

Fig. S46. A molecular phylogeny of pGC (or Gucy, guanylate cyclase), inferred from maximum-likelihood analysis (829 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.

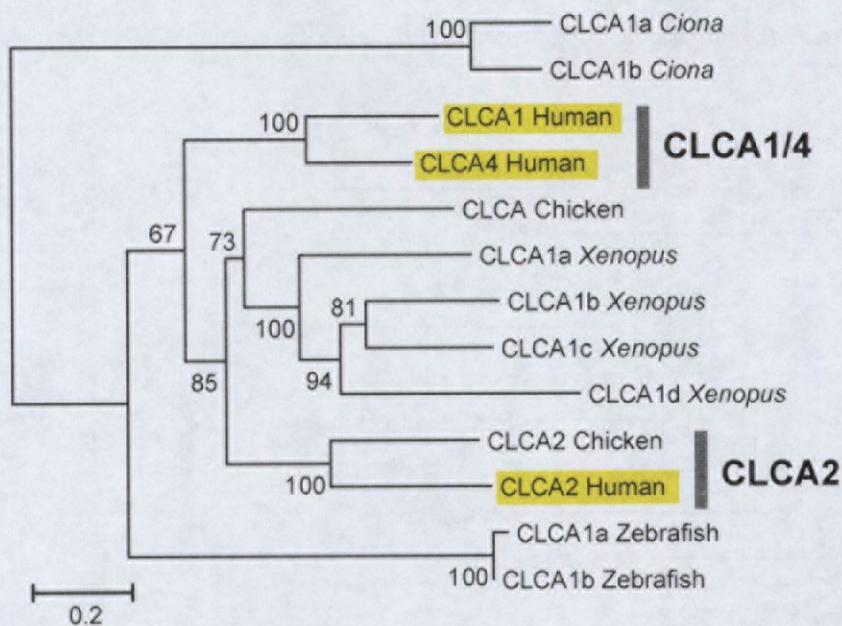
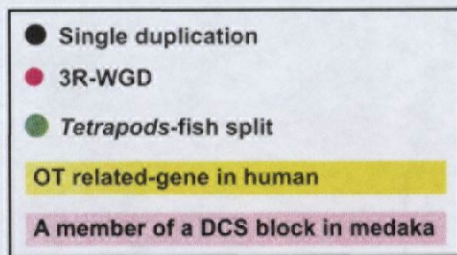


Fig. S47. A molecular phylogeny of CLCA (chloride channel, calcium activated), inferred from maximum-likelihood analysis (536 amino acid sites were used; WAG+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

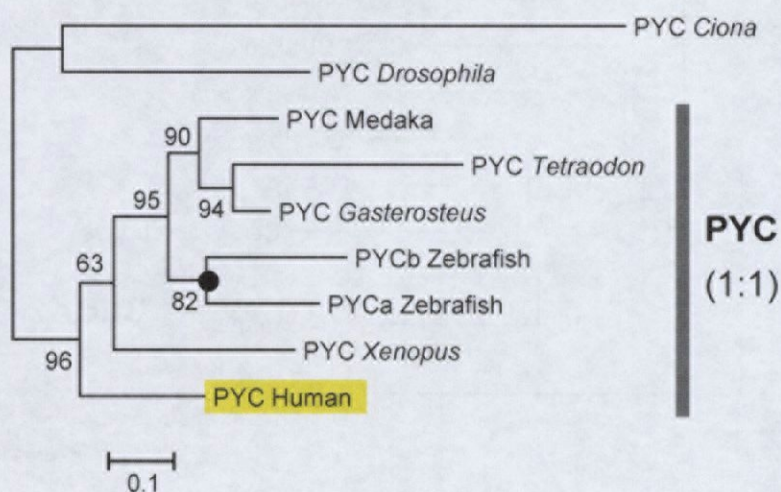
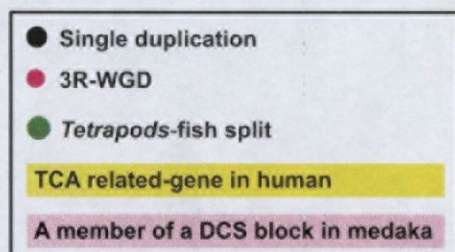


Fig. S48. A molecular phylogeny of PYC (pyruvate carboxylase, E.C. 6.4.1.1), inferred from maximum-likelihood analysis (1290 nucleotide sites were used; GTR+I+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

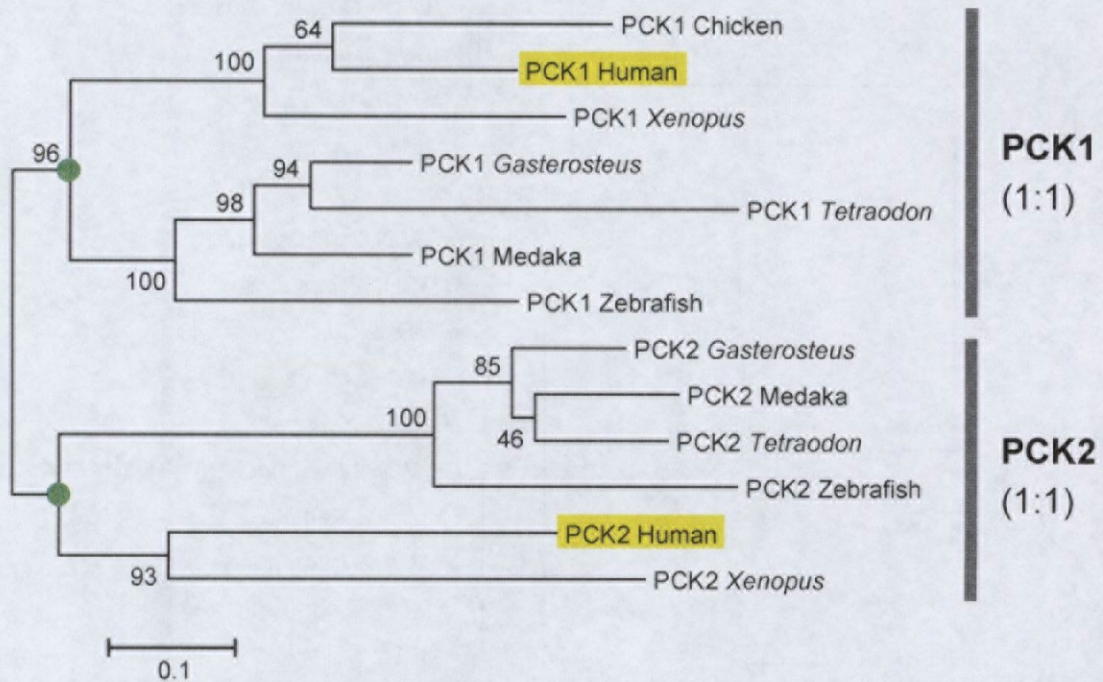
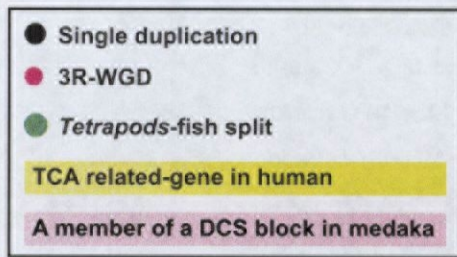


Fig. S49. A molecular phylogeny of PCK(phosphoenolpyruvate carboxykinase, soluble, E.C. 4.1.1.32), inferred from maximum-likelihood analysis (1810 nucleotide sites were used; GTR+I+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the

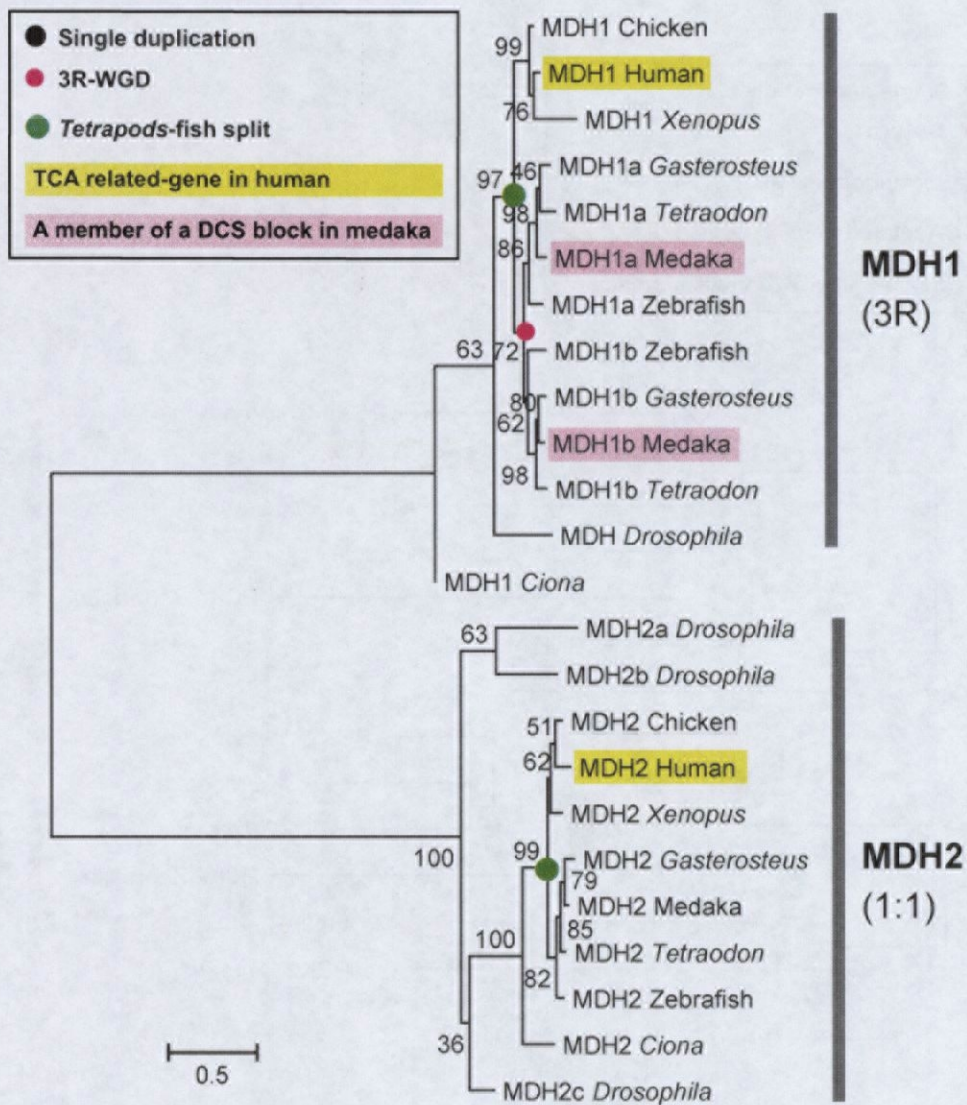


Fig. S50. A molecular phylogeny of MDH (malate dehydrogenase 1, NAD, soluble, EC:1.1.1.37), inferred from maximum-likelihood analysis (245 amino acid sites were used; WAG+I). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

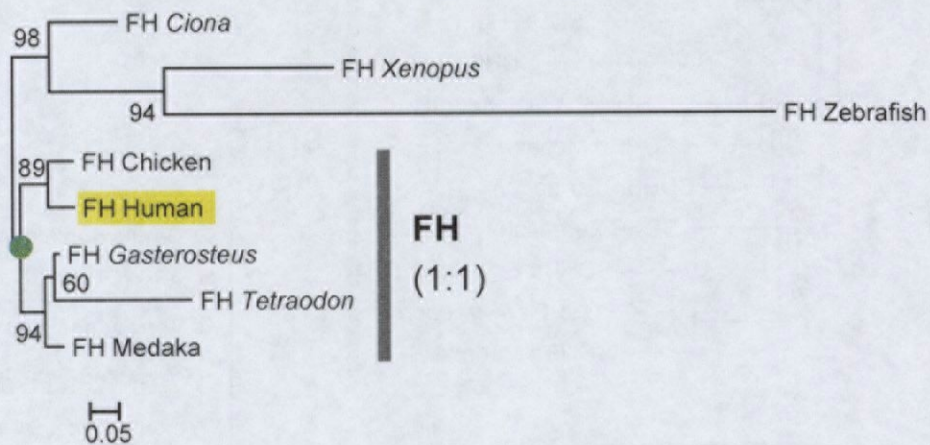
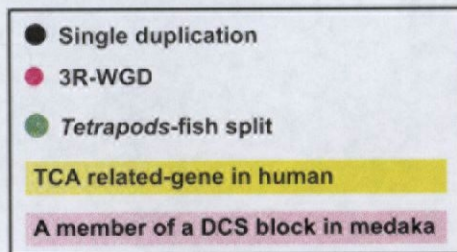


Fig. S51. A molecular phylogeny of FH (fumarate hydratase, E.C. 4.2.1.2), inferred from maximum-likelihood analysis (361 amino acid sites were used; WAG+Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

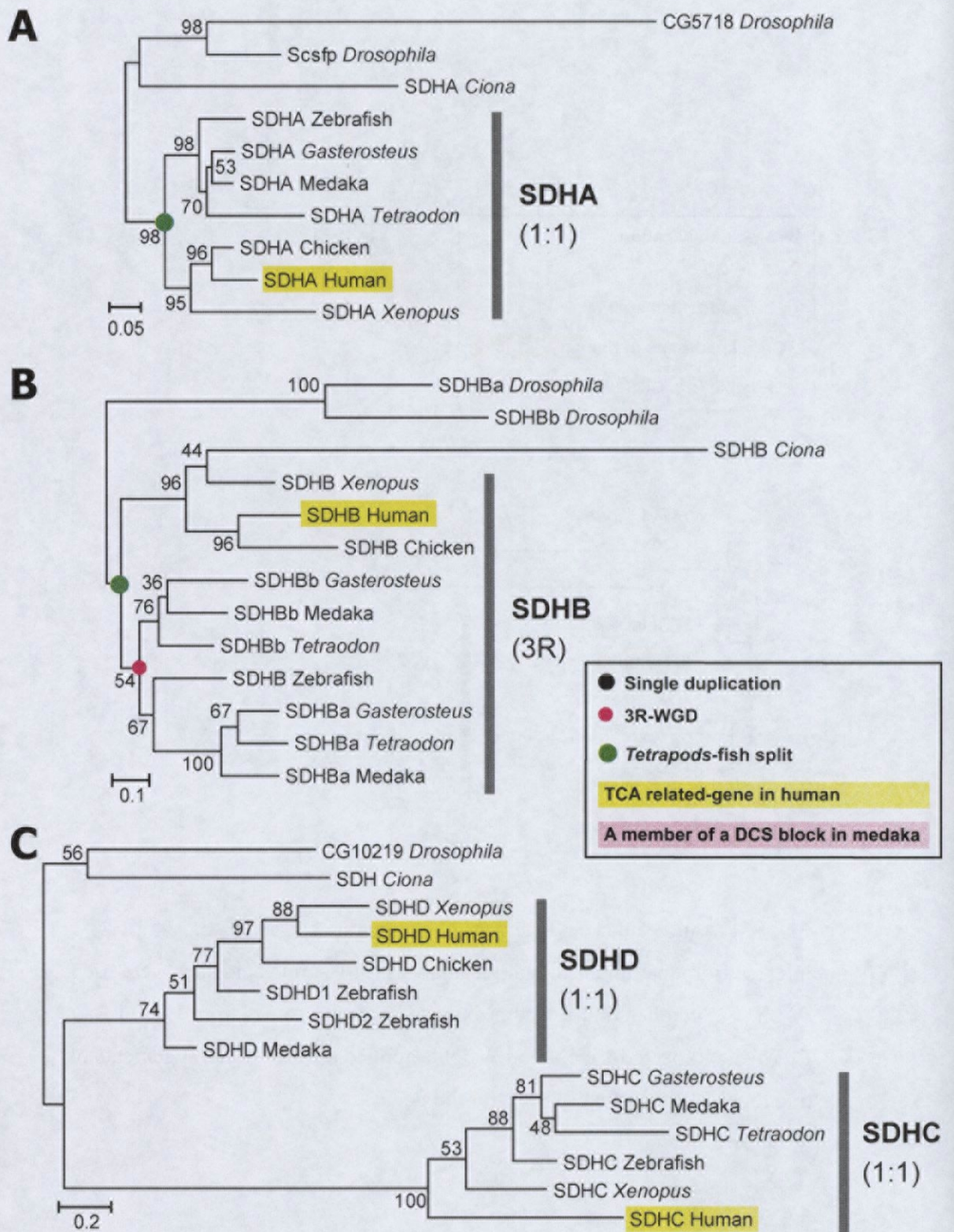


Fig. S52. A molecular phylogeny of SDH (succinate dehydrogenase complex, E.C. 1.3.5.1), inferred from maximum-likelihood analysis (panel A: 635 amino acid sites were used with WAG+ Γ ; panel B: 744 nucleotide sites were used with TrN+H+ Γ ; panel C: 343 nucleotide sites were used with HKY+ Γ). Numbers 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.

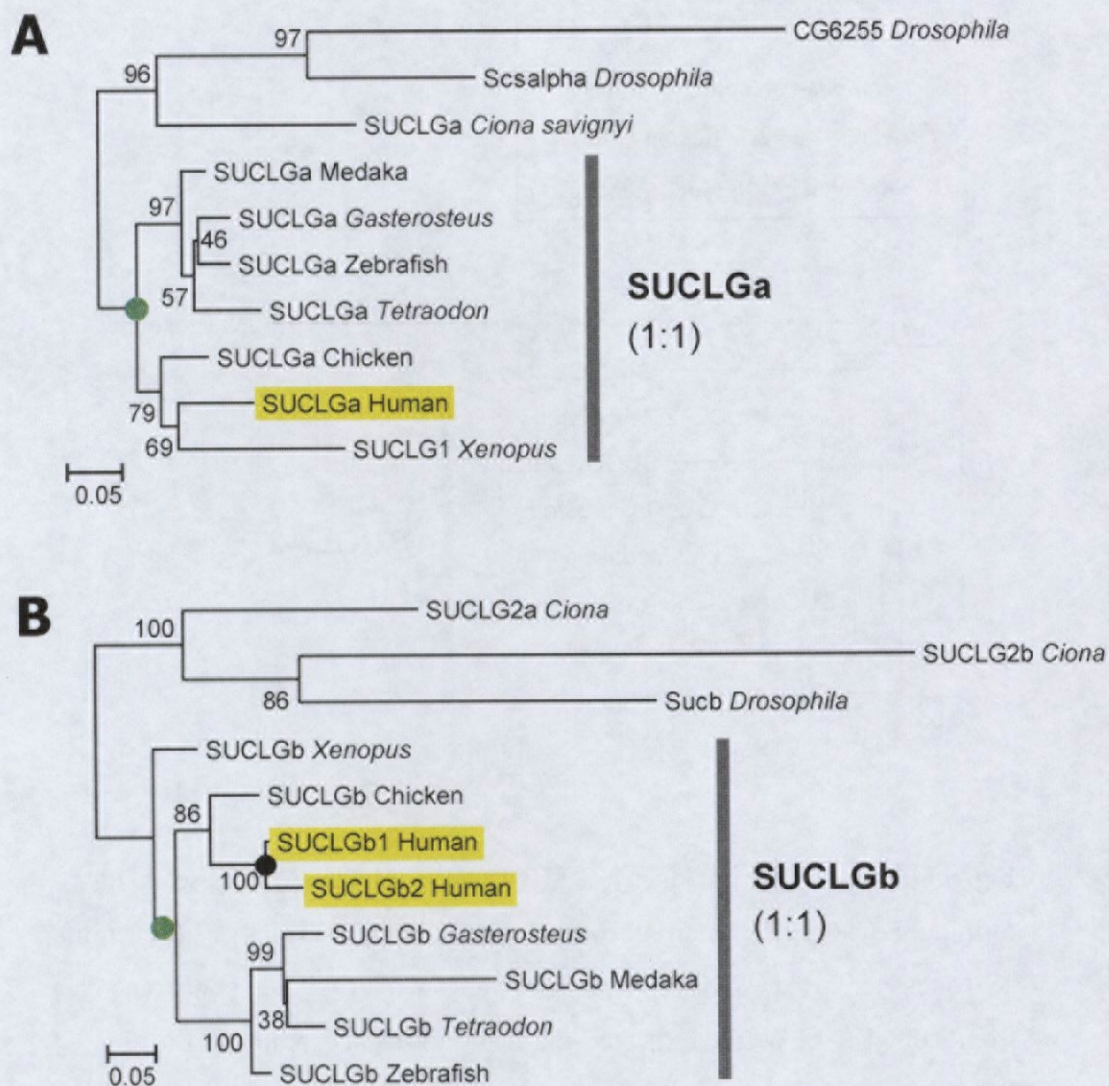
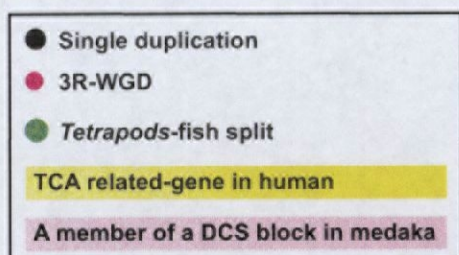


Fig. S53. A molecular phylogeny of SUCLG (succinate-CoA ligase, GDP-forming, E.C. 6.2.1.4), inferred from maximum-likelihood analysis (panel A: 298 amino acid sites were used with WAG+ Γ ; panel B: 345 amino acid sites were used with WAG+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

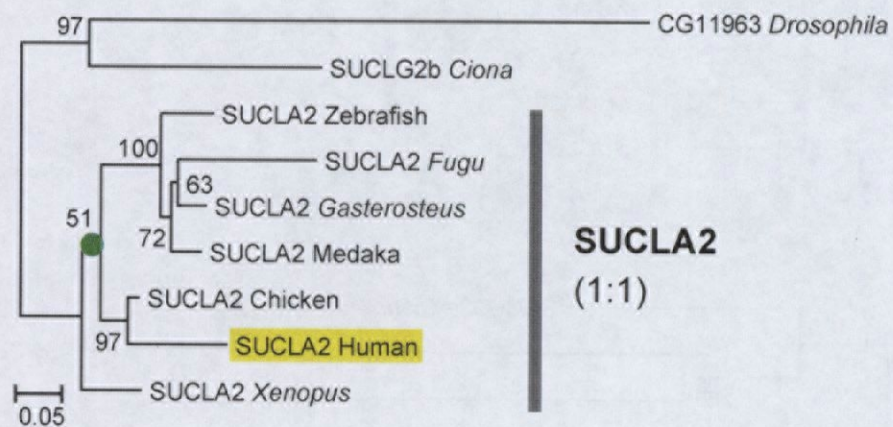
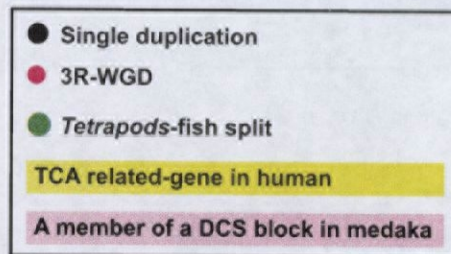


Fig. S54. A molecular phylogeny of SUCLA2 (succinate-CoA ligase, ADP-forming, E.C. 6.2.1.5), inferred from maximum-likelihood analysis (419 amino acid sites were used; WAG+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.

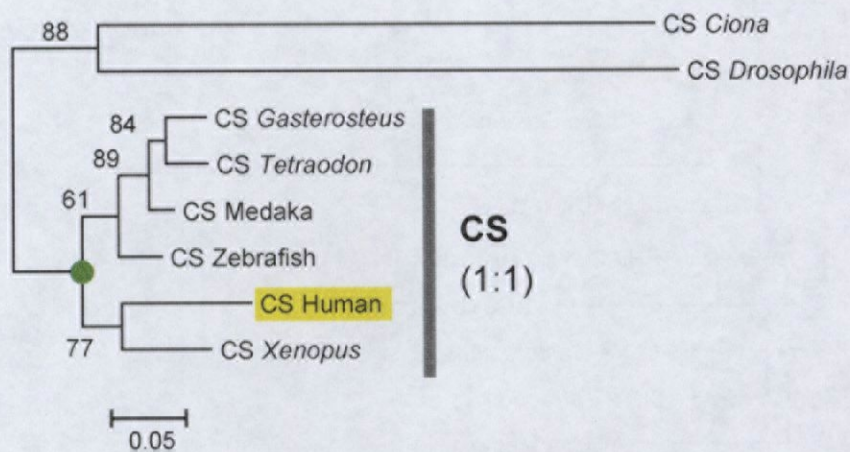
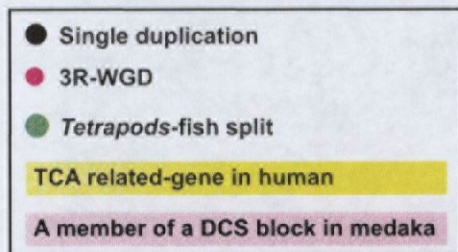


Fig. S55. A molecular phylogeny of CS (citrate synthase, E.C. 2.3.3.1), inferred from maximum-likelihood analysis (461 amino acid sites were used; WAG+ Γ). Numbers indicate approximate bootstrap values from 1,000 LR-ELW (the Expected-Likelihood Weights applied to Local Rearrangements of tree topology) tests that support for the nodes.