Appendices

Appendix 1. Molecular phylogenies of the 130 human genes and their putative orthologs obtained from other animal genome sequences (shown as Fig S1–S63). Abbreviations used in these figures are as follows: LPT, long-term potentiation; TT, Taste transduction; OT, olfactory transduction; TCA, TCA cycle; 3R-WGD, third-round whole genome doubling; 3R, orthologous genes group that appears to be duplicated through the 3R-WGD; 1:1, orthologous gene groups that show 1 to 1 orthologous relationships between tetrapods and teleosts.

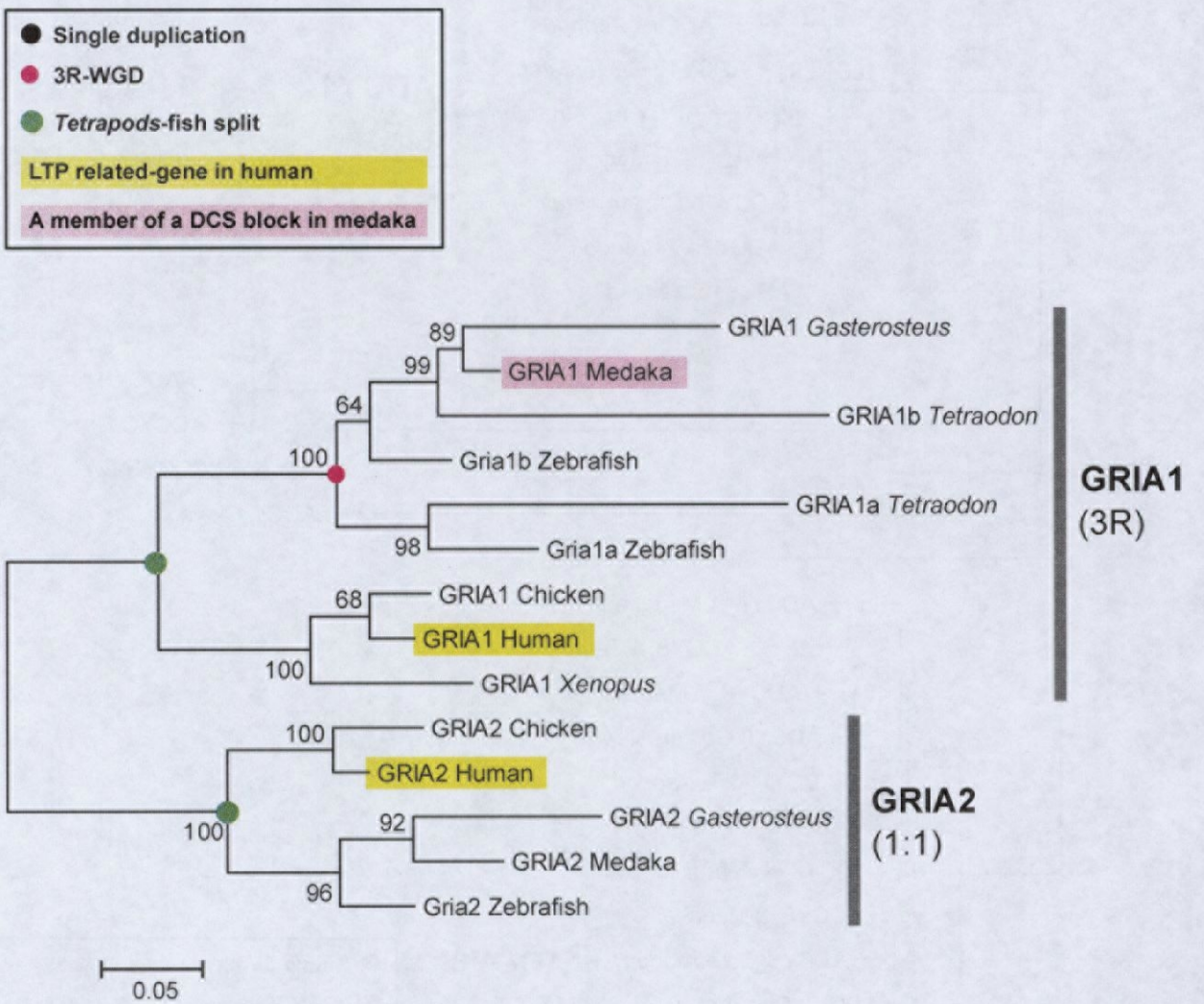

Fig. S1. A molecular phylogeny of AMPAR (glutamate receptor, ionotropic) inferred from maximum-likelihood analysis (606 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

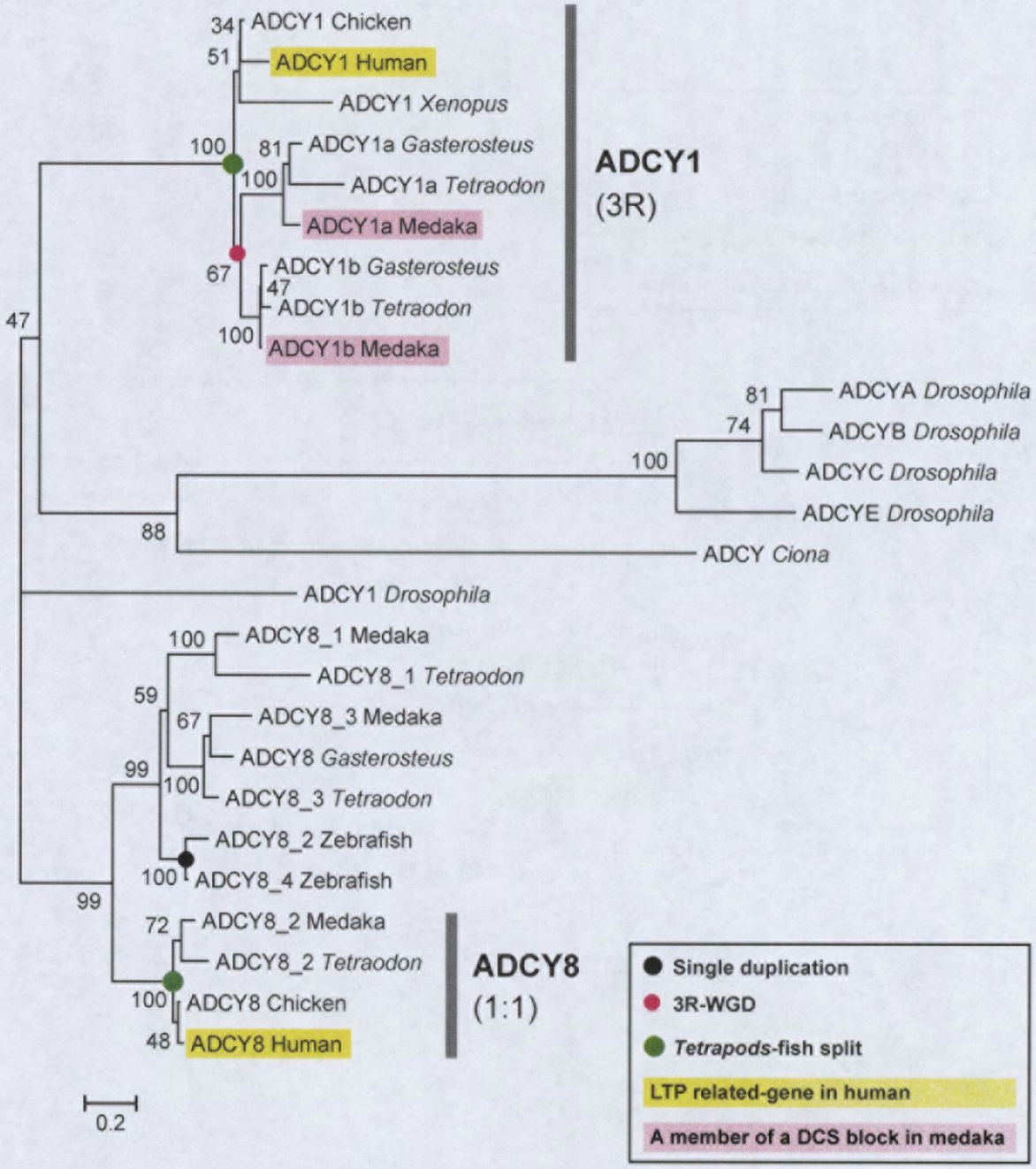

Fig. S2. A molecular phylogeny of AC1 and AC8 (adenylate cyclase 1 and 8, EC: 4.6.1.1) inferred from maximum-likelihood analysis (342 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

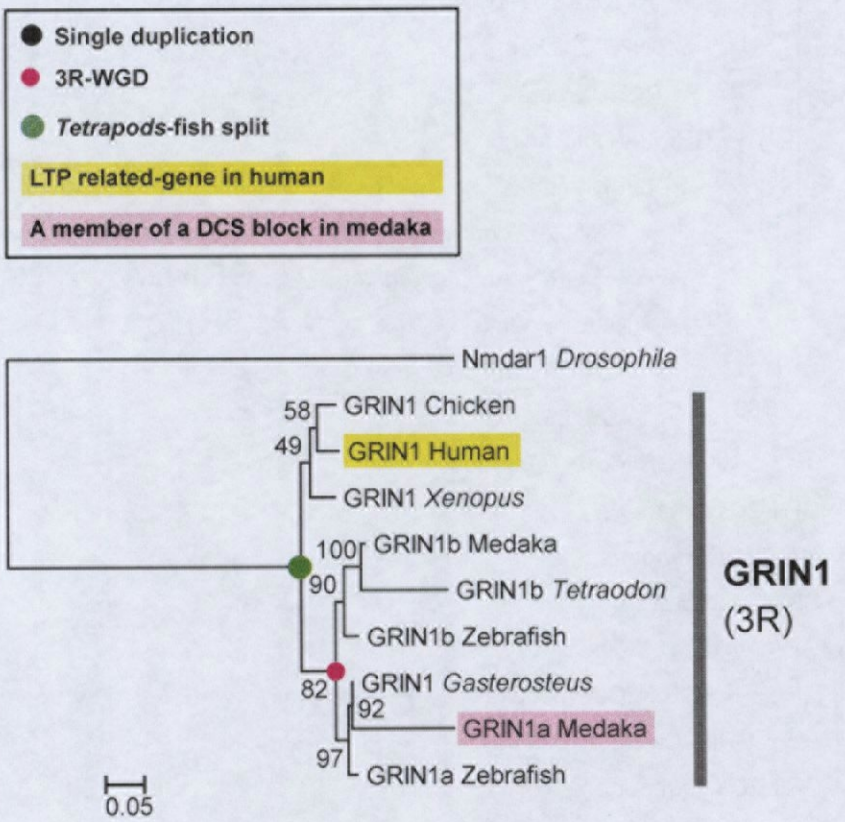

Fig. S3. A molecular phylogeny of NMDAR (glutamate receptor, ionotropic, N-methyl D-aspartate) inferred from maximum-likelihood analysis (752 amino acid sites were used; WAG+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

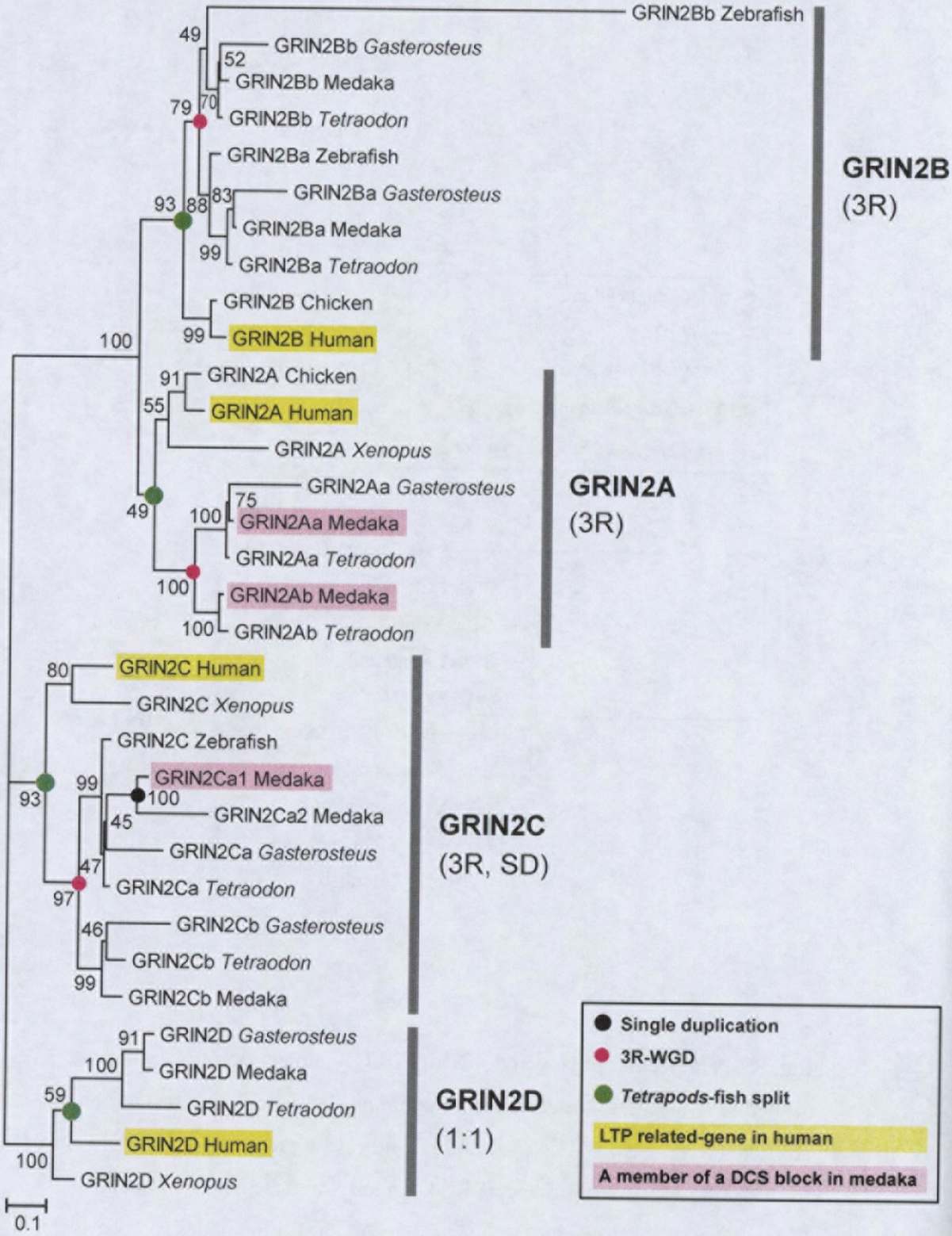

Fig. S4. A molecular phylogeny of NMDAR (glutamate receptor, ionotropic, N-methyl D-aspartate) inferred from maximum-likelihood analysis (321 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

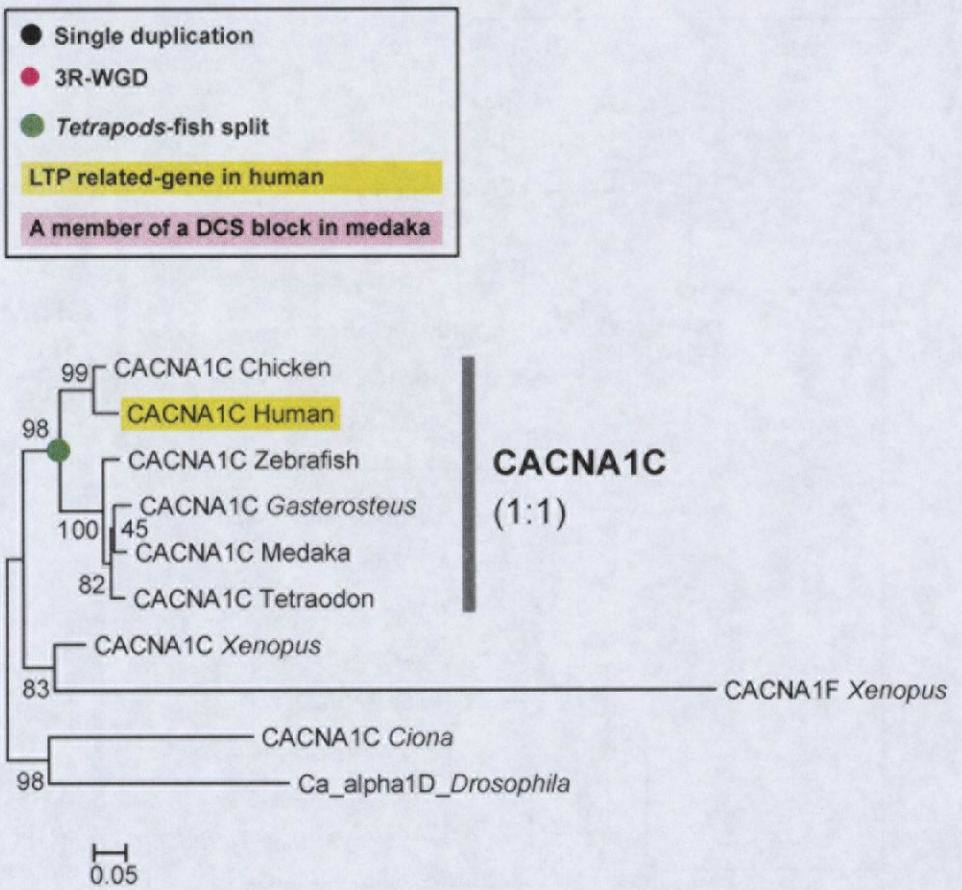

Fig. S5. A molecular phylogeny of VDCC (or CACNA1C, calcium channel, voltage-dependent, L type, alpha 1C subunit), inferred from maximum-likelihood analysis (530 amino acid sites were used; Blosum62+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests

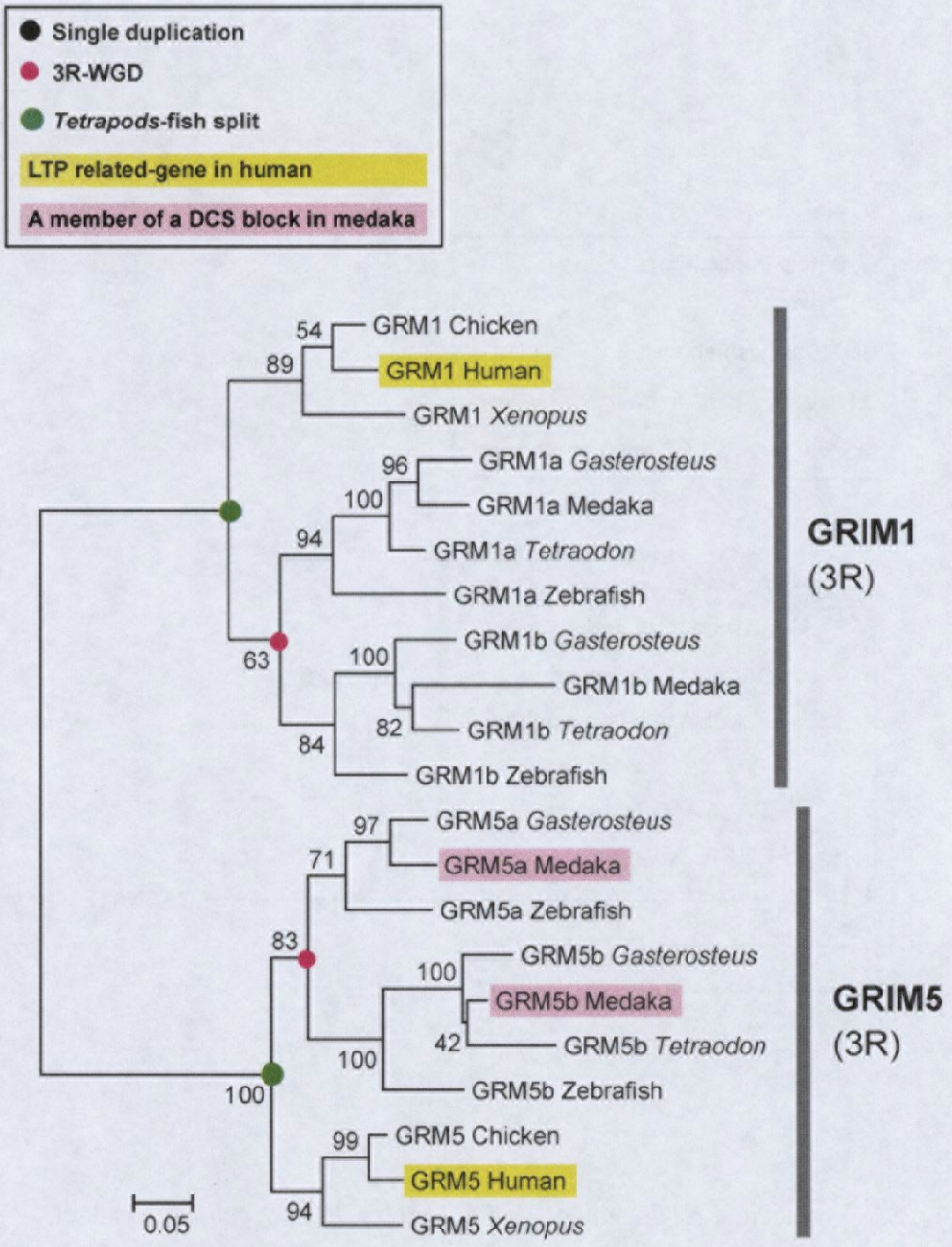

Fig. S6. A molecular phylogeny of mGluR (or GRM, glutamate receptor, metabotropic), inferred from maximum-likelihood analysis (529 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

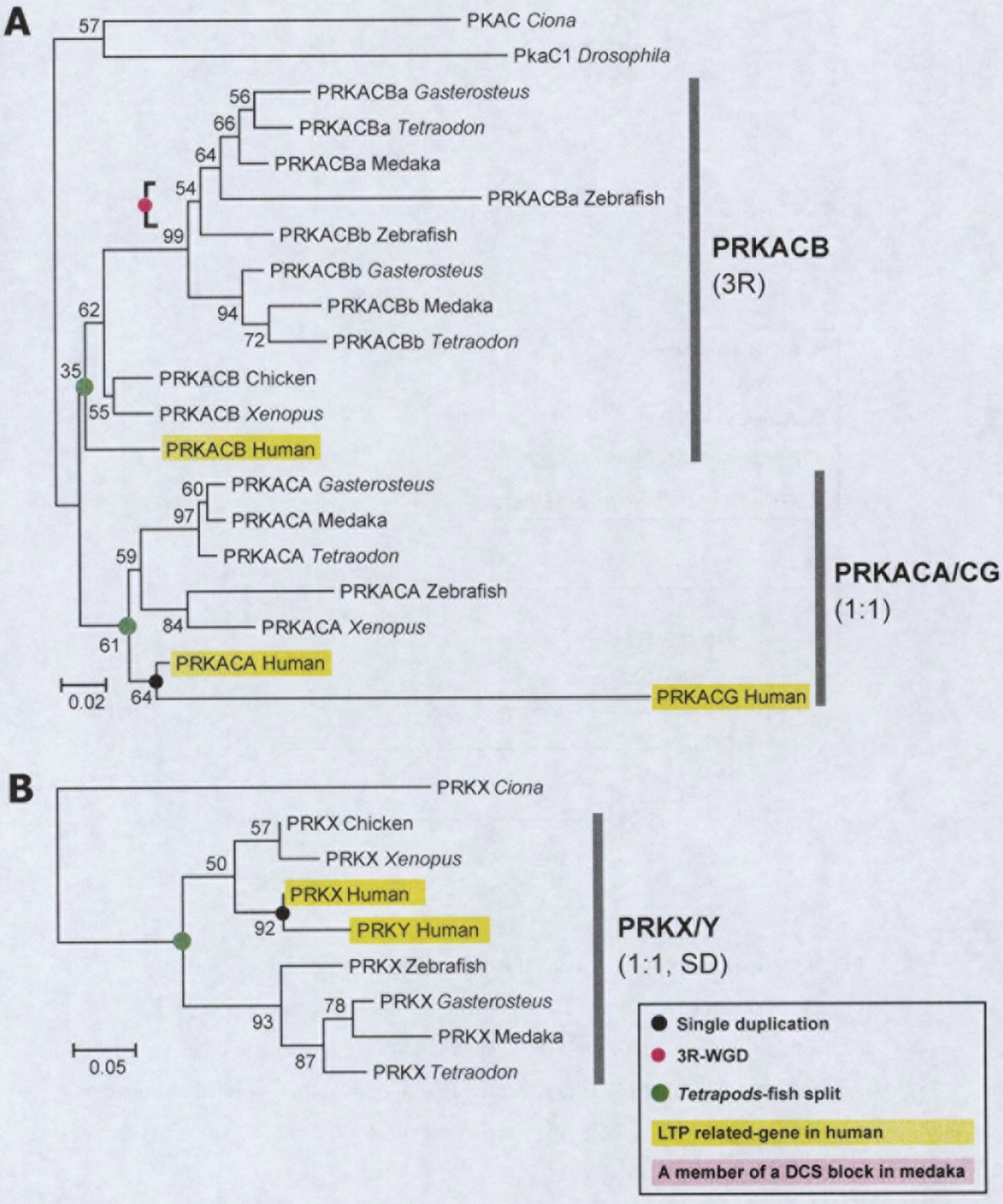

Fig. S7. A molecular phylogeny of PKA (protein kinase), inferred from maximum-likelihood analysis (panel A: 295 amino acid sites were used with JTT+Γ; panel B: 213 amino acid sites were used with JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

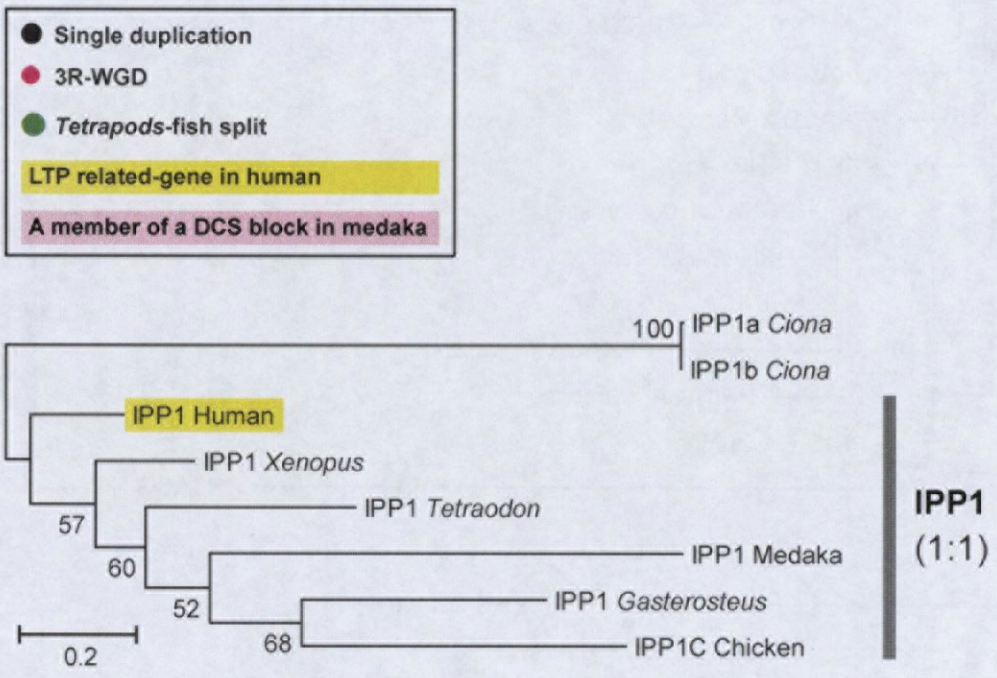

Fig. S8. A molecular phylogeny of IPP1 (protein phosphatase 1, regulatory [inhibitor] subunit 1A), inferred from maximum-likelihood analysis (307 nucleotide sites were used; TrN+I). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.