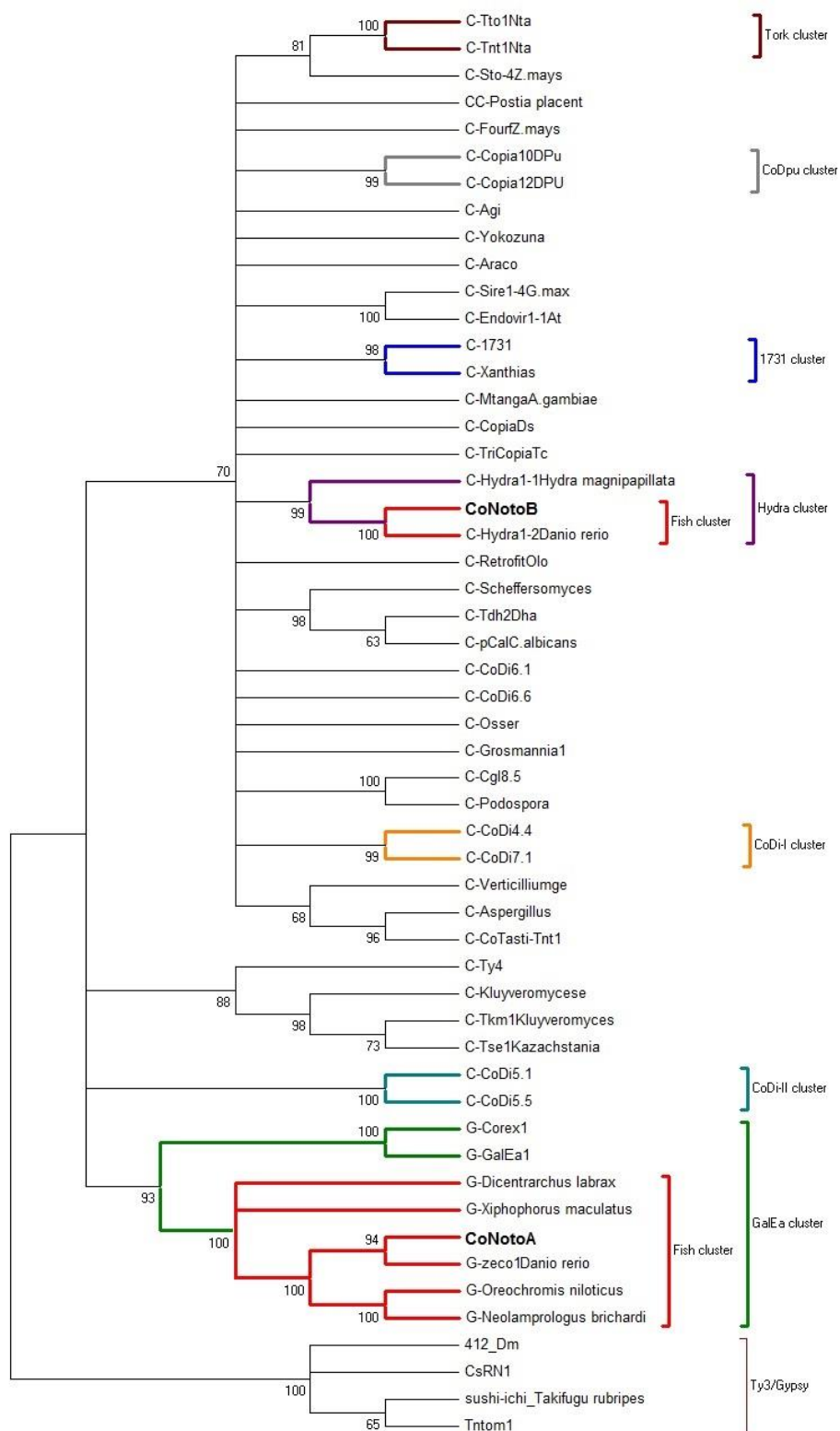




Additional file 5: NJ bootstrap consensus tree for *Copia* based on the RT/RH amino acid sequences.

Complement of Figure 3. The *GalEa* and *Hydra* families identified in nototheniid genomes (**bold font**) group with the other bony fish *Copia* sequences: *Dicentrarchus labrax*, *Xiphophorus maculatus*, *Danio rerio*, *Oreochromis niloticus* and *Neolamprologus brichardi*. Distances were calculated with the JTT model and the gamma distribution correction for amino acid. Support for individual clusters was evaluated using non-parametric bootstrapping with 1 000 replicates. Only bootstraps over 60 are presented. Nodes with bootstraps <60% were collapsed.