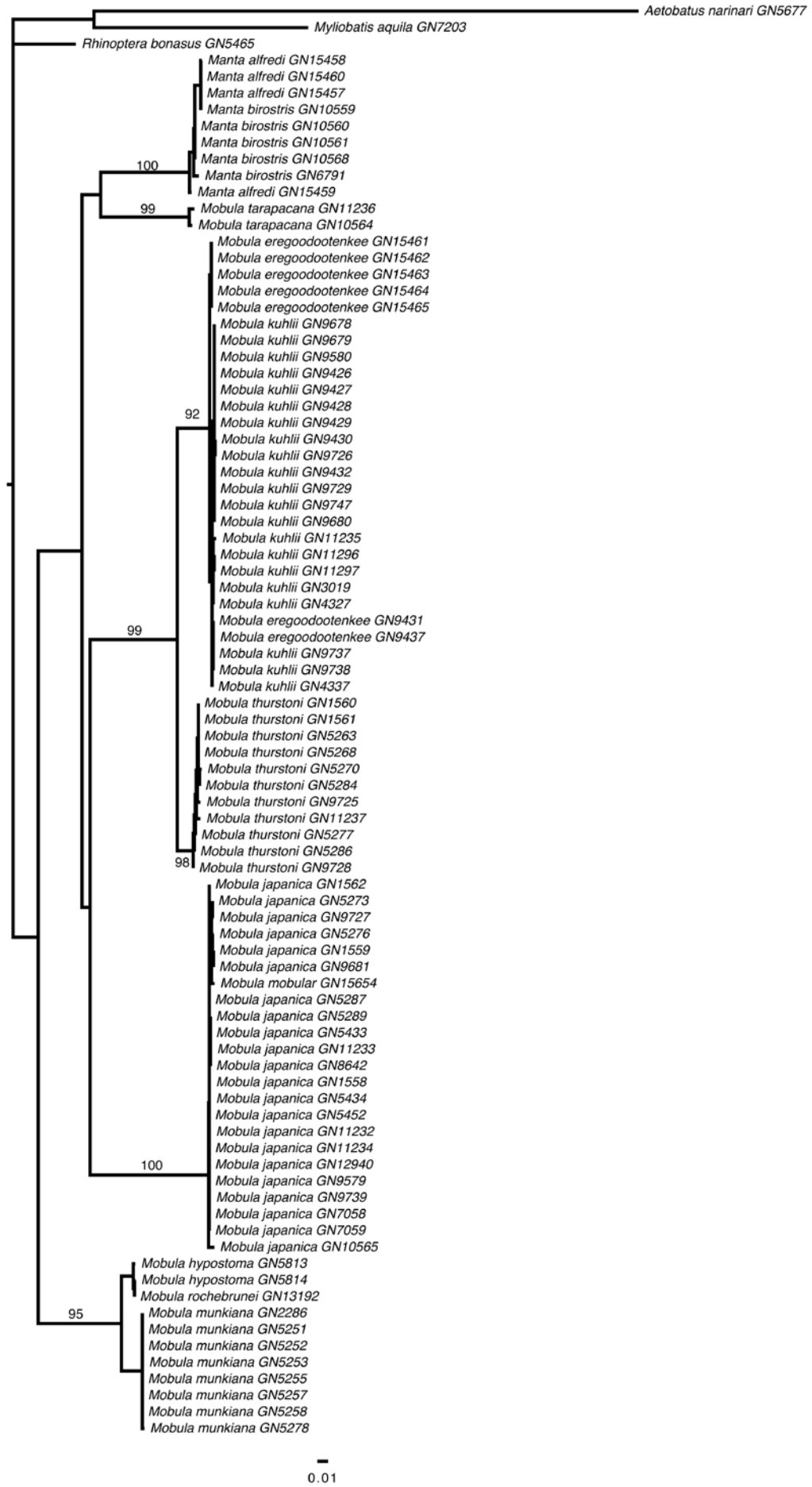

Figure 1. Maximum Likelihood tree showing nominal identifications of mobulid specimens and the relationships among them, relative to three outgroups (*Aetobatus narinari*, *Myliobatis aquila* and *Rhinoptera bonasus*). The tree was derived from an alignment of mitochondrial NADH2 sequences (1044 sites) under a TVM+I+G model of molecular evolution.