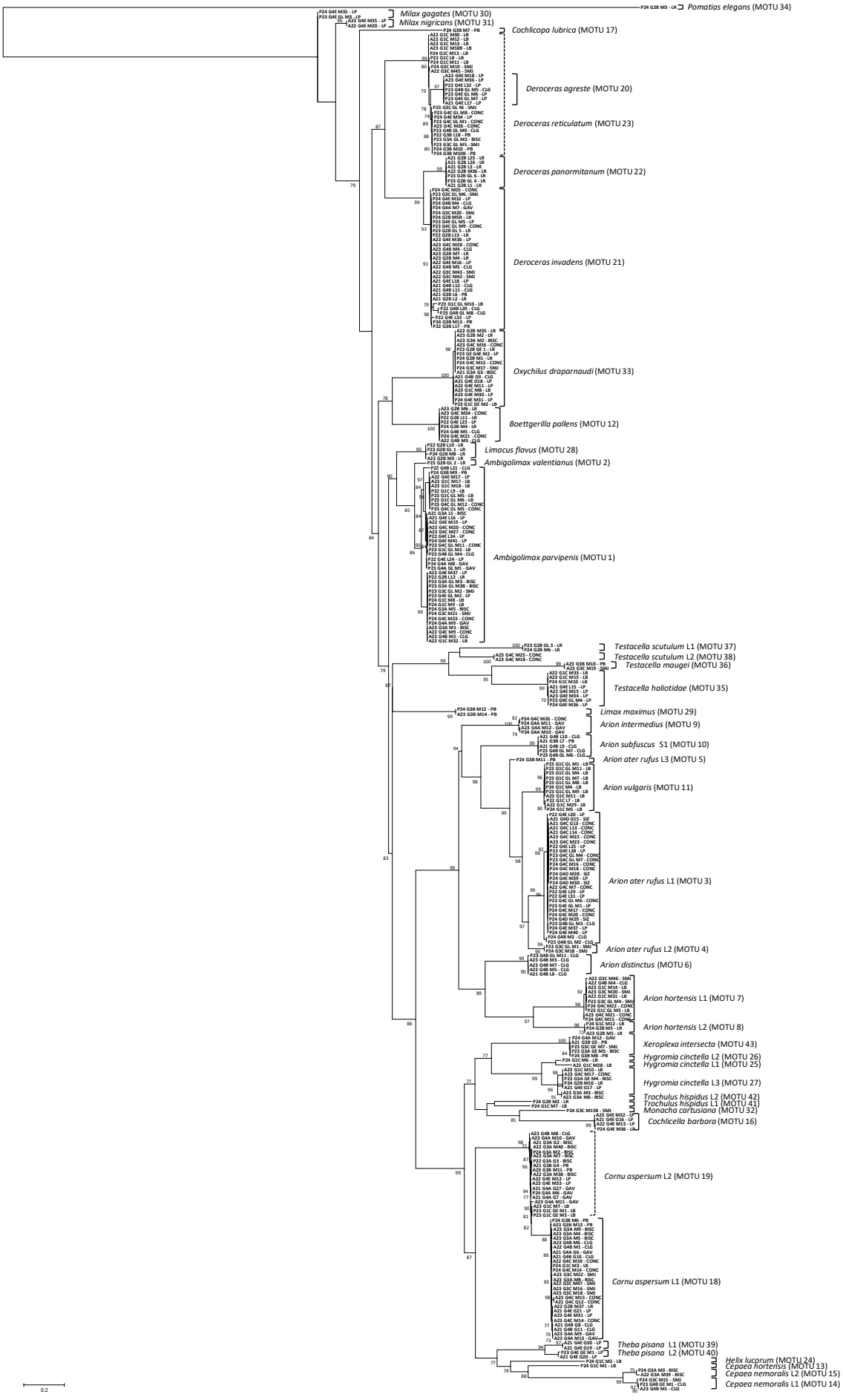

Milax gagates (MOTU 30)
Milax nigricans (MOTU 31)
Cochlicopa lubrica (MOTU 17)
Deroceras agreste (MOTU 20)
Deroceras reticulatum (MOTU 23)
Deroceras panormitanum (MOTU 22)
Deroceras invadens (MOTU 21)
Oxychilus draparnaudi (MOTU 33)
Boettgerilla pallens (MOTU 12)
Limacus flavus (MOTU 28)
Ambigolimax valentianus (MOTU 2)
Ambigolimax parvipenis (MOTU 1)
Pomatias elegans (MOTU 34)
Testacella scutulum L1 (MOTU 37)
Testacella scutulum L2 (MOTU 38)
Testacella maugei (MOTU 36)
Testacella haliotidae (MOTU 35)
Limax maximus (MOTU 29)
Arion intermedius (MOTU 9)
Arion subfuscus S1 (MOTU 10)
Arion ater rufus L3 (MOTU 5)
Arion vulgaris (MOTU 11)
Arion ater rufus L1 (MOTU 3)
Arion ater rufus L2 (MOTU 4)
Arion distinctus (MOTU 6)
Arion hortensis L1 (MOTU 7)
Arion hortensis L2 (MOTU 8)
Xeroplexa intersecta (MOTU 43)
Hygromia cinctella L2 (MOTU 26)
Hygromia cinctella L1 (MOTU 25)
Hygromia cinctella L3 (MOTU 27)
Trochulus hispidus L2 (MOTU 42)
Trochulus hispidus L1 (MOTU 41)
Monacha cartusiana (MOTU 32)
Cochlicella barbara (MOTU 16)
Cornu aspersum L2 (MOTU 19)
Cornu aspersum L1 (MOTU 18)
Theba pisana L1 (MOTU 39)
Theba pisana L2 (MOTU 40)
Helix lucorum (MOTU 24)
Cepaea hortensis (MOTU 13)
Cepaea nemoralis L2 (MOTU 15)
Cepaea nemoralis L1 (MOTU 14)
0.2

Figure S2. Maximum likelihood (ML) tree reconstructed from the COI sequences obtained in this study. The tree is rooted with the COI sequence of *Pomatias elegans*. The numbers indicated at the nodes correspond to bootstrap values greater than 70. At the end of each sample name, an abbreviation indicates the site of origin: LB: Limeil-Brévannes; LR: La Rochelle; BISC: Biscarrosse; PB: Parentis-en-Born; SMJ: Saint-Médard-en-Jalles; GAV: Gâvres; CLG: Cléguer; CONC: Concarneau; SIZ: Sizun; LP: Lampaul-Plouarzel. MOTU numbers refer to the Automatic Barcode Gap Discovery (ABGD) analysis.