

Fig. S36. A molecular phylogeny of KCN (or KCNB1, potassium voltage-gated channel, Shab-related subfamily, member 1), inferred from maximum-likelihood analysis (337 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

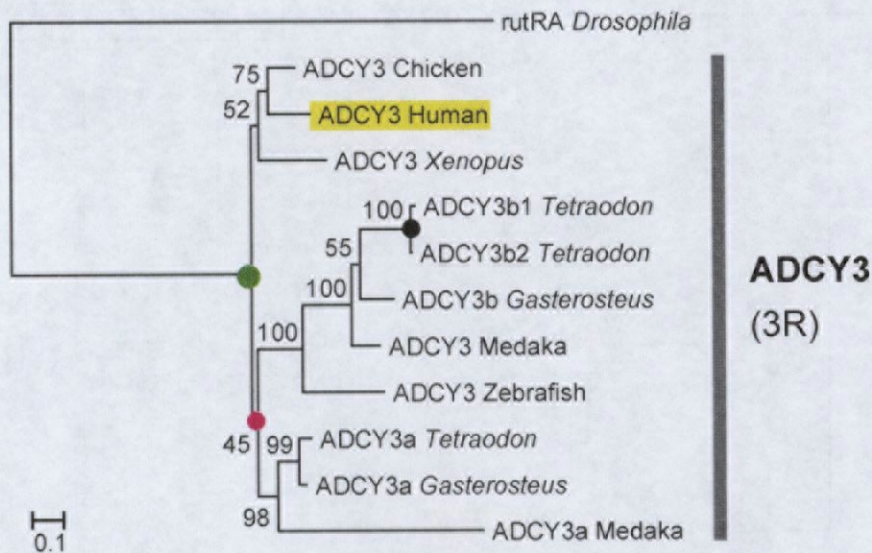
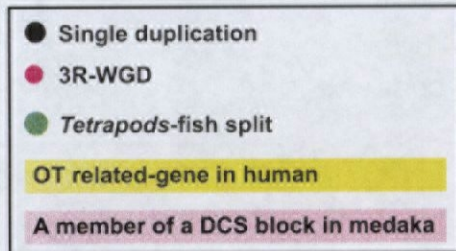


Fig. S37. A molecular phylogeny of AC3 (or ADCY3, adenylate cyclase 3, EC:4.6.1.1), inferred from maximum-likelihood analysis (549 amino acid sites were used; JTT+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

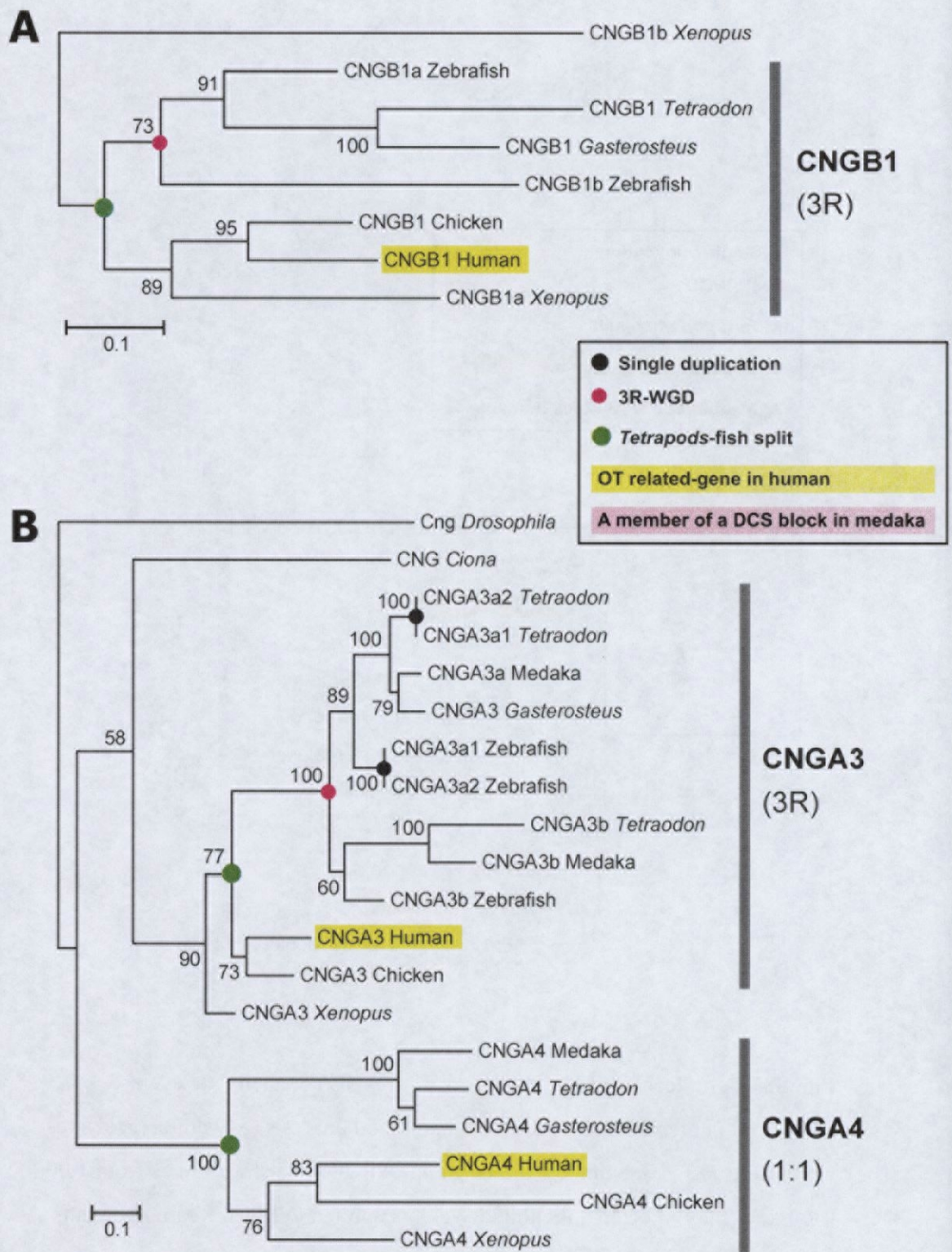


Fig. S38. A molecular phylogeny of CNGA and CNGB (cyclic nucleotide gated channel alpha and beta), inferred from maximum-likelihood analysis (panel A: 460 amino acid sites were used with WAG+ Γ ; panel B: 390 amino acid sites were used with JTT+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

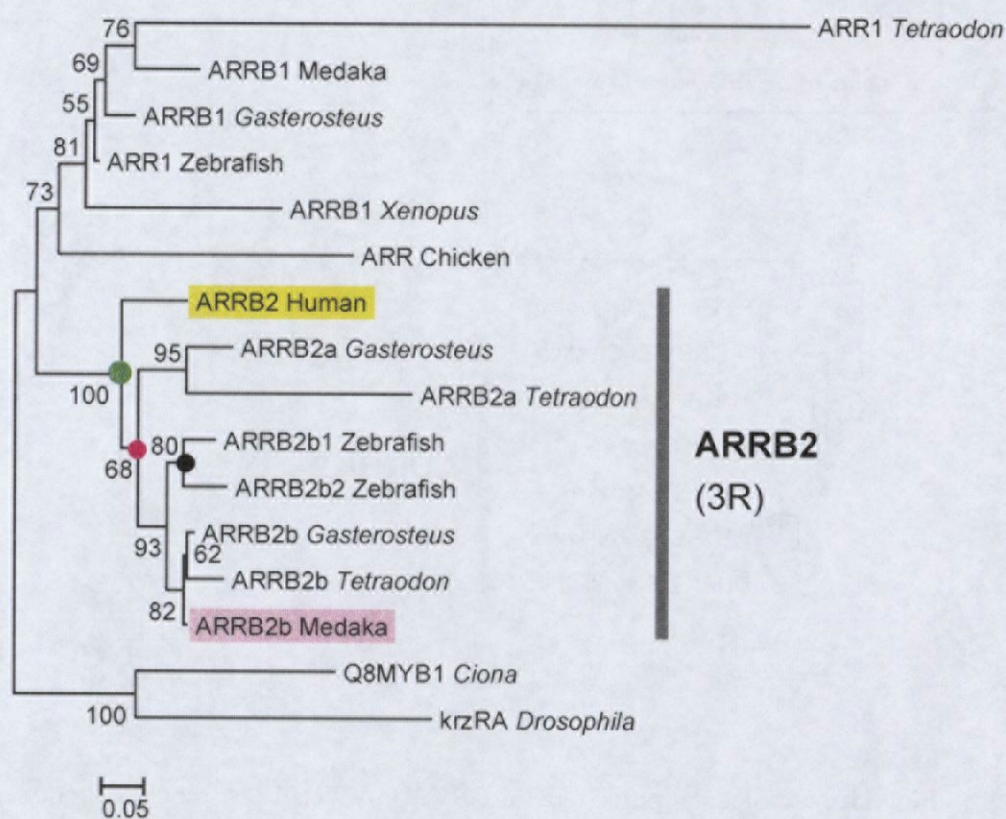
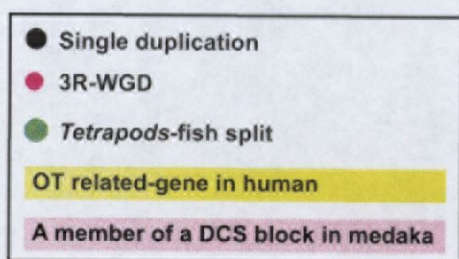


Fig. S39. A molecular phylogeny of ARRB2 (arrestin, beta 2), inferred from maximum-likelihood analysis (297 amino acid sites were used; JTT+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

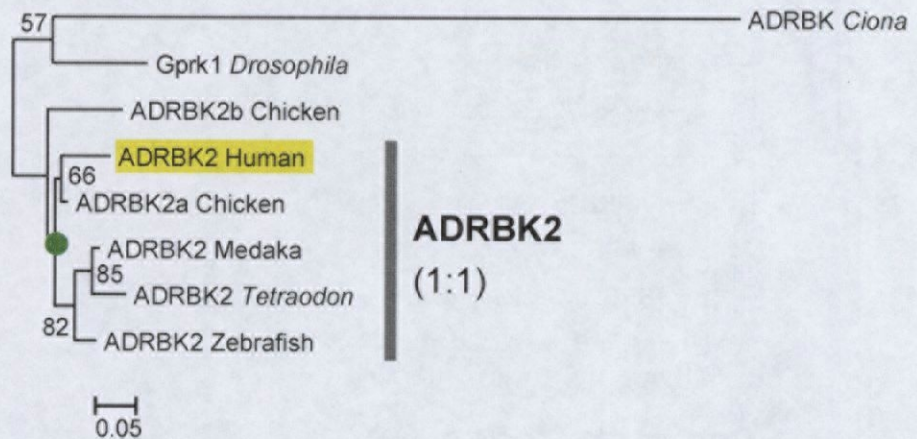
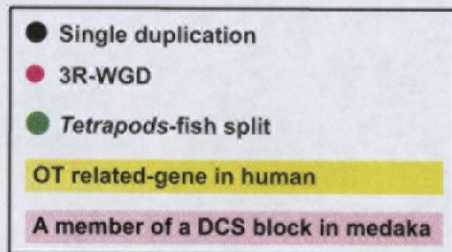


Fig. S40. A molecular phylogeny of GRK (or ADRBK2, adrenergic, beta, receptor kinase 2), inferred from maximum-likelihood analysis (147 amino acid sites were used; JTT+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

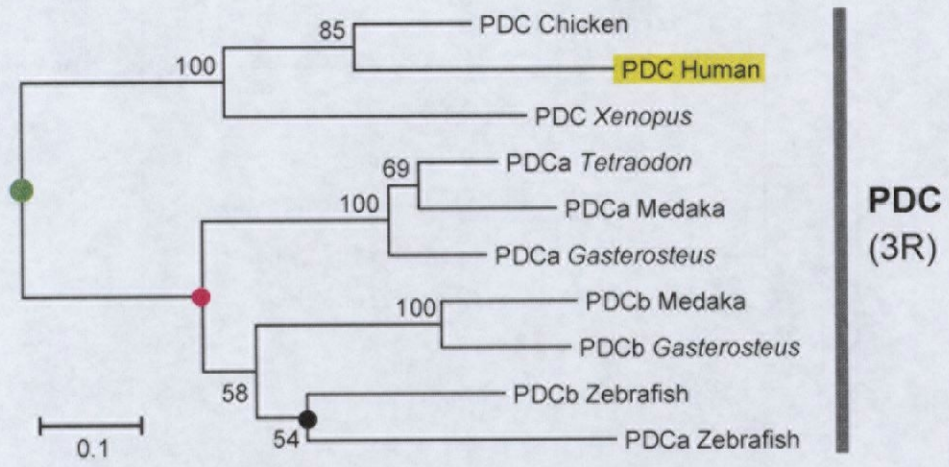
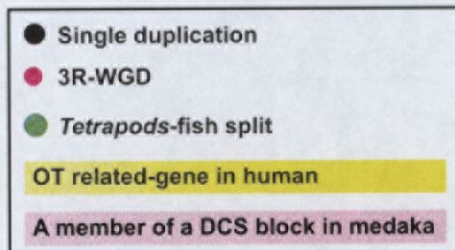


Fig. S41. A molecular phylogeny of PDC (or Phd, phosducin), inferred from maximum-likelihood analysis (638 nucleotide sites were used; TrN+I+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

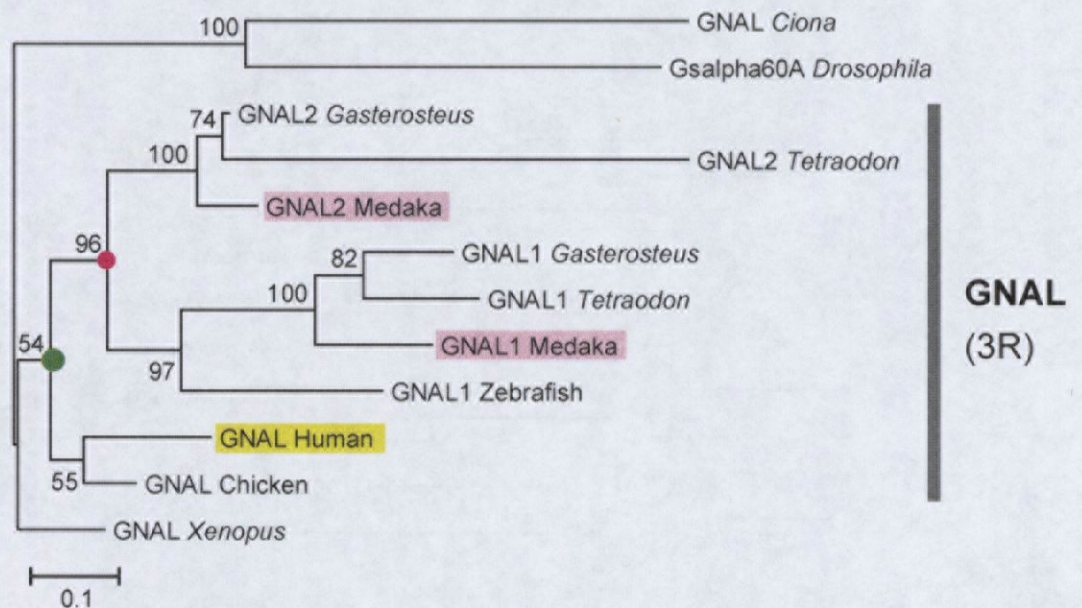
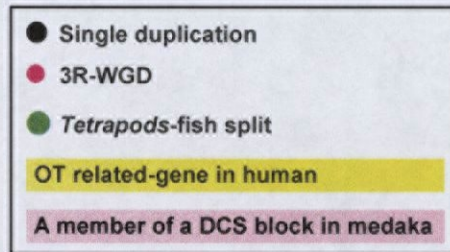


Fig. S42. A molecular phylogeny of GNAL(or Golf, guanine nucleotide binding protein [G protein], alpha activating activity polypeptide, olfactory type), inferred from maximum-likelihood analysis (790 nucleotide sites were used; TrN+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree

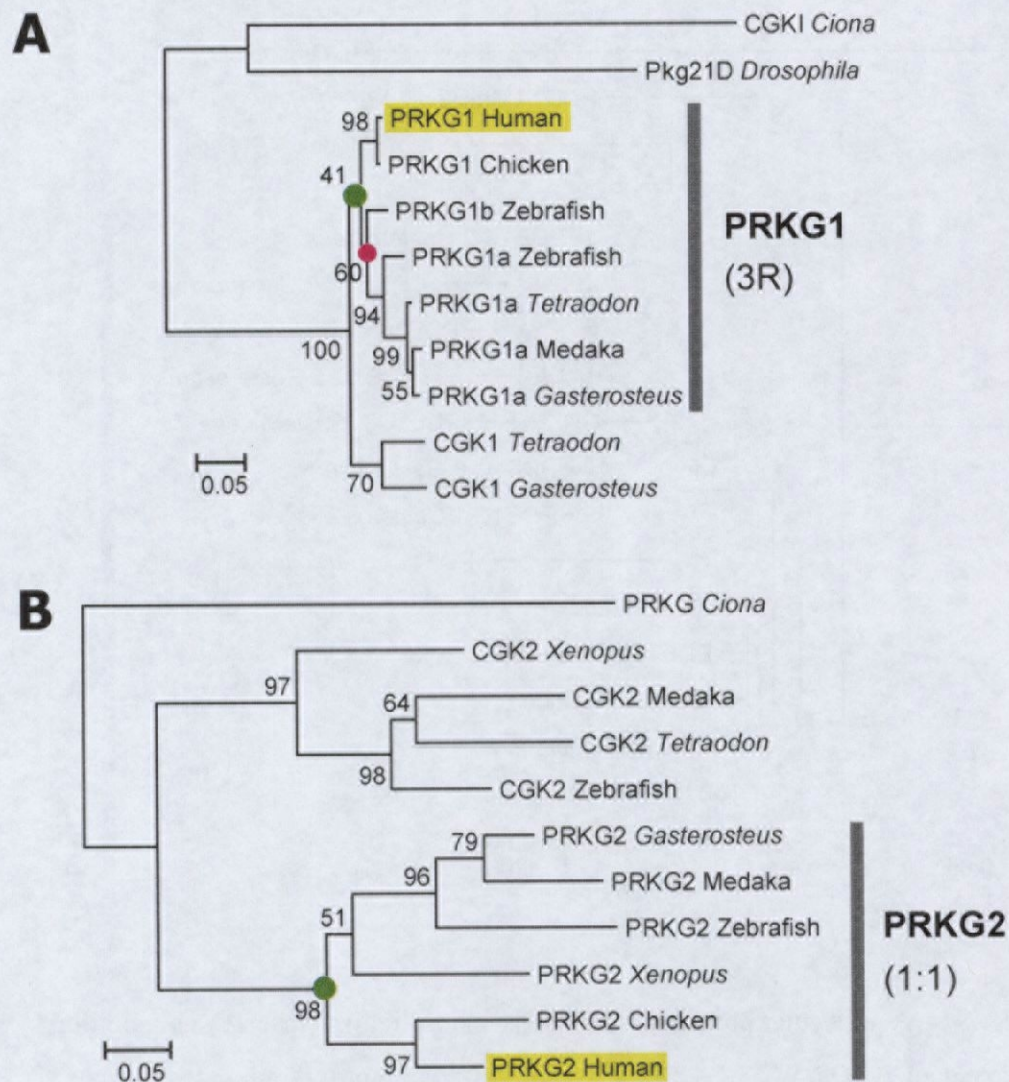
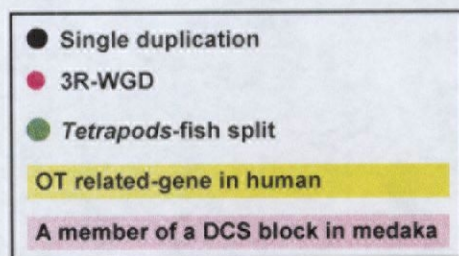


Fig. S43. A molecular phylogeny of PKG (protein kinase, cGMP-dependent, type I and type II), inferred from maximum-likelihood analysis (panel A: 327 amino acid sites were used with JTT+ Γ ; panel B: 291 amino acid sites were used with JTT+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

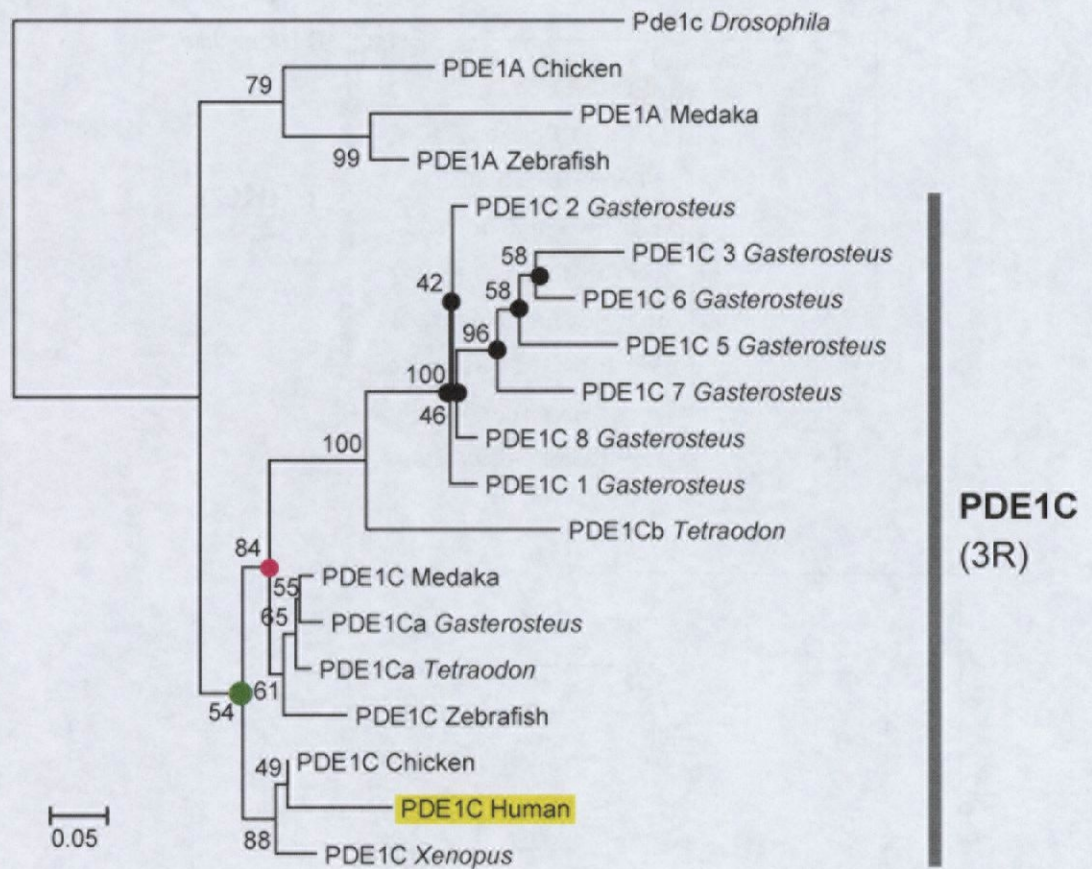
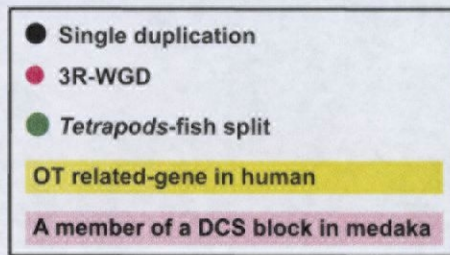


Fig. S44. A molecular phylogeny of PDE1C phosphodiesterase 1C, calmodulin-dependent 70kDa, EC:3.1.4.17), inferred from maximum-likelihood analysis (311 amino acid sites were used; JTT+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

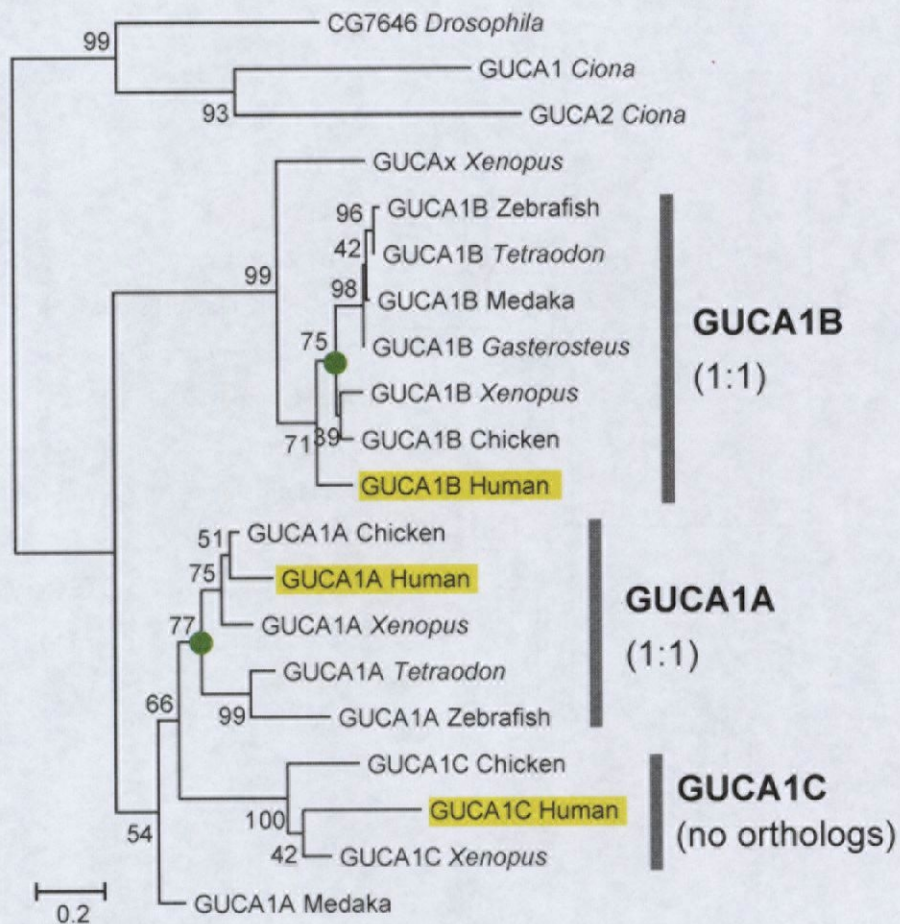
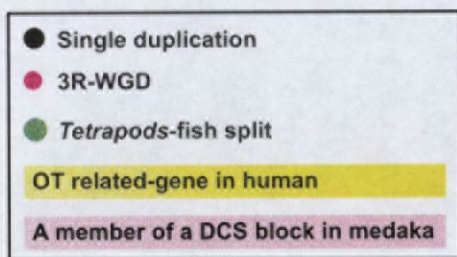


Fig. S45. A molecular phylogeny of GCAP (or GUCA, guanylate cyclase activator), inferred from maximum-likelihood analysis (139 amino acid sites were used; JTT+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.