Supplemental Table 1. Accession data for individual gene information (all from Li et al. 2007) downloaded from the ENSEMBL Genome Browser (Hubbard et al., 2007), the UCSC genome browser (Kent et al., 2002) and GenBank (Benson et. al., 2005).

LOCUS	**Accession number for template *Oryzias latipes***
zic1	EF032914.1
myh6	EF032927.1
RYR3	EF032940.1
Ptr	EF032953.1
tbr1	EF032966.1
ENC1	EF032979.1
Glyt	EF032992.1
SH3PX3	EF033005.1
plag12	EF033018.1
sreb2	EF033031.1

Supplemental Table 2. Branch lengths and the corresponding 95% Bayesian credible intervals (BCI) based on phylogenetic reconstruction using the ten protein coding genes (Li et al., 2007) or Ultra Conserved Elements (UCEs) and the corresponding flanking regions. See Materials and Methods and Supplemental Figure 2 for details.

Branch	**Protein Coding Average**	**Lower 95% BCI**	**Upper 95% BCI**	**UCE Average**	**Lower 95% BCI**	**Upper 95% BCI**
(Root,3)	0.0268	0.0158	0.0389	0.0198	0.0191	0.0205
(Root,1)	0.0268	0.0158	0.389	0.0198	0.0191	0.0205
(1,2)	0.0648	0.0531	0.0767	0.0528	0.0521	0.0536
(2,4)	0.0083	0.0049	0.0117	0.0046	0.0044	0.0048
(4,6)	0.0037	0.002	0.0056	0.0024	0.0023	0.0025
(3,5)	0.1736	0.1451	0.2054	0.1202	0.119	0.1214
(3, *G. aculeatus*)	0.0837	0.0678	0.0984	0.1041	0.1031	0.1051
(5, *T. rubripes*)	0.1305	0.1084	0.1547	0.0539	0.0531	0.0546
(5, *T. nigrovirides*)	0.1435	0.1205	0.1681	0.0739	0.073	0.747
(1, *O. latipes*)	0.1334	0.1154	0.1517	0.167	0.1656	0.1683
(2, *O. niloticus*)	0.0069	0.0037	0.0101	0.0055	0.0053	0.0057
(4, *N. brichardi*)	0.0048	0.0028	0.0069	0.0046	0.0028	0.0069
(6, *P. nyererei*)	0.0029	0.0015	0.0045	0.0021	0.002	0.022
(6, *H. burtoni*)	0.0013	0.0004	.0024	0.0019	0.0018	0.0019

FIGURE 4. Average PI per nucleotide for the UCE flanking regions versus average PI per nucleotide for the UCE core regions. Linear regression results: adjusted $R^2 = 0.14$; p-value = $<2.2\text{x } 10^{-16}$; slope = 0.7081; and Y-intercept = $1.196 \text{ x}10^{-3}$.

FIGURE 5. Average PI for each UCE plotted against upstream and downstream flank length.

ONLINE APPENDIX FIGURES

Supplemental Figure 1. *In silico* time calibrated phylogeny used in TAPIR analysis. Time axis is in millions of years before the present.

Supplemental Figure 2. Phylogenetic reconstruction of the eight percomorph species used in our analysis based on ten protein coding genes from Li et al. (2007) and 988 UCEs. The posterior probabilities for all internal nodes were near 1 (See Supplemental Table 2 for details).

Supplemental Figure 3. Linear regression of maximum PI per nucleotide against average PI per nucleotide for the core and flanking regions. a) Core Regions: adjusted $R^2 = 0.91$; slope = 1.212; and Y-intercept = $3.225\text{x}10^{-6}$. b) Flanking Regions: adjusted $R^2 = 0.99$; slope = 1.277; and Y-intercept = $-1.364\text{x}10^{-4}$.