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

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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 chondrichtyan species, elephant shark (*Callorhinchus 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 vertbrates *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 tetra-paralogon 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 SST*s, as well as their counterparts from other chondrychthyans, 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 introducted by Tostivint *et al.* (2008) then extended by Liu *et al.* (2010). Nevertheless, the correspondence bewteen 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 Tm 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 Tm of the primers, 30 sec; and extension 72°C, 30 sec) and a final extension of 72°C for 7 min. The *S. canicula Egf1* 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 NH2-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 NH2-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 AGCKNFFWKTFTSC 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 view 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 likehood 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 actinopteygian 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. Gnathotostome 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 *STTe* were found, in addition to the three *SST* genes, *SSTa*, *SSTb* and *SSTc*, previoulsly 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 SST*s without prejudice to their evolutionary relationships with other vertebrate *SST*s (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 chondrichtyan *SSTc* and *SSTe* also led us to redefine the relationships between *SST2* and *SST6*. The *SST2* gene was been 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 though, 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 sarcoperygians 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.

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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. Polyadenylylation 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^5]-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^7, Gly^{10}]-somatostatin-14 from the endocrine pancreas of rainbow trout, *Oncorhynchus mykiss*. Gen. Comp. Endocrinol. 98, 253–261.

Muffato, M., Louis, A., Poisnel, C.E, Roest Crollius, 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-Fernàndez, 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. 3rd, 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 Crollius, H., 2018 Chromosome evolution at the origin of the ancestral vertebrate genome. Genome Biol. 19, 166.

Tostivint, H., Lihrmann, 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., Lihrmann, I., Ekker, M., Vaudry, H., 2004. Chromosomal localization of three somatostatin genes in zebrafish. Evidence that the [Pro^2]-somatostatin-14 isoform and cortistatin are encoded by orthologous genes. J. Mol. Endocrinol. 33, R1–R8.

Tostivint, H., Lihrmann, 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., Lihrmann, 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., Lihrmann, 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^{2}, Met^{13}]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 1

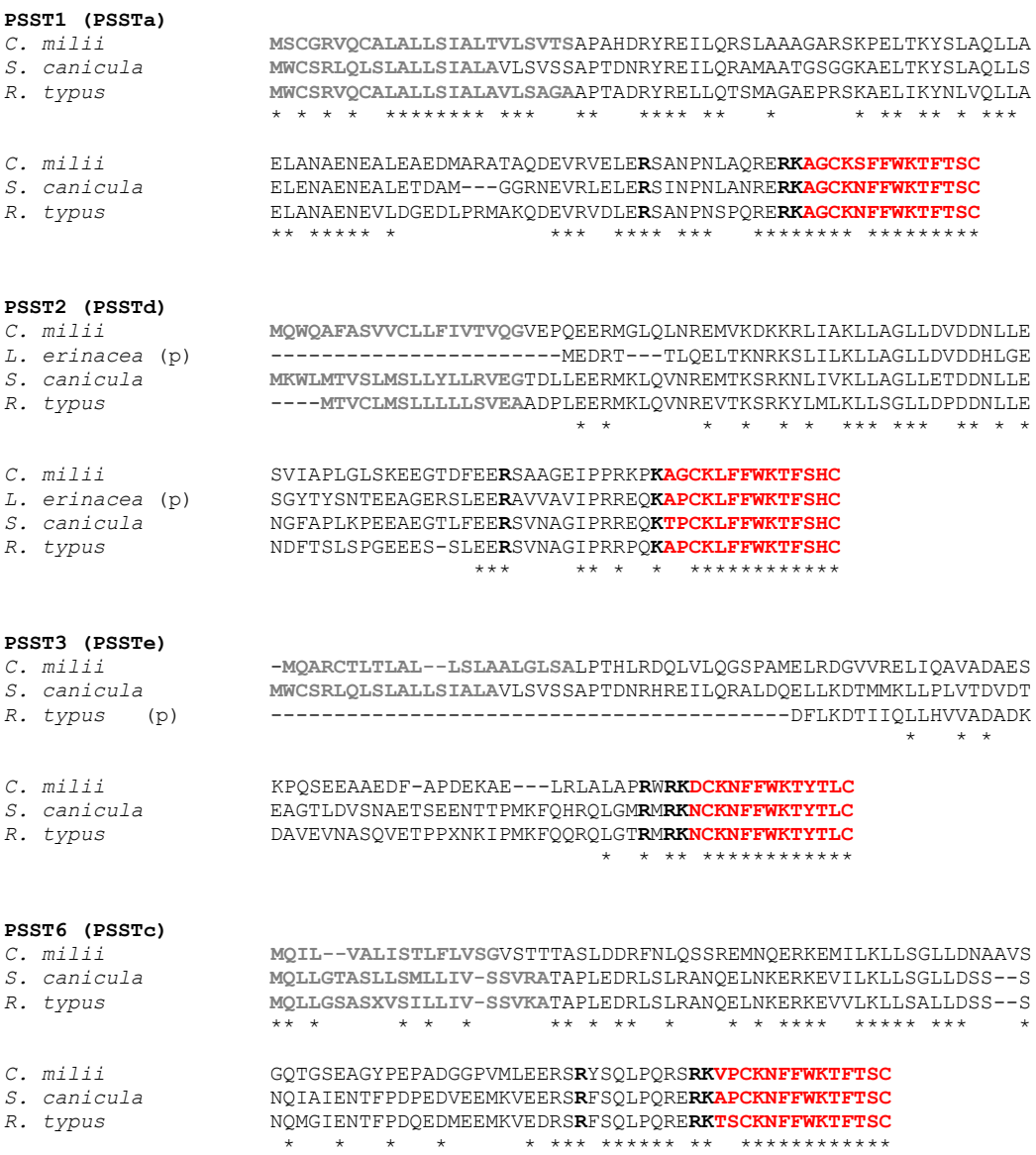

PSST1 (PSSTa)
C. milii MSCGRVQCALALLSIALTVLSVTSAPAHDRYREILQRSLAAAGARSKPELTKYSLAQLLA
S. canicula MWCSRLQLSLALLSIALAVLSVSSAPTDNRYREILQRAMAATGSGGKAELTKYSLAQLLS
R. typus MWCSRVQCALALLSIALAVLSAGAAPTADRYRELLQTSMAGAEPRSKAELIKYNLVQLLA
C. milii ELANAENEALEAEDMARATAQDEVRVELERSANPNLAQRERKAGCKSFFWKTFTSC
S. canicula ELENAENEALETDAM---GGRNEVRLELERSINPNLANRERKAGCKNFFWKTFTSC
R. typus ELANAENEVLDGEDLPRMAKQDEVRVDLERSANPNSPQRERKAGCKNFFWKTFTSC
PSST2 (PSSTd)
C. milii MQWQAFASVVCLLFIVTVQGVEPQEERMGLQLNREMVKDKKRLIAKLLAGLLDVDDNLLE
L. erinacea (p) ----------MEDRT---TLQELTKNRKSLILKLLAGLLDVDDHLGE
S. canicula MKWLMTVSLMSLLYLLRVEGTDLLEERMKLQVNREMTKSRKNLIVKLLAGLLETDDNLLE
R. typus ----MTVCLMSLLLLLSVEAADPLEERMKLQVNREVTKSRKYLMLKLLSGLLDPDDNLLE
C. milii SVIAPLGLSKEEGTDFEERSAAGEIPPRKPKAGCKLFFWKTFSHC
L. erinacea (p) SGYTYSNTEEAGERSLEERAVVAVIPRREQKAPCKLFFWKTFSHC
S. canicula NGFAPLKPEEAEGTLFEERSVNAGIPRREQKTPCKLFFWKTFSHC
R. typus NDFTSLSPGEEES-SLEERSVNAGIPRRPQKAPCKLFFWKTFSHC
PSST3 (PSSTe)
C. milii -MQARCTLTLAL--LSLAALGLSALPTHLRDQLVLQGSPAMELRDGVVRELIQAVADAES
S. canicula MWCSRLQLSLALLSIALAVLSVSSAPTDNRHREILQRALDQELLKDTMMKLLPLVTDVDT
R. typus (p) ----------DFLKDTIIQLLHVVADADK
C. milii KPQSEEAAEDF-APDEKAE---LRLALAPRWRKDCKNFFWKTYTLC
S. canicula EAGTLDVSNAETSEENTTPMKFQHRQLGMRMRKNCKNFFWKTYTLC
R. typus DAVEVNASQVETPPXNKIPMKFQQRQLGTRMRKNCKNFFWKTYTLC
PSST6 (PSSTc)
C. milii MQIL--VALISTLFLVSGVSTTTASLDDRFNLQSSREMNQERKEMILKLLSGLLDNAAVS
S. canicula MQLLGTASLLSMLLIV-SSVRATAPLEDRLSLRANQELNKERKEVILKLLSGLLDSS--S
R. typus MQLLGSASXVSILLIV-SSVKATAPLEDRLSLRANQELNKERKEVVLKLLSALLDSS--S
C. milii GQTGSEAGYPEPADGGPVMLEERSRYSQLPQRSRKVPCKNFFWKTFTSC
S. canicula NQIAIENTFPDPEDVEEMKVEERSRFSQLPQRERKAPCKNFFWKTFTSC
R. typus NQMGIENTFPDQEDMEEMKVEDRSRFSQLPQRERKTSCKNFFWKTFTSC

Figure 2

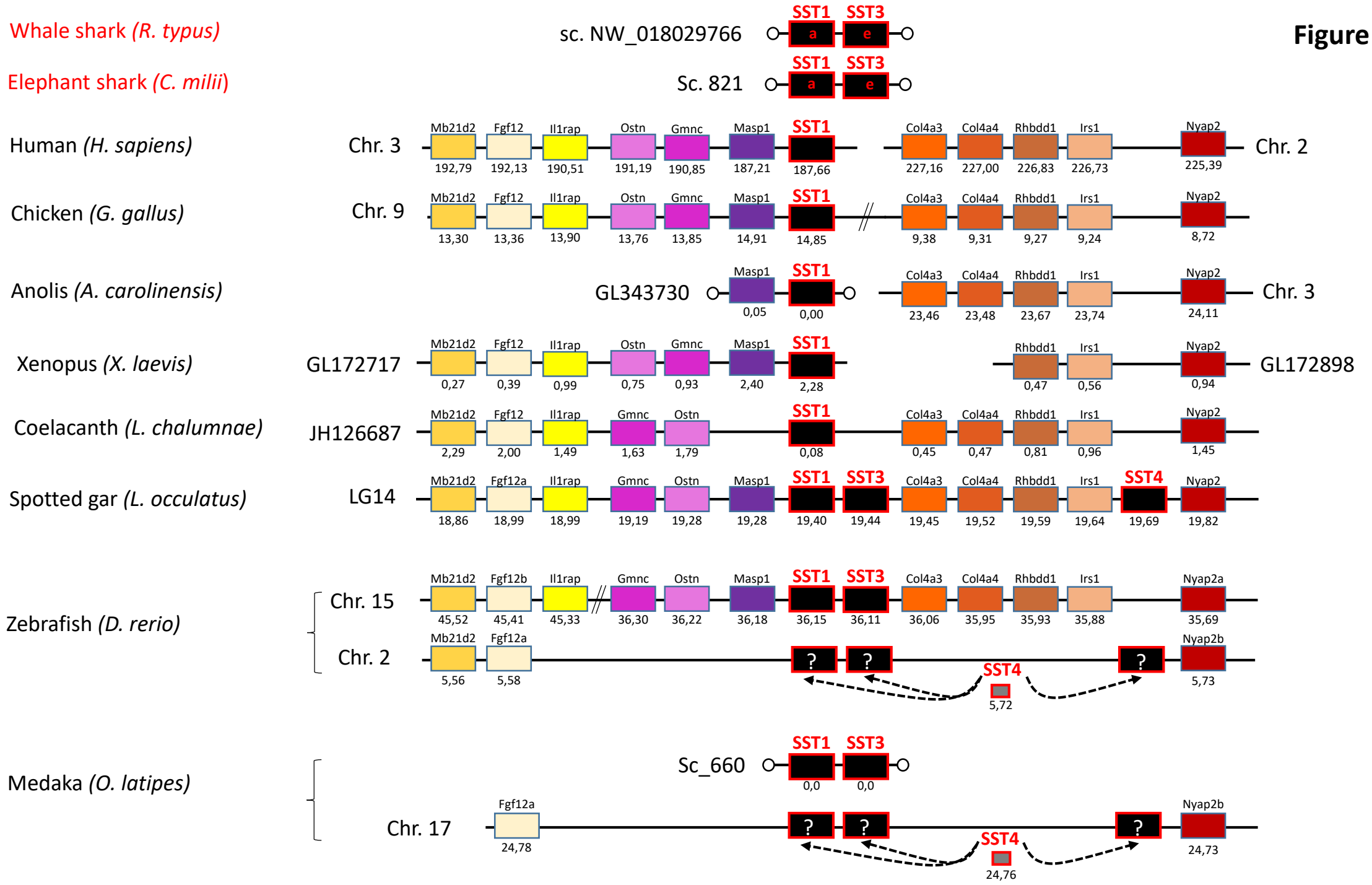

Whale shark (R. typus)
sc. NW_018029766
SST1 SST3
a e
Elephant shark (C. milii)
Sc. 821
SST1 SST3
a e
Human (H. sapiens)
Chr. 3
Mb21d2 Fgf12 Il1rap Ostn Gmnc Masp1 SST1 Col4a3 Col4a4 Rhbdd1 Irs1 Nyap2
192,79 192,13 190,51 191,19 190,85 187,21 187,66 227,16 227,00 226,83 226,73 225,39
Chr. 2
Chicken (G. gallus)
Chr. 9
Mb21d2 Fgf12 Il1rap Ostn Gmnc Masp1 SST1 Col4a3 Col4a4 Rhbdd1 Irs1 Nyap2
13,30 13,36 13,90 13,76 13,85 14,91 14,85 9,38 9,31 9,27 9,24 8,72
Anolis (A. carolinensis)
GL343730
Masp1 SST1 Col4a3 Col4a4 Rhbdd1 Irs1 Nyap2
0,05 0,00 23,46 23,48 23,67 23,74 24,11
Chr. 3
Xenopus (X. laevis)
GL172717
Mb21d2 Fgf12 Il1rap Ostn Gmnc Masp1 SST1 Rhbdd1 Irs1 Nyap2
0,27 0,39 0,99 0,75 0,93 2,40 2,28 0,47 0,56 0,94
GL172898
Coelacanth (L. chalumnae)
JH126687
Mb21d2 Fgf12 Il1rap Gmnc Ostn SST1 Col4a3 Col4a4 Rhbdd1 Irs1 Nyap2
2,29 2,00 1,49 1,63 1,79 0,08 0,45 0,47 0,81 0,96 1,45
Spotted gar (L. occulatus)
LG14
Mb21d2 Fgf12a Il1rap Gmnc Ostn Masp1 SST1 SST3 Col4a3 Col4a4 Rhbdd1 Irs1 SST4 Nyap2
18,86 18,99 18,99 19,19 19,28 19,28 19,40 19,44 19,45 19,52 19,59 19,64 19,69 19,82
Zebrafish (D. rerio)
Chr. 15
Mb21d2 Fgf12b Il1rap Gmnc Ostn Masp1 SST1 SST3 Col4a3 Col4a4 Rhbdd1 Irs1 Nyap2a
45,52 45,41 45,33 36,30 36,22 36,18 36,15 36,11 36,06 35,95 35,93 35,88 35,69
Chr. 2
Mb21d2 Fgf12a ? ? ? Nyap2b
5,56 5,58 SST4 5,72 5,73
Medaka (O. latipes)
Sc_660
SST1 SST3
0,0 0,0
Chr. 17
Fgf12a ? ? ? Nyap2b
24,78 SST4 24,76 24,73

Figure 3

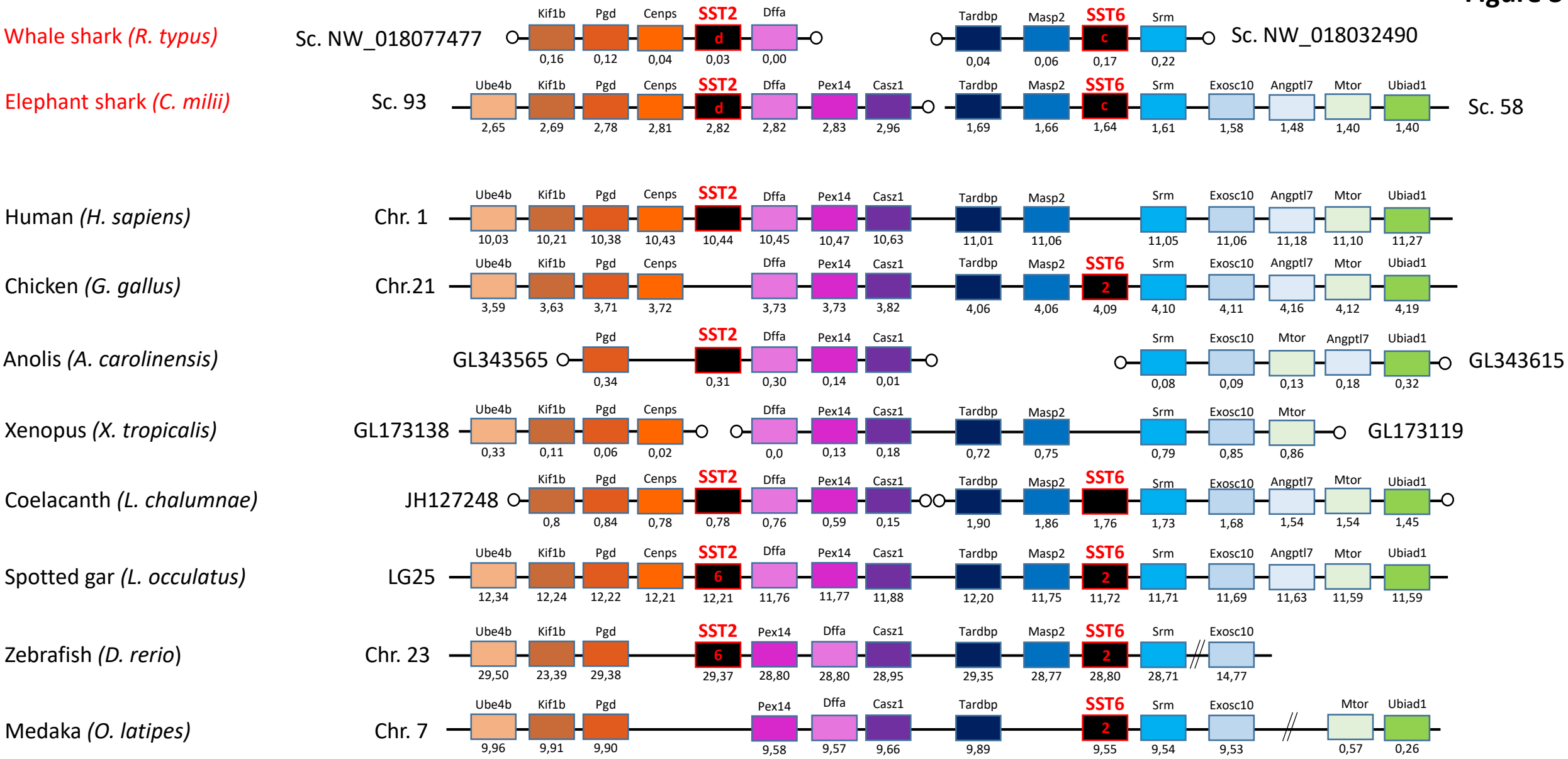

Whale shark (R. typus)
Sc. NW_018077477
Kif1b Pgd Cenps SST2 Dffa
0,16 0,12 0,04 d 0,03 0,00
Tardbp Masp2 SST6 Srm
0,04 0,06 c 0,17 0,22
Sc. NW_018032490
Elephant shark (C. milii)
Sc. 93
Ube4b Kif1b Pgd Cenps SST2 Dffa Pex14 Casz1
2,65 2,69 2,78 2,81 d 2,82 2,82 2,83 2,96
Tardbp Masp2 SST6 Srm Exosc10 Angptl7 Mtor Ubiad1
1,69 1,66 c 1,64 1,61 1,58 1,48 1,40 1,40
Sc. 58
Human (H. sapiens)
Chr. 1
Ube4b Kif1b Pgd Cenps SST2 Dffa Pex14 Casz1
10,03 10,21 10,38 10,43 10,44 10,45 10,47 10,63
Tardbp Masp2 Srm Exosc10 Angptl7 Mtor Ubiad1
11,01 11,06 11,05 11,06 11,18 11,10 11,27
Chicken (G. gallus)
Chr.21
Ube4b Kif1b Pgd Cenps Dffa Pex14 Casz1
3,59 3,63 3,71 3,72 3,73 3,73 3,82
Tardbp Masp2 SST6 Srm Exosc10 Angptl7 Mtor Ubiad1
4,06 4,06 2 4,09 4,10 4,11 4,16 4,12 4,19
Anolis (A. carolinensis)
GL343565
Pgd SST2 Dffa Pex14 Casz1
0,34 0,31 0,30 0,14 0,01
Srm Exosc10 Mtor Angptl7 Ubiad1
0,08 0,09 0,13 0,18 0,32
GL343615
Xenopus (X. tropicalis)
GL173138
Ube4b Kif1b Pgd Cenps Dffa Pex14 Casz1
0,33 0,11 0,06 0,02 0,0 0,13 0,18
Tardbp Masp2 Srm Exosc10 Mtor
0,72 0,75 0,79 0,85 0,86
GL173119
Coelacanth (L. chalumnae)
JH127248
Kif1b Pgd Cenps SST2 Dffa Pex14 Casz1
0,8 0,84 0,78 0,78 0,76 0,59 0,15
Tardbp Masp2 SST6 Srm Exosc10 Angptl7 Mtor Ubiad1
1,90 1,86 1,76 1,73 1,68 1,54 1,54 1,45
Spotted gar (L. occulatus)
LG25
Ube4b Kif1b Pgd Cenps SST2 Dffa Pex14 Casz1
12,34 12,24 12,22 12,21 6 12,21 11,76 11,77 11,88
Tardbp Masp2 SST6 Srm Exosc10 Angptl7 Mtor Ubiad1
12,20 11,75 2 11,72 11,71 11,69 11,63 11,59 11,59
Zebrafish (D. rerio)
Chr. 23
Ube4b Kif1b Pgd SST2 Pex14 Dffa Casz1
29,50 23,39 29,38 6 29,37 28,80 28,80 28,95
Tardbp Masp2 SST6 Srm Exosc10
29,35 28,77 2 28,80 28,71 14,77
Medaka (O. latipes)
Chr. 7
Ube4b Kif1b Pgd Pex14 Dffa Casz1
9,96 9,91 9,90 9,58 9,57 9,66
Tardbp SST6 Srm Exosc10 Mtor Ubiad1
9,89 2 9,55 9,54 9,53 0,57 0,26

Figure 4

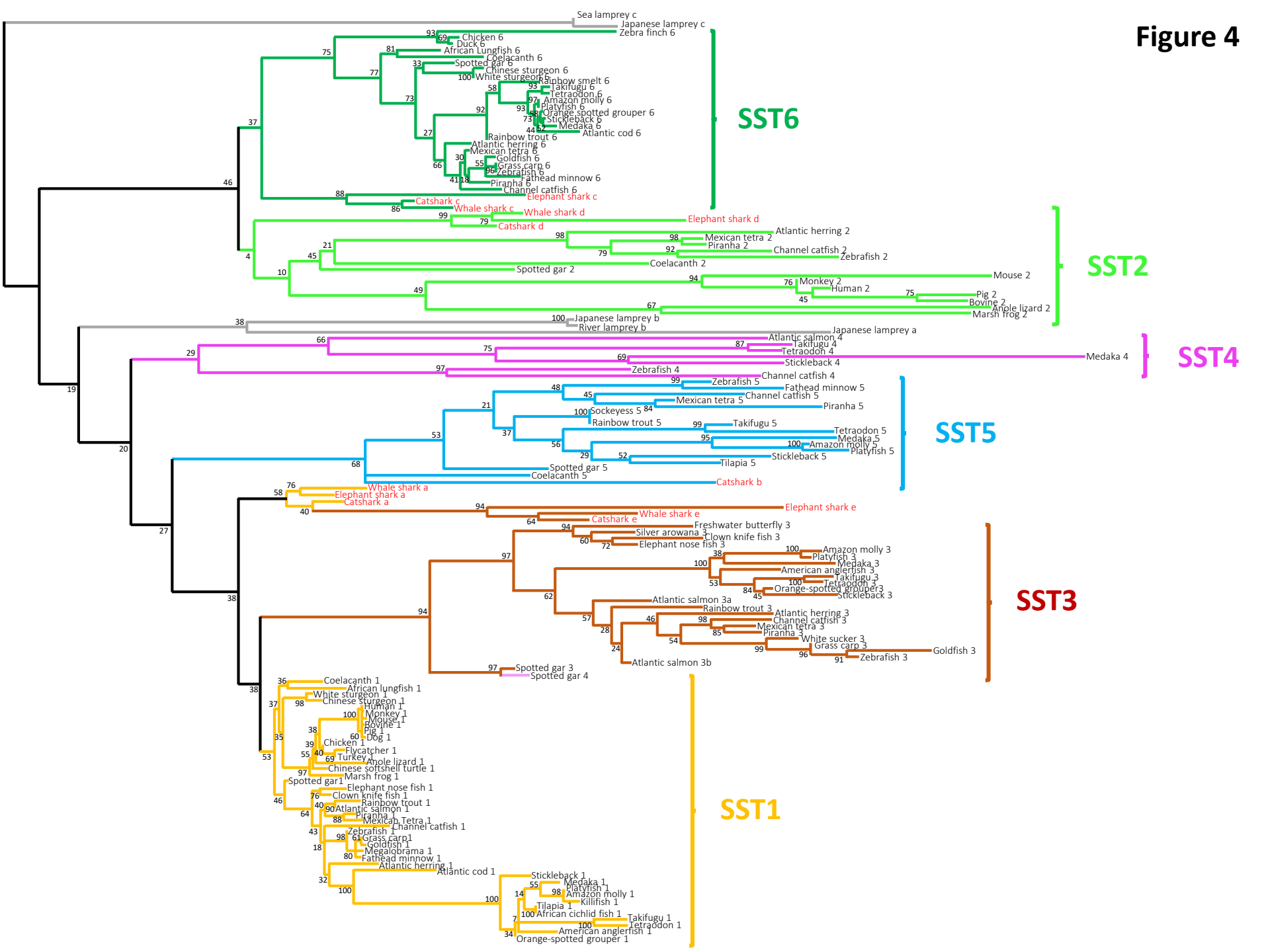
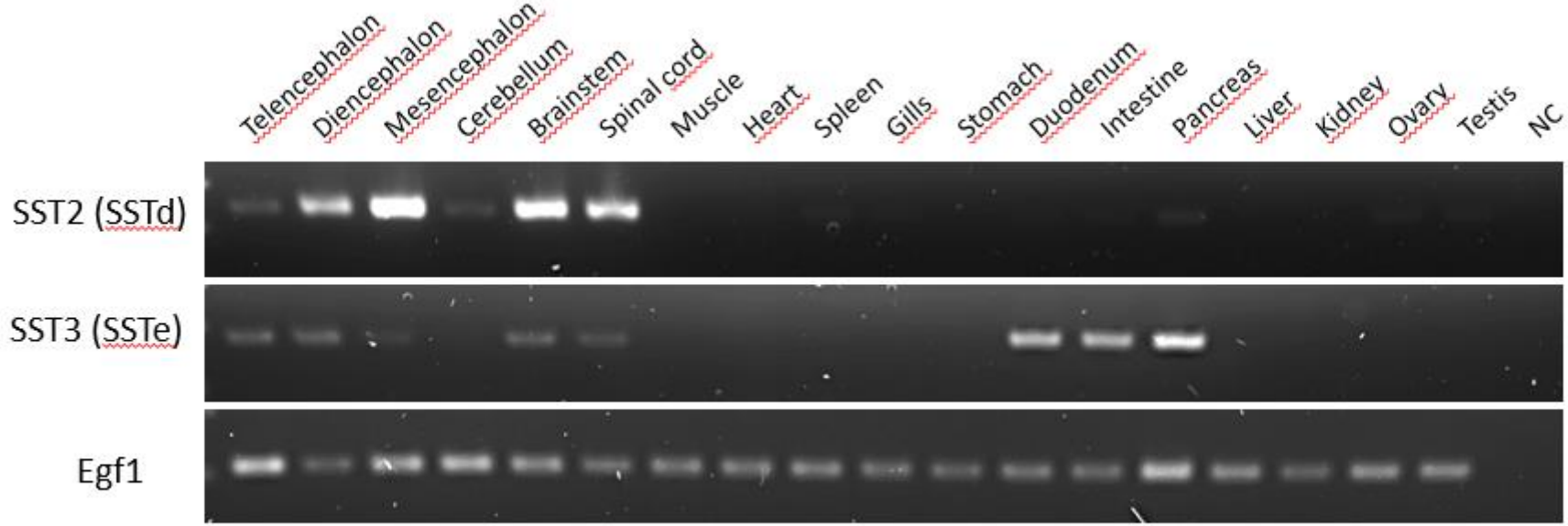

Sea lamprey c
Japanese lamprey c
Zebra finch 6
Chicken 6
Duck 6
African Lungfish 6
Coelacanth 6
Spotted gar 6
Chinese sturgeon 6
White sturgeon 6
Rainbow smelt 6
Takifugu 6
Tetraodon 6
Amazon molly 6
Platyfish 6
Orange spotted grouper 6
Stickleback 6
Medaka 6
Atlantic cod 6
Rainbow trout 6
Atlantic herring 6
Mexican tetra 6
Goldfish 6
Grass carp 6
Zebrafish 6
Fathead minnow 6
Piranha 6
Channel catfish 6
Elephant shark c
Catshark c
Whale shark c
Whale shark d
Elephant shark d
Catshark d
SST6
Atlantic herring 2
Mexican tetra 2
Piranha 2
Channel catfish 2
Zebrafish 2
Coelacanth 2
Spotted gar 2
Mouse 2
Monkey 2
Human 2
Pig 2
Bovine 2
Anole lizard 2
Marsh frog 2
SST2
Japanese lamprey b
River lamprey b
Japanese lamprey a
Atlantic salmon 4
Takifugu 4
Tetraodon 4
Stickleback 4
Medaka 4
Zebrafish 4
Channel catfish 4
SST4
Zebrafish 5
Fathead minnow 5
Channel catfish 5
Mexican tetra 5
Piranha 5
Sockeyess 5
Rainbow trout 5
Takifugu 5
Tetraodon 5
Medaka 5
Amazon molly 5
Platyfish 5
Stickleback 5
Tilapia 5
Spotted gar 5
Coelacanth 5
Catshark b
SST5
Whale shark a
Elephant shark a
Catshark a
Elephant shark e
Whale shark e
Catshark e
Freshwater butterfly 3
Silver arowana 3
Clown knife fish 3
Elephant nose fish 3
Amazon molly 3
Platyfish 3
Medaka 3
American anglerfish 3
Takifugu 3
Tetraodon 3
Orange-spotted grouper3
Stickleback 3
Atlantic salmon 3a
Rainbow trout 3
Atlantic herring 3
Channel catfish 3
Mexican tetra 3
Piranha 3
White sucker 3
Grass carp 3
Goldfish 3
Zebrafish 3
Atlantic salmon 3b
Spotted gar 3
Spotted gar 4
SST3
Coelacanth 1
African lungfish 1
White sturgeon 1
Chinese sturgeon 1
Human 1
Mpnkey 1
Mouse 1
Bovine 1
Pig 1
Dog 1
Chicken 1
Flycatcher 1
Turkey 1
Anole lizard 1
Chinese softshell turtle 1
Marsh frog 1
Spotted gar1
Elephant nose fish 1
Clown knife fish 1
Rainbow trout 1
Atlantic salmon 1
Piranha 1
Mexican Tetra 1
Channel catfish 1
Zebrafish 1
Grass carp1
Goldfish 1
Megalobrama 1
Fathead minnow 1
Atlantic herring 1
Atlantic cod 1
Stickleback 1
Medaka 1
Platyfish 1
Amazon molly 1
Killifish 1
Tilapia 1
African cichlid fish 1
Takifugu 1
Tetraodon 1
American anglerfish 1
Orange-spotted grouper 1
SST1

Figure 5


Telencephalon
Diencephalon
Mesencephalon
Cerebellum
Brainstem
Spinal cord
Muscle
Heart
Spleen
Gills
Stomach
Duodenum
Intestine
Pancreas
Liver
Kidney
Ovary
Testis
NC
SST2 (SSTd)
SST3 (SSTe)
Egf1

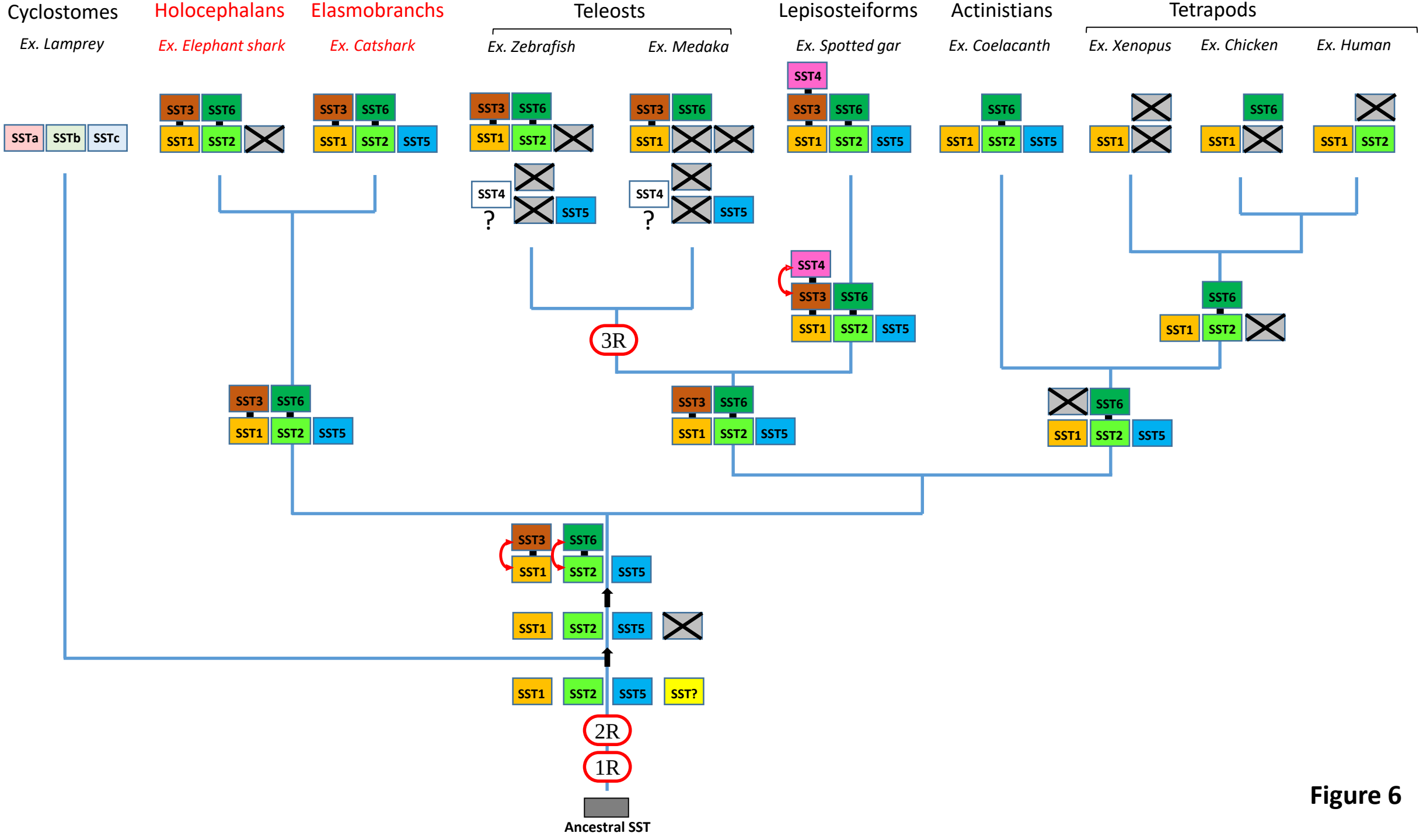

Cyclostomes
Ex. Lamprey
Holocephalans
Ex. Elephant shark
Elasmobranchs
Ex. Catshark
Teleosts
Ex. Zebrafish
Ex. Medaka
Lepisosteiforms
Ex. Spotted gar
Actinistians
Ex. Coelacanth
Tetrapods
Ex. Xenopus
Ex. Chicken
Ex. Human
SSTa
SSTb
SSTc
SST1
SST2
SST3
SST4
SST5
SST6
SST?
?
3R
2R
1R
Ancestral SST

Figure 6

Figure S1

Somatostatin 1

Primates

>Human *(Homo sapiens)* SST1 (BC032625)
MLSCRLQCALAALSIVLALGCVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTENDALEPEDLSQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC
>Monkey (*Macaca fascicularis*) SST1 (XP_005545499)
MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTENDALEPEDLSQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC

Other mammals

>Bovine (*Bos taurus*) SST1 (NP_776385.1)
MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTEIDALEPEDLSQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC
>Dog *(Canis lupus familiaris)* SST1 (NP_001003307.1)
MLSCRLQCALAALSIVLALGGVTCAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTENDALEPEDLSQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC
>Mouse *(Mus musculus)* SST1 (NP_033241.1)
MLSCRLQCALAALCIVLALGGVTGAPSDPRLRQFLQKSLAAATGKQELAKYFLAELLSEPN
QTENDALEPEDLPQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC
>Pig SS1 (*Sus scrofa*) SST1 (AAT02532.1)
MLSCRLQCALAALSIVLALGGVTGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPN
QTENDALEPEDLSQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC

Birds

>Flycatcher (*Ficedula albicollis)* SST1 (ENSFALT00000007767.1)
MLSCRLQCALALLSIALALGTVSAAPSDPRLRQFLQKSLGGGGGGGELAKYFLAELLSEPSQ
TENEALESEDLSRGAEQDEVRLELERSANSNPALAPRERKAGCKNFFWKTFTSC
>Chicken *(Gallus gallus)* SST1 (CN210817.1)
MLSCRLQCALALLSIALAVGTVSAAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPSQ
TENEALESEDLSRGAEQDEVRLELERSANSNPALAPRERKAGCKNFFWKTFTSC
>Turkey (*Meleagris gallopavo)* SST1 (ENSMGAT00000008507.2)
KELAKYFLAELLSEPSQTENEALESEDLSRGAEQDEVRLELERSANSNPALAPRERKAGCKN
FFWKTFTSC

Reptiles

>Anole lizard (*Anolis carolinensis)* SST1 (XP_003228868)
MLPCRLPCALALLSLALALGSGAAAPADPRLRQFLQKSLAAAAAGKQELAKYFLAELLSEP
GQAENEALEPEELSRGGGAEQDEVRLELERSASLNPALEPRVRKAGCKNFFWKTFTSC
>Chinese softshell turtle (*Pelodiscus sinensis)* SST1 (ENSPSIT00000016437.1)
MLSCRLQCALALLSLALAVSSVSGAPSDPRLRQFLQKSLAAAAGKQELAKYFLAELLAEPS
QPENEALEPEDLSRGPEQDEVRLELERSANPNPALAPRERKAGCKNFFWKTFTSC

Amphibians

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

Lobe-finned fish

>Coelacanth (*Latimeria chalumnae*) SST1 (XP_005992512.1)
MLSSRLQCAFAFLSLALVVSNISAAPSDLRLRQLLQKSLAAAAGKQEVSKYSLAELLAELAQ
AENEALESDDFSKTSDQDEVRLELERSANGNPALAPRERKAGCKNFFWKTFTSC
>African lungfish *(Protopterus annectens)* SST1 (AAD39138.1)

MLSCRFQCALVLLSLAVVFSKVSAAPSDLRLRQLLQRSLAAAAGKQELTKYSLAELLSELA
QSENDALDSSDLSRGADQDEVRLELDRSANSSPLAARERKAGCKNFFWKTFTSC

Euteleosts

>Orange-spotted grouper *(Epinephelus coioides)* SST1 (AAU93565.1)
MKMVSSSRLRCLLLLLLSLTASISCSSAAQRDSKLRLLLHRTPLLGSKQDMSRASLAELLLSD
LLQVENEALEEENFPLAEGEPEDVHVDLERAAAAGSGPLLAPRERKAGCKNFFWKTFTSC
>Killifish *(Fundulus heteroclitus)* SST1 (EV461374.1)
MKMFSSLSLRCLLLLLLCLSASISCSAAAQRDSKLRLLLHRTPLLSSQQDVSRSSLAELLLSD
LLQMENEALEEDGFTLPEGEPEDIRVDLERAASSGPLLAPRERKAGCKNFFWKTFTSC
>Atlantic cod *(Gadus morhua)* SST1 (AAZ85702.1)
MMSVRSTLLLLSCAAMLSGSSAAPSDTKLRQLLQRSLLAPMPGQEETVRYTLAQLLSELAQ
AENEALGTDDQDDERMDLERAAGPMMAPRERKAGCKNFFWKTFTSC
>Stickleback *(Gasterosteus aculeatus)* SST1 (KT235748)
MVSSRLRCLLLLLLSLTASISCSSTAQRDGKLHLLLHRTPLLSSKQDMSRASLVELLLSDLLQ
VQNEALEEENLAPAGGEPEEVHLDLERAADAGPLLGPRERKAGCKNFFWKTFTSC
>African cichlidfish *(Haplochromis burtoni)* SST1 (AAS97964.1)
MNSSSRLRCLLLLLVSLTASISCTSAAQRDSKLRLLLHRTPLLGSKQDMSRSSLAELLLSDLL
QVENEALEEENFPLADGEPEDIRVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC
>American anglerfish *(Lophius americanus)* SST1 (P01169.1)
MKMVSSSRLRCLLVLLLSLTASISCSFAGQRDSKLRLLLHRYPLQGSKQDMTRSALAELLLS
DLLQGENEALEEENFPLAEGGPEDAHADLERAASGGPLLAPRERKAGCKNFFWKTFTSC
>Rainbow trout *(Oncorhynchus mykiss)* SST1 (CA364601.1)
MLSTRVQCALALLSLALAISSVSAAPSDAKLRQLLQRSLMAPAGKQELARNTLVELLSELAH
VENEAIELDDMSHGVEQEDVDLELERAPGPVLAPRERKAGCKNFFWKTFTSC
>Tilapia (*Oreochromis niloticus)* SST1 (ENSONIT00000001338.1)
MNSSSRLRCLLLLLVSLTASISCTSAAQRDSKLRLLLHRTPLLGSKQDMSRSSLAELLLSDLL
QVENEALEEENFPLADGEPEDIRVDLERAAGSGPLLAPRERKAGCKNFFWKTFTSC
>Medaka *(Oryzias latipes)* SST1 (XP_004084505.1)
MMSSSSRLLLLLLSLTASISCSSAAQRDSKLRLLLQRTPLLGSKQDMSRSSLAELLLSDLLQM
ENEVLEEDGFPLSDGEPEDVRVDLERAAASGPLLAPRDRKAGCKNFFWKTFTSC
>Amazon molly (*Poecilia formosa)* SST1 (ENSPFOT00000005658.1)
MKMLSSLSLRCLLLLLLSLSASISCSSAAQRDSKLRLLLHRTPLLSSKQDASRSSLAELLLSDL
LQMENEALEEDGFGLPEGEPEDIRVDLERAASSGPLLAPRERKAGCKNFFWKTFTSC
>Atlantic salmon *(Salmo salar)* SST1 (CB509644.1)
MLSTRVQCALALLSLALAISSVSAAPSDAKLRQLLQRSLMAPAGKQELARYTLAELLSELAQ
AENEAIESDDLSRGVEQEDVRLELERAAGPVLAPRERKAGCKNFFWKTFTSC
>Takifugu *(Takifugu rubripes)* SST1 (ENSTRUG00000010048)
MFSSNSMCLLMLLLSLSASFSCSSAAHRDFKLPLLLQSNALMGNKQEMTRSSLANLLLSDLL
QVGNEALEENLALAEGEPEEVHIDMERAAAAGIGPFLTPRERKAGCKNFFWKTFTSC
>Tetraodon *(Tetraodon nigroviridis)* SST1 (KT235747)
MKMFSNSCCLLMLLLSLSASFSCSSAAHRDSKLALMLPPNPLLGHRQEMSRSSLADLLLSDL
LQVENQALDENFPLVEGEPEEVHVDMERAADAGIGPFLTPRERKAGCKNFFWKTFTSC
>Platyfish (*Xiphophorus maculatus)* SST1 (ENSXMAT00000014478.1)
MKMLSSLSLRCLLLLLLSLSASISCSSAAQRDSKLRLLLHRTPLLSSKQDASRSSLAELLLSDL
LQMENEALEEDGFPEGEPEDIRVDLERAASSGPLLPRERKASCKNFFWKTFTSC

Other teleosts

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

>Goldfish *(Carassius auratus)* SST1 (Q9YGH5.1)
MLSTRIQCALALLSLALAVCSVSAAPTDAKLRQLLQRSLLNPAGKQELARYTLADLLSELVQ
AENEALEPEDLSRAVEKDEVRLELERAAGPMLAPRERKAGCKNFFWKTFTSC
>Clown knife fish *(Chitala chitala)* SST1 (AAK97070.2)
MLSTRIQCALALLSLALAVSSVYAAPSDLKLRQLLQRSIIAPASKQELARYTLAELLSELAQV
ENEALESDDLSRGADQEEVRLELERAAGPPLAPRERKAGCKNFFWKTFTSC
>Atlantic herring (*Clupea harengus*) SST1 (XP_012673158.1)
MLSLRLQCALALLSIVLAISCISAAPTDVKLRQLLQRSLFAPGGKQELARLTLAELLSELAQA
ENEALESEDMSRGAEGEDVRYELERSAGSMLAPRERKAGCKNFFWKTFTSC
>Grass carp *(Ctenopharyngodon idella)* SST1 (ACB69423.1)
MLSTRIQCALALLSLALAVCSVSAAPTDAKLRQLLQRSLLNPAGKQELARYTLADLLSDLV
QAENEALEPEDLSRAVEKDDVRLELERAAGPMLAPRERKAGCKNFFWKTFTSC
>Zebrafish *(Danio rerio)* SST1 (AAH76254.1)
MLSTRIQCALALLSLALAVSSVSAAPSDAKLRQLLQRSLLSPAGKQELARYTLADLLSDLVQ
AENEALEPEDLSRGAEKDDVRLELERAAGPMLAPRERKAGCKNFFWKTFTSC
>Elephant nose fish *(Gnathonemus petersii)* SST1 (AF292652)
MLSSRIQCALALLSLALAVSSVSAAPSDLKLRQLLQRSLLAPASKQDLARNPLEELLSEMVR
VENEALEPDDLSRGADQEEVRLELERAAGPALAPRERKAGCKNFFWKTFTSC
>Channel catfish *(Ictalurus punctatus)* SST1 (CAA23877.1)
MPSTRIQCALALLAVALSVCSVSGAPSDAKLRQFLQRSILAPSVKQELTRYTLAELLAELAQ
AENEVLDSDEVSRAAESEGARLEMERAAGPMLAPRERKAGCKNFFWKTFTSC
>Megalobrama *(Megalobrama pellegrini)* SST1 (AAO92644.1)
MLSTRIQCALALLSLALAVSSVSAAPSDAKLRQLLQRSLLNPAGKQELARYTLTDLLSDLVQ
AENEVLEPEDLSRAVEKDEVRLELERAAGPMLAPRERKAGCKNFFWKTFTSC
>Fathead minnow *(Pimephales promelas)* SST1 (DT100930)
MLSTRIQCALALLSLALAISSVSAAPSDAKLRQLLQRSLLNPAGKQELARYTLADLLSELVQ
AENEALEPEDLSRAVEKDDVRLELERAAGPMLAPRERKAGCKNFFWKTFTSC
>Red-bellied piranha (*Pygocentrus nattereri)* SST1 (XP_017539070.1)
MLSTRVQCALALLSLALALSSVSGAPSDAKLRQFLQRSLIGPSGKQELARYTLAELLSELAQ
AENEALEAEDMPRGAEQEDVRMELERAAGPVLAPRERKAGCKNFFWKTFTSC
Other ray-finned fish
>White sturgeon *(Acipenser transmontanus)* SST1 (AAL13248.1)
MLSSRLQCALAFLSLALAVSSVSAAPSDPRLRQLLQRTLAASAGKQELLKYSIAELLSELAQS
ENDALASDELSRAAEQNDVRLELERSANGNPAMAPRERKAGCKNFFWKTFTSC
>Chinese sturgeon *(Acipenser sinensis)* SST1 (FJ792687.1)
MLSSRLQCALALLSLALAVSSVSAATSEPRIRQLLQRALVASAGKQDLLKYSLAELLSELAQ
SENDALASDELSRAAEQNDVRLELERSANGNPAMAPRERKAGCKNFFWKTFTSC
>Spotted gar (*Lepisosteus oculatus*) SST1 (XP_006637937.1)
MLSSRVQCALALLCLALAVSSVSAAPSDLRLRQLLQRSLAASAGKQELARYTLAELLSELA
QSENEALESDDLSRAAEQDEVRLELERSANPALAPRERKAGCKNFFWKTFTSC
Cartilagonous fish
>Elephant shark (*Callorhinchus milii)* SSTa (XP_007910586.1)
MSCGRVQCALALLSIALTVLSVTSAPAHDRYREILQRSLAAAGARSKPELTKYSLAQLLAEL
ANAENEALEAEDMARATAQDEVRVELERSANPNLAQRERKAGCKSFFWKTFTSC
>Whale shark (*Rhincodon typus)* SSTa (XP_020365362.1)
MWCSRVQCALALLSIALAVLSAGAAPTADRYRELLQTSMAGAEPRSKAELIKYNLVQLLAE
LANAENEVLDGEDLPRMAKQDEVRVDLERSANPNSPQRERKAGCKNFFWKTFTSC
>Catshark (*Scylorhinus canicula*) SSTa (JX964750)
MWCSRLQLSLALLSIALAVLSVSSAPTDNRYREILQRAMAATGSGGKAELTKYSLAQLLSEL
ENAENEALETDAMGGRNEVRLELERSINPNLANRERKAGCKNFFWKTFTSC

Somatostatin 2

Primates

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

> Monkey (*M. fascicularis*) SST2 (XP_015298230)
MPLPPGLLLLLLSGATATAALPLEGSPTGPDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASA
GPLIGEEAREVARRQEGAPPQQSARRDRTPCKNFFWKTFSSCK

Other mammals

> Bovine (*B. taurus*) SST2 (NP_001191825)
MLPLCLLLPLLLLPSGATTALSPEGGLAGHESGHMQEVAEIKTNSLLTFLAWWYEWASQAR
AVPFVGGEAREVSKRQEGAPLHQSTRQDKTPCKNFFWKTFSSCK

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

> Pig (*S. scrofa*) SST2 (NP_001191865)
MLPPLCLLLLLLLPPLGATTALPLEGGLTSHDRDSGHMQEVAEIKKNSLLTFLAWWHEWMS
QAREVPFVGGETREMPKKQEGLPRQQASRGDRTPCGNFFWKTFSSCK

Reptiles

>Anole lizard *(A. carolinensis)* SST2 (XP_008119733.1)
MAFLVHPPPSAPFLLALLSFSRLMGAAPAAVLPIPGGLAWKHNEGSADLGRDELLAFLSGLV
DRASRRHGMPLSKQEKVVRSPREERVPFFRHPVREKAPCKNFFWKTFSSC

Amphibians

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

Lobe-finned fish

>Coelacanth (*L. chalumnae)* SST2 (NW_005819697)
MQPLILLVPLVLMAWNLGVAAVPKEERLMLYDKVNRETTGFGEERKQFLSNMLDALIGLN
TLENDTPLLGTKEQEEHNLSERSAFKYSSLKKAPCRNFFWKTFSSC

Teleosts

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

>Atlantic herring (*C. harengus*) SST2 (XP_012681486.1)
MGVLARVDPCSVAQSARITMRVLTSLVPLILIVWSGSQTGALPVREKPLRNESLADEERILLL
KILAGLTEKNLTEENLTGHDLEGLLNGTLKGGSVPTPQERSPCKNFFWKTFSSC

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

>Channel catfish (*I. punctatus*) SST2 (XP_017341959.1)
MALGGRINLYQAVDSPMFTMRVLLSLIPLLFVAWSANNADALPVQDKLPNSNEVLTKEQK
DFMTQFLANLAELNMTIKDLETMDHEQLSKLSERAAFGLPPAREKSQCNFFWKTFSSC

> Red-bellied piranha (*P. nattereri)* SST2 (XM_017706353.1)
MALAVGGTSCGGADGGMFIMRMLLSLVPLLLIAWSGTSTDALPVENKLPQSNEVLTKEQK
DLLIKIMSDLAELNMTVKDLGALDLEQLLSGKLGERSVFGLPAQEKSPCKNFFWKTFSACQ
H

Other ray-finned fish

>Spotted gar (*L. oculatus)* SST2 (NC_023203.1)
MHLLSSLVPLALLVWSLKCAAAVPSEERRALQSNGGLAKERKDVLLKVLSGLLVSNLLRKE
QSAVDSEQLKSSLMGERSVFGPSVSRERTPCKNFFWKTFSSC

Cartilaginous fish

>Elephant shark (*C. milii*) SSTd (XP_007900347.1)
MQWQAFASVVCLLFIVTVQGVEPQEERMGLQLNREMVKDKKRLIAKLLAGLLDVDDNLLE
SVIAPLGLSKEEGTDFEERSAAGEIPPRKPKAGCKLFFWKTFSHC
>Whale shark (*R. typus*) SSTd (XP_020390988.1)
MTVCLMSLLLLLSVEAADPLEERMKLQVNREVTKSRKYLMLKLLSGLLDPDDNLLENDFTS
LSPGEEESSLEERSVNAGIPRRPQKAPCKLFFWKTFSHC
>Catshark (*S. canicula*) SSTd (MK491629)
MKWLMTVSLMSLLYLLRVEGTDLLEERMKLQVNREMTKSRKNLIVKLLAGLLETDDNLLE
NGFAPLKPEEAEGTLFEERSVNAGIPRREQKTPCKLFFWKTFSHC

Somatostatin 3

Euteleosts

>Orange-spotted grouper (*E. coioides*) SST3 (AAU93566.1)
MQCIRCPTILVLVALVLCSPGVFSQPDRDQDQYQNQDLDLELRHHRLLQRARSAGLLSQEW
SKRAVEDLLAQMSLPEADTQREAEVVSMATGGRMNLERSVDPPNNLPPRERKAGCKNFYW
KGFTSC
>Stickleback *(G. aculeatus)* SST3 (KT235756)
MQYTRCPAILVLVGLVLCGPGVSSQRNRDQDQDQYQNQDLDPRPHLLLQRARGAGLLSQD
WSKRAVEDLLAQMSLPEADSQLGAEVVSAATGGRLHLERSVDPPNNLPARERKAGCKNFY
WKGFTSC
>American anglerfish (*L. Americanus*) SST3 (P01170.2)
MQCIRCPAILALLALVLCGPSVSSQLDREQSDNQDLDLELRQHWLLERARSAGLLSQEWSK
RAVEELLAQMSLPEADVQREAEDASMATGGRMNLERSVDSTNNLPPRERKAGCKNFYWK
GFTSC
>Rainbow trout (*O. mykiss)* SST3 (Q91194.1)
MKVCRIHCALALLGLALAICSQGAASQPDLDLRSRRLLQRARAAAWPHRSGVSERWRTFYP
NCPCLRPRKVKCPAGAKEDLRVELERSVGNPNNLPPRERKAGCKNFYWKGFTSC
>Medaka (*O. latipes*) SST3 (AU168379.1)
MQHARGPAFVVLAALALSSLGVSSQSDRDQDQFQNHDLDLELRHHRLLQRARSAGLLSQD
WSKRAIENMLARMPDPEAEAEREAEVGRNNMERSVDANVPPRNRKDGCKNFYWKGFTSC
>Amazon molly (*P. formosa)* SST3 (ENSPFOT00000005672.2)
MHHARCPTILVLAALAALSLGVSSQADRDQDPYQNQNLDLDLELRHHRLLQRARSAGLLS
QDWSKRAVEDLLAQMSRSAVEAQQDDPEAASKGTDSRLNLERSVETTARERKAGCKNFY
WKGLTSC
>Atlantic salmon *(S. salar)* SST3a (DW531645.1)
MKFSQIHCALALLGLALAICSQGAASQPDLDLRSRRLLQRARAASIATQEWSKRVMEDVLS
KLSLPDVEAQKSVGSTADAKEDLERSVDNSNNLPPRERKAGCKNFYWKGFTSC
>Atlantic salmon *(S. salar)* SST3b (CB505007.1)

MKVCRIHCALALLGLALAICSQGAASQPDLDLRSRRLLQRARAAGIATQEWSKRAVEDILS
QLSWPEAQESEVSPAGAKEDLRVELERSVGNPNNLPPRERKAGCKNFYWKGFTSC

>Takifugu (*T. rubripes*) SST3 (ENSTRUT00000025350.1)

MQRIHSSTILMLTTLVLCIQGVSSQPDRDLNQNQDLEMEVRHHRLLQHVHGAGLLSQEWSK
RAVEDLIAQMSMPEGTGQRDTEVVSMATGGRMNLERSVDTTNNLSPPERKAGCKNFYWK
GPTSC

>Tetraodon (*T. nigroviridis*) SST3 (ENSTNIT00000001563.1)

MPGVRSSTILVLTALVLSIQAVSSQPDRDLDQNQDLDQEVRRHRLLQRAHGAGLLSQDWSK
RAVEDLIAQMSLPEGTGQRDTEVVSMATGGRMNLERSVDTTNNLPPRKAGCKNFYWKGFT
SC

>Platyfish (*X. maculatus*) SST3

MHHARYPAILVLAALAALSLGVSSQADRDQDPYQNQNLDLDLELRHHRLLQRARSAGLLS
QDWSKRAVEDLLAQMSRSEVEAQQDGPEAASRGTGSRLNLERSVETTARERKAGCKNFY
WKGLTSC

Other teleosts

>Mexican tetra (*A. mexicanum*) SST3 (ENSAMXT00000006711.1)

MKVCVLQCGLVLLGLALVLCSSGASSQPDLDLDLDVDLRHRRLLQRARALGIAAQEWKKR
EMEDLLSQLTLPESEFQESEISTLGSKQDVRVEMDRSAENPNSLPPRERKAGCKNFYWKGFT
SC

>Goldfish (*C. auratus)* SST3 (AAF15306.1)

MRLCELHCYLALLGLSLVLCGRCANSQLEPDLDFRHHRLLQRASATGQATRWDFTKRDVE
KLLSLLSIPEMEMREKGLSMAGESEDLRLEQERSAESSNQLPTRVRKEGCKNFYWKGFTSC

>White sucker (*Catostomus commersonii*) SST3 (AAK97071.2)

MRLCELHCYLALLGLSLVLCDRGADSQLEPDMDFRHRRLLQRARAIGLATQDWTKKDIEEL
LSQLSLPEIEARENGVSTTGGNDDLHLELERSAENTNQLYPRERKAGCKNFYWKGFTSC

>Clown knife fish (*C. chitala*) SST3 (AAV48555.1)

MKNCQAQCILALMGLFLGLCWPSDASQPDLRYRSLLQRAHSAPASPQDWTRRTVEDLLAR
LPPPEGEFTPVEDVPAADEGEEVRVELERSVDPNNLPPRERKAGCKNFYWKGFTSC

>Atlantic herring (*C. harengus*) SST3 (XP_012693360.1)

MMRFSGIHCSLALLGLSLVLCSHSASSQPDLDLDLDLRHHRLLQRARAAGMSTQEWSKRAV
EDLLSQLSLPEEETQDREVSTVGAAKDDLHMERSAETNNIPPKDRKSGCKNFFWKGRTSC

>Grass carp (*C. idella*) SST3 (ACB69424.1)

MRLCELQCYLALLGLSLVLCGRSANSQLEPDLDFRHRRLLQRARAIGQATQDWTKKDVEEL
LSLLSMPEMEMRENDISTVDENEDLRVELERSAESSNHIPARERKAGCKNFYWKGFTSC

>Zebrafish (*D. rerio*) SST3 (XP_694143.1)

MRLCELQCYLALLGLSLVLCGRSANSQLEPEMDFRHHRLLQRARAIGQAQEWTKKDVEEL
LSLLSMPEMQMRESDLSTTDENEDLRVELERSAESSNHIPARERKAGCKNFYWKGFTSC

>Channel catfish (*I. punctatus*) SST3 (CK424149.1)

MRTCVLQCCLTLLGLSLVLCSNGVSSQPDLDLRHRRLLQRVQALGVAAQEWTKNDLKAIL
AQLTMPESEFQESDVSTLGTKQDLTVELERSAEDPNSLPPRERKAGCKNFYWKGFTSC

>Elephant nose fish *(G. petersii)* SST3 (AAV48556.1)

MKTCQVHCVLVLLGLVLGLCYPSAASQPDLRYRSFMQRAHTAAMSPQDWSRRVVEDLLSR
LAPPEDDTPQSEMSTAEEGEETRVELERSVEPNNLPPRERKAGCKNFYWKGFTSC

>Silver arowana (*Osteoglossum bicirrhosum*) SST3 (AAK97067.1)

MKICQIHCTLVLLGLVLGLYCPSAASQPDLRYRSFLQRAHAAAMSPQDWSKQAVEELLSRL
APAQGEVPQGAVSAADEEEDVRVDLERSLELNNLPPRERKAGCKNFYWKGFTSC

>Freshwater butterfly fish (*Pantodon buchholzi*) SST3 (AAK97068.2)

MKLCQVHCILALLGLVLGMCGSSSATQLDSRYRSLVQRARAASMGPQQDWGKLSVEDLSL
LAATEADMPFGDMSAAEESEGAHLDLERSVEPGNVPPRERKAGCKNFYWKGFTSC

> Red-bellied piranha (*P. nattereri)* SST3 (XP_017539071.1)
MRVCVLQCCLALLGLSLVLCGNGASSQPDLDMDVDVDLDPRYHRLLQRARALGMAAQD
WRKREMEDLLSQLTLPESEFKESEITSLGAKHDVRVELERSAENPNNLPPRERKAGCKNFY
WKGFTSC

Other ray-finned fish

>Spotted gar (*L. oculatus*) SST3 (ENSLOCT00000011545.1)
MLSYRVHCTLALFGLVLAFCCVSAVSHSDLRFRRFLQKAKAAGLNKQDSSKYAIEDLISQL
VQSDSEALENEMSVLDENSDARLELERSTEIGKEIPPRERKAGCRNFYWKTFTSC

Cartilaginous fish

>Elephant shark *(C. milii)* SSTe (XP_007910587.1)
MQARCTLTLALLSLAALGLSALPTHLRDQLVLQGSPAMELRDGVVRELIQAVADAESKPQS
EEAAEDFAPDEKAELRLALAPRWRKDCKNFFWKTYTLC
>Whale shark (partial) (*R. typus*) SSTe (XP_020365363.1)
DFLKDTIIQLLHVVADADKDAVEVNASQVETPPXNKIPMKFQQRQLGTRMRKNCKNFFWK
TYTLC
>Catshark *(S. canicula) SSTe* (MK491630)
MWCSRLQLSLALLSIALAVLSVSSAPTDNRHREILQRALDQELLKDTMMKLLPLVTDVDTE
AGTLDVSNAETSEENTTPMKFQHRQLGMRMRKNCKNFFWKTYTLC

Somatostatin 4

Euteleosts

>Stickleback *(G. aculeatus)* SST4 (KT235754)
MAHILCVFALLCFAFCAAQDGETQRGFKDNRLQRDSLPWLDKLQDEQDSTKKLNLIEWLYS
FYKFDNGNIVKGPTDAEEPEKNRRGLGKTTRRFGCRVFFWKSWSPC
>Medaka (*O. latipes*) SST4 (KT235752)
MANVLCVLAFLCFAVCVVQNTEIMVESEDLPAGQGLLSSFDRISDFQQSVETGILMNLLYKL
SRPDSAITLQQVRDSEKQEKNRRGVEIATQRPCRVFYWKSWAKC
>Atlantic salmon (*S. salar*) SST4 (CA039604.1)
MALTGIWCAFVLVCVTLCQMGKVDSFVNEDKPTWLETLQDKQVSAADDKYNLVWLLYKL
SQSHHDNTFKINFPPHGPESVGKPESRRETIPQDSRVRKEGCKVFFWKSWTAC
>Takifugu (*T. rubripes*) SST4 (NC_018911.1)
MARALCILVLLCFAPCCAENSKTEHRFNDLQVQEDLLSWLKPQEKWEPSKRQTLEDLLYKL
TNYKSENRILPQQPGDTENQEKNRRDLDNLRVQQRQFGCRMFFWKSWTYC
>Tetraodon (*T. nigroviridis*) SST4 (KT235753)
MARALCFLVLLCFASRCAGNSKTEHRLKDLQVEEDVLPWLNSQEKWEPSKGQNLEDLLYK
LTNYRSENRIVSQQPSDTNQEKNRRGLDNLKVQQRQAGCRIFFWKSWTSC

Other teleosts

>Zebrafish (*D. rerio*) SST4 (NP_571802.1)
MASSQLHLTATLLCLAMMAGIICGRSHMLLNSALQASRGTSADEEIPERYSLSELEWLLSNS
DPAVFQPDSSSLGSLHSGLELMRRDTKEERKTGCKNYFWKSRTAC
>Channel catfish (*I. punctatus*) SST4 (P01172.1)
MSSSPLRLALALMCLVSAVGVISCGRPHVVLNSALEEARNVPFGEEVPERLTLPELQWMLS
NNELTPVQVEEAPRSRLELVRRDNTVTSKPLNCMNYFWKSRTAC

Other ray-finned fish

>Spotted gar *(L. oculatus)* SST4 (ENSLOCT00000011651.1)
MLSYRVHCTLALFGLVFAFCCVSAVSNSDLRFRRFLQKAKAASLSTRDSSKYALEDLISQIA
QSDNEALENEMSVLDENSDARLELERSADMGKVIPPRERKAGCRNYYWKTITSC

Somatostatin 5

Lobe-finned fish

>Coelacanth (*L. chalumnae)* SST5 (XP_005999859.1)
MMCSHVQSLLAVLSASLLLVGVGGLPKGEVLTDLFQGQGAEGKEDFSRMLMLKMVSNLL
KSENDVLVPSAEDTASQDELTRRLAPSRERKAGCKNFFWKTFTSC

Euteleosts

>Stickleback *(G. aculeatus)* SST5 (ALD51533.1)
MQVLLVALFSSVLLVQVSGAPRGDMPTQRGDPADNKDLAYSMLLKFVSELTAARGGETLL
VPEQEEEEAEGGRQEVMRRHLPLTQRERKAGCRNFFWKTFTSC
>Rainbow trout *(O. mykiss)* SST5 (BX909872.3)
MLCSQLQVLLVALSASVFLARVSAAPHRDMLAELLRADSTKGNEDLSRTLLLKMMSDLMS
AAVGENEVLPDLEEALGVREEVRQLPLSHRERKAGCRNFFWKTFTSC
>Sockeyess *(Oncorhynchus nerka)* SST5 (EV380196.1)
MLCSQLQVLLVALSASVFLARVSAAPHRDMLAELLRADTTKGNEDLSRTLLLKMMSDLMS
TAVGENEVLPDLEEALGVREEVVRQLPLSHRERKAGCRNFFWKTFTSC
>Tilapia (*O. niloticus)* SST5 (XP_005464163.1)
MLRSQVLLVALGLSVLLVRVSTAPYSDMLTETLRADLTNDKDLTHWLLLKFMAELMAARG
DETRRGREEVTRRHLSLSQRERKAGCRNFFWKTFTSC
>Medaka *(O. latipes)* SST5 (XP_020567335.1)
MLLAALGLSLLMACVSGAPQRNPLTHTKQLQLLKSEVDPTRLLLMKLVLELVALRRQEML
QELEEEELGGRERLMKRHIRFTQRERKAGCRNFFWKTFTSC
>Amazon molly (*P. formosa)* SST5 (XP_007551472.1)
MLCSQMKVLFVALCSSMLALHVSSAPQMDELTETLQAELISDKDLTGLLLLRFMSELMASR
GEEMLREKQEEEEEELGGRQRLMRRHIRFSHRERKAGCRNFFWKTFTSC
>Takifugu *(T. rubripes)* SST5 (N.D.)
MLSQVQLLLVTSFSSMLLMEVSSAPRKHMPSELLPADPLKDKDLAILILLRIISEVMAAEREM
LLLPQEGEEEAGVREGEVMMRRQVPFSQRDRKAGCRNFFWKTFTSC
>Tetraodon *(T. nigroviridis)* SST5 (ALD51532.1)
MTRSQLLLAASFSFLLLMEAGGTPRKHKFLPADSVKDKDLALVTSLKFAFEGTAAQREMLL
LLQEDEEDAGVREMMMMMRRQIPFSQRERKAGCRNFFWKSYTSC
>Platyfish (*X. maculatus)* SST5 (XP_005804860.3)
MLCSQMKVLVVALCSSMLALHVSSAPQMDELTETLQAELISDKDLTGLLLLRLMSELTASR
GEEMLREQEEEEEDELGGRQRLMRRHIRFTHRERKAGCRNFFWKTFTSC

Other teleosts

> Mexican tetra *(A. mexicanum)* SST5 (XP_007243346.1)
MCSQLQVVLVALSVLVLVSRVSAAPRGDVLTQLLQNEADTKENEDISRMLMLKLLSELEVA
GENEVLSGADVRNDVVRQLPFSQRERKTGCRNFFWKTFTSC
>Zebrafish *(D.rerio)* SST5 (XP_001333082.1)
MFSRLQVVVVTLWVSLLLCRVSSAPRGDLLFQLLRSQVDPKENELQDLSRLLLLKQLSESVT
PEEKDALDSIDELDVRNEVVRQIPVSQRERKAGCRNFYWKTFTSC
> Channel catfish (*I. punctatus*) SST5 (XP_017327476.1)
MSSQMQIVVLAVSLLVLVSRVRTAPRTDLLAHMLQNEADGKEDLSRILLLKLISELKIPDEN
DTLSDDDMELNRILRHLPLTTRERKAGCRNFFWKTFTSC
>Fathead minnow *(P. promelas)* SST5 (DT105503.1)
MFSPLQMVVATLSLSLLLCSVSSAPGGDMLIQLLRSEVEPKEIELQDFFRLLLLKQLSESAAP
EEKQPRESIDDDPEVHNEVVRQIPLSHRERKTGCRNFYWKTFTSC
> Red-bellied piranha (*P. nattereri)* SST5 (XP_017578562.1)
MNFEVKSSLLSRAAGRSASTPVIQTFEEFEYFKSICLLNHLITRVSAAPRGDILAQLQADPKG
NEELSRMLILKLLSDLEIPGDNEVLSGTDVRSDMVRQLPFPQRERKTGCRNFFWKTFTSC

Other ray-finned fish

>Spotted gar (*L. oculatus*) SST5 (XP_006627411.2)

MSTGQPSLPPAPAPNQGFQQHKLQVLLVALSVSVLLARVSGVPQRDRLADLLRAEVPEGKE
DLSRMLLLKIFSDLLRAENEIPPGSAEDAGIRSDVPRQLPLAQRERKAGCRNFFWKTFTSC
Cartilaginous fish
>Catshark (*S. canicula*) SSTb (JX964751)
MPRSQTQVLLTLVTVALLLLRGSSTARVQGLPDILQERNDEGTEELSRTMVLNLLSELLHAG
DKGLPSTERRGLPQAEIVRRWNSPRDRKAGCKNFFWKTFTSC

Somatostatin 6

Birds
>Duck *(Anas platyrhynchos)* SST6
MQLVASLVSVLLLVWSVRATALPGEERLALQNSREQTKLRKDAILKMLAGLLESVDVASPD
LEEEGKLEEERATLGRLAQLSQRDRKAPCKNFFWKTFTSC
>Chicken *(G. gallus)* SST6 (DQ279789)
MQLVASLVSVLLLVWSVRATALPGEERLALQNSREQTKLRRDALLKMLAGLLESSDVASP
DLEEEGKLEEERAALGRLAQLSQRDRKAPCKNFFWKTFTSC
>Zebra finch (*Taeniopygia guttata)* SST6
MQLVASLASVLLLLWSVRATALPGQEGLQSTREQSTARKDVILKMLAGLLGSVDAGAEVA
FPAGQEKARLEEDQAALGRLAQLSQRDRKAPCKNFFWKTFTSC
Lobe-finned fish
>Coelacanth (*L. chalumnae*) SST6 (XP_005994063.1)
MQLLTSLVSFLLVVWSVRATALPIEEKLMSHNNVELTKERKELMLKMIAGLLEGIDSPPMG
GEVGSMDLEEPVEPKLEERAAFNRLPQLPQRDRKAPCKNFFWKTFTSC
>African lungfish *(P. annectens)* SST6 (Q9W7E9.1)
MQFLASLVSFLLVVWSVKATALPVEDRLSVHSNRDLTREREEMILKMISGLLDGSDNSLFG
GEVTSMDIEEPLENKLEERAAYNALPQLPQRDRKAPCKNFFWKTFTSC
Euteleosts
>Orange-spotted grouper *(E. coioides)* SST6 (AAU93567.1)
MQLLVVLAALMGVLFSVRAAAVLPVEDRSSIHVNRELSKERKELILKLVSGLLDGALDTNM
LPGEAAPVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC
>Atlantic cod *(G. morhua)* SST6
MQLMVVLAALMGVLFSVRAAALLPVEDRSNFHSSRELSKERKELILKLVSGLLEGSPDSNM
LPGELSPVELEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC
>Stickleback *(G. aculeatus)* SST6 (ENSGACG00000007077)
MQLLVVLATLMGVLFSVRAAAVLPMEDRSSINVNRELSKERKELILKLVSGLLDGAADAN
MLPGEAAPVDFEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC
>Rainbow trout *(O. mykiss)* SST6 (CX153272.1)
MQLLVILASLMGVLYSVRAAAVLPVEERSPLLNRELSKERKELILKLVSGLLDGATDTNMLP
GEGVSPVDLEEPLESRLEERAAYNRLSQLPQRDRKAPCKNFFWKTFTSC
>Medaka *(O. latipes)* SST6 (BJ885293.1)
MQLLVVLAALMGVLFSVRAAAVLPVEDRSSIHVNRELSKERKELILKLVSGLLDGSLDTNM
LPGEAAPVDFEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC
>Rainbow smelt *(Osmerus mordax)* SST6 (EL519905.1)
MQLLVVLAALMGVLYSARAAAVLPVEERSPIQANRELSTERKQLILKLVSGLLDGASDSNM
LPGDVSPLDLEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC
>Amazon molly (*P. formosa)* SST6
MQLLVVLAALMGVLFSVRAAAVLPLEDRSPIHANRELSKERKELILKLVSGLLDGALDTNM
LPGEAAPVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC
>Takifugu *(T. rubripes)* SST6 (ENSTRUG00000012370)
MQLLVVLAALTGVLLSIRAAAVLPVEERSPVHLNRELSKERKELILKLVSGLLDGALDTNML
PMETVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC

>Tetraodon *(T. nigroviridis)* SST6 (ENSTNIG00000015178)
MQLLVVLAALTGVLLSVRAAAVLPVEERIPLHLNRELSKERKELMLKLVSGLLDGALDTNM
LPMEAVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC
>Platyfish (*X. maculatus)* SST6
MQLLVVLAALMGVLFSVRAAAVLPLEDRSPIHANRELSKERKELILKLVSGLLDGALDTNM
LPGEAAPVDLEEPLESRLEERAVYNRLSLPQRDRKAPCKNFFWKTFTSC
Other teleosts
> Mexican tetra (*Astyanax mexicanus*) SST6 (ENSAMXT00000013526.1)
MQILASLVSLLLVLYSVRAAAVLPVEERSPAHTRELSKERKELILKLVSGLLDGVDNSVLGG
DLVPMEAEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC
>Goldfish *(C. auratus)* SST6 (AAD09631.1)
MQLLSSLVSLLLVLYSVRAAAVLPVEERNPAQSRELSKERKELILKLISGLLDGVDNSVLDG
EIAPVPFDAEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC
> Atlantic herring (*Clupea harengus*) SST6 (XP_012681579.1)
MQLLASLVSLMLVLYSIRAAAVLPVDERSPAHARELSKERKELILKLVSGLLDGVESNMLPG
DEAPLDLEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC
>Grass carp *(C. idella)* SST6 (ACB69425.1)
MQLLASLVSLLLVLYSVRAAAVLPVEERNLAQSRELSKERKELILKLISGLLDGVDNNVLAG
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>Zebrafish *(D. rerio)* SST6 (BG307388)
MQLLASLVSLLLVLYSVRAAAVLPLEERNPAQSRELSKERKELILKLISGLLDGVDNSVLAG
EIAPVPLDVEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC
> Channel catfish (*I. punctatus*) SST6
MQLLASLVSLLLVLYSVRAAVVLPAEERSPAHTREPSKERKEMILKMVSSLLDGVDNNMLA
GDLLPLEEEEPIDSRLEERAVYNRLAQLPQRDRKAPCKNFFWKTFTSC
>Fathead minnow *(P. promelas)* SST6 (DT250237.1)
MQLLASLVSLMLVLYSVRAAALLPVEERNLAQSRELSKDRKELILKLISGLLDGVDNSVLAG
EIAQVPMDAEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC
Other ray-finned fish
>White sturgeon *(A. transmontanus)* SST6 (AAL13249.1)
MQLRARLVSLMLVVYSLRVVAVLPGEERLSVHSNRELSKERKEGFLKLLSGLLDRVDSSVV
LGEDVSPMDLEEPLDSRLEERAIYNRLSQLPLRARKAPCKNFFWKTFTSC
>Chinese sturgeon *(A. sinensis)* SST6 (FJ792688.1)
MQLRASLVSLMLVVYSLRVVAVLPGEERLSVHSNRELSKERKEGFLKLLSGLLDGVDSSVV
LGEDVSPMDLEEPLDSRLEERAVYNRLSQLPQRARKAPCKN
>Spotted gar (*L. oculatus*) SST6 (XP_006642047.1)
MQLLASLASLMLVVYSVRAAAVLPGEERATLHTKELSKDRKELILKLISGLLDGADSAMLA
GDVASVDLEEPLESRLEERAVYNRLSQLPQRDRKAPCKNFFWKTFTSC
Cartilaginous fish
>Elephant shark (*C. milii*) SSTc (XP_007895974.1)
MQILVALISTLFLVSGVSTTTASLDDRFNLQSSREMNQERKEMILKLLSGLLDNAAVSGQTG
SEAGYPEPADGGPVMLEERSRYSQLPQRSRKVPCKNFFWKTFTSC
>Whale shark *(R. typus)* SSTc (XP_020368528.1)
MQLLGSASXVSILLIVSSVKATAPLEDRLSLRANQELNKERKEVVLKLLSALLDSSSNQMGIE
NTFPDQEDMEEMKVEDRSRFSQLPQRERKTSCKNFFWKTFTSC
> Catshark (*S. canicula*) SSTc (JX964752) = SST6
MQLLGTASLLSMLLIVSSVRATAPLEDRLSLRANQELNKERKEVILKLLSGLLDSSSNQIAIE
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Other somatostatins

Lampreys

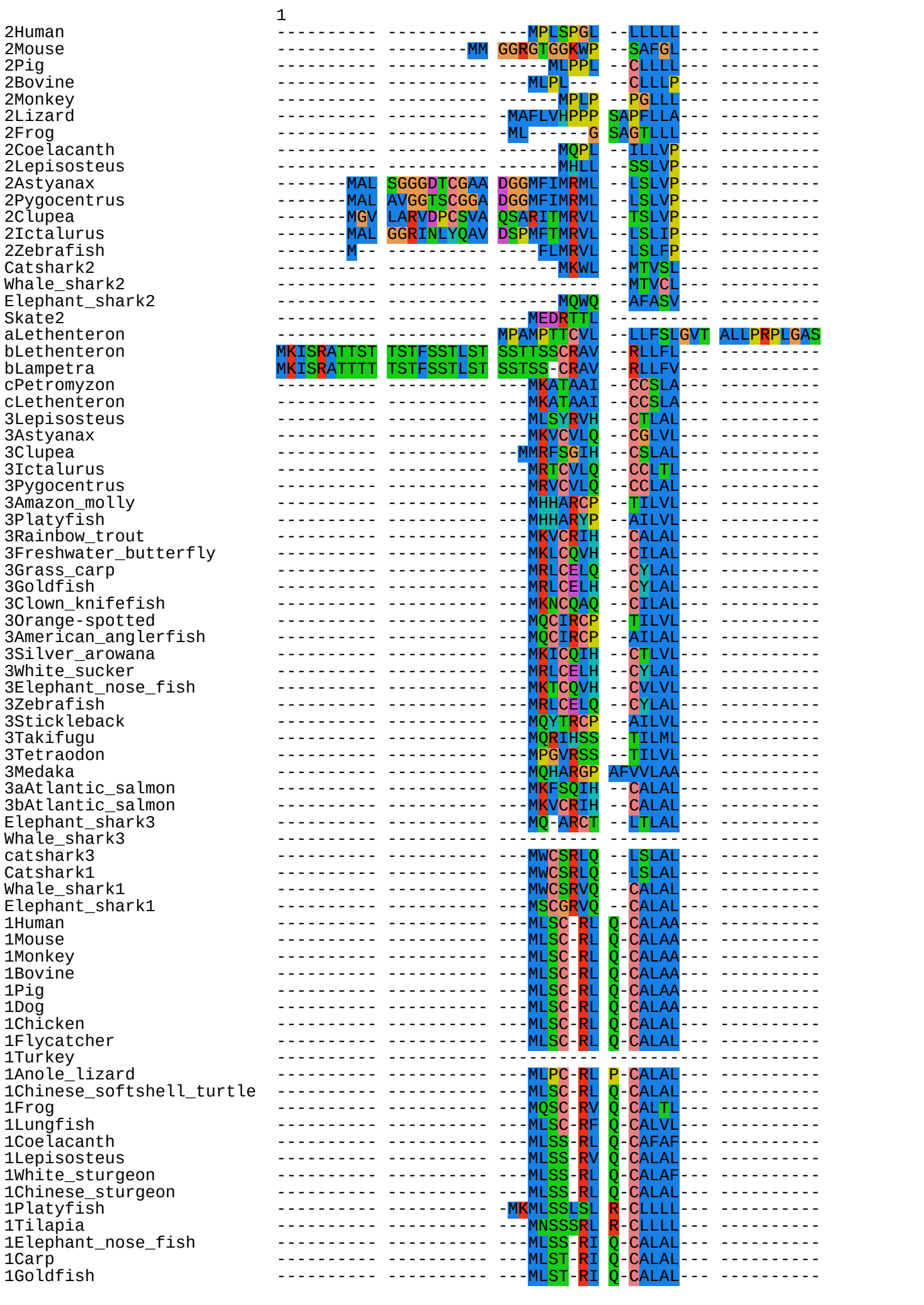
>Japanese lamprey (*Lethenteron japonicum*) SSTa (KU522234)
MPAMPTTCVLLLFSLGVTALLPRPLGASPFRRPAEGSSLAGLGAWALGPGAGXGGAGLIDD
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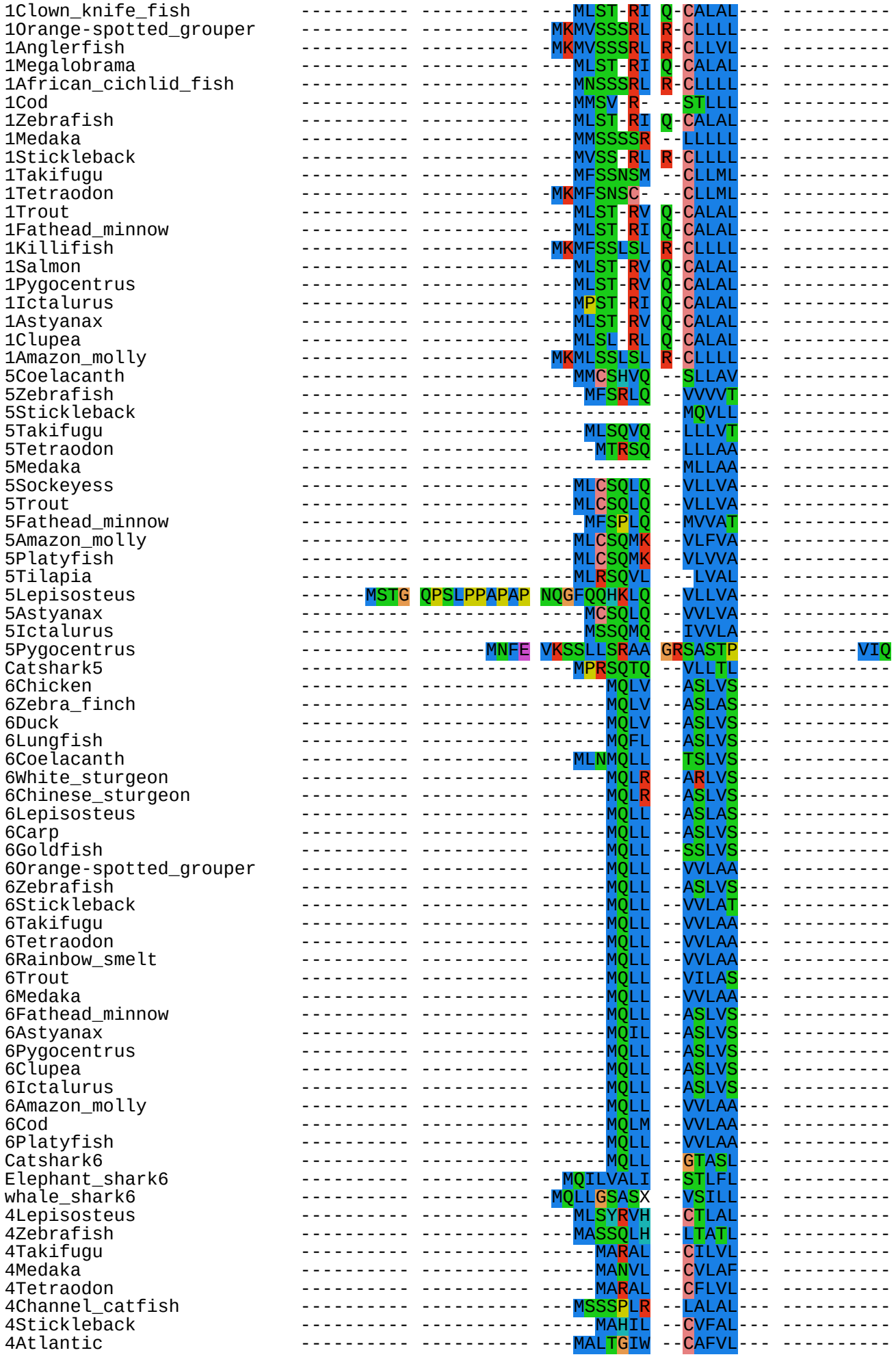
>River lamprey (*Lampetra fluviatilis*) SSTb (KX345282)
MKISRATTTTTSTFSSTLSTSSTSSCRAVRLLFVLPMLSVVLGSVTADVRPLHVRMALERVM
DGPGMENLDQDQKQFLVRLLAAIDSSADETNELNHSEDGSLPEVLVARALRAAAAPGAAG
GAQLPLGNRERKAGCKNFFWKTFSSC

>Japanese lamprey (*Lethenteron japonicum*) SSTb (KU522235)
MKISRATTSTTSTFSSTLSTSSTTSSCRAVRLLFLLSVLSVVLGSVTADVRPLHARMALERVM
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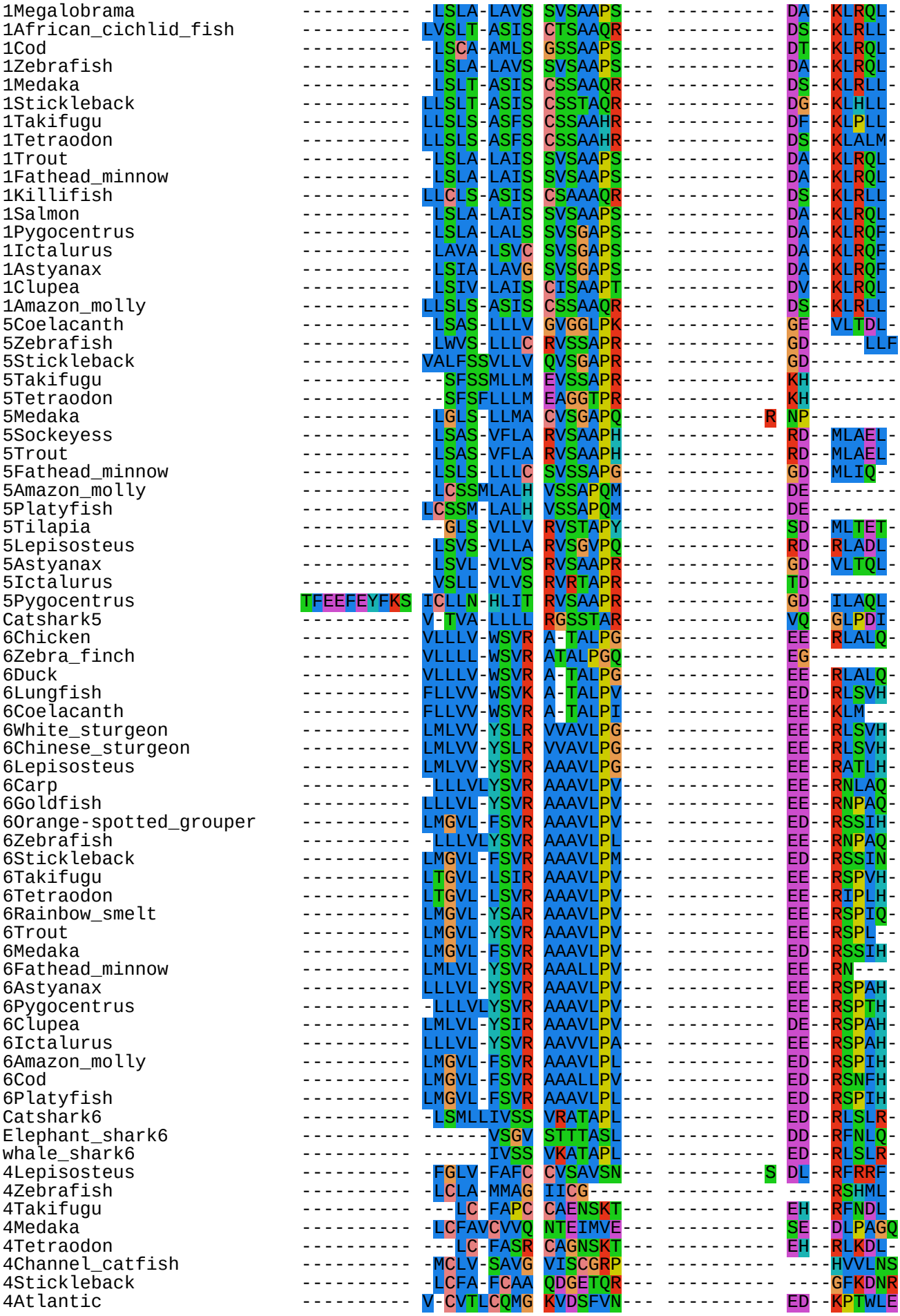
>Japanese lamprey (*Lethenteron japonicum*) SSTc (KU522236)
MKATAAICCSLALVLVATGGRRGGGLHAASIGRSAILRAPASYRQLEAHPDLQMGDQDDSQ
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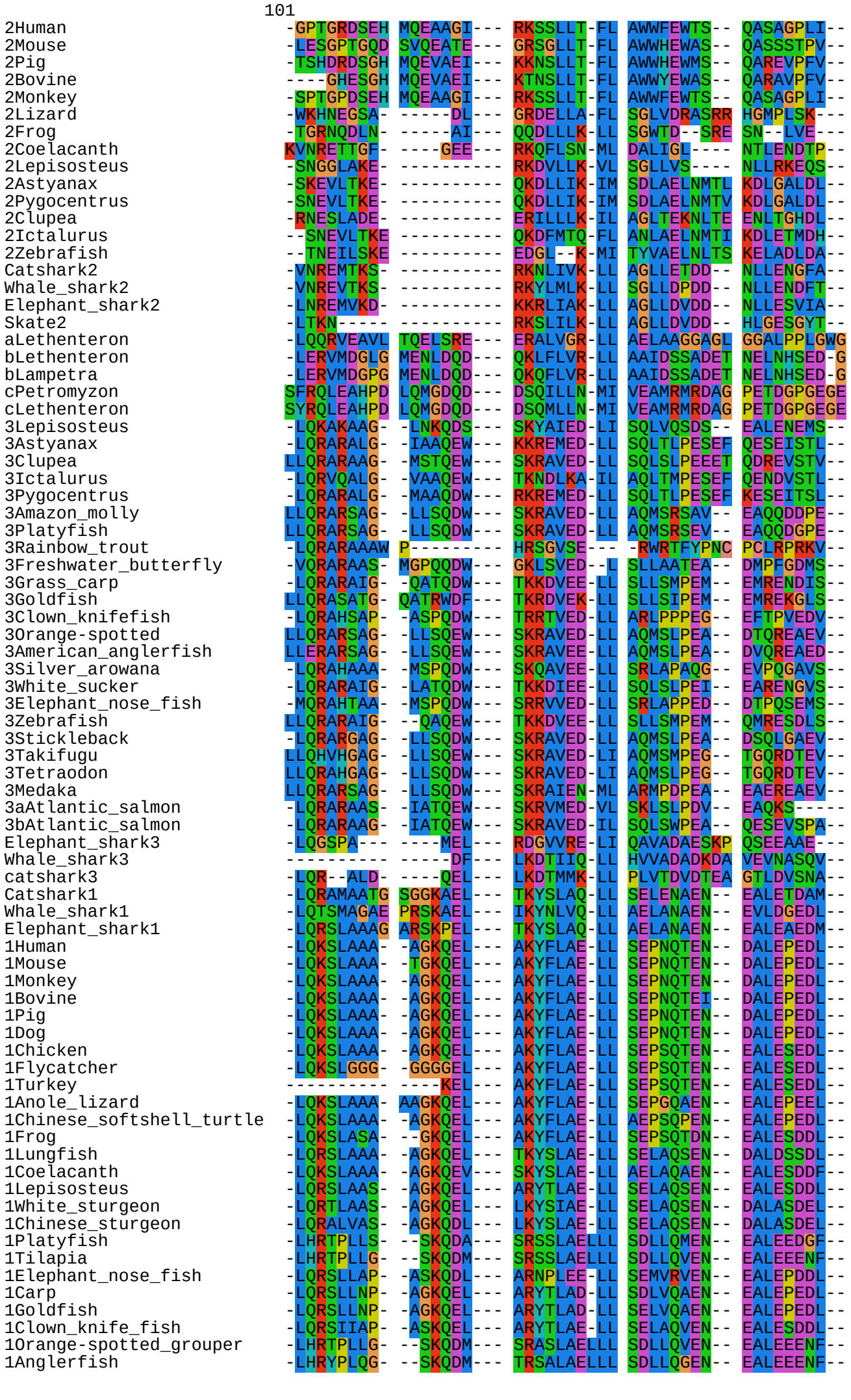
>Sea lamprey (*Petromyzon marinus*) SSTc (KU529940)
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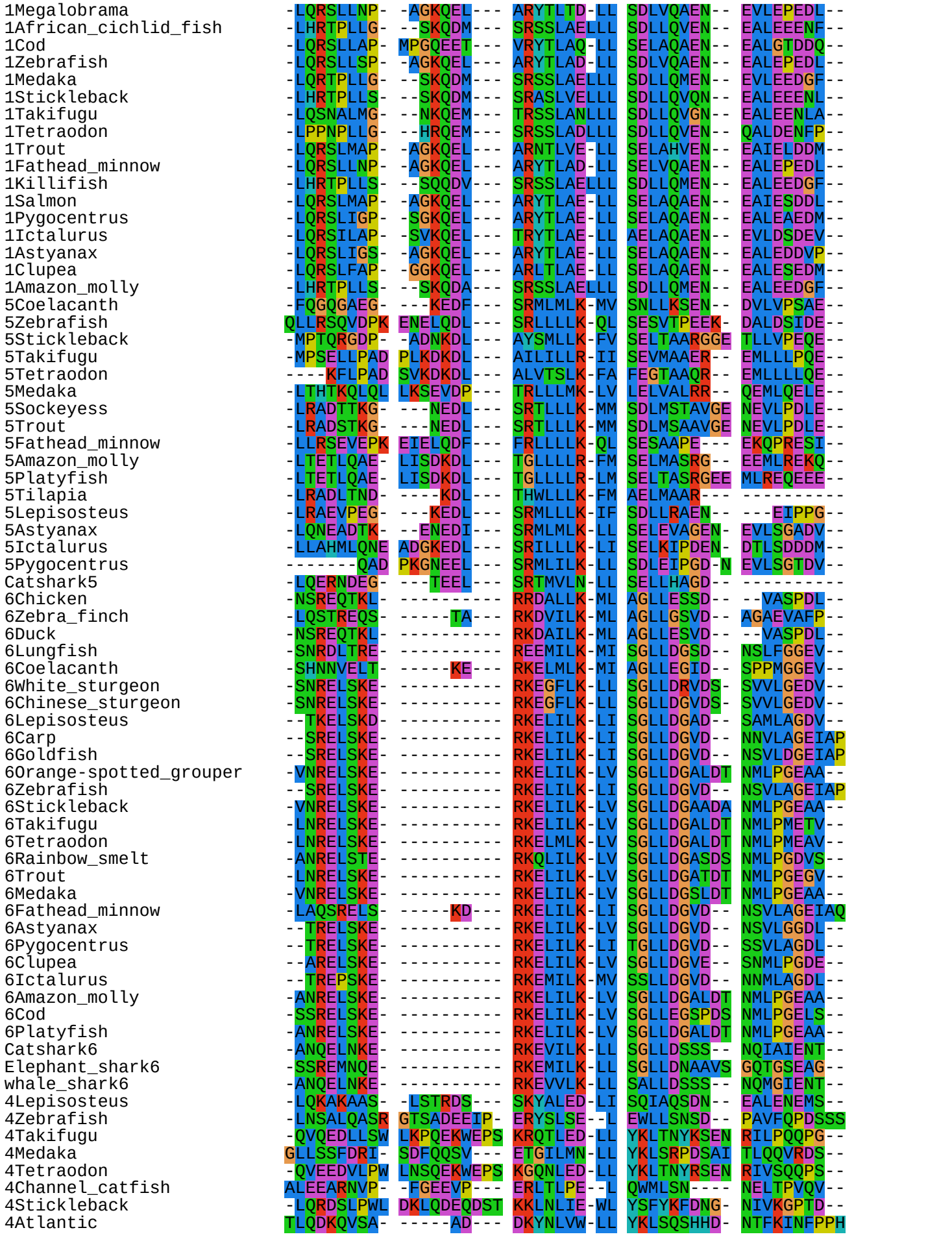

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2Monkey
2Lizard
2Frog
2Coelacanth
2Lepisosteus
2Astyanax
2Pygocentrus
2Clupea
2Ictalurus
2Zebrafish
Catshark2
Whale_shark2
Elephant_shark2
Skate2
aLethenteron
bLethenteron
bLampetra
cPetromyzon
cLethenteron
3Lepisosteus
3Astyanax
3Clupea
3Ictalurus
3Pygocentrus
3Amazon_molly
3Platyfish
3Rainbow_trout
3Freshwater_butterfly
3Grass_carp
3Goldfish
3Clown_knifefish
3Orange-spotted
3American_anglerfish
3Silver_arowana
3White_sucker
3Elephant_nose_fish
3Zebrafish
3Stickleback
3Takifugu
3Tetraodon
3Medaka
3aAtlantic_salmon
3bAtlantic_salmon
Elephant_shark3
Whale_shark3
catshark3
Catshark1
Whale_shark1
Elephant_shark1
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1Bovine
1Pig
1Dog
1Chicken
1Flycatcher
1Turkey
1Anole_lizard
1Chinese_softshell_turtle
1Frog
1Lungfish
1Coelacanth
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1Chinese_sturgeon
1Platyfish
1Tilapia
1Elephant_nose_fish
1Carp
1Goldfish

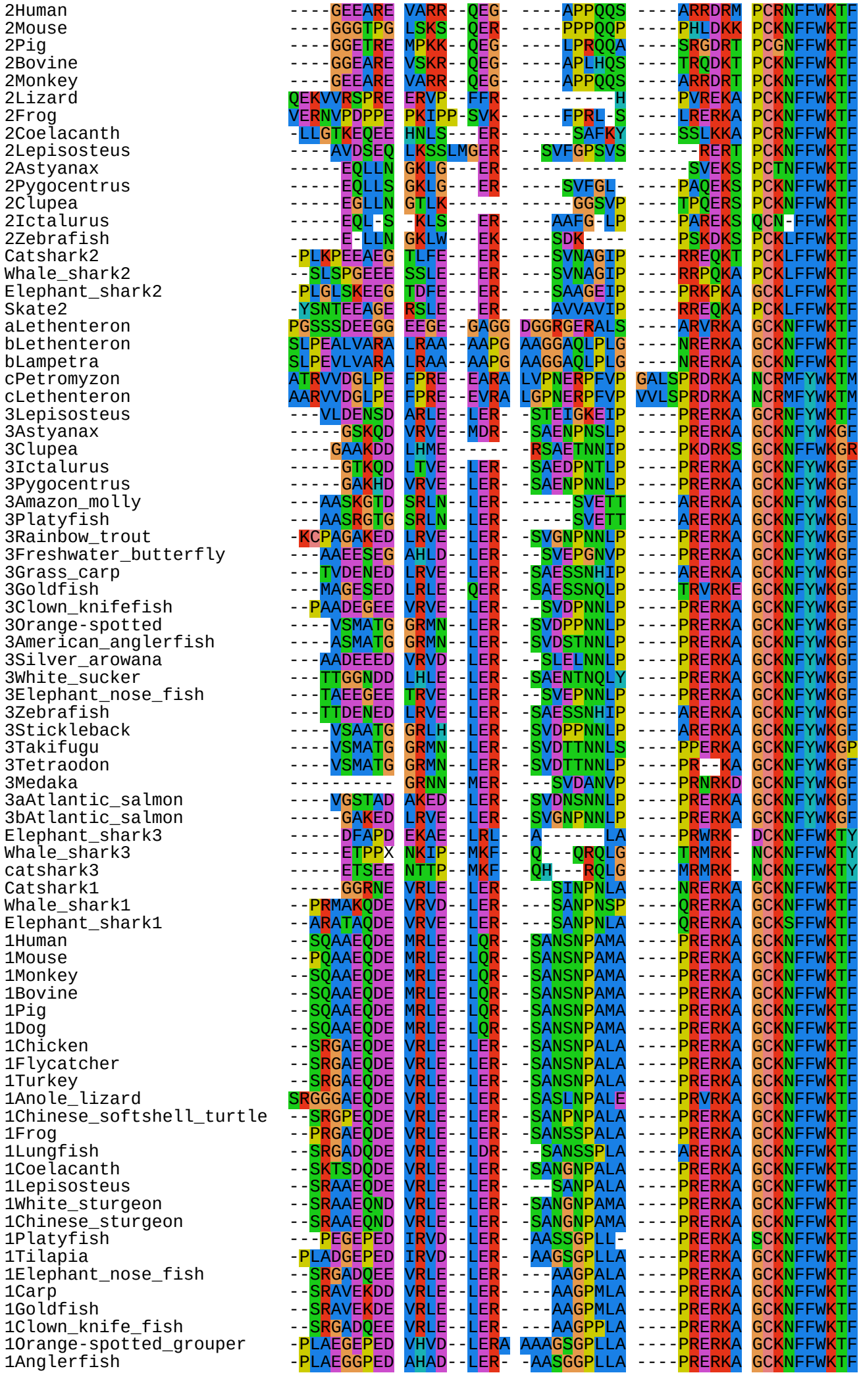

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1Anglerfish
1Megalobrama
1African_cichlid_fish
1Cod
1Zebrafish
1Medaka
1Stickleback
1Takifugu
1Tetraodon
1Trout
1Fathead_minnow
1Killifish
1Salmon
1Pygocentrus
1Ictalurus
1Astyanax
1Clupea
1Amazon_molly
5Coelacanth
5Zebrafish
5Stickleback
5Takifugu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

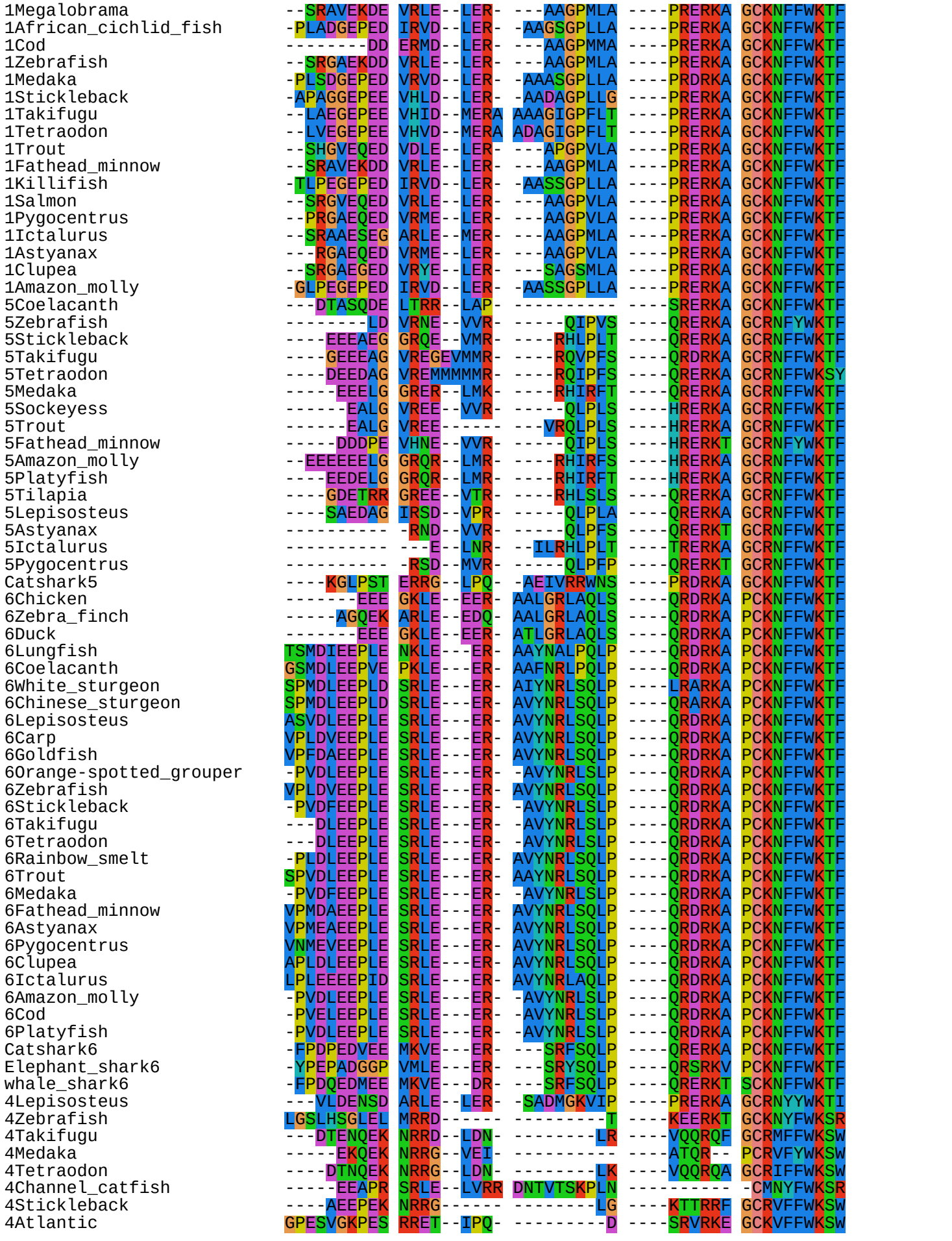

51
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2Mouse
2Pig
2Bovine
2Monkey
2Lizard
2Frog
2Coelacanth
2Lepisosteus
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2Pygocentrus
2Clupea
2Ictalurus
2Zebrafish
Catshark2
Whale_shark2
Elephant_shark2
Skate2
aLethenteron
bLethenteron
bLampetra
cPetromyzon
cLethenteron
3Lepisosteus
3Astyanax
3Clupea
3Ictalurus
3Pygocentrus
3Amazon_molly
3Platyfish
3Rainbow_trout
3Freshwater_butterfly
3Grass_carp
3Goldfish
3Clown_knifefish
3Orange-spotted
3American_anglerfish
3Silver_arowana
3White_sucker
3Elephant_nose_fish
3Zebrafish
3Stickleback
3Takifugu
3Tetraodon
3Medaka
3aAtlantic_salmon
3bAtlantic_salmon
Elephant_shark3
Whale_shark3
catshark3
Catshark1
Whale_shark1
Elephant_shark1
1Human
1Mouse
1Monkey
1Bovine
1Pig
1Dog
1Chicken
1Flycatcher
1Turkey
1Anole_lizard
1Chinese_softshell_turtle
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1Lungfish
1Coelacanth
1Lepisosteus
1White_sturgeon
1Chinese_sturgeon
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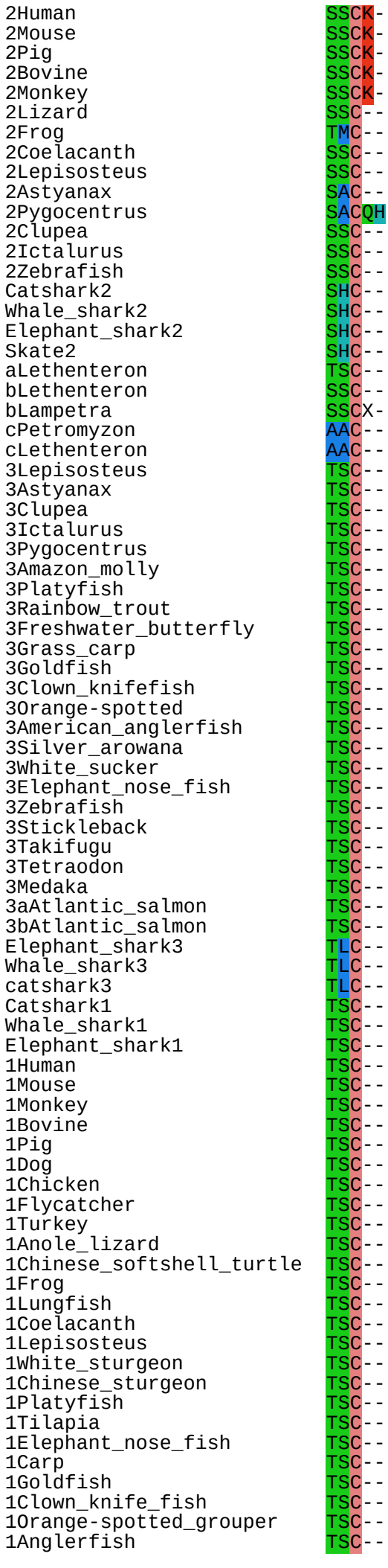

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1Stickleback
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5Astyanax
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Catshark5
6Chicken
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6Goldfish
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6Takifugu
6Tetraodon
6Rainbow_smelt
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6Fathead_minnow
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Catshark6
Elephant_shark6
whale_shark6
4Lepisosteus
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4Medaka
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4Channel_catfish
4Stickleback
4Atlantic


101
2Human
2Mouse
2Pig
2Bovine
2Monkey
2Lizard
2Frog
2Coelacanth
2Lepisosteus
2Astyanax
2Pygocentrus
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2Ictalurus
2Zebrafish
Catshark2
Whale_shark2
Elephant_shark2
Skate2
aLethenteron
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bLampetra
cPetromyzon
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3Clown_knifefish
3Orange-spotted
3American_anglerfish
3Silver_arowana
3White_sucker
3Elephant_nose_fish
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3Stickleback
3Takifugu
3Tetraodon
3Medaka
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3bAtlantic_salmon
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catshark3
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1Anole_lizard
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1White_sturgeon
1Chinese_sturgeon
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1Tilapia
1Elephant_nose_fish
1Carp
1Goldfish
1Clown_knife_fish
1Orange-spotted_grouper
1Anglerfish


1Megalobrama
1African_cichlid_fish
1Cod
1Zebrafish
1Medaka
1Stickleback
1Takifugu
1Tetraodon
1Trout
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1Astyanax
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Catshark5
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151
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1Anglerfish


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Catshark6
Elephant_shark6
whale_shark6
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4Medaka
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4Stickleback
4Atlantic


201
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2Bovine SSCK-
2Monkey SSCK-
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2Frog TMC--
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Catshark2 SHC--
Whale_shark2 SHC--
Elephant_shark2 SHC--
Skate2 SHC--
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bLampetra SSCX-
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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--

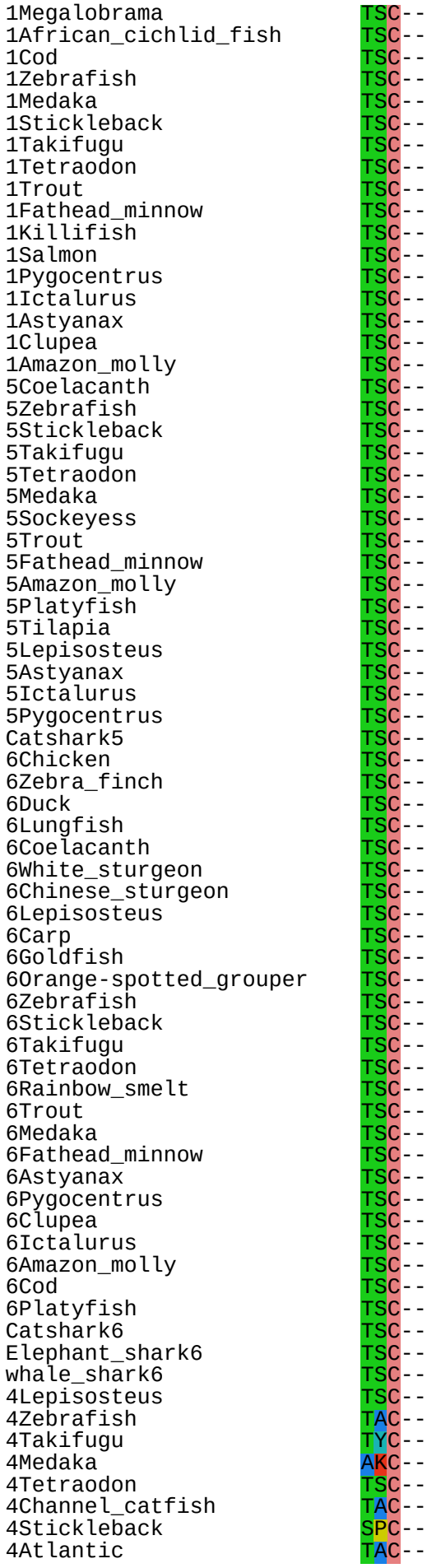

1Megalobrama TSC--
1African_cichlid_fish TSC--
1Cod TSC--
1Zebrafish TSC--
1Medaka TSC--
1Stickleback TSC--
1Takifugu TSC--
1Tetraodon TSC--
1Trout TSC--
1Fathead_minnow TSC--
1Killifish TSC--
1Salmon TSC--
1Pygocentrus TSC--
1Ictalurus TSC--
1Astyanax TSC--
1Clupea TSC--
1Amazon_molly TSC--
5Coelacanth 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)

```
        gctgtccacagagccagtgctgaaaccaccgccaatttcaaagcgtttgtaaa
atgtggtgcagccgccttcagttgagcctggctctcctctccatcgccctggcagtactg
 M  W  C  S  R  L  Q  L  S  L  A  L  L  S  I  A  L  A  V  L
agtgtcagctcagcacccacagacaacaggtatcgcgaaatcctgcagagagccatggca
 S  V  S  S  A  P  T  D  N  R  Y  R  E  I  L  Q  R  A  M  A
gccacaggaagcggagggaaagcggagttgacgaaatattccctcgcccaactgctctcc
 A  T  G  S  G  G  K  A  E  L  T  K  Y  S  L  A  Q  L  L  S
gaactggaaaacgcggagaatgaagctctggaaacggatgcaatgggcggacgcaacgag
 E  L  E  N  A  E  N  E  A  L  E  T  D  A  M  G  G  R  N  E
gtgcggctcgaactggagagatcgataaatcccaacctggcgaacagggagcgaaaagcg
 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  -
gcaacccacacactcagaatgtggcattcagataactaaataaatcatgtggtgaatgat
tctatttgaattatgtaagagaagacaattggtttgaattgtccaatagcaggccagttt
gaatggtgactggatagagtcgctatttttcattaatctgttgcaataaaatctctgttt
gaaattg
```

B. Catshark SST2 (SSTd)

```
                                  tttagcattttgtccaggagtgctcgaagattcagc
atgaagtggctaatgacagtgagcctgatgtctctgctgtaccttctgagagtcgagggt
 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
aagaatctgattgtaaagctactggctggcttgttggagactgatgataatctcttggag
 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
gttaacgctggaattccacgcagggagcaaaaaaccccatgcaaactgttcttctggaaa
 V  N  A  G  I  P  R  R  E  Q  K  T  P  C  K  L  F  F  W  K
acctttcccactgttaataaccgtgtagcggatttttctaaagcagtgggagtatgaaa
 T  F  S  H  C  -
gaaaaatgggtgtaaaggcttaactttaaaactatcgaaaatacactgcaatcatgtttt
tctctatcccaaatatttaattcaaatttacaggaaatgcttgcaataaagttaacctga
aagttacacctttaagacatgtgaaattattgtgttttaaatgagatagcaatccagtt
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cctgggattccgtactctccccctcgctttacctttccctctttcgctagacgaatgttt
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tgccagacacaatttgggatattttctgagttaaagcctatatatatgttgacagtgacc
tttcctcttgatcgtgagatctgagcatattgtaatggtgttaattgttttgaccagtct
atctgcatacaatgtacatacttatctcgaaatatcctgtgagtaatgctaacaataaaa
agaca
```

C. Catshark SST3 (SSTe)

```
                                                        acatgg
ggagagacagtgctgaaacgccctctccactttccgtcggcttcttcgccttgtgcagag
atgtggtgcagccgccttcagttgagcctggctctcctctccatcgccctggcagtactg
 M  W  C  S  R  L  Q  L  S  L  A  L  L  S  I  A  L  A  V  L
agtgtcagctcagccccacagacaacaggcatcgcgaaatcctgcagagagccttggat
 S  V  S  S  A  P  T  D  N  R  H  R  E  I  L  Q  R  A  L  D
caggaacttctgaaggacacaatgatgaaactgttgcctttggttactgatgtagacact
 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
aaattccagcatcgtcagttgggaatgagaatgcggaaaaactgcaagaacttcttttgg
 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 -
gtaccccac

D. Catshark SST5 (SSTb)

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atgccgagatcgcagactcaagtcctcctcactctggtcactgtcgctctgctgttactg
M P R S Q T Q V L L T L V T V A L L L L
cggggatcgagtacagccagagtgcaggggctgcccgatatcttacaggagaggaacgac
R G S S T A R V Q G L P D I L Q E R N D
gaggggactgaggagctgtccaggaccatggtgctgaacctcctctccgagctgctccat
E G T E E L S R T M V L N L L S E L L H
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A G D K G L P S T E R R E L P Q A E I V
cgccggtggaactcaccgcgggaccgcaaagcaggctgcaagaacttcttttggaaaacc
R R W N S P R D **R K** A G C K N F F W K T
ttcacctcttgttaacgtgcggagagagagagggaaagagaaagtgagccggcgggggga
F T S C -
gagatataaagagaattcctccctctcccaaaacccatcttcagctcctgaagggaggca
aaaaaaaatcaattgcctctaacttgtagattttaagattcacaaatcccaaccacctcc
gtccctcgaaagattgcctcccccttgggctgcctctccgctgaggatttctctgtgtc
tttatccaaggtgtttgtaaatgattgacttgtttgctttgttctctgagcatggacttg
ctctcacatcataaaatatctttatttctcagcaaaaaaaaaaaaaa

E. Catshark SST6 (SSTc)

tcgaccctcgcgtccgccaaggtcgaggcaca
ttgagaagatctcggccaggctccgcttcattccaacttcacaagatcgagagtgtcagc
atgcagttgctgggaacggcgagcctcctgtccatgctgctcatcgtgtccagtgtgagg
M Q L L G T A S L L S M L L I V S S V R
gccacggcacctttggaagatcggctgagtctgcgggcaaatcaggagctgaacaaagaa
A T A P L E D R L S L R A N Q E L N K E
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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
tcccgcttcagccagttaccgcagagagagcgcaaggctccctgcaaaaacttcttttgg
S R F S Q L P Q R E **R K** A P C K N F F W
aaaaccttcacctcctgctgacgacagacaatgccacctggctgccaactaaagccgccg
K T F T S C -
agaaaggaactgatttagcactgtacataagctgcttttattttattcatctgtgaggg
gtggtggaggtgggggggggttaatattttctgtcgtgcacaagaaaaataaaaagagc
atgattgtgtgatttcaccgcaacctgtatgtatttatttttctttcccagtaatgttgtc
gcgctcaacctgccagagcaataaagtggatccgagataaaaaaaaaaaa

Figure S4

A. Catshark SST1 = SSa (scaffold122178)

AACAGAAGTAAAATGATACCTGGTCCCAGTGTGTAAATCTGTAACAGCCCCATTTCTGTGGCATTTCAAT
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GGGCCACAAAGAGAACACGCTGTTAAAATCACAAACTACACACAATTATTCAGATGGCAGCGAGTCTTTC
CCCAGGAAACATTCCTTTATTCTGTCTCACTCAGTCTCTAACTTTGTACATTCAGTTCACTGGGATTACC
CAACCCATTCCCCACTGATCCAGTGTGTTCAATGCTCAAGGAAGATTGAGATTTATGGATGAGGGTGTTT
ACTGGGGATTGATGTTCACTTTTTCCACGGATTTTCTAGTTGAAGACTTGGCTGCATTCATTTTGTGATC
GACACGAACCAATACAATCGTAGGGCCAGCTGCCAACACGCGATAGGGTGTCCACATTGAGACTCCATGG
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CATCTCCTGGGACCCTCCTCCCAACGTGTGAGCTGGTGTGAAGGCGGCTTTAAAAGGAGCTTCCCCGATT
GCAGGGACAGAAGGAGCGGAGCTGTCCACAGAGCCAGTGCTGAAACCACCGCCAATTTCAAAGCGTTTGG
AAACTGCTCTCCTTCTCGCTGTCTCTCCCGTTGATCTTCGCCTTGTGCAGAGATGTGGTGCAGCCGCCTT
M W C S R L
CAGTTGAGCCTGGCTCTCCTCTCCATCGCCCTGGCAGTACTGAGTGTCAGCTCAGCACCCACAGACAACA
Q L S L A L L S I A L A V L S V S S A P T D N
GGTATCGCGAAATCCTGCAGAGAGCCATGGCAGCCACAGGAAGCGGAGGGAAAGCGGTAAGGACCCAGCA
R Y R E I L Q R A M A A T G S G G K A
AAAAGTCACATTCAATAGAAATGGTAGTTTGTGTTCATCCCGTTCACCTCGAATAGAAACAGGGACTGGG
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GAAGATAAATGAAGATAATTTCACAAAGTTGAATTTAATTCATTGTAGATTTATTCGCGGGAGTTTGCAA
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TGTTCTCAGGAGTTGACGAAATATTCCCTCGCCCAACTGCTCTCCGAACTGGAAAACGCGGAGAATGAAG
E L T K Y S L A Q L L S E L E N A E N
CTCTGGAAACGGATGCAATGGGCGGACGCAACGAGGTGCGGCTCGAACCGGAGAGATCGAGAAATCCCAA
E A L E T D A M G G R N E V R L E P E R S N P N
CCTGCCGAACAGGGAGCGAAAAGCGGGATGTAAGAACTTATTTTGGAAAACCTTCACATCCTGTTAACTC
L P N R E **R K A G C K N L F W K T F T S C** -
TCCGAATTCTCCATAGCAACCCACACACTCAGAATGTGGCATTCAGATAACTA**AATAAA**TCATGTGGTGA
ATGATTCTATTTGAATTATGTAAGAGAAGACAATTGGTTTGAATTGTCCAATAGCAGGCCAGTTTGAATG
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GTTGGATTTTGTTCTCTGGGAGATGGGGCAATATAACAAGGGACAGAATTAACTCGGCTAGTTTTCAACA
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GGGTGGAATCGCTCTGGGTCACTGTCTCTGATCTGGGAAATGTGTTGCTGGAAGTTCCTCCGCGTATTCA
AACTCAGAGGAGACAATGAATGGACGGATATTAAAGGGGGTTCTGCTCTGTCCAATGCAACCGTGCTCTG
TGAGTGCTGTAATCTGCAGGAGAGCAAACTATTCACCTGCATCACACTGGTAAAAGTCTAACCCTGGTCA
ATGAAAGCATCAATCCACAAATCACAAACCTGCTTCCAGCCTTCCCTTGTAAAGCCGGTTTCCATTCTAA
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CTTGGGTCACTGTCCATGCGGAGTCTGCACGTTCTCCCCGTGTCTGCGTGGGTTTCCTCCGGGTGCTCCG
GTTTCCTCCCACAAGTCCCGAAAGACGTGCTGTTGGGTAATTTGGACATTCGGAATTCTCCCTCTCTGTT
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GTCTAGAAACATAGAAAATAGGTGCAGGAGGAGGTCATTTGGCCCTTTGAGCCTGTTCTGCCATTCATTA
TGATCATGGCTGATCATCCAGCTCAATAGCCTTCTCCAGCGTTCCCCCATATCCTTTGATCTCCTTCACC
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CCACAAGGAGAAACCCCGTTGACCAGCTGGCGAAACGGAGAATCCCGATGGCATATGGTGGGACAGAGAA

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B. Catshark SST2
(scaffold 83887)

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AGGTAATGGGGTGCAAGGTTGTTGGGGGTAGGCGGGAGATTACAGTCCGATGGGCCATGATCTTATTGAA
TGGCAGATCAGGCTCGAAGGGCCGAGTGGCCTACACGTGCTCTTAGTTCCTATGTCTGTAACATCCGACA
CTTTGGAGAAGAATATTTTTGATTGTGTCAGGAATCCAGCCCTCCCAGAATTTTCCAGGGTGCTAATAAT
CAGTTTTTACTTAGATTTCTAGTCAACCTACAGGTTTTAGATTTTAGTTTTCTTATACTGCATTGGAGGG
TCAGTTGTTGAACAGCATCCATCCAATTCCACTTTTATAACTTCTAAAAATATAATTTTGTTTAAATGGC
TGGAACATTCTTGGATTGGAGGCTATAAAGCTCTTTAATGGCTGCTTCATTCAAATTGAACTGCAATTTT
AACTGTCCACATTACAGATCCTTCATCTACTTGCCCATAAATTTACAGAACGTAAAAGTGTAATATAATC
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M K W L M T V
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S L M S L L Y L L R V E G T D L L E E R M K L
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Q V N R
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TGAAAGGACCTGTGGACCTGAACAAGCTCGACACTCATTTTTGCCTTTAATCTAATGTCCTTCAGGGAAT
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TGGCATCAACAAACAAGTGCCTTGCAATGAAATGAAAACGAAAGCTTTCTATTCTCTGTTTATCCACA**AG**
GAAATGACAAAAAGCAGGAAGAATCTGATTGTAAAGCTACTGGCTGGCTTGTTGGAGACTGATGATAATC
E M T K S R K N L I V K L L A G L L E T D D L
TCTTGGAGAATGGCTTTGCACCTTTGAAACCGGAAGAGGCAGAAGGGACTTTGTTCGAAGAGAGGTCGGT
D L L E N G F A P L K P E E A E G T L F E E R S
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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**TAACCGTGTAGCGGATTTTTCTAAAGCAGTGGGAGTATGAAAGAAAAATGGGTGTAAAGGCTTA
H C -
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AAATGCTTGC**AATAAA**GTTAACCTGAAAGTTACACCTTTTAAGACATGTGAAATTATTGTGTTTTAAATG
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CCTGCCCCTGACACAGCCGGCTGGGACTTCTGGAAGCACTTGAATTTTGCCAGACACAATTTGGGATATT

TTCTGAGTTAAAGCCTATATATATGTTGACAGTGACCTTTCCTCTTGATCGTGAGATCTGAGCATATTGT
AATGGTGTTAATTGTTTTGACCAGTCTATCTGCATACAATGTACATACTTATCTCGAAATATCCTGTGA…

C. Catshark SST3
(scaffold121269)

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NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
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CCTGAAGTGAGTCATTCTTTCTGCATAGCTGTACAACAAACTAAAATATTAGGGTTTTGGTCCAGTATCC
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D. Catshark SST5 = SSb

(scaffold 888145)

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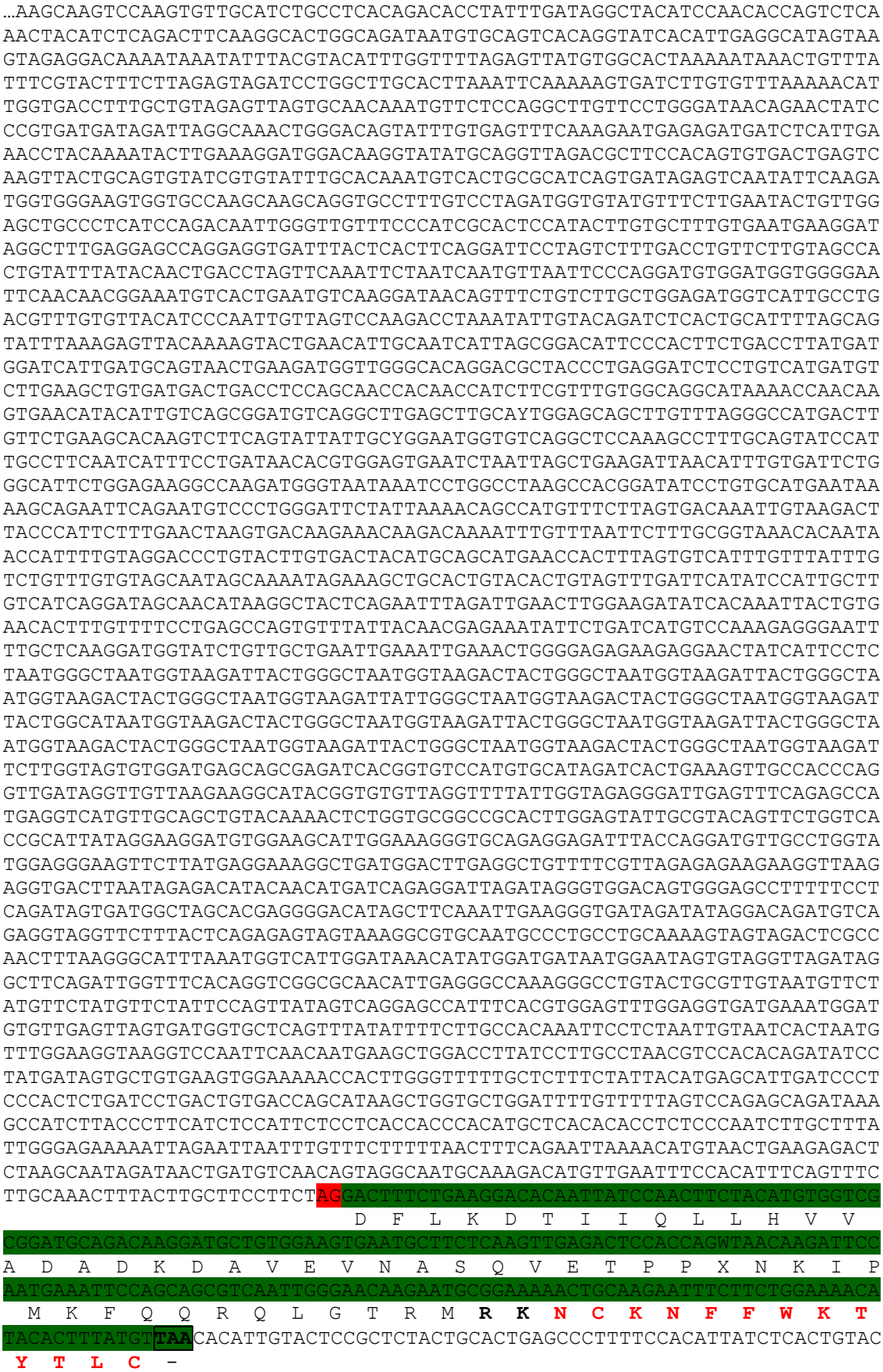
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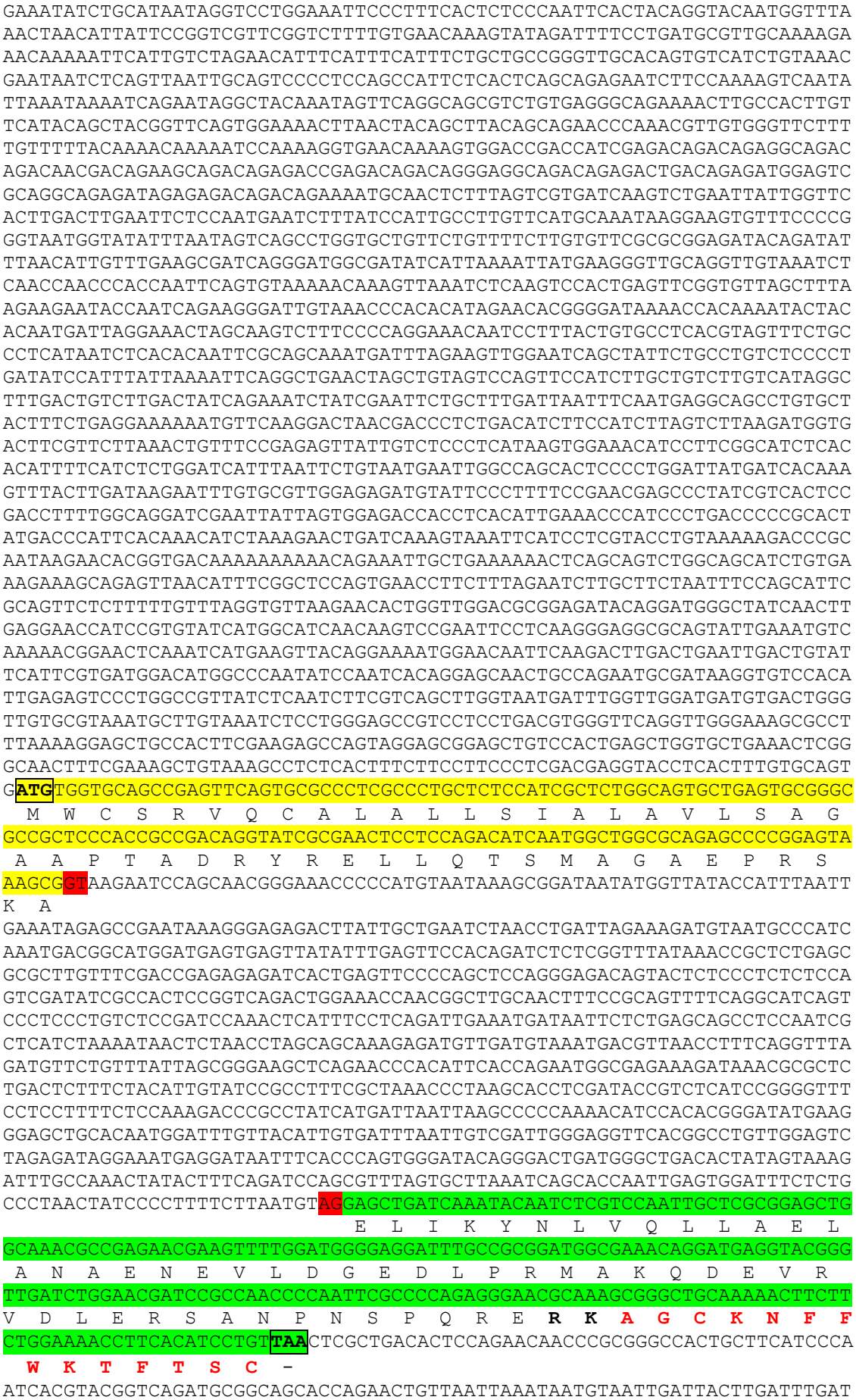
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E L N K E R K E V I L K L L S G
TGCTTGACTCCAGCAGCAATCAAATCGCGATTGAGAACACTTTCCCGGATCCAGAGGATGTGGAGGAGAT
L L D S S S N Q I A I E N T F P D P E D V E E M
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K V E E R S R F S Q L P Q R E R K A P C K N F
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F W K T F T S C -
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ACCAGGTTTGTAAATGTAAACACAATACTGTTTATTTATAACAAAAACTATCTTGAAACAAATGCAGTA…

Figure S5

A. Whale shark SST1/3 (NW_018029766.1)



CTCACTGCATCCTGTTTGTCCACAGTGCCCTTCTCTGTGCTCAACGTAGTGGACTTTGCCTCACTGTACC
ATAATGACTCCTTCCCATTGTGCCTCATCGTAGCCTATTATCCTCTACTGTACCTCATTATACCACATTG
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V D L E R S A N P N S P Q R E R K A G C K N F F
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B. Whale shark SST2 (NW_018077477.1)

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GCCCAGGAGAGGAAGAGAGTTCGCTTGAAGAGAGGTCGGTTAACGCTGGCATCCCTCGTAGACCGCAGAA
S P G E E E S S L E E R S V N A G I P R R P Q **K**
GGCACCGTGTAAATTGTTCTTCTGGAAAACATTCTCGCACTGT**TAA**TTATTGATGGATTTCTAAACCAGT
A P C K L F F W K T F S H C –
AGAACTGTATTTAAACAAAATGGCTTCTGAAGAAGGGTCTAGGCCCAAAATGTCAGCCTTCCTGCTTCTC
TCATGCTGCTTGGCCTGCTGTGTTCATCCAGCTCTACACCTTGTTATCTCTGTTTTCCTGTAAAGGCTTA
ACTTTAAAATGATCAAAAACTTGCATGCAATTCTGTTCTTTTTCGATATCAATATTTACAACATGTGCCT
GCAATGAATTTAAGCGGAGAGCGACCTGTGAAACCCCCTGTCAAATCATGTTTTCGCAAATCAAACCCAG
GTTAAACTTTCTAAGTTTTTGTGTTAAGGAAGGTTATTCTTTGGCATGTGATTCCGGGCACTTTCCTGCC
GTTTTTCCCCCTCTATTCCCCACCCTAGCATTATTATTTCTTCATCTCCCTGATTTCCCTGTCCCCAAAA
GGGTAGTCCTGGATCCAGTTTCCCTCCCTCCCTGATTCAAACCCCATACTGATAGTTTCAGAGAAGGACC
TGGACGTAGAGATTCTCTGTCTCACACACACAGTCTCTCAAGTCTGTCAAACTGAGGAGACAGTGTCATT
TGGATTTGATTGTGATACATGAATGTATAGAACATACAGTCTATCTGCATTGAATGTATATACTTACCAA
GCAGTGTGATGCCAAC**AATAAA**AGTATACATTCACACCTGTGTATTAAGCATTGTTATTCTTTTCTATCT
CAAACAAAAAGGTAAACAAAAACACTCTGCTCCTTCTGTCTTCCTTGTGTTGAATTTGCAGCACCAACAG
AACCGGTCTTTAACCCTTTTATTTATTGATACCAATGTTTCAGCTCTCACCGTCAATTACTCACAACCGT
TACAGTTTTGCTATCCTAGGGGTGAGGTTGCACAAGCCAGGTGTGTGTGCTCATTGGGCTGTGTGGATTC
CGGGGTGATCTGATTTTGCTGATTACAGGGTCCGATAGAATGCACTCTGTCTGAAATTAACTTTCGAGCC
AATCTGTTCAGGGTTGACGCCACAAAGAGCTAATCCACACAAAGGTCAATGAGAGGCAATTTAAAATCCC
CCCTCACTCCCCTACTTTCTGACCCTCCTCCGCCCACAACACAAAAAAAATTACAAAAAGAAGTGGAAGG
GTGATCTAATCTTTAAAACGGTCAGTGGTTTTGATGGAATGAATACACAGATTAAAAATAATCTTAAAAA
TATCTTAAAACTAAACAACTTCTTTTCAGAATATGCCGAAGAATCGAGCAAGTACTGTTTGTAGTGTTAA

ACAGTCATTACTTGCAGAGCAACAGTATTCAAACTAGGATACAAACTGGAAATTCATGATGAGCTGATAC
TAGAGATCTTCAAGATTGATTTTGTTTTGACCTGCTGGTTGTCATTTCTGCTGCTGTGAGATAGTTAAGT
GTTTGTCCTTGCAAATCATCTCCCTGTCTTTTGGAAGTAAGGACAGGGGCTCCTGGCAATATGTCGATT…

C. Whale shark SST6 (NW_018032490.1)

…CCTTGGCATAGGAAAGGGAGAATGTACTTATTTCCAGGTTCCTAACTGCTACACAGTAATGCCTAGTG
AGGCATCGGGCACCAGCTGTAATGCTGGCATAGTTGAATAATTTGCTAGCATCCATCACCCAGACTCATA
TGTGAAAAAGGGGCACTTGGAAGGAATACTGCAGTACAATCTCCTTGTATGAAACTGTTCTCGCCAAGGA
TAAAACATGTCCAGGAAAGGCAGGTGAACAAAAAGGGAGTAGGGAACCTGTTTAATTTGTGAAAACAAAA
CAATCCAATTCACTGGAAATCAGTTTTTGACACAAATATACCATCAGATTTAGCATGTTTTAAAAAATTC
AGTCATCAAATAATATCCCACAAATGTCATGAGGAAGATCTTTTGATCATATTTTAAAGACCTTATTAGA
TATAGTGACAGTCATTTACATTTGCTCAATCTTTCAAAAATCCTTAGCACAAAGAAAAATTCTCACGGAG
AAATGACCATCACTCCCTGAACATTTTAACGTTTTTCCCGAAGAAAAGGATCCTGCCTTAAAACTGCAGA
CAGAAATTCAACATTGAATTTAATTTTGAATTGAAGACTTCCTCCTCAGTGCTTCTGCAGGCAGAGAATT
GCACTATTTCAACATATCTGATTGGATGACCTGGTTCTAAACTAAATCTGGTCAGTGAATGGTTAATCTT
GGACTGGGTGTAATTGTGTGTCTTTGATGGAGTCTTAATGTTTAATGAAGCTTTGGTCTGTGCGTCAGTG
AGTGGGGCTGTACTGGGTTATAAAAGGGGGTTGGAGACTGTCAAAACCACACAGAGACTTCAAGGGTCGA
GGCACATTGCAAAGATCTCGAAAAGGCACCACTTCAATCCAATTCCAAGCGACTGAGAGAAGAGGCAGC**A**
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
TTTGGAAGACAGACTGAGTCTTCGGGCAAATCAGGTGAGTAAAGTCTTAAAATGTGGGAGCAGTACGTGA
L E D R L S L R A N Q
CCAAAAGATAAATCAGTGGAGAGAATAAGTAAGAACCTTAAAGGAATCAAGGAGTAAGAATCAGTGTGGG
AGAGAGGTAGATGAATTTAGTTGGCAATTATAGAAAGTGAAATTCGTAGACAAACAAATGACATACATCG
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TGAAAGTAATAGTGAGAGAGAATGGGGCTAAAATGAGAGTACGAGAAAATAACAGGTAAATGGAAGAGTG
CAGTAAGAGAGTGGGCATGTTAAAATGGGAGGGAACAAGTGCATGAGACAGAAAAAAAACAAAAAACGAA
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TCTACACCTTGTTATCTCTTAATAGTGCAAATACCATGTTCACATGAGCAGTTTCTCAGAATTCGACTTA
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CAAGTGCAGGACTCTCCCTGTTGCTGAGTTGAAGGGAACAGTCCCTGGCAGATGTTACAACTTTGTATTG
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CAAACCTATTTTCTGTACGAGGGGCAGGAAACAGCAAGGGAGTTTCGGTGAGGGCTGGGGGTGGGGGGTG
CGGTGGTGGGCAGTGGTGCGTGGGATGTGGGGTAAGGGAATTAAGAGGCAGAGTGGGGACTGTGACTGGG
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AGGCCAAGCAGCATCAGGGGAGCAGGGGTCTCGACCTGAAACGTCAGCCTTCCTGCTCCTCTGATGCTGC
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ATGAGGTAGTTTCCTCCCATCTTCCTTGTGTGCTTAAAGGAAATGCAGATGCTCTCCTGCATCCCTTGCC
TGTAAGCAGCTTGTTTCTAGAGGTTCTACCAACATTACCAACACTGGCTTACAGCCTTCAGCATGGCACC
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AAATAACGTTGCTGAGATTATATTCCACTGGGCTAAAGGCTAAATGTTTCATAGATACCACTGAACAATC
CCCCTTTCAGACTAAAACTCAGTCATTCCTTGGTTTGTTATAATATGCAGAATTTTACAGTTTCGGCATG
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CCATGAGATATGCAGGATTACAGGAATAAGGTAGGGGTTGGGTCTGGGTGGGTTGCTCTTCGGAGGGCCA
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AATATCTGATCATGTAAGTATAGGTCTAGAGAGGGGAATAATTACCAATTGAACGTTATCTTATTTTCGC
CTGGAGTTCACAAGCATTAATTTTTTAGTGGAATGTAAAATATTAATAGACACCCTCTGGTCATTTGCAG
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GCTCTATAAGAAAGTGCTGGGATTGTTCATATTTTACTGAGCTGTTATTCAGCTAACTTCCAGGCTCCAA
TCAACTAGGTAACTGAAGGAAACATTAAATAGCGAGTGCAGGAAGACAGAAGAAATTCTCTCCAACAGCC
TGTGTATTATTTTATTAAAATATTGAAATGGCGGAAGGCTTTGTTTAAGCTGAGTGCTATACGACTTTAC
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TCCTGGATTTTTCCTACCAGTAAATGAGCTAATCTGAATGTTCCAGATCATTCCTTGGGCTCTGCTGGAT
TGGTTAATCTTAGTTGGAGAAGTGGCTTTGATGTTACAGTCGGTTGAACCCATCAGATTAAGGGCTGGGT
AACATGGGGAGGCGATGGCCTGTTGGTATTATTGCTGGATTGTTGACCCAGATAATGTTCTGGGGACCCA
GGTTTGAATCCTGCTATGGCAGATGGTGAAATTTGAAATCAATAAATATCTGGAATTAAGATGACCATGA
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TGGCCTGTCTGAATCCAGACCCACAGCAATGTGTTTGATTCTTAACTGCCCTCTGGGCAATTAGGGATGA
GCAATAAATGCTGCCTGGCCATTGACGCCCTCATCCCATGAATGAATGAAGGAAAAAAAAAATCCTGGTTA
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TTTGGCACAGGTTTTCACAGAGCGGCAAACACGAATAGTTCTGAGGAAGCATCACTGGACCTGAAACGTT
TACTCTGATTTCTTACCATAGATAATACCAGACCTTTTCCAGCAATTCCTGTTCTTGTTTCCGATTTACA
ACTTCCACAGTTCTTTCGGTTTTTGTGAATGAGTTTCGTGTTTGTCTTTAACAGGAGCTGAATAAAGAAA
E L N K E
GGAAAGAGGTTGTTCTCAAGCTGTTATCTGCACTGCTTGACTCCAGCAGCAATCAAATGGGGATTGAGAA
R K E V V L K L L S A L L D S S S N Q M G I E N
CACGTTCCCAGATCAGGAGGACATGGAAGAGATGAAAGTGGAAGACAGGTCCCGCTTCAGTCAGTTACCA
T F P D Q E D M E E M K V E D R S R F S Q L P
CAACGAGAGCGGAAGACATCCTGCAAAAACTTCTTCTGGAAAACCTTCACCTCCTGCTAACGTCAGACGA
Q R E **R** **K** **T** **S** **C** **K** **N** **F** **F** **W** **K** **T** **F** **T** **S** **C** -
TGACATGTCGCTAGGAACTGATTTAGCACTGTACATAAGCTGGTGTTGTTTATTTTCTTTGTTTCTTGGG
GGTTACATTTCTTTCATGCACAAGAAAAATTTAAAAAAAAAGCATGAATGTGTGTAATTTTGCTGCAACT
TGTATGTATTTCTTTTCCAGCAATGTGGTGCCGCTCGTTCTGTTAGAGC**AATAAA**GTGGATCCGAAATAA
TCAAATTTGATTTGATCGTTTACTGACTTGGCCTTTCCAAAGCTCTGTTTGAGATCTGTTCAGGGGATTG

ATGTCTTAAGTGAGAGAGGGAAGTCATAGTCAAAGCTACAGGGGAGGCAATGGCCTGGTGGTATTATCRG
TGGGCTGTTAATCCAGAGATCCAGGTAATATTTTGGGGACCCGGGTTTGAATCCTGCCATGGCAGATGGT
GGAATTTGAATTCAGTATAAAGAAAAATCTAGCTGGTGCTCTGGTTTCCTCCCACAGCCCAAAGATGTGC
AGGCTAGGTGGATTGGCCATGCTAAATTGCCTATAGTGTTCAGGGGTGTGTAGATTAGGTCGGTTATAG…

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
agtgcgggcgccgctcccaccgccgacaggtatcgcgaactcctccagacatcaatggct
 S  A  G  A  A  P  T  A  D  R  Y  R  E  L  L  Q  T  S  M  A
ggcgcagagccccggagtaaagcggagctgatcaaatacaatctcgtccaattgctcgcg
 G  A  E  P  R  S  K  A  E  L  I  K  Y  N  L  V  Q  L  L  A
gagctggcaaacgccgagaacgaagttttggatggggaggatttgccgcggatggcgaaa
 E  L  A  N  A  E  N  E  V  L  D  G  E  D  L  P  R  M  A  K
caggatgaggtacgggttgatctggaacgatccgccaaccccaattcgccccagagggaa
 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
atgacagtgtgcctgatgtccctgctgcttcttctaagtgttgaggcagcagacccactg
 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
ttaaaactgctgtctgggctgttggatcctgatgataatctcttggaaaatgacttcacg
 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
cctcgtagaccgcagaaggcaccgtgtaaattgttcttctggaaaacattctcgcactgt
 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)

```
gactttctgaaggacacaattatccaacttctacatgtggtcgcggatgcagacaaggat
 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
caaagatctcgaaaaggcaccacttcaatccaattccaagcgactgagagaagaggcagc
atgcagctactggggtcagcgagcttkgtgtctatactgctcattgtgtccagtgtgaag
 M  Q  L  L  G  S  A  S  X  V  S  I  L  L  I  V  S  S  V  K
gccacagcacctttggaagacagactgagtcttcgggcaaatcaggagctgaataaagaa
 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
tcccgcttcagtcagttaccacaacgagagcggaagacatcctgcaaaaacttcttctgg
 S  R  F  S  Q  L  P  Q  R  E  R  K  T  S  C  K  N  F  F  W
aaaaccttcacctcctgctaacgtcagacgatgacatgtcgctaggaactgatttagcac
 K  T  F  T  S  C  -
```

tgtacataagctggtgttgtttatttctttgtttcttgggggttacatttctttcatgc
acaagaaaa

Figure S7

A. Elephant shark SST1 (Sc_821)

…TTTAGTGGATGGTATGTTGTGGATGCTGTATAGGGGATTGTGTGTAATGGATTGTGTGTAAGGGATGGT
GTGTAGTGGTTGGTGTGTAGAGGATAGTGTGTAGTGGATGGTGTGTGGTGGTTGGTTTGTAGAGGATAGT
GTATAGTGGACGGTGTGTGGTGGTTGGTGCGTTGGGCATGGTGTGCGGAGGATGGTGTTCGCGATGGTGT
GTAGAAGACTGTTTGTAGAGGATGCTGTGCAGTGAAGGGTGTGTTGGGGATGGTATGTAGTGAATGGTGT
GTAATGGATAGTGTTAAGGGATGGTGTATATGGGATGGTGTGTAGAGGATGGTGTGTTGGGGATGGTGTG
TTCAGGATGTCCTTCTAATATTTTGCACTACAGTATTAGAATTGAAAAGTTTGCCTCTTGTTTTTGCTCT
GTATTTAAATCCATAGAATTAATAAGAAAAAAAATGTAATATTTAAGAGGAGGTGGACGTGGTACGAATC
TCTGCCCTAATCTTAAAAGCCTCGTCACGGCCGGATGGGTGGGGGTGGGAGAGTCAACGTATCGGAGGCG
ATAACATCCCCAAGTGGCGAGGTTATGGACATTATCTCAATACTCGTCACGTGGGTTATTATTTTGTTCG
ATGATGTGACTAAATTGAGCATAAATTGCTTAAATCTCTGAGGACATTTGCTTTTGACGTCAGAAGGTGG
CGTGAGGCGGCTTTATAAGGCGAGTCTATGGACACCAGGACCAGAAGATCCAGACGAGGCAGAGCGTCCA
GAGAGCCGGTGCTGAACCACGAGCGTTCCTCCGTTCCTCTCTCGCTCCTCCTTTGACAGTTTGGTGCCGT
CGCCCCGAG**ATG**TCGTGCGGCCGAGTGCAGTGCGCCCTGGCGTTGCTCTCCATCGCCCTGACAGTGCTGA
M S C G R V Q C A L A L L S I A L T V L
GTGTCACCTCGGCGCCAGCACACGACAGGTACCGCGAAATCCTGCAGCGATCACTGGCCGCGGCGGGAGC
S V T S A P A H D R Y R E I L Q R S L A A A G A
CAGGAGTAAACCGGTAAGACAGCCGATTCCACACTGGGTAATTAATATCTGACAAGGTTGCTAAATACAC
R S K P
ATATTTACAACATTGACCTGTATTTCTAAAGTACATTCATTTGGGATTTTTGACTGGAGCTAATTATCCG
ACCGTCAGATTTTATTTCCTCATTTCTGTAATTCTGAATATAGCGCATTTCAGATGTCAGTCTATAACTG
TAAAGGAGATATCACGGTAACTCGTCTCTAACTTGCACAGAGGCAGATGCGCACCTGCCAGGATCGCCGA
TGGCCCCAGAGACACACCCCGATCTGGAGCCCCGGTACCGCGGCTCTCGGGCTCTGAGGATAACATTCCA
AACCATCAGATTACCGCACTCTCAGTCTCAGGGCAACTGCTCAGTGCCGCCGAGGACCCATAGCTCCCGA
GCGCTCCGTGTCAGTCGTGTAGTTGGAACCGTTGACACCTTGAGAGCCATTCATTCGTCTAAACCAGTTT
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TGGTGCATTTCTGGGCACAATAGAGAGGACTCCAGACTCCAGGCTGAAAACCTTACATCTTTCTTACATT
TACTAAAACATTGATATCTCCTAAGCTGAGAGAGCACATCCGTGTTCACCCCCCACCCCCACCCCCACCC
CGGAGCGCTGGCCTCTCATGTAGCCAATGGCTTAGAACCTATTTCTCCGGGAAAGTGAATGCTCGTGATT
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GAGTTTGACGTATATAGGAGGTGGGAGTCACTGAGCCATAAACAGACAAACACGCTGATTTTCCTGATCT
TCACACAAACAGCCAAAGCTGGAGAGGAAACTGCGCCAAACGATACATTTTTGTGAATGTAGTCATTAAT
CCGGGTTGAGTAATCAGCCATCAGCTGCTTGCCATGTGTACATGTGCCTCACTGATTACTGTTCTCTTGT
GTTACTGTTCTC**AG**GAGCTGACCAAGTACAGCCTGGCTCAGCTGTTGGCGGAATTGGCCAACGCGGAGAA
E L T K Y S L A Q L L A E L A N A E N
CGAGGCGCTGGAGGCGGAGGACATGGCCCGAGCAACCGCACAGGACGAAGTAAGGGTTGAATTGGAGAGA
E A L E A E D M A R A T A Q D E V R V E L E R
TCGGCCAACCCCAACCTGGCGCAGAGAGAGCGCAAAGCGGGCTGTAAAAGCTTCTTCTGGAAAACCTTCA
S A N P N L A Q R E **R K A G C K S F F W K T F**
CTTCCTGC**TAA**CTCTGAGCAGCCCCCACCACCCCTCTCACACACACTCATACACACACTTTCCCTGACCC
T S C –
CCACCCCTCCCATCCCCACCCTACACACAAAGTTTTCCCGATCCCCCGCCACACACACACACACACACAT
TGTATTTGTCTTACGCTACG TGGTCTGTTCTGATTTTAACATACTGTA**AATAAA**ACACATGGTGATGATA
ATTCAACCTAATTTATTGTGACAGAACCTTTAGATGGGGTTGTGACTGTATAGTTACCCACTCTTTCTGG
CTAGAGGTGTATGTATTATTTTTTAATTTGTATGTCGCAATGAAATACATGTTTGAAACTGAAACCATCTC
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GCAATTGGCTGCCGCGTTCGCCCACAAATATACAGTCAATTCACTTTACAGTGTGTTCTGTGAAGTGCTT
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B. Elephant shark SST2 (Sc_58)

…TACTTATTTTTTTCACATAATAATAATAATCCTTGCATTTGATATAGCGCTTTTCACGTCGGGAGGACA
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ATTGCGCACAGCAATGTCCCACAAACAGTCGTAGACTGAAAATAACCAATTTATTATTGTTTTGTTTTTT
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CAATGAGGTTTTGAATGAAGAAACAATTAACAATCCTGTTTGAGACTGAAATCTTCCGACTTGATATGAC
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M Q W Q A F A S V V C L
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L F I V T V Q G V E P Q E E R M G L Q L N R
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E M V K D K K R L I A K L L A G L L D V D D N
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L L E S V I A P L G L S K E E G T D F E E R S
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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**TGGATTTGTCAAAGATAAACATTTTTTAAAAATCCAGTTTGTGTTTTCCTGTTGATATGTAAA
C –
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CTTCCATACATCAAACGATTTGTAAATATTCACTGA**AATAAA**ACTGGAAAATAAATAGGTGGCTTTCTAA
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C. Elephant shark SST3 (Sc_821)

…TGGGCAGGGCATTTGGGAATAAATTAATCAAATTATTAATCAGGGTGGGTAGGGCATTGGGATTAAATTA
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M Q A R C T L T L A L L S L A A L G L S
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A L P T H L R D Q L V L Q G S P A M
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E L R D G V V R E L I Q A V A D A E S
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K P Q S E E A A E D F A P D E K A E L R L A L A
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P R W **R K D C K N F F W K T Y T L C** –
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D. Elephant shark SST6 (Sc_58)

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M Q I L V A L I S T L F L V S G V S T T T
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A S L D D R F N L Q S S R
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E M N Q E R K E M I L K L L S G L L D N A
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A V S G Q T G S E A G Y P E P A D G G P V M L E
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E R S R Y S Q L P Q R S **R K V P C K N F F W K**
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T F T S C –
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A. Elephant shark SST1 (SSTa)

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cgagcgttcctccgttcctctctcgctcctcctttgacagtttggtgccgtcgccccgag
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 S  V  T  S  A  P  A  H  D  R  Y  R  E  I  L  Q  R  S  L  A
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 E  L  A  N  A  E  N  E  A  L  E  A  E  D  M  A  R  A  T  A
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 Q  D  E  V  R  V  E  L  E  R  S  A  N  P  N  L  A  Q  R  E
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 R  K  A  G  C  K  S  F  F  W  K  T  F  T  S  C  -
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catccccaccctacacacaaagttttcccgatcccccgccacacacacacacacacacat
tgtatttgtcttacgctacgtggtctgttctgattttaacatactgtaaataaaacacat
ggtgatgataattcaacctaatttattgtgacagaacctttagatggggttgtgactgta
tagttacccactctttctggctagaggtgtatgtattatttttaatttgtatgtcgcaat
gaaatacatgtttgaaactgaaa
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B. Elephant shark SST2 (SSTd)

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                                                                a
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ctatacgaatgtaatcttcttgtggaaatgttacaaaactcagagctggctaaatgtttg
ttctacagacaaattccccatgaagagtcccaacatcccataagctgctgaacccttatt
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tcagcctcactgattccttatcagtctttgaaaacaatgactttctgagttgtgaaaatc
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 K  R  L  I  A  K  L  L  A  G  L  L  D  V  D  D  N  L  L  E
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 S  V  I  A  P  L  G  L  S  K  E  E  G  T  D  F  E  E  R  S
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 T  F  S  H  C  -
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C. Elephant shark SST3 (SSTe)

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                                                                gcagca
atgcaggctcggtgcaccctcactctagccctcctctccctggcagcgcttggcctcagt
 M  Q  A  R  C  T  L  T  L  A  L  L  S  L  A  A  L  G  L  S
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 A  L  P  T  H  L  R  D  Q  L  V  L  Q  G  S  P  A  M  E  L
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 R  D  G  V  V  R  E  L  I  Q  A  V  A  D  A  E  S  K  P  Q
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 S  E  E  A  A  E  D  F  A  P  D  E  K  A  E  L  R  L  A  L
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 A  P  R  W  R  K  D  C  K  N  F  F  W  K  T  Y  T  L  C  -
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tcattgtgaattcttaatcaagtgtttactgttacg
```

D. Elephant shark SST6 (SSTc)

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                                                          cgctctccc
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 M  Q  I  L  V  A  L  I  S  T  L  F  L  V  S  G  V  S  T  T
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 T  A  S  L  D  D  R  F  N  L  Q  S  S  R  E  M  N  Q  E  R
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 K  E  M  I  L  K  L  L  S  G  L  L  D  N  A  A  V  S  G  Q
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 T  G  S  E  A  G  Y  P  E  P  A  D  G  G  P  V  M  L  E  E
cgatctcgctacagccaactgccccagcgaagccgcaaagtcccctgtaagaacttcttc
 R  S  R  Y  S  Q  L  P  Q  R  S  R  K  V  P  C  K  N  F  F
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 W  K  T  F  T  S  C  -
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ctcgctcac
```

Figure S9

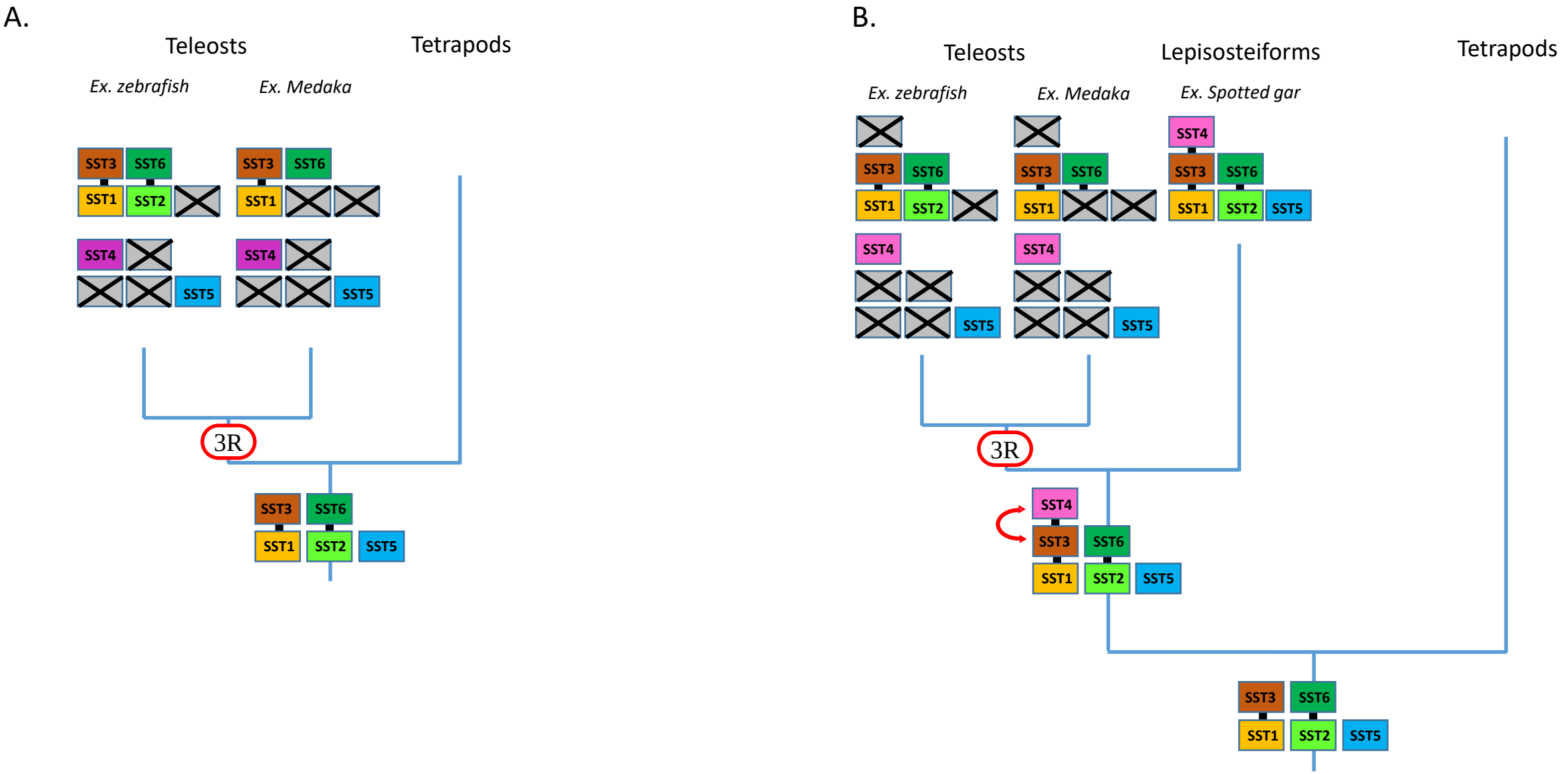

A.
Teleosts
Tetrapods
Ex. zebrafish
Ex. Medaka
SST3
SST6
SST1
SST2
SST4
SST5
3R
B.
Teleosts
Lepisosteiforms
Tetrapods
Ex. zebrafish
Ex. Medaka
Ex. Spotted gar

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	GGTCAAACTGCTCCCAGAAG

Table S2

Name	Sequence	Species
SST1	AGCKNFFWKTFTSC	*Most vertebrates, including catshark (SSTa)*
	AGCKSFFWKTFTSC	*Elephant shark, ratfish (SSTa)*
SST2 (*previously known as SST6)	MPCRNFFWKTFSSCK	*Human*
	PCKNFFWKTFSSCK	*Mouse, rat*
	TPCKNFFWKTFSSCK	*Bovine, monkey*
	TPCGNFFWKTFSSCK	*Pig*
	APCKNFFWKTFTMC	*Frog*
	APCKNFFWKTFSSC	*Anolis*
	APCRNFFWKTFSSC	*Coelacanth*
	SPCTNFFWKTFSAC	*Mexican tetra**
	SPCKNFFWKTFSAC	*Piranha**
	TPCKNFFWKTFSSC	*Spotted gar**
	SPCKLFFWKTFSSC	*Zebrafish**
	SPCKNFFWKTFSSC	*Herring**
	APCKLFFWKTFSHC	*Whale shark, skate (SSTd)*
	TPCKLFFWKTFSHC	*Catshark (SSTd)*
	AGCKLFFWKTFSHC	*Elephant shark (SSTd)*
SST3	AGCKNFYWKGFTSC	*Most teleosts*
	AGCKNFYWKGLTSC	*Tilapia*
	AGCKNFYWKGPTSC	*Takifugu*
	DGCKNFYWKGFTSC	*Medaka*
	AGCRNFYWKTFTSC	*Spotted gar*
	SGCKNFFWKGRTSC	*Herring*
	NCKNFFWKTYTLC	*Whale shark, catshark (SSTe)*
	DCKNFFWKTYTLC	*Elephant shark (SSTe)*
SST4	FGCRVPFWKSWSPC	*Stickleback*
	PCRVFYWKSWAKC	*Medaka*
	QFGCRMFFWKSWTYC	*Takifugu*
	QAGCRIFFWKSWTSC	*Tetraodon*
	TGCKNYFWKSRTAC	*Zebrafish*
	PLNCMNYFWKSRTAC	*Catfish*
SST5	AGCRNFFWKTFTSC	*Most actinopterygians*
	AGCRNFFWKSYTSC	*Tetraodon*
	TGCRNFFWKTFTSC	*Piranha, mexican tetra**
	AGCRNFYWKTFTSC	*Zebrafish*
	AGCKNFFWKTFTSC	*Coelacanth, catshark (SSTb)*
SST6 (*previously known as SST2)	APCKNFFWKTFTSC	*Chicken*, lungfish*, coelacanth*, actinopterygians*, catshark (SSTc)**
	TSCKNFFWKTFTSC	*Whale shark (SSTc)*
	VPCKNFFWKTFTSC	*Elephant shark (SSTc)*
Others		
SSTa	AGCKNFFWKTFTSC	*Lampreys*
SSTb	AGCKNFFWKTFSSC	
SSTc	ANCRMFYWKTMAAC	

Table S3

SST1 (SSTa)	Csh	Wsh	Esh
Catshark		66.37	73.45
Whale shark			74.14
Elephant shark			

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

SST3 (SSTe)	Csh	Wsh
Catshark		38.14
Elephant shark		

SST6 (SSTc)	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	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000180611	3	192,796,815 - 192,918,161
		G. Gallus	ENSGALG00000007218	9	13,300,318 - 13,348,379
		X. tropicalis	ENSXETG00000002143	GL172717.1	276,599 - 277,885
		A. carolinensis			
		L. chalumnae	ENSLACG00000017691	JH126687.1	2,299,815 - 2,301,095
		L. oculatus	ENSLOCG00000009364	LG14	18,861,293 - 18,899,827
		D. rerio	ENSDARG00000077316	15	45,527,281 - 45,538,773
			ENSDARG00000077690	2	5,563,077 - 5,581,772
		O. latipes			
Fgf12	Fibroblast growth factor 12	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000114279	3	192,139,395 - 192,767,764
		G. Gallus	ENSGALG00000036971	9	13,369,379 - 13,557,972
		X. tropicalis	ENSXETG00000002144	GL172717.1	393,833 - 521,960
		A. carolinensis	ENSACAG00000012985	GL343683.1	253,412 - 268,830
		L. chalumnae	ENSLACG00000017275	JH126687.1	2,003,413 - 2,283,293
		L. oculatus	ENSLOCG00000009371	LG14	18,996,717 - 19,055,669
		D. rerio	ENSDARG00000113925	15	45,414,883 - 45,510,977
			ENSDARG00000027957	2	5,587,495 - 5,681,658
		O. latipes	ENSORLG00000016010	17	24,782,508 - 24,802,926
Il1rap	Interleukin 1 receptor accessory protein	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000196083	3	190,514,051 - 190,659,750
		G. Gallus	ENSGALG00000007253	9	13,905,930 - 13,926,342
		X. tropicalis	ENSXETG00000015044	GL172717.1	998,488 - 1,097,171
		A. carolinensis	ENSACAG00000017733	GL343380.1	208,166 - 264,200
		L. chalumnae	ENSLACG00000016241	JH126687.1	1,498,996 - 1,521,106
		L. oculatus	ENSLOCG00000009378	LG14	19,120,504 - 19,150,963
		D. rerio	ENSDARG00000114719	15	45,338,623 - 45,356,635
		O. latipes			
Gmc	Geminin coiled-coil domain containing	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000205835	3	190,852,877 - 190,892,429
		G. Gallus	ENSGALG00000026907	9	13,853,476 - 13,857,367
		X. tropicalis	ENSXETG00000026307	GL172717.1	934,067 - 936,733
		A. carolinensis	ENSACAG00000008004	GL343380.1	1,488,188 - 1,492,009
		L. chalumnae	ENSLACG00000016600	JH126687.1	1,636,912 - 1,645,473
		L. oculatus	ENSLOCG00000009396	LG14	19,190,052 - 19,196,340
		D. rerio	ENSDARG00000068719	15	36,309,070 - 36,316,825
		O. latipes			
Ostn	Osteocrin	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000188729	3	191,199,241 - 191,265,615
		G. Gallus	ENSGALG00000007226	9	13,761,297 - 13,772,476
		X. tropicalis	ENSXETG00000015042	GL172717.1	750,574 - 755,484
		A. carolinensis			
		L. chalumnae	ENSLACG00000016886	JH126687.1	1,792,819 - 1,800,129
		L. oculatus	ENSLOCG00000009421)	LG14	19,280,012 - 19,292,855
		D. rerio	ENSDARG00000054055	15	36,228,835 - 36,249,087
		O. latipes			
Masp1	Mannan binding lectin serine peptidase 1	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000127241	3	187,217,285 - 187,292,022
		G. Gallus	ENSGALG00000007419	9	14,910,364 - 14,927,972
		X. tropicalis	ENSXETG00000019757	GL172717.1	2,406,583 - 2,454,003
		A. carolinensis	ENSACAG00000006732	GL343730.1	51,210 - 227,647
		L. chalumnae	ENSLACG00000018650	JH127453.1	681,716 - 776,581
		L. oculatus	ENSLOCG00000009432	LG14	19,284,195 - 19,341,321
		D. rerio	ENSDARG00000068726	15	36,187,434 - 36,223,417
		O. latipes			
SST1	Somatostatin 1	*R. typus*	XM_020509773.1	NW_018029766	122,914 - 124,407
		C. milii	XM_007912395.1	Sc_821	7,008 - 9,515
		H. sapiens	ENSG00000157005	3	187,668,906 - 187,670,399
		G. Gallus	ENSGALG00000007361	9	14,852,386 - 14,853,973
		X. tropicalis	ENSXETG00000019777	GL172717.1	2,228,041 - 2,229,578
		A. carolinensis	ENSACAG00000006722	GL343730.1	4,342 - 23,375
		L. chalumnae	ENSLACG00000003574	JH126687.1	88,278 - 90,189
		L. oculatus	ENSLOCG00000009439	LG14	19,404,762 - 19,407,399
		D. rerio	ENSDARG00000040799	15	36,156,986 - 36,158,851
		O. latipes	ENSORLG00000019152	scaffold660	2,344 - 3,701
SST3	Somatostatin 3	*R. typus*	XM_020509774.1	NW_018029766	131,096 - 160,273
		C. milii	XM_007912396.1	Sc_821	17,287 - 22,746
		H. sapiens			
		G. Gallus			
		X. tropicalis			
		A. carolinensis			
		L. chalumnae			
		L. oculatus	ENSLOCG00000009445	LG14	19,441,987 - 19,443,409
		D. rerio	ENSDARG00000033161	15	36,115,955 - 36,120,277
		O. latipes	ENSORLG00000019158	scaffold660	8,674 - 10,556
Col4a3	Collagen type IV alpha 3 chain	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000169031	2	227,164,565 - 227,314,792
		G. Gallus	ENSGALG00000038612	9	9,384,943 - 9,430,089
		X. tropicalis			
		A. carolinensis	ENSACAG00000004217	3	23,464,166 - 23,573,541
		L. chalumnae	ENSLACG00000009918	JH126709.1	458,799 - 567,615
		L. oculatus	ENSLOCG00000009454	LG14	19,454,926 - 19,507,683
		D. rerio	ENSDARG00000003395	15	36,054,864 - 36,112,794
		O. latipes			
Col4a4	Collagen type IV alpha 4 chain	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000081052	2	227,002,711 - 227,164,453
		G. Gallus	ENSGALG00000004946	9	9,318,986 - 9,370,173
		X. tropicalis			
		A. carolinensis	ENSACAG00000003770	3	23,583,599 - 23,670,714
		L. chalumnae	ENSLACG00000012078	JH126709.1	673,429 - 787,527
		L. oculatus	ENSLOCG00000009493	LG14	19,522,370 - 19,590,210
		D. rerio	ENSDARG00000002831	15	35,951,888 - 36,055,401
		O. latipes			
Rhbdd1	Rhomboid domain containing 1	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000144468	2	226,835,581 - 226,999,215
		G. Gallus	ENSGALG00000004957	9	9,276,974 - 9,300,051
		X. tropicalis	ENSXETG00000020088	GL172898.1	477,735 - 505,838
		A. carolinensis	ENSACAG00000003827	3	23,670,816 - 23,710,982
		L. chalumnae	ENSLACG00000013155	JH126709.1	816,263 - 961,971
		L. oculatus	ENSLOCG00000009504	LG14	19,592,741 - 19,635,912
		D. rerio	ENSDARG00000021046	15	35,933,094 - 35,944,902
		O. latipes	ENSORLG00000001341	13	2,545,608 - 2,553,109
Irs1	Insulin receptor substrate 1	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000169047	2	226,731,317 - 226,799,759
		G. Gallus	ENSGALG00000004959	9	9,244,127 - 9,248,424
		X. tropicalis	ENSXETG00000020086	GL172898.1	560,083 - 563,337
		A. carolinensis	ENSACAG00000003830	3	23,742,830 - 23,746,420
		L. chalumnae	ENSLACG00000014111	JH126709.1	963,541 - 1,032,531
		L. oculatus	ENSLOCG00000017412	LG14	19,644,120 - 19,647,356
		D. rerio	ENSDARG00000054087	15	35,888,549 - 35,930,070
		O. latipes			
SST4	Somatostatin 4	*R. typus*			
		C. milii			
		H. sapiens			
		G. Gallus			
		X. tropicalis			
		A. carolinensis			
		L. chalumnae			
		L. oculatus	ENSLOCG00000009520	LG14	19,696,596 - 19,698,886
		D. rerio	ENSDARG00000014190	2	5,726,353 - 5,728,843
		O. latipes	ND	17	24,768,840-24,769,036
Nyap2b	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2	*R. typus*			
		C. milii			
		H. sapiens	ENSG00000144460	2	225,399,710 - 225,654,018
		G. Gallus	ENSGALG00000004966	9	8,727,389 - 8,844,775
		X. tropicalis	ENSXETG00000005150	GL172898.1	945,276 - 992,671
		A. carolinensis	ENSACAG00000003843	3	24,114,255 - 24,276,004
		L. chalumnae	ENSLACG00000016098	JH126709.1	1,453,451 - 1,537,068
		L. oculatus	ENSLOCG00000009528	LG14	19,821,041 - 19,871,639
		D. rerio	ENSDARG00000079581	15	35,698,508 - 35,895,161
			ENSDARG00000093357	2	5,734,870 - 5,776,030
		O. latipes	ENSORLG00000016004	17	24,738,491 - 24,749,441