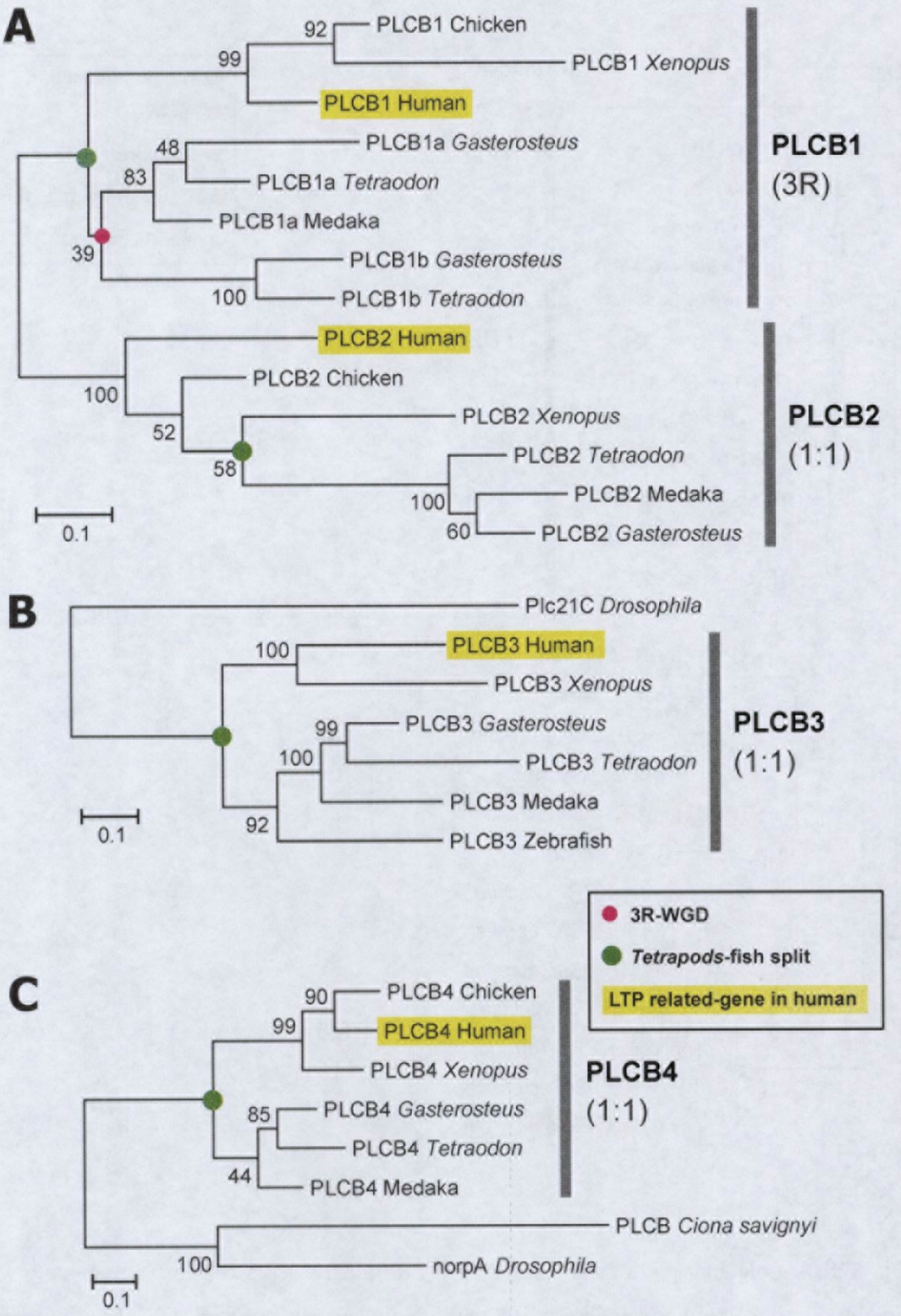

Fig. S27. A molecular phylogeny of PLCB (phospholipase C, beta), inferred from maximum-likelihood analysis (panel A: 394 nucleotide sites were used with HKY+I+Γ; panel B: 3116 nucleotide sites were used with GTR+I+Γ; panel C: 1066 nucleotide sites were used with GTR+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

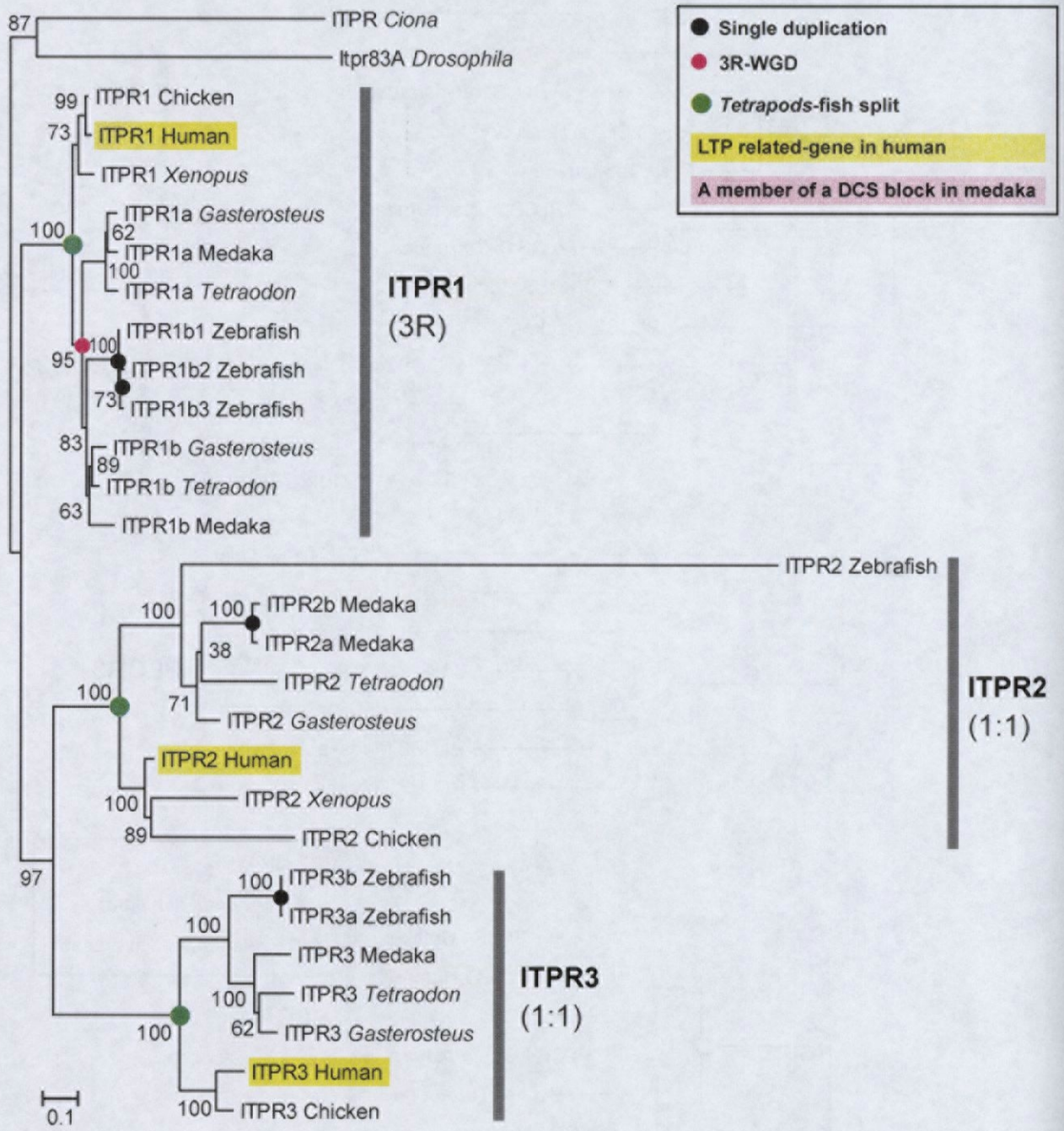

Fig. S28. A molecular phylogeny of IPR (or ITPR, inositol 1,4,5-triphosphate receptor), inferred from maximum-likelihood analysis (1022 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

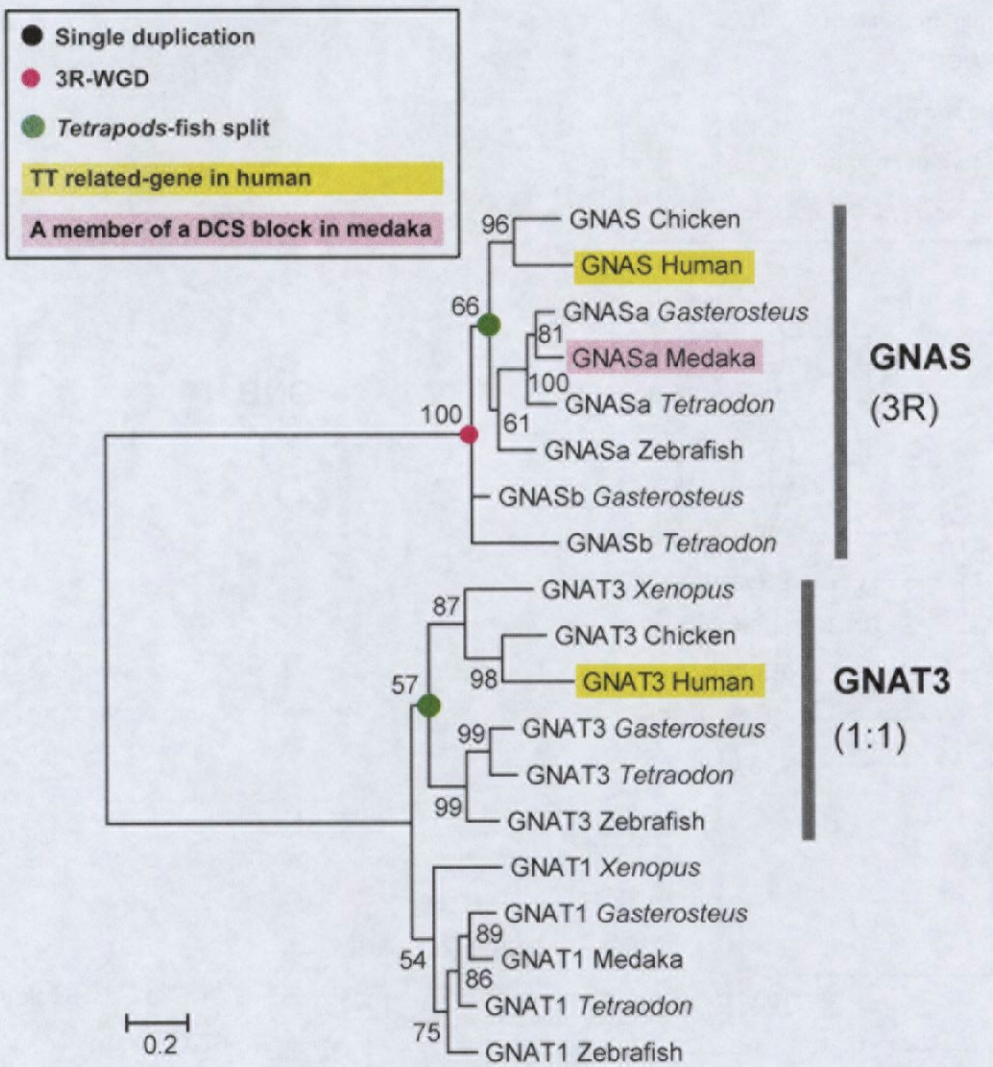

Fig. S29. A molecular phylogeny of Gα (guanine nucleotide binding protein, alpha transducing), inferred from maximum-likelihood analysis (744 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

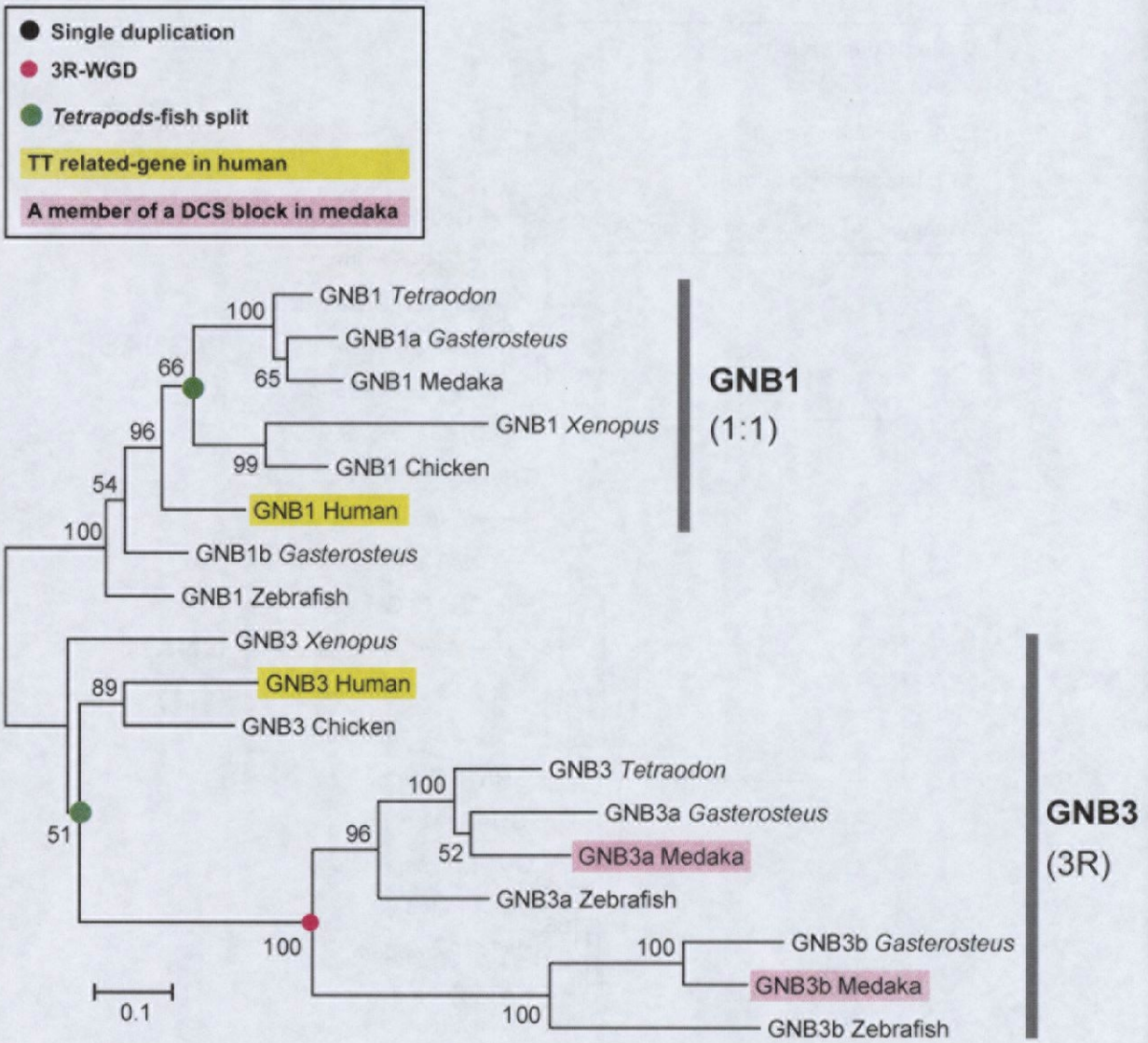

Fig. S30. A molecular phylogeny of GNB (guanine nucleotide binding protein, beta polypeptide), inferred from maximum-likelihood analysis (934 nucleotide sites were used; GTR+I+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

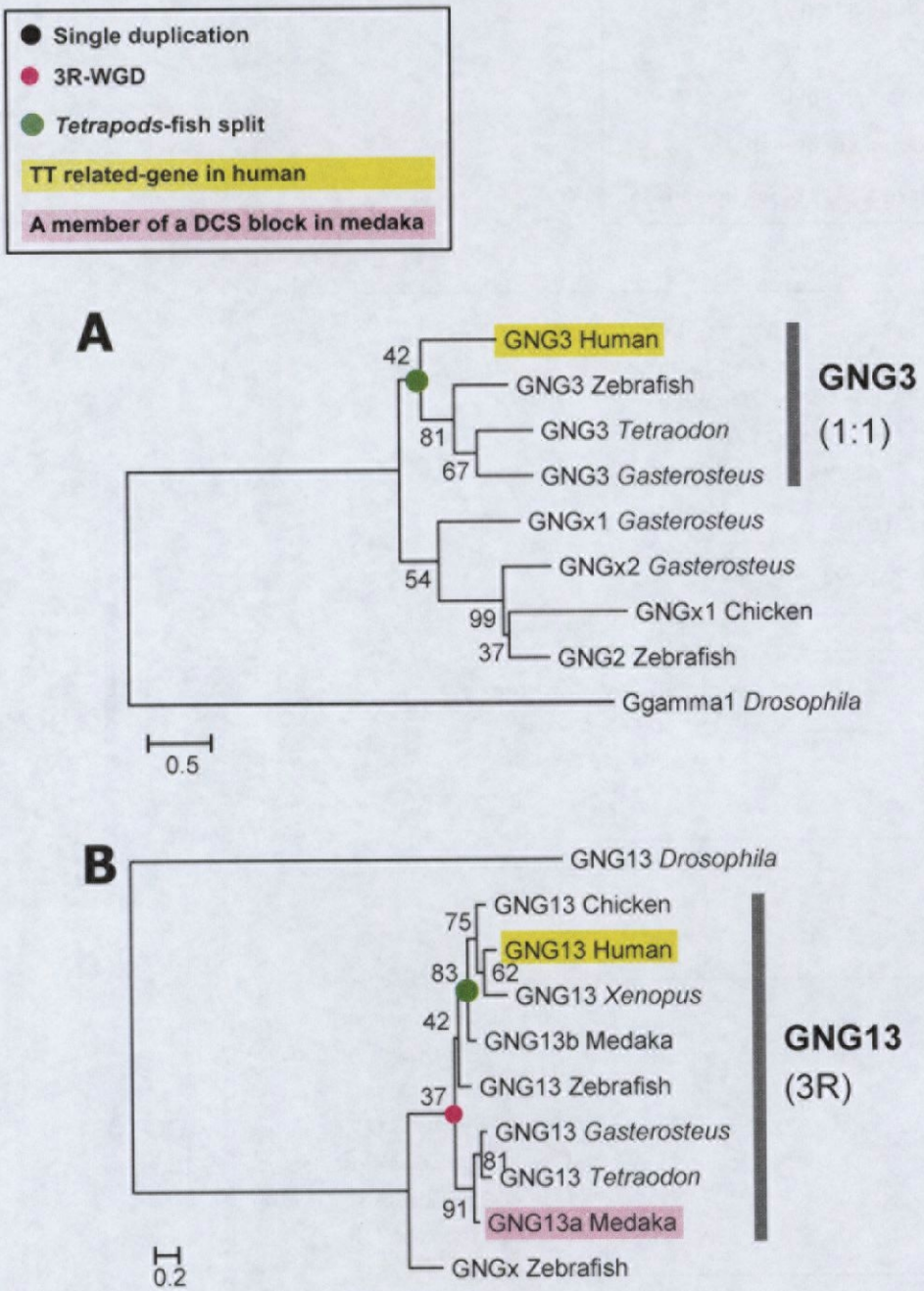

Fig. S31. A molecular phylogeny of GNG3 and 13 (guanine nucleotide binding protein, gamma polypeptide 3 and 13), inferred from maximum-likelihood analysis (panel A: 531 nucleotide sites were used with GTR+I+Γ; panel B: 204 nucleotide sites were used with TrN+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

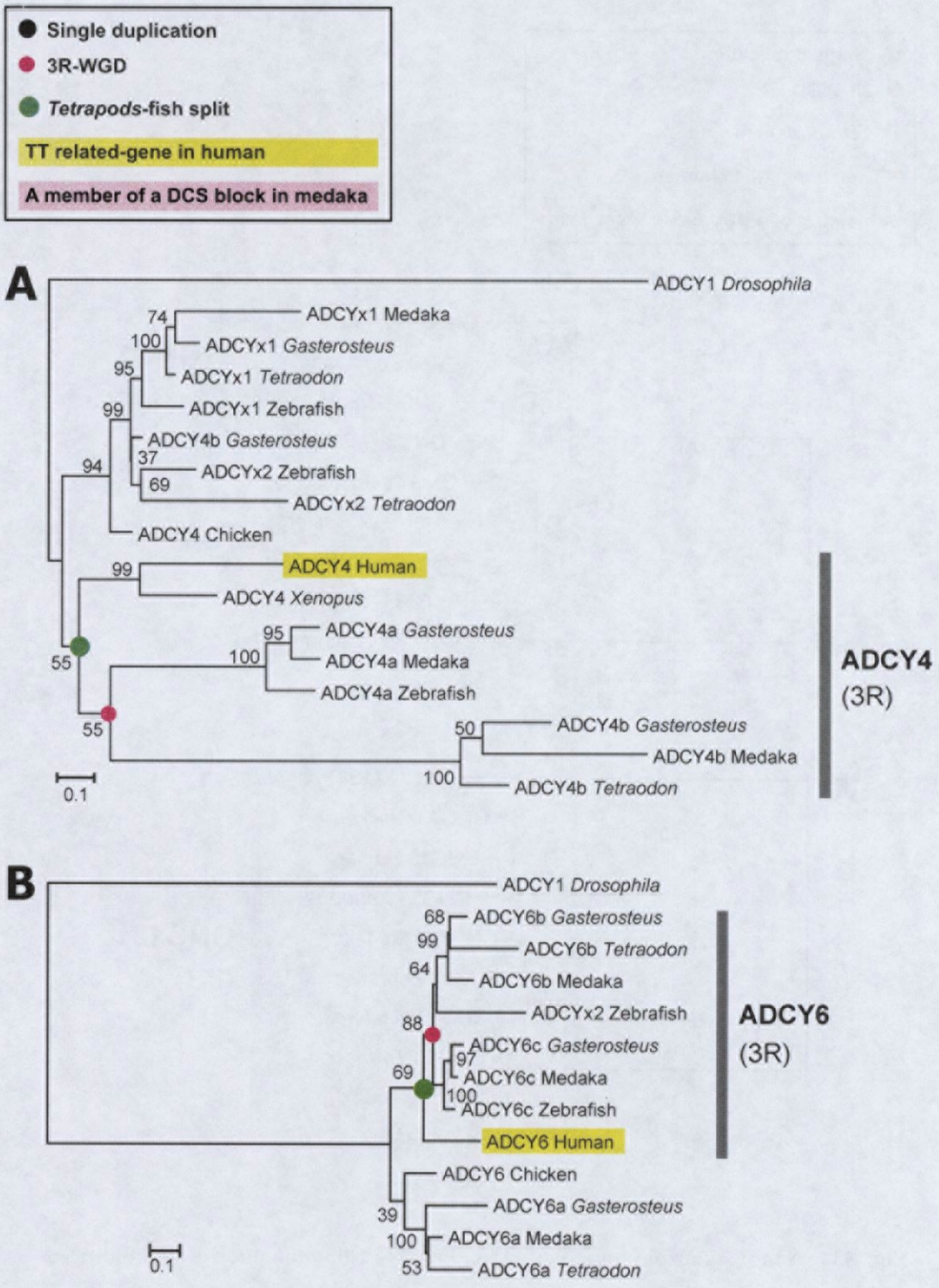

Fig. S32. A molecular phylogeny of AC (adenylate cyclase, EC:4.6.1.1), inferred from maximum-likelihood analysis (panel A: 571 amino acid sites were used with JTT+Γ; panel B: 680 amino acid sites were used with Blosum62+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

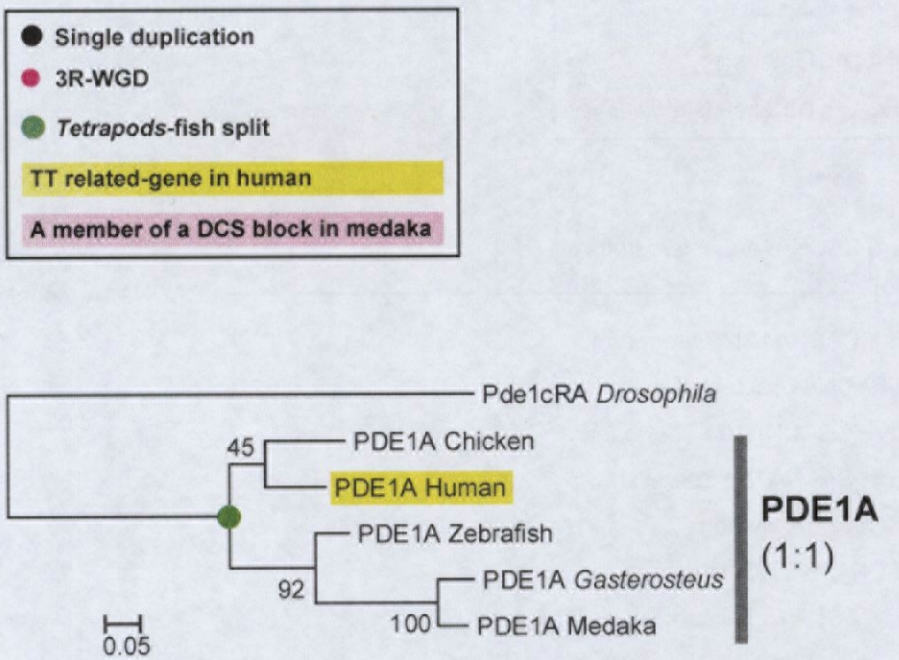

Fig. S33. A molecular phylogeny of PDE1A (phosphodiesterase 1A, calmodulin-dependent, EC:3.1.4.17), inferred from maximum-likelihood analysis (435 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

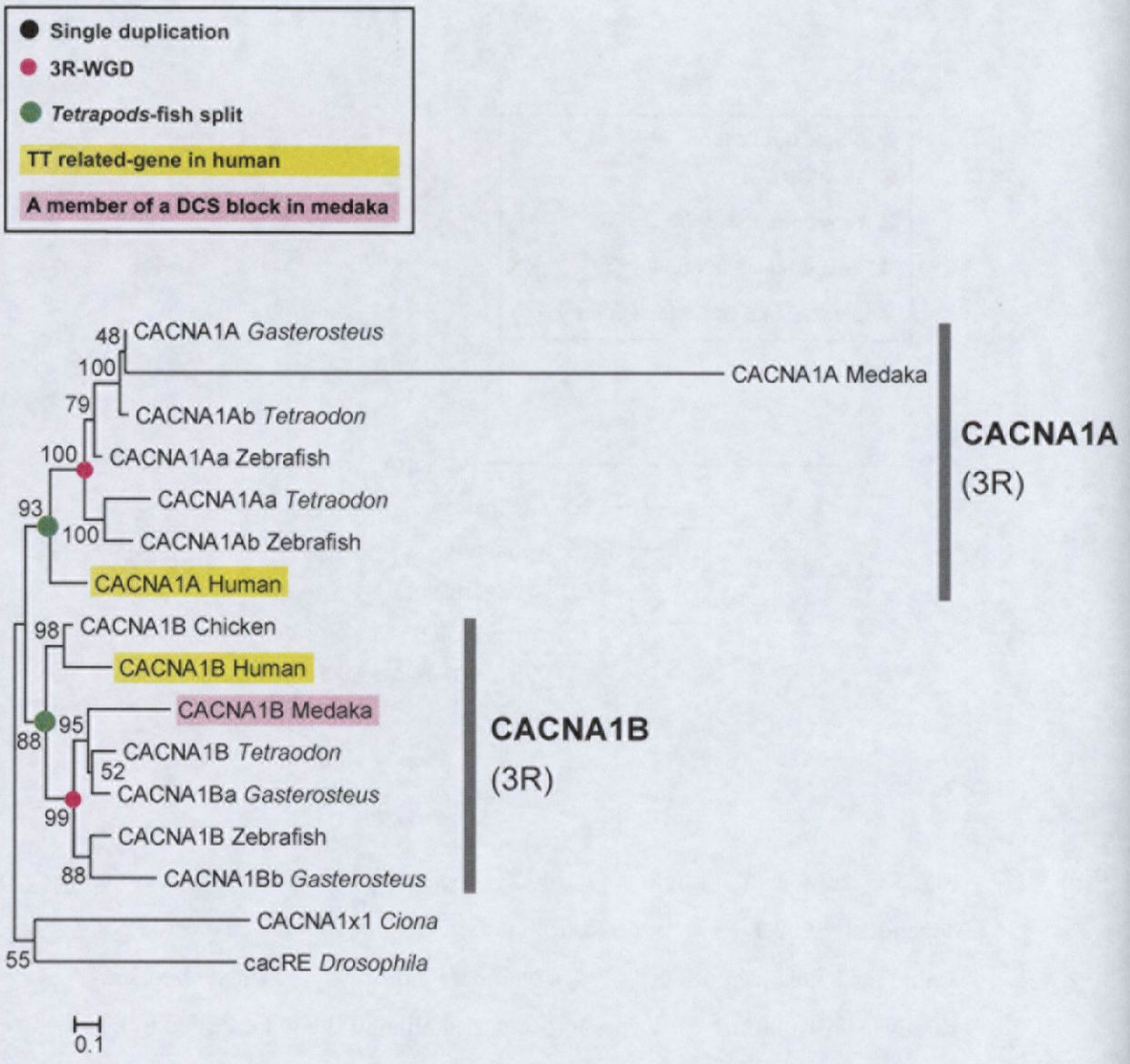

Fig. S34. A molecular phylogeny of CACN (calcium channel),, inferred from maximum-likelihood analysis (343 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

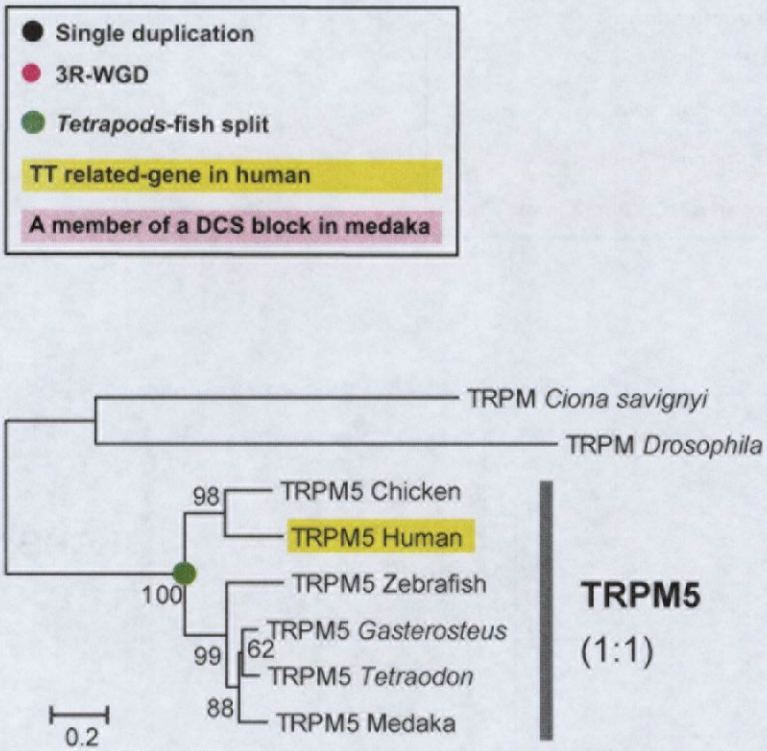

Fig. S35. A molecular phylogeny of TRPM5 (transient receptor potential cation channel, subfamily M, member 5), inferred from maximum-likelihood analysis (865 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the