Fig. S1. Maximum likelihood (ML) phylogenetic tree for betanodavirus RNA1 partial sequence, inferred using MEGA X software (Kumar et al. 2018). Black Sea isolate from the present study is marked (◆)
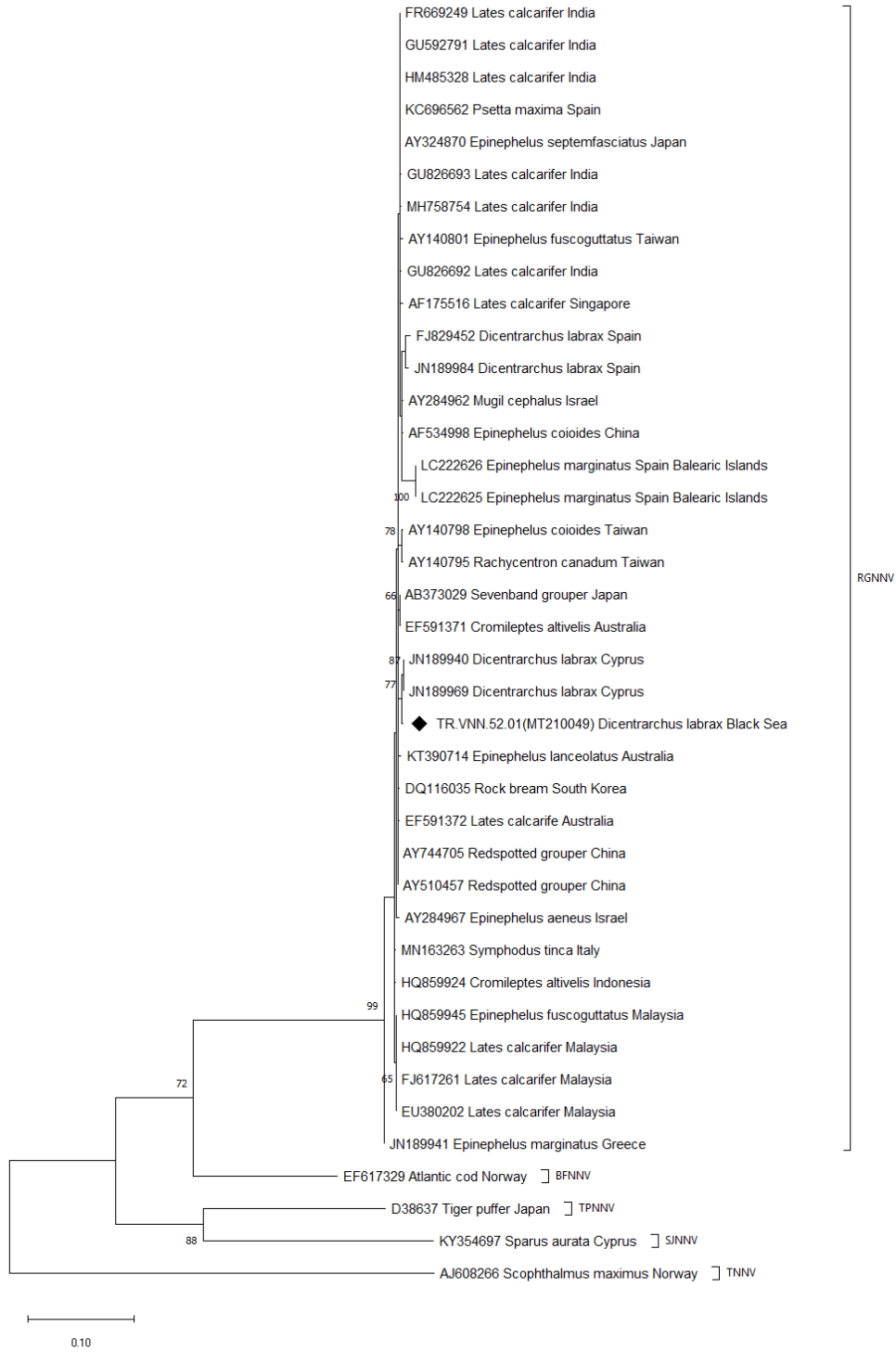
Fig. S2. Maximum likelihood (ML) phylogenetic tree for betanodavirus RNA2 partial sequence. Details as in Fig. S1