

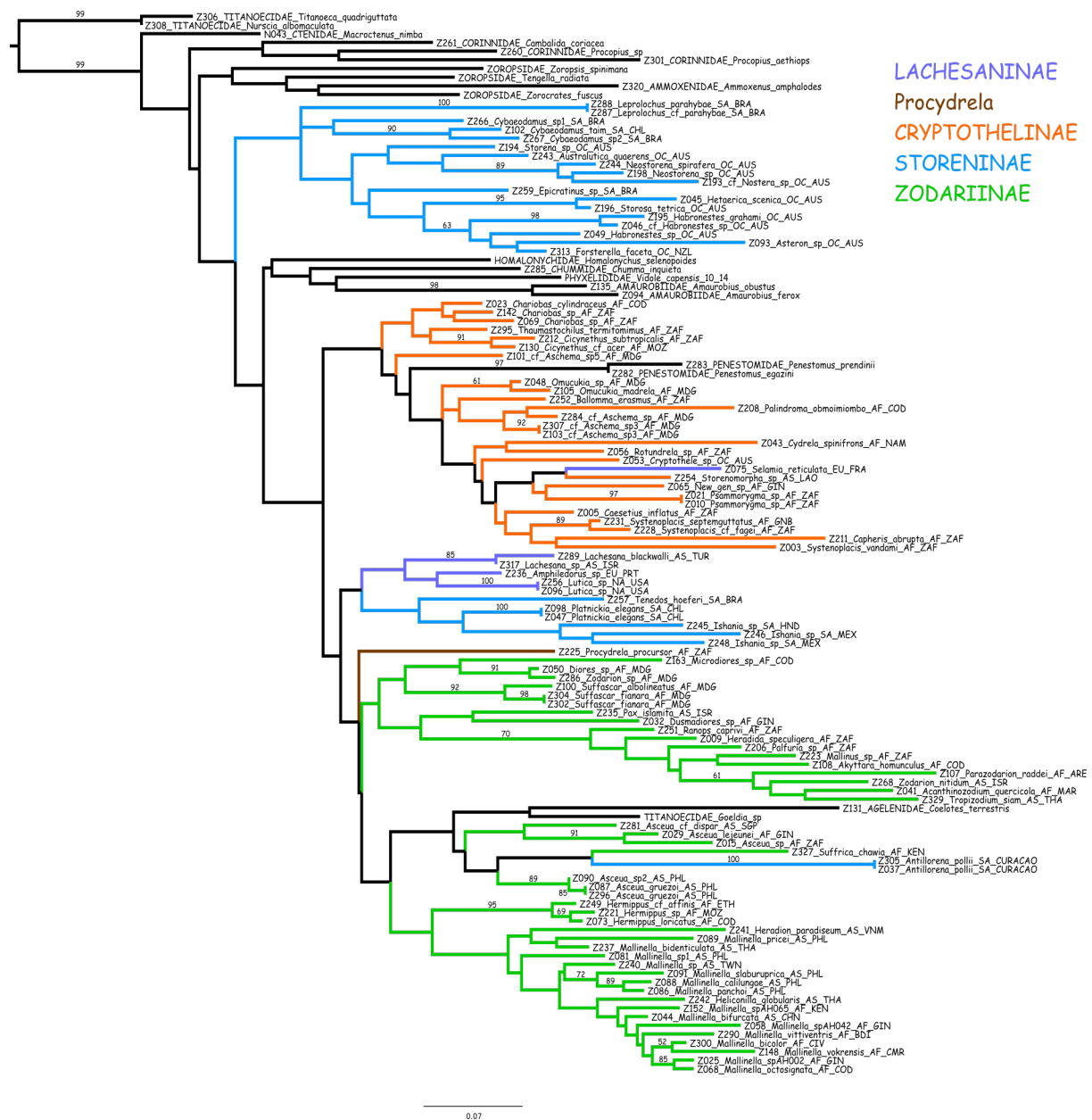
Appendix 13. Phylogeny reconstruction based on the COI alignment

Support values (>50) are summarized here on the best ML tree performed with GARLI.



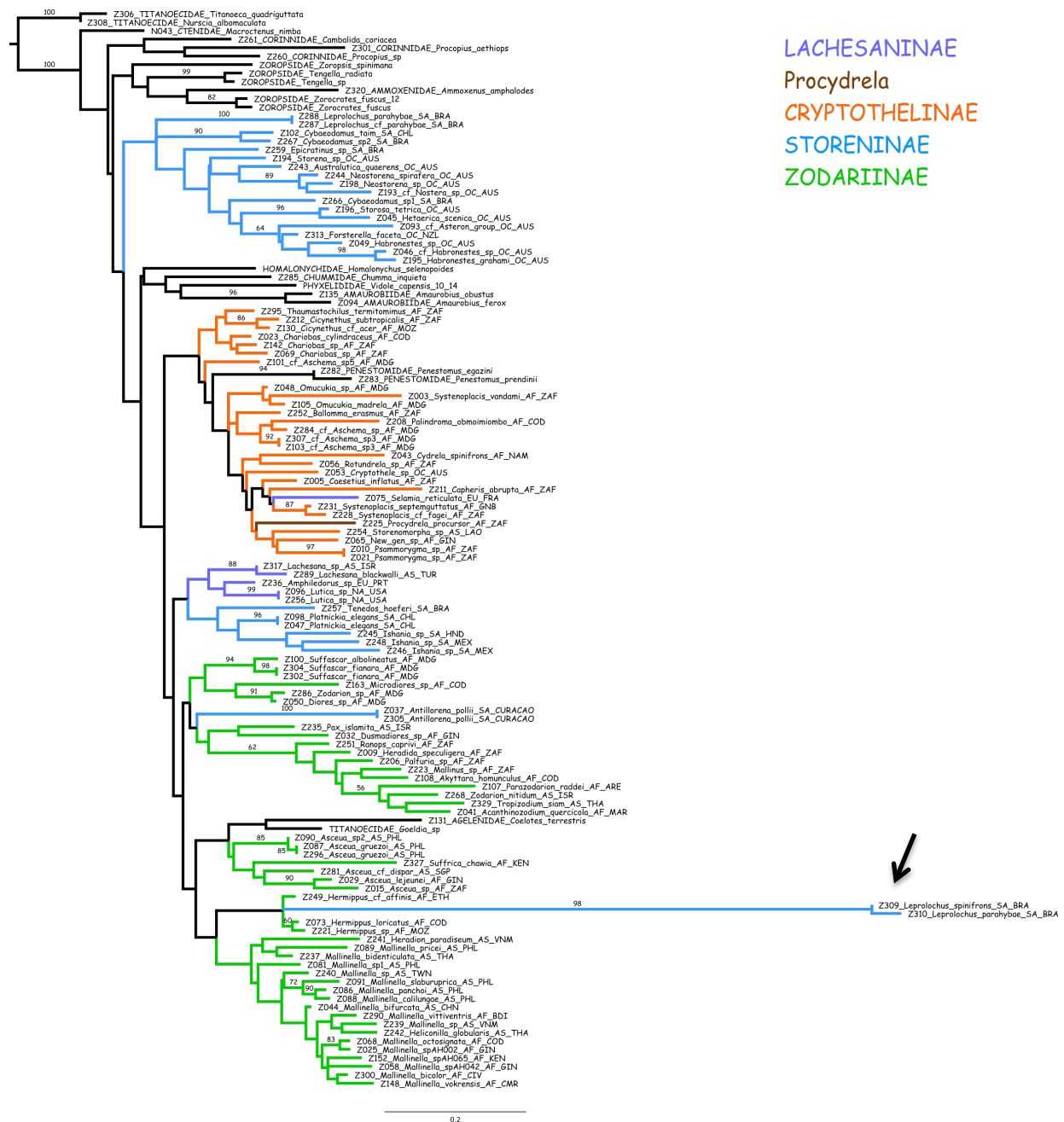
Appendix 14a. Phylogeny reconstruction and based on the H3 alignment

(supposed paralogous not included) Support values (>50) are summarized here on the best ML tree performed with GARLI.



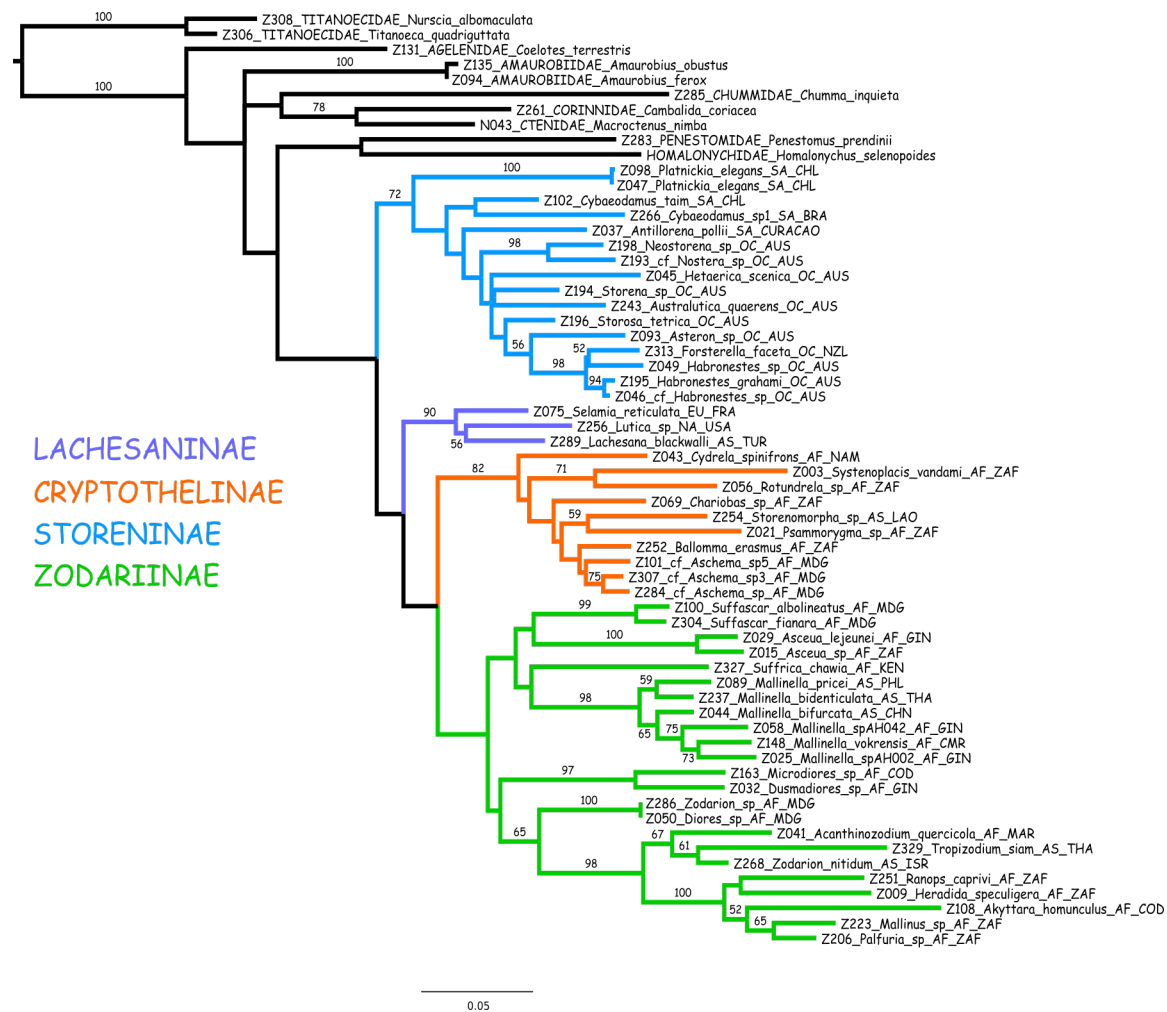
Appendix 14b. Phylogeny reconstruction and based on the H3 alignment (supposed paralogous included)

(i.e. Z309 and Z310 indicated by the arrows). Support values (>50) are summarized here on the best ML tree performed with GARLI.



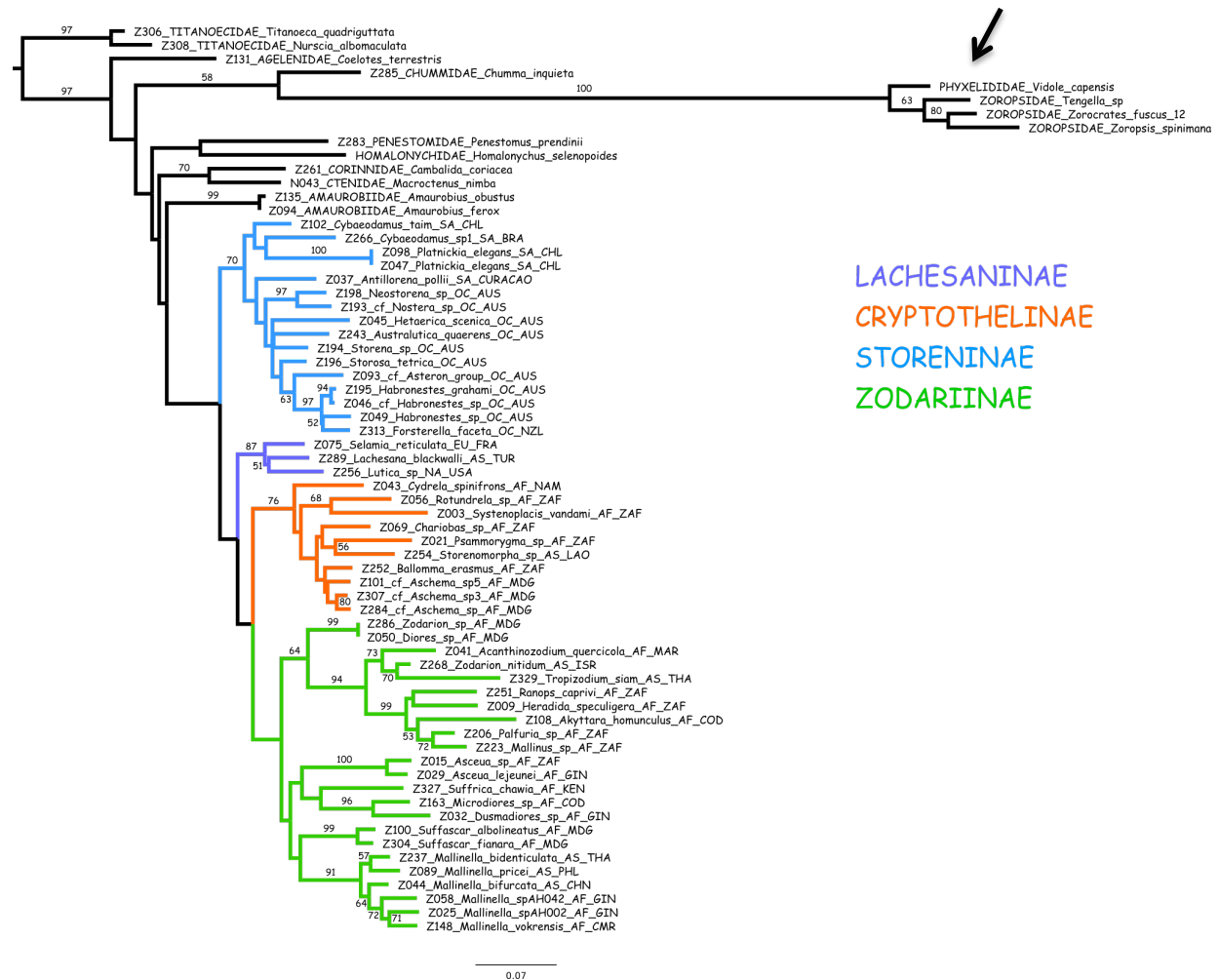
Appendix 15a. Phylogeny reconstruction based on the Act5C alignment

(supposed paralogous not included) Support values (>50) are summarized here on the best ML tree performed with GARLI.



Appendix 15b. Phylogeny reconstruction based on the Act5C alignment (supposed paralogous included)

(supposed paralogous are indicated with the arrow). Support values (>50) are summarized here on the best ML tree performed with GARLI.



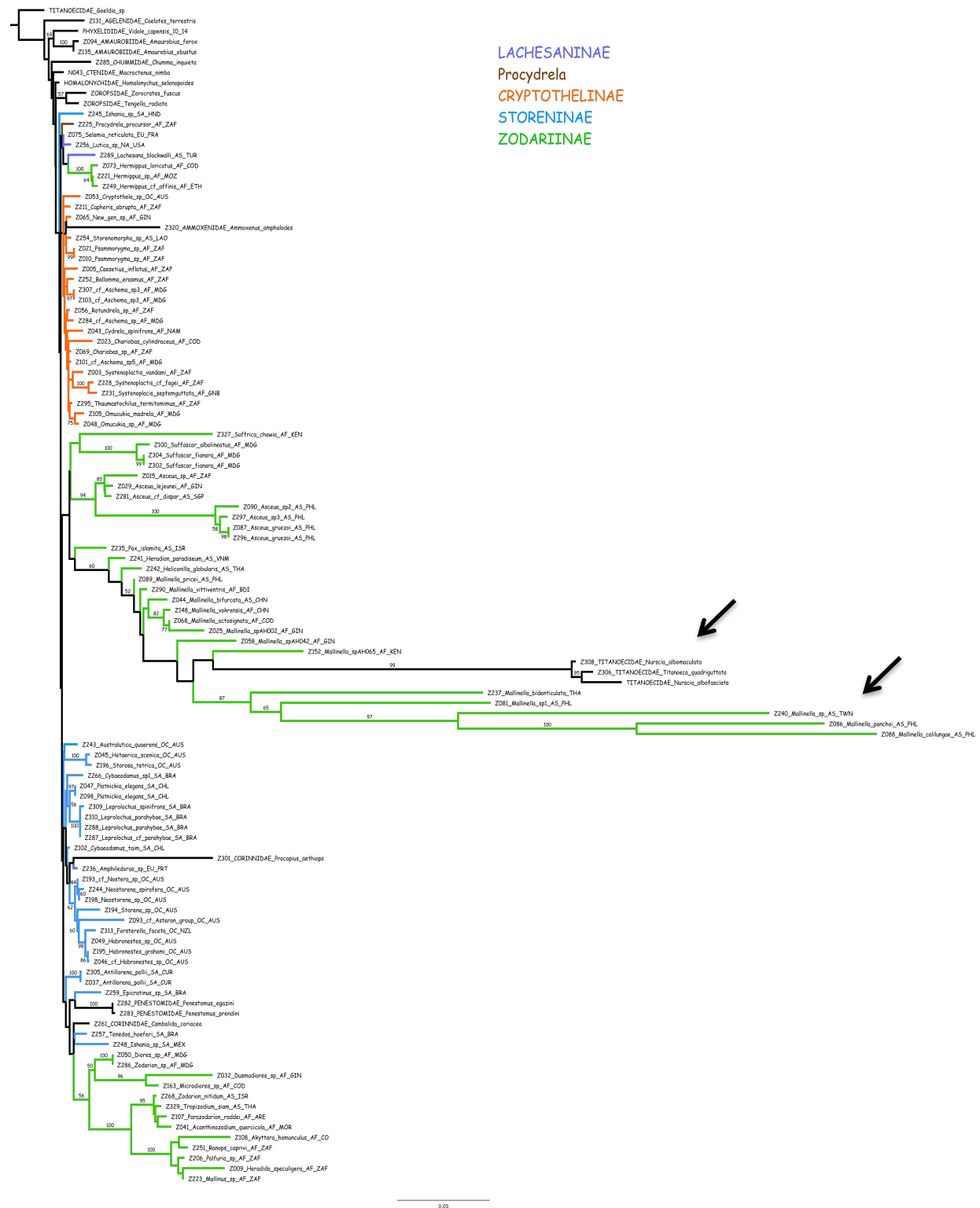
Appendix 16a. Phylogeny reconstruction based on the 18S alignment

(supposed paralogous or sequences generating too long branches not included). Support values (>50) are summarized here on the best ML tree performed with GARLI.



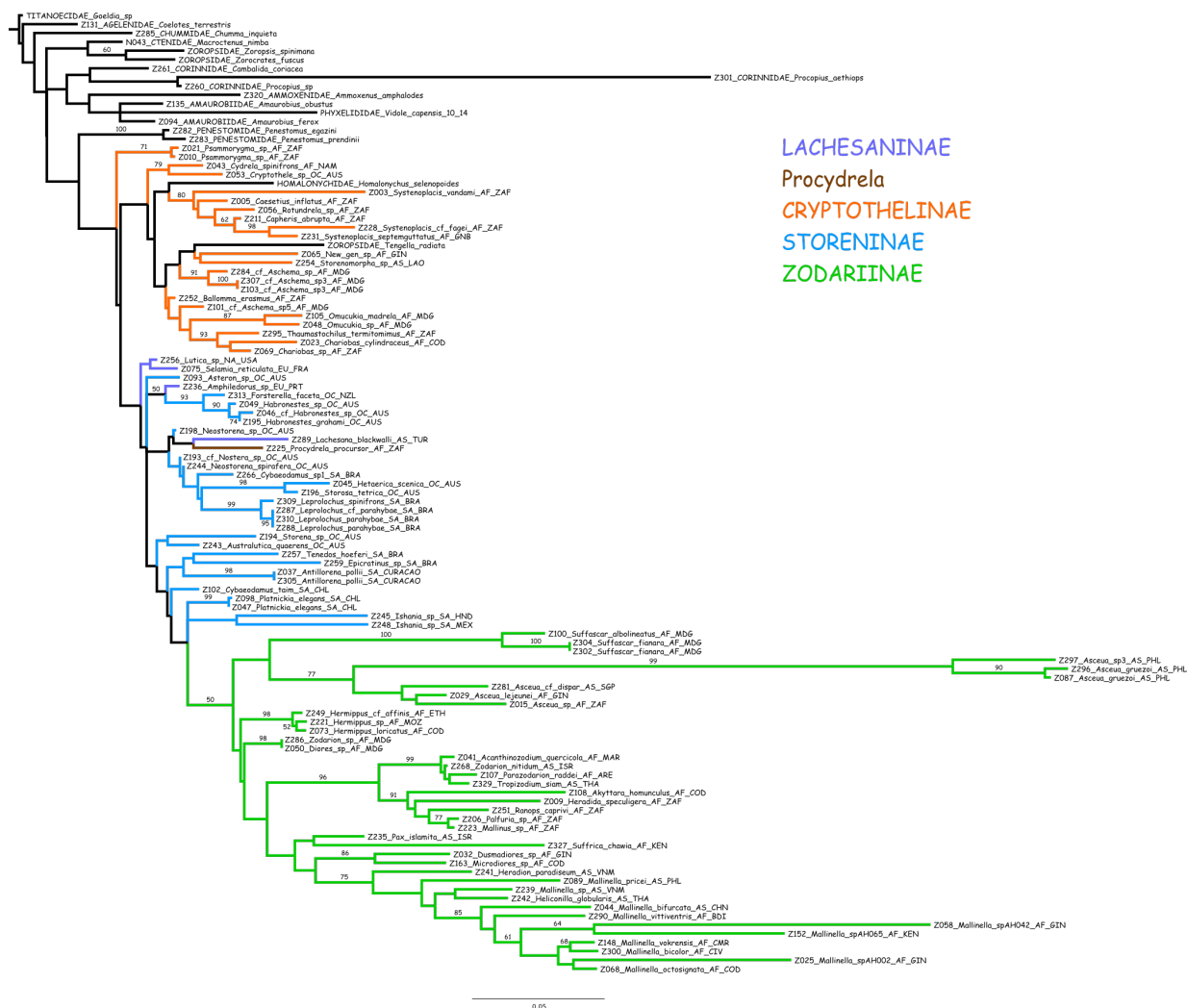
Appendix 16b. Phylogeny reconstruction based on the 18S alignment (supposed paralogous included)

(supposed paralogous or sequences generating too long branches are indicated with arrows). Support values (>50) are summarized here on the best ML tree performed with GARLI.



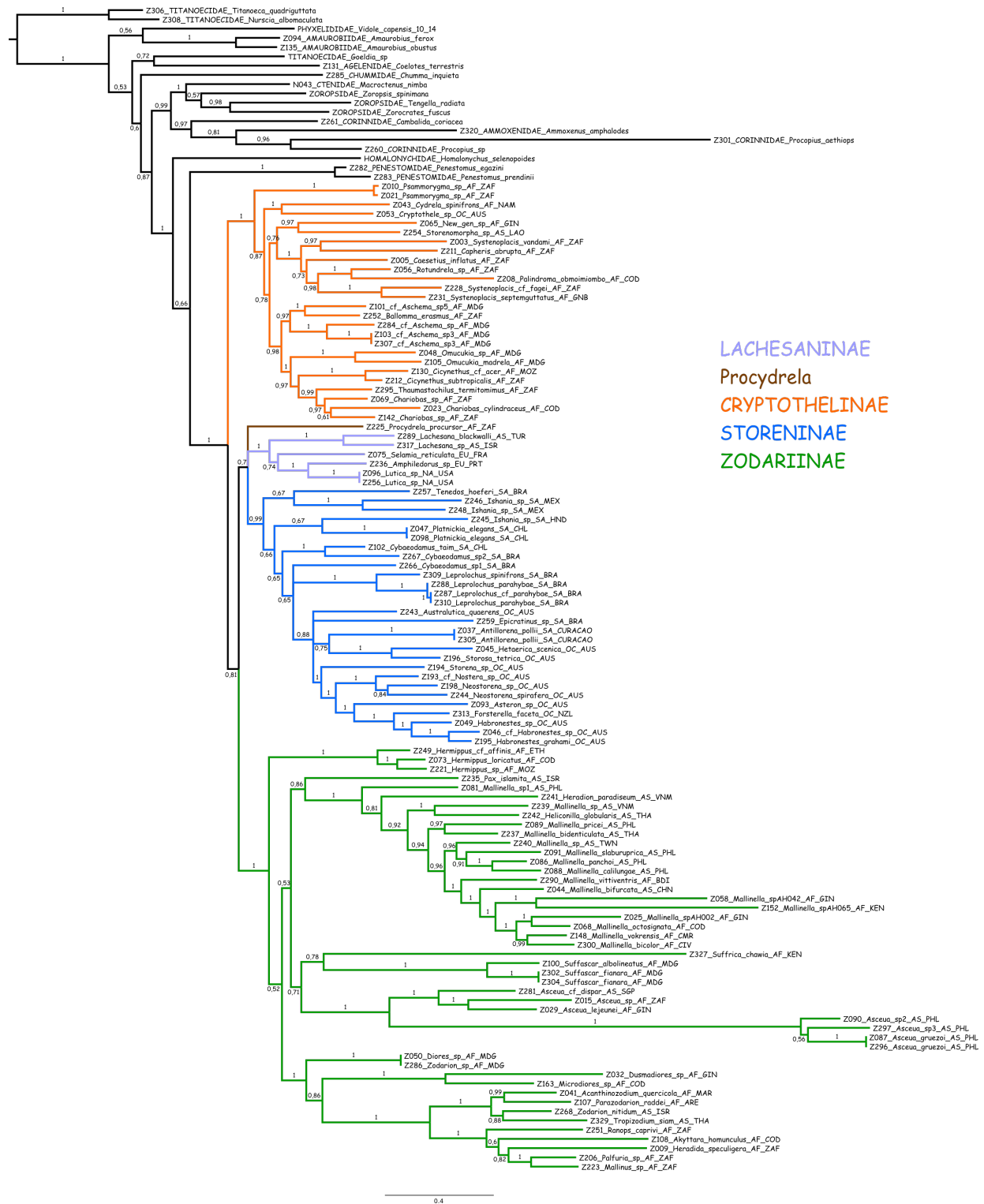
Appendix 17a. Phylogeny reconstruction based on the 28S alignment

(supposed paralogous or sequences generating too long branches not included). Support values (>50) are summarized here on the best ML tree performed with GARLI.

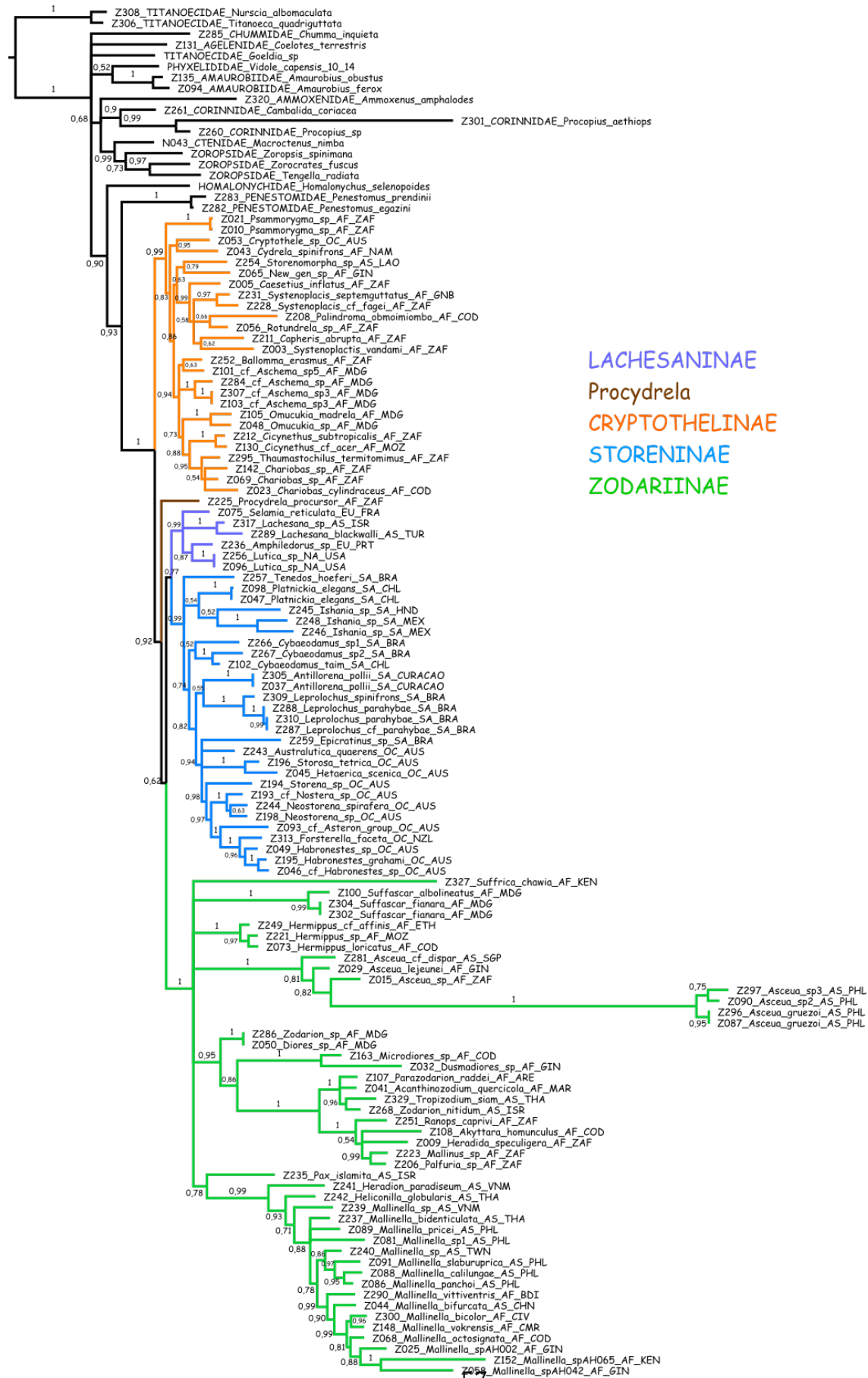


(supposed paralogous or sequences generating too long branches are indicated with arrows). Support values (>50) are summarized here on the best ML tree performed with GARLI and.

Appendix 18. Majority rule consensus Bayesian tree obtained with MrBayes (MB) with the FINAL multigene alignment



Appendix 19. Majority rule consensus Bayesian tree obtained with PhyloBayes (PB) with the FINAL multigene alignment.



Appendix 20. Phylogeny reconstruction based on the multigene alignment (supposed paralogous included)

(supposed paralogous or sequences generating long branches included except H3 for Z309 and Z310). Support values (>50) are summarized here on the best ML tree performed with GARLI.

