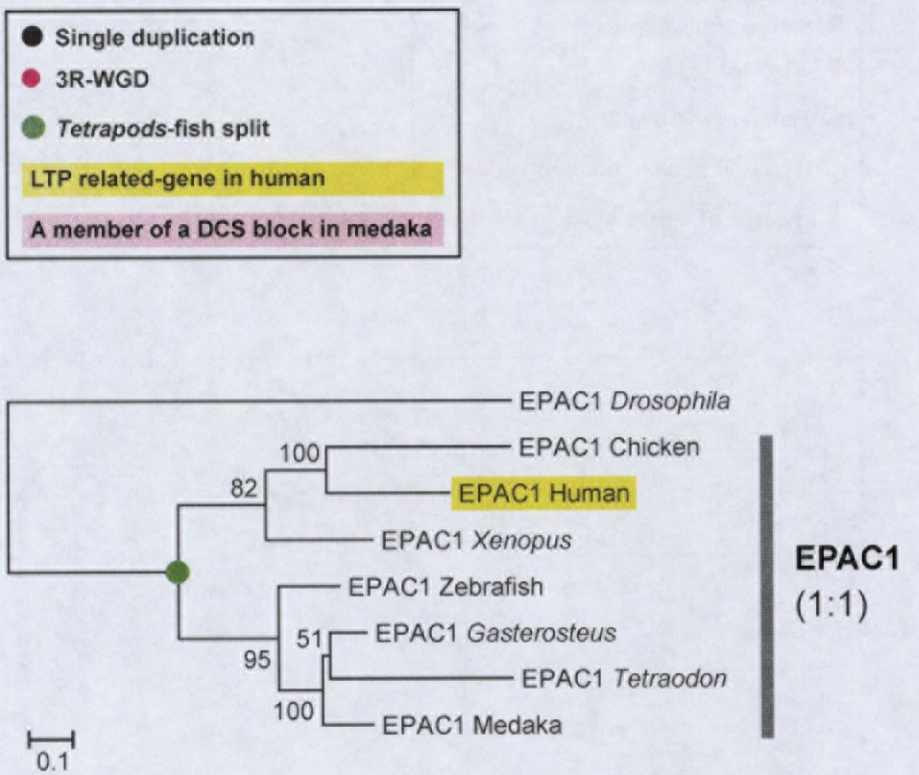

Fig. S9. A molecular phylogeny of EPAC1 (Rap guanine nucleotide exchange factor 3), inferred from maximum-likelihood analysis (701 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

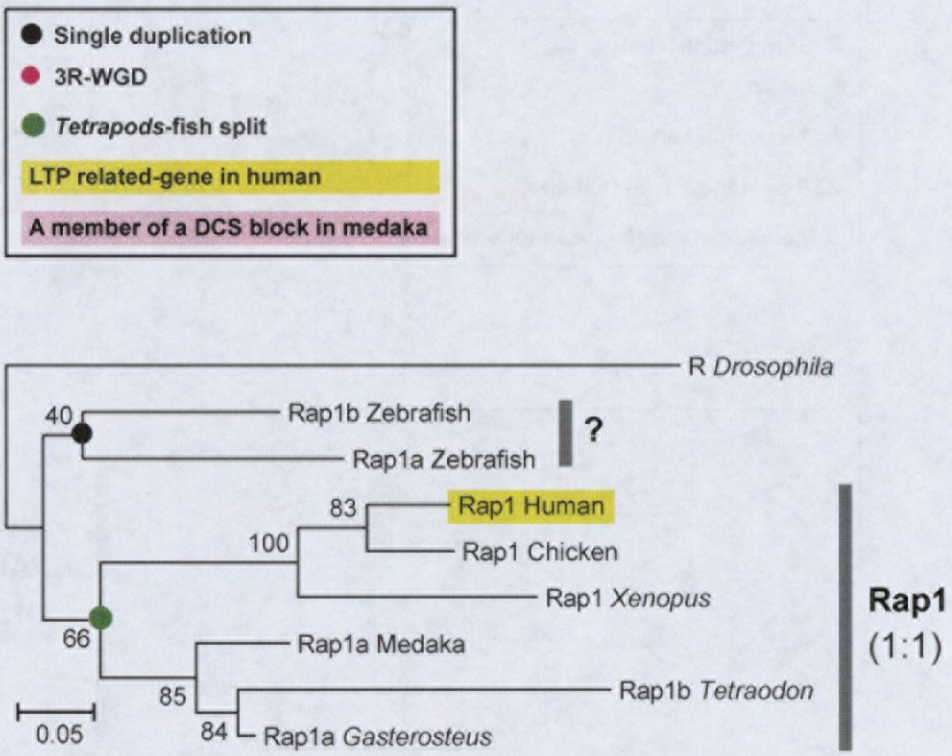

Fig. S10. A molecular phylogeny of Rap1 (or RAP1A, member of RAS oncogene family), inferred from maximum-likelihood analysis (548 nucleotide sites were used; GTR+I+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

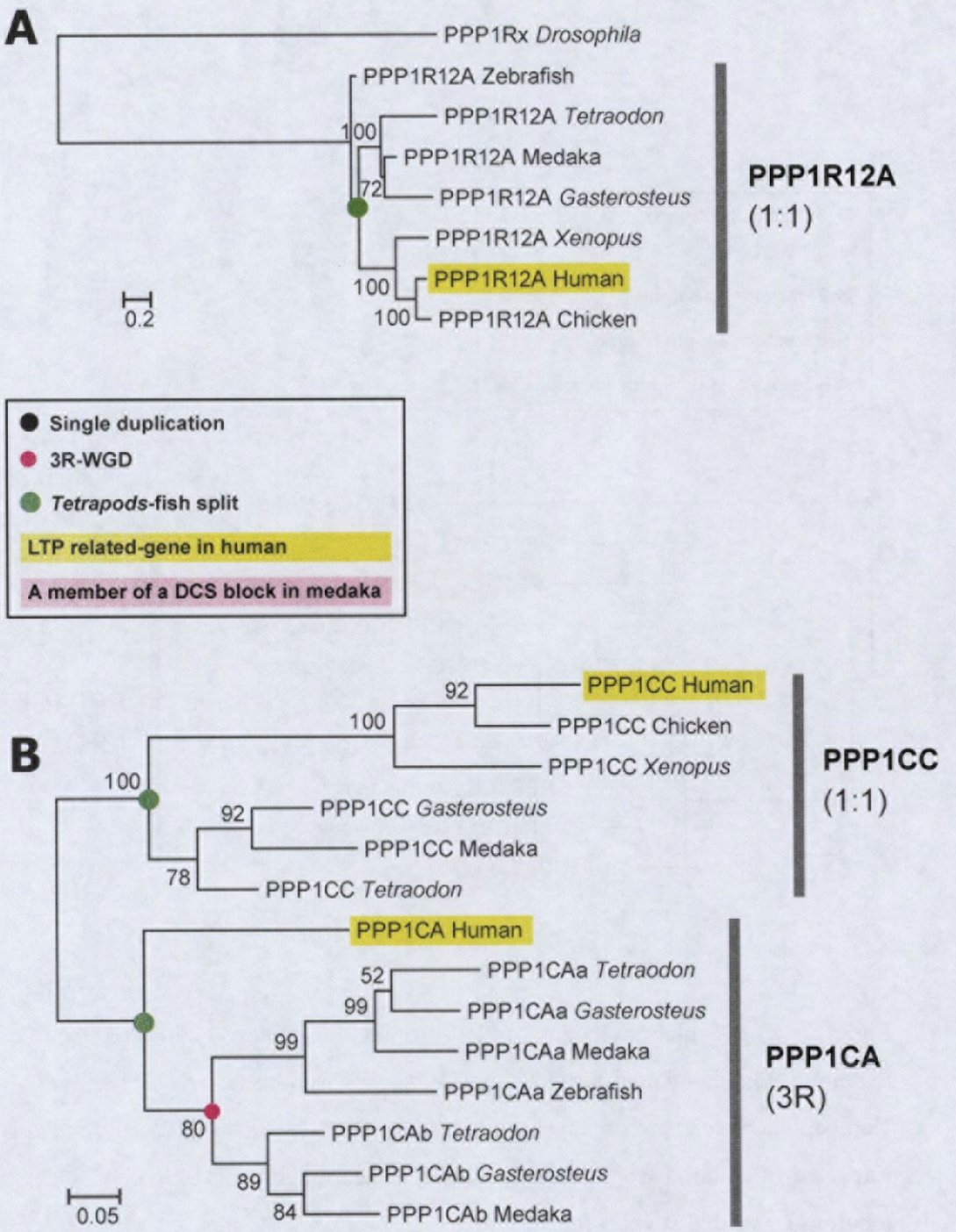

Fig. S11. A molecular phylogeny of PP1 (protein phosphatase 1), inferred from maximum-likelihood analysis (panel A: 807 amino acid sites were used with JTT+Γ; panel B: 909 nucleotide sites were used with TrN+I+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

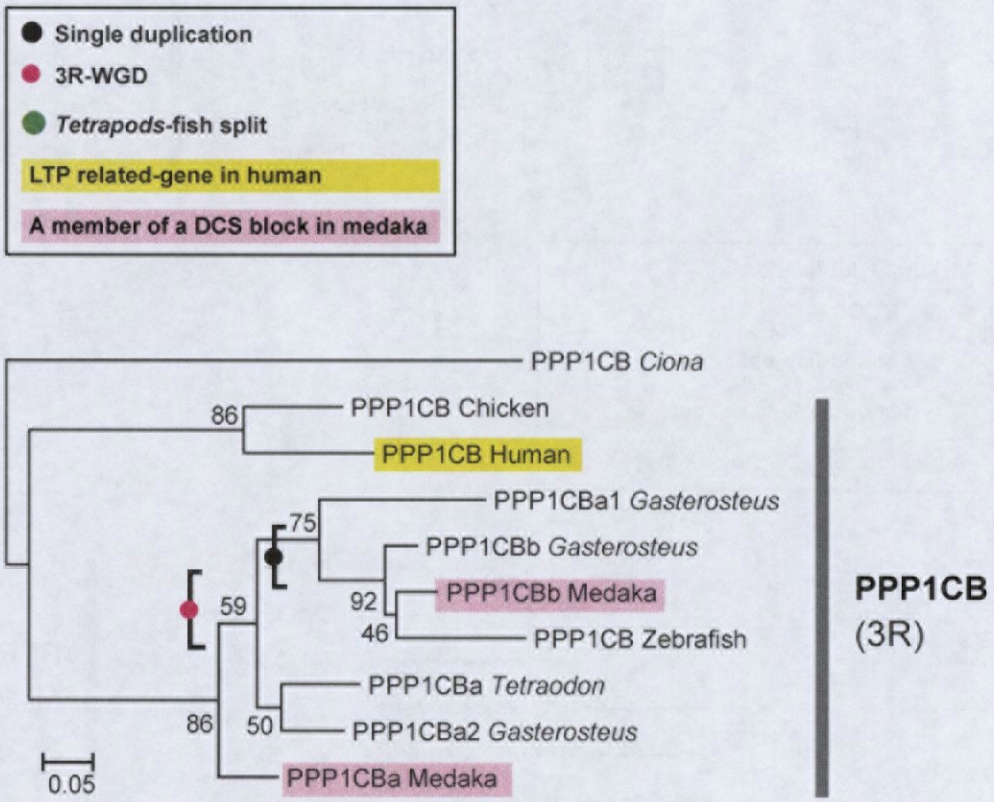

Fig. S12. A molecular phylogeny of PP1 (protein phosphatase 1), inferred from maximum-likelihood analysis (699 nucleotide sites were used; TrN+I+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

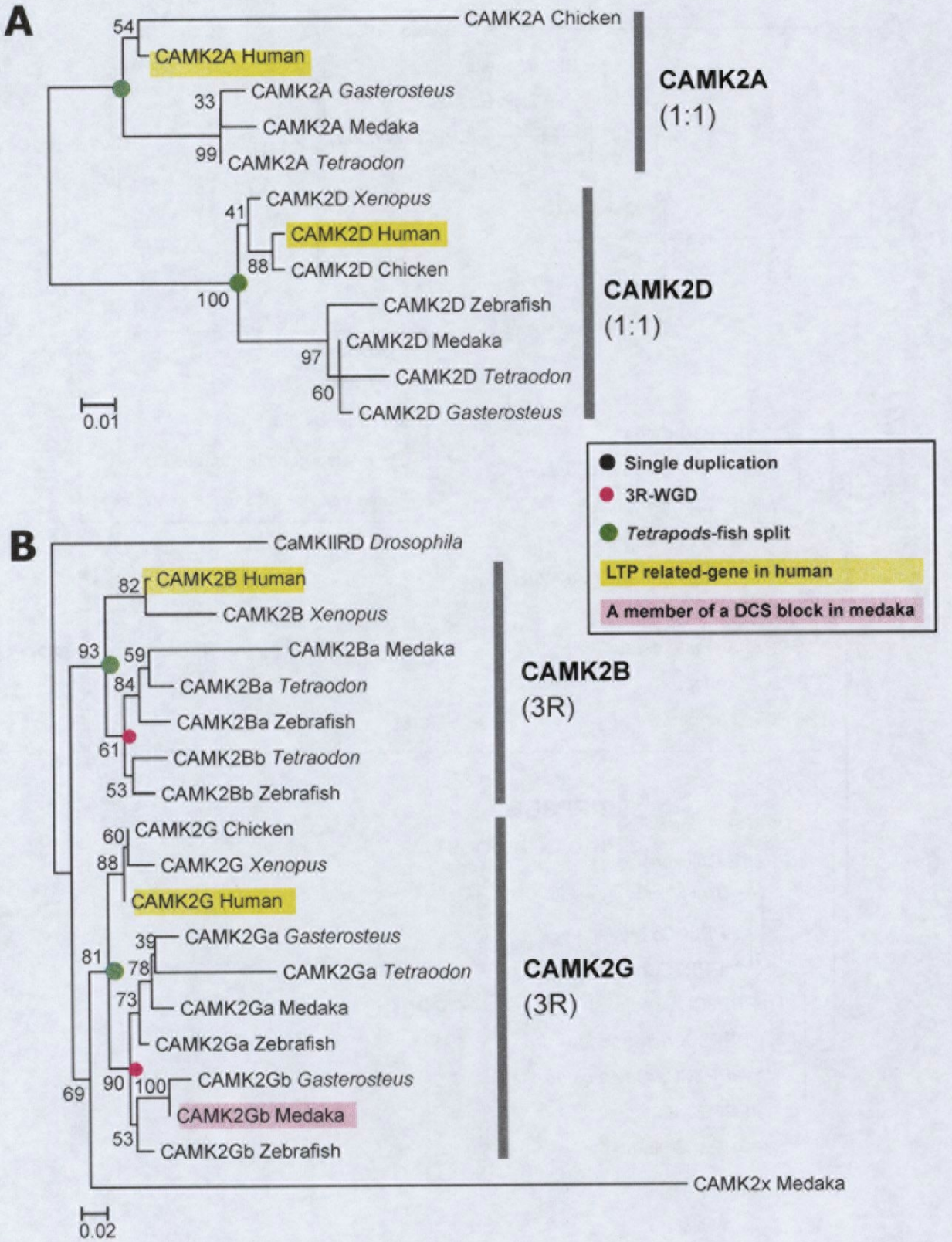

Fig. S13. A molecular phylogeny of CAMK2 (calcium/calmodulin-dependent protein kinase 2), inferred from maximum-likelihood analysis (panel A: 289 amino acid sites were used with JTT+Γ; panel B: 317 amino acid sites were used with JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

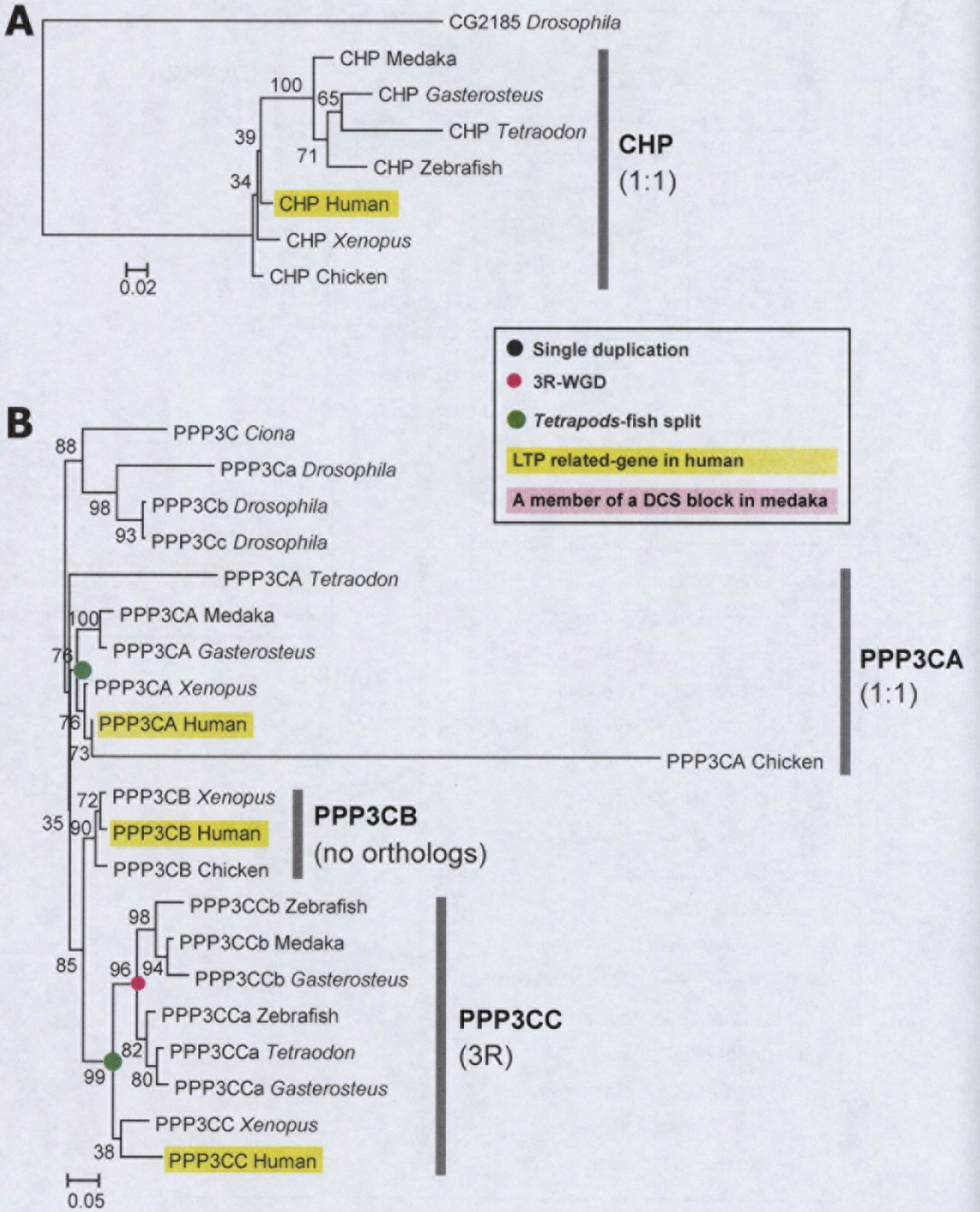

Fig. S14. A molecular phylogeny of CaN (calcium binding protein P22 and protein phosphatase 3), inferred from maximum-likelihood analysis (panel A: 186 amino acid sites were used with JTT+Γ; panel B: 352 amino acid sites were used with JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

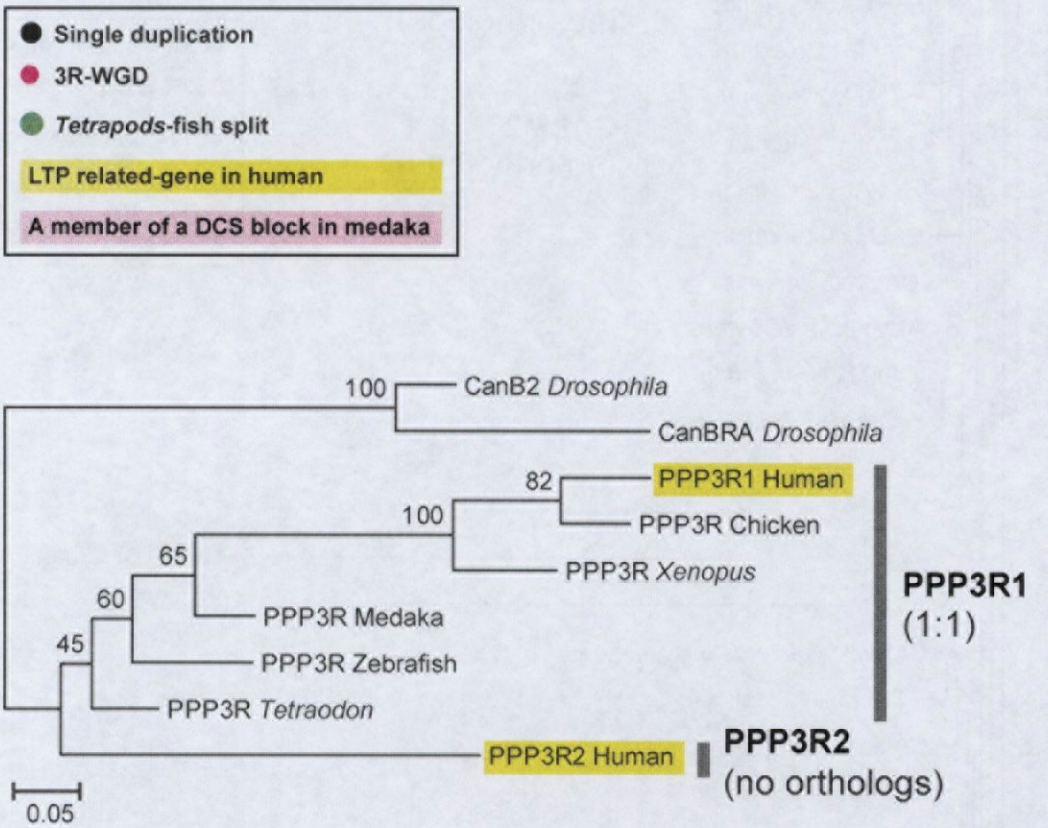

Fig. S15. A molecular phylogeny of CaN (calcium binding protein P22 and protein phosphatase 3), inferred from maximum-likelihood analysis (494 nucleotide sites were used; TrN+I+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

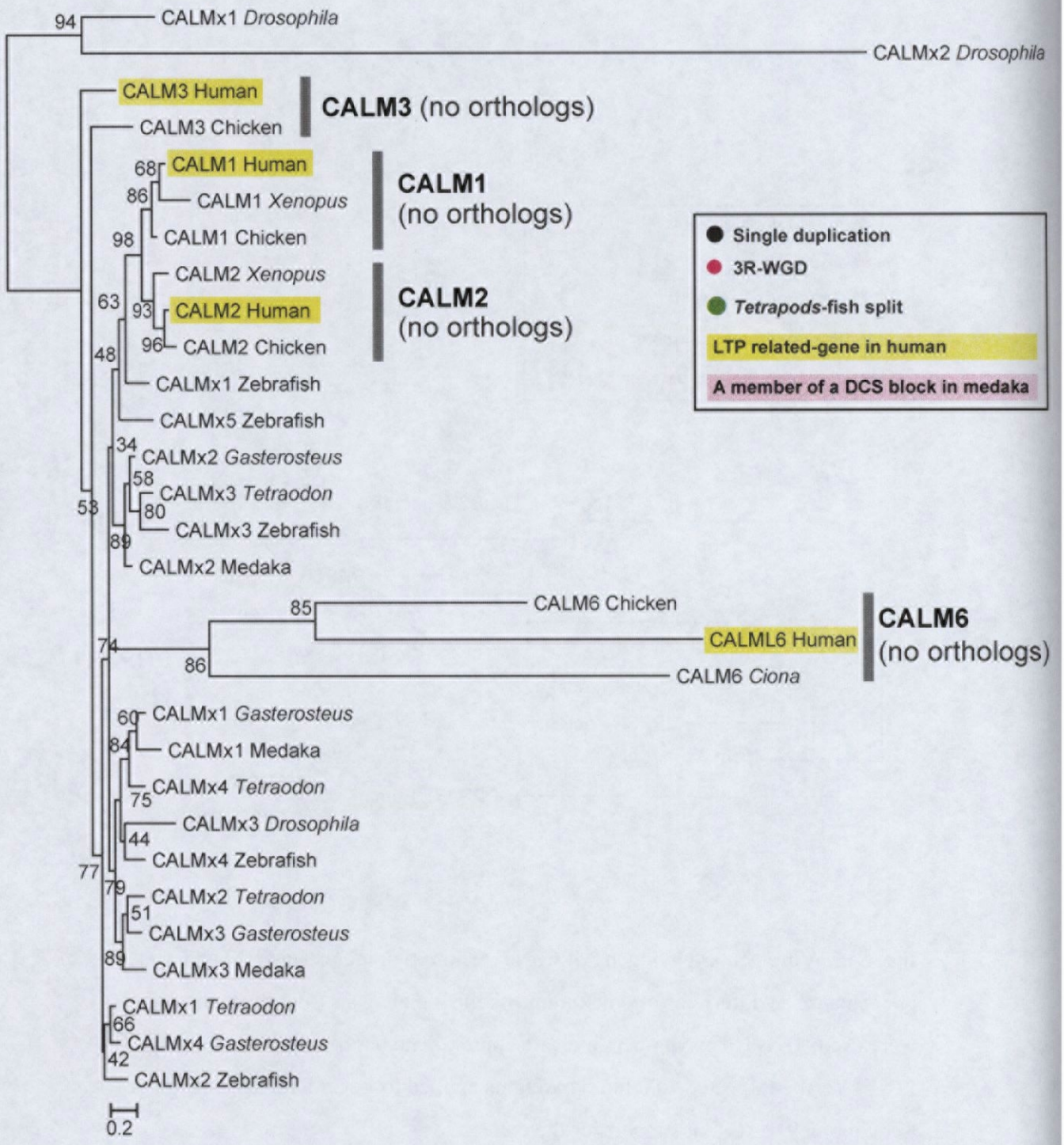

Fig. S16. A molecular phylogeny of CAM (calmodulin), inferred from maximum-likelihood analysis (408 nucleotide sites were used; TrN+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

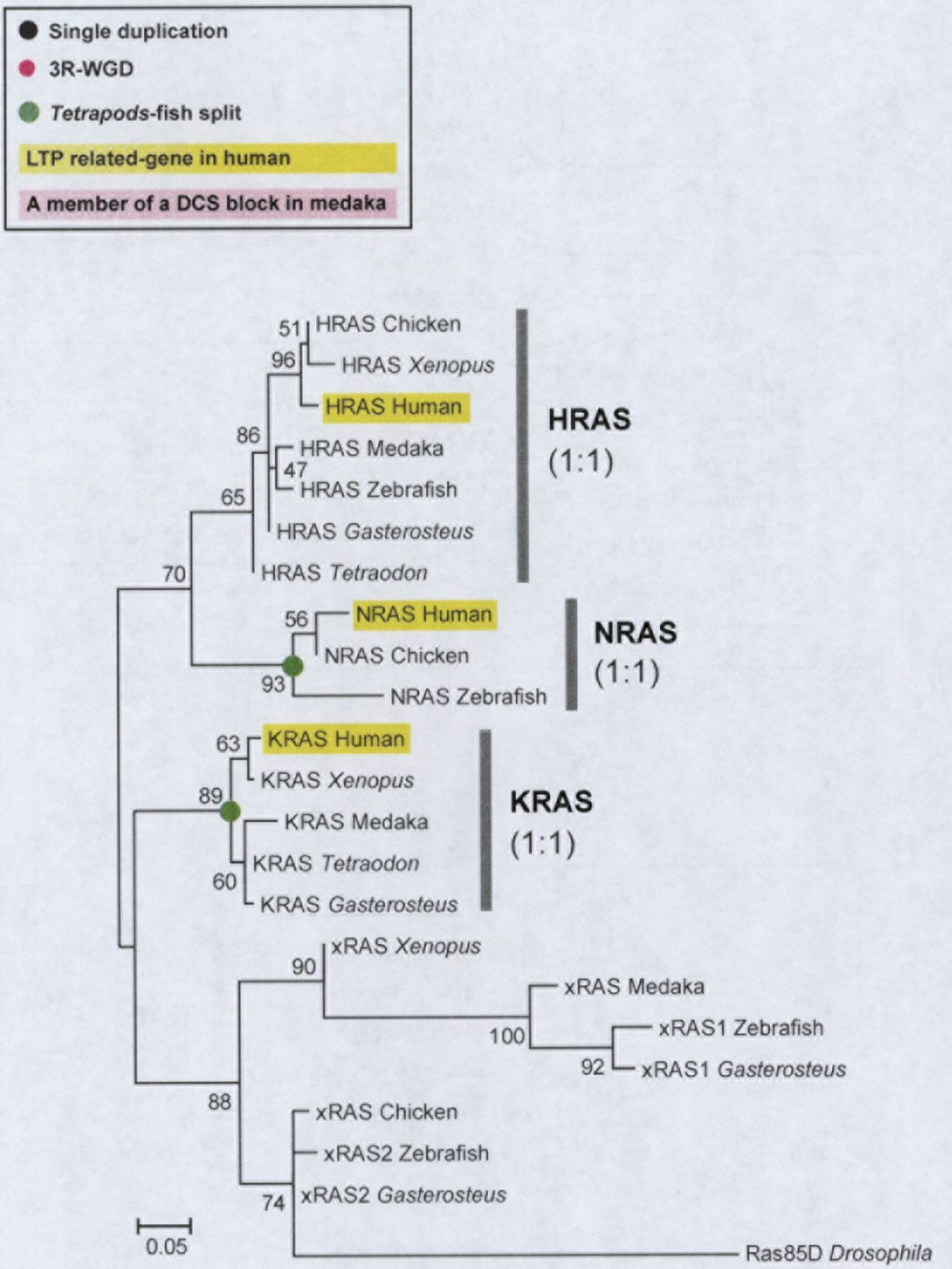

Fig. S17. A molecular phylogeny of Ras, inferred from maximum-likelihood analysis (182 amino acid sites were used; JTT+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.