Fig. S1. Maximum Likelihood (ML) consensus tree reconstructed for Alainites spp. (Baetidae). Deeper nodes are labelled above branches with Maximum Likelihood bootstrap support (BS) and under branches with Bayesian posterior probability (PP) only for BS > 50 and PP > 0.5. Tip labels: the first two letters indicate the taxon name (AL = Alainites; BA = Baetis gr. alpinus). Two digit code: sample number. Last group of letters: origin of the material (CO = Corsica; SA = Sardinia; FR(ME) = France Mercantour; FR(MV) = France Mont Ventoux; IT(AP) = Italy Appeninno; IT(LI) = Italy Liguria; IT(TO) = Italy Toscana; CAN = Canary Islands; CH = Switzerland; FR = France; HU = Hungary; TU = Tunisia).
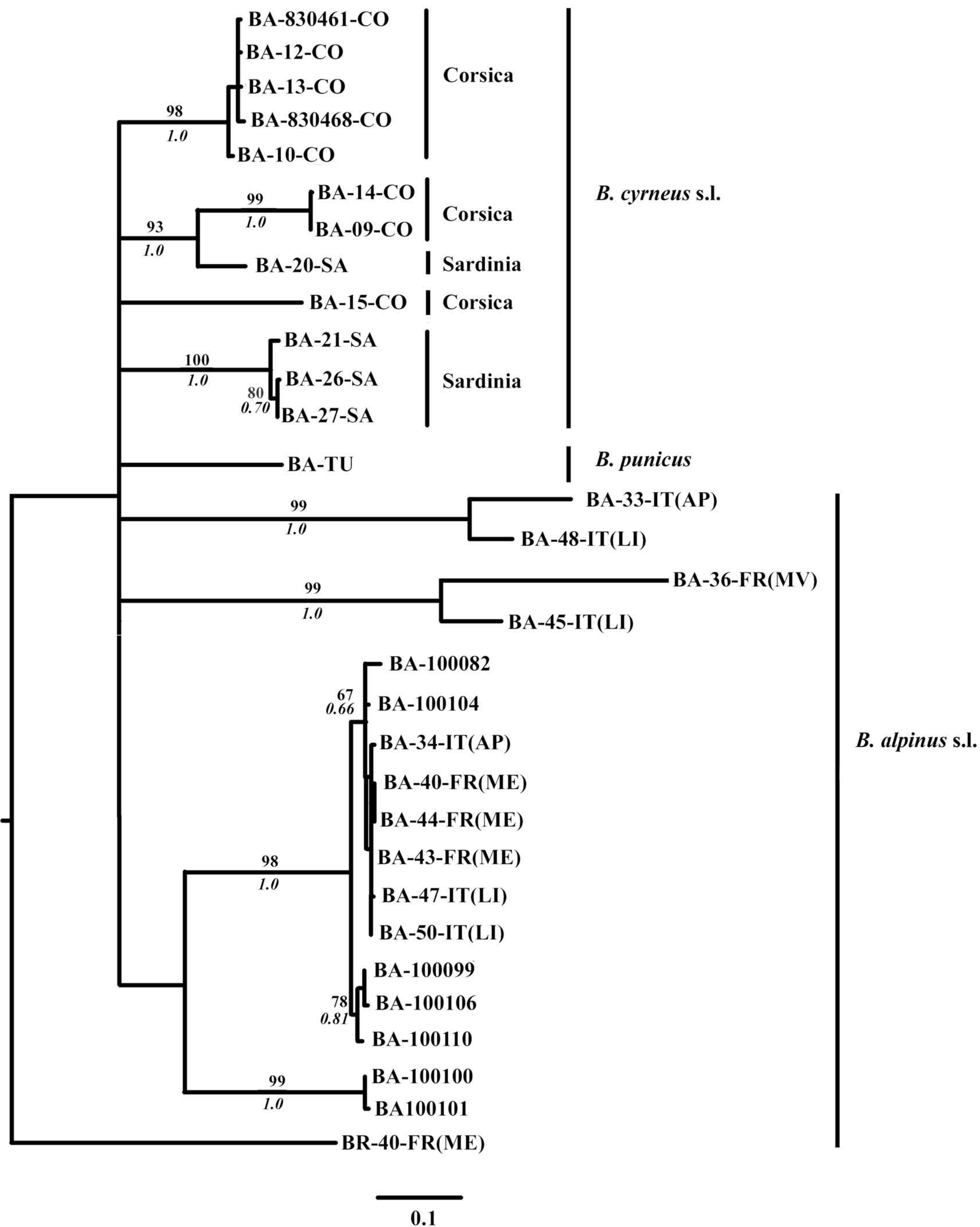
Fig. S2. Maximum Likelihood (ML) consensus tree reconstructed for Baetis gr. alpinus (Baetidae). Deeper nodes are labelled above branches with Maximum Likelihood bootstrap support (BS) and under branches with Bayesian posterior probability (PP) only for BS > 50 and PP > 0.5. Tip labels: the first two letters indicate the taxon name (BA = Baetis gr. alpinus; BR = Baetis gr. rhodani). For other codes see Fig. S1. Other tip labels refer to additional material (GenBank and unpublished data).
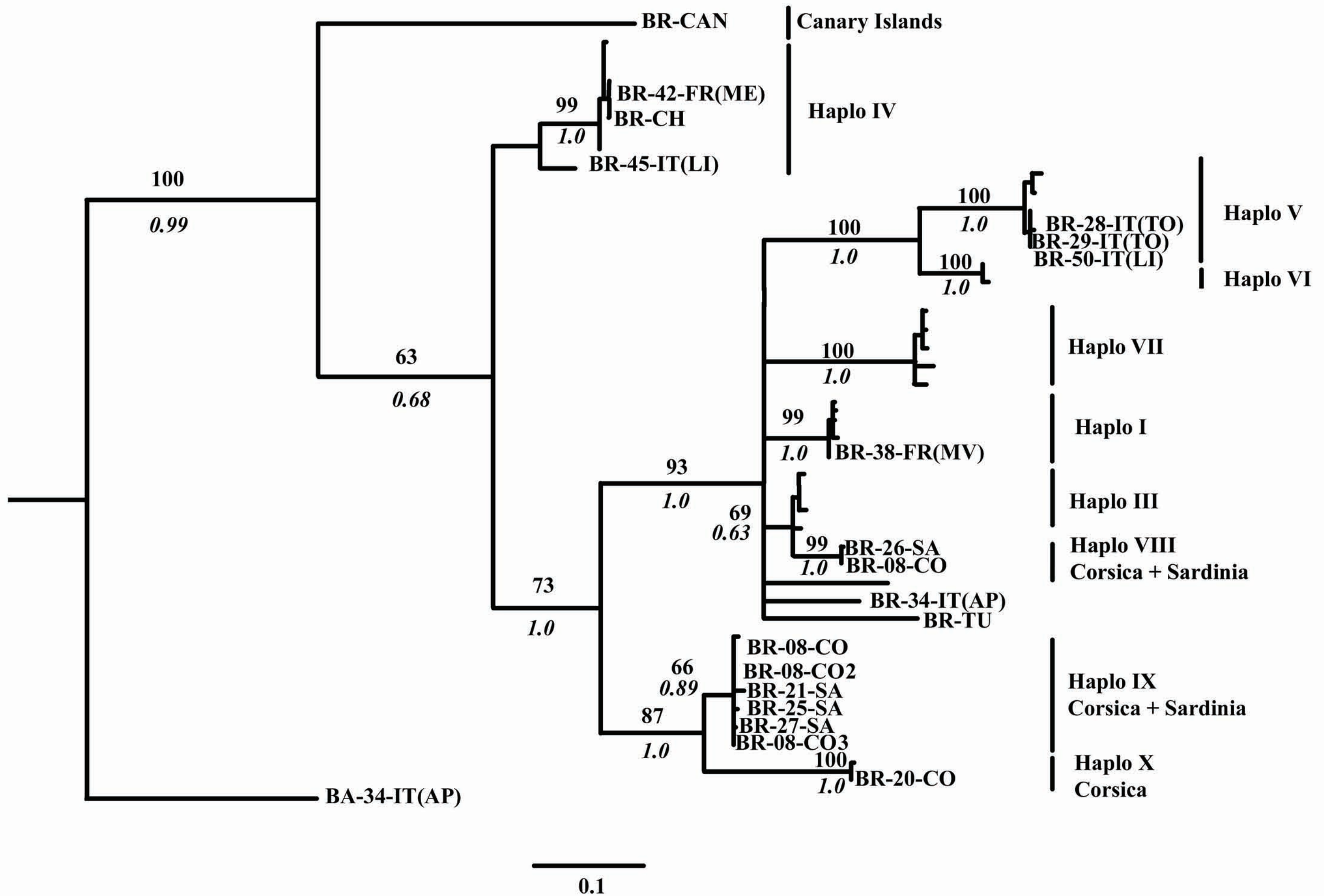
Fig. S3. Maximum Likelihood (ML) consensus tree reconstructed for Baetis gr. rhodani (Baetidae). Deeper nodes are labelled above the branch with Maximum Likelihood bootstrap support (BS) and under the branch with Bayesian posterior probability (PP) only for BS > 50 and PP > 0.5. Tips labels are generated as follows: Two first letters indicated the taxon name (BR = Baetis gr. rhodani; BA = Baetis gr. alpinus). Other codes see Fig. S1. Tip without labels refer to additional material (GenBank and unpublished data).
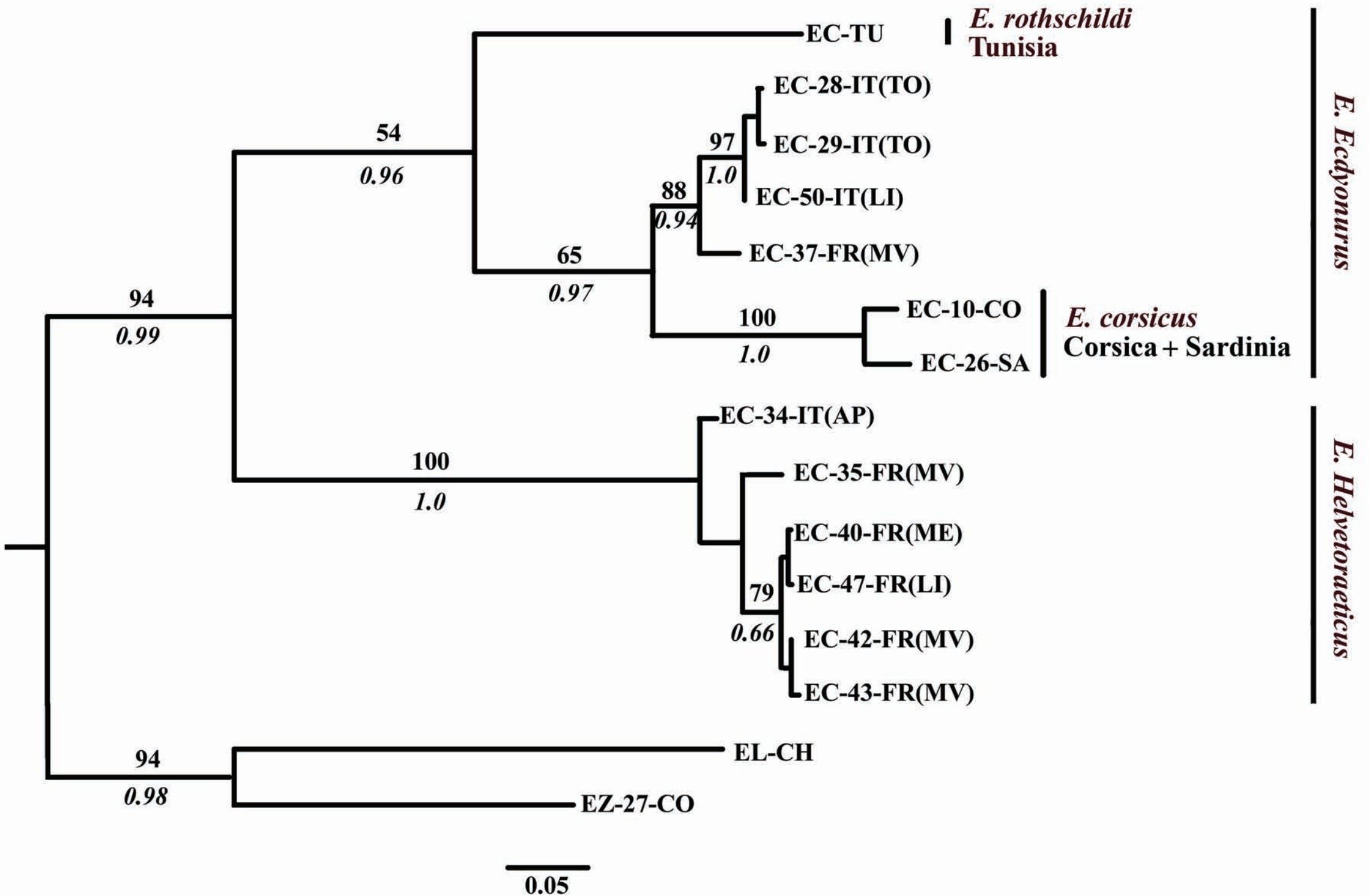
Fig. S4. Maximum Likelihood (ML) consensus tree reconstructed for Ecdyonurus spp. (Heptageniidae). Deeper nodes are labelled above the branch with Maximum Likelihood bootstrap support (BS) and under the branch with Bayesian posterior probability (PP) only for BS > 50 and PP > 0.5. Tips labels are generated as followed: Two first letters indicated the taxon name (EC = Ecdyonurus spp.; EL = Electrogena sp.; EZ = Electrogena zebrata). Other codes see Fig. S1.
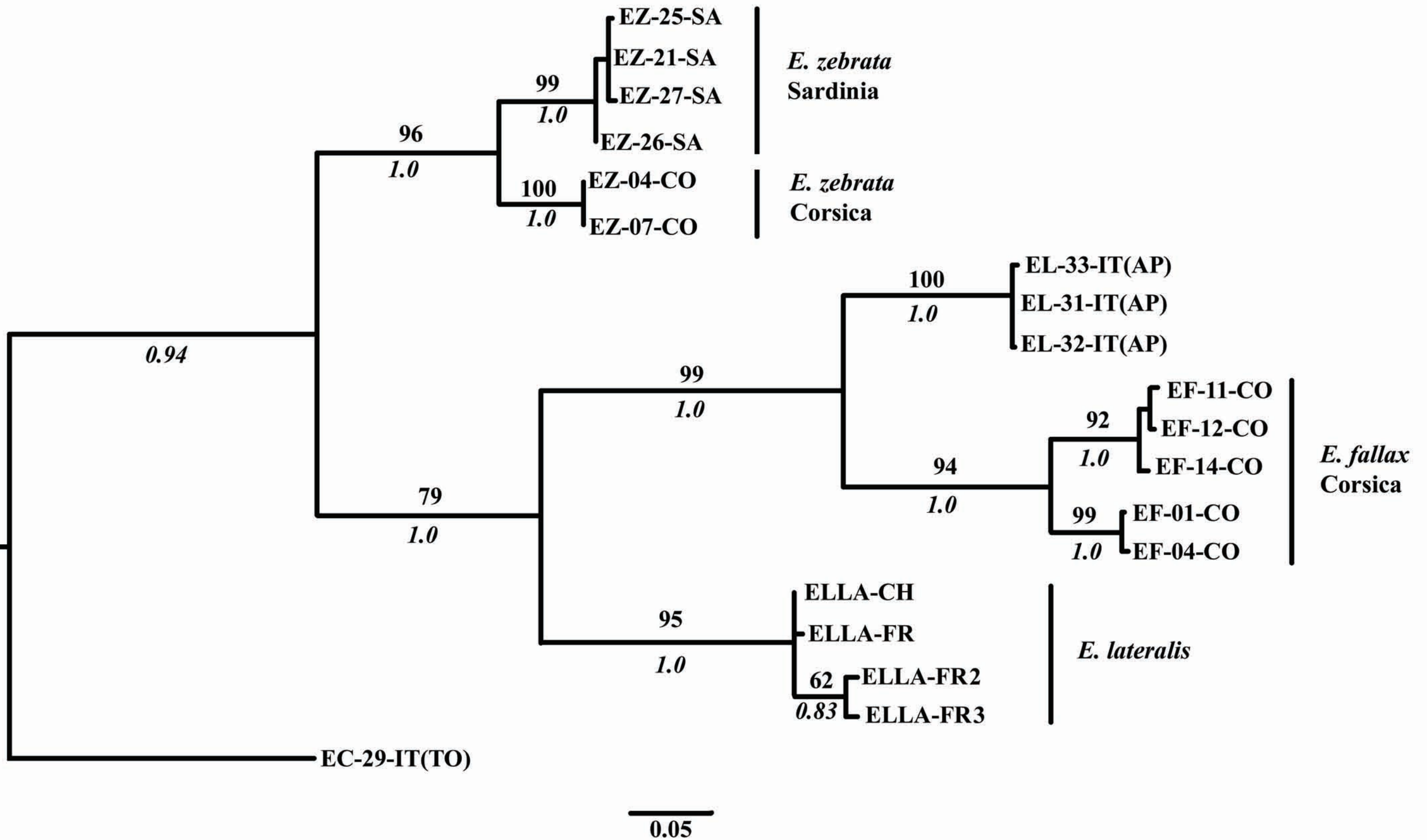
Fig. S5. Maximum Likelihood (ML) consensus tree reconstructed for Electrogena spp. (Heptageniidae). Deeper nodes are labelled above branch with Maximum Likelihood bootstrap support (BS) and under the branch with Bayesian posterior probability (PP) only for BS > 50 and PP > 0.5. Tips labels are generated as followed: Two first letters indicated the taxon name (EF = Electrogena fallax; EZ = Electrogena zebrata; ELLA = Electrogena lateralis; EL = Electrogena spp.). Other codes see Fig. S1.
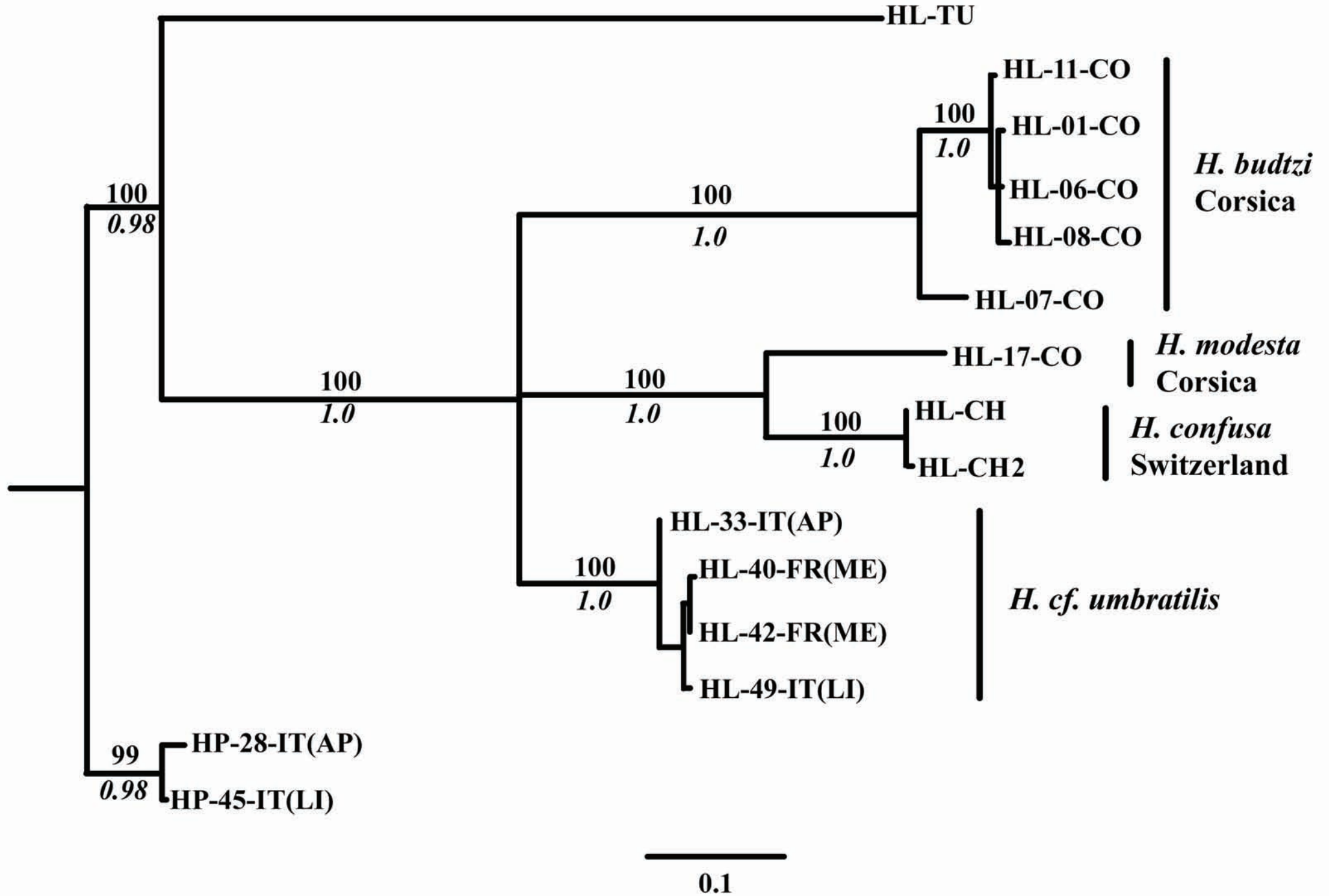
Fig. S6. Maximum Likelihood (ML) consensus tree reconstructed for Habroleptoides spp. (Leptophlebiidae). Deeper nodes are labelled above the branch with Maximum Likelihood bootstrap support (BS) and under the branch with Bayesian posterior probability (PP) only for BS > 50 and PP > 0.5. Tips labels are generated as followed: Two first letters indicated the taxon name (HL = Habroleptoides spp.; HP = Habrophlebia spp.). Other codes see Fig. S1.
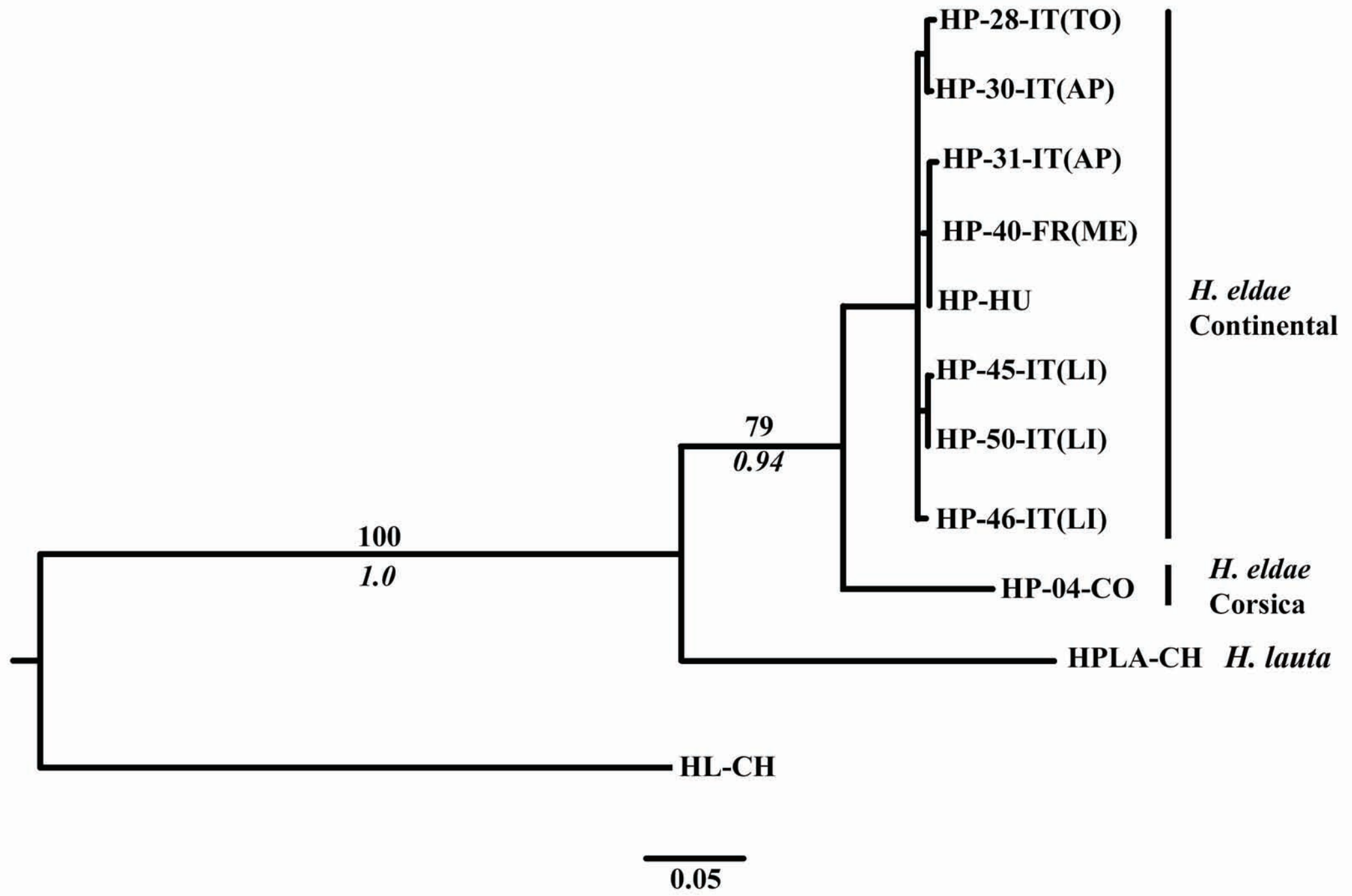
Fig. S7. Maximum Likelihood (ML) consensus tree reconstructed for Habrophlebia spp. (Leptophlebiidae). Deeper nodes are labelled above the branch with Maximum Likelihood bootstrap support (BS) and under the branch with Bayesian posterior probability (PP) only for BS > 50 and PP > 0.5. Tips labels are generated as followed: Two first letters indicated the taxon name (HP = Habrophlebia eldae; HPLA = Habrophlebia lauta; HL = Habroleptoides sp.). Other codes see Fig. S1.
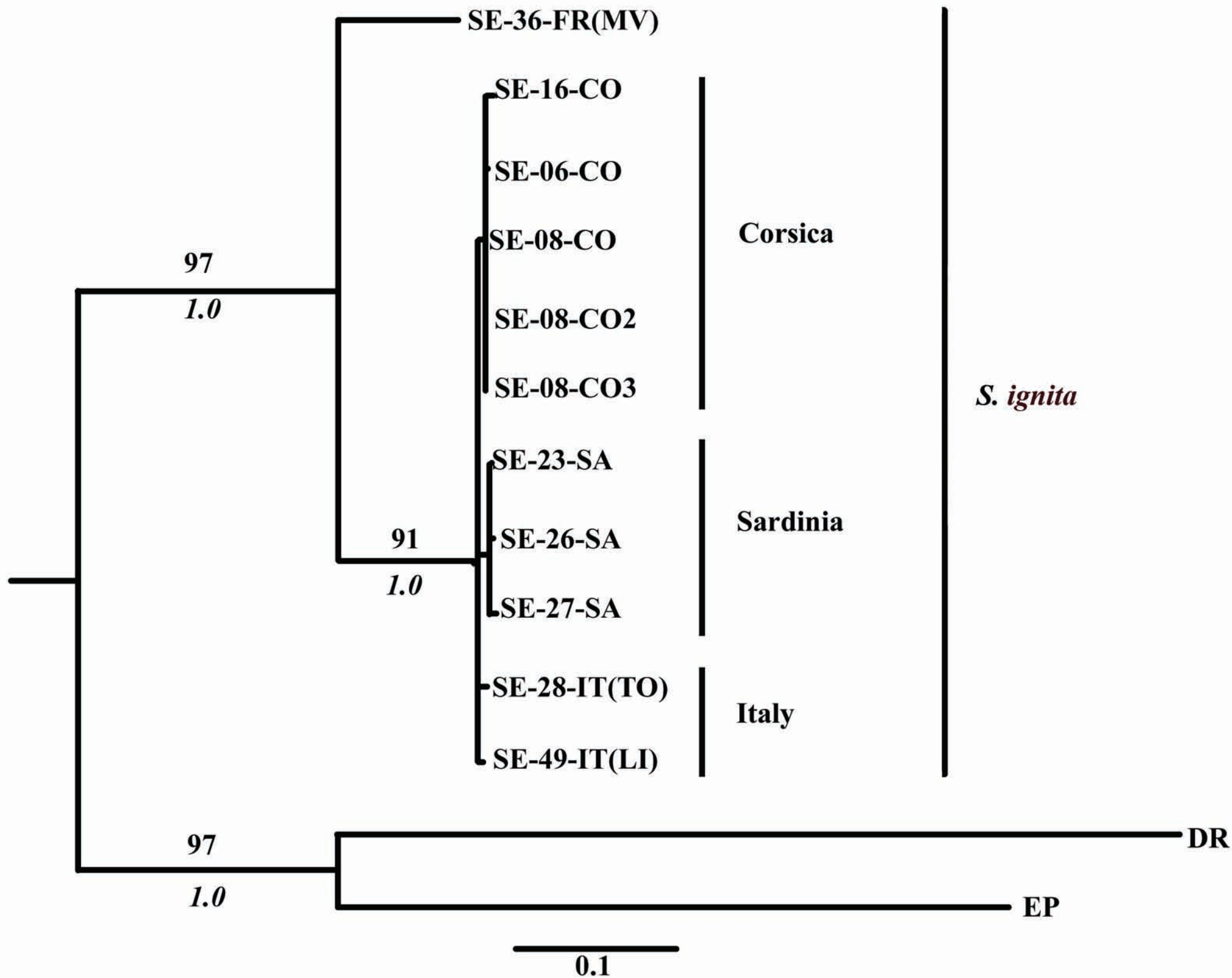
Fig. S8. Maximum Likelihood (ML) consensus tree reconstructed for Serratella ignita (Ephemerellidae). Deeper nodes are labelled above the branch with Maximum Likelihood bootstrap support (BS) and under the branch with Bayesian posterior probability (PP) only for BS > 50 and PP > 0.5. Tips labels are generated as followed: Two first letters indicated the taxon name (SE = Serratella ignita; DR = Drunella sp; EP = Ephemerella sp.). Other codes see Fig. S1.