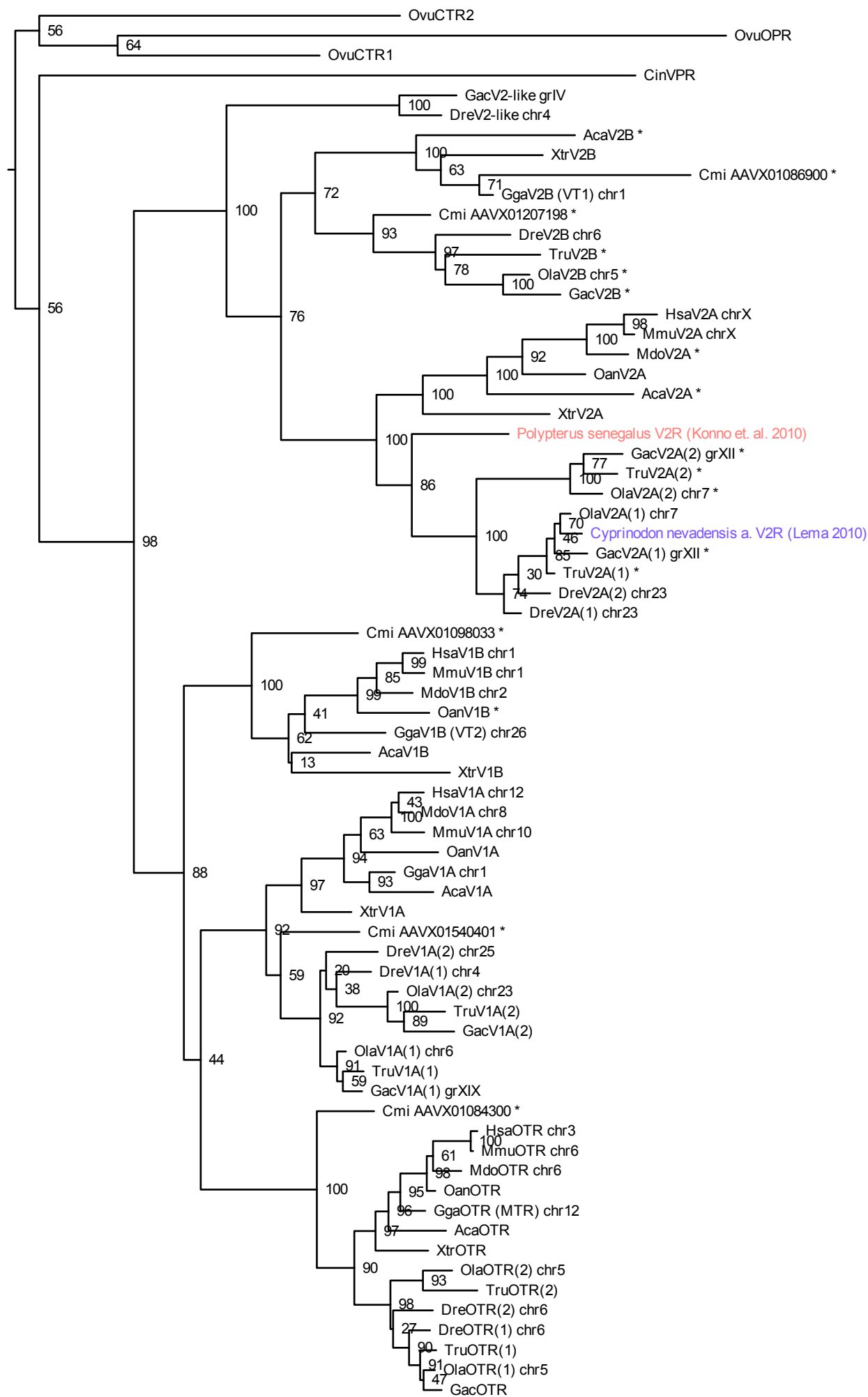


SUPPLEMENTARY MATERIAL 5

Phylogenetic maximum likelihood (PhyML) tree of the oxytocin and vasopressin receptor family including the published V2R sequences from *Polypterus senegalensis* (gray bichir) and *Cyprinodon nevadensis amargosae* (Amargosa pupfish). The gray bichir and Amargosa pupfish V2R sequences (accession nos. AB539139 and GQ981414, respectively) were aligned to the final OT/VP receptor amino acid sequence alignment described in section 2.2 of Methods using the profile alignment function in ClustalX version 2.0. The tree was constructed as described in section 2.2 of Methods. Species abbreviations are applied: Aca (anole lizard), Dre (zebrafish), Cin (tunicate), Cmi (elephant shark), Gac (stickleback), Gga (chicken), Hsa (human), Mdo (opossum), Mmu (mouse), Oan (platypus), Ola (medaka), Ovu (octopus), Tru (fugu), Xtr (frog). Where known, the chromosome assignments of the identified receptor sequences are given next to the sequence name. For the elephant shark sequences, the scaffold IDs are shown (see section 3.4). Accession IDs and detailed locations for all sequences can be found in Supplementary Material 1. Sequences marked with an asterisk are fragments and in some cases do not span the entire length of the sequence alignment used to construct this tree (see Table 1 and Supplementary Material 3). Branch support is shown for each node (out of 100 bootstrap iterations).



0.2