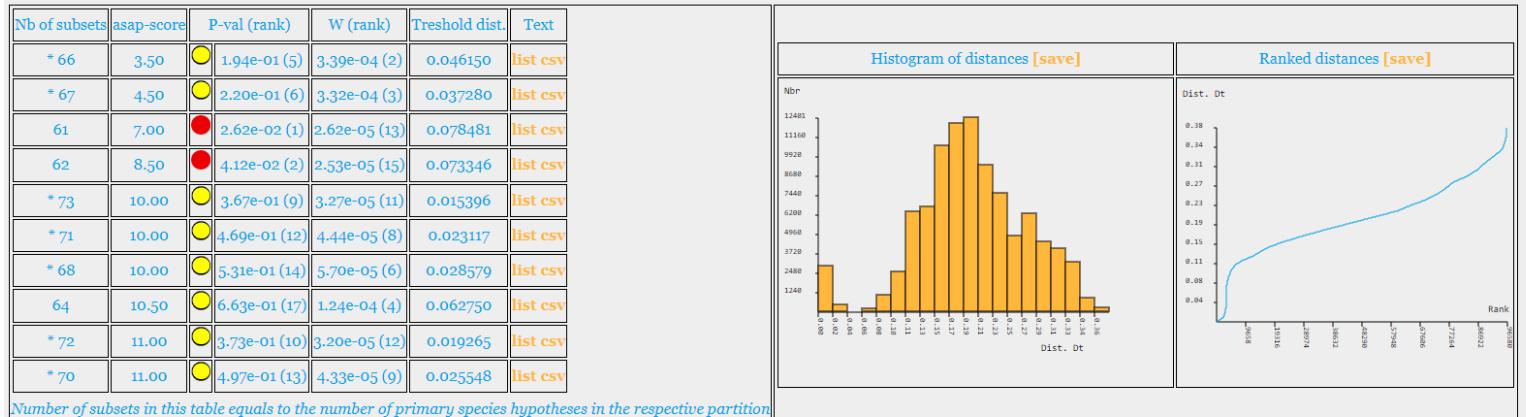
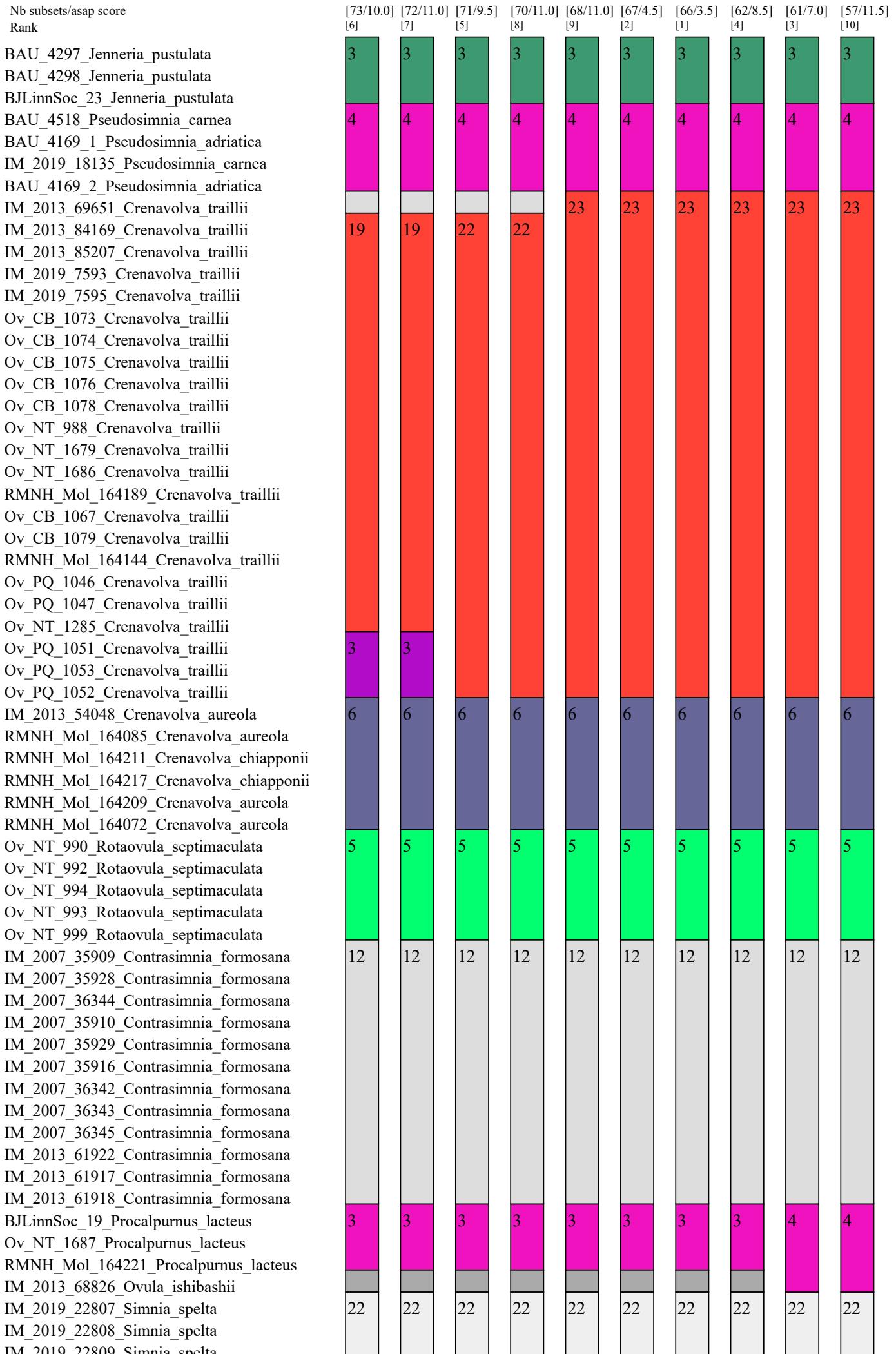
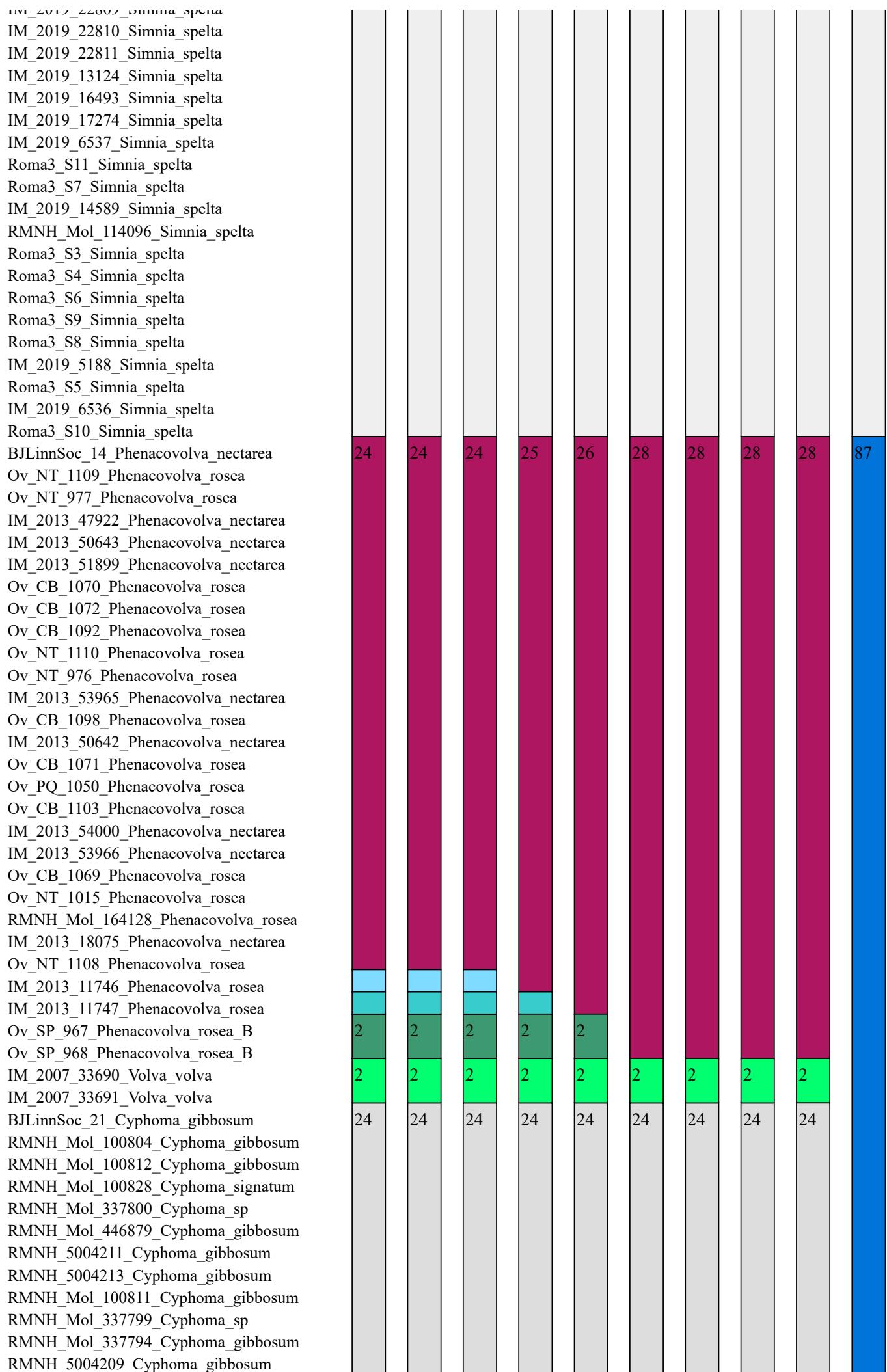


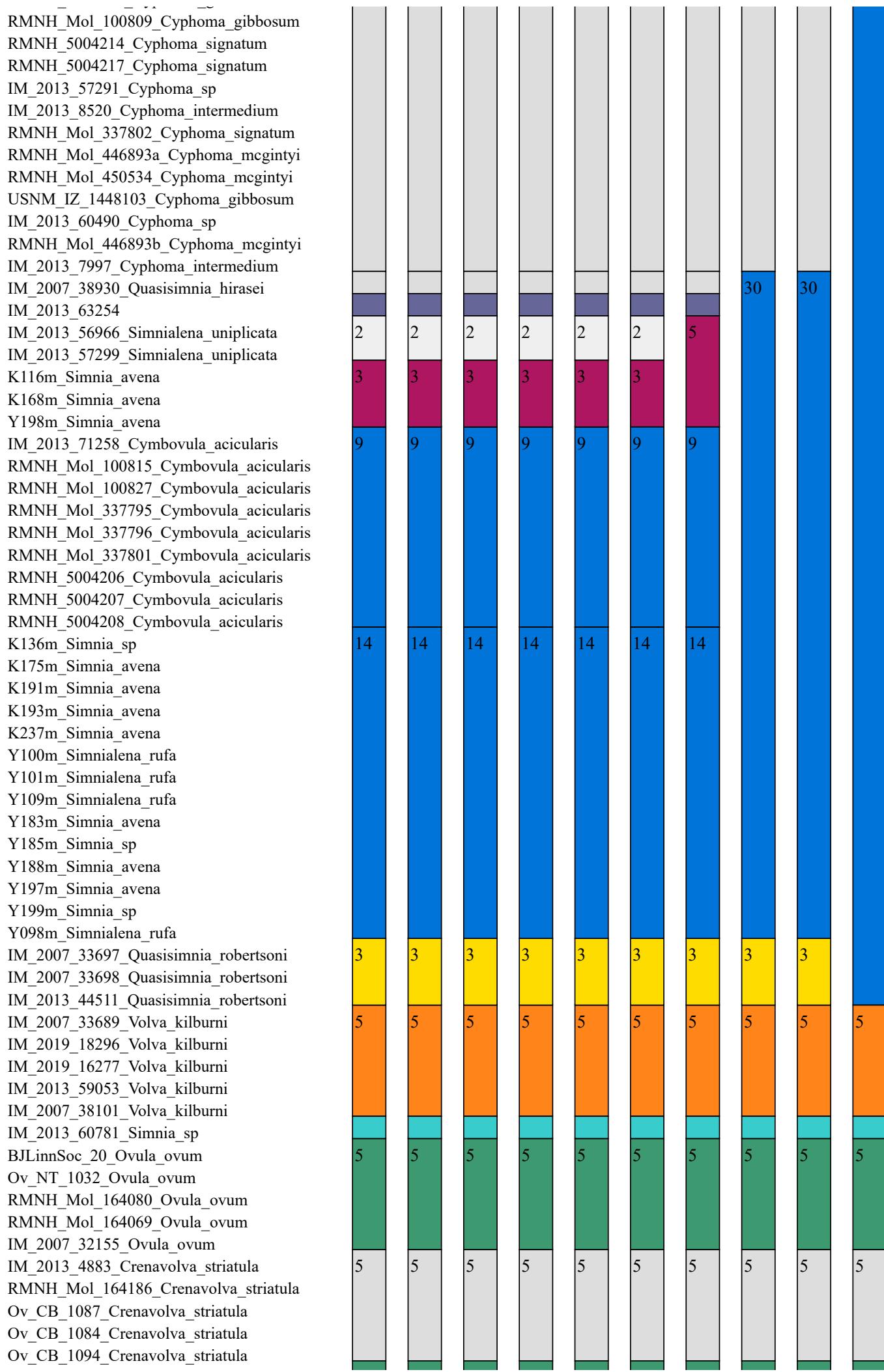
Figure S1. ASAP analysis of the COI dataset. Upper left, ASAP ten best partitions; upper central, ASAP ranked genetic distances; upper right, ASAP histogram of genetic distances; down left, voucher numbers; down right, the ten best partition identified by ASAP (each box correspond to one hypothetical species, the number of specimens included in each group is reported at the top of the box). On the top for each partition is reported the total number of hypothetical species found “Nb groups” and the ASAP score “Score”. “W” = Relative Barcode Gap Width.

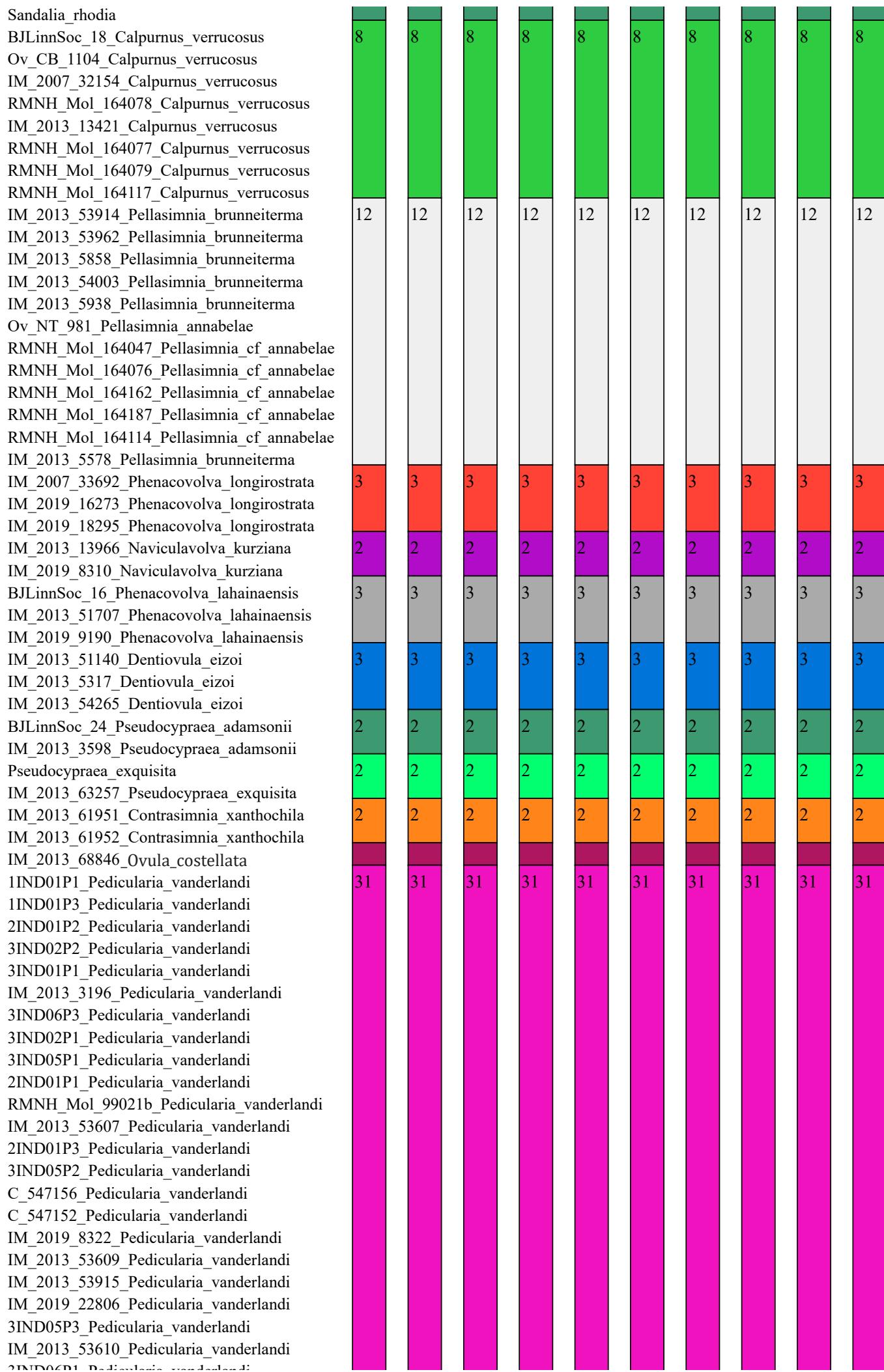


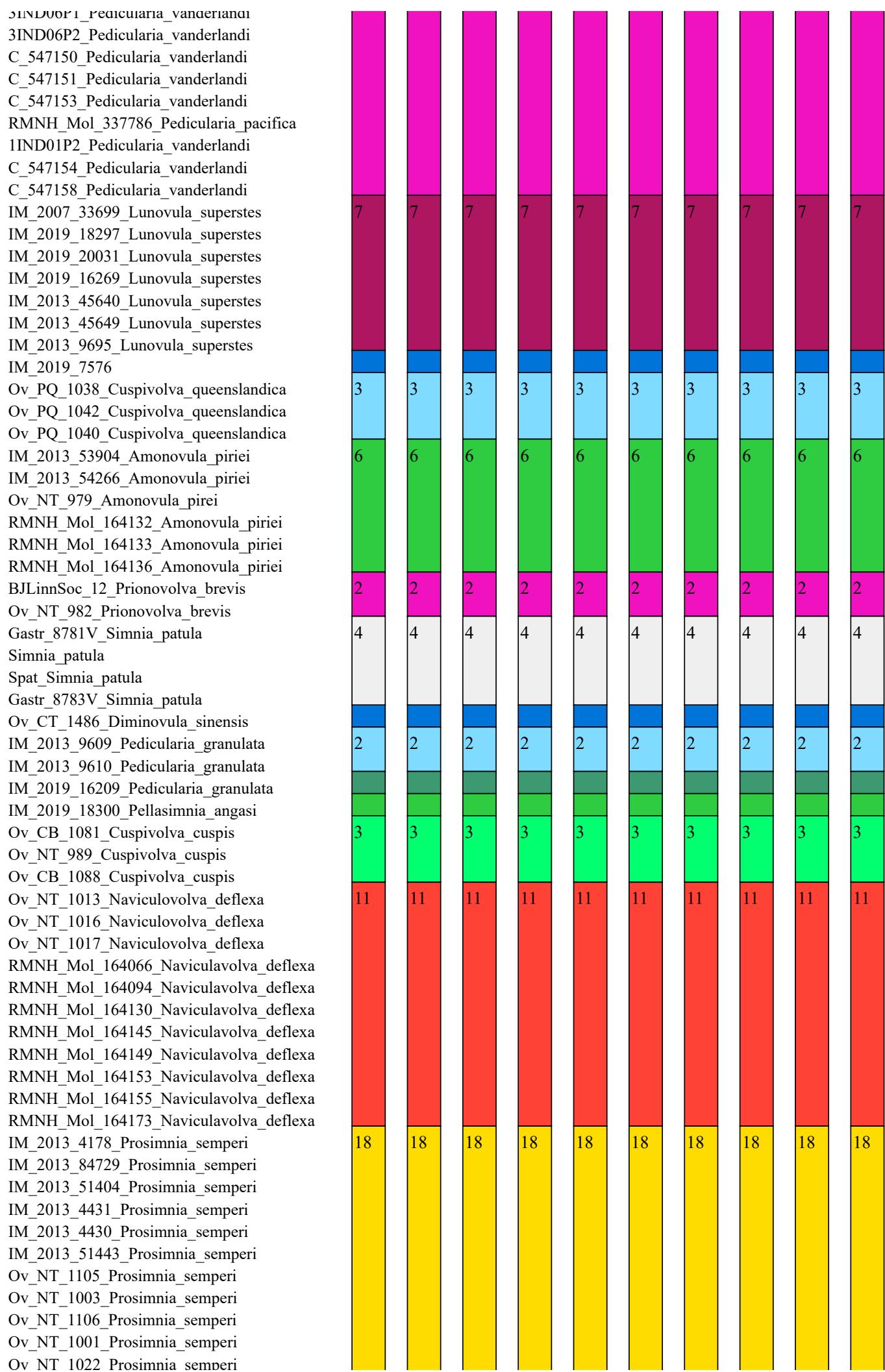
Nb subsets/asap score
Rank

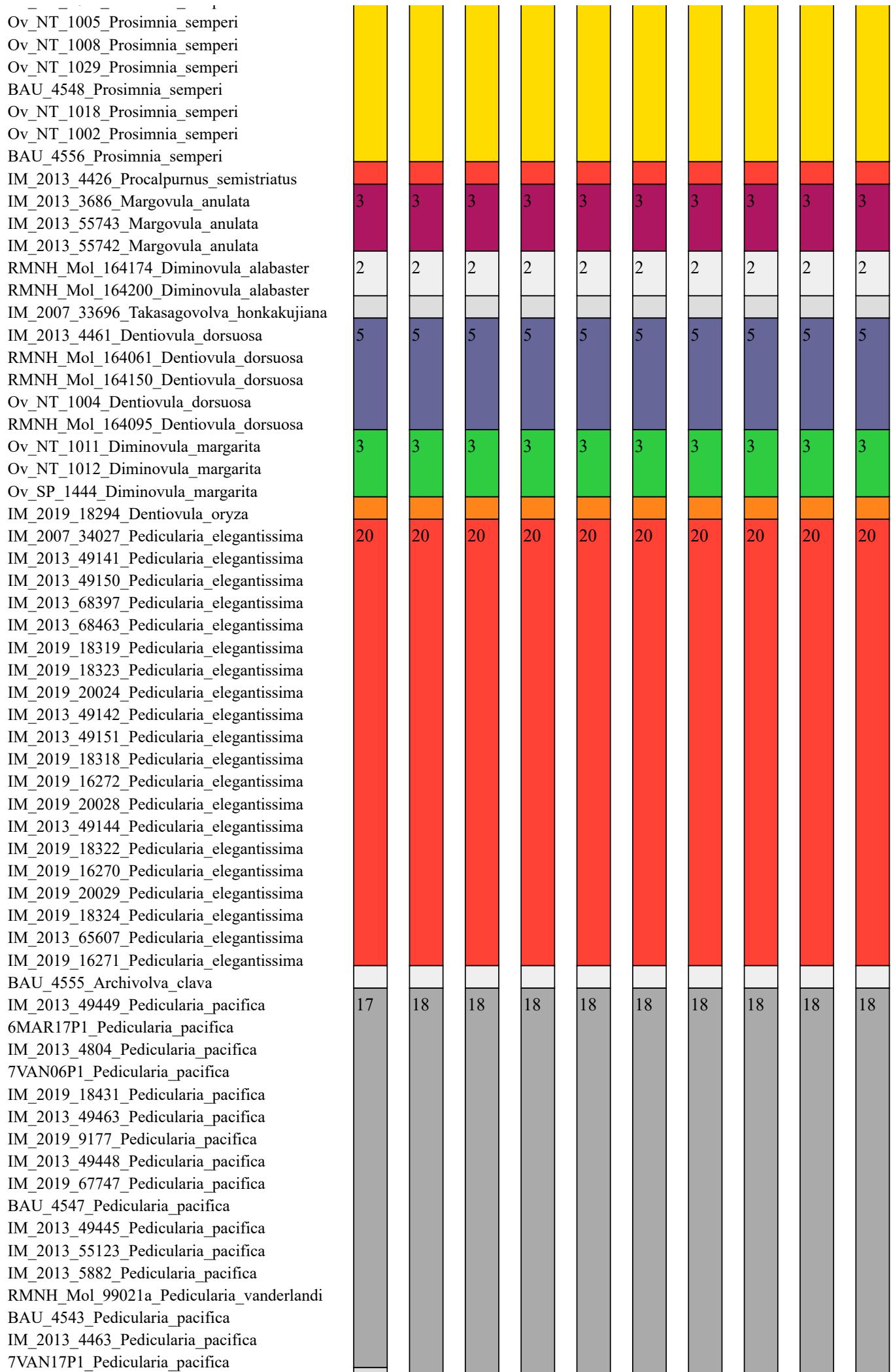


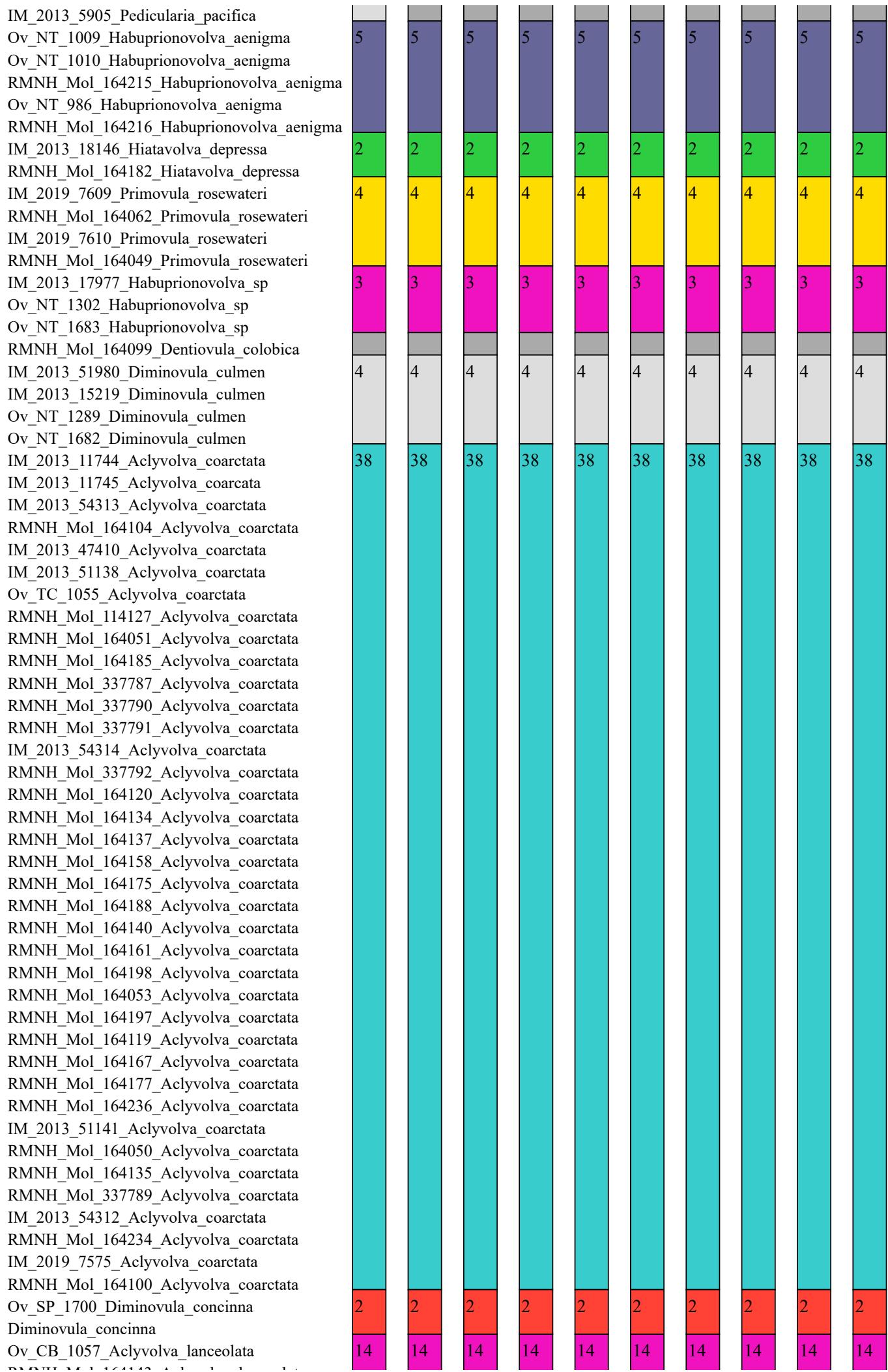












RMNH_Mol_164143_Aclyvolva_lanceolata
RMNH_Mol_164152_Aclyvolva_lanceolata
RMNH_Mol_164154_Aclyvolva_lanceolata
RMNH_Mol_164179_Aclyvolva_lanceolata
RMNH_Mol_164183_Aclyvolva_lanceolata
RMNH_Mol_164190_Aclyvolva_lanceolata
RMNH_Mol_164195_Aclyvolva_lanceolata
RMNH_Mol_164169_Aclyvolva_lanceolata
RMNH_Mol_164192_Aclyvolva_lanceolata
RMNH_Mol_164165_Aclyvolva_lanceolata
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RMNH_Mol_337788_Aclyvolva_lanceolata

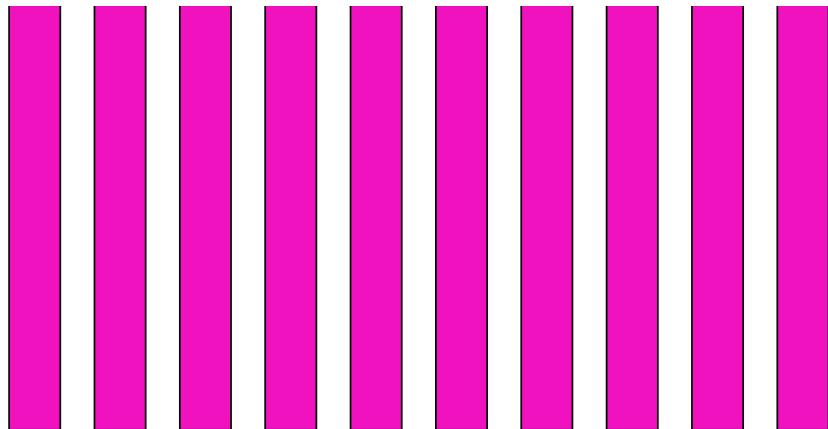


Figure S2. Maximum Likelihood phylogenetic inference on the combined COI-16S-28S combined dataset. Numbers at nodes indicate ultrafast bootstrap values.

```

graph LR
    Root --- Alvania_angioyi
    Root --- Clade[ ]
    Alvania_angioyi --- Clade
    Clade --- Surrepifungium_costulatum
    Clade --- MCZ_DNA101389_Littorina_littorea
    Clade --- MHN_IM_2013_56653_Tonna_galea
    Clade --- BAU_2406_1_Trivia_arctica
    Clade --- BAU_2536_1_Lamellaria_latens
    subgraph Node1 [ ]
        Alvania_angioyi
        Clade
    end
    subgraph Node2 [ ]
        MCZ_DNA101389_Littorina_littorea
        MHN_IM_2013_56653_Tonna_galea
        BAU_2406_1_Trivia_arctica
        BAU_2536_1_Lamellaria_latens
    end
    Alvania_angioyi --- Node1
    Clade --- Node2
    Node1 --- Node2
    
```

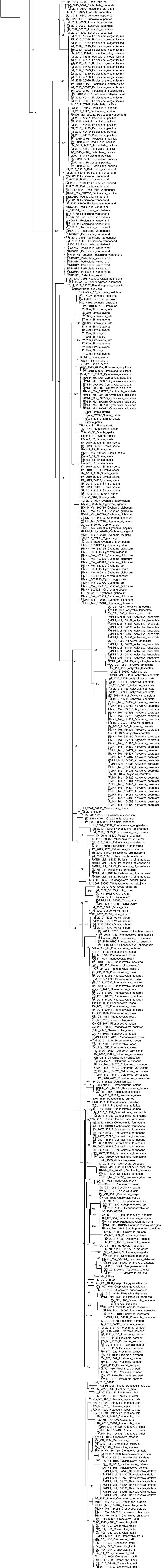


Figure S3. Maximum Likelihood phylogenetic inference on the COI dataset. Numbers at nodes indicate ultrafast bootstrap values.



Figure S4. Maximum Likelihood phylogenetic inference on the 16S dataset. Numbers at nodes indicate ultrafast bootstrap values.

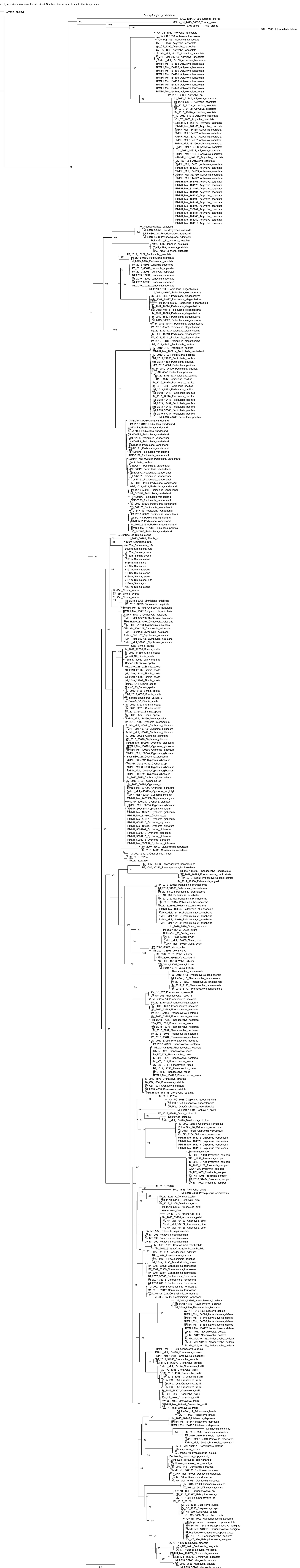


Figure S5. Maximum Likelihood phylogenetic inference on the 28S dataset. Numbers at nodes indicate ultrafast bootstrap values.



Figure S6. Bayesian phylogenetic inference on the COI-16S-28S combined dataset. Numbers at nodes indicate posterior probability value

```

graph LR
    Root --- Alvania_angioyi
    Root --- Surrepifungium_costulatum
    Alvania_angioyi --- MCZ_DNA101389_Littorina_littorea
    Alvania_angioyi --- MNHN_IM_2013_56653_Tonna_galea
    Alvania_angioyi --- BAU_2406_1_Trivia_arctica
    Alvania_angioyi --- BAU_2536_1_Lamellaria_latens
    Alvania_angioyi --- IM_2012_16292_Dendrodoa_rubris
    MCZ_DNA101389_Littorina_littorea --- MNHN_IM_2013_56653_Tonna_galea
    MNHN_IM_2013_56653_Tonna_galea --- BAU_2406_1_Trivia_arctica
    BAU_2406_1_Trivia_arctica --- BAU_2536_1_Lamellaria_latens
    
```

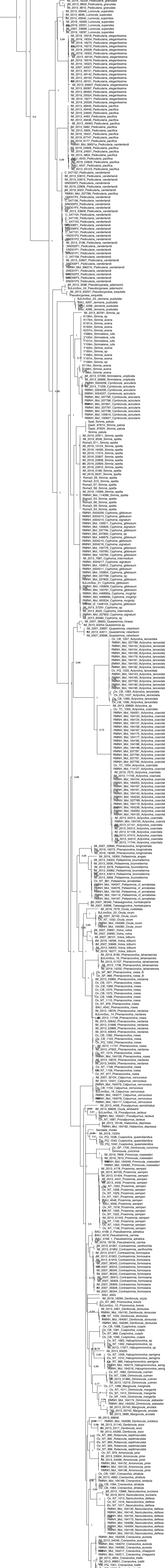


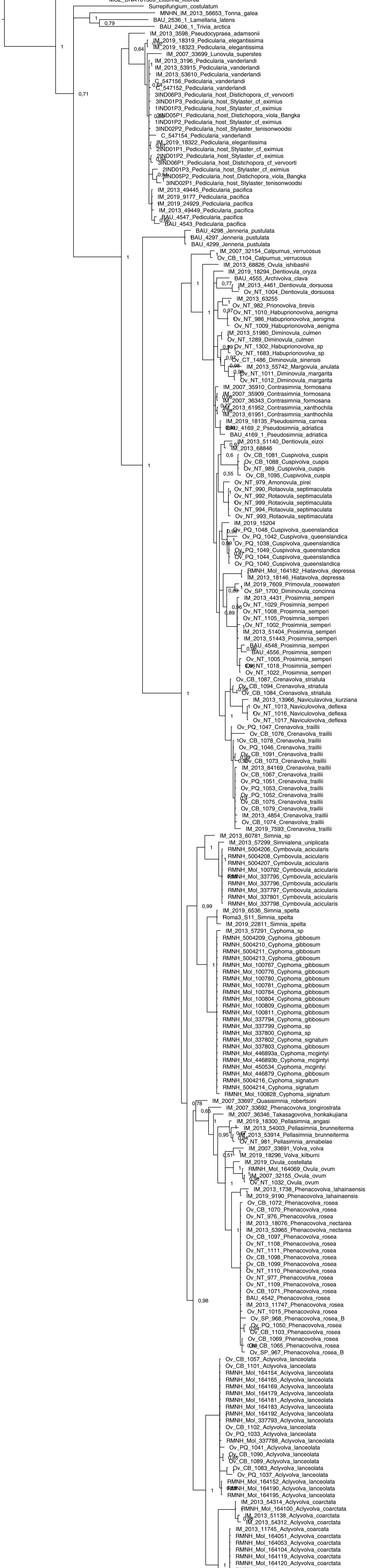
Figure S7. Bayesian phylogenetic inference on the COI dataset. Numbers at nodes indicate posterior probability values.



Figure S8. Bayesian phylogenetic inference on the 16S dataset. Numbers at nodes indicate posterior probability values.



Figure S9. Bayesian phylogenetic inference on the 28S dataset. Numbers at nodes indicate posterior probability values.



0.03

Supplementary Material: tables

Table S1. List of gastropod samples used in this study, along with voucher registration numbers, collection localities, number of localities corresponding to orange points on the map (Fig. 2), cnidarian hosts and GenBank accession numbers for sequences; the names correspond to the morphological identification of each specimen (PSH); * indicates samples included in the combined dataset used for the macroevolutionary analysis; ° indicates identification of the coral host based on both morphology and molecular data.

Table S2. List of cnidarians associated with ovulids samples used in this study, along with voucher registration numbers, collection localities, and GenBank accession numbers for sequences.