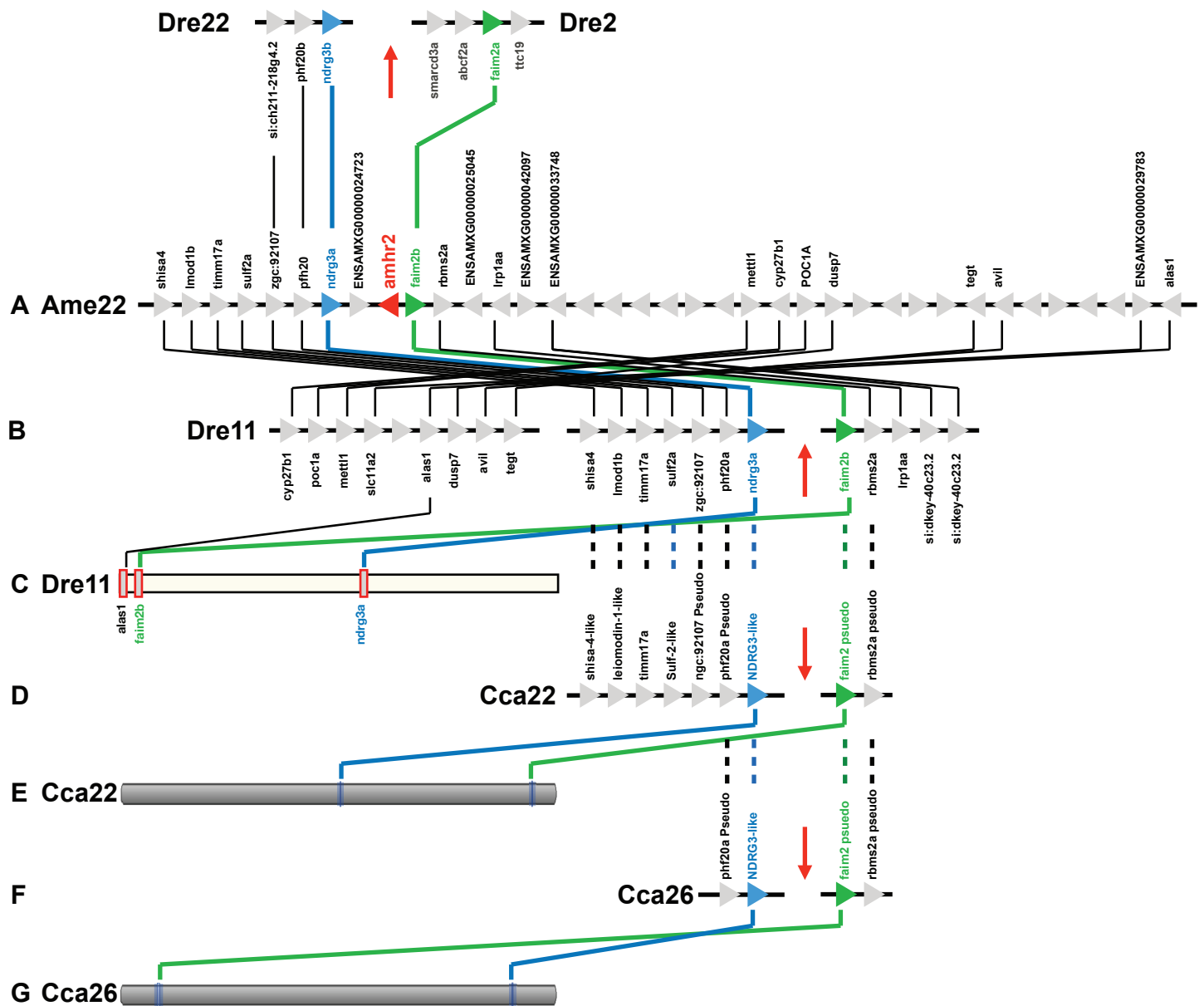


Figure S2



Supplemental Figure S2. Conserved syntenies and loss of the zebrafish *amhr2* gene. A. A portion of chromosome 22 (Ame22) from the cavefish *Astyanax mexicanus* containing *amhr2*. B. Three portions of zebrafish chromosome 11 (Dre11) containing regions with conserved syntenies to the *amhr2*-containing portion of the cavefish genome showing that the breakpoint of a chromosome rearrangement lies at the predicted location of *amhr2*. The portion of the figure above part A shows that paralogs of the zebrafish genome from Dre22 and Dre2 contain ohnologs derived from the teleost genome duplication and also lack *amhr2*. C. The three regions of the zebrafish genome shown in in part B occupy different positions along the entire chromosome Dre11. D. Portions of the common carp (*Cyprinus carpio*) genome on two parts of Cca22 with orthology to the *amhr2*-containing part of cavefish, which are broken at the expected site of the *amhr2* gene as in zebrafish. E. Positions of regions shown in part D on chromosome Cca22. F. The duplicated region from the carp genome duplication event co-orthologous to zebrafish chromosome Dre11. G. Positions of regions shown in part F on chromosome Cca22. Results show that *amhr2* loss occurred associated with a chromosome rearrangement breakpoint that is a shared feature of cypriniforms that occurred after cypriniform otophysans diverged from characiform and siluriform otophysans.