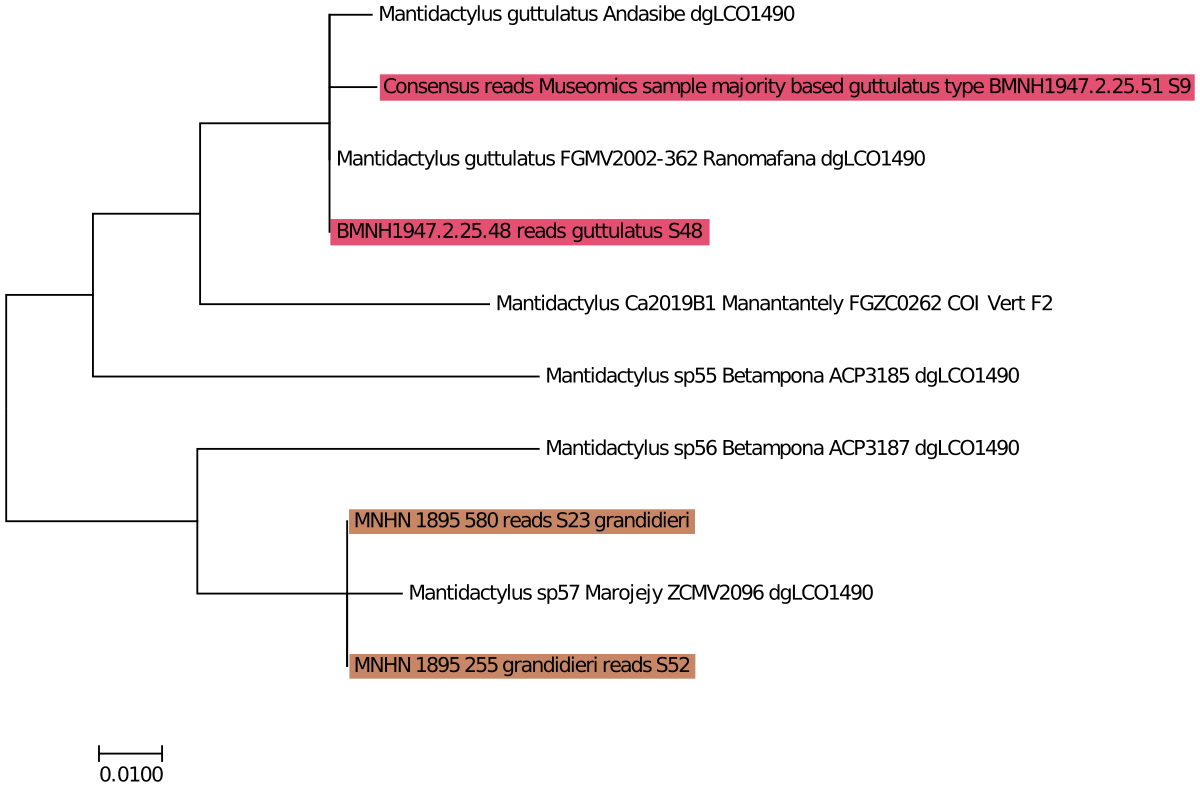
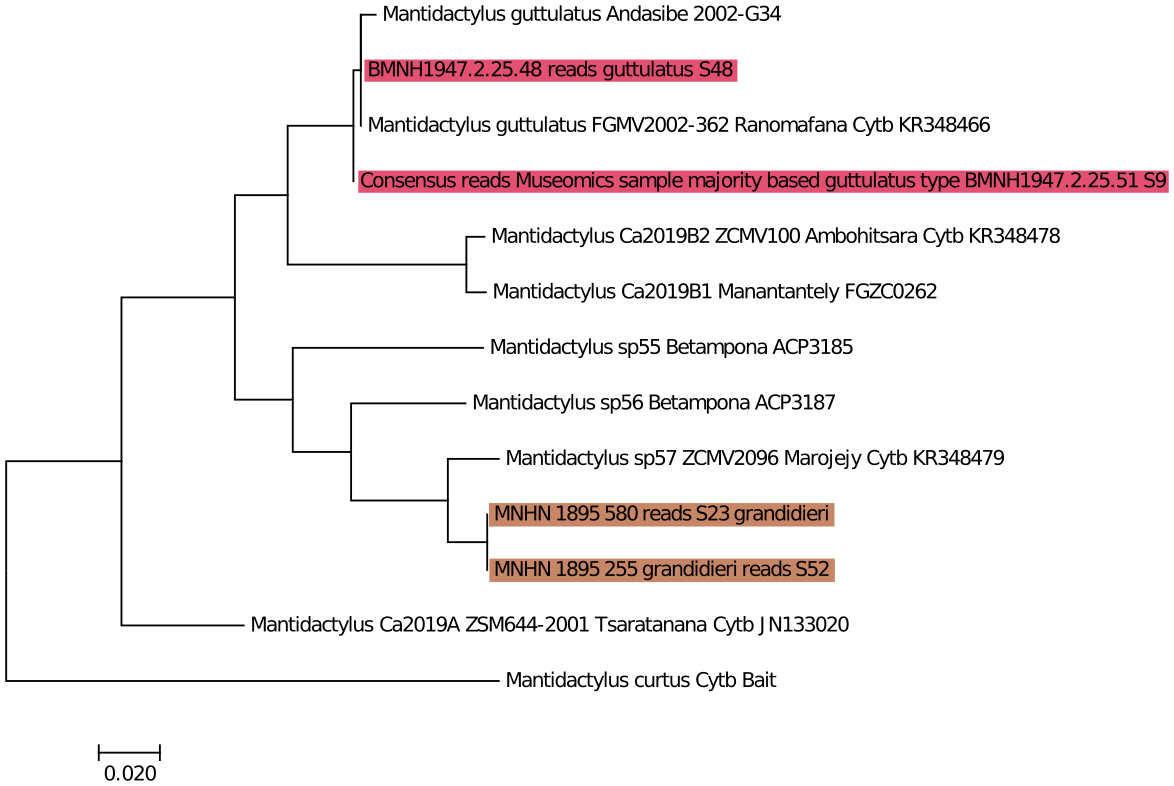
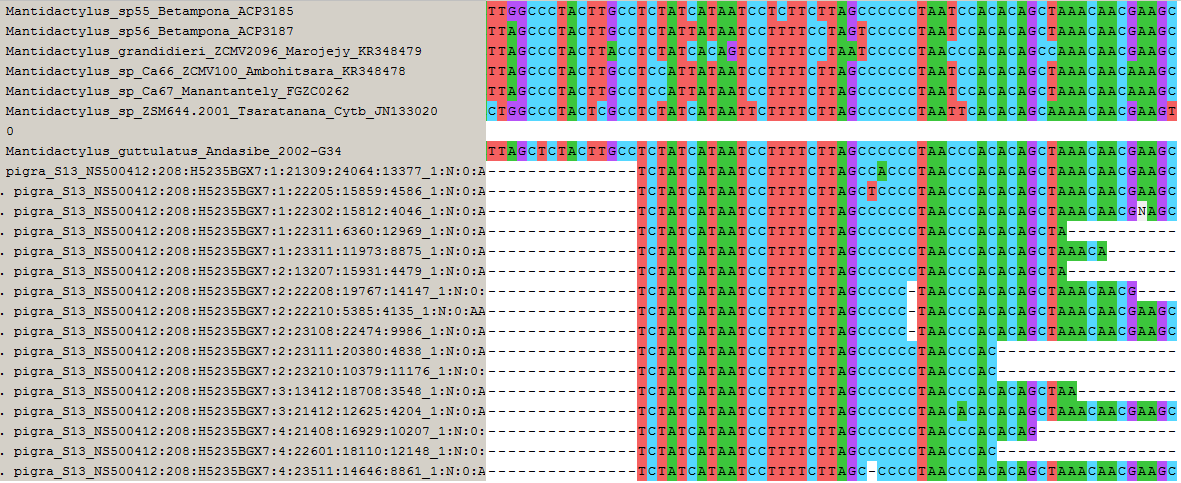
**Figure S1.** Graphical summary of the bioinformatic pipeline used to assign museum specimens to a lineage based on illumina reads.

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**Figure S2.** Tree based on cytochrome oxidase subunit 1 (cox1) sequences, including consensus sequences of four historical type specimens (in red: *Mantidactylus (M.) guttulatus*; in light brown: *M. (M.) grandidieri*).



**Figure S3.** Tree based on cytochome b (cob) sequences, including consensus sequences of four historical type specimens (in red: *Mantidactylus (M.) guttulatus*; in light brown: *M. (M.) grandidieri*).



**Figure S4.** Alignment of 16 reads derived from bait capture of the holotype of *Rana pigra* (MNHN 1899.410) that matched the terminal part of the cytochrome b fragment analysed. These reads best match the sequence of the lineage considered to be *Mantidactylus (M.) guttulatus.*