTTCCGAGTTGGCAAGATATGCAGAGGGTAGCAACGAGTAAACTGTAACAAAACCTGGGTCAATGGTGGGAA  
TAATGGTTGGAATAAAGTGTAAAAGACAATAAAGAGCTGAGCTAGATCTGAGTGAGTGATTCATGTT  
TGGCATCAACAAACAAGTGCCTTGCAATGAAATGAAAACGAAAGCTTTCTATTCTCTGTTTATCCACAAG

GAAATGACAAAAGCAGGAAGAATCTGATTGTAAAGCTACTGGCTGGCTTGTGGAGACTGATGATAATC

E M T K S R K N L I V K L L A G L L E T D D L

TCTTGGAGAATGGCTTTGCACCTTTGAAACCGGAAGAGGCAGAAGGGACTTTGTTCGAAGAGAGGTCCGGT

D L L E N G F A P L K P E E A E G T L F E E R S

TAACGCTGGAATTCACGCAGGGAGCAAAAACCCCATGCAAACTGTTCTTCTGGAAAACCTTTTCCCAC

V N A G I P R R E Q K T P C K L F F W K T F S

TGT TAA TAACCGTGTAGCGGATTTTTCTAAAGCAGTGGGAGTATGAAAGAAAAATGGGTGTAAGGCTTA

H C -

ACTTTAAACTCGAAAATACACTGCAATCATGTTTTTCTCTAGCCCCAAATATTTAATTCAAATTTACAGG  
AAATGCTTTGC AATAAA GTTAACCTGAAAGTTACACCTTTTAAAGCATGTGAAATTAATTGTGTTTTAAATG  
AGATAGCAATCCAGTTAAACTTTCTCAGTTTGTCTTATCATGCCTGTTATTTCCCTGTTTTTCCAGCAT  
TGTTTTCTTCTCAGTTCTCGCTTTTCTTTGGCATGTTAGCCCCCTCTCTTCCCACAGAATGCTCCTG  
GGATTCCGTAATCTTCCCCCTCGCTTTTACCTTTTCCCTCTTTCCCTAGACGAATGTTTCTGAAAAGATTGCA  
CCTGCCCTGACACAGCCGGCTGGGACTTCTGGAAGCACTTGAATTTTGCAGACACAATTTGGGATATT

TTCTGAGTTAAAGCCTATATATATGTTGACAGTGACCTTTCCTCTTGATCGTGAGATCTGAGCATATTGT  
AATGGTGTTAATTGTTTTGACCAGTCTATCTGCATACAATGTACATACTTATCTCGAAATATCCTGTGA...



TCCCCAAGTCCCAACGTCTCAAATATATCCATAACAACCTGAATTTCAACAGAATTGTGACAACGCAGAAAAG  
AGCCCTTTTGACCCATGGTGTGGTGGCTCTCAAATCAGCATCATGATAATGAAATGAAATGAAAAT  
CGCTTATTGTACAGAGTAGGCTTCAATTAAGTTACTGTGAAAAACCCCTAGTTGCCACATTCTGGCGCCT  
ATCCAGGGAGGCTGGTATGGGAATCGAACCATGCTGCTAGCCTGCTTGGTCTGCTTTAAAAAGCCAGCGAT  
TTAGCCCAGTGAGCTAAACCAGCCCCTATTTTGTGCCAATCCCTTGCAATTTCCCTACTCCTGAACATT  
GTTTCTGTTCAAGTAACCATCTAAAGCCCTCTTGAACCTCTCAATTGAACCTGGCTCCCCACACTACTA  
GACAGTGCATTCCAGACCCAACCACTCACTGTGTGAAAAAAAATCTAACATTACATTTGTTTCTTTTAC  
AAATCGCATTAAATCTGTGCCCTCTCATTCTTGATCTTTTACCTGCGGAAACAGTTTCTCCCCGTCTACT  
CTGTCCGGCCCCCTCATGGTTTTTAAGCATCTCTATCAAAGCTCCTCTCAGCCTTCTCTCCAAGGGGAACA  
GTCCCAACCTCCCAATCTATCCTCACAACCTGAAGTTTCTCATCCCTGCAACTGTTTTTGTGAACCTCTT  
CTGCCCTCTCTCTACAATACATTACATCCTTCTATGGTGTGGTGTACAGAACGGTGCACAATACATCA  
ATTGAGAGTCTATGTTAATGTCTTGTATAAAATTTAACATAACCACATTACTCTTGTACTCTATTCCCTTG  
TTTCTAAAGCCTGGTATACTGTGTATTCACTAAGCTCTCCATCTGTTGTACCACCTTCAATGATCT  
ATACATACACACAGGTCTCTCTGCTCCTGCACCCCTTAAAGAAATTTTATGCTTGATTTTATATTGTCTCTC  
CATTGTGGGCAGCACGGTAGCACAGTGGTTAGCACTGTTGCTTACAGCACCAGGGTCCAGGTTTGTATT  
CCCGGCTTGGGTCACTATCTGTGTGGAGTCTGCATGTTGTCCCATGTCTGCATGGGTTTCTCCGGGTG  
CTCCAGTTTCTCCACAAGACCCAAAAGACATGCTGTTGGGTGATTGAGCATTCTGAATTCTCCCTTC  
GTGTACACAAACAGACGCAGGAGTGTGGCAACTAGGGGCTTTTACAGTAACCTCATTGCAGAGTTAATG  
TACAACCTGTGACAATAAAATATTATTATTATTATTATGTGACTCCTCCCAAAATCCATCACCTCACACT  
TCTATGCACTGAACCTCTATCTGCCATCTATCTGCCCACTCCACCAACTTGCCATGTCTTTTGGAGGTT  
TATACTGTCTCCTCACAGTTTACAATACTTTCAAGTTTTGTATCATCCACAAACTTTGAAATTTGTTGGG  
CAGCACAATGGCGCAGTGGTTAGCTCTGGGACTGCAGCACCGAGGACCCGGGTTTGAATCTCAGCCCTGG  
TCACTGTCTGTGGAGTTTACACAGAACATAGGGCAGCACGGTAGCATTGTGGATAGCACAATTGCTACAC  
AGCTCCAGGGTCCCAGGTTTGTATTCTGGCTTGGGTCACTGTCTGTGTGGAGTCTGCACATCTCCCCGTG  
TGTGCGTGGGTTTCTCCGGGTGCTCCGGTTTCTCCACAGTCCAAAGATGTGCAGGTTAGGTGGATTG  
GCCATGATAAATTGCCCTTAGTGTCCAAAATTGCCCTTAGTGTGGTGGGATTACTGGG

(scaffold 604248)

GTACGAGACAAGTTTTTACACAGAGGGTAGTGGGTGCCTGGAACCTCGCTGCCGGAGGAGGTGGTGGAAAGC  
AGGGACGATAGTGACGTTTTATGGGGCATCTTGACAAACACATGAATATAGTGACACAGTGGTTAACACTG  
TTGCTTACAGTTCCAGGGTCTCGGGTTTGATTCTGGCTTGGGTCACTGTCTGTGTGGAGTCTGCACGT  
TCTCCCATGTCTGCGTGGGTTTCTCCGGGTGCTCCGGTTTCTCCACAGTCCAAAGGCGTGCAGGTT  
AGGTGGATTGGCCGTGATAAATTGGCCTCAGTGACCAAAAGGATAGCTGGGATAACGGGGATAGGGTGA  
GGTGTGGGCTTAGGTAGGATGCTCTTTCCAGGGGATGGTGCAGACTCGATGGGCCGAATGGCACTGTAAA  
TTCTATGATCCTATGGTGAGGATGGGAATAGAGGGATACGGACCCCGGAAGTGCAGAAGATTTTAGTTTA  
GACGGGCAGCATGGTGGGCGCAGGCTTGGAGGGCCGAAGGGCCTGTTCTGTGCTGACTTTTCTTTCTT  
CTTAAGCACCTAACGTGACACCAAGCAACTGAAACACAAAGGATTCAAATTAATTTGAACAGGAGTCC  
TGTTGGATTCCGAGATTTCTTTCCACAGAAGCTGCCGGACTTTCTGGATTTCTCCAGCATTTTATTATT  
TTACATTGCACAATCCAAACTTCTGTTTCTAACAGACTTTAATTGCTTCCTTTCAAGAACTTCTGAAGGA  
E L L K D  
CACAAATGATGAAACTGTTGCCTTTGGTTACTGATGTAGACACTGAGGCCGGAACACTGGATGTTTCCAAT  
T M M K L L P L V T D V D T E A G T L D V S N  
GCTGAGACTTTCAGAAGAAAACACAACACCGATGAAATTTCCAGCATCGTCAAGTTGGGAATGAGAATGCGGA  
A E T S E E N T T P M K F Q H R Q L G M R M R  
AAAACCTGCAAGAACTTCTTTTGGAAAACCTACACTTTATGCTAAATCCACTGTACCCAGTGAGCCCTTCTC  
K N C K N F F W K T Y T L C -  
ACTGGACCCTGCTGTACCCCACTGCACCCCACTGACTCCATCCCACTGTACCC



D. Catshark SST5 = SSb

(scaffold 888145)

GTGGAGAGTGTACGGGGCTAGGGGAAGAACCTTGAGGTGGGGCGATGAAAATCTCTCTTTCCCTCACATCGT  
ATTGAGTGGGGGGTGGCAGGGGGCATGAAACAGAAATCAGATAGAAAAGCAAATGGGTTTTCTCTTCATTG  
AGTGAGAGGGGCATGCCNACTGATTGGTACACCGTCCGCCCAATTAATTCGCAGCACCAATCAGAGAGTGA  
GGAGCGTGGGGGGCTTTGCTTGTGACGTGATTGCTACCTCGCCTGAGGGGGTATATAAAGCAGGTAAATC  
GCAGGGCTGGAGTTGGTCAGAGCAGTTACACAGAGAAGCTCGCCTCTCGCCCACTGCCCGACGAGACA  
GTTTGCCAATCGCTCCCATCCGCAGTAAGAAAATCAGAGCTCGAGATGCGAGATCGCAGACTCAAGTCC  
M P R S Q T Q V  
TCCTCACTCTGGTCACTGTGCTCTGCTGTTACTGCGGGGATCGAGTACAGCCAGAGTGCAGGGGCTGCC  
L L T L V T V A L L L L R G S S T A R V Q G L P  
CGATATCTTACAGGAGAGGAACGACGAGGGGACTGAGCTAAGACAGATACCCCTATAAAATCTCCATCCT  
D I L Q E R N D E G T E  
GTTGCGCTGGCGCAGGTTAACCCCGACACTCCATTCTGCACTCTATTTAACCCGTTAAGATCCAGCACT  
TAACATAATTTAAATGCATAATTTTGTGTTAGTTTATTGCTGGAATCCATCT

(scaffolds 31600)

TTCGGCCCTCGATGTTGCGCCGACCTGTGAAACCATTCTAAAGCCCATCTACACTATTCAAATGCCAGTG  
TTGTGTTGTGTTTACAGGAGCTGTCCAGGACCATGGTGTGTAACCTCCTCTCCGAGCTGCTCCATGCTGG  
E L S R T M V L N L L S E L L H A G  
GGACAAGGGGTGCCCAGCACCGAGAGACGGGAGCTTCCCCAGGCTGAGATCGTCCGCCGTGGAACCTCA  
D K G L P S T E R R E L P Q A E I V R R W N S  
CCGCGGGACCGCAAAGCAGGCTGCAAGAACTTCTTTTGAAAACCTTCACCTCTGTAAACGTCGCGGAGA  
P R D R K A G C K N F F W K T F T S C -  
GAGAGAGGGAAAGAGAAAGTGTAGCCGGCGGGGGGAGAGATATAAAGAGAATTCCTCCCTCTCCCAAAACC  
CATCTTCAGCTCCTGAAGGGAGGCAAAAAAATCAATTGCCTCTAAGTGTAGATTTTAAGATTCACAAA  
TCCCAACCACCTCCGTCCTCGAAAGATTGCCTCCCCCTTTGGGCTGCCTCTCCGCTGAGGATTTCTCTG  
TGTCTTTATCCAAGGTGTTTGTAAATGATTGACTTGTGTTGCTTTGTTCTCTGAGCATGGACTTGCTCTCA  
CACAAATAATATCTTTATTTCTCAGCAACCTCCACGACTTTGTGTTTCTTTCTGCCCTCTCCCTGACTG  
GGAATCCATCCCTGCACCACCTTCCACACTCATACCCAGCTCCCCTCTAAAAATCTAATCGGTTATGTGA  
ACATTTTGGGTTGTGGGGGGTGAACCCACGCAGACACAGGGAGAATGTGCAAACCTCCACACGGACAGT  
GACCCAGAGCCGGGATCGAACCTGGGACCTCGGCGCCATGAGGCAGCAGGGCTAACTCAATGCGCCACCG  
TGCTGCCTTCATAGGCTGTTAATGACCTCATCCTCCCTAAACAAGCGAAAGAGGGGTTGCAGCTGTAA  
CGACTATGAAGTACCGTCCATAACTGTATTCCCAAGAACTTCTCCACTCGGAAAATTACGGCTAGTCCCTT  
TTTCTCCATATGAGAATTAAGCTTTTTTCGGCATCAGTCCGAGTCTCGCACAGGCAATAGGCCACCTTAA  
ATGATAAAACCGCTCCGATTCTGGGTGAGAATGATCGCTATTAGCGGGGAGTGGGGGGAGGGGGGATTC  
TAAATGAATAAGAACTGGATGACTGGAAAGCTAGTTTGCACCTGTTAAAAGGTTTACTTCTGATGTTCTC  
TCCAATACCACCTCTGCTGCTTCTTGAGCAATGTGTGTAGGGGTGCCAACATTACAGAAAAGATTAGGAAT  
AAATCTTCCGTAACCATTCACCATTCCTGAAGAAAATTTTCAGTTCACACATTTTTTGGGAGCTGGTGCTT  
CCTTCGATATTCTCCTACATTGGTTGCAGCCCTTGGGCGTCTACCCTGAACCCCAAATACTTCACTCGAT  
GAACCTGGAACGTGCACCTTTTCAATTTTTAAGACTTTTTAAAACCTTCTCTAATTCATATTGTTGGCACGC  
TAGCCTCATACAAAGTTTAGTGTGAGTTAAACCTGCTAATTTAACAATATAAGTCTTCGATTCTTGATATT  
GAGTAACCTGCCAATTTTGTGCGCAGTTTACGGTTAATTTATAACCGCACATATCTCAATGGTTCCATC  
TGTTTTAACACAGGCACGATGGGTGCTGCCCACTCCGAAAACCTGCATAGATCTGATGATGCTTCATTCT  
TCCAATGTCTTGAATTCAGGTTCAACCTTCTCATGTAAGGCACGGGGGTATGGGCCAGGCTCTGTAATAAC  
TAGGATCCACAAGCAAATTTAATTTGACGATAAGAGCCCCAGGGGAGACGATAGCGGCATTCACGGCGTA  
CCTAAGACAAACAGCTGAGTGTGCAAGCTCGGGTCTGCGCTCAACGACATGTTGAGAGACCGGTTTCATC  
CATGGCGTTACCGACATGGCCAAATTAAGTACTAGCAGAGGCATAGATTACCTCATAATAATCTTTATATATT  
TATAATCGTTATTAGTGTCAAGTAGGCTTACATTAACACTGCAATGAAGTTACTGTGGAAAACCC

**E. Catshark SST6 = SSc  
(scaffold 66610)**

...GTAATAAGGGGAAGGAAAAATACACTAAGGTCCTCGATTGCTACACACCAATGCCAAATAAGGC  
ACCAAGATCGGGCTGTGATGCAGCCACAGTTGAATAGTTTGTCTAACATCCATGGTCCATGCTTGCATAAG  
AGAATAAGGGCACTCGATAGAGATACTGGAGTGCAGTGCAGCATCTGTGAAGCTGTACTCAGTAAAGATAAA  
ACATTTTTCAGAGAAGCAGGTGAAGGAACATGGAATGTGTTTCTGGTCTGAAAACATAGAATCCAATTCAC  
TTGACATTGCTTTTTCTTTAAGTATAAAAACACAATATCAGATTTGGGACTTTTCAAATCATCAAATAATA  
TTCCACAAATGGCATCAAGAAAAAACGTTTAAATCATATTTAATTTCCATATATACCATGATAGATATTT  
ATATTTGCTCAGTGCTGAACCTCTCCAACAAATTTGTTAGCACAAAAAGAATTTCTGACTGGGAAATGTCCG  
ATGTTAAATGTTGCCTGAGCATTAAAAATTTGTCCCTGAAGCAAAGGTTCTTGCCTTAAGTCTGGAGACA  
GAAATTC AACATTTAATTTAATTCAGAATTTAAAACCTTTCTCCTCAGTGCTTCTTATCTTCAGGCAGAAA  
ATTGCAGAAATTC AACGCAATAAGACTCTTGTATTGACCGATGTGTTTGTGAAGCAAACCTGGTCAGCTA  
AGGGTTAATCTTGGACCGAGTGTAAATGTTTGGCTTTGATGGAGCCCTGATGTTAATGAAGCTTTGGTC  
TGTGCGTCACTGACTGGGGCTGCGCTGGGTTATATAAAGGGTTAGAGATTGTCAAAGCCACACAGAGACT  
CCAAGGTCGAGGCACATTGAGAAGATCTCGGCCAGGCTCCGCTTCATTCCAACCTCCACGAGATCGAGAGT  
GTCAGC **ATG**CAGTTGCTGGGAACGGCGAGCCTCCTGTCCATGCTGCTCATCGTGTCCAGTGTGAGGGCCA

M Q L L G T A S L L S M L L I V S S V R A  
**CGGCACCTTTGGAAGATCGGCTGAGTCTGCGGGCAAATCAG** **G**GAGTGAAAACCTTAAGCGAGGGGAAAAAT  
T A P L E D R L S L R A N Q

CTGCAAAGGGTACACGGCCGGAAGGGAATGACAGAACGAAGAAAAGAGAGGGAGACGACAAAAAAGAACA  
CACAAGACAAAGCAAGGAGACAAGGAGCGAGAGGCAGATGGCGTGGGAGAGAAGTCGAGGTGCATATGAA  
TCGGGGTGACAATTACAGAAGGGGGAAAGGCAGCTAGAAAATGAGAGGGGGATGGAGGTAGGAAGAAAAC  
CTGAGCAACGAATGATTTACAGAAGAGGAAATCTGTGAGAAGAAAAGAAAGTTTCAGTCAGTAAAGTGG  
CATGGGTGTGGGTTAGAGTGAAGGAACTGAAAGTAACAGTGCACAAAGGCTGGGGATAAAAATGAGAGAGA  
GAGAGAGAAAATAACAGGTGGCGGGGATGGCAGAAAAGAGACCTAGCAAAGGGGCAAGAAGTGTGGGTGAG  
GGGGAAAAAAGTAGAGGGATGAACAGAAAAAATGTGAGGGAGAAGTAGAAAATGAGAGTACTCTGGA  
AGAGCGACAGAGGTGGAATAATAGAGAAAAAGCAACTGACAGAGGTTAAAGGGAAAAAATAAATGAGA  
CAAACATGCACACCAGAAAGTGAAGAATAACAGAGAGGTGGTGAAGAGGGACAGAAGAAGAGTACGAGAA  
TTTTTTTTTTGAGTTGGCTGATATCCATGACTGGTTTCTTGGGGGGAGGGATTGTGATAGTTATCCCGG  
GATGCACAAAGATTTTAGTGTCTGAGTCTGCCTCTGGAATAAGAGTTAGTCATGCCGACACTGTACTCAC  
ACAAGCAGCTTCCCACCCCTTTAATCACATTTAGTTTTGGTGCTTTAAGTTTCTTGGAGATTCTGTTC  
CTTTGATGCAGTACCCCTTTAATGGCAGCCTCTTCATTTCTCCCCAACCTTGTGATTTTAGATTTTGT  
GGTTACCTCAAAGAAGCACACCAGTTTCCCAGAATCCGACTTAAACATGCATCAGTGTAAAAGTGGCA  
AAAGAGATGCAGCAAGAGGGAAAAAGGACAGATAATTTTTTTTTAAAACACACAAAGAGAGAACTAAATG  
AAAAGATTAGGGTGCCAGAAAAGAATCTTTTTCATTCCGATGCTGAATGCGGAGGAGACAATATCCTTTGA  
ATCGAAGTGTAGCATGCAGTAACTAGGAGAGTGAAGTGCATGAAGCACAAAAACAGAGCAAGACAGGTG  
GAACAGTAATAAGTAAGCCATGACAAGCAATAAATGCAAACCTGTGTGTTCTTACCTCCCTGGCGCACA  
TGTTTCGAAGATGCCTACCCCTTATTATTAGTCTAATAGGTCACCTCGGTCAATGTTTGTCTCATGGTAGC  
TTAGCTCCACTCACTGACGCCAAAACGTTCCCTCATCTTCACTTCTCAGTGCTGTGTGGCTTAAAAATGA  
TCCCAAACATATAAATTAAGTGTGCTGTTGTAATTTGATGAAGACTTTGTGTACTCCCTCTGATTCGCC  
TCTGGGTTAGCAGAGCTGTATACGTGCGAGTGTGGACTTTTGAATAGATACTCGACATTTTACCGTGTGT  
TTTCTGTGTTAAGTGTCTTTGCTGCTATCTCCAACAGGTGCTCCTGTCCCCTTAAACCCCACTCAT  
TATTCAGGGGGTTTTCTGTTCAATTATACATGACCGAGGGCAGCAAGTGGGAGCCCCCTCCCTGTTGAGTT  
GAAGGGGAGGGGGTCTTTGGCAGGTGAAACAACCTTTGTGCTGGATACTTGGGTAAGGATAGACTTAGAG  
ACAATGGGCTGGATTCTCCGTCCCGGTTTCAGCACGCCGGCACGATGCTCCGTTTCGCCAGCTGGTCACTG  
TGGGCAGGTCCCATAACCGTCGGGAAACCTCCGGGTTGCCAGCAAAATGGAGAATCCAACGGCGGAGAAT  
CTAGCCCAAAGTTAAAGAGAGAGCGAGTTTTATATGATCACGAAGGAGTCCACATCGAGTAGTTCAAAGA  
AACTTAGTTTTATTTACAATCACTATTATATACATCACACGGCAGATCCCAACTGGGTCTGCCTTGCTGAT  
GCCAAACTGGCCAGCTTTATACATCGTCCAATAATATATTGTTTAGAGGTCCCCACACCCTTAACGGGG  
GAGCTCGTATTCCGCAAGGTTTCATGGGGAAGCTAATTGCCCTCACCCCTTTAGACCCCTTGCGGGTATATA  
TGAGAGAGAGGGATTGCAGCCGTGAAGATCGGTCTCTAGATTAATAATAAAAATGCCTATCAGGTACTGAT  
TTCCAGCCAGGCGGTGCTATAGCATCATTGCTCAGTCCATGTGGACACCCCTTCCATTTGAAGACGGCGC  
TAATTTAATGTATCTCAGACAGATGAAGGGCAAAGCCACTTTTCCCTTGACAAGTATACGGAAATCGGGCT  
TGATTTTTGACCCCGTTTTCTGTTTATCTAAATGTTGATCAGAAATGACCGGTTTTCTCATTTTAGACAT  
TTAGACACAGGTACAGAGCAAGGCGGCTCTTTACCCCTACCTTGTCCCAGCAATTAATTTCCCCCTT  
TCTCAAGACAGAAGTACCCACCGCTTTTACAAGGATGAATTTTTTCCATTCTGTAGTCTCTAAGTTGT  
GATTTGCTGTGGTGTGTTTCTGCTGTTGAACTGTGGCCGATTCTGTCCACGAACCTCCGAAACAAAGCAT  
TGGCTTGGAGTTCCCGTTTAAACAGAGAGTGCCTAAACATTTGTAAGCTTGAAGCTTGAAGCTTGAACCCATC  
TTAACAAAACAGGATGGCCATTATCACAAATGTATTATATTTGAGATGGAGTTGATAGTACTATATGTT  
GGGATGCATTAGCAGAAGATTCTAGCACATCATTTGTTTACGAGGTTTCAGTATGTATCGCAGCTCAGTA  
ACTTACGGCAAGGTCAAAGGTCACGAGAGCAACTTGATCCAATCTCTAAAATTTCTGGCAGCAATGAATC



Figure S5

A. Whale shark SST1/3 (NW\_018029766.1)

...AAGCAAGTCCAAGTGTTCATCTGCCTCACAGACACCTATTTGATAGGCTACATCCAACACCAGTCTCA  
AACTACATCTCAGACTTCAAGGCACTGGCAGATAATGTGCAGTCACAGGTATCACATTGAGGCATAGTAA  
GTAGAGGACAAAATAAATATTTACGTACATTTGGTTTTAGAGTTATGTGGCACTAAAAATAAACTGTTTA  
TTTCGTACTTTCTTAGAGTAGATCCTGGCTTGCACTTAAATTCAAAAAGTGATCTTGTGTTTAAAAACAT  
TGGTGACCTTTGCTGTAGAGTTAGTGCAACAAATGTTCTCCAGGCTTGTTCCTGGGATAACAGAACTATC  
CCGTGATGATAGATTAGGCAAACCTGGGACAGTATTTGTGAGTTTCAAAGAATGAGAGATGATCTCATTGA  
AACCTACAAAATACTTGAAGGATGGACAAGGTATATGCAGGTTAGACGCTTCCACAGTGTGACTGAGTC  
AAGTTACTGCAGTGTATCGTGTATTTGCACAAATGTCACTGCGCATCAGTGATAGAGTCAATATTCAGA  
TGGTGGGAAGTGGTGCCAAGCAAGCAGGTGCCTTTGTCCTAGATGGTGTATGTTTCTTGAATACTGTTGG  
AGCTGCCCTCATCCAGACAATTGGGTTGTTTCCCATCGCACTCCATACTTGTGCTTTGTGAATGAAGGAT  
AGGCTTTGAGGAGCCAGGAGGTGATTTACTCACTTCCAGGATTCCTAGTCTTTGACCTGTTCTGTAGCCA  
CTGTATTTATACAACCTGACCTAGTTCAAATTTCAATCAATGTTAATTTCCAGGATGTGGATGGTGGGGAA  
TTCAACAACGGAAATGTCACTGAATGTCAAGGATAACAGTTTCTGTCTTGCTGGAGATGGTCATTGCCCTG  
ACGTTTGTGTTACATCCCAATTGTTAGTCCAAGACCTAAATATTGTACAGATCTCACTGCATTTTAGCAG  
TATTTAAAGAGTTACAAAAGTACTGAACATTGCAATCATTAGCGGACATTTCCACTTCTGACCTTATGAT  
GGATCATTGATGCAGTAACTGAAGATGGTTGGGCACAGGACGCTACCCTGAGGATCTCCTGTATGATGT  
CTTGAAGCTGTGATGACTGACCTCCAGCAACCACCAATCTTCGTTTGTGGCAGGCATAAAAACCAAA  
GTGAACATACATTGTGAGCGGATGTGAGGCTTGGAGTTGCAYTGGAGCAGCTTGTTTAGGGCCATGACTT  
GTTCTGAAGCACAAGTCTTCAGTATTATTGCGYGAATGGTGTGAGGCTCCAAAGCCTTTGCAGTATCCAT  
TGCCTTCAATCATTTTCTGATAACACGTGGAGTGAATCTAATTAGCTGAAGATTAACATTTGTGATTCTG  
GGCATTCTGGAGAAGGCCAAGATGGGTAATAAATCCTGGCCTAAGCCACGGATATCCTGTGCATGAATAA  
AAGCAGAATTCAGAATGTCCCTGGGATTCTATTTAAAACAGCCATGTTTCTTAGTGACAAAATGTAAAGACT  
TACCCATTCTTTGAACTAAGTGACAAGAAACAAGACAAAATTTGTTAATTCTTTGCGGTAAACACAATA  
ACCATTTTGTAGGACCCTGTACTTGTGACTACATGCAGCATGAACCCTTTAGTGTCAATTTGTTTATTTG  
TCTGTTTGTGTAGCAATAGCAAAATAGAAAGCTGCAGTGTACACTGTAGTTTGAATTCATATCCATTGCTT  
GTCATCAGGATAGCAACATAAGGCTACTCAGAATTTAGATTGAACTTGAAGATATCACAATTTACTGTG  
AACACTTTGTTTTCTGAGCCAGTGTATTATACAACGAGAAATATTCTGATCATGTCCAAAGAGGGAATT  
TTGCTCAAGGATGGTATCTGTTGCTGAATTGAAATTTGAAACTGGGGAGAGAAGAGGAACATATCATTCCCTC  
TAATGGGCTAATGGTAAGATTACTGGGCTAATGGTAAGACTACTGGGCTAATGGTAAGATTACTGGGCTA  
ATGGTAAGACTACTGGGCTAATGGTAAGATTATTGGGCTAATGGTAAGACTACTGGGCTAATGGTAAGAT  
TACTGGCATAATGGTAAGACTACTGGGCTAATGGTAAGATTACTGGGCTAATGGTAAGATTACTGGGCTA  
ATGGTAAGACTACTGGGCTAATGGTAAGATTACTGGGCTAATGGTAAGACTACTGGGCTAATGGTAAGAT  
TCTTGGTAGTGTGGATGAGCAGCGAGATCACGGTGTCCATGTGCATAGATCACTGAAAGTTGCCACCCAG  
GTTGATAGTTGTTAAGAAGGCATACCGTGTGTAGGTTTTATTGGTAGAGGGATTGAGTTTCAGAGCCA  
TGAGGTATGTTGCAGCTGTACAAAACCTCTGGTGCAGCCGCACTTGGAGTATTGCGTACAGTTCTGTTCA  
CCGCATTATAGGAAGGATGTGGAAGCATTGGAAGGGTGCAGAGGAGATTTACCAGGATGTTGCCTGGTA  
TGGAGGGAAGTTCTTATGAGGAAAGGCTGATGGACTTGAGGCTGTTTTTCGTTAGAGAGAAGAAGGTTAAG  
AGGTGACTTAATAGAGACATAACAATGATCAGAGGATTAGATAGGGTGGACAGTGGGAGCCTTTTTTCTCT  
CAGATAGTGATGGCTAGCACGAGGGGACATAGCTTCAAATTTGAAGGGTGATAGATATAGGACAGATGTCA  
GAGGTAGGTTCTTTACTCAGAGAGTAGTAAAGGCGTGAATGCCCTGCCTGCAAAAAGTAGTAGACTCGCC  
AACTTTAAGGGCATTAAATGGTCATTGGATAAACATATGGATGATAATGGAATAGTGTAGGTTAGATAG  
GCTTCAGATTGGTTTACAGGTCGGCGCAACATTGAGGGCCAAAGGGCCTGTACTGCGTTGTAATGTTCT  
ATGTTCTATGTTCTATTCCAGTTATAGTCAGGAGCCATTTACGTGGAGTTTGGAGGTGATGAAATGGAT  
GTGTTGAGTTAGTGATGGTGTCTCAGTTTATATTTTCTTGCCACAAAATTCCTCTAATTGTAATCACTAATG  
TTTGGAAAGGTAAGGTCCAATTCACAATGAAGCTGGACCTTATCCTTGCCTAACGTCCACACAGATATCC  
TATGATAGTGCTGTGAAGTGGAAAAACCACTTGGGTTTTTGTCTTTTCTATTACATGAGCATTGATCCCT  
CCCCTCTGATCCTGACTGTGACCAGCATAAGCTGGTGTCTGGATTTTGTTTTTAGTCCAGAGCAGATAAA  
GCCATCTTACCCTTCATCTCCATTCTCCTCACCACCCACATGCTCACACACCTCTCCCAATCTTGCTTTA  
TTGGGAGAAAAATTAGAATTAATTTGTTTCTTTTTAACTTTTCAAGATTTAAAACATGTAAGTGAAGAGACT  
CTAAGCAATAGATAACTGATGTCAACAGTAGGCAATGCAAAGACATGTTGAATTTCCACATTTCACTTCT  
TTGCAAACCTTTACTTGTCTTCTTCT

CGGATGCAGACAAGGATGCTGTGGAAGTGAATGCTTCTCAAGTTGAGACTCCACCAGWTAACAAGATTC  
A D A D K D A V E V N A S Q V E T P P X N K I P  
AATGAAATTTCCAGCAGCGTCAATTTGGGAACAAGAATGCGGAAAAACTGCAAGAAATTTCTTTGGA  
M K F Q Q R Q L G T R M R K N C K N F F W K T  
TACAATTTATGTTAAACATTTGACTCCGCTCTACTGCACTGAGCCCTTTTCCACATTATCTCACTGTAC  
Y T L C -

CTCACTGCATCCTGTTTGTCCACAGTGCCCTTCTCTGTGCTCAACGTAGTGGACTTTGCCTCACTGTACC  
ATAATGACTCCTTCCCATTGTGCCTCATCGTAGCCTATTATCCTCTACTGTACCTCATTATACCACATTG  
AATTTCAATTGTACTTCACTGTGTCTACTGTACCCTAATGCACTGCTCTGTACCTCACAATGTCACATTA  
ACTCTTTCCCACTGTACCTACTATACAGTATTATACCACATTATGCCACATTGTAGTGCACCTTGTACCCC  
ACTGTTCCACACTACAGGCAACTGTATCCCCTATAAAGTATGGAGTCTTCCACTACATCCCAATCTA  
CCACAGTGTGTACTAATGAGCTCTTCCCTATTTTATCTATTGTAATCTGACAATAGTTGCATTTAATCTGC  
AGTATAACTGAAGCTTCAGTTTAACTATTTGACACACACATTCTTTACTTTTTGTTTTGCATTTGTACT  
CAAAGTCTGCATTACGCTTTCAACATGCTGCAATAAAAATGGTTTCACATTTGAAGATTATGCTGCAGT  
CTCTGTCTAGTTGAAATTTATCATGGTGAGAATCCACAGATTGTAACCTTACCGAGAATCCAGTTATGGG  
AGTCTGAGGTGGCAATTCACGCAGTACTGAGGGAGCATTGCATTGCCATTGGTGTCACTTTCTGACG  
GTCCGTCTGTTTCAGCTAAACGTGGAAATGTCACAGCACCAGTTGAAGAAGACCAGAGAGTCTTTGCCATT  
AAATGACATCATGTGTGATGTGTTTTCTGTTTTGAATTCCACATTCCCCTCTGTACCCAGCAATCCTTTATT  
CCCTTGCAATTATTTGTGGATATCTCCCCGTAATTGTCCCCTCTTCTTCTGTGCATGCACCTATTTTCCACA  
CAAAACCAAAACTCGCATCCAAAATAGTGAATCCATAAGCAGATCTAACTAATTAATTTCTGAAATGTGC  
ATCTAAAATAAACAGCTAATTGAAACCTTGATTTAATGCATATCATATCAAATTTGTGAAGACACTCCCC  
CATATCTCATTCTAAAGCAAAATATTTTGGATGCTGGAAATCTTGGTTAAGAACAAAAATGCTGGAAAA  
TGCAGTACACAAGGCAGGGCCCATTGAGAAAGAAACACATTTAACATTTAATGTGAAAATTAATTCGTT  
TCTCTCCATAGGTAGTCCCAATTTGCTGAGACTTTTTAAATGTATGTTGTTACTGTGCAACTCATAATGA  
ATTTGAAATGAACTCCAAATAGTACCTTTGTTATTAATCTATAAATATGTTGTCTAAATACATATTTTC  
TAATTTGAAATCTGAACTTCAGCTGTCTTGATGTTTTAAACAAAAGTTCCAATAACCATAAACATAACAT  
AGTAAGAACACTCAGCAGGTGAGGCCCTACCCTCAGGAAGAGAAAACAGATTTAGGGAAAAATAATGTAATC  
CAATTTTTAAGAAAGAAGCATTCTGGAACCAAAAATATAAATAATGACCAATATCAATTTGAAATGGAAAG  
TGTTGCCTGATCAACTTAATTGGACTCTGAATCATCAGCAGAGTTTAGAAAAGACAATGAGGTAGATATA  
ATAATTTATATTTCTAAATGACATTCAAAAAGTGACATTTAATAAACTATTCAATAAAGTATGCAGATA  
CATAGTACAGCATCAGAATGGATACAAATGACTGTACACAGAAAGTAGAGAGTGGGGATAACTAGCTGC  
TCAAAGTACAGAAGCTAGGGAAGTAGAGTTGTCTAGAAACAGGTAATGTTATTTCAATTTACATTAAT  
GACTTTAAATCAAAGCACAAATTTAGAAATATGCAGATGTTTTCCAAATTCGCTGAGTAAATAGTTGAT  
TTCAAGGCAAAACAGAAACACATTTCAAGAGGATATTAATACAATTTTAGAATAGACATGTTGTAATTTTC  
AATACAGATTGAAAATAAAGAGCCATATATTTTGAATTAACATTAGACTAGAGGAAGCAGGATTGGCACA  
GACATGGATTAGTAAGAGTTGCACAGTAGCCCACTAAGGCCATAAGAAAAGTAAAAGTAAAATGCTCAGAGT  
TCCAAAGGTGAGTCATTAGACTCAAAATGTTCAATTTTTCTCTTTCCACAAATGCTGCCAGGCCCTGTT  
GTGTTTTCTCTGGCACTTTCCATTTTTATTTTTCAGATCTCTAGTATCTGCAGTATTTTCGATTTTATTTAAGA  
TGAAGTAACGGGGAGATGGTATAGGAAAGTCCCTCAGTGGTACCTTGACGGTTTCTACCACCAGAGCTATT  
TTTCTAGCAGCAGAAAAGATATCAAATTAACATCTTCCCAGAACCAAACTGAATAATTTGGCTAGTTAAG  
GGGGTGAGTGGGGTTTTGGAAAGGATGCTATGTGGGGCCGTGGACCAATTAACCTGGCAGCCTGACAGCA  
GGCTCTGGGATTAGGCATCAACTACTCACAGCTCAACTGGTGCATCATTACGGGCGCTACCATCAATGCAT  
CTTCATGCACTGAGTGCACAAGCACAAGTGGCCATCCTAGCAAGGTGCTGTTGAACTGCCAACCTTTGA  
TTTTGGACATTCATTCTTTGGGGTTCAGGCCATTGTACATAGGAGAAAACAAAAGTTCCAACATAGCTGCTTAA  
CTGGTTGCAGAGGCCATAATGAAATCACATTGCCAATGCACAGGGGTCCGACCAATAAAGGTAATACCT  
CACATCTATCAATGTTGAAATTTATTGGGCTTCATGTCAATTTCTACCTCACTGTGTTGACTTTTCATG  
TCCTAAACCCTCACACCTCACTGAGCTGTAACCTAGGTTCTTATTCCCTCCCCACTCTGCTGTAACCCTG  
GATCTTATACTTAGTCTCAATTAGTTATAACACATGCGACCTATAACATTACCCCATCACCTCACTGTGC  
TGAATCTCTGGTCTTATAATCTCCTTTATTGCATTGTAATCCTTGATCTATTACCTCCCTCACTGGTC  
TGTAACCTCTGGATATTATGTGCTTCCACTAGGAAGTGTAAACATATGCCTTATACTCTCCCTGATTGTGTT  
ATAACCTTGTGCTCTACAACCACCAGCCCCATTCTCCTCAATGTGCTCTAACCCAACTACTATAAACC  
CTTAATCTTGTACCGTTTCATCATTATACTGTAATGCTGGGTCTATTAACCTGCACATCCCCACACCCCCA  
CCTCCCACTCAGTGCTATATCCCTGGGACTTATACCCTACCTCACTGTGCTGCACACCTGGATCTACTAC  
ACTCACTCAGTGCTGTAACCTTCTGTACCTTCCCTTGCTGGTCTTATACTCCCCCTCCCTCTCTGTGCTG  
TAACTCTGAATTTTGTACCCTTCCCCATTACGCTGCAATCCAGCCTCATTCAATAATTTGTGCACCCATG  
CCCCGAGGTGCTCTTGTTCCTCTGGAGTTGCATTCTCTATTTTATACTGTTTCTCCGTTTCATTCACC  
AGAATGAATCGCTTCACATTTTATTGAATTAATTCGCTCTGTAACGTCTGTCAATTCACCAGCCTTTC  
TACGTTTTTGGAACTTCTACACTATCCTCCTCACAGTTCGCAATGCTTTCAAATTCGCTCATCAGTACAT  
TTTGAATCATCTAATGTACAGAAAAATCTCGATTGTTAATATAGATCAGGAAAATTAATGGTGATGAAA  
CTGATCAACTCGGCCATCTGATGGCATCACCTGTTTGAAGGTGCCATTCTCTTGGTCCACTCTACAATA  
CAAGAGGTTAATGTCGATTCTGCCCCGTGTTTCGACACCGTCTCAATGTCAAGGTTGAGAAAAATCCCAG  
TTGTACGACCCCCAAGTGAGATGCCTCATTGTCTGCCATTCTAAAATGATGTCCATTTAATGAAATAAGCG  
ATTCATTTTCGACAGTTCCTTTCCATTTGAGACGGTTCAGTTGACTAGAGTTTCCCCTCACTGATCAACA  
GTTCAATTAATCTCCCGAGCCACTAGCACTGCACACTAACGGTGAGAAGACTTTCTGCCTTGCCCTCGTGTC  
AAGATAAATGACATGTGGTATCATAGAGCTCCCTGGCGCTACTACCCGTAACAGGACAGAGGTCCACTCA  
TGCTGATAGGTTTCTACTTATCTTGTCAAACACACCAACTTGTAATAACAATTACTGCTCCCTTAATA  
TATTCATCAGCACTCAGCACGCAAGCCGCTTCCACAACCTATTTCTCAAGTTCCTTCCCATTGATTAACA

GAAATATCTGCATAATAGGTCCTGGAAATTCCTTTCACTCTCCCAATTCCTACTACAGGTACAATGGTTTA  
AACTAACATTATTCCGGTTCGTTTCGGTCTTTTGTGAACAAAGTATAGATTTTCTGATGCGTTGCAAAAAGA  
AACAAAAATTCATTGTCTAGAACATTTTCATTTCTGCTGCCGGGTTGCACAGTGTCACTGTAAAC  
GAATAATCTCAGTTAATTGCAGTCCCCTCCAGCCATTCTCACTCAGCAGAGAATCTTCCAAAAAGTCAATA  
TTAAATAAAATCAGAATAGGCTACAAATAGTTTCAGGCAGCGTCTGTGAGGGCAGAAAACTTGCCACTTGT  
TCATACAGCTACGGTTCAGTGGAAAACCTTAACTACAGCTTACAGCAGAACCCAAACGTTGTGGGTTCTTT  
TGTTTTTACAAAACAAAAATCCAAAAGGTGAACAAAAGTGGACCGACCATCGAGACAGACAGAGGCAGAC  
AGACAACGACAGAAGCAGACAGACAGACAGACAGGAGGCAGACAGAGACTGACAGAGATGGAGTC  
GCAGGACAGAGATAGAGACAGACAGAAAAATGCAACTCTTTAGTCGTGATCAAGTCTGAATTATTGGTTC  
ACTTGACTTGAATTCTCCAATGAATCTTTATCCATTGCCTTGTTCATGCAAATAAGGAAGTGTTCCTCCCG  
GGTAATGGTATATTTAATAGTCAGCCTGGTGTCTGTTTTCTTGTGTTTCGCGCGGAGATACAGATAT  
TTAACATTGTTTTGAAGCGATCAGGGATGGCGATATCATTAAAAATTATGAAGGGTTGCAGGTTGTAAATCT  
CAACCAACCCACCAATTTCAGTGTAAAAACAAAGTTAAATCTCAAGTCCACTGAGTTCGGTGTAGCTTTA  
AGAAGAATACCAATCAGAAGGGATTGTAAACCCACACATAGAACACGGGGATAAAAAACACAAAAATACTAC  
ACAATGATTAGGAACTAGCAAGTCTTTCCCGAGAAACAATCCTTTACTGTGCCTCACGTAGTTTCTGC  
CCTCATAATCTCACACAATTCGCAGCAAATGATTTAGAAGTTGGAATCAGCTATTCTGCCTGTCTCCCT  
GATATCCATTTATTAATAATTCAGGCTGAACTAGCTGTAGTCCAGTTCATCTTGTCTGTCTGTATAGGC  
TTTGACTGTCTTGACTATCAGAAATCTATCGAATTCTGCTTTGATTAATTTCAATGAGGCAGCCTGTGCT  
ACTTTCTGAGGAAAAAATGTTCAAGGACTAACGACCCTCTGACATCTTCCATCTTAGTCTTAAGATGGTG  
ACTTCGTTCTTAAACTGTTTTCCGAGAGTTATTGTCTCCCTCATAAGTGGAAACATCCTTCGGCATCTCAC  
ACATTTTCATCTCTGGATCATTTAATTCTGTAATGAATTGGCCAGCACTCCCCTGGATTATGATCACAAA  
GTTTACTTGATAAGAATTTGTGCGTTGGAGAGATGTATTCCCTTTTCCGAACGAGCCCTATCGTCACTCC  
GACCTTTTGGCAGGATCGAATTATTAGTGGAGACCACCTCACATTGAAACCCATCCCTGACCCCCGCACT  
ATGACCCATTACAAAACATCTAAAGAAGTATGATCAAAGTAAATTCATCTCGTACCTGTAAAAAGACCCGC  
AATAAGAACACGGTGCACAAAAAAGAGAAATTTGCTGAAAAAAGTACAGCAGTCTGGCAGCATCTGTGA  
AAGAAAGCAGATTAACATTTCCGGCTCCAGTGAACCTCTTTAGAAATCTTGTCTTAATTTCCAGCATTC  
GCAGTTCTCTTTTTGTTTAGGTGTTAAGAACACTGGTTGGACGCGGAGATACAGGATGGGCTATCAACT  
GAGGAACCATCCGTGTATCATGGCATCAACAAGTCCGAATTCCTCAAGGGAGGCGCAGTATTGAAATGTC  
AAAAACGGAACCTCAAATCATGAAGTTACAGGAAAATGGAACAATTCAGACTTGACTGAATTGACTGTAT  
TCATTCGTGATGGACATGGCCCAATATCCAATCACAGGAGCAACTGCCAGAATGCGATAAAGGTGTCCACA  
TTGAGAGTCCCTGGCCGTTATCTCAATCTTCGTGAGCTTGGTAATGATTTGGTTGGATGATGTGACTGGG  
TTGTGCGTAAATGCTTGTAAATCTCCTGGGAGCCGTCCTCCTGACGTGGGTTGAGGTTGGGAAAAGCGCCT  
TTAAAAGGAGCTGCCACTTCGAAGAGCCAGTAGGAGCGGAGCTGTCCACTGAGCTGGTGTGAAACTCGG  
GCAACTTTCGAAAGCTGTAAAGCCTCTCACTTTCTTCCCTCGACGAGGTACCTCACTTTGTGCAGT  
G**ATG**TGGTGCAGCCGAGTT**CAGTGCGCCCTCGCCCTGCTCTCCATCGCTCTGGCAGTGTGAGTGCGGGG**  
M W C S R V Q C A L A L L S I A L A V L S A G  
**GCCGCTCCACCCGCGACAGGTATCGCGAACTCCTCCAGACATCAATGGCTGGCGCAGAGCCCCGAGTA**  
A A P T A D R Y R E L L Q T S M A G A E P R S  
**AAGCGT**AAGAATCCAGCAACGGGAAACCCCATGTAATAAAGCGGATAATATGGTTATACCATTTAATT  
K A  
GAAATAGAGCCGAATAAAGGGAGAGACTTATTGCTGAATCTAACCTGATTAGAAAAGATGTAATGCCCATC  
AAATGACGGCATGGATGAGTGAATTTAGTTCACAGATCTCTCGGTTTATAAACCGCTCTGAGC  
GCGCTTGTTCGACCGAGAGAGATCACTGAGTTCCCCAGCTCCAGGGAGACAGTACTCTCCCTCTCTCCA  
GTCGATATGCGCCACTCCGGTCAGACTGGAACCAACGGCTTGCAACTTTCCGAGTTTTAGGCATCAGT  
CCCTCCCTGTCTCCGATCCAAACTCATTTCCTCAGATTGAAATGATAATCTCTGAGCAGCCTCCAATCG  
CTCATCTAAAATAACTCTAACCTAGCAGCAAAAGAGATGTTGATGTAATGACGTTAACCTTTAGGTTTA  
GATGTTCTGTTTTATTAGCGGAAGCTCAGAACCCACATTCACCAGAATGGCGAGAAAAGATAAACCGCCTC  
TGACTCTTTCTACATTGTATCCGCCTTTTCGCTAAACCTAAGCACCTCGATAACCGTCTCATCCGGGGTTT  
CCTCCTTTTCTCCAAAGACCCGCTATCATGATTAATTAAGCCCCAAAAACATCCACACGGGATATGAAG  
GGAGCTGCACAATGGATTTGTTACATTGTGATTTAATTGTGATTGGGAGGTTACAGGCTGTGGAGTC  
TAGAGATAGGAAATGAGGATAATTTACCCAGTGGGATACAGGACTGATGGGCTGACACTATAGTAAAG  
ATTTGCCAAACTATACTTTAGATCCAGCGTTTGTGCTTAAATCAGCACCAATTGAGTGGATTTCTCTG  
CCCTAACTATCCCTTTTCTTAATGT**AGGAGCTGATCAAATACAATCTCGTCCAATTGCTCGCGGAGCTG**  
E L I K Y N L V Q L L A E L  
**GCAAACGCCGAGAACGAAGTTTTGGATGGGGAGGATTTGCCGCGGATGGCGAAAACAGGATGAGGTACGGG**  
A N A E N E V L D G E D L P R M A K Q D E V R  
**TTGATCTGGAACGATCCGCCAACCCCAATTGCCCCAGAGGGAACGCAAAGCGGGCTGCAAAAACTTCTT**  
V D L E R S A N P N S P Q R E **R K A G C K N F F**  
**CTGGAACCTTCACATCCTGT****TAA**CTCGCTGACACTCCAGAACAACCCGCGGGCCACTGCTTCATCCCA  
**W K T F T S C -**  
ATCACGTACGGTCAGATGCGGCAGCACCAAGTGTAAATTAATAATGTAATTGATTACTTGATTTGAT

TTATTTGACACAAGAGTTTAAAGTTTGAATTGTTTCAGCAGACCAGTCCTCATTGAAACTAGGTAGGACCGG  
TTTGATTAAAGAGGCTCTTTCTCATTGAAATAAAAATCTTTGAAAGTGGAATATTGTGTTTCGTGTTTTATG  
TGGTGGGAACCTGTGGGCAATATACCTGAGTGGGCAGAAACAAATCAAGGTTTTCGCGAAGCCCAGTCGTTT  
TGGGAAGGTACAATGCGCGGAATTAAGCGCTCACAGTTAGAACAATGTGGCCATCAGCTAGTGGGAATCG  
CTTTGAGTCCCATTCCCGGAATCTGTTTTGTCTTAAGTTGCTCCGTTACCAAGAGGCAGTGACAATCAGC  
CTTATCTATATGAAGGGGGTCTACACCAGGTCTTCGTGCGCATTGTGTCTGTTAGAAGCTATATGGGAG  
AAGACCCACAGTGCAGGCATCAGGACCCAACCGCTTCAATGTAACCAACAATCCACAAAGCGTAAATTTG  
CACTCCGCAAACCGCGGCCAGTCTCTCATTTC AACGGCGGTTTTCTCTTAAAACCTGCCATTTGTCTTTG  
TGCCGTTTTGCTGCCAATCTCAGTGTCTGAGTGGAGGGAAACATAGTGTTCAGCTGGGGATAGTGTG  
CTGGTGGTGGTGAAGGGATCGGGGCGGGGAGTTGGGGGAGGTGGGTATTGGGAAGGGGATCCATTCCTCA  
TTCTTCATCTAACAGGATCCAGGAAATAAAGACACAGGGTGGTTCAATCAGCAAGTGCCCATATCAGTA  
ATTGCAATCCTGAACTTCAGACAGATCACGGGAGCGCTGACMGTGAGGAAAAGCTATCGTTTTTACGAAGGG  
AATAACAACCTGATAACAGACTTTACCAAGGGTGTCTGTGTCCCATCAGCAACGCAGACCCGTCGGGTCA  
AAGTGAGATGCTAAGCGTGGGAGGGGTTGGTTTTCTCGAGGAAATTTCCGATCAAGCACCCACTTCCTGC  
CTTAACAACTAAGTTTCATTATGATATACAGCGGCACGCGGGGAAATAGAACGTACACGAATGCAGAGT  
TAAAGTGCAACGTCACAACAACACACATGCCTAGGGCACATCTGATCACTATAACCGCTGGCAGGAGGGAG  
AACCACGCACTCCTTAAGAATGCAAAGCATTGTCTTTAGCAAGCCTTCAAGGTGCATCACACCCACATGC  
TGAGTGTGTACAGACTGACGCTAAATCACCACGGTCAATGACACACTATGGGCCATTAATTTTGAAGAA  
TTGTA AACCGCCACAATGTCTAACCTCGTGGCGGAGCGTACCTTCCAGTCTTCCACAATCATCTGTCCAG  
TCGGCTGTGGAAGAATTATGGGAATGCCATCGCCCTCCCGTTCTCTCCAAGCTACTCACCATTCTGATT  
TGGAGACATATTGTTACTGGGTCAAACCTGCAAGAACTTCTTCCAAGCCATTCTGGATGACCTTACCTC  
CCAGGAATTTCTGCAGTTGAAAATGGCAGCTCACCACAACGTTCTTTCAGAATAATTAGAGGTGGGTTATA  
AATGTTGGGCCAGCTACAGACATCCACATCCCATCATTGAGCAACAGGAAGGGATATCAGGAATAGCAGC  
AATCTCATTTAGAAAAGAGACACAGAATTATTCAAGCTGTAACATCGAGATATCTGTGAGAGCCAGCTGA  
TCAGAACAAGCACTGTTGTCTTATATACCCGGTGAAGAATAGCAGTGACTAAGGAGGTAGCGAGAGGA  
TTAGAATGAAATAACATGAAAATATCCATTACAATGATGAAGTCCGGCTCATGAGTGTTAGGGACA  
AAGCTGAAAGTTGTAATACTTTTTCTGGAAGTGAACGTGACTATATCTTGTGAGACTCCGAGGAT  
CCAGTAGGTGAATGAATCATGAGCAAAGAATAGTTCTTTAAGTGTATTGCTGCAAATTCCTCAATTCGTC  
TGTAAGATCTAATCTCAATTCCTGACTTTTTCTAACTATTGACGGACCTTTGTTTTTACATTTCTTCAATC  
TTTTATCTGCGATTTCTTCAATCATTTAATGCTGAGAGAATGCAGATTGCTGTGACTGAGCAACCAGTAG  
GAGGTAGAATTCAGTCTGAACTCACAATTAATGGCAATTTTCTTCCAAGTGAACAGTACCCTTTATTT  
TGGACGAGCAACATCCAATGGTTAATAAAAAATCGATACATCCAAAAGAAAAGGATACGTTTCCCTTATCAT  
CTGTCAACCCACATCTTCAATTTGTGATTAATAAACATGAGGTAGTTCACTCACAAGTAACAAACTCA  
GAAAGTGATGACATTGGCTGTAAAATGCATTCTTTTTACACTAATCCACATCCAAACTGTGGAAGCAAG  
CCATTTACTACCCTGGAAATCTTTTTCTCTGAGATTCTAAGAAATAGGAACAGGAGTGAGTCAGTCAGT  
CCTCTGAGCCTGCTCTGCCATTC AACAAAATCTGGGAAGATAAAAAAAAACCTGTTTAGCTGATTAAGGTT  
TGGCTCCATTTAATGTCAATTCATGTACAATTGGATATGGGCAATTCGTAAATCAATGAATTCCTCAACAT  
AGCCACCTCCACCCCATCTAATAAATGGTGCTTTTCTAACTTTAACCCTGACATGTGGTTCTCTACTC  
AAGGTACACTGCAGTGTTC AATATTTTAATCAGTCACCAATTCATTGATTTTCAAGTGTGATTGCCTGTGT  
GGCTCAATATTTACACTTTTCTGAAACCAATGAAGATTATGAATTCAGTCTGACTTCAGAGGCTTCA  
GAATAATACCCAAGCAGGAGCTATTCTTTTGAACCACATTCATTCAAGAAAAGCAGCTGGAATTCACTTCC  
ACTGACTGCAGATATCAAATGAAAAAATGGCGTCAAATTTGCTCATGATCAAAAATCTGTCTTTGGTATAC  
TGAATAAATATGCCAACTAGATTCAAACATTTTATTGATTGAGATTATACTGACCTTAGAGAGCTCATCTG  
TTGCCTCCCCGCATCAATCCCAGTGTCTCCACTTAATATTCCAATCACCCATCTATTAGCCTTGGCAG  
ATTTTTTAAAAAATGAACTCACCTGATAAACCAAAGATTCATCTCCATCTAGTACCTGCCAAAACCTGCTT  
CTAGGATTATTCAATGTCTCTGAAATCTAAAGTTCTGATAATGTGCAATGAAATCTAATCAAATATCTT  
GTAAAACGTAAGTCTGCTGCTCATCAATTGCCACCAAAAAGATAGTCTTGGTTAGTGGAACTTGCAGTTAGA  
ATCAGTGTAAATTTGTAGTTTGGACAGAGTAACTCTTCAGACTTAGTACAACCTGAATGCTAGCATAARCTG  
TTGTCTGTGTAACCTCAATACTTACACAATGTGTTGCCAGTGTAAATCTGTGGCATTGTATTTTGGTGTG...

**B. Whale shark SST2 (NW\_018077477.1)**

...AATGTTGATTACATAACAATTGAACCAGAAAGGAAAAAAGACTGCATTTGAATAGCATCTTTTCATGATCT  
CAATACACCCCAAAGCAACTGAGTTAATTTTAAATTTGTTTTTACAATAGTGTAGGAAACATGGTTCGGCCA  
ATTTGTACTATGGAATGTGTTGAACAAGCAGGGATGTTTATTGAGGGATAAATATTGGTCAGGAGAAAGG  
GGAGGAGAACTCTGCTCTTCTCTTAAATGTTATTTCCACCTCTGAGGGCAGGTTTAAACACATTGGTTTAA  
TGTCTGTTCTGAAACCAGACAAGTTTTATAGACTAAATCAATTA AAAACCTACCAAAAAATGGCTAAAGTAT  
GCACCCCATTTGGCAATTCATCAACACACATGAACACGGTTAAATGGATGCCCAAGCAATGTGCAGTGAA  
TGGTGGGCAGATATCATTATATCAGCTTGTGCAATAAATTTGAAAACCTGAAGTAAAAACGAGAAGAAG  
AATTGATTTTTCAGTACAGTATATAGATTA AAAATGACAAATCCTTGACCAGTGTTTTAAAGAAGAAATTTCC  
AGGAAACAACCTTACCTCAGAACTCTCTAAGGTGCTGACGATCAGCTGTTATGATTAATTTCTAGTCAGCCC  
ATGGGTTTTGATAACGCTTGTACTGCATTAGATGGTCTATCTAACATCTAGCTCCACTTTGAAACAGCTA  
AGAATATATTTTTGCTGATATGGTTAGAATGTTTCTAGATTGGAAACTATAAAAACCTCTTAATGAGTAAT

TGTA CTTCAATTTTAA C C A T C C A T A T T A C A G A C C T T T C A G A C A C T T T C A T A A T A A A T T T A C A A A A C T T A T  
A G C G G C A A T A T T A T T A T T A G T C A G T T A T G T T C T T T G T A A A T T A G C A T T T T T C C A T T T A C G A T A A C A C A A A C C T  
G T C G C T C T T T A T A T A C A C C G A G A T T C C A G G C C T T T A T T G G G T T A A T G A T G C A C T T G A C T A T T A G G C T T T A  
A T T G T A T C A T T A A T T T T G T G C G T C A G A G A G T T G G T T C T G C T G T G C T A T A A A A G A A C T G G A A A A G C A T C C A  
G T A A A A A A G G A T T G A G G T G T T C A C G A C A C A T T G A G C A T T T T A T T C G G G A G A G C T T G G A G C T T C A G T A T G  
A A G T G G C A A **A T G** A C A G T G T G C C T G A T G T C C C T G C T G C T T C T T C T A A G T G T T G A G G C A G C A G A C C C A C T G G

M T V C L M S L L L L L S V E A A D P L

**A G G A A C G A A T G A A A C T C C A G G T A A A T A G G** G T G A G T A A A A G G T A A T T A C G G A A T T T G C A A A T G T G G C A G G T  
E E R M K L Q V N R  
A G G G A C C A G G C A G A A T C A A T A A T T G T A A C A A G C A A A A T A G A A A C A G A A G T G T G A T G G A A G T G A A A A A  
A A G A C A G A A G G A A T C C C A C T G G A G A G A A G A A C A G A A C T T T T T A T T T A A A G C A G G T A T T G C G G A A G A G A  
A T T G G C A G T G A A T T A A C A G T A A T A C T G C T G A T G C T G G A T A T C T G A A A T A T A A A C A G A A A C T G T T G G G G A  
A G A A A C T T G G C A C T G T G G A G A G A G A G A A A A T A G A G T A A A T G T T T C A C G T T T T A G T T C A G A T T T C C A G C A  
C C T G C A G T A T T C T G T T T T T T A A C A G A A A G G A G A G A A T T G A A G T A A T A G T T T T G G G G A A A T T G T A G A G A G  
A A A T G A C A G A A G G T G G G A T T G T T C T C T A G A A C A C T G A G A A A G C G G A G G G A A A A T T T A A T A G A G A C T G T T A A  
A A T C T T G A A G A G G G A A T A A G T G C A A G T G G T T T C C A C T G A T A G C A G A C C G G T A G C C A G A G G T C A C A A T T T T  
A A G T T G G T T T A G A G A G A G A A T T T T T T T T T G C A C A G T G C A T T G T T A T A A T C T G G A A T A T G G T G C C T A A A A  
G T T G A G G G A A T G A G A T T C A G C A G T A A C T T T T A G A A G G A A A T T T G A T A T A T A A A G G A T G G T A A A T T G C A C G  
G C T G T G G G G A A G A A A C A G G G A A T G G G A C T A A C T G G C C A G C T A T T C C A C A A G G A C T A G T A C A G G G A T G A T  
T G A A T G A A T G G T G T T G T T C T T T T C T G T A G G A T T C T A T G A A A G C C A A C A T T G G C A T C A A G A G A T A T T G A G T  
A C A T T A G T T A T C T C T C A G G A C T G G T A T T A T A T A G G T C T G A G T T A A T A A A C C A G A G A A T T T G A G T T C A A A G  
A C C A C T T A T T T G A G A A C T T G A A A T T G G T T T G A A A A C A A A A T G C A G A A A C A C A A A G C T G G T T C C A G C A A A A  
G T A A G C G T G A A G C T G T C A G A C C G T A A T A A A T C C C C A A C T G G T T C A C A A A T T T C C T T T A A G G A A A G A A G T T  
G A T C T G A T A C A T G G C C C A C A G C T G C T C C A G A G C C A A T C T G G A T G G C T A T T A A C T G C C T T G T G A A G T G G T C  
C A G T A A A T C A C T C A A A T G T A C G G G G A G C T G A A C A A A A A T A T A G G C A T C T G T T G A C A T T G A A A A C C T A C T C  
A A G A T T A G A A A A T C C A G T G C G G C T G T G C T T T T G A A A G A C T T G T T G A T T A T A C T T A A C T A G A T A G T G G A A C  
A T T A T T G A A A A G C C A G T A A A C C T T A A C A A C T G A G G G A T T T T G A T T T T G C A C A A A T A C T T C G G C A G G A C  
A G G A G G A T C A G G G T T A A G A A G T G T T C A T T G G C A A A G A C A G C A G T G A G G A G T T T T A T T A T T A T T A T T G T G  
G G A T G T A G G C A T T A C T G C C T G G G C C A G C A T T T C T T G C C C A T C C C T A G T T G C C C T T A A G A A G G T G G T G G T G  
A G C T A C T T T T T G A A C C G C T G C A G T C C T C T G C T G T G G G T T G A C G C A C A A T T A T G T T A G G G A G G A A T T C  
C A G G A T T T T G A C C C A G C A A C A G T G A A A G A A C G G T G A T T T A T T T C T A A G T C A G G A T A G T T A A T G G C T T G G A  
G G A G A A C T T G T G G G T G A T G G T G T T C C C A T G T A T C A G C T G C C C T T G T C C T T C T A G G T G G A A G T G T T T G T G A  
G T T T G G A A G G A G C T A C G T G A G G A T C T T T G A T T T T C T G C A G T G C A T C T T G T A G A T A G T A C A C A C T G C T G C A  
A C T G C A G T A A A C T G C A A T A A A G C A G G T C G A T G G T G G G G A A G G T G C T G C T A T A A A C T A T G A A A A G C A T T C A  
G G A C A A C T G A G C A C A A T T T G A G T A A G C A A A T G A T G C T T G C A T C A A T G G A C A A A T G G C T T G T G T T G T A T A A  
A G A T A A A C A A A A G T T T T T T C T C T C T C T C G G T T T G T C C A C A **A G G A A G T T A C A A A A A G C A G G A A G T A T C T G**

E V T K S R K Y L

**A T G T T A A A A C T G C T G T C T G G G C T G T T G G A T C C T G A T G A T A A T C T C T T G G A A A A T G A C T T C A C G T C T T T G A**  
M L K L L S G L L D P D D N L L E N D F T S L  
**G C C C A G G A G A G A G A G A G T T C G C T T G A A G A G A G G T C G G T T A A C C G T G G C A T C C C C T C G T A G A C C G C A G A A**  
S P G E E E S S L E E R S V N A G I P R R P Q K  
**G G C A C C G T G T A A A T T G T T C T T C T G G A A A A C A T T C T C G C A C T G T T A A** T T A T T G A T G G A T T T C T A A A C C A G T

A P C K L F F W K T F S H C -

A G A A C T G T A T T T A A A C A A A A T G G C T T C T G A A G A A G G G T C T A G G C C C A A A A T G T C A G C C T T C C T G C T T C T C  
T C A T G C T G C T T G G C C T G C T G T G T T C A T C C A G C T C T A C A C C T T G T T A T C T C T G T T T T C C T G T A A A G G C T T A  
A C T T T A A A A T G A T C A A A A C T T G C A T G C A A T T C T G T T C T T T T C G A T A T C A A T A T T A C A A C A T G T G C C T  
G C A A T G A A T T T A A G C G G A G A G C A C C T G T G A A A C C C C T G T C A A A T C A T G T T T T C G A A A T C A A A C C C A G  
G T T A A A C T T T C T A A G T T T T G T G T T A A G G A A G G T A T T C T T T T G G C A T G T G A T T C C G G G C A C T T T C C T G C C  
G T T T T T C C C C C T C T A T T C C C C A C C T A G C A T T A T T A T T T C T T C A T C T C C C T G A T T T C C C T G T C C C C A A A A  
G G G T A G T C C T G G A T C C A G T T T C C C T C C C T G A T T C A A A C C C C A T A C T G A T A G T T T C A G A G A A G G A C C  
T G G A C G T A G A G A T T C T C T G T C T C A C A C A C A G T C T C T C A A G T C T G T C A A A C T G A G G A G A C A G T G T C A T T  
T G G A T T T G A T T G T G A T A C A T G A A T G T A T A G A A C A T A C A G T C T A T C T G C A T T G A A T G T A T A T A C T T A C C A A  
G C A G T G T G A T G C C A A C **A A T A A A** A G T A T A C A T T C A C A C C T G T G T A T T A A G C A T T G T A T T C T T T T C T A T C T  
C A A A C A A A A A G G T A A A C A A A A A C A C T C T G C T C C T T C T G T C T T C C T T G T G T T G A A T T T G C A G C A C C A A C A G  
A A C C G G T C T T T A A C C T T T T A T T T A T T G A T A C C A A T G T T T C A G C T C T C A C C G T C A A T T A C T C A C A A C C G T  
T A C A G T T T T G C T A T C C T A G G G G T G A G G T T G C A C A A G C C A G G T G T G T G T G C T A T T G G G C T G T G T G G A T T C  
C G G G G T G A T C T G A T T T T G C T G A T T A C A G G G T C C G A T A G A A T G C A C T C T G T C T G A A A T T A A C T T T C G A G C C  
A A T C T G T T C A G G G T T G A C G C C A C A A G A G C T A A T C C A C A C A A A G G T C A A T G A G A G G C A A T T T A A A A T C C C  
C C C T C A C T C C C C T A C T T T T C T G A C C C T C C T C C G C C C A C A C A A A A A A A T T A C A A A A A G A A G T G G A A G G  
G T G A T C T A A T C T T T A A A A C G G T C A G T G G T T T T G A T G G A A T G A A T A C A C A G A T T A A A A A T A A T C T T A A A A A  
T A T C T T A A A A C T A A A C A A C T T C T T T T C A G A A T A T G C C G A A G A A T C G A G C A A G T A C T G T T T G T A G T G T T A A



ACAGTCATTACTTGCAGAGCAACAGTATTCAAACCTAGGATACAAACTGGAAATTCATGATGAGCTGATAC  
TAGAGATCTTCAAGATTGATTTTGTGTTTGGACCTGCTGGTTGTCATTTCTGCTGCTGTGAGATAGTTAAGT  
GTTTGTCTTGCAAATCATCTCCCTGTCTTTTGGAAAGTAAGGACAGGGGCTCCTGGCAATATGTCGATT...

**C. Whale shark SST6 (NW\_018032490.1)**

...CCTTGGCATAGGAAAGGGAGAATGTACTTATTTCCAGGTTCCCTAACTGCTACACAGTAATGCCTAGTG  
AGGCATCGGGCACCAGCTGTAATGCTGGCATAGTTGAATAATTTGCTAGCATCCATCACCCAGACTCATA  
TGTGAAAAGGGGCACTTGGAAAGGAATACTGCAGTACAATCTCCTTGTATGAAAAGTTCTCGCCAAGGA  
TAAAACATGTCCAGGAAAGGCAGGTGAACAAAAAGGGAGTAGGGAACCTGTTAATTTGTGAAAAACAAA  
CAATCCAATTCAGTGGAAATCAGTTTTTGGACACAAATATACCATCAGATTTAGCATGTTTTAAAAAATTC  
AGTCATCAAATAATATCCACAAATGTCATGAGGAAGATCTTTTGTATCATATTTTAAAGACCTTATTAGA  
TATAGTGACAGCTCATTACATTTGCTCAATCTTTCAAATACTTTAGCACAAAGAAAAATTTCTACGGAG  
AAATGACCATCACTCCCTGAACATTTTAACGTTTTTCCCGAAGAAAAGGATCCTGCCTAAAACCTGCAGA  
CAGAAATTC AACATTGAATTTAATTTTGAATTTGAAGACTTCCCTCCTCAGTGCTTCTGCAGGCAGAAAT  
GCACTATTTCAACATATCTGATTGGATGACCTGGTTCTAAACTAAATCTGGTCAGTGAATGGTTAATCTT  
GGACTGGGTGTAATTTGTGTGCTTTTGTGAGTCTTAATGTTTAAATGAAGCTTTGGTCTGTGCGTCAGTG  
AGTGGGGCTGTACTGGGTTATAAAAGGGGTTGGAGACTGTCAAAACCACACAGAGACTTCAAGGGTCGA  
GGCACATTGCAAAGATCTCGAAAAGGCACCCTTCAATCCAATTC AAGCGACTGAGAGAAGAGGCAGCA

**TGCAGCTACTGGGGTCAGCGAGCTTKGTGTCTATACTGCTCATTGTGTCCAGTGTGAAGGCCACAGCACC**

M Q L L G S A S X V S I L L I V S S V K A T A P

**TTTGAAGACAGACTGAGTCTTCGGGCAAAATCAG**GTGAGTAAAGTCTTAAAATGTGGGAGCAGTACGTGA

L E D R L S L R A N Q

CCAAAAGATAAATCAGTGGAGAGAATAAGTAAGAACCTTAAAGGAATCAAGGAGTAAGAATCAGTGTGGG  
AGAGAGGTAGATGAATTTAGTTGGCAATTATAGAAAGTGAATTCGTAGACAAACAAATGACATACATCG  
GGGGTGTGATTGGAGATAAAAAATGTGAATAGTACATGATTTTATTACAGAGCAGTGAAATAATATTTT  
TAACCCCTTATGCAGAAAGAATTAATCCTTCAGAAGAGGAAACCAGCGAGTGAATCAGATTGAGAGGAGC  
TGAAAGTAATAGTGAGAGAGAATGGGGCTAAAATGAGAGTACGAGAAAATAACAGGTAAATGGAAGAGTG  
CAGTAAGAGAGTGGGCATGTTAAAATGGGAGGGAAACAAGTGCATGAGACAGAAAAAAAAACAAAAACGAA  
TAGAAAGGGACAATAGAAAAAATAGAAGACGAGAGAGGAAGTAGTGGAAATAGTAAAAATTAATTTGACA  
AATGTTAAAGAGAGAAAAGACAAAACCTGMGGGTAAGGATGCACATCAGAACTGAGAATGACAGAGTGAGA  
TGGTGAACAAGGGGCAGAAGCGCAGTGTAGGGGAATCAAAAACCTGCTTTTACACAGGAGCTAGTTTTGTT  
TGGATGTACAGAGACTGAATTTGCATGACGAGTCTCTTGTGTTTTATTCCCAATAGTTATCGCCGTGGTAA  
GTTTGTAAACCCCTCAAAATTTAGCAGCACAAGCCAGGCTCTGGAATAAGACAACCAGAATTAATAGTGC  
AAATGTCTAGGCCCGAAACCTCAGCTTTGCTGCTCCTCTGATGCTGCTTACCTGCTGTTTCACTCCAGC  
TCTACACCTTGTATCTCTTAATAGTGCAAATACCATGTTTCATGAGCAGTTTCTCAGAATTCGACTTA  
AACCTGCGTCTCTATAGAAGTGGGAAAAGAATGAGAGTGAAAAGAGATCAGAAGACAGAAAAGACAAATTTG  
AACAGATAAGCTGGGAGTAAGTGAATAAACCTTTTCAATCCCTCACACAGAATATCTTTTGAAGAGTAG  
TAAGGCTTACAGTAAGTAGGAGAGTGAGTGACAGAGACAAAAAAAAACCTGAAAGGCAGATGGAGAACT  
AATAAGCAGAGAGACTTGGCTCTGACAAGCAATAACAGTGCAAACTAYATGGTCTGACCTCCCTGGTGCA  
CAATCTCTGCAAAGACTGCCCTTGTATGAGACTAAGTCACTTCAGTCACTGTTAGTGTACGGCAGCT  
TACTCACCAGCTCTGCTCATTGATGCCACACCATTCCCCTTATTGTTTCACTTCTCAGTGCCGTGTAGCTA  
AAAGTGATTTCCAAACTACAAATTAAGTGTGCAAGTGTGTAATTTGACGAACGTTTTCATGCACTCATATCTG  
ACTCTCCTCTGGCTCAGCAGAGCTGTTAAAATGTTAATAATACAACAATGTGAATGCAAGTCTGGACTTC  
CAAGTACAGGTTCTAGTTTTTATAGTGTGATTTCCACATTAATTTTCCCTTTGCTGTTATCTCTAACAGG  
TGCTCCTGTCTAATAAATCGATCGCATTGTGCTATGCATTTCTATTTAATTATAAAGGAGCAAGGAAAC  
CAAGTGCAGGACTCTCCCTGTTGCTGAGTTGAAGGGAACAGTCCCTGGCAGATGTTACAACCTTTGTATTG  
GATACATGGCTAAGGAGAGATTTAAAGATAAGGGACAGTCTGCTGTTGAGATCAGTCTTTATTAATAAT  
ATTATGCTTATTACATGCTGATTTCCATTTATATTATCAATGGTCAGCATAGCTAGGTCCACACAGTCCAC  
CTGTTTTTATCTTATATCTCAAGATGAGTGAAGAGTGAGCCTTCATAGAACCATTTGCTCCAGCTTTGG  
GTGACATATTTACAGATTTCTGTGCATCAGTTCAAAGGCTCATCAATCAGACTTGCTTTTGTGAACTTT  
GTGCTATCAAAATGACCAAAAATTAATAGTGTCTCATTTTAAAGGAGCAATGTCTCTCACAGGTCAG  
GTCTGCCACAGATACAGCTCCTTCTGTGCTGTCCCAACAATATACCTTTAACTTCAGTCCCTCGGTCAA  
AACAGGCACGAGAGTAAAGATTTTCTTTTTTCACTCCAGTCAATTCCTGTCTATCTCTGAGTGTCCAATTTG  
CTGCTAAGGTGGKTCGGTATGTGAGTCTCTGAAAAGCATTGGCTGAGCCTTTTGTTTAGCAGAAAGCTAAC  
AAGATTGAAAAGCTGATTATCCTGTGCTTTTTAAAACATGCTTGTAGGCCATTAATTTAATAATTTTACAA  
GATGGAGTTATTAATCCATTGGAATATTGGGTATCATTTTTTGGAGGTTGAGCATATCTTGAAGCACTGT  
AATGTCAGGTAATGAGCTCAACTTCACTCTAAGTATTTTGGCAGCAGGAAATTTCCCATCTCGTA  
CAAACCTATTTTCTGTACGAGGGGCAGGAAACAGCAAGGGAGTTTCGGTGAGGGCTGGGGGTGGGGGTG  
CGGTGGTGGGCAGTGGTGCCTGGGATGTGGGGTAAGGGAATTAAGAGGCAGAGTGGGGACTGTGACTGGG  
ACTGACTCCACTCCAGAAGTGACTTTGCGTCTGTCTATAGATAACAAGGTGTAGAGCTGGATGAACACAGC  
AGGCCAAGCAGCATCAGGGGAGCAGGGGTCTCGACCTGAAACGTGAGCCTTCCTGCTCCTCTGATGCTGC  
TTGGCCTGCCGTGTTTATCCAGCTCTACACCTTGTATCTCAGATTTCTCCAGCATCGGCAGTTCTGACTA

TCTCTTGCATCTGTCTATAAGTTGCTGGCCAATCAGATTCCCTTGCTAAAGGGGAATGTGCTGCACTGGGGA  
AACAGATAAATGAGGCAAGTGGACGAATCACATTGTTTTCTACAGAGAGTAGAGGGAAGCAAAGATGCATG  
ATCTTTTGTGACCTTAAAAAATCTTTCTCCCCAGTTATTCCACCTCAAGATATTTGCCACTAAATAAGACT  
TAAGACCGACATTAATGTGCAGAAGGAATAAATAGTGGTGGTATTATCCACCCAAGGGCAGGACTCCGG  
CTTATTTCTCTTTGCTTTGTGGTACTGAGGTGTCCTGCCTGGTTGGCAATCTGACTAGGCAAGAGGGGAC  
ATGAGGTAGTTTCTCCCATCTTCCCTTGTGTGCTTAAAGGAAATGCAGATGCTCTCCTGCATCCCTTGCC  
TGTAAGCAGCTTGTCTTAGAGGTTCTACCAACATTACCAACACTGGCTTACAGCCTTCAGCATGGCACC  
CTCAGCTGGGCTGGCTCCGTCTCAAGAAAGGATAGGAAAAATCTGTCCCTAAAACCTCAAATGACCAGT  
AAATAACGTTGCTGAGATTATATCCACTGGGCTAAAGGCTAAATGTTTCATAGATACCACTGAACAATC  
CCCCTTTCAGACTAAAACCTCAGTCATTCCCTGGTTTGTATAAATATGCAGAATTTTACAGTTTCGGCATG  
TGACTGTCTTTTGTGCAAATTGGCCTTGCTCCAAGTTTTCTCTGGCAGTGGTTAGAGGGGCAGCACGGT  
GGGTCAGTGGTTAACACTGCTGCCTCACAATGCCATGGGGCTGGGTTTGATTTACCGTTGAGCGACTG  
TCAGTGTGGAGTTTGCATATTCTCCCCGTGTCTGCTTGGGTTTCTCCTGGTGTCCAGTTTCTCCCAC  
ATTCAAAGATGTGGATTGGCCTTGCTAAATTGCCACAGTGTCCAGTGATGTGTAGGTTAGGTGGATTAG  
CCATGAGATATGCAGGATTACAGGAATAAGGTAGGGGTTGGGTCTGGGTGGGTTGCTCTTCGGAGGGCCA  
TTGTGGGGTCAATGGGCCGAATGGCTTGCTTCCACACAGTGGGGGTTCTGTGTTTTCCCTCTCTGTTC  
TTAAGGTGATGACCAATGGCAAAATGTGGGAACCTTCTAATAACCCACTTGAGTGTGAGGCTGGACTATG  
AATATCTGATCATGTAAGTATAGGTCTAGAGAGGGGAATAATTACCAATTGAACGTTATCTTATTTTCGC  
CTGGAGTTCACAAGCATTATTTTTTAGTGGAAATGTAAAATATTAATAGACACCCCTCTGGTCATTTGCAG  
CTGGACTGTTTTGTTGAGGTGAGCTAAAAGCATTCCGAGACTGTGTGGCTCAGGACCACAGCAGAAGGA  
GTGTCTGATGATTGATTTATGTGATATGTGGCCATCAGCTCTTTTAGCCCTCAATACCTTGATTCTGTT  
GCTCTATAAGAAAGTGTGGGATTGTTTCATATTTTACTGAGCTGTTATTCAGCTAACTTCCAGGCTCCAA  
TCAACTAGGTAACCTGAAGGAAACATTAATAGCGAGTGCAGGAAGACAGAAGAAATTTCTCTCCAACAGCC  
TGTGTATTATTTTATTAATAATTGAAATGGCGGAAGGCTTTGTTAAGCTGAGTGTATACGACTTTAC  
ATGGAAGGTAATAATGTTTCATCTTTAATATCCTGCGTGCAGCTTTACTTTGTTGTACGTGTTGGCACCT  
TTTATACTTGTATCCTGCCTCTGCAGAAAATTACGCTGAGTGCCTGTGGTGAAGTATCTCCGAGATTAT  
AAAAACTACAATCACAATGCAGTCATTACATCAGCAACATAAATCTGACAGTATTTTAAATGCTGCTCTG  
TGAAAGCTTTAAGTGTAGCCAGTTATTTTATTTAGAAAAGGCACTTATTCATGGTTATCGTAGAATCTTA  
CAGCAGAGGAGGCCATTACAGCCATTGTGCCTGCAATGGGTTTTAGAAAATACCTATCCAATAAGTCCCAT  
TCCTGGATTTTTCTACCAGTAAATGAGCTAATCTGAATGTTCCAGATCATTCCTTGGGCTCTGCTGGAT  
TGGTTAATCTTAGTTGGAGAAGTGGCTTTGATGTTACAGTCGGTTGAACCCATCAGATTAAGGGCTGGGT  
AACATGGGGAGGCGATGGCCTGTTGGTATTATTGCTGGATTGTTGACCAGATAATGTTCTGGGGACCCA  
GGTTTGAATCCTGCTATGGCAGATGGTGAATTTGAAATCAATAAATATCTGGAATTAAGATGACCATGA  
ATCAAACAAATCTGGTTCCTAATGTCTTTAGGGAAGGAACTGCTGCGTGTACTCCATCTGGCTTGCA  
TGGCCTGTCTGAATCCAGACCCACAGCAATGTGTTTGAATCTTAACTGCCCTCTGGGCAATTAGGGATGA  
GCAATAAATGCTGCCTGGCCATTGACGCCCTCATCCCATGAATGAATGAAGGAAAAAAAAAATCCTGGTTA  
TCATTCTGCAACACTTGTAGAGAAGTCTCCGTGAATAAAGAGTCTGCTGACTCTCACTCTCTGGACTGAA  
ACACTCAGCTGATGTTTTAGAAAGATAGCATGTACTGAGTAAACTATTCAACCAGCAAGAGATGCCGCGTC  
TTGTGCAGGAGTGGGACGGGGGATTGGGGTAATGGGAACAGAAAAACAATGTGACACTCAGCACTGTCA  
TGTCTGAGTCAGAGTATTCAATCCCATTCACAGAGCTGACCACATAATTTAGGCCAAAAAGTACTGTG  
AGGATGTGCTGTCTTGTGTTGAGGCATCTTTTCCAAGACAAGATGTCAAACAGAGGCCCTGCCAGATGAAT  
GTAGACTATCCCACATCAAGTCAGAAATTGCTGGAGAATCTCAGCAGGTCTGGCAGTGTCTAAGAGAGAG  
AGAAGCAGAGTTAACGTTTCAAGTCCAGTGACCCTTCCCTCAGAACAGTAAACTATCCCGTGTGTTTCTG  
ACCAATATTTGCCTCAATCAACATTACTGTTACTCGCCCTTCTGAGTGTAAATTTGATGCTGCATT  
TCTGAAAAAAWTTCTTAATTGCGATTAAGTGTCTCTAGAAGAGCAAAGATGCAACATAAATGCAAGTTA  
TTTTCTTTAACC GGATGTGTACAAAGGCTCAGGTTGGGGAAAAAAAAAATTACTCTTTTACACATGGCAGGC  
CACCCATCACGTGTACAAAATAAACCTCCACCTCAGCCAAAATAAATGGGCTCAATCCTTCAGAGTGCAA  
TTTGGCACAGGTTTTACAGAGCGGCAAAACACGAATAGTTCTGAGGAAGCATCACTGGACCTGAAACGTT  
TACTCTGATTTCTTACCATAGATAATACCAGACCTTTTCCAGCAATTCCTGTTCTTGTTCGGATTTACA  
ACTTCCACAGTTCTTTGCGTTTTTGTGAATGAGTTTCGTGTTTGTCTTTAAC

E L N K E

GGAAAGAGGTTGTTCTCAAGCTGTTATCTGCACTGCTTACTCCAGCAGCAATCAAATGGGGATTGAGAA  
R K E V V L K L L S A L L D S S S N Q M G I E N  
CACGTTCCAGATCAGGAGGACATGGAAGAGATGAAAGTGGAAAGACAGGTCCCGCTTCAGTCAGTTACCA  
T F P D Q E D M E E M K V E D R S R F S Q L P  
CAACGAGAGCGGAAGACATCCTGCAAAAACCTTCTTCTGGAAAACCTTCACTCCTGCTAA

Q R E R K T S C K N F F W K T F T S C -  
TGACATGTCGCTAGGAACTGATTTAGCACTGTACATAAGCTGGTGTGTTTATTTTCTTTGTTTCTTGGG  
GGTTACATTTCTTTTCATGCACAAGAAAAATTTAAAAAAAAGCATGAATGTGTGTAATTTTGTGCAACT  
TGTATGATTTCTTTTCCAGCAATGTGGTGGCCTCGTTCTGTGTAGAGCAATAAAGTGGATCCGAAATAA  
TCAAATTTGATTTGATCGTTTACTGACTTGGCCTTTCAAAGCTCTGTTTGTGATCTGTTCAAGGGATTG

ATGTCTTAAGTGAGAGAGGGAAGTCATAGTCAAAGCTACAGGGGAGGCAATGGCCTGGTGGTATTATCRG  
TGGGCTGTTAATCCAGAGATCCAGGTAATATTTTGGGGACCCGGGTTTGAATCCTGCCATGGCAGATGGT  
GGAATTTGAATTCAGTATAAAGAAAAATCTAGCTGGTGCTCTGGTTTCCTCCCACAGCCCAAAGATGTGC  
AGGCTAGGTGGATTGGCCATGCTAAATTGCCTATAGTGTTTCAGGGGTGTGTAGATTAGGTCGGTTATAG...

## Figure S6

### A. Whale shark SST1 (SSTa)

atgtggtgcagccgagttcagtgcgccctcgccctgctctccatcgctctggcagtgctg  
M W C S R V Q C A L A L L S I A L A V L  
agtgcggggcgccgctcccaccgcccagcaggtatcgcgaaactcctccagacatcaatggct  
S A G A A P T A D R Y R E L L Q T S M A  
ggcgcagagccccggagtaaagcggagctgatcaatacaatctcgtccaattgctcgcg  
G A E P R S K A E L I K Y N L V Q L L A  
gagctggcaaacgcccgagaacgaagttttggatggggaggatttgccgcgatggcgaaa  
E L A N A E N E V L D G E D L P R M A K  
caggataggtaggggttgatctggaacgatccgccaacccaattcgccccagaggaa  
Q D E V R V D L E R S A N P N S P Q R E  
cgcaaagcgggctgcaaaaacttcttctggaaaaccttcacatcctgttaa  
R K A G C K N F F W K T F T S C -

### B. Whale shark SST2 (SSTd)

gaagtggcaa  
atgacagtgtgcctgatgtccctgctgcttcttctaagtgttgaggcagcagaccactg  
M T V C L M S L L L L L S V E A A D P L  
gaggaacgaatgaaactccaggtaaatagggaagttacaaaaagcaggaagtatctgatg  
E E R M K L Q V N R E V T K S R K Y L M  
ttaaactgctgtctgggctggttgatcctgatgataatctcttgaaaaatgacttcacg  
L K L L S G L L D P D D N L L E N D F T  
tctttgagcccaggagaggaagagagttcgcttgaagagaggtcggttaacgctggcatc  
S L S P G E E E S S L E E R S V N A G I  
cctcgtagaccgcagaaggcaccggtgtaaattgttcttctggaaaacattctcgcactgt  
P R R P Q K A P C K L F F W K T F S H C  
taattat  
-

### C. Whale shark SST3 (SSTe) (exon 2 only)

gactttctgaaggacacaattatccaacttctacatgtgggctcgcggatgcagacaaggat  
D F L K D T I I Q L L H V V A D A D K D  
gctgtggaagtgaatgcttctcaagttgagactccaccagwtaacaagattccaatgaaa  
A V E V N A S Q V E T P P X N K I P M K  
ttccagcagcgtcaattgggaacaagaatgcggaaaaactgcaagaatttcttctggaaa  
F Q Q R Q L G T R M R K N C K N F F W K  
acatacactttatgttaa  
T Y T L C -

### D. Whale shark SST6 (SSTc)

aaccacacagagacttcaagggtcgaggcacattg  
caaagatctcgaaggcaccacttcaatccaattccaagcgactgagagaagaggcagc  
atgcagctactggggctcagcgagcttkgtgtctatactgctcattgtgtccagtggaag  
M Q L L G S A S X V S I L L I V S S V K  
gccacagcacctttggaagacagactgagtccttcgggcaaatcaggagctgaataaagaa  
A T A P L E D R L S L R A N Q E L N K E  
aggaaagaggttgttctcaagctgttatctgcactgcttgactccagcagcaatcaaatg  
R K E V V L K L L S A L L D S S S N Q M  
gggattgagaacacgttcccagatcaggaggacatggaagagatgaaagtggaagacagg  
G I E N T F P D Q E D M E E M K V E D R  
tcccgttctcagtcagttaccacaacgagagcggaagacatcctgcaaaaacttcttctgg  
S R F S Q L P Q R E R K T S C K N F F W  
aaaacttcacctcctgctaactgacgatgacatgtcgttaggaactgatttagcac  
K T F T S C -

tgtacataagctgggtggtggtttatcttctttggttcttgggggttacatttctttcatgc  
acaagaaa

Figure S7

A. Elephant shark SST1 (Sc\_821)

...TTTAGTGGATGGTATGTTGTGGATGCTGTATAGGGGATTGTGTGTAATGGATTGTGTGTAAGGGATGGT  
GTGTAGTGGTTGGTGTGTAGAGGATAGTGTGTAGTGGATGGTGTGTGGTGGTTGGTTTGTAGAGGATAGT  
GTATAGTGGACGGTGTGTGGTGGTTGGTGCCTGGGCATGGTGTGCGGAGGATGGTGTTCGCGATGGTGT  
GTAGAAGACTGTTTGTAGAGGATGCTGTGCAGTGAAGGGTGTGTTGGGGATGGTATGTAGTGAATGGTGT  
GTAATGGATAGTGTAAAGGGATGGTGTATATGGGATGGTGTGTAGAGGATGGTGTGTTGGGGATGGTGTG  
TTCAGGATGTCCTTCTAATATTTTGCCTACAGTATTAGAATTGAAAAGTTTGCCTCTGTTTTGCTCT  
GTATTTAAATCCATAGAATTAATAAGAAAAAAATGTAATATTTAAGAGGAGGTGGACGTGGTACGAATC  
TCTGCCCTAATCTTAAAAGCCTCGTCACGGCCGGATGGGTGGGGGTGGGAGAGTCAACGTATCGGAGCG  
ATAACATCCCCAAGTGGCGAGGTTATGGACATTATCTCAATACTCGTCACGTGGGTTATTATTTTGTTCG  
ATGATGTGACTAAATTGAGCATAAATTGCTTAAATCTCTGAGGACATTTGCTTTTACGTCAGAAAGGTGG  
CGTGAGGCGGCTTTATAAGGCGAGTCTATGGACACCAGGACCAGAAGATCCAGACGAGGCAGAGCGTCCA  
GAGAGCCGGTGTGAACCACGAGCGTTTCCCTCCGTTTCTCTCGCTCCTCCTTTGACAGTTTGGTGCCGT  
CGCCCCGAGATGTCGTCGCGGCGAGTGCAGTGCAGCCTGGCGTTGCTCTCCATCGCCCTGACAGTGCCTGA  
M S C G R V Q C A L A L L S I A L T V L  
GTGTCACCTCGGCCAGCACACAGGATACCGCGAAATCCTGCAGCGATCACTGGCCGCGCGGGAGC  
S V T S A P A H D R Y R E I L Q R S L A A A G A  
CAGGAGTAAACCGGTAAAGACAGCCGATCCACACTGGGTAATTAATATCTGACAAGGTTGCTAAATACAC  
R S K P  
ATATTTACAACATTGACCTGTATTTCTAAAGTACATTCAATTTGGGATTTTTGACTGGAGCTAATTATCCG  
ACCGTCAGATTTTATTTCTCATTCTGTAAATCTGAATATAGCGCATTTTCAAGTGTGAGTCTATAACTG  
TAAAGGAGATATCACGGTAACTCGTCTCTAACTTGCACAGAGGCAGATGCGCACCTGCCAGGATCGCCGA  
TGGCCCCAGAGACACACCCCGATCTGGAGCCCCGGTACCGCGCTCTCGGGCTCTGAGGATAACATTTCCA  
AACCATCAGATTACCGCACTCTCAGTCTCAGGGCAACTGCTCAGTGCAGGCGGAGGACCCATAGCTCCCGA  
GCGCTCCGTGTGAGTGTAGTTGGAACCGTTGACACCTTGAAGCCATTCAATCGTCTAAACAGTTT  
TATTTTAATGATTAATGCATCAATTGGCATCAAACGACAATTTTAACTTTCAAGATTTGAGACAGTTTCT  
AACTGAACCTCCCCAAAATCTCTTCCGACAATTTGTCACCAATAAACAGAAACCTCCCGAACACAGCACAA  
GAACCAAGTTAAACAGCTACAGATTGTAAGTAGCTGTCAAACAACCGCGTAACTAGTAACTAGTCCGGT  
TGGTGCATTTCTGGGCACAATAGAGAGGACTCCAGACTCCAGGCTGAAAACCTTACATCTTTCTTACATT  
TACTAAAACATTGATATCTCCTAAGCTGAGAGAGCACATCCGTGTTACCCCCACCCCCACCCCCACCC  
CGGAGCGCTGGCCTCTCATGTAGCCAATGGCTTAGAACCTATTTCTCCGGGAAAGTGAATGCTCGTGATT  
TACATTCGGTCTTGAATTGAGTGATTTTTCAGACATTTCTTGTCTTAGTGAGTAGTTTGGACTGAGGAG  
GAGTTTGCAGTATATAGGAGGTGGGAGTCACTGAGCCATAAACAGACAAACACGCTGATTTTCTGATCT  
TCACACAACAGCCAAAGCTGGAGAGGAAACTGCGCCAAACGATAACATTTTGTGAATGTAGTCAATTAAT  
CCGGTTGAGTAATCAGCCATCAGCTGCTTGCATGTGTACATGTGCCTCACTGATTACTGTTCTCTTGT  
GTTACTGTTCTCAGGAGCTGACCAAGTACAGCCTGGCTCAGCTGTTGGCGGAATTGGCCAACCGGAGAA  
E L T K Y S L A Q L L A E L A N A E N  
CGAGGCGCTGGAGGCGGAGGACATGGCCGAGCAACCGCACAGGACGAAGTAAGGGTTGAATTGGAGAGA  
E A L E A E D M A R A T A Q D E V R V E L E R  
TCGGCCAACCCCAACCTGGCGCAGAGAGCGCAAAGCGGGCTGTAAAAGCTTCTTCTGGAAAACCTTCA  
S A N P N L A Q R E R K A G C K S F F W K T F  
CTTCCTGCTAACTCTGAGCAGCCCCACCACCCCTCTCACACACTCATAACACACTTTCCCTGACCC  
T S C -  
CCACCCCTCCCATCCCCACCCTACACACAAAGTTTTCCCGATCCCCCGCCACACACACACACACACAT  
TGTATTTGTCTTACGCTACG TGGTCTGTTCTGATTTTAAACATACTGTAATAAACACATGGTGTATGATA  
ATTCAACCTAATTTATTGTGACAGAACCTTTAGATGGGGTTGTGACTGTATAGTTACCCACTCTTTCTGG  
CTAGAGGTGTATGTATTTTTTAAATTTGTATGTCGCAATGAAATACATGTTTGAACCTGAAACCATCTC  
TTCTCTTTCTTGCCTGACGTGTGAAAGTCGCTGGTTACCCGGCTCAGCTCCATCACTGACGGCAAAGCGT  
AGCTGTAACATTACACGAGTTCTATATATTTATATCACTTTCTCAAAACGTAAACCATTTGATCACAGAT  
GTCTTTTACGCGATGTGGAGTCTGTAGCTCAGTGGTTAGAGCACTCGCTTTGCAAGTGAGAGACCTGAG  
TTCAATCCCCGGGGGTGAGGGCCAAACCTCGGGCAAGTTTCTTACTCCACACAGAGCCTAATAATAAT  
CCTCCAAAACCAAAAACAATAATAAATTTGGTCAATTTCAATCTACGACTGTTTGTGGGACATTTGCTGTG  
GCAATTTGGCTGCCCGTTTCGCCACAAATATACAGTCAATTTCACTTTACAGTGTGTTCTGTGAAAGTGTCT  
TGGGACATCTCCGACGTGAAAAGCGCTATATCAAATGCAAGGATTATTATTATTATTTATTTATTTGCTCAGAC  
AGATCTGCCATAGTCTTTCACTGTGTGATTGACATTTTCGGCTCTCATTTCACCAACTCCAGAACAGCTCA  
CTGGAAGCGATCATTGAAACACAGCAATGACCGGGGGCGACCCCCACCGTCTGTCTCAATGTAATCCTCA  
CTCTTGTCTGCTCTCACTCTCGCACTCCTTCCCTCAACCATTCCATCACCAGATGGTTATCTCATACTC...



**B. Elephant shark SST2 (Sc\_58)**

...TACTTATTTTTTTTACATAATAATAATAATCCTTGCATTTGATATAGCGCTTTTCACGTCGGGAGGACA  
TCCCAAAGCGCTTACAGAACACACTGTAAAGTGAATTGACTGTATATTTGTGGGCGAACCGCGCAGCCA  
ATTGCGCACAGCAATGTCCCACAAACAGTCGTAGACTGAAAATAACCAATTTATTATTGTTTTGTTTTT  
GGAGGGATTATTGTGGTTGCTTGTGGTTGCCCTGTTGTGAGTTTAATTAGCTTATCTTGTAAAAAGAAA  
CAATGAGGTTTTGAATGAAGAAACAATTAACAATCCTGTTGAGACTGAAATCTTCCGACTTGATATGAC  
TTGTGTGAGGTTTTTACTCTATTTCATACCCTTGCTGTTGAGTCTAAGTGTATAACTTAATCGACCTTC  
TTGCAGTACTTAGATTTTTGTGCACACCTCACCTCATAATAGAAAGAAGCACTTGTAAATTTATAGTACC  
TTAACATGTTGAAGTGGCTCAAAATGCTTTACGGTATTGAGTGTGCTGTAATGGAAATAATGATAATAGT  
ACTTGCATTGCACCTTATATTGTCTGTTGAGACGTCTCAAAGCAAGCGCTTACAGACTATAATGTAAAGT  
GGATTGACTGTAGTTTTGTGGTGAAGTATCAGAAATCCTGATAACCGTCTACGACAGATGTATGAACAC  
TATCAACCGAGCTGAATTAATACCCATTAATGTGGGCAAATCACTAACGAGGCCACTTTTTTTAGTCTTT  
TTGAAACTGATAGTAACCAAAGTCTCAAACCTCAGCCTAAGGATAATTTGCCACTGTATAGGCAAAAGGAG  
CTCTAGTGAGAAAAGTTCACGTTTGTAGATATTGTTTGGAGGAATGTATTTAAAGTTCTAATAATAAAATTA  
TGAAACAGCACCTCATGACATCGTACCGACAACCTCAAAGCACTTACAGAAATTTACCGTACAGTGTAGT  
CAATGTGTGTAGGCAAACGCGACAACCAGAACAACCGATGTCCACGAACAGCATGATGTCAATCTAGA  
CTGAGTACAAAGTCCCAACATGGGGCTTGAACCCATGATCTTCTGACTCAGATGAGAACAGTTAGTGACA  
TTTTGAAGACAATCTTGTGGTGAAGGATGGCGTTTAAACCTTATTTCTACTTGTGAGGAAAGAGTAAGTG  
TAAAACGCAAAGGTCAAATTTCTTTAATTTACGTAATGGTACTGATATGTCCCTTGTAAATGTCAGGGCT  
ATTCAAGTGAACATTAGGGCATATATCAGACCTTACACGTGACCCACAAACCAGACTATAAAACAAGACC  
TGCTATTTCAATCTTTCCAGTTTCTTTCAGCAAAATCGATACGGCCAATTGAGAAATTAATAACTATAAT  
TGATGTAGATCACCCAAATCACAACCTGTTTGTGGGGCACTGTTGTGCGTAATTGGCTGCCTCGTTTTACC  
CACAAAATGTACAGTATATTCTGTGAATCACTTTGAGACATCTTGAAGATGTGATAAGGTACTATATCAA  
ATGCAAGGATTATTATTATATTGATATTGAGACGTCTTCCCGATGTGAAAAGCACTATACGAATGTAATC  
TTCTTGTGAAATGTTACAAAACCTCAGAGCTGGCTAAATGTTTGTCTACAGACAAATTTCCCATGAAGA  
GTCCCAACATCCCATAAAGCTGCTGAACCCCTTATTTAGTAAACTGGAGGTCAATCATGTAATACTGTGGAC  
CTTTCTGGCTCATGTATCAGATCGCCCAACGAGAGCTATCAAAGAGAATTGTCTCAGTCCACTAGTCA  
TGTTAGATTGGTGTGGCATCACCCCTTTCTCAGAGTTGTCCCATGACATCAATTTCTCCGCAAACTCA  
GGCTTCAGCCTCACTGATTCCTTATCAGTCTTTGAAAACAATGACTTTCTGAGTTGTGAAAATCTTATGT  
TCTGTAACAGGCATTATTTCTGTTAGGGTCATCAAGTGGTATTGCCAAGGGGAGCCACTTTTTTTAATA  
GATCAGATGACAGATTGGTTAATGTCTCATTTGAAGGACAGATGATTCATGGTAAGACGAAAAAGTTTC  
ATTTCTTGTGGATTCTAGAGCTGGAACAATTTCTACCTCCACTTTAATTCGTAGAAGTGTTTTTTGTGT  
GTTGGATATTATAGAAGATTGATGTTGAAAGCTCTATACAAAACACACAAAGACTGACTCATTTCTAAAT  
GGAAAGCTCTTTAATTATCAGTGTCTAATCTTTGATGCAAATCGAAATGGAAAATATAAAAATAAATC  
AATTATGATCTTTCTAAATTAACATTTTTTTCCAGTTGTTGACTTTGTCATTTTTTTAATGTTCCAGTTA  
ATGGTTCTCATTGTATATTAGTGTCTGATTATAGCACTAATTTTGCACGTGAGCGAGTGTATAATTGTG  
CTGCATTATAAAGCAGGACAATTAGAGTTTTCTCAGCAAAACAGGGAAAGAGTCAGTGAAGCTCGACA  
GATCCATTGAAAAGAGAGAAAGTTTGTAGTCCAGC**ATG**CAGTGGCAAGCATTTCGCAAGTGTCTGTGTCTG  
M Q W Q A F A S V V C L  
TTGTTTCAATTGAACTGTTTCAAGGAGTTGAACCACAGGAGGAACGAATGGGTCTTTCAGCTGAACAGG**CT**GA  
L F I V T V Q G V E P Q E E R M G L Q L N R  
GTAAAATAATAATAATCCTTGCATTTGATATCGCGCATTATCACGTCGTTGATATGTCTCAACGCCCTTC  
ACAGAATGTACTGTAAAGTGGTGAATTTGGGGCCAAATTCGGCAGTCAGTTGCGCACAGCTGTGTCCC  
ACCATCAGTCTGTGATTAAACTCGCATGAATTTTACCAAAAAAAAAAAGTTTCTTCTCTCCATCCAACA  
**CGAGATGGTAAAGGACAAGAAACGCCTGATTGCGAAGCTGCTGGCGGGATTGTTGGACGTGGATGACAAT**  
E M V K D K K R L I A K L L A G L L D V D D N  
**CTGTTAGAAAGTGTCTCGCCCCATTGGGTCTGAGCAAAGAAGAGGGGACTGATTTGAGGAGAGATCAG**  
L L E S V I A P L G L S K E E G T D F E E R S  
**CTGCCGGTGAATCCCTCCCAGAAAACCGAAGGCAGGGTGCAAACCTGTTCTTCTGGAAAACCTTCTCGCA**  
A A G E I P P R K P K A G C K L F F W K T F S H  
**CTGT****TAG**TGGATTTGTCAAAGATAAACATTTTTTAAAAATCCAGTTTGTGTTTTCTGTTGATATGTAA  
C -  
CACTTCCCCCCCCCACTGCCCAATTCCTGCACCCCTCCTCTCCACTCCCTCCCCCCCCCCCCACCC  
CTTCCATACATCAAACGATTTGTAAATATTTCACTGA**AAATAAA**ACTGGAAAATAAATAGGTGGCTTTCTAA  
AAGGCGACGTAAATGATTACATTTTAATAAATGGAAATTTCTGCATTAGAATTCACAGTGTCTTGTGCGT  
TTTTTTAAAGGAAAAGAATCTGAATTAATCCCATGTTCCCTTTAATCATCCGCTGCGCTAAAGAGATGC  
ACAGGTCCTGCTCAGCGCATCCCAGCGGAGTGAAGCTCATATCTTAACCTCATACCACAGCCACAACCT  
TTCTGACTCAGAGGCAAGAGTGAACCAACTGAGCCAGACTGACACCTGTGACTAATAGTAATTTCAATTT  
CAGACATCTTATCACATCTTCAAACATCTCAAAGCGATTACACGATATACTGTAAAGCGCAGTACTA  
TTTTCAAGAGTGTATTGTTGCATTTTGAAGGGTTGTGTGTCAGCCTGGCTCAGTCCGTAATGTTTTCA...



C. Elephant shark SST3 (Sc\_821)

...TGGGCAGGGCATTGGGAATAAATTAATCAAATTATTAATCAGGGTGGGTAGGGCATTGGGATTAATTA  
GACATCTTGCTCTGACAGCCTGTACAGAATCAATAAACTGAATGGACTCCTTCTGCACTGTAAATTTCTG  
TGTCTCTGAGTTGAGTCAGTCGGTGAGATTTTTGAAGCGTTTTCCAATCCCACGTAATTGTGTATCATTA  
TTATATATATTATATATGCTTACATGTGTCTAACATTTTTTGTGTGGGTGTGTATGAGAGATATGCATGTA  
TTGTATAGCACCTCATGGATAGTACTCGTTATGCCGCTACACATGGATAAACTGAAGTTTTGCTTTGAGTG  
TCCATCAACCTTAATCTGTCTGGACAGGTGGCTGTTTGAGATGAATTATAAAAAATCTGTCCACCTTCT  
GGGTAATATTTGCTAATTAGTTGTGTTTGCAATAAGTGAGTGGATCAGCTGAAACCAGAAAGCCATTAT  
CACATTTTACCTGAAATTTAAATTTGCTCAGTGAACCACTCAGCCCTACCACATGGGAGCTGTGTCCAGC  
ATTCACGGGGGAGGGGCAGCTAGTGAGGGCTACTGATTGCACACACAGTCAAGGGAAGAAACACTCAC  
TTGGCAGCTGCTGATGGACATTCATTGTGCTGATTCCAGTGCTTTTTATGCTGGAAATTGGAAGACTTGAGT  
TGAGTCAGTAAGTGAGTTAATGGAGTGGCTCCAATCCCATCTAATTGTTAATGAATAGAGATGGGCTG  
AGGCAGAAGGTGGGAGTCAAGCGGCTAAATTTGATGGAAGAGCTCTCCATTTAAATTTCCAAGCCTCTTGT  
GTTTAATTGACAGCAGAAATTCACAGACCATTTAAAGCTGTAACATACTTTTACACCGTTTCACTTCCGC  
TTTTGACAGAAACAAACATTTACAGTCAAAGCACTAGACCAATTCTCAATACTATTTCCATAACATATTT  
AACAAAGGCCCAATAACTTTTCCACAACACGCAAGGAGAACATTTATTACATGTGATTTGATAGTTATCA  
ACAGTGAGACTGTGTGCAATGGGGGAAGTTCTCTGTCTAAGTGAGTGTGGGTGGGGTGGATATGGGTGT  
ATGTTTGTGTGTGTTCCGTGGGGGCTGTGATCGGAGGCTGACTGTTGCTTTACCTTATGATCTGGGTTA  
AATCTTCAGTGGTAGGGGTGACTGACTGTGAGCACCTGACAGGGGAGGGAAATTGGGGCCAATCCTAAT  
AGCTGTGCACAAAGCTGGCCCTGGCCTGGACCTTGCTCAGGCGGTCTCGTGTGGGAAATGGAAGTTCATG  
GTTGAGAATAGGGAGCCTGAGGGTAATGGAGGAGATACCCTGAGCGATCTAAGCACTGACTGGTTTCCCT  
GCATTTGATCAGTATCTGTGATGATCAGCCTGACAGAGGAGGGTAATTGTGCATAAATGTCAGGTCCTC  
TCCCCAGGTGTTATTTAACATCAGGTGATTATGCGAGAGTGGCTTTATAAAGCAGGACATAGGGTACCCC  
CACAGTGCAGTGATCGGATCAGCATTGCTGACAGTTTGGAGCTGACACACATTGCAGACTGTGCTCCGGT  
GTTGGCAGCAATGCTCAGGCTCGGTGCACCCTCACTCTAGCCCTCCTCTCCCTGGCAGCGCTTGGCCCTCAGT  
M Q A R C T L T L A L L S L A A L G L S  
GCTTTGCCACACCTCAGGGACCAGCTCGTTCTCCAGGGATCACCAGCAATGCTAAGTAAGCTTCACC  
A L P T H L R D Q L V L Q G S P A M  
TCACCAGCTTTTCCCTCTAGGCCCTCAACCAAGCTTGAGTTATTTCTAATTGACAACCTGCCTTCACTC  
AAGATTAACAGTAAGGATTTGATTAGTGGCTCATAGAATCACAGAATTATACAGCACAGAAGAAGGCCA  
TCGTGTCTGTGCTGAATCTTTTTAAAGAGCTATCCAAATCAATCCTACTCCCCCGCTCTCCCTATAGCCC  
TGCAATCTGTCTTTTCCAAATAATTATCTATTTCTCTCTTAAAAGTTGTTATTAAATCAGCTTCCACCA  
GCCTTTTCCAGGCAATGCATTTTCCAGATCCAAAATTGAATTGAAAACATCTATTAAGTCTCCTCTTAACTTC  
TCTGCTCCAAGGAGAATAATCCAGCTTCTCTACCTCTCATGATAACTGAAGTCCCTCATTCCTGGTACC  
ATTCCGGTCAATCTCCTTTTACACCCTCTCCAATGCCTTGACATCCTTCTTAAAGTGTGGGGCCAGAACT  
GAACCGAGTCTCTCGCTGAGGCCTAACCAAGTGTTTTATATAAAGGTTTATCATAACTTCTGACTTGTGT  
ATTCTAAGCCCTATTTATAAAGCCAGTATCCCCTGATGTTTTTTTTTAAACAGCTGTATCTACCTGTCT  
GCTGCCTTCAAAGATTTTCTTATATGACCCCCAGGTCTCTCTGTTTCTTCAACCCCTTACGATTTACC  
ATCAGCTTATATTGCCTCTCCTCATTCCTTCCCAATTGCATCACTTTGCATTTCTCCACATTAACCT  
TCATTTGCCACGTGTCTGCCCATGTTACCAGTCTGTCTGAAAACCTTGGAAATTGTAAGTCCCTATAGT  
CCAGGTCATTTATATAGATAAAAAAACATCAGTGGTCCCAATACTGACCCCCGGGGGGACACCCTGTA  
CACTTCCCTCCAGTCAGCAAAAACACCGTTCCCCACACTCTCTGCTTTCTGTCTCCAGTTCTGTATCCG  
CTGCCACTGTCCCTTAAATACCGGGGATTTTTATTTTGCTTACAAGTCTCTTATGTGTCACTTTATCAAA  
TGCCTTTTGAATCCATATAAACTACATCAACTGCACTACCTTCAATCCGCCCTCTCCGTTACTTCACTCA  
AAAACCTATCAGGTTTGTAGACATGATTTGCCTTTAACAATCTGTGCTGGCTGTGATACTGTGGCA  
TTGACTGCATCTTTTATCAAGAAAGTACTATTAGTACGTCAGCCGTGCCCGCTGCCTCCACAAGAAGA  
TTTTCCCTTTAGTCCCTTATTGAGCCACCTTACCTTTGACTAACCTTTTATTCTTTATATGCTTATAAA  
ATACCTTAGGTTTCCCTTTTATGTTACCTGCTAATCTTTTCTCATAACAATCTCTTTGCCCTTTTGTTC  
CTTCTTCCAGTTCTTCTCTATACTTTCTATATTCTATTTGATTATCTTGTGTTGTATTGAAGTGTTCACAT  
GTTTCGATTGAATTGTGAGCCTGTCTCACTCTTGCCTTTGAGCCAGAAATAGAGGGTTAAAGCCTCATGC  
CAGGGAGCTTAGCACAGAGATTTGATGGAATACAATTTTATCCTGTGATACATAGAATGATATGGAACAG  
AAACAGATCATTCCGTACAGCTAATCTGTATTTGACATAACTTGCCTTTTCAAGTGCCTTCACTCCCTGAA  
ACTGCCCCAGCTTGTAACTACAGTCATTGCTTGTGACAAAACCTTCTGGAGCAATGAGCAGCGAGAGAGAT  
CCCTGTTATTGCAAACGGGAGGATTCTCTGAGCCCAAGAGGAACTCAGTAAAAACATGTCATCTGTCCG  
TTACTCAGCATGTGCCTTAAACAAAATAAATCTTTTTTCTTACAGCTGCTAGGCAAAATAAAAAATGAATCC  
AATTTTTTCAACCTAAGGTGAGATAATTGACTCTTTTATTCACTTCTGCTGTGCAAAATCAAAAGTGA  
TAGACTGCTGATGTAAGTACAGGAGATGGCACACATCTCTCTTGTACTTTATAAAGCAGCCATTAAAC  
ACTCTGATCACCATTGAATGGAAAGCTCACAAATAATTGTCACTGAGAGGTAATAATAATAATAATCCGTG  
CATTTGATATAGCACTTTTACAGTCTTCCAGATGTCTCAAAGCGCTTACAGAAATAGACTATAAAGTGA  
TTGACTGTATATTTGTGGGCGAAACGCAGCAGCCACTTGTGCACAGCAGTGTCCACAAACGGTCTGGA  
TTGGAATGACCAATTTATTTTTTTTTGAGGAATTATTATTAGGCGTGTGGAGTAAGGAACTTGCCCAAGG

TTTTGCCCTGCCGGGAATCGAACTCAGGTCTCTCACTTGTAAATCACCACAGTTTTTAAATACCCCTTTAAAT  
AAATGCCCATTAATACCCCTTTGAAGGAATATCCTCTAAATACCTCTGAGCAATGGAATACCCGCAGAAA  
TGCCACAGATGTCCATTTGAAAGGCCAGACCCCTAGTACTGACGAAAGGTCATCGACCTGAAACGTTAAC  
TTATTTTCTTCTCTCCATAGATACTGCCAGACCTGCTGAGTGTTCACAGCAATTTCTGTTTTTATCCCAA  
GGCTCGGTGTTTTGTTGGTGTGAGTGCAGTGCAGAAAGTACTCGTACAAAGTGCCTTGTGTGCGGGACTACCATCTC  
AAATGGTCTAGGCCAGTGTATGGCCAACCTGCAGCCTGCGTGACTAATTTACACGTGTGTATTGTAAGTTG  
GTCATCCCTGGCGAGGCTGACACTGCAAATCAGCCGTCTTTTGGAGAGTTTCAACAGCATAATGATGCCA  
TGTGTAATAATGGACCTTTAAGCAGGGATTAATTACATTGTCTGTGTAATAATCACTTGACAGCAATT  
AATCATGAAGCATTGGGAGCGATTTGACGTGATAAGGTGCTATAAAAAAATTGGATTTGACTTGTGTGTC  
ATGTCTAACAAATCTAATAGAAATTTTTGTAGTACGAGTACGGAGAGGGTGGATAAAGGTAGTGCAGTTGAT  
GTCGTTTTATATGGACTTTCAAAGGCATTTGACAAAGTGCCACATGAAAGACTTGTAAAGAAAGATAGAAG  
CCAATGGTATAAAAGGGGCAGCGGATCCCGAACGGGCGGGGAGACAGAAAGCAGAGAGTGGTGGTGAACG  
GCTGCTTTTCTGACTGGAGGGAAGTGTACAGTGGCGTTCGCGAGGAATCGGTATTAGGACCCTGCTCTT  
CTTAATATATATAAACTTGGACTTGGGTATAGCAAGTACCATTTCCAAGTTTGTGGATGACACAAAAGTTA  
GGGAGGGGGTAAACAGTGAAGAGGACAGGAACCAACTGCAGGAAGACATAGACAGAATGGTACAATGGGC  
GACACATGGCAGATGAGTTTCAATGTAGAGAAATGTGAGGTAATGCATTTTGGTAGAAAGAATGAGGGGC  
AATATAGGCGTAATACAATCTTAAGGGGGTAAAAGAACAGAGAGACCTGGGGGTGCAGGTAAATGAATC  
CTTGAAGGTGGAGGGACAGGTAGATACAGCTGTAAAAAGGGCATCTGGGATACTGGGCTTTATAACAGG  
GGCATAGAGTACAAGAATCAGGAGATTATGATTAACCTTATATAAAACACTGGTTAGGCTTCAGTTAGAAT  
ACTGCGCCAGTTCTGGGCACCCGACTATAGGAAGGATGTTAAGGCATTGGAAAGGGTACAGAGGAGATT  
TACGAGGATGGTACCAGGAATGAGGGACCTTGATGATGAGGAAAGGGTAGAGAGGCCGAGATTATTCTCA  
TTGGAGCAGAGAAGGTTACGAGGACCTGATAGAGGTCTTCAAAAATCAAAAATCATTTGATAGGTTAGAAAAG  
GGAACAACCTGTTCCACTGGTGGGTGTGTGCGGTGACTCGAGGTCACAGATTCAAAAATAGTCTCTAAAAAG  
AGCCGAGGGGAGGGGAGAAGACATTTTTCACGCAGCGAGTTGTTGGAATCTGGAAGCCATTACCTGAAAG  
GGCGGTGAGGGCCGATTTCGATAACTACTTTTTAAAAACGCGGTGGACGGGTATTTGAGGAGGACGGGTTTG  
CAGGTTATGGGGTAAGGGCCGGGAGTGGGATGACATTAATTGCTCTATTCAAAGAGCCGCACAGACTCG  
ATGGGCCGAATGGCCTCTTTTTGTGCTGTACGATTCTATGATTCTATGATTCTATGTGCTGACTGGAG  
GGTGTGTGTCAGCAGGCGCGCTCTGCCCTCGCTGGGTACTGCTGTTTTTACATTATTATAGACATTGA  
GAAGCAGATCAGAAATCTCCGCTTATTAACACTATAGTGAGGACAGAATGCTGACGCGCTGCTCTTAA  
ACTCAGATAGGGGTGAGAGAGGTGACACTATGTAATTACAGAGAAACAAATGTCAAAAATAAACTAGGTTGC  
CCTATTTAGAATGTTCCAGAAAGTTTAGAGTCTAATGTAGCTACTCAGGGTGCAGCAGGGACGGAGGAGA  
CTGGGAGGGAAAGGATGGATTGTGATAGTGTTTAATAATAATAATCCCTGCATTTGATATAGTGCCTTA  
TCACGTCTTTGAGATGTCTCAAAGCGCTTCACAGAATATACTGTAAAGTGAAATAACAGTAGTTGCTGGG  
AACACACAGCAGATCAGGCTGCATCTAAGGAGAGAGGAAAGTGAGGTCATGTTTCAGGTAACGATGACCT  
TTCATCAGAACTGGAAGTGAATTGACTGTATATTTTATACAGTATTTTATGTGACAACACGCTGATTT  
CAGCACAATCAGTTGAATCTCAACGACACTGGCTGTTACGTCAGTAATCTCAGCATCTCAGGGGTGAGT  
GATGGAGTGCAGGAGGGGGACAGTGTGCGGAGGTGAGAGATTGTGTTCACTCTGTGATTGGCCGATG  
CTATTCATGTTATGAGCCACTCAGTCTGTCTGCGTTGTGTGGCCGCCAGCGGGTGACTTTGCTCTCACC  
GCTTGTTTGCAAGGAGCTGCGGGATGGTGTGGTCCGGGAGCTGATACAGGCAGTGGCCGATGCAGAGAGCA

E L R D G V V R E L I Q A V A D A E S

AACCCAGAGTGAGGAGGCAGCAGAGGACTTCGCTCCAGATGAAAGGCTGAACTACGGCTTGGCGTGGC  
K P Q S E E A A E D F A P D E K A E L R L A L A

TCCACGGTGGCGGAAAGATTGTAATAAATTTCTTCTGGAAAACCTTACACTTTGTGCTAAATCCTGTGCCAGC

P R W R K D C K N F F W K T Y T L C -

GTTAAAGCCTGACTGAACCACAACCGTCTGGCTGGCGAGAGGTCTTAATTAATGTGTAATATGAATTGTT  
TGCTATTTAGCATGCCTCAATTATTGTTAATCCTTTACTCATTGTGAATTCTTAATCAAGTGTACTGT  
TACGGGGAACAAATAATCATCATCATAGCTATATTCTGCAATGTGTGAAATATTTGTAACGATTTGGTG  
ATTTTTTAAATGTTGATTCAAGTGACAACCTGTCAATGTTGGGAACTAAAGTTTCAGGGCTCAACGTC  
GCTCTGCACTCACACTTCGATTGAGGCCATTCTGGACTGCAGGAAGGATGTCAAGGCCAAAAGTAGGGC  
ACATTCAGTGGACATCTCATTCTTTTATCCAACAGCCTCCATCACTGCTGCACCCAGACAATAGTCACGG  
CAGAACCATAGACATTTAAAGCACAGGAGAAGACCATTCTGCCATAGTCTCTGTGTTCCCTTAAAGAG  
CAACCTTTTGGGGCCATTTATATGCCCATTTCCAAAACCTGTAATTTAATCTATCTACCATTCCATCT  
CAACCTGCCTTTTCTACTGACCTGATCAAAGTACAAAATAACATTTCTTTTCTCAGCGTCTTGACC  
TCTCTGCCACCTACCACACGTAACCTCTATCTCTGTCTTACCCTTGATTCCAGGACCCTGTTGAACT  
GACCGGTTGTCTTTTGGACATCCTGGATGTCTGGATGAGAGCTAAACTTTCTCTAGTTAAATGTTGACA  
AGACATCAACACCTTTTCACTTCAGGTAACAGCATCAATCCACACAGGTGCACTCTCCACCTCATGGA  
AAGCGTGATGAAAGCATGGATCAGGGTCTCGGGGGCCTGCGGTGAGAGGCAGTGTGAGGTTGGGCAATA  
CTGCGGAGGTGGTGAAGCCGGAACGGGTACAGCAGCAATGTGGGGTTTGAAGGATAGCTGAGGGTCTGA  
AAAGGACTCCGAGGTTTTGGATTGACTCAGTGAAGAGCACAGCCGTGGGTGGGGATAATGCAGT...

D. Elephant shark SST6 (Sc\_58)

...TAATTAATTCATAAATTAATTAAGATGAATTGATCATCCACCTCATGACTGGTGTGTAAGATCTTGCTT  
TGCACAAAACGGCTGCCACATTTGCCACGGAATACACAGTCACTACACCTGAGCAGTTGGTGAAGTGGT  
GAATCAAAAGAGGCAGCAAAGATCTTATAGTCAATTCACCTTACAGTGTATTCTGTGAAGTGCTTTGAAA  
CGTCTTGAAGACGCAATAAGGCACAATATCAAACAGCAATGATTATTATTATTACATTGTGATATTGTAA  
AGTTTATTTTAATACTAAAGAGGATCAGAGCAGATTGTGTGCGAAATATTCAAGATTCTTAAGGGTAATGT  
AATCCAAGTCTCCCCATATCCCCAGTCTCACCGCCCCCACCCCCACCCTCTCTCTATCACCATAGCC  
TCTCGACGCTGGAGCAAATCAAAGAGCAAATAAAAAAGGATAAAAAAATGAGAAGACTTTTTCTGGTCT  
AATTACAAATAAGTTAGGAAATAATATCTTGGGATACAGTATATAGTTTGGGACACGACATGTCAATCCA  
CGGCCAGGATGGTGGAAAGTGAACACTACATGGACTTCGTCTTCCAGTGAATTGTTATGACTTATGGTCAG  
TGTGACAGAAAACACGATGAGCTCCTGTTCCACTGTCCCCAGAAAACCAACCGGAACGAGAATTAACA  
AGTGACGGGACTTTTCAGCCACTGAACAAACTCCAGGAGGGAAATGCTGAGCTCTGCGAGATGCCACCTG  
CATGAAGGCGTTGGGTAACACAAGCTGTGCGTTGATGAGAGAAGTAGCAAGTGGTTTTGGGAGGAGATGCCA  
ATGGAGTCACCCCCACACCCCACTCCCTCCACTCTCCGCCCTCCCCACGAGACCAGATTC  
ACTCCACTAACGTAATGTTTTAGAGCGACCAGGATTTGGCAGATTGTCAGCCACTGTATGTAGTTTGGGA  
GCTGTGAGTGTGTGTGTGTGCGGAGTATGTTTGGTGGGAGTGTATGTATGAGGGTGTGAGTGTGAG  
TGTGTGAGGATGTGTGAAAGT  
AAATCCCCCAAAAAATGTGTACGAACGAATTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
AAAGATGGTCTATCACTTCAGAAGGATGTCTCACAGTGAAGAGCAGTGAATTGTGTGTCTGCAGGCAACA  
CAAAGATTGTGCCCCGCAACGTCCACAAACAACGTGAAACTAATCCTGGACCTCTGTACACTCCCTGG  
GCGGAGAGAGAGCGAGAAAAGAGAGAGAGACACAGACAGACAGAGTTAAAGAGAGAGAGGGGGACCGCTT  
GGTGAATCTCAGCCTCCATCAATCTGAAGGATGGCGCTCACAAATTTTTATTGCGGAAATGAATTATGG  
GCGGCAATGCGGAAATGTAATAAGCCATTTGCTTCGTGCTTTAAAACTTTCACTGTGTTTCTGCGGAGAA  
TGTGCCCTGGGGCGGGTGTGCGAGCCACGTATGATTGGAACGGACAGACCGAAAAGAGAGAGAGAGAGA  
AAGCAGGAGCTGTAGTGAATTGACGGCTGAGTGGCTGATTCTGATCTGGGCGTTATTGTATGTGTGTTTGA  
TGGACTCTGGAGTTCTAATGAAGCTTTACGTCAAGTGCCTGGGCTTCAGCGGCTTATAAAAGGGGCCGGAG  
AAAGACTGAGAGAGACAGACCGAGGCTTCCGCTCTGCGCTGTTCTCTCTGCTCTCCCTCGCTCCGCTCTC  
TCACCCCTCGCTCTCCCTCACTCGCCCTGCTCCTGTTCCCTCTGCTCTGCTCTCTCTCTGCTCTGCTCTG  
CACACC **ATG**CAGATCCTCGTCGCTCTTATCTCCACTCTCTTCTCGTGTCCGGGGTGAGCACCACCCTG  
M Q I L V A L I S T L F L V S G V S T T T  
**CCTCGTGGAGACAGATTCAACCTCCAGAGCAGCCGGT**GAGTGGAGCGGACCGGGAGAGAGAGAGAG  
A S L D D R F N L Q S S R  
AGGAGAAAGAGGATGATGAAGAGAGAGTGTGAAAAGAGAGAATGAGAATGACAGTGAAGAGAGAGAGAGAAA  
CCGAAAGAGTGTGAAAAAAGAAAGACAGCAAGAGAGAGGGGGAGAAAAGACGATGATGGAGCTGGTGTATGG  
AGCAAGAGCGAGGGAAAGAGAATGGGAAAGAGGAAAGGAGGGAGGACGAGGGTGTATCGAGAGAGAGAATG  
ACAGAGAGAGAGAAAAGGAAACAAAGGGGACGAGAGATAAAGAATGACAGAGAGAGCAGGATACAGCGG  
AGAAAGGAAGTGAAGGAGGATGATGGAAAGAGAGAGAATGACAGGAAAAGAGAAAGGGAGAGAGAATG  
ATAGAGAAAGCGAGAGAGGGAACAAAGGAGACAGAGACAAGAGAGAGACACAAAGACAAATGGGTAGATA  
AAGAGAATGGCAGTGAAGAAAGACTGAGAGAGAAAGAGCGGAGTAGAGAGAGAATGATAGGGAACGAGC  
GAGAGGAGTCAAGGGGATAGAAAAGAGAGAATGACAGAGAGAGAGACGCTGATAAAAAGTATGTGATGGCAT  
GTGAATGACAGCGAGCAAGGGAGAGAAAAATACTTGCTGGAGAGGAGAAAAGTGTCTGAGAGAAAAGATGA  
GGGAGAGATAGAAAAGTAATGTTAACAGAAAAGGAGAGAAAAGACAGGAGGGAGAGAGGAGTGAAGAGAA  
TAGGGAGAGTGAACAAGATGAACAGTGTGAAAAGAGAAAATGGAACAAGGAGTGAACAGAGAGCGATAG  
GCAGAAAAGAGGAGAGAGAAAATTGAGACAGACAAGAGTGAAGGAAAATGAAGAGAGAGGAAAAGAGATAG  
AATGAGAGAATGAGAGAGATAGACAGAGACAGCGGAGAGAGAGAAAAGTGTGAGAGAGAAAAGAGGAGAA  
TGAGAAAAGAGATGGAGTAACTGAGACAGAAAAGAGAAAGGATTTGTGGAGCAGAAAAGCAGCTGTGGCTCAGGA  
GTCAAATAGAAAAGTGAAGAGAAAAGACACAGCACAACAGGAGACAGAGGGAGAGAGAGAGAGAGAGG  
GGGGAGACAGGGAGATAGATAGAAGGGAGAGAGAGATTGAGAGAAAACCGAGAAAAGACAAAGAGAGACACA  
GAGGGCAGGAGACAGAGAGAGATAGAGAAGAGAGAGAAAAGGAGACAGAGGGAGAGATAGAGAGAAGAGA  
GAGGAGAGAGTGAAGACAGAAATGGAGAGAGACAGAGAGGAGAGAGCAAGGAGATAAAAAGAGAGACAAAAG  
CTGACAGAGGGAGAGATAGAGGTGTTGTGTTGGTACCTGTGGAGCTCACTGACAAAAGGTTGAGACAGAG  
CTAAACTGAGGTAAAGGCTCTCACATCACAGCGCTGTCTACACTCTCACTCACTAGGACTTGTCTCTCTC  
TGTGTGTCTCTCTATCTCTCTCTGCTCTTTCTCTGTCTCCTGCTCTCTGTGTCTCTCCCCGCTTTTCTC  
AGCGCCCTGGGACGTCCTCCTCATGTGAAAAGCACTTACAAAATATAATTTGGCGTATGTTGTGCTTTCT  
CTCTCCTTCCCTCTCTCTGTCTCCAGTCTGTGCGGGAGTGTGTGTGTGTGTCTCTCAGTTTTTCTA  
TTTGACGTCTGAATAACAGCTATTTTTCTGCTCCACAATCTTTCTCTTTCTGTCTCAGTTCTCTGTGCT  
TTCTCTCATTCTGTTTACCTCTGTTTGTGTTGATCGGCGGATCGCTTTTCTGCGGATAATAACCCCTTAAA  
AAAAATTATCATTGGTCAAGACTGTTTGTGGGACGCTGCTGTGCGCATTTTCGCCACAAAACATACAG  
TCAATTCACCTTACAGTATATACTGTGAAGCGCTTTGAGACATATAGAAGACGTGATAAGGCGCTGTATC  
AAATGCAAGGATTATTATTATTATTATGCTTTCTCTCTCACACTCTTTCTCTCTCTGGCTGCTTCTTCT

ACCTCTCTATTCTCTCAGTCTGTCTCTTCTCGTGACGGTGCCATCTATAAAACACCAATACAATGTGTT  
TGTGACAGCACAATGAAAGAGTTAAGTCAGAGAGGGATAACATACAGTATTTCTTACTGGGAAAATGGGCA  
ATCATTGAATTTATAACCGTTATTGGAGACAATCTTCAGCTCAGTCTTGTGAGAAGGACGAGTTTTCTCAT  
TAAGAATTGGGTTTTAAGAAATAGCACAAAGTTGGATCCCCGACCATGTGCAGATGTAGAAAAATTGCTTTAAA  
CTTTGCAAAAATAATGATCTCTGCATTTCGATATAGTGCCTTAGCGCATCTTCGAGACGTCTCAAAGCGCT  
TCACAGAAATATACTGTAGAGTTCGAGCCCCCTCAGTACTCAAGAAGTTAATGAACGTGCGTCCAGCTG  
TTTTAAATCAAACGATCCCCGGAATGCTCCGCCACGAGGTCCCCTGAGGCAGAGCAATAAAATTCACT  
GTAAATTGTCCAACACCGTACGGAGAGAGCAGCTTCCATTTACACAGCCTCTGCCACAACAGACAGTGG  
GGGAGTGACACCAGCACAGATGCGATGGGGGAGAGAGAGAGAGAGAGAGACAGGAATGGGGTTAGAGT  
AGAGAGCTTAGTGGGGGAGTGGCCCCAGCACAGACACAATGGGGGAGAGTGGAGCAAGATGGGGTT  
AGAGTAGGGCTCAGTACGATGGCTTCTCTCCCCAGTCTCATTGATTCTGTACCTGTTGTTGACACTATT  
TTAC

**AGGAGATGAATCAGGAAAGGAAAGAGATGATCCTCAAGCTGTTGTCAGGTCTCCTGGACAATGCCG**  
E M N Q E R K E M I L K L L S G L L D N A  
**CGGTGAGTGGGACGCGGGGAGCGAGGCCGTTACCCTGAGCCCCCGGATGGGGGGCCGTGATGTTGGA**  
A V S G Q T G S E A G Y P E P A D G G P V M L E  
**GGAACGATCTCGCTACAGCCAATGCCCGAGCGGAAGCCGAAAGTCCCCTGTAAGAACTTCTTCTGGAAA**  
E R S R Y S Q L P Q R S **R K V P C K N F F W K**

**ACATTCACCTCCTGTTGA**CGATAAACAGTACAGACCTCCTACACCCCCTCTCCCCGTCCTCTTTCCCC  
**T F T S C -**

TCCCTCTTCCCCCCACCCACCCACACAACCTAAAGCACGGGATGAAACCCACCAGTAACTAAACTGTTTFA  
GCACTGTACATTTGCTGCTGCTGTTTTTATTTTTATTTCATCTGTGAAGTGAATTCCTTTCTTGGGCAGC  
GAAATAATTAAGAAAGCATAACCATAACGTTCACTGCCTGGTGTCTTTCTTTCTTCTGGTGACAGAGCGAGC  
GAGGGAGGGAGGATGGAGGGAGAGAGAGAGAGGGGGGAAGGAGAGAGGGAGGTGGTACCTGAGCTCATAGC  
ATCTCCCACTTACACAGGGAGCGGATATCTCAATCGCACCTACACACAATCGCACACACTCACACTCGCT  
CACCCACACACACAGCACCTCTAAAGTCTCAACATTTCAAAGCTATAACGGGATGCACTGTAAAAGTGACT  
GTGTATTTTGGAGGTGAAGCTGGCCTATGCCAATTTGCTCAAAGCGACGTCCACAAAACAGCCGGGAGGG  
GAATAATCTAATTTAACACTTGTGGCCGTGACGCTGGGAGAAATTTCTTCTGTTTTGAAACAGCTCC  
CGGGATCTTTAACGCCACCTGATCAGGTGACAGGTCAGCAGGTAACGGTAAATGTCTTCTGAAAGCACG  
CGGCTTTGACTGGTGTGAGTACAGCTGGCCTGACCTGAGCTGAGCTTCTCACTGAGCCGAGCTGCCCTCACACT  
CAACACACAGGATGAACAGTACAATTAACATTTACACAGCGCCTGTAGCTCCAGAGGGAGGGTGTCTCA  
AAGCCCTCAACGCTGCTGCCATTGGCTTACCAATCACAGTGGGCTTACAGGATTAACGTTTTTTTGAAGA  
TTCAATGATAGATTTCAAATGGGAATTGGATAGGAACTTAAGAAGGAAAAATGTGCCGGACTATGGGGAG  
AGTGCGGGGAGTGGGACTATTTGGAAGCTCTTTTCAAAGAACCGGCACAGGCACAGTGGGCTGAACGGTC  
TCCTTTTGTGCTGTAAAATTTCTATGATTCCATGAAGTGCTTCATGAGATGATGGGGTCACTGGGCGAGG  
AGAAGAGGGCATTGAGAGTCCATTGAAAGCATGTTAGAGAGAATAAGAGAAAAGAAAAGAAAAGAAAAG  
AAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAGAGAAAGGGAAAGAGAG  
AGTGTGAAGAGTGAAGAGAGTGAAGCAAGAGAGAGAACAAGAGGGACTGAGAATGTAAGAGCAAGTGC  
AAGAGAGACAGCGCGAGAGAGATAGAAAAGAGAGCCTGAAATGGTGTATAATAATAATAATAATCTTTGC  
GTTTGATATAAGGCTTTTCACGTCTTCGAGATGTCTCATTGCCCTTAACAGAATAGACTGTAAATTTGTC  
GGCGAAACACGGCAGCCAAATGCGCACAGCCTAAGATTTGCCCCGCCATATATCACAAAAGTGTAGTGAC  
TGTATGTGTTGTGGGCGAAACCGCGCAGCAAGTTGCACGTAGCAGTGTCCACAAAACAACCTTGGACTGA  
GTGATCAACTTTGTTTGGGGGATTGTTGGAGTCCGGTAACTCAGTGGTGTAGAGCCCTCGCCTCGCAAGTG  
AGAGGACCTGGGTTTGATTCCCGGGCAGGGTGAACGCTGGGCAAGTTTCCTTACTCCACACGCCTCTGT  
TTTCCCAGCAGTGTGACAGGAACCCGTTGTAGTGTGATTGGCAGATTGATTTTCCCGGAATAGTAATTGC  
TTCAAAGAGTTTTTAAT**AATAAA**TTTGACTCACTCAATCCAGACTGTGGGACGCTGTGTACGCAATTG  
GCTGCCACGTTTTGTCTCACAAAATATTTCTGTGAAGTGCTTTGAGACGCCTTGAAGACATGATAAGGCAT  
GTAACAAGTGCAAAGATTGTATTATTATCTTAAATAGTAAAGGAACTATACTATTTGCCCGTGAGTCT  
GATCTGTTGAAATGCTTTGACGATGAGCTTTGAAGCAGAAATCTATCTGATCAATATCATACTGATCTCT  
CGTTTGTGCACAATTAGTGATTTTCATAATAATAATCCTTGCATGTGATTCCATAGATTTTTTTTCATAGA  
ATGTTACAGCACAGAAGGAGGCCATTCGGCCCATCGAGTCTGTGCGGCTCTTTGACAGAGCGTCACTTTC  
ACTAACCCCAATCACCAGCTTTCTCCCCATAACTCTGCAAACCCATCCTTCCCCGATACCTGTCCAGTTC  
TCTCTTAAAGCTGTTATCGAATCGGACTTCACTGCCCTTTCGGGCGGATCATTCAAATCCAACAACCT  
CGCTGAGTGAAAACATTTCTTCTAACCTCTCCTCTGCTTCTTTTGGTAGATATCTTAAAGACTGTAACCAC  
AGGTCACAGACACACCTACCAGCGGAAACAGCTTTCCCTATCTCGCCTGTGCGAAACCTTTCATGATCTTG  
AAGACCTCTATCAGGTCCCACGTAACCTTCTCTGTCTAATGGGAAAAGTCCCTAAGTCTCCACTGTCC  
TCATAGCTAAGGTTCTCATTCCGTGGTATCATTCTCGTGAATCTCCTCTGCACCCCTTTCCAGTGCCTTAA  
TATCCTTCCGTGAGGTAAGGTGCCCGAAGTGGACACAGTACTCCAGCTGAGGCCTAACCAGTGTFTTTGTA  
TAGATTAACCATAACCCCTACTCTTATACTCTATGCCCTACTAATGAAGCTCAGTACACCAAATGCCCTT  
TTTCTGCCCTATCTACCTGCCCCACTACCTTTAATGATTGCTTACTTTGAACGCACAGATCTCTCTGTAT  
GTTACCCCTTAAAGATTGAGCTCCAAGTCTATATTGCTCCTATCATTFTTCCCACCTAAGTGTATCA  
CCTCACACTTATCCACATTGAAATCCATCTGCCACATGTCAGCCCATCCACCATTCTGTGTGTGTCG...



**A. Elephant shark SST1 (SSTa)**

agactgttttagagggatgctgt  
gcagtgaaggggtgtgttggggatgaaggtggcgtgagggcgtttataaaggcgagtctat  
ggacaccaggaccagaagatccagacgaggcagagcgtccagagagccgggtgctgaacca  
cgagcgttccctccgttccctctctcgtcctcctttgacagtttggtgccgtcgccccgag  
atgtctgctgcccagagtgcagtgccctggcgttgcctcctccatcgccctgacagtgctg  
M S C G R V Q C A L A L L S I A L T V L  
agtgtcacctcggcgccagcacacgacaggtaccgcgaaatcctgcagcgatcactggcc  
S V T S A P A H D R Y R E I L Q R S L A  
gcgggcgggagccaggagtaaaccggagctgaccaagtacagcctggctcagctgttggcg  
A A G A R S K P E L T K Y S L A Q L L A  
gaattggccaacgcggagaacgagggcgtggaggcggaggacatggcccagcaaccgca  
E L A N A E N E A L E A E D M A R A T A  
caggacgaagtaagggttgaattggagagatcggccaaccccaacctggcgcagagagag  
Q D E V R V E L E R S A N P N L A Q R E  
cgcaaagcgggctgtaaaagcttcttctggaaaaccttcaacttctgtaactctgagca  
**R K A G C K S F F W K T F T S C -**  
gccccaccacctctcacacacactcactcactttccctgacccccacctcc  
catccccaccctacacacaaagtttcccgatcccccgccacacacacacacacacat  
tgtatgttcttacgctacgtggctgttctgattttaacatactgtaaataaaaacacat  
ggtgatgataattcaacctaatatttattgtgacagaaccttttagatgggggttgtgactgta  
tagttaccactcttctggctagaggtgtatgtatttttaatttgtatgtcgcaat  
gaaatacatgtttgaaactgaaa

**B. Elephant shark SST2 (SSTd)**

a  
tatcaaagcaaggattattattatattgatattgagacgtcttcccgatgtgaaaagca  
ctatacgaatgtaatcttcttgtggaaatgttacaaaactcagagctggctaaatgtttg  
ttctacagacaaaattccccatgaagagtccaacatcccataagctgctgaacccttatt  
tagtaaaactggaggtcaatcatgtaatactgtggaccttctggctcatgtatcagatcg  
cccaacgagagctctatcaaagagaattgtctcagctccactagtcagtttagattgggtg  
tggcatcacccttctcagagttgtcccagatcaattctcctccgcaaactcaggct  
tcagcctcactgattccttatcagctcttggaaaacaatgacttctgagttgtgaaaatc  
ttatgttctgtaacaggcattatcttctgttagggctcatcaagtggattgccaagggga  
gccacttttttaatagatcagatgacagattggtttaatgtctcatttgaaggacagat  
gattcatggtaagacgaaaaagtttcatttcttgtggatttctagagctggaacaatttc  
tacctccactttaattcgtagaagtgttttttgtgtgttggatattatagaagattgatg  
ttgaaagctctatacaaaacacacaaaagactgactcattctaaattggaaagctctttta  
attatcagtggttctaattctttgatgcaaactcgaaattggaaaatataaaataaacaatt  
atgatcttctaaattaacattttttccagttgttggactttgtcatttttttaatgttc  
cagttaatgggttctcattgtatattagtgtctgattatagcactaattttgcacgtcagc  
gagtgctataattgtgctgcattataaaagcaggacaattagagtttctcagcaaaaaca  
gggaaagagtcagtgaaagctcgacagatccattgaaaagagagaaagtttgagtccagc  
atgcagtggaagcattcgaagtgctgctgtgtctgttgttctcattgtaactgttcaggga  
M Q W Q A F A S V V C L L F I V T V Q G  
gttgaaccacaggaggaacgaatgggtcttcagctgaacagggagatggtaaaggacaag  
V E P Q E E R M G L Q L N R E M V K D K  
aaagcctgattgcaagctgctggcgggattgttggacgtggatgacaatctgttagaa  
K R L I A K L L A G L L D V D D N L L E  
agtgtcatcgccccattgggtctgagcaagaagaggggactgatttcgaggagagatca  
S V I A P L G L S K E E G T D F E E R S  
gctgccggtgaaatccctcccagaaaaccgaaggcagggtgcaaactgttcttctggaaa  
A A G E I P P **R K P K A G C K L F F W K**  
accttctcgcactgttagtgatttgtcaaagataaacatttttttaaaaatccagtttgt  
**T F S H C -**  
gttttctgtttagatgtaaacacttccccccccccact

C. Elephant shark SST3 (SSTe)

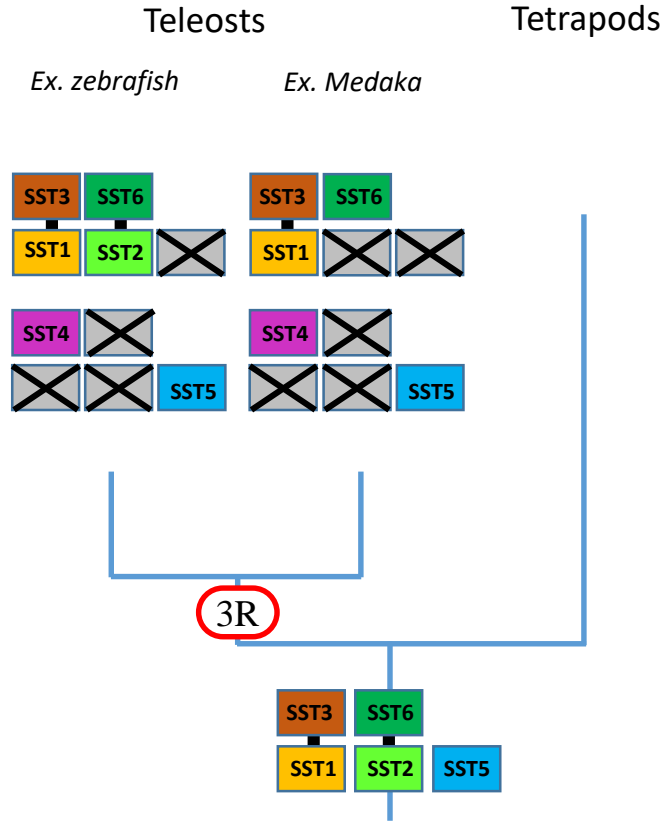
gcagca  
atgcaggctcgggtgcaccctcactctagccctcctctccctggcagcgcttggcctcagt  
M Q A R C T L T L A L L S L A A L G L S  
gctttgcccacacacctcagggaccagctcgttctccagggatcaccagcaatggagctg  
A L P T H L R D Q L V L Q G S P A M E L  
cgggatgggtggtccgggagctgatacaggcagtgccgatgcagagagcaaaccacag  
R D G V V R E L I Q A V A D A E S K P Q  
agtgaggaggcagcagaggacttcgctccagatgaaaaggctgaactacggcttgcgctg  
S E E A A E D F A P D E K A E L R L A L  
gctccacgggtggcggaaagattgtaaaaatttcttctggaaaacttacactttgtgctaa  
A P R W **R K D C K N F F W K T Y T L C** -  
tcctgtgccagcgtaaagcctgactgaaccacaaccgtctggctggcgagaggtcttaa  
ttaatgtgtaatatgaattgtttgctatttagcatgcctcaattattgttaatcctttac  
tcattgtgaattcttaatcaagtgtttactgttacg

D. Elephant shark SST6 (SSTc)

cgctctccc  
tcactcgccttgctcctggtcctctcgcctctctctcgcctcgccttcgctccgctcacacc  
atgcagatcctcgtcgcctcttatctccactctcttctcgtgtccggggtgagcaccacc  
M Q I L V A L I S T L F L V S G V S T T  
actgcctcgcctggacgacagattcaacctccagagcagccgggagatgaatcaggaaagg  
T A S L D D R F N L Q S S R E M N Q E R  
aaagagatgatcctcaagctggtgacaggtctcctggacaatgccgcggtgagtgggcag  
K E M I L K L L S G L L D N A A V S G Q  
acggggagcagggccggttacacctgagcccgggatggggggccggtgatggtggaggaa  
T G S E A G Y P E P A D G G P V M L E E  
cgatctcgcctacagccaactgccccagcgaagccgcaaagtcccctgtaagaacttcttc  
R S R Y S Q L P Q R S **R K V P C K N F F**  
tgaaaacattcacctcctggtgacgataaacagtacagacctcctacacccccctctcc  
**W K T F T S C** -  
ccgtccctctttccctcctcttccccccccccccacccccacacacctaagcagggatg  
aaaccaccagtaactaaactgtttagcactgtacatttgctgctgctgtttttatTTTT  
attcatctgtgaagtgaaattcctttcttgggacggaaataattaagaaagcataacc  
atagttcactgcctggtgtttcttcttctggtgacagagcagcagggaggaggat  
ggaggagagagagagaggggggaaggagagagggagggtggtacctgagctcatagcatct  
cccacttacacagggagcggatctcaatcgcacctacacacaatcgcacacactcaca  
ctcgtcac

Figure S9

A.



B.

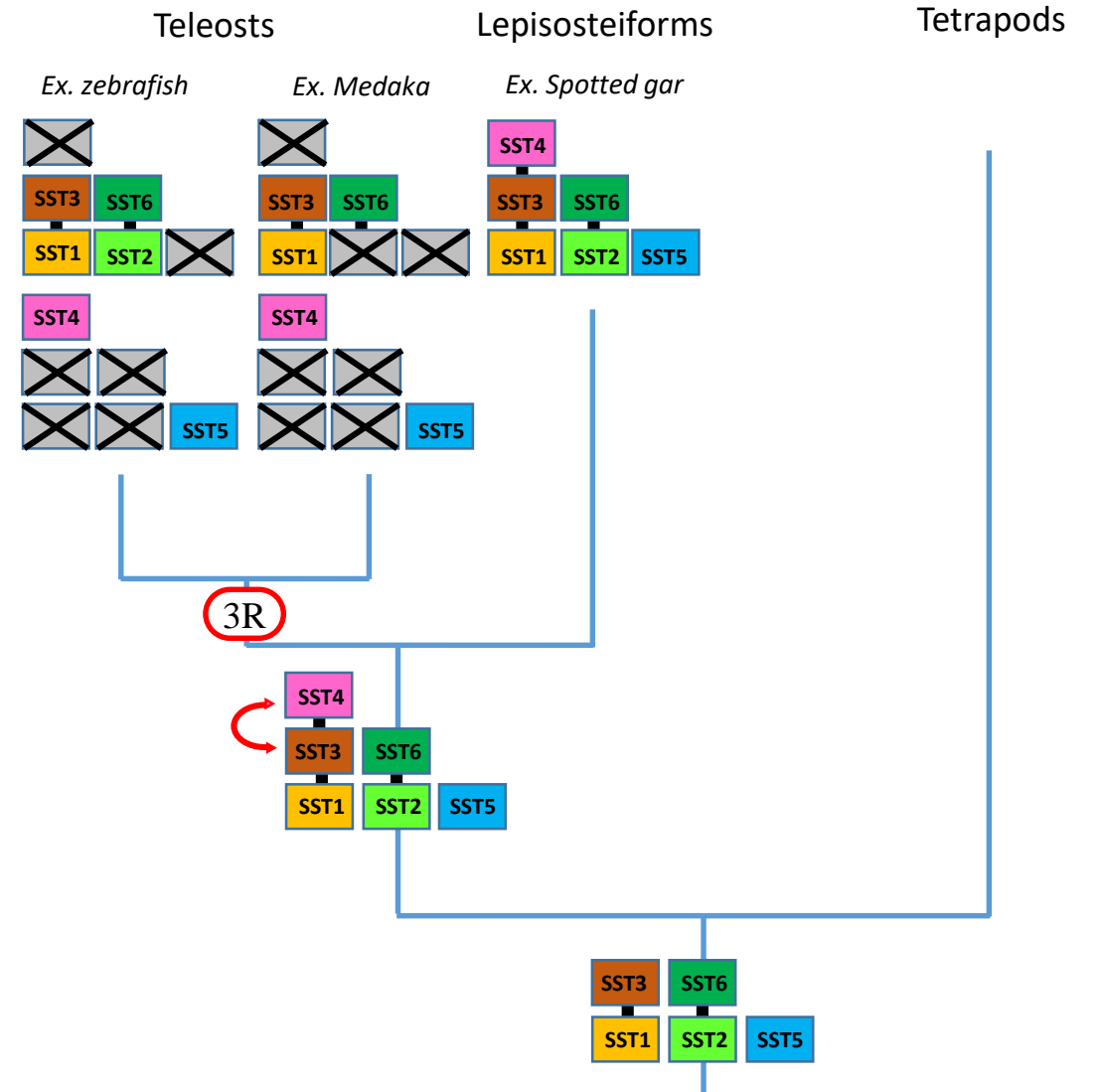




Table S1.

Molecular cloning		
Catshark SST3 (SSTe)	CshSSTe Rev	CAGTGGGATGGAGTCAGTGGGGTGCA
	CshSSTe Rev Nest	GGAGTCAGTGGGGTGCAGTGGGGTAC
Tissue distribution analysis		
Catshark SST2 (SSTd)	CshSSTd For	TTGTCCAGGAGTGCTCGAAGA
	CshSSTd Rev	GTCCCTTCTGCCTCTTCTGGT
Catshark SST3 (SSTe)	CshSSTd For	ATGTAGACACTGAGGCCGGAA
	CshSSTd Rev	AGAAGGGCTCACTGGGTACA
Egf1	Egf1 For	CTTTCGCTCACCTACCCAAG
	Egf1 Rev	GGTCAAAGTCTCCCAGAAG

**Table S2**

Name	Sequence	Species
<b>SST1</b>	AGCKN <b>FFWKTF</b> TSC	Most vertebrates, including <i>catshark (SSTa)</i>
	AGCKS <b>FFWKTF</b> TSC	<i>Elephant shark, ratfish (SSTa)</i>
<b>SST2</b> (*previously known as SST6)	MPCRN <b>FFWKTF</b> SSCK	Human
	PCKN <b>FFWKTF</b> SSCK	Mouse, rat
	TPCKN <b>FFWKTF</b> SSCK	Bovine, monkey
	TPCGN <b>FFWKTF</b> SSCK	Pig
	APCKN <b>FFWKTF</b> TMC	Frog
	APCKN <b>FFWKTF</b> SSC	Anolis
	APCRN <b>FFWKTF</b> SSC	Coelacanth
	SPCTN <b>FFWKTF</b> SAC	Mexican tetra*
	SPCKN <b>FFWKTF</b> SAC	Piranha*
	TPCKN <b>FFWKTF</b> SSC	Spotted gar*
	SPCKL <b>FFWKTF</b> SSC	Zebrafish*
	SPCKN <b>FFWKTF</b> SSC	Herring*
	APCKL <b>FFWKTF</b> SHC	<i>Whale shark, skate (SSTd)</i>
	TPCKL <b>FFWKTF</b> SHC	<i>Catshark (SSTd)</i>
	AGCKL <b>FFWKTF</b> SHC	<i>Elephant shark (SSTd)</i>
<b>SST3</b>	AGCKN <b>FYWKGF</b> TSC	Most teleosts
	AGCKN <b>FYWKGL</b> TSC	Tilapia
	AGCKN <b>FYWKGP</b> TSC	Takifugu
	DGCKN <b>FYWKGF</b> TSC	Medaka
	AGCRN <b>FYWKTF</b> TSC	Spotted gar
	SGCKN <b>FYWKGR</b> TSC	Herring
	NCKN <b>FYWKTY</b> TLC	<i>Whale shark, catshark (SSTe)</i>
	DCKN <b>FYWKTY</b> TLC	<i>Elephant shark (SSTe)</i>
<b>SST4</b>	FGCRV <b>FFWKS</b> WSPC	Stickleback
	PCR <b>V</b> FY <b>WKS</b> WAKC	Medaka
	QFGCR <b>MFFWKS</b> WTYC	Takifugu
	QAGCR <b>IFFWKS</b> WTSC	Tetraodon
	TGCKN <b>FYWKS</b> RTAC	Zebrafish
	PLNC <b>MNYFWKS</b> RTAC	Catfish
<b>SST5</b>	AGCRN <b>FFWKTF</b> TSC	Most actinopterygians
	AGCRN <b>FFWKS</b> Y <b>T</b> SC	Tetraodon
	TGCRN <b>FFWKTF</b> TSC	Piranha, mexican tetra*
	AGCRN <b>FYWKTF</b> TSC	Zebrafish
	AGCKN <b>FFWKTF</b> TSC	Coelacanth, <i>catshark (SSTb)</i>
<b>SST6</b> (*previously known as SST2)	APCKN <b>FFWKTF</b> TSC	Chicken*, lungfish*, coelacanth*, actinopterygians*, <i>catshark (SSTc)</i> *
	TSCKN <b>FFWKTF</b> TSC	<i>Whale shark (SSTc)</i>
	VPCKN <b>FFWKTF</b> TSC	<i>Elephant shark (SSTc)</i>
<b>Others</b>		
<b>SSTa</b>	AGCKN <b>FFWKTF</b> TSC	Lampreys
<b>SSTb</b>	AGCKN <b>FFWKTF</b> SSC	
<b>SSTc</b>	ANCR <b>M</b> FY <b>W</b> K <b>T</b> MAAC	

**Table S3**

<b>SST1 (SSTa)</b>	Csh	Wsh	Esh
Catshark		66.37	73.45
Whale shark			74.14
Elephant shark			

<b>SST2 (SSTc)</b>	Csh	Wsh	Sk	Esh
Catshark		76.0	62.03	58.1
Whale shark			62.82	53.0
Skate				51.9
Elephant shark				

<b>SST3 (SSTe)</b>	Csh	Wsh
Catshark		38.14
Elephant shark		

<b>SST6 (SSTc)</b>	Csh	Wsh	Esh
Catshark		86.79	58.65
Whale shark			53.85
Elephant shark			

Table S4

Gene	Designation	Species	Ensembl ID	Chromosome location	Position (Mb)
Mb21d2	Mab-21 domain containing 2	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000180611	3	192,796,815 - 192,918,161
		<i>G. gallus</i>	ENSGALG00000007218	9	13,300,318 - 13,348,379
		<i>X. tropicalis</i>	ENSXETG00000002143	GL1272717.1	276,599 - 277,885
		<i>A. carolinensis</i>	ENSACAG00000000000		
		<i>L. cholerae</i>	ENSLACG000000017691	JH126687.1	2,399,815 - 2,301,095
		<i>I. oculatus</i>	ENSLOGG000000009364	LG14	18,861,293 - 18,899,827
		<i>D. rerio</i>	ENSNDARG00000077316	15	45,527,281 - 45,538,773
		<i>O. latipes</i>	ENSNDARG00000077690	2	5,563,077 - 5,581,772
Fgf12	Fibroblast growth factor 12	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000114279	3	192,139,395 - 192,767,764
		<i>G. gallus</i>	ENSGALG000000036973	9	13,369,379 - 13,557,972
		<i>X. tropicalis</i>	ENSXETG00000002144	GL1272717.1	393,833 - 521,960
		<i>A. carolinensis</i>	ENSACAG00000000000		
		<i>L. cholerae</i>	ENSLACG000000017275	JH126687.1	2,003,413 - 2,283,293
		<i>I. oculatus</i>	ENSLOGG000000009371	LG14	18,996,717 - 19,055,889
		<i>D. rerio</i>	ENSNDARG000000113325	15	45,414,883 - 45,510,977
		<i>O. latipes</i>	ENSNDARG00000027957	2	5,587,495 - 5,681,658
Il1rap	Interleukin 1 receptor accessory protein	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000196083	3	190,514,051 - 190,659,750
		<i>G. gallus</i>	ENSGALG000000007253	9	13,905,930 - 13,926,342
		<i>X. tropicalis</i>	ENSXETG000000015044	GL1272717.1	998,488 - 1,097,171
		<i>A. carolinensis</i>	ENSACAG00000000000		
		<i>L. cholerae</i>	ENSLACG000000016241	JH126687.1	1,498,996 - 1,521,106
		<i>I. oculatus</i>	ENSLOGG000000009378	LG14	19,120,504 - 19,150,963
		<i>D. rerio</i>	ENSNDARG000000114719	15	45,338,623 - 45,356,635
		<i>O. latipes</i>	ENSNDARG00000016010	17	24,782,508 - 24,802,926
Gmc	Geminin coiled-coil domain containing	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000205835	3	190,852,877 - 190,892,429
		<i>G. gallus</i>	ENSGALG000000026907	9	13,853,476 - 13,857,367
		<i>X. tropicalis</i>	ENSXETG000000026307	GL1272717.1	934,067 - 936,733
		<i>A. carolinensis</i>	ENSACAG00000000000		
		<i>L. cholerae</i>	ENSLACG000000016600	JH126687.1	1,636,912 - 1,645,473
		<i>I. oculatus</i>	ENSLOGG000000009396	LG14	19,190,052 - 19,196,340
		<i>D. rerio</i>	ENSNDARG000000068719	15	36,309,070 - 36,316,825
		<i>O. latipes</i>	ENSNDARG000000068719	17	24,782,508 - 24,802,926
Ostrn	Osteonin	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000188729	3	191,199,241 - 191,265,615
		<i>G. gallus</i>	ENSGALG000000007226	9	13,761,297 - 13,772,476
		<i>X. tropicalis</i>	ENSXETG000000015042	GL1272717.1	750,074 - 755,484
		<i>A. carolinensis</i>	ENSACAG00000000000		
		<i>L. cholerae</i>	ENSLACG000000016886	JH126687.1	1,792,819 - 1,800,129
		<i>I. oculatus</i>	ENSLOGG000000009421	LG14	19,280,012 - 19,292,855
		<i>D. rerio</i>	ENSNDARG000000054055	15	36,228,853 - 36,249,087
		<i>O. latipes</i>	ENSNDARG000000054055	17	24,782,508 - 24,802,926
Masp1	Mannan binding lectin serine peptidase 1	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000127241	3	187,217,285 - 187,292,022
		<i>G. gallus</i>	ENSGALG000000007819	9	14,910,864 - 14,927,922
		<i>X. tropicalis</i>	ENSXETG000000019757	GL1272717.1	2,406,583 - 2,454,003
		<i>A. carolinensis</i>	ENSACAG000000006732	GL343730.1	51,210 - 227,647
		<i>L. cholerae</i>	ENSLACG000000011850	JH127453.1	611,754 - 796,681
		<i>I. oculatus</i>	ENSLOGG000000009432	LG14	19,284,195 - 19,341,321
		<i>D. rerio</i>	ENSNDARG000000068726	15	36,187,434 - 36,223,417
		<i>O. latipes</i>	ENSNDARG000000068726	17	24,782,508 - 24,802,926
SST1	Somatostatin 1	<i>R. typos</i>	XM_020509773.1	NW_018029766	122,814 - 124,407
		<i>C. millii</i>	XM_007912395.1	Sc_821	7,008 - 9,515
		<i>H. sapiens</i>	ENSG00000157895	3	187,668,906 - 187,670,399
		<i>G. gallus</i>	ENSGALG000000007361	9	14,872,386 - 14,883,973
		<i>X. tropicalis</i>	ENSXETG000000019777	GL1272717.1	2,228,041 - 2,229,578
		<i>A. carolinensis</i>	ENSACAG000000006722	GL343730.1	4,342 - 23,375
		<i>L. cholerae</i>	ENSLACG000000003574	JH126687.1	88,278 - 90,189
		<i>I. oculatus</i>	ENSLOGG000000009439	LG14	19,284,195 - 19,407,399
		<i>D. rerio</i>	ENSNDARG000000040799	15	36,156,986 - 36,158,851
		<i>O. latipes</i>	ENSNDARG000000019152	scaffold660	2,344 - 3,701
SST3	Somatostatin 3	<i>R. typos</i>	XM_020509774.1	NW_018029766	131,096 - 160,273
		<i>C. millii</i>	XM_007912396.1	Sc_821	17,287 - 22,746
		<i>H. sapiens</i>	ENSG00000157895	3	187,668,906 - 187,670,399
		<i>G. gallus</i>	ENSGALG000000007361	9	14,872,386 - 14,883,973
		<i>X. tropicalis</i>	ENSXETG000000019777	GL1272717.1	2,228,041 - 2,229,578
		<i>A. carolinensis</i>	ENSACAG000000006722	GL343730.1	4,342 - 23,375
		<i>L. cholerae</i>	ENSLACG000000003574	JH126687.1	88,278 - 90,189
		<i>I. oculatus</i>	ENSLOGG000000009439	LG14	19,284,195 - 19,407,399
		<i>D. rerio</i>	ENSNDARG000000040799	15	36,156,986 - 36,158,851
		<i>O. latipes</i>	ENSNDARG000000019152	scaffold660	2,344 - 3,701
Col4a3	Collagen type IV alpha 3 chain	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000169031	2	227,164,565 - 227,314,792
		<i>G. gallus</i>	ENSGALG000000038612	9	9,384,943 - 9,430,089
		<i>X. tropicalis</i>	ENSXETG000000004217	3	23,464,166 - 23,573,541
		<i>A. carolinensis</i>	ENSACAG000000009918	JH126709.1	458,799 - 547,615
		<i>L. cholerae</i>	ENSLACG000000009454	LG14	19,454,926 - 19,507,683
		<i>I. oculatus</i>	ENSLOGG000000003395	15	36,054,864 - 36,112,784
		<i>D. rerio</i>	ENSNDARG00000003395	15	36,054,864 - 36,112,784
		<i>O. latipes</i>	ENSNDARG00000003395	17	24,782,508 - 24,802,926
Col4a4	Collagen type IV alpha 4 chain	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000081052	2	227,002,711 - 227,164,453
		<i>G. gallus</i>	ENSGALG00000004946	9	9,318,986 - 9,370,173
		<i>X. tropicalis</i>	ENSXETG000000003770	3	23,883,599 - 23,670,714
		<i>A. carolinensis</i>	ENSACAG000000012078	JH126709.1	673,429 - 787,527
		<i>L. cholerae</i>	ENSLACG000000009493	LG14	19,522,370 - 19,590,210
		<i>I. oculatus</i>	ENSLOGG000000002831	15	35,951,888 - 36,055,401
		<i>D. rerio</i>	ENSNDARG00000002831	15	35,951,888 - 36,055,401
		<i>O. latipes</i>	ENSNDARG00000002831	17	24,782,508 - 24,802,926
Rhbod1	Rhomboid domain containing 1	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000081052	2	227,002,711 - 227,164,453
		<i>G. gallus</i>	ENSGALG00000004946	9	9,318,986 - 9,370,173
		<i>X. tropicalis</i>	ENSXETG000000003770	3	23,883,599 - 23,670,714
		<i>A. carolinensis</i>	ENSACAG000000003827	JH126709.1	816,263 - 961,971
		<i>L. cholerae</i>	ENSLACG000000013155	LG14	19,592,741 - 19,635,912
		<i>I. oculatus</i>	ENSLOGG000000009504	15	35,933,094 - 35,944,902
		<i>D. rerio</i>	ENSNDARG00000021046	15	35,933,094 - 35,944,902
		<i>O. latipes</i>	ENSNDARG00000021046	17	24,782,508 - 24,802,926
Irs1	Insulin receptor substrate 1	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000169047	2	226,731,317 - 226,799,759
		<i>G. gallus</i>	ENSGALG00000004957	9	9,276,974 - 9,300,051
		<i>X. tropicalis</i>	ENSXETG000000020086	GL127898.1	477,755 - 505,839
		<i>A. carolinensis</i>	ENSACAG000000003830	3	23,742,830 - 23,746,420
		<i>L. cholerae</i>	ENSLACG000000014111	JH126709.1	963,541 - 1,032,531
		<i>I. oculatus</i>	ENSLOGG000000017412	LG14	19,644,420 - 19,647,336
		<i>D. rerio</i>	ENSNDARG000000054087	15	35,888,549 - 35,930,070
		<i>O. latipes</i>	ENSNDARG000000054087	17	24,782,508 - 24,802,926
SST4	Somatostatin 4	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000169047	2	226,731,317 - 226,799,759
		<i>G. gallus</i>	ENSGALG00000004957	9	9,276,974 - 9,300,051
		<i>X. tropicalis</i>	ENSXETG000000020086	GL127898.1	477,755 - 505,839
		<i>A. carolinensis</i>	ENSACAG000000003830	3	23,742,830 - 23,746,420
		<i>L. cholerae</i>	ENSLACG000000014111	JH126709.1	963,541 - 1,032,531
		<i>I. oculatus</i>	ENSLOGG000000017412	LG14	19,644,420 - 19,647,336
		<i>D. rerio</i>	ENSNDARG000000054087	15	35,888,549 - 35,930,070
		<i>O. latipes</i>	ENSNDARG000000054087	17	24,782,508 - 24,802,926
Nyp2b	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	<i>R. typos</i>			
		<i>C. millii</i>			
		<i>H. sapiens</i>	ENSG00000144400	2	225,399,710 - 225,654,018
		<i>G. gallus</i>	ENSGALG00000004986	9	8,727,389 - 8,844,775
		<i>X. tropicalis</i>	ENSXETG000000005150	GL127898.1	945,276 - 992,671
		<i>A. carolinensis</i>	ENSACAG000000003843	3	24,114,255 - 24,276,004
		<i>L. cholerae</i>	ENSLACG000000018098	JH126709.1	1,453,451 - 1,537,668
		<i>I. oculatus</i>	ENSLOGG000000009528	LG14	19,821,041 - 19,871,639
		<i>D. rerio</i>	ENSNDARG000000079581	15	35,698,508 - 35,895,161
		<i>O. latipes</i>	ENSNDARG000000093357	2	5,734,870 - 5,776,030
<i>O. latipes</i>	ENSNDARG000000093357	17	24,782,508 - 24,789,441		