

The evolution of vertebrate somatostatin receptors and their gene regions involves extensive chromosomal rearrangements

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SUPPLEMENTAL FIGURES 1-3

Figure S1: Bootstrapped phylogenetic maximum likelihood tree of the SSTR gene family. The topology of the tree is supported by a non-parametric bootstrap analysis with 100 replicates (see Methods). Branch support is shown at the nodes. The tree is rooted with the human kisspeptin receptor 1 sequence (not shown). Comprehensive information about the sequences is available in Additional file 7, Table S1.

Figure S2: aLRT-supported phylogenetic maximum likelihood tree of the SSTR gene family. The topology of the tree is supported by an SH-like approximate likelihood ratio test (see Methods). Branch support is shown at the nodes. The tree is rooted with the human kisspeptin receptor 1 sequence (not shown). Comprehensive information about the sequences is available in Additional file 7, Table S1.

Figure S3: Identification of additional known teleost SSTR sequences. Additional teleost sequences from goldfish, grass carp, orange-spotted grouper, black ghost knifefish and rainbow trout (see Discussion) were added to the sequence alignment described in our results. The NCBI accession IDs of these sequences can be seen in the sequence names (in colors) and in Additional file 7, Table S1. The tree was made using the neighbor joining method supported by 100 bootstrap replicates (see Methods). Branch support is shown at the nodes. The tree supports the hypothesis that both the goldfish and rainbow trout have retained duplicates genes from the respective 4R whole genome duplications that occurred in their individual lineages. The goldfish has 4R duplicates of *SSTR1* (GenBank:AAF08613.1 and GenBank:AAF08614.1) and *SSTR5a* (GenBank:AAN76495.1 and GenBank:AAM18805.1), and the rainbow trout of *SSTR6* (GenBank:NP_001118006.1 and GenBank:NP_001118115.1, misidentified as *SSTR1a* and *-b* in the literature) and *SSTR2a* (GenBank:ADH59744.1 and NP_001182111.1).

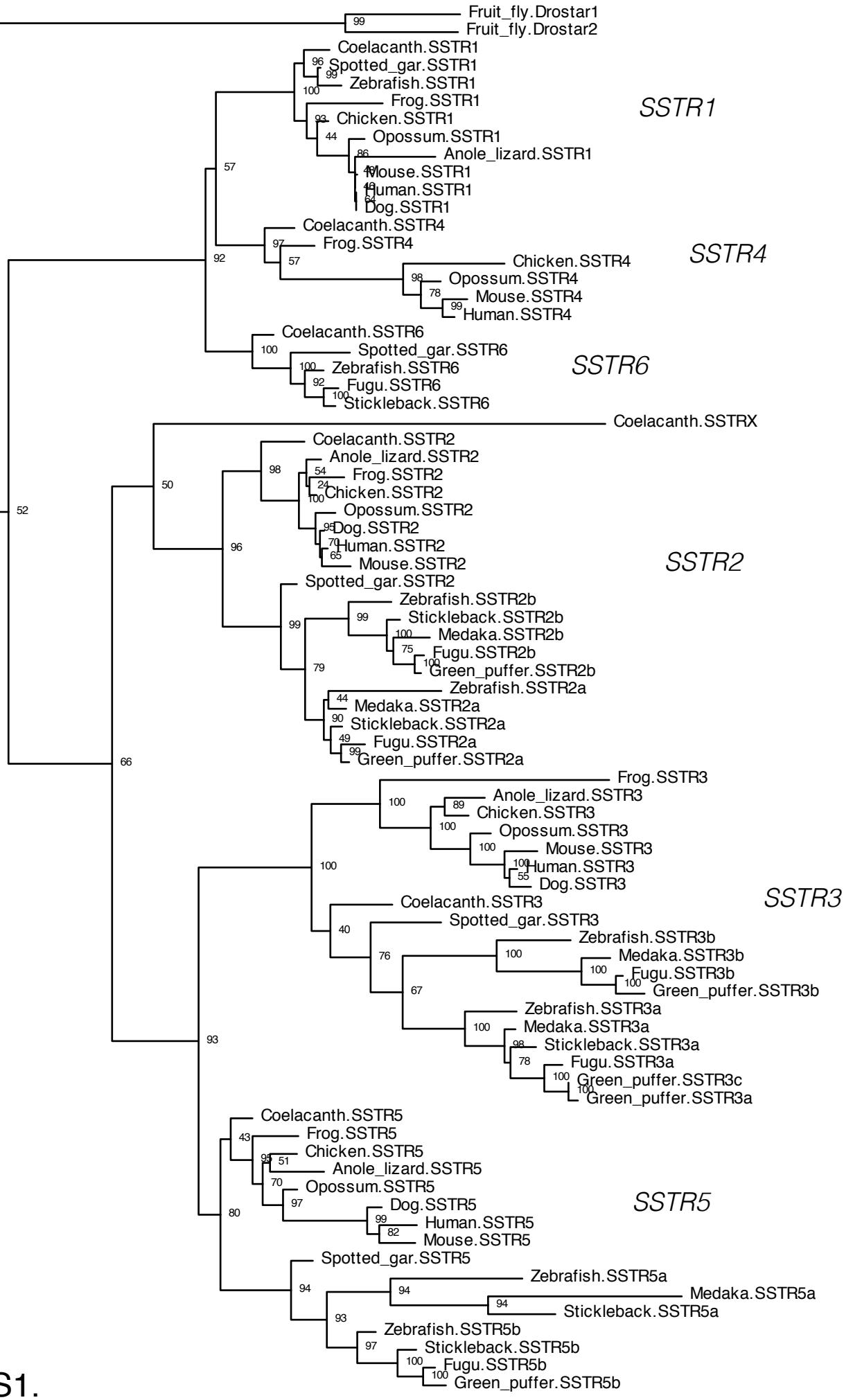


Figure S1.

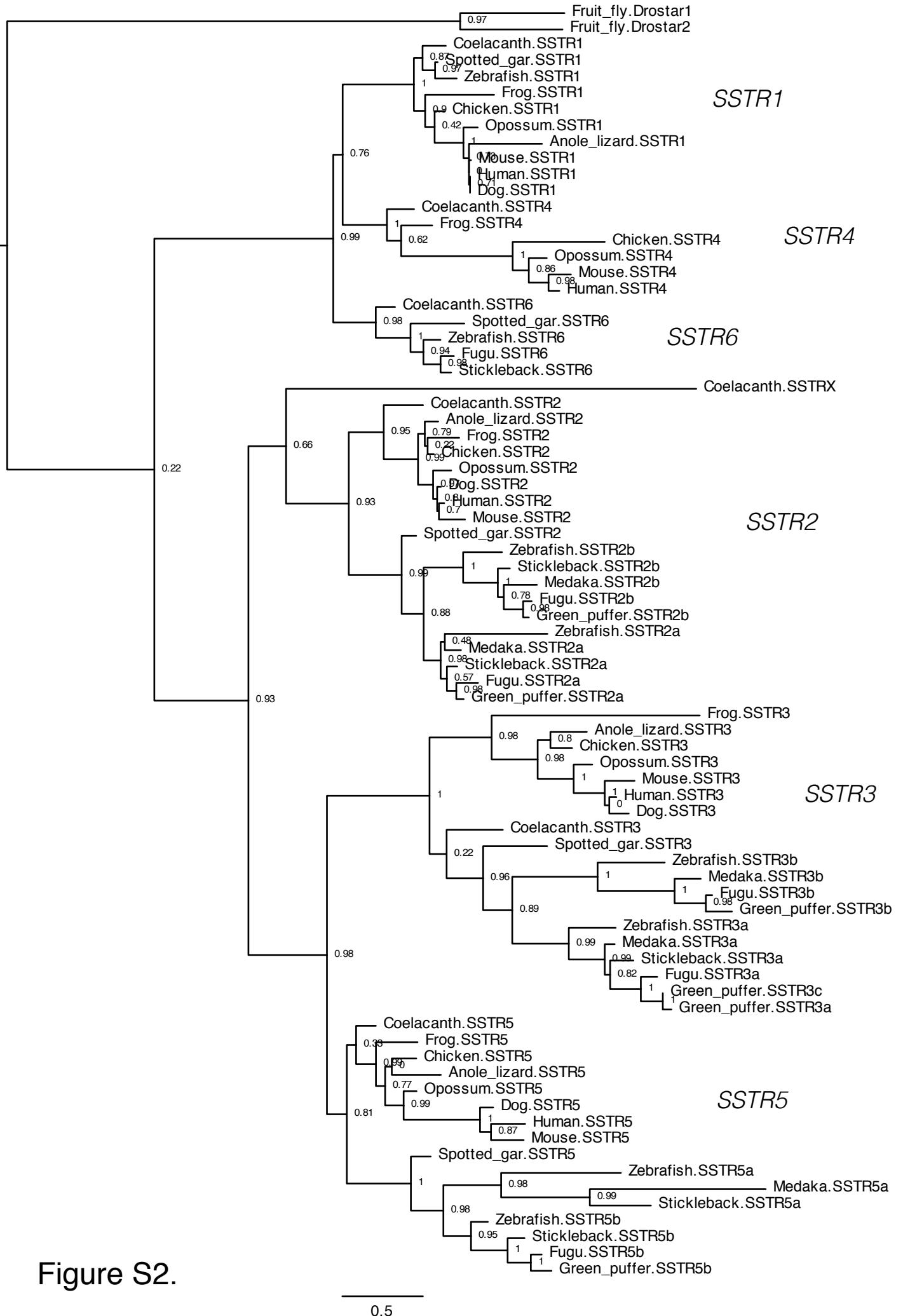


Figure S2.

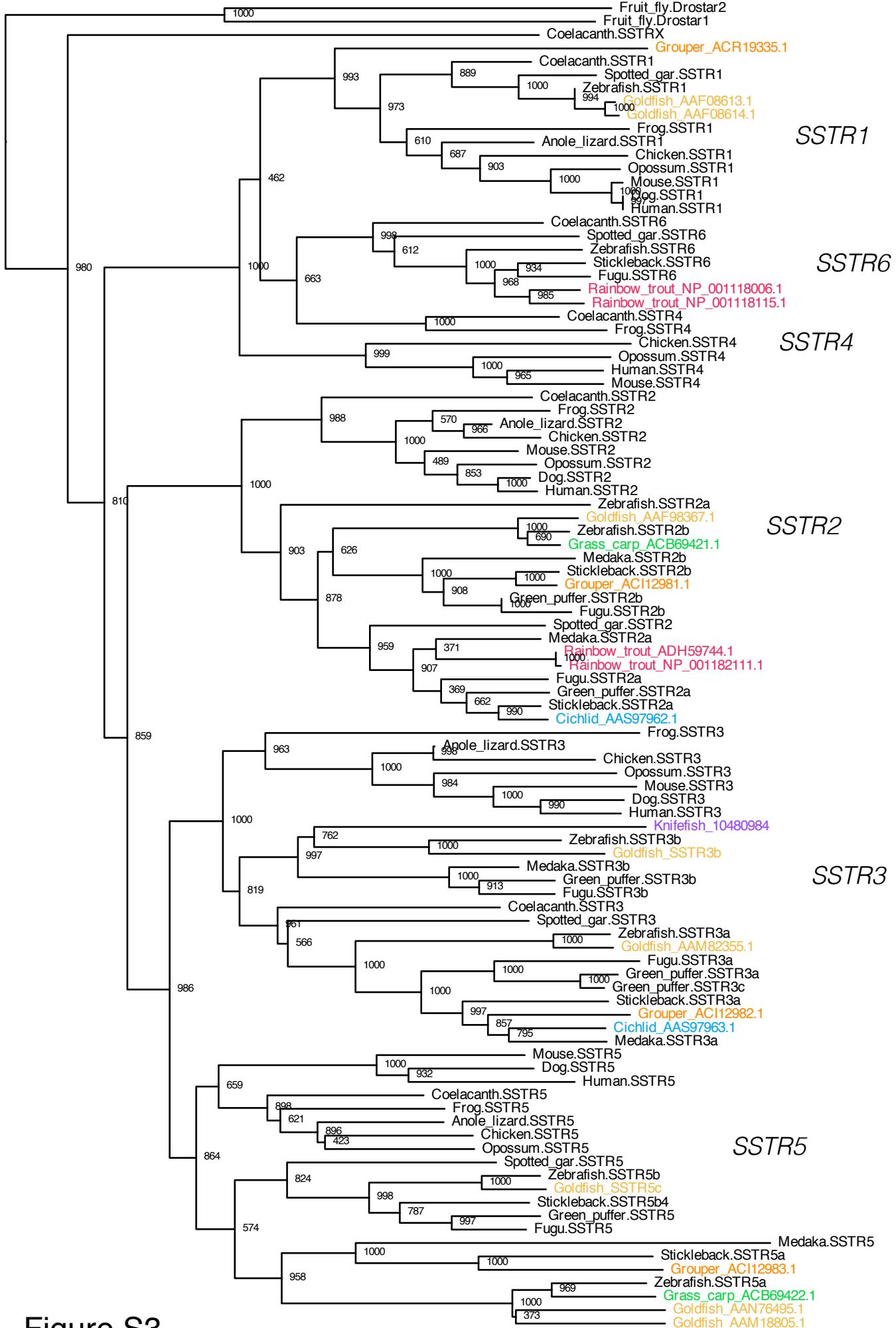


Figure S3.

0.05