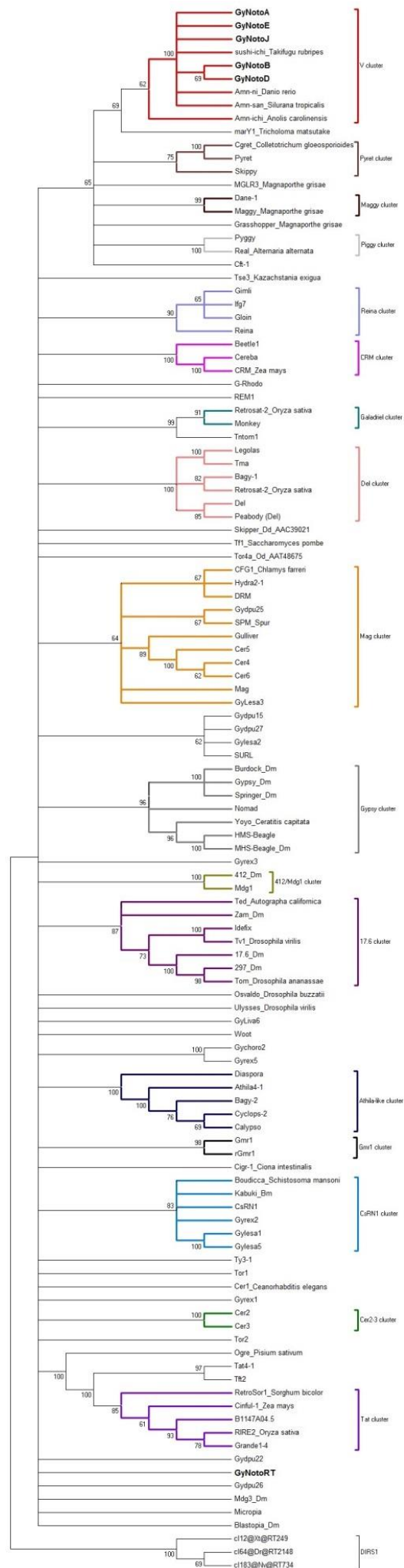
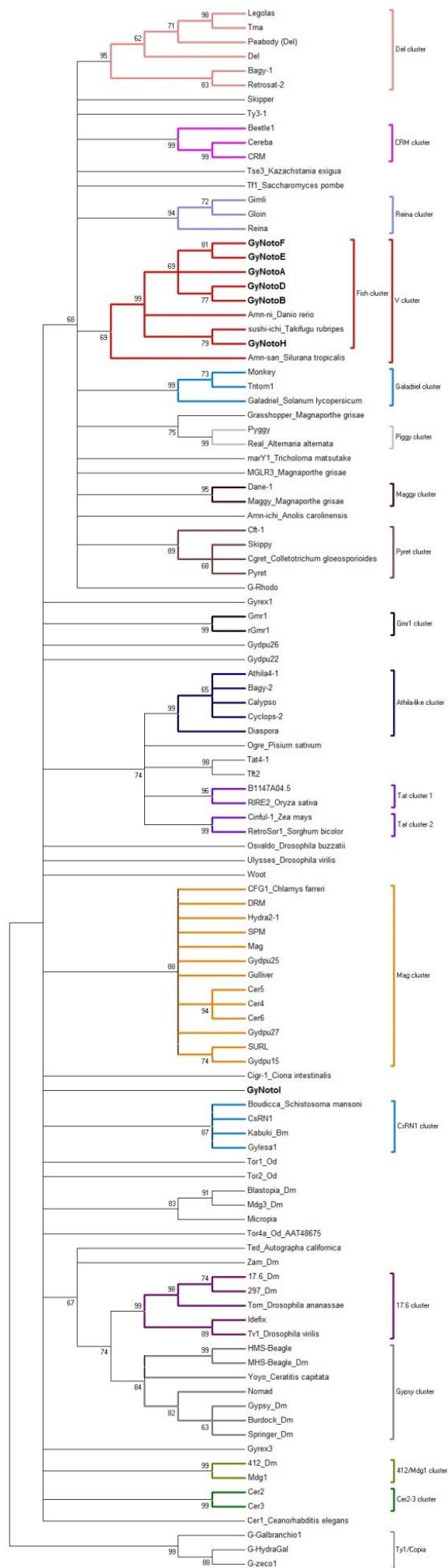


a)



b)



Additional file 4: NJ bootstrap consensus tree for Gypsy based on the amino acid sequences of the RT/RH (a) and INT (b) regions. Complement of Figure 2. Except for *GyNotoI* and *GyNotoRT*, the families identified in nototheniid genomes (**bold font**) group with the other vertebrate: *Xenopus/Silurana tropicalis*; and particularly with bony fish *Gypsy* sequences: *Tetraodon rubripes* -sushi-ichi, *Danio rerio* -Amn-ni. 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.