S5 Appendix. Multispecies coalescent approach

A comparative approach for species delimitation based on multiple methods of multi-locus DNA sequence analysis: a case study of the genus *Giraffa* (Mammalia, Cetartiodactyla)

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Table A. Summary of BPP results obtained in the analyses of the dataset including 21 introns for 66 giraffes.

| Putative species | Bayesian Phylogenetics and Phylogeography (PP) |
|------------------|---------------------------------------------|
|                  | 3S  | 4S  | 5S  | 6S  |
|                  | 1   | 2   | 3   | 1   | 2   | 3   | 1   | 2   | 3   |
| (C) camelopardalis | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (R1) rothschildi  | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (A1) antiquorum   | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (P1) peralta      | -   | -   | -   | -   | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| (A1 R1) antiquorum & rothschildi | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (C R1) camelopardalis & rothschildi | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (C A1) camelopardalis & antiquorum | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (C R1 A1) camelopardalis, rothschildi & antiquorum | -   | -   | -   | -   | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| (C R1 A1 P1) *Giraffa camelopardalis* sensu stricto B | -   | -   | -   | -   | 1.0 | 1.0 | 1.0 | -   | -   |
| (R2) reticulata   | -   | -   | -   | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| (C R1 A1 P1 R2) *Giraffa camelopardalis* sensu stricto A | 1.0 | 1.0 | 1.0 | -   | -   | -   | -   | -   | -   |
| (T1) tippelskirchi| -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (T2) thornicrofti  | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (T1 T2) *Giraffa tippelskirchi* | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 0.74 | 0.6 | 0.65 |
| (G) giraffa       | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (A2) angolensis   | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| (G A2) *Giraffa giraffa* | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |

PP: average posterior probability values; "-": not found.
**Fig A.** MSC species-tree constructed from the nuDNA-G274O6 dataset using *BEAST with the posterior probability values indicated for each node (outgroup taxa *Bos, Ovis, Okapia* not shown).