



**S1 Fig:** Evolutionary relationships of taxa. The evolutionary history was inferred using the Neighbor-Joining method [1]. The evolutionary distances were computed using the Maximum Composite Likelihood method [2]. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA7 [3].

## References

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3. Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. *Mol Biol Evol* 33:1870–1874. <https://doi.org/10.1093/molbev/msw054>