

**Figure S1.** Searching patterns for vertebrate telomerase RNA. Initial search pattern derived from the Chen et al., 2000 alignment. Each conserved sequence block is represented by a PWM displayed here as its sequence logo drawn using WebLogo (Crooks et al., Genome Res 14, 1188-90, 2004). A PWM is a matrix of score values that gives a weighted match to any given residue in the sequence. It calculates scores at each position independently from the residues at other positions. Three of the eight PWMs were allowed to match with 1 indel, and seven intervening intervals with prescribed length range. The numbers above the block are the required pwm-match-score (Kel et al., Nucleic Acids Research 31, 3576-9, 2003) and the maximal number of deletions in the genomic DNA. Dotted lines between the blocks represent unmatched genomic DNA, the numbers above the lines defining the minimal and maximal length of the intervening sequence, respectively. Starting with the most informative PWM, fragrep2 matches the PWM to the genomic DNA sequence and then collects combinations matches that obey the length restrictions on the intervening sequence using a dynamic programming algorithm.

Supplemental Table S1: Genomic locations of teleost telomerase RNAs

<b>Species</b>	<b>Assembly</b>	<b>Coordinates</b>		<b>Upstream gene</b>	<b>Downstream gene</b>
Zebrafish	Zv6	Chr:25	10426622-10426938 (+)	TMEM178	HPCAL4
Medaka	MEDAKA1	Chr:8	5329954-5331990 (-)	Arf-like	-, LASP1
Stickleback	BROAD1	Group:XI	6569094-6569441 (+)	Arf-like	PLXDC2, LASP1
Fugu	FUGU 4.0	Scaffold_15	1952644-1952968 (+)	Arf-like	PLXDC2
Tetraodon	Tetraodon-7	Chr:3	13151278-13151605 (+)	Arf-like	PLXDC2
Human		Chr:3	170965092-170965529 (-)	ARPM1	MDS1

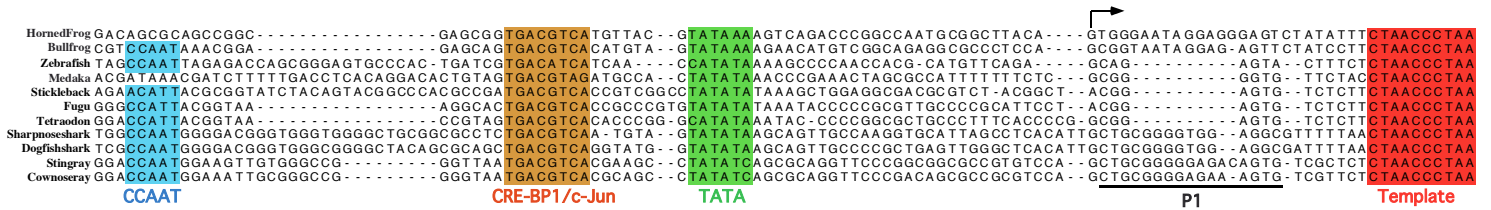


Figure S2. Cis-acting regulatory elements in the promoter region of fish telomerase RNA genes. The sequences were aligned based on the CCAAT element, TATA element and template sequence of the telomerase RNA gene. The putative CRE-BP1/c-Jun element is predicted by using the Transcription Element Search System (TESS) at <http://www.cbil.upenn.edu/tess/>. The CCAAT, CRE-BP1/c-Jun, TATA element and the template region are shaded in blue, orange, green and red, respectively. The transcription initiation site of the telomerase RNA genes is indicated with an arrow above the sequence alignment.

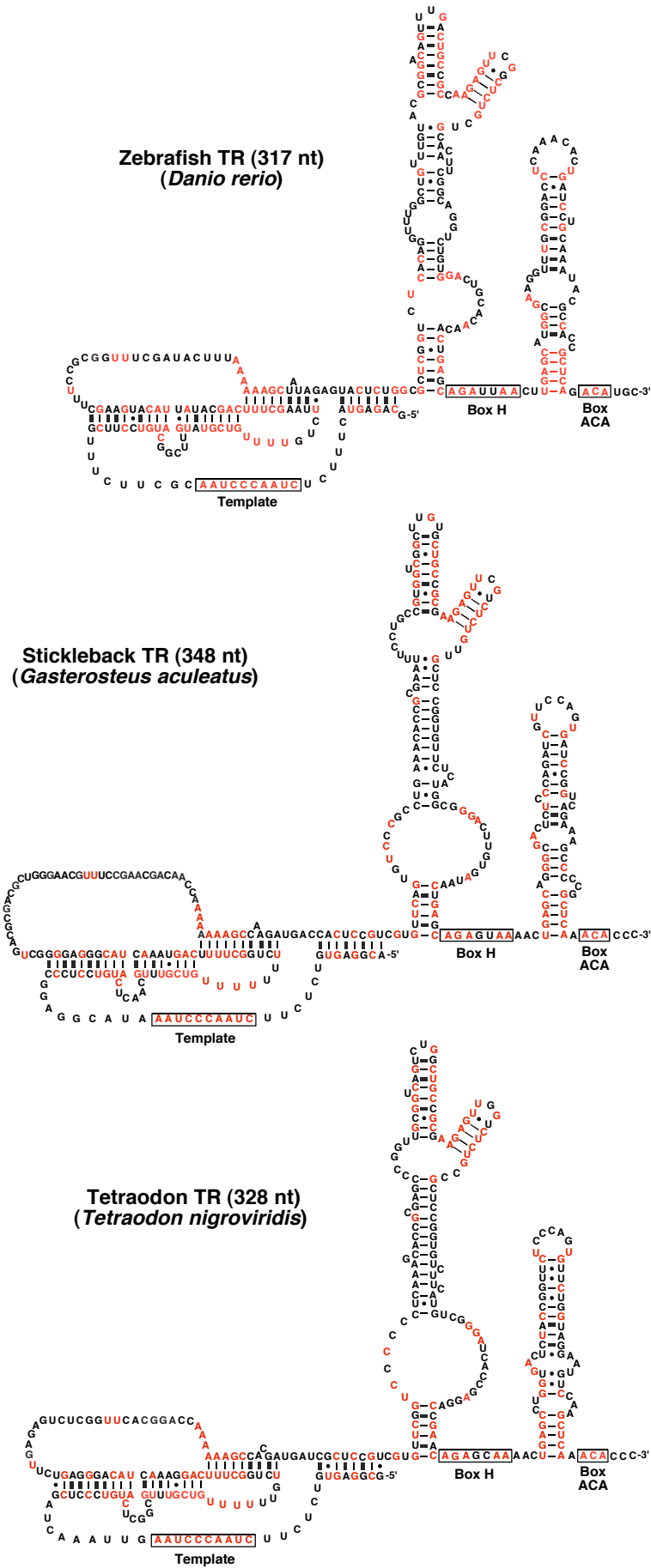


Figure S3. Secondary structure models of zebrafish, stickleback and Tetraodon telomerase RNAs. Residues conserved in all five teleost TRs are shown in red. Conserved nucleotides in the template region, box H and ACA motifs are indicated in black boxes.