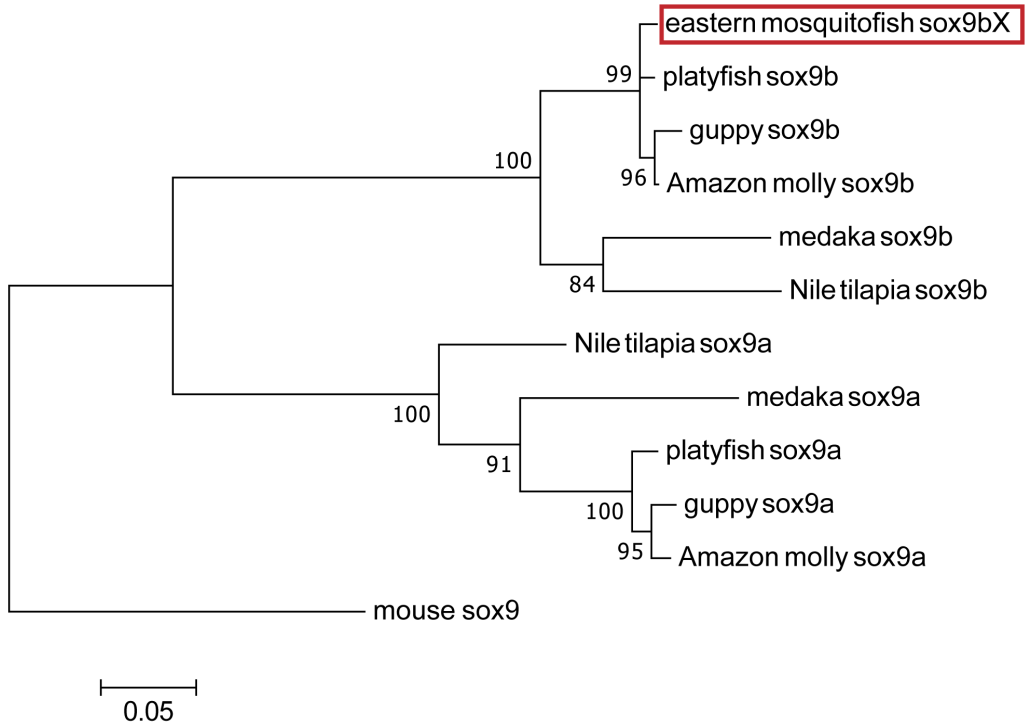

Figure S3 Molecular phylogeny of fish *sox9*.

Maximum Likelihood phylogenetic tree based on the Tamura-Nei model of fish *sox9* rooted on mouse (*Mus musculus*). The tree with the highest log likelihood (-6494.64) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches (1000 bootstrapping replicates). Branch lengths correspond to the number of substitutions per site. Only ORF sequences were used to build the tree. GenBank accession numbers: AY870394.1 (medaka *sox9a*), AY870393.1 (medaka *sox9b*), XM_005807350.2 (platyfish *sox9a*), XM_005801437.2 (platyfish *sox9b*), XM_008437952.2 (guppy (*Poecilia reticulata*) *sox9a*), NM_001297444.1 (guppy *sox9b*), XM_007560257.2 (Amazon molly (*Poecilia formosa*) *sox9a*), XM_007556363.2 (Amazon molly *sox9b*), XM_005447985.2 (Nile tilapia (*Oreochromis niloticus*) *sox9a*), XM_003450119.4 (Nile tilapia *sox9b*), NM_011448.4 (mouse *sox9*). Note that the NCBI databank refers to *sox9b* as *sox9* in all of the used sequences except for medaka.