

# Files changed

This file lists all changes that were made in the project directory (corresponding to the ~/Grive/Slater\_Lab/Charadriiformes path referenced in the bash and R scripts) between the original submission (July 16, 2021, also corresponding to the bioRxiv preprint) and the revised submission (June 2, 2022). Changed files are in **black**; deleted files are in **red**; newly added files are in **blue**. The list is organized in the order in which the corresponding analyses are described in the paper.

## Taxonomy and data assembly (section 2.1)

### [./Changelog.pdf](#)

- This file added.

### [./charadriiformes\\_sampling.numbers](#)

- Removed as redundant with respect to Coverage.csv

### [./Coverage.csv](#)

- *Actophilornis africanus*: sequence data added (ADNH: DQ674656.1)
- *Actophilornis albinucha*: sequence data added (CytB: accession number to be decided)
- *Aethia cristatella*: sequence data replaced (Cox1: changed from EF380315.1 to MN337912.1, CytB: changed from U37087.1 – misrecorded as “ACU37087.1” to MN337912.1, ND6: changed from X73928.1 to MN337912.1)
- *Aethia psittacula*: incorrect accession number fixed (CytB: from CPU37296.1 to U37296.1)
- *Aethia pusilla*: incorrect accession number fixed (CytB: from APU37104.1 to U37104.1)
- *Aethia pygmaea*: incorrect accession number fixed (CytB: from APU37286.1 to U37286.1)
- *Alca torda*: sequence data replaced (12S: changed from EF373065.1 to MN356408.1, 16S: changed from EF380281.1 to MN356408.1, Cox1: changed from EF380318.1 to MN356408.1, CytB: changed from U37288.1 – misrecorded as “ATU372288.1” – to MN356408.1, Myo2: changed from AY339074.1 to VZSD01016873.1 from whole-genome shotgun sequence, ND2: changed from EF373220.1 to MN356408.1, ND5: changed from AJ242683.1 to MN356408.1, ND6: changed from X73916.1 to MN356408.1). The new Myo2 sequence is slightly longer.
- *Alca torda*: sequence data added (ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L: MN356408.1, from whole-genome shotgun sequence: ADNH: VZSD01003049.1, ALDOB: VZSD01012097.1, BDNF: VZSD01002125.1, c-mos: VZSD01000344.1, FGB7: VZSD01011907.1, GAPDH: VZSD01009222.1, NTF3: VZSD01016944.1)
- *Alle alle*: incorrect accession number fixed (CytB: from AAU37287.1 to U37287.1)
- *Anous minutus*: sequence data added (12S: AY631320.1)
- *Anous stolidus*: sequence data added (12S: AY631321.1)
- *Anous tenuirostris*: sequence data replaced (12S: changed from EF373066.1 to AY631322.1, ND2: changed from EF373223.1 to KU601378.1). The new 12S sequence is substantially longer. The old ND2 sequence was misidentified, as it grouped with *Gallinago stenura* rather than other species of *Anous* or any other larid.
- *Arenaria interpres*: sequence data replaced (12S: changed from NC\_003712.1 to AY074885.2, 16S: changed from AY074885.1 to AY074885.2, Cox1: changed from NC\_003712.1 to AY074885.2, CytB: changed from AF417928.1 – misrecorded as “AF417120.1” – to AY074885.2, ND2: changed from AY074885.1 to AY074885.2, ND3: changed from AY074885.1

to AY074885.2, ND4: changed from AY074885.1 to AY074885.2, ND4L: changed from AY074885.1 to AY074885.2, ND5: changed from AY074885.1 to AY074885.2, ND6: changed from AF411401.1 to AY074885.2, NTF3: changed from EU740247.1 to VXAK01012496.1 from whole-genome shotgun sequence). Note that while “NC\_003712” and “AY074885” refer to the same sequence, NC\_003712.1 represents an older version of it than AY074885.2. The new NTF3 sequence is slightly longer.

- *Arenaria interpres*: sequence data added (FGB7: EU739369.1, from whole-genome shotgun sequence: ADNH: VXAK01013147.1, c-mos: VXAK01012117.1, GAPDH: VXAK01007474.1)
- *Attagis malouinus*: sequence data added (CytB: JQ963041.1, ND2: JQ963018.1)
- *Burhinus bistriatus*: sequence data replaced (12S: changed from DQ674587.1 to MN356222.1, 16S: changed from DQ674625.1 to MN356222.1, Cox1: changed from JQ174203.1 to MN356222.1, FGB7: changed from AY695198.1 to VYXH01002573.1 from whole-genome shotgun sequence, RAG1: changed from AY339103.1 to VYXH01005721.1 from whole-genome shotgun sequence). The new FGB7 and RAG1 sequences are substantially longer.
- *Burhinus bistriatus*: sequence data added (ATP6, ATP8, Cox2, Cox3, CytB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: MN356222.1, from whole-genome shotgun sequence: c-mos: VYXH01000819.1)
- *Burhinus capensis*: sequence data added (Cox1: MF580171.1)
- *Burhinus grallarius*: sequence data removed (12S: DQ385270.1, 16S: DQ385287.1, ALDOB: JX470583.1, ATP6: DQ385236.1 – misrecorded as “DW385236.1”, ATP8: DQ385253.1, BDNF: JX470604.1 – misrecorded as “JX4700604.1”, Cox1: DQ385168.1, Cox2: DQ385185.1, Cox3: DQ385202.1, CytB: DQ385219.1, ND1: DQ385066.1, ND2: DQ385083.1, ND3: DQ385100.1, ND4: DQ385134.1, ND4L: DQ385117.1, ND5: DQ385151.1, NTF3: JX470668.1, RAG1: AY228769.1). GenBank classifies the ALDOB, BDNF, and NTF3 sequences as *B. grallarius*, but the original paper of Baker et al. (2012) clarifies that they come from the Beach thick-knee *Burhinus magnirostris*. The same applies to the mitochondrial sequences, where the original paper (Paton & Baker 2006; doi:10.1016/j.ympev.2006.01.011) also lists the species in question as the Beach thick-knee *Burhinus magnirostris*. Finally, the RAG1 sequence also suffers from the same problem; the original paper (Paton et al. 2003; doi:10.1016/S1055-7903(03)00098-8) once again lists the species as the Beach thick-knee *Burhinus magnirostris*. Despite the convoluted history of the scientific name *Burhinus magnirostris*, the English vernacular name makes it clear which species was meant: the Beach stone-curlew (= Beach thick-knee) *Esacus magnirostris*. This problem has been pointed out to us by John Boyd. Corresponding row not deleted (the species is valid, only unsampled).
- *Burhinus oediconemus*: sequence data replaced (FGB7: changed from EF552756.1 to VFFE01007663.1 from whole-genome shotgun sequence). The new sequence is substantially longer.
- *Burhinus oediconemus*: sequence data added (Cox3: AF076345.1, from whole-genome shotgun sequence: ADNH: VFFE01007878.1, ALDOB: VFFE01007614.1, BDNF: VFFE01007173.1, c-mos: VFFE01007699.1, GAPDH: VFFE01006113.1, Myo2: VFFE01006550.1, NTF3: VFFE01006620.1, RAG1: VFFE01009229.1). Note that only a short fragment of the ADNH sequence could be obtained.
- *Burhinus superciliaris*: sequence data added from BOLD (Cox1: BROM211-06)
- *Burhinus vermiculatus*: sequence data added from BOLD (Cox1: BROM391-06)
- *Calidris acuminata*: sequence data added (ATP8: EU826414.1)
- *Calidris alpina*: sequence data replaced (12S: changed from KF041183.1 to MN122893.1, Cox1: changed from KF009520.1 to MN122893.1, CytB: changed from KC969154.1 – misrecorded as “KC060154.1” – to U34686.1, ND2: changed from AY156135.1 to MN122893.1). The new CytB sequence is slightly longer.
- *Calidris alpina*: sequence data added (16S, ATP6, ATP8, Cox2, ND1: MN122893.1)
- *Calidris bairdii*: missing accession number added (ND2: KC969093.1). The sequence itself was used but not listed.
- *Calidris canutus*: sequence data replaced (12S: changed from KF041185.1 to MT183697.1, Cox1: changed from DQ432799.1 to MT183697.1, CytB: changed from KC969156.1 to MT183697.1, ND2: changed from KC969094.1 to MT183697.1)
- *Calidris canutus*: sequence data added (16S, ATP6, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MT183697.1). Note that the mitogenome does not include an ATP8 sequence.
- *Calidris himantopus*: sequence data added (12S: KF041188.1)

- *Calidris pusilla*: sequence data added (12S: KF041195.1)
- *Calidris pygmaea*: sequence data replaced (Cox1: changed from KF009532.1 to KY434065.1)
- *Calidris pygmaea*: sequence data added from whole-genome shotgun sequence (ADNH: QJSC01013933.1, ALDOB: QJSC01007472.1, BDNF: QJSC01026553.1, c-mos: QJSC01026092.1, FGB7: QJSC01023112.1, GAPDH: QJSC01029153.1, Myo2: QJSC01008973.1, NTF3: QJSC01018987.1)
- *Calidris ruficollis*: sequence data replaced (Cox1: changed from KF009527.1 to MG736926.1, CytB: changed from FJ499023.1 to MG736926.1)
- *Calidris subminuta*: missing accession number added (RAG1: KC969132.1). The sequence itself was used but not listed.
- *Calidris tenuirostris*: sequence data replaced (12S: changed from KF041199.1 to MK992912.1, ATP6, ATP8: changed from EU826406.1 to MK992912.1, Cox1: changed from KF009530.1 to MK992912.1, CytB: changed from KC969170.1 to MK992912.1, ND2: changed from KC969108.1 to MK992912.1, ND6: changed from AF411396.1 to MK992912.1)
- *Calidris tenuirostris*: sequence data added (16S, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5: MK992912.1)
- *Catharacta antarctica*: incorrect accession numbers fixed (12S: from CAU76771.1 to U76771.1, CytB: from CAU76793.1 to U76793.1)
- *Catharacta antarctica*: sequence data replaced (12S: changed from U76771.1 – misrecorded as “CAU76771.1” – to U76774.1). The latter sequence belongs to another subspecies (*Stercorarius antarcticus hamiltoni*) and is 8 bp longer.
- *Catharacta chilensis*: incorrect accession numbers fixed (12S: from CCU76770.1 to U76770.1, CytB: from CCU76779.1 to U76779.1)
- *Catharacta chilensis*: sequence data added from BOLD (Cox1: BROM637-07)
- *Catharacta hamiltoni*: row deleted. This taxon is now considered to represent a subspecies of *Stercorarius antarcticus* (formerly *Catharacta antarctica*) by both Boyd (2019) and Clements et al. (2021). Note that the taxon did not have to be removed from the analysis, as this was already done during taxonomic reconciliation. Upon its removal from the table, we merely checked that its locus coverage is redundant with respect to *S. antarcticus* (yes: 12S, CytB sampled for both) and that its sequences for the overlapping loci (12S: U76774.1 – misrecorded as “CHU76774.1”, CytB: U76796.1 – misrecorded as “CHU76796.1”) are of the same length or shorter. The 12S sequence turned out to be longer, and so replaced the original sequence of *C. antarctica* for this locus (see above).
- *Catharacta longbergi* [sic]: row deleted. This taxon (correct spelling: *Catharacta lonnbergi*) is now considered to represent a subspecies of *Stercorarius antarcticus* (formerly *Catharacta antarctica*) by both Boyd (2019) and Clements et al. (2021). Note that the taxon did not have to be removed from the analysis, as this was already done during taxonomic reconciliation. Upon its removal from the table, we merely checked that its locus coverage is redundant with respect to *S. antarcticus* (yes: 12S, CytB sampled for both) and that its sequences for the overlapping loci (12S: U76769.1 – misrecorded as “CLU76769.1”, CytB: U76786.1 – misrecorded as “CLU76786.1”) are of the same length or shorter.
- *Catharacta maccormicki*: incorrect accession number fixed (CytB: from KM201546.1 to KM401546.1)
- *Catharacta skua*: sequence data replaced (CytB: changed from U76810.1 – misrecorded as “CSU76810.1” – to DQ385227.1)
- *Catoptrophorus semipalmatus*: sequence data removed (ATP6, ATP8, Cox2, Cox3, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: MF036175.1, 12S: KF041200.1, 16S: AY894156.1, c-mos: AY894190.1, Cox1: NC\_036016.1, CytB: AY894224.1, RAG1: AY894207.1). The mitogenome MF036175.1 (for which NC\_036016.1 is just an alternative reference) actually belongs to subspecies *Tringa* (formerly *Catoptrophorus*) *semipalmata inornata* (Bi 2017; doi:10.1080/23802359.2017.1339213), recently raised to the species status (Oswald et al. 2016; doi:10.1642/AUK-15-232.1; see below). The 16S, c-mos, CytB, and RAG1 sequences all come from the same study (Pereira & Baker 2005; doi:10.1093/condor/107.3.514) and voucher specimen (RCA87-181), and have been removed because after the separation of *T. inornata* from *T. semipalmata sensu stricto*, they are no longer identifiable to the species level. The same applies to the 12S sequence from Gibson & Baker (2012; doi:10.1016/j.ympev.2012.03.008); these authors did not identify their isolate to the subspecies level, either.

- *Catoptrophorus semipalmatus*: sequence data added (Cox1: BROM064-06 from BOLD, ND2: KU854970.1). The Cox1 sequence is specifically attributed to the subspecies *semipalmata* in BOLD; the ND2 sequence was confirmed by Oswald et al. (2016) to specifically come from *T. semipalmata semipalmata*.
- *Cepphus carbo*: incorrect accession number fixed (CytB: from CCU37292.1 to U37292.1)
- *Cepphus carbo*: sequence data replaced (Cox1: changed from EF380324.1 to GQ481535.1). The former sequence incorrectly nested the taxon within *Brachyramphus*.
- *Cepphus grylle*: sequence data replaced (12S: changed from AJ242688.1 to MN356419.1, Cox1: changed from GU571326.1 to MN356419.1, CytB: changed from U37294.1 – misrecorded as “CGU37294.1” – to MN356419.1, ND5: changed from AJ242688.1 to MN356419.1, ND6: changed from X73917.1 to MN356419.1)
- *Cepphus grylle*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND2, ND3, ND4, ND4L: MN356419.1, from whole-genome shotgun sequence: ADN1: VZUD01000029.1, ALDOB: VZUD01001033.1, BDNF: VZUD01000014.1, c-mos: VZUD01000002.1, FGB7: VZUD01000029.1, GAPDH: VZUD01000118.1, Myo2: VZUD01000109.1, NTF3: VZUD01000177.1, RAG1: VZUD01000303.1)
- *Cerorhinca monocerata*: incorrect accession number fixed (CytB: from CMU37295.1 to U37295.1)
- *Cerorhinca monocerata*: sequence data replaced (Cox1: changed from EF380326.1 to EU525337.1). The former sequence incorrectly nested the taxon within *Synthliboramphus*.
- *Charadrius alexandrinus*: sequence data replaced (Cox1: changed from NC\_041118.1 to MF565382.1, CytB: changed from AF417931.1 to MF565382.1, FGB7: changed from KM001428.1 to VUYV01000031.1 from whole-genome shotgun sequence, Myo2: changed from KM001172.1 – misrecorded as “KM001171.1” – to VUYV01000082.1 from whole-genome shotgun sequence, ND3: changed from AM941579.1 to MF565382.1, ND6: changed from AF411407.1 to MF565382.1, RAG1: changed from KM001510.1 to VUYV01000240.1 from whole-genome shotgun sequence). Note that while the study that sequenced the mitogenome MF565382.1 (Chen et al. 2018; doi:10.1007/s13258-018-0703-3) did not identify the voucher specimen to the subspecies level, we can nevertheless be reasonably confident that it belongs to *C. alexandrinus* rather than *C. dealbatus*, since it was collected from Rudong, Jiangsu Province, which falls outside the range of the latter species (Sadanandan et al. 2019; doi:10.1038/s41598-019-44996-5; Wang et al. 2019a; doi:10.1186/s12862-019-1449-5; see also Clements et al. 2021). Similarly, Dos Remedios et al. (2015) report in their Supplementary Table 1 that their sequence data (including ADN1) come from a specimen collected at Cape Verde, i.e., completely outside of the geographic range of *C. dealbatus*. For the whole-genome shotgun sequence, Feng et al. (2020: Supplementary Table 1) state they were unable to determine the subspecies identity of the specimen from which it was extracted, and the locality they give (Xitou, Yangjiang County, Guangdong Province) lies well within the breeding range of *C. dealbatus*. However, Wang et al. (2019b; doi:10.3389/fgene.2019.00919) confirm that this specimen was in fact *C. alexandrinus*.
- *Charadrius alexandrinus*: sequence data added from whole-genome shotgun sequence (ALDOB: VUYV01000023.1, BDNF: VUYV01000218.1, c-mos: VUYV01000158.1, GAPDH: VUYV01000166.1, NTF3: VUYV01000280.1).
- *Charadrius alticola*: incorrect accession number fixed (Myo2: from KM00175.1 to KM001175.1)
- *Charadrius alticola*: sequence data added from the unpublished data of Dos Remedios et al. 2015 (RAG1: RAG1\_alticola1a)
- *Charadrius asiaticus*: sequence data added from the unpublished data of Dos Remedios et al. 2015 (ADN1: ADH5\_asiaticu3a, FGB7: FGB7\_asiaticu1a, Myo2: MYO2\_asiaticu3a)
- *Charadrius australis*: incorrect accession number removed (ND5: JX470680.1). This number refers to the already listed NTF3 sequence.
- *Charadrius australis*: sequence data added from BOLD (Cox1: BROM690-07)
- *Charadrius bictinctus*: incorrect accession number fixed (Myo2: from KM00178.1 to KM001178.1)
- *Charadrius bicinctus*: sequence data added (CytB: AH003633.2, from the unpublished data of Dos Remedios et al. 2015: FGB7: FGB7\_bicinctu1a)
- *Charadrius dealbatus* **[added species]**: sequence data added (ATP6 and ATP8: MK830738.1, ND3: MK830754.1). Note that it is difficult to determine which sequences belong to *C. alexandrinus* and which to *C. dealbatus* (see below); in GenBank, all are referred to simply as *C.*

*alexandrinus*, and in their paper (or the supplement thereto), Wang et al. (2019a) do not provide any table that breaks down the accession numbers by species, either. However, their Table 1 shows that each species was sampled from a distinct set of localities, and the letters in the names of the GenBank isolates represent the syllabic acronyms of these localities. The ATP6/ATP8 and ND3 sequences both come from isolate BH\_1; BH refers to the Beihai locality, from which only *C. dealbatus* was sampled (see Wang et al. 2019a: Table 1).

- *Charadrius dubius*: incorrect accession number removed (12S: KM001185.1). This number refers to the already listed Myo2 sequence.
- *Charadrius forbesi*: sequence data added from the unpublished data of Dos Remedios et al. 2015 (ADNH: ADH5\_forbesi01a, FGB7: FGB7\_forbesi01a, ND3: ND3\_forbesi02a, RAG1: RAG1\_forbesi01a)
- *Charadrius hiaticula*: incorrect accession number fixed (Cox1: from KGU571811.1 to GU571811.1)
- *Charadrius marginatus*: sequence data added (ATP8: AM941618.2)
- *Charadrius modestus*: sequence data added (ATP6: FM995619.1)
- *Charadrius mongolus*: sequence data replaced (12S: changed from LC104770.1 to MW298528.1, Cox1: changed from GQ481570.1 to MW298528.1, CytB: changed from AF417927.1 to MW298528.1, ND3: changed from KM001377.1 to MW298528.1, ND6: changed from AF411400.1 to MW298528.1)
- *Charadrius mongolus*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND2, ND4, ND4L, ND5: MW298528.1)
- *Charadrius obscurus*: sequence data added from the unpublished data of Dos Remedios et al. 2015 (ADNH: ADH5\_obscurus1a, Myo2: MYO2\_obscurus2a, ND3: ND3\_obscurus1a)
- *Charadrius peronii*: sequence data added (ATP6: FR822417.1, from the unpublished data of Dos Remedios et al. 2015: ADNH: ADH5\_peroni001a, FGB7: FGB7\_peroni001a, Myo2: MYO2\_peroni001a, RAG1: RAG1\_peroni001a)
- *Charadrius placidus*: sequence data removed (12S, 16S, ATP6, ATP8, Cox1, Cox2, CytB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: KY419888.1). The complete mitogenome is misidentified and actually belongs to *Charadrius alexandrinus* (Sangster & Luksenburg 2021; see also Päckert 2021; doi:10.1111/ibi.13005).
- *Charadrius placidus*: sequence data added (Cox1: MT602072.1, from the unpublished data of Dos Remedios et al. 2015: ADNH: ADH5\_placidu02a, FGB7: FGB7\_placidus1a, Myo2: MYO2\_placidus1a)
- *Charadrius semipalmatus*: sequence data added (RAG1: KM001568.1).
- *Charadrius tricoloris*: sequence data added (FGB7: KX371208.1)
- *Charadrius veredus*: sequence data replaced (Cox1: changed from KM001332.1 to BROM681-07 from BOLD). The former sequence incorrectly nested the taxon within the Glareolidae.
- *Charadrius vociferus*: sequence data replaced (12S: changed from DQ485792.1 to MN356113.1, 16S: changed from DQ385286.1 to MN356113.1, ADNH: changed from KM001164.1 to JMF02045512.1 from whole-genome shotgun sequence, ATP6: changed from DQ385235.1 to MN356113.1, ATP8: changed from DQ385252.1 to MN356113.1, Cox1: changed from DQ385167.1 to MN356113.1, Cox2: changed from DQ385184.1 to MN356113.1, Cox3: changed from DQ385201.1 to MN356113.1, CytB: changed from DQ485890.1 to MN356113.1, FGB7: changed from KM001503.1 to JMF02077956.1 from whole-genome shotgun sequence, Myo2: changed from KM001251.1 to JMF02023182.1 from whole-genome shotgun sequence, ND1: changed from DQ385065.1 to MN356113.1, ND2: changed from DQ385082.1 to MN356113.1, ND3: changed from KM001420.1 to MN356113.1, ND4: changed from DQ385133.1 to MN356113.1, ND4L: changed from DQ385116.1 to MN356113.1, ND5: changed from DQ385150.1 to MN356113.1). The new ADNH, FGB7, and Myo2 sequences are longer.
- *Charadrius vociferus*: sequence data added (ND6: MN356113.1, from whole-genome shotgun sequence: JMF02064083.1)
- *Chionis albus*: sequence data added from BOLD (Cox1: BROM503-07)
- *Chionis minor*: sequence data replaced (12S: changed from DQ385272.1 to MN356383.1, 16S: changed from DQ385289.1 to MN356383.1, ATP6: changed from DQ385238.1 to MN356383.1, ATP8: changed from DQ385255.1 to MN356383.1, Cox1: changed from DQ385170.1 to MN356383.1, Cox2: changed from DQ385187.1 to MN356383.1, Cox3: changed from DQ385204.1 to MN356383.1, CytB: changed from DQ385221.1 to MN356383.1, ND1: changed

from DQ385068.1 to MN356383.1, ND2: changed from DQ385085.1 to MN356383.1, ND3: changed from DQ385102.1 to MN356383.1, ND4: changed from DQ385136.1 to MN356383.1, ND4L: changed from DQ385119.1 to MN356383.1, ND5: changed from DQ385153.1 to MN356383.1)

- *Chionis minor*: sequence data added (ND6: MN356383.1, from whole-genome shotgun sequence: ADN: VZSF01000004.1, ALDOB: VZSF01001212.1, BDNF: VZSF01006330.1, c-mos: VZSF01009658.1, FGB7: VZSF01008499.1, GAPDH: VZSF01009116.1, Myo2: VZSF01010064.1, NTF3: VZSF01010994.1)
- *Chlidonias albostratus*: sequence data added (12S: AY631331.1)
- *Chlidonias hybrida*: sequence data added (12S: AY631323.1)
- *Chlidonias leucopterus*: sequence data replaced (12S: changed from EF373073.1 to AY631324.1). The new sequence is substantially longer.
- *Chlidonias niger*: sequence data added (12S: AY631325.1)
- *Chroicocephalus poiocephalus* **[added species]**: sequence data added (ATP6 and ATP8: AY584119.1, ND2: AY590395.1, ND5: AY590415.1). The sequences all come from voucher specimen MKP 1477, which is listed in Table 1 of Given et al. (2005) as belonging to *L. cirrocephalus poiocephalus*.
- *Coenocorypha aucklandica*: sequence data removed (12S: EF373075.1, ATP6 and ATP8: GQ452548.1, Cox1: GQ452686.1, Cox2: GQ452472.1, CytB: EF373126.1, ND2: EF373233.1, RAG1: EF373177.1). The 12S, CytB, ND2, and RAG1 sequences (all from Baker et al. 2007) have all been removed because after the separation of *C. huegeli* from *C. aucklandica sensu stricto*, they are no longer identifiable to the species level. The Cox1 and Cox2 sequences (both from Baker et al. 2010; doi:10.1007/s10592-009-9965-2) have been removed for the same reason. The ATP6 and ATP8 sequences have been removed because they belong to *C. huegeli* rather than *C. aucklandica* (see above).
- *Coenocorypha aucklandica*: sequence data added (ATP6 and ATP8: GQ452502.1, Cox1: GQ452606.1, Cox2: GQ452398.1)
- *Coenocorypha huegeli* **[added species]**: sequence data added (ATP6 and ATP8: GQ452548.1, Cox1: GQ452652.1, Cox2: GQ452444.1)
- *Coenocorypha pusilla*: sequence data added (CytB: JQ963042.1)
- *Creagrus furcatus*: sequence data added from BOLD (Cox1: BROM401-06)
- *Cursorius cursor*: sequence data added from BOLD (Cox1: SIBSI010-19)
- *Dromas ardeola*: incorrect accession number fixed (BDNF: from EU7380000.1 to EU738000.1)
- *Dromas ardeola*: sequence data replaced (12S: changed from HM369462.1 to MN356323.1, Cox1: changed from KU722492.1 to MN356323.1, CytB: changed from HM369461.1 to MN356323.1, ND2: changed from HM369460.1 to MN356323.1)
- *Dromas ardeola*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MN356323.1, from whole-genome shotgun sequence: ADN: VYZM01014165.1, ALDOB: VYZM01001791.1, c-mos: VYZM01022238.1, GAPDH: VYZM01000086.1)
- *Elseya melanops*: sequence data added (Cox1: MK262581.1)
- *Erythrogonys cinctus*: sequence data added from BOLD (Cox1: BROM688-07)
- *Esacus giganteus*: sequence data added (12S: DQ385270.1, 16S: DQ385287.1, ALDOB: JX470583.1, ATP6: DQ385236.1, ATP8: DQ385253.1, BDNF: JX470604.1, Cox1: DQ385168.1, Cox2: DQ385185.1, Cox3: DQ385202.1, CytB: DQ385219.1, ND1: DQ385066.1, ND2: DQ385083.1, ND3: DQ385100.1, ND4: DQ385134.1, ND4L: DQ385117.1, ND5: DQ385151.1, NTF3: JX470668.1, RAG1: AY228769.1). Note that "*Esacus giganteus*" is an obsolete synonym of the Beach Stone-Curlew *Esacus magnirostris*, which is also confusingly referred to as *Burhinus magnirostris* (see above).
- *Fratercula arctica*: sequence data replaced (CytB: changed from AJ004176.1 to DQ385228.1)
- *Fratercula arctica*: sequence data added from whole-genome shotgun sequence (ADN: CAJHIB020000004.1, ALDOB: CAJHIB020000026.1, BDNF: CAJHIB020000005.1, c-mos: CAJHIB020000002.1, FGB7: CAJHIB020000004.1, GAPDH: CAJHIB020000001.1, Myo2: CAJHIB020000001.1, NTF3: CAJHIB020000001.1)
- *Fratercula cirrhata*: incorrect accession number fixed (CytB: from FCU37298.1 to U37298.1)
- *Fratercula cirrhata*: sequence data added from whole-genome shotgun sequence (ADN: BMBE01031848.1, ALDOB: BMBE01026396.1, BDNF: BMBE01020939.1, c-mos: BMBE01031431.1, FGB7: BMBE01021660.1, GAPDH: BMBE01027361.1, Myo2: BMBE01029814.1, NTF3: BMBE01025889.1)

- *Fratercula corniculata*: incorrect accession number fixed (CytB: from FCU37299.1 to U37299.1)
- *Gabianus scoresbii*: incorrect accession number fixed (Cox1: from FM209924.1 to FJ027709.1). The original number referred to an alternative CytB sequence.
- *Gallinago delicata*: sequence data replaced (CytB: changed from JQ963043.1 to FJ603651.1). The original sequence appears to suffer from sequencing errors, as pointed out by Laurent Raty at <https://www.birdforum.net/threads/scolopaci.171100/page-2>.
- *Gallinago gallinago*: sequence data replaced (12S: changed from DQ674576.1 to MZ157405.1, 16S: changed from DQ674614.1 to MZ157405.1, ATP6: changed from FJ603658.1 to MZ157405.1, Cox1: changed from FJ582605.1 to MZ157405.1, CytB: changed from FJ787309.1 to MZ157405.1, ND2: changed from EF373240.1 to MZ157405.1). Note that the paper describing the mitogenome (Yang et al. 2021; doi:10.1080/23802359.2021.1972870) confirms that it specifically comes from *G. gallinago gallinago*, ruling out the possibility that it could instead come from *G. delicata* (occasionally regarded as a subspecies of *G. gallinago*)
- *Gallinago gallinago*: sequence data added (ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MZ157405.1)
- *Gallinago hardwickii*: sequence data added (Cox1: AB842791.1)
- *Gallinago imperialis*: sequence data added (Cox1: KF009533.1)
- *Gallinago paraguaiiae*: sequence data removed (CytB: JQ963047.1). This sequence has been removed due to data quality issues. Even though the CytB sequences provided by Baker et al. (2009: FJ603655.1) and Gibson & Baker (2012: JQ963047.1) are supposed to come from the same voucher specimen (L50137), they differ in 16 out of the 621 overlapping nucleotides. In contrast, the 12S sequences, which are also provided by both studies (Baker et al. 2009: FJ603668.1, Gibson & Baker 2012: KF041202.1), can be aligned so that they match up perfectly, as long as we assume that the Gibson & Baker (2012) sequence contains gaps. This problem has first been pointed out by Laurent Raty at <https://www.birdforum.net/threads/scolopaci.171100/>.
- *Gallinago paraguaiiae*: sequence data checked to ensure they really come from this taxon and not from *G. magellanica*, which was formerly considered to be its subspecies. None of the records in GenBank report the subspecies affinity of the samples, but in their paper that separated *G. magellanica* from *G. paraguaiiae sensu stricto*, Miller et al. (2020; doi:10.1111/ibi.12795) show that the two species have non-overlapping geographic ranges separated by the Monte Desert in central Argentina, which *G. paraguaiiae* occurs to the north of and *G. magellanica* to the south of (Miller et al. 2020: Figure 1). The Cox1 sequence (FJ027605.1) comes from a specimen collected near Corrientes in northernmost Argentina, and can therefore be safely attributed to *G. paraguaiiae*. The 12S (FJ603668.1), ATP6 (FJ603662.1), ND2 (JQ963024.1), and RAG1 (JQ963005.1) sequences come from two different studies (12S, ATP6: Baker et al. 2009; doi:10.1111/j.1755-0998.2009.02650.x; ND2, RAG1: Gibson & Baker 2012) but the same voucher specimen (L50137), whose provenance Baker et al. (2009: Table S1) report to be Lagoa do Peixe, Brazil. Therefore, these sequences can be attributed to attributed to *G. paraguaiiae* as well.
- *Gallinago solitaria* **[added species]**: sequence data added from BOLD (Cox1: YIOB072-15)
- *Gallinago stenura*: sequence data replaced (Cox1: changed from GQ481955.1 to KY056596.1)
- *Gallinago undulata*: sequence data added (Cox1: JQ174906.1)
- *Glareola maldivarum*: sequence data replaced (12S: changed from EF373083.1 to MW579776.1, Cox1: changed from AB843529.1 to MW579776.1, CytB: changed from EF373133.1 to MW579776.1, ND2: changed from EF373241.1 to MW579776.1)
- *Glareola maldivarum*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MW579776.1)
- *Glareola pratincola*: sequence data replaced (12S: changed from EU372667.1 to MN356161.1, Cox1: changed from JF498778.1 to MN356161.1, CytB: changed from EU372674.1 to MN356161.1, ND1 and ND2: changed from EU372681.2 to MN356161.1)
- *Glareola pratincola*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND3, ND4, ND4L, ND5: MN356161.1, from whole-genome shotgun sequence: ADN: VWPO01002410.1, ALDOB: VWPO01001368.1, BDNF: VWPO01003955.1, c-mos: VWPO01003021.1, FGB7: VWPO01000294.1, GAPDH: VWPO01003135.1, Myo2: VWPO01002423.1, NTF3: VWPO01000072.1, RAG1: VWPO01000511.1). Note that the mitogenome does not include an ND6 sequence.



- *Gygis alba*: sequence data replaced (Cox1: changed from JQ174974.1 to BROM414-06 from BOLD). The new sequence is both longer (900 bp instead of 647 bp) and more reliably identified as *G. alba* rather than *G. microrhyncha*, as it comes from the southern Atlantic (the range of *G. microrhyncha* is restricted to the Marquesas, the Phoenix Islands, and the Line Islands, i.e., the southern Pacific). The remaining sequences have been checked to ensure they really come from *G. alba* and not from *G. microrhyncha*, which is often considered to be its subspecies. The FGB7 and Myo2 sequences were obtained from a specimen collected in the South Atlantic Ocean (ZMUC 113340), and therefore reliably belong to *G. alba*. The 12S and RAG1 sequences were obtained from specimen C1066 housed at the University of Copenhagen Zoological Museum. While GenBank provides no further information about this record (neither subspecies nor provenance), the same specimen was also used to obtain a Cox1 barcode stored in BOLD (BROM414-06), which shows that the specimen was also collected in the southern Atlantic (“Saint Helena, Ascension and Tristan da Cunha”). The CytB and ND2 sequences were published by Bridge et al. (2005; doi:10.1016/j.ympev.2004.12.010), who reported the provenance of their *Gygis* specimen to be Hawaii in their Table 2; these should therefore also be attributed to *G. alba* (more specifically, *G. alba rothschildi* according to Yeung et al. 2009; doi:10.1111/j.1095-8312.2009.01299.x), although Olson (2005; Bull. Br. Orn. Club. 125(2):155–7) did report a single case of a storm-driven vagrant *G. microrhyncha* from Hawaii.
- *Gygis microrhyncha* **[added species]**: sequence data added (CytB: EU516519.1, ND2: EU516656.1)
- *Haematopus ater*: sequence data replaced (12S: changed from AY074886.1 to AY074886.2, 16S: changed from AY074886.1 to AY074886.2, Cox1: changed from AY074886.1 to AY074886.2, CytB: changed from NC\_003713.1 to AY074886.2, ND2: changed from AY074886.1 to AY074886.2, ND3: changed from AY074886.1 to AY074886.2, ND4: changed from AY074886.1 to AY074886.2, ND4L: changed from AY074886.1 to AY074886.2, ND5: changed from AY074886.1 to AY074886.2). Note that while “NC\_003713” and “AY074886” refer to the same sequence, NC\_003713.1 represents an older version of it than AY074886.2.
- *Haematopus ater*: sequence data added (c-mos: JX533080.1)
- *Haematopus chathamensis* **[added species]**: sequence data added and replaced (12S: EF514930.1, Cox1: changed from EF514934.1 to the longer sequence MK262366.1). The CytB sequence (EF514926.1) has been checked and confirmed to belong to the taxon. Note that *H. chathamensis* was already present in the table, but was erroneously dropped from the final taxon sample during the taxonomic reconciliation process.
- *Haematopus finschi*: sequence data added (12S: EF514931.1, Cox1: MK262329.1, CytB: EF514927.1)
- *Haematopus fuliginosus*: sequence data added from BOLD (Cox1: ROMC012-06)
- *Haematopus leucopodus*: incorrect accession number fixed (BDNF: from KX470611.1 to JX470611.1)
- *Haematopus leucopodus*: truncated accession number fixed (NTF3: from “JX47064” to JX470674.1)
- *Haematopus longirostris* **[added species]**: sequence data added from BOLD (Cox1: ROMC036-06)
- *Haematopus moquini*: sequence data added (Cox1: LR595935.1, CytB: LR595942.1, ND2: LR595934.1)
- *Haematopus osculans* **[added species]**: sequence data added (12S, 16S, ATP6, ATP8, Cox1, Cox2, Cox3, CytB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: KY419886.1)
- *Haematopus ostralegus*: sequence data removed (12S: EU167052.1, 16S, Cox1, Cox2, Cox3, ND1, ND2: ND3, ND4, ND4L, ND5, ND6: KY419886.1, CytB: EU166998.1, Myo2: AY339084.1, RAG1: AY339111.1). The mitogenome KY419886.1 belongs to *Haematopus osculans* (Lee et al. 2017; doi:10.1080/23802359.2017.1292474). The 12S and CytB sequences published by Brown et al. (2008) have been removed because after the separation of *H. osculans* from *H. ostralegus sensu stricto*, they are no longer identifiable to the species level. The same problem also applies to the Myo2 and RAG1 sequences published by Ericson et al. (2003), with the additional problem that while these authors claim they sampled the “Eurasian Oystercatcher” (vernacular name for *H. ostralegus*), they list the scientific name as *H. ater*. An examination of the 930-bp RAG1 sequence (AY339111.1) reveals that it is 100% identical to that of *H. ater* (AY228794.1), so the latter identification may be correct.



- *Haematopus ostralegus*: sequence data added (Cox1: LR595929.1, CytB: LR595930.1, ND2: LR595931.1). These sequences all come from the same specimen (isolate HO03), which comes from Scotland and can therefore be safely attributed to *H. ostralegus ostralegus*. This attribution is further made explicit by Senfeld et al. (2019; doi:10.1111/ibi.12778) in their Figure S3.
- *Haematopus palliatus*: sequence data checked to ensure they really come from this taxon. This concerned the ALDOB, BDNF, Myo2, and NTF3 sequences, which were published by Hackett et al. (2008), who report them both in their Supplementary Table 1 and in the original alignment files deposited in TreeBase to come from *H. ostralegus* instead. GenBank classifies them as *H. palliatus*, but the annotation contains no mention of an earlier misidentification. However, Hackett et al.'s (2008) Supplementary Table 1 also shows that the sequences were obtained from specimen LSUMNS 163409 (as does the GenBank annotation), although the catalogue number is given with a question mark in the table. The Louisiana State University Museum of Natural Science shows this specimen to belong to *H. palliatus*, an identification further confirmed by the fact that the individual was collected in Panama (<http://portal.vertnet.org/o/lsuzmz/birds?id=urn-catalog-lsumz-birds-163409>), completely outside the geographic range of *H. ostralegus*.
- *Haematopus unicolor*: sequence data replaced (12S: changed from EF514930.1 that actually belongs to *H. chathamensis* to EF514933.1, Cox1: changed from EF514937.1 to the longer sequence MK262500.1). The CytB sequence (EF514929.1) has been checked and confirmed to belong to the taxon.
- *Heteroscelus brevipes*: sequence data added (Cox3: AY894259.1)
- *Heteroscelus incanus*: sequence data added (Cox3: AY894264.1)
- *Himantopus himantopus*: incorrect accession number removed (RAG1: EF373193.1). This number actually refers to the RAG1 sequence of *Calidris himantopus*. Note that despite its erroneous inclusion in the table, the sequence was not used for the actual analyses.
- *Himantopus leucocephalus* [**added species**]: sequence data added (CytB: HQ007646.1, from whole-genome shotgun sequence: ADN: RSEF01000001.1, ALDOB: RSEF01000031.1, BDNF: RSEF01000005.1, c-mos: RSEF01000002.1, FGB7: RSEF01000004.1, GAPDH: RSEF01000001.1, Myo2: RSEF01000001.1, NTF3: RSEF01000001.1, RAG1: RSEF01000005.1). Note that GenBank classifies the CytB sequence as *H. novaeseelandiae*, but the original paper of Steeves et al. (2010; doi:10.1111/j.1365-294X.2010.04895.x) clarifies that CytB haplotype A is exclusive to “poaka” (*H. leucocephalus*, then classified as *H. himantopus leucocephalus*). Note also that *H. leucocephalus* was already represented in the table by one sequence (Cox1: EU525421.1), but due to the failure of the taxonomic reconciliation process, did not make it into the final alignment, and is therefore marked as “added species” here.
- *Himantopus melanurus* [**removed species**]: sequence data removed (Cox1: EU525423.1). This taxon is now considered to represent a subspecies of *H. mexicanus* by both Boyd (2019) and Clements et al. (2021). Corresponding row deleted.
- *Himantopus mexicanus*: sequence data replaced (12S: changed from DQ674564.1 to MN356245.1, 16S: changed from DQ674602.1 to MN356245.1, ATP6: changed from DQ385234.1 to MN356245.1, ATP8: changed from DQ385251.1 to MN356245.1, Cox1: changed from DQ385166.1 to MN356245.1, Cox2: changed from DQ385183.1 to MN356245.1, Cox3: changed from DQ385200.1 to MN356245.1, CytB: changed from EU167022.1 to MN356245.1, FGB7: changed from AY695203.1 to VXBK01005257.1 from whole-genome shotgun sequence, ND1: changed from DQ385064.1 to MN356245.1, ND2: changed from DQ385081.1 to MN356245.1, ND3: changed from DQ385098.1 to MN356245.1, ND4: changed from DQ385132.1 to MN356245.1, ND4L: changed from DQ385115.1 to MN356245.1, ND5: changed from DQ385149.1 to MN356245.1). Note that while Feng et al. (2020; Supplementary Table 1) state that the mitogenome as well as the nuclear genome shotgun sequence belong to *Himantopus himantopus* (consistent with the GenBank annotation), they also specify that they belong to the subspecies *mexicanus*. This clearly refers to what we treat as a separate species *H. mexicanus*, since *H. himantopus sensu stricto* does not have recognized subspecies (Clements et al. 2021). The new FGB7 sequence is substantially longer.
- *Himantopus mexicanus*: sequence data added (ND6: MN356245.1, from whole-genome shotgun sequence: ALDOB: VXBK01005922.1, BDNF: VXBK01011442.1, c-mos: VXBK01007183.1, Myo2: VXBK01006790.1, NTF3: VXBK01007093.1)

- *Himantopus novaezelandiae* **[added species]**: sequence data added (Cox1: MK262058.1; CytB: HQ007648.1). Steeves et al. (2010) confirm that CytB haplotype C is exclusive to “kaki” (*H. novaezelandiae*).
- *Hydrophasianus chirurgus*: sequence data replaced (12S: changed from EF373085.1 to MH219929.1)
- *Hydroprogne caspia*: sequence data replaced (12S: changed from DQ674569.1 to MN122905.1, 16S: changed from DQ674607.1 to MN122905.1, Cox1: changed from EU525429.1 to MN122905.1, CytB: changed from AY631300.1 to MN122905.1, ND2: changed from AY631372.1 to MN122905.1)
- *Hydroprogne caspia*: sequence data added (ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MN122905.1)
- *Ibidorhyncha struthersii*: sequence data replaced (12S: changed from EF373086.1 to MN356371.1, CytB: changed from EF373136.1 to MN356371.1, ND2: changed from EF373244.1 to MN356371.1)
- *Ibidorhyncha struthersii*: sequence data added (16S, ATP6, ATP8, Cox1, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MN356371.1, from whole-genome shotgun sequence: ADN: VZSZ01002972.1, ALDO: VZSZ01002484.1, BDNF: VZSZ01008030.1, c-mos: VZSZ01007024.1, FGB7: VZSZ01011087.1, GAPDH: VZSZ01010964.1, Myo2: VZSZ01001853.1, NTF3: VZSZ01010522.1)
- *Ichthyaelus leucophthalmus* **[added species]**: sequence data added (CytB: AY964939.1)
- *Irediparra gallinacea*: sequence data added (ND5: AF146630.1)
- *Jacana jacana*: sequence data replaced (12S: changed from EU167053.1 to KJ631049.1, 16S: changed from DQ385290.1 to KJ631049.1, ATP6: changed from DQ385239.1 to KJ631049.1, ATP8: changed from DQ385256.1 to KJ631049.1, Cox1: changed from DQ385171.1 to KJ631049.1, Cox2: changed from DQ385188.1 to KJ631049.1, Cox3: changed from DQ385205.1 to KJ631049.1, ND1: changed from DQ385069.1 to KJ631049.1, ND4: changed from DQ385137.1 to KJ631049.1, ND4L: changed from DQ385120.1 to KJ631049.1, ND5: changed from DQ385154.1 to KJ631049.1)
- *Jacana jacana*: sequence data added (FGB7: EU739430.1, from whole-genome shotgun sequence: ADN: VZTM01023040.1, c-mos: VZTM01008011.1, GAPDH: VZTM01005299.1)
- *Jacana spinosa*: sequence data replaced (12S: changed from DQ485796.1 to KJ631048.1, 16S: changed from DQ485834.1 to KJ631048.1, Cox1: changed from DQ433701.1 to KJ631048.1, CytB: changed from DQ485894.1 to KJ631048.1)
- *Larosterna inca*: sequence data added (12S: AY631328.1, Cox1: BROM093-06 from BOLD)
- *Larus argentatus*: sequence data replaced (16S: changed from FJ465237.1 to MN122936.1, Cox1: changed from GU571445.1 to MN122936.1, CytB: changed from FM866243.1 to MN122936.1, ND2: changed from FN543388.1 to MN122936.1). The GenBank annotation gives no catalogue number for the voucher specimen, the locality it was collected from, or the exact subspecies it belongs to. In theory, the sequence could therefore also belong to *L. mongolicus*, *L. smithsonianus*, or *L. vegae*, all of which are occasionally regarded as mere subspecies of *L. argentatus* (e.g., Clements et al. 2021). However, the annotation shows that the sequence was extracted as part of the DNAmark project (Margaryan et al. 2020; doi:10.1002/edn3.138), which aims to sequence the mitogenomes of Danish vertebrates. Of the species for which it could be potentially mistaken, only *L. argentatus* occurs in Denmark (*L. mongolicus* breeds in Mongolia and the neighboring regions of Russia and China, and winters to eastern Asia; *L. smithsonianus* breeds in North America and winters to Central America; *L. vegae* breeds in northeastern Siberia and winters to eastern Asia), and the mitogenome can therefore be safely assigned to this species.
- *Larus argentatus*: sequence data added (12S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MN122936.1)
- *Larus belcheri*: sequence data added from BOLD (Cox1: BROM592-07)
- *Larus brachyrhynchus* **[added species]**: sequence data added (Cox1: DQ433746.1). Note that GenBank classifies this sequence as *L. canus*, but Johnsen et al. (2010; doi:10.1007/s10336-009-0490-3) clarify that it belongs to North American *L. canus*, then classified as *L. canus brachyrhynchus* and now as *L. brachyrhynchus*. Note also that *L. brachyrhynchus* was already present in the table, but was erroneously dropped from the final taxon sample during the taxonomic reconciliation process. Its remaining sequences (CytB: FN543288.1, ND2:

FN543357.1) were checked against Sternkopf (2011; <https://tinyurl.com/2xay4pwc>: Appendix D) to confirm that they really belong to *L. brachyrhynchus* rather than *L. canus*.

- *Larus brunnicephalus*: incorrect accession number fixed (ND5: from KX155863.1 to JX155863.1)
- *Larus bulleri*: sequence data added (ATP8: AY584122.1, Cox1: MK261879.1)
- *Larus canus*: sequence data removed (12S: X76361.1). This sequence has been removed because after the separation of *Larus brachyrhynchus* from *Larus canus sensu stricto*, it is no longer identifiable to the species level. The GenBank annotation lists neither the subspecies identity nor the geographic provenance of the voucher specimen, and neither does the original paper (Moum et al. 1994; doi:10.1073/pnas.91.17.7912).
- *Larus canus*: sequence data replaced (Cox1: changed from GU571447.1 to MN122843.1, CytB: changed from FN543287.1 to MN122843.1, ND2: changed from FN598881.1 to MN122843.1, ND6: changed from X73932.1 to MN122843.1). The GenBank annotation gives no catalogue number for the voucher specimen, the locality it was collected from, or the exact subspecies it belongs to. In theory, the sequence could therefore also belong to *L. brachyrhynchus*, which was until recently regarded as a subspecies of *L. canus* (see above). However, the annotation shows that the sequence was extracted as part of the DNAmark project (Margaryan et al. 2020), which aims to sequence the mitogenomes of Danish vertebrates. Since only *L. canus* occurs in Denmark (as opposed to *L. brachyrhynchus*, which is restricted to North America), the mitogenome can be safely assigned to this species.
- *Larus canus*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5: MN122843.1)
- *Larus cirrocephalus*: sequence data removed (CytB: FM209906.1). This sequence has been removed because after the separation of *Chroicocephalus poiocephalus* from *Chroicocephalus* (formerly *Larus*) *cirrocephalus sensu stricto*, it is no longer identifiable to the species level. Moreover, the study cited for the sequence – Sternkopf et al. 2008, “A revision of the taxonomic relationships in Gulls (Laridae) based at [sic] nuclear and mitochondrial DNA analysis” – has apparently never been published, making it impossible to check the details of the sequence. The remaining sequences have been checked to ensure they really come from *C. cirrocephalus* and not from *C. poiocephalus*, which is often considered to be its subspecies. The ATP6 and ATP8 (AY584118.1), ND2 (AY590394.1), and ND5 (AY590414.1) sequences all come from voucher specimen C373-112647, which is listed in Table 1 of Given et al. (2005; doi:10.1093/auk/122.1.268) as belonging to *L. cirrocephalus cirrocephalus*.
- *Larus cirrocephalus*: sequence data added from BOLD (Cox1: KPARG447-08). This sequence comes from a specimen (MACN-Or 71415) collected in Buenos Aires, Argentina, and so can be reliably attributed to *C. cirrocephalus sensu stricto*, which has an exclusively South American distribution.
- *Larus crassirostris*: sequence data replaced (CytB: changed from AB208753.1 to KM507782.1)
- *Larus delawarensis*: sequence data added (12S: AY631327.1)
- *Larus dominicanus*: sequence data replaced (CytB: changed from AJ508121.1 to AY293619.1, ND2: changed from FN543383.1 to AY293619.1)
- *Larus genei*: sequence data added (ATP8: AY584130.1, from BOLD: Cox1: BROM614-07)
- *Larus hartlaubi* [sic]: sequence data added (ATP8: AY584120.1, from BOLD: Cox1: BROM788-07)
- *Larus heermanni*: incorrect accession number fixed (12S: from LHU88012.1 to U88012.1)
- *Larus maculipennis*: sequence data replaced (CytB: changed from FM209915.1 to MN356336.1, ND2: changed from AY590405.1 to MN356336.1, ND5: changed from AY590425.1 to MN356336.1, ND6: changed from AY584128.1 to MN356336.1)
- *Larus maculipennis*: sequence data added (12S, 16S, ATP6, ATP8, Cox1, Cox2, Cox3, ND1, ND3, ND4, ND4L: MN356336.1, from whole-genome shotgun sequence: ADNH: VYZF01000105.1, ALDOB: VYZF01000729.1, BDNF: VYZF01000416.1, c-mos: VYZF01000579.1, FGB7: VYZF01000246.1, GAPDH: VYZF01000064.1, Myo2: VYZF01000082.1, NTF3: VYZF01000292.1, RAG1: VYZF01000213.1)
- *Larus marinus*: sequence data replaced (12S: changed from EF373088.1 to MN122906.1, Cox1: changed from GU571453.1 to MN122906.1, CytB: changed from AJ508140.1 to MN122906.1, ND2: changed from KX534740.1 to MN122906.1)

- *Larus marinus*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5: MN122906.1, FGB7: EU739431.1). Note that the mitogenome does not include an ND6 sequence.
- *Larus modestus*: sequence data added from BOLD (Cox1: BROM799-07)
- *Larus novaehollandiae*: sequence data added (ATP8: AY584124.1)
- *Larus philadelphia*: sequence data added (ATP8: AY584114.1)
- *Larus poiocephalus*: sequence data added from BOLD (Cox1: BROM778-07). This sequence comes from a specimen (ROM 156971) collected in KwaZulu-Natal, South Africa, and so can be reliably attributed to *C. poiocephalus*, which has an exclusively Afro-Madagascan distribution.
- *Larus relictus*: sequence data added (12S: KC760146.1)
- *Larus scolopinus* [sic]: sequence data added (ATP8: AY590313.1, Cox1: MK262155.1)
- *Larus serranus*: sequence data added (ATP8: AY584131.1, from BOLD: Cox1: BROM814-07)
- *Larus smithsonianus*: sequence data replaced (Cox1: changed from DQ433741.1 to MN356257.1, CytB: changed from FM866259.1 to MN356257.1, ND2: changed from FN543389.1 to MN356257.1)
- *Larus smithsonianus*: sequence data added (12S, 16S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MN356257.1, from whole-genome shotgun sequence: ADNH: WAAC01013541.1, ALDOB: WAAC01000317.1, BDNF: WAAC01000499.1, c-mos: WAAC01006819.1, FGB7: WAAC01008783.1, GAPDH: WAAC01003668.1, Myo2: WAAC01002072.1, NTF3: WAAC01016345.1, RAG1: WAAC01006558.1)
- *Larus thayeri* **[removed species]**: sequence data removed (Cox1: HM033523.1, CytB: FN543338.1). This taxon is now considered to represent a subspecies of *L. glaucooides* by both Boyd (2019) and Clements et al. (2021). Corresponding row deleted.
- *Larus vegae*: sequence data removed (12S, 16S, ATP6, ATP8, Cox2, Cox3, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: KT943749.1). The mitogenome is misidentified and actually belongs to the procellariiform *Calonectris leucomelas* (Sangster & Luksenburg 2021). Note that the sequence given for Cox1 (GQ482043.1) is unproblematic, but in the analyses, it was erroneously replaced by the Cox1 subsequence of KT943749.1.
- *Limnodromus scolopaceus*: sequence data removed (CytB: AF285819.1). This sequence appears to suffer from sequencing errors. This problem has first been pointed out by Laurent Raty at <https://www.birdforum.net/threads/scolopaci.171100/page-2>, and it is confirmed by our own CytB tree. Note that the available alternative sequence, EF373140.1, is also problematic (probably misidentified).
- *Limnodromus scolopaceus*: sequence data replaced (12S: changed from EF373090.1 to AF285806.1). This appears to be a misidentified *Phalaropus tricolor* sequence. This problem has first been pointed out by Laurent Raty at <https://www.birdforum.net/threads/scolopaci.171100/page-2>, and it is confirmed by our own 12S tree.
- *Limosa haemastica*: sequence data replaced (12S: changed from EF373091.1 to MT188757.1, Cox1: changed from KF009541.1 to MT188757.1, CytB: changed from AF285821.1 to MT188757.1, ND2: changed from EF373249.1 to MT188757.1)
- *Limosa haemastica*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5, ND6: MT188757.1)
- *Limosa lapponica*: sequence data replaced (ND6: changed from AF411403.1 to KX371106.1)
- *Limosa lapponica*: sequence data added from whole-genome shotgun sequence (ADNH: LXVZ01065852.1, ALDOB: LXVZ01032106.1, BDNF: LXVZ01057585.1, FGB7: LXVZ01003606.1, GAPDH: LXVZ01044967.1, Myo2: LXVZ01001042.1, NTF3: LXVZ01086250.1, RAG1: LXVZ01041335.1). Note that no BLAST hit was found for c-mos.
- *Lymnocyrtus minimus*: sequence data removed (RAG1: EF373192.1). Laurent Raty pointed out at <https://www.birdforum.net/threads/gruiformes-and-charadriiformes.391066/page-2#post-4209907> that the first 907 bp of this sequence are identical to *Limosa haemastica*, suggesting that it might be chimerical. However, BLASTing the remaining 1829 bp against the NCBI *nr/nt* database still shows a greater percent identity with various species of *Limosa* (in this order: *fedoa*, *limosa*, *haemastica*) than with *Limnodromus* – the sister taxon of *Lymnocyrtus* in the mitochondrial gene trees and in the tree of Baker et al. (2007). As a result, the sequence probably comes from one or more species of *Limosa*, being either simply misidentified, or both misidentified and chimerical. Finally, note that a conflict between RAG1 and mitochondrial data could constitute a genuine case of gene tree–species tree discordance, and in itself would not

be sufficient to exclude the sequence. Rather, we exclude EF373192.1 because we cannot reproduce the results of Baker et al. (2007) with it. The latter authors obtained a high posterior probability (0.97) for a sister-group relationship between *Lymnocyrtes* and *Limnodromus* in an analysis based on the concatenated sequence data from 12S, CytB, ND2, and RAG1. However, in our concatenated analyses, despite the inclusion of one more locus that supports its close affinity with *Limnodromus* (Cox1), *Lymnocyrtes* instead resulted sister to *Limosa*, due entirely to RAG1 overriding the other loci. This demonstrates that whatever RAG1 sequence Baker et al. (2007) used for *Lymnocyrtes* could not have had the same effect, but rather must have agreed with the mitochondrial loci in allying *Lymnocyrtes* with *Limnodromus*.

- *Metopidius indicus*: sequence data replaced (12S: changed from KF289820.1 to MW482963.1, 16S: changed from KF289827.1 to MW482963.1, Cox1: changed from KJ442627.1 to MW482963.1, CytB: changed from KF289833.1 to MW482963.1, ND5: changed from AF146628.1 – misrecorded as “AF146628.10” – to MW482963.1)
- *Metopidius indicus*: sequence data added (ATP6, ATP8, Cox2, Cox3, ND1, ND2, ND3, ND4, ND4L, ND6: MW482963.1)
- *Numenius hudsonicus* [**removed species**]: sequence data removed (12S: JQ962995.1, CytB: JQ963053.1, ND2: HM776965.1, RAG1: JQ963015.1 – truncated to “JQ963015”). This taxon is now considered to represent a subspecies of *N. phaeopus* by both Boyd (2019) and Clements et al. (2021). Upon its removal from the table, we merely checked that its locus coverage is redundant with respect to *N. phaeopus* (yes: 12S, CytB, ND2, RAG1 sampled for both) and that its sequences for the overlapping loci are of the same length or shorter. The RAG1 sequence turned out to be longer, and so replaced the original sequence of *N. phaeopus* for this locus (see below). Corresponding row deleted.
- *Numenius madagascariensis*: sequence data replaced (12S: changed from JQ962994.1 to MW930394.1, Cox1: changed from GQ482250.1 to MW930394.1, CytB: changed from AF417925.1 to MW930394.1, ND2: changed from JQ963033.1 to MW930394.1, ND6: changed from AF411397.1 to MW930394.1)
- *Numenius madagascariensis*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L, ND5: MW930394.1)
- *Numenius phaeopus*: sequence data replaced (CytB: changed from AF417930.1 to KP308149.1, ND2: changed from HM640836.1 to KP308149.1, ND6: changed from AF411405.1 to KP308149.1, RAG1: changed from KC969138.1 to JQ963015.1)
- *Numenius tahitiensis*: sequence data removed (12S: JQ962997.1). This appears to be a misidentified *Limosa limosa* sequence. This problem has first been pointed out by Laurent Raty at <https://www.birdforum.net/threads/scolopaci.171100/page-2>, and it is confirmed by our own 12S tree.
- *Pedionomus torquatus*: incorrect accession number fixed (CytB: from DQ385525.1 to DQ385225.1)
- *Pedionomus toquatus*: sequence data replaced (FGB7: changed from AY695174.1 to VZRU01011443.1 from whole-genome shotgun sequence, NTF3: changed from EU740331.1 to VZRU01014671.1 from whole-genome shotgun sequence). The new sequences are slightly longer.
- *Pedionomus torquatus*: sequence data added from whole-genome shotgun sequence (ADNH: VZRU01020087.1, c-mos: VZRU01016814.1)
- *Phaetusa simplex*: sequence data added (12S: AY631329.1, from whole-genome shotgun sequence: ADNH: VZZW01000298.1, ALDOB: VZZW01003093.1, BDNF: VZZW01001470.1, c-mos: VZZW01000827.1, FGB7: VZZW01001927.1, GAPDH: VZZW01000405.1, Myo2: VZZW01000877.1, NTF3: VZZW01000822.1)
- *Phalaropus lobatus*: missing accession number added (ND4: KY765409.1). The sequence itself was used but not listed.
- *Phalaropus lobatus*: sequence data removed (RAG1: KC969139.1). The sequence may be a chimera or suffer from other unidentified problems based on its position in our RAG1 tree. See also the comment by Laurent Raty regarding AY894222.1 at <https://www.birdforum.net/threads/scolopaci.171100/page-2>.
- *Phalaropus lobatus*: sequence data replaced (16S: changed from AY894171.1 to KY765409.1, ND1: changed from AY894290.1 to KY765409.1, ND5: changed from AY894256.1 to KY765409.1)
- *Phegornis mitchellii*: sequence data added from BOLD (Cox1: BROM438-06)

- *Philomachus pugnax*: sequence data replaced (12S: changed from KF041205.1 to MN956840.1, Cox1: changed from JQ251265.1 to MN956840.1, CytB: changed from KC969173.1 to MN956840.1, ND2: changed from EF373258.1 to MN956840.1, ND5: changed from JQ251374.1 to MN956840.1, ND6: changed from GQ255993.1 to MN956840.1)
- *Philomachus pugnax*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L: MN956840.1, from whole-genome shotgun sequence: ADNH: LDEH01000866.1, BDNF: LDEH01017300.1, c-mos: CZLE01001126.1, FGB7: LDEH01001119.1, GAPDH: LDEH01020432.1, Myo2: LDEH01032077.1, NTF3: LDEH01004939.1)
- *Pinguinus impennis* **[added species]**: sequence data added (12S, 16S, ATP6, ATP8, Cox1, Cox2, Cox3, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: KU158188.1)
- *Pluvialis apricaria*: sequence data replaced (Cox1: changed from GU571580.1 to MN122928.1)
- *Pluvialis apricaria*: sequence data added (12S, 16S, ATP6, ATP8, Cox2, Cox3, CytB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: MN122928.1, from whole-genome shotgun sequence: ADNH: JAGGDW010001059.1, ALDOB: JAGGDV010000006.1, BDNF: JAGGDW010000678.1, c-mos: JAGGDV010000001.1, FGB7: JAGGDW010000082.1, GAPDH: JAGGDW010000415.1, Myo2: JAGGDW010000105.1, NTF3: JAGGDV010000002.1, RAG1: JAGGDW010000677.1)
- *Pluvialis fulva*: sequence data added (CytB: KX639757.1)
- *Pluvialis squatarola*: sequence data replaced (12S: changed from EF373101.1 to MT561267.1, Cox1: changed from EF515746.1 to MT561267.1, CytB: changed from EF373151.1 to MT561267.1, ND2: changed from HM640798.1 to MT561267.1, ND3: changed from KM001391.1 to MT561267.1, ND6: changed from AF411399.1 to MT561267.1)
- *Pluvialis squatarola*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND4, ND4L, ND5: MT561267.1)
- *Pluvianellus socialis*: sequence data replaced (12S: changed from DQ385271.1 to MN356314.1, 16S: changed from DQ385288.1 to MN356314.1, ATP6: changed from DQ385237.1 to MN356314.1, ATP8: changed from DQ385254.1 to MN356314.1, Cox1: changed from DQ385169.1 to MN356314.1, Cox2: changed from DQ385186.1 to MN356314.1, Cox3: changed from DQ385203.1 to MN356314.1, CytB: changed from DQ385220.1 to MN356314.1, ND1: changed from DQ385067.1 to MN356314.1, ND2: changed from DQ385084.1 to MN356314.1, ND3: changed from DQ385101.1 to MN356314.1, ND4: changed from DQ385135.1 to MN356314.1, ND4L: changed from DQ385118.1 to MN356314.1, ND5: changed from DQ385152.1 to MN356314.1)
- *Pluvianellus socialis*: sequence data added (ND6: MN356314.1, from whole-genome shotgun sequence: ADNH: VZTS01001126.1, ALDOB: VZTS01013762.1, BDNF: VZTS01023129.1, c-mos: VZTS01003301.1, FGB7: VZTS01027929.1, GAPDH: VZTS01024330.1, Myo2: VZTS01019160.1, NTF3: VZTS01013524.1)
- *Pluvianus aegyptius*: sequence data added from BOLD (Cox1: BROM444-06)
- *Procelsterna albivitta* **[added species]**: sequence data added (ND2: KU601380.1, CytB: KU601393.1)
- *Procelsterna cerulea* **[added species]**: sequence data added (Cox1: JQ175981.1, CytB: KU601395.1, ND2: KU601379.1)
- *Prosobonia leucoptera* **[added species]**: sequence data added (CytB: JQ012743.1, ND2: JQ012744.1)
- *Prosobonia parvirostris*: incorrect accession number fixed (JQ012745.1 is a CytB rather than a Cox1 sequence)
- *Ptychoramphus aleuticus*: incorrect accession number fixed (CytB: from PAU37302.1 to U37302.1)
- *Recurvirostra americana*: sequence data removed (ND2: EF373262.1). See Laurent Raty's comment in this BirdForum thread for justification: <http://www.birdforum.net/threads/banded-stilt.302939>
- *Recurvirostra avosetta*: incorrect accession number fixed (ND5: from KT623657.1 to KY623657.1)
- *Recurvirostra avosetta*: sequence data replaced (Cox1: changed from KP757766.1 to KY623657.1, CytB: changed from AF417926.1 to KY623657.1, ND6: changed from AF411398.1 to KY623657.1, RAG1: changed from AY339117.1 to SAYO01033914.1 from whole-genome shotgun sequence)
- *Recurvirostra avosetta*: sequence data added from whole-genome shotgun sequence (ADNH: SAYO01000882.1, ALDOB: SAYO01003494.1, BDNF: SAYO01013748.1, c-mos:

SAYO01027612.1, FGB7: SAYO01033122.1, GAPDH: SAYO01028658.1, NTF3: SAYO01033797.1)

- *Recurvirostra novaehollandiae*: sequence data added from BOLD (Cox1: BROM224-06)
- *Rhinoptilus africanus*: sequence data replaced (12S: changed from DQ674574.1 to MN356261.1, 16S: changed from DQ674612.1 to MN356261.1, FGB7: changed from AY695196.1 to VXBO01013636.1 from whole-genome shotgun sequence, RAG1: changed from AY339118.1 to VXBO01002207.1 from whole-genome shotgun sequence). The new FGB7 and RAG1 sequences are substantially longer.
- *Rhinoptilus africanus*: sequence data added (ATP6, ATP8, Cox1, Cox2, Cox3, CytB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: MN356261.1, from whole-genome shotgun sequence: ALDOB: VXBO01008438.1, BDNF: VXBO01009389.1, c-mos: VXBO01005791.1, NTF3: VXBO01013149.1)
- *Rhinoptilus chalcopertus*: sequence data added from BOLD (Cox1: BROM447-06)
- *Rissa tridactyla*: sequence data replaced (12S: changed from DQ385280.1 to MN356420.1, 16S: changed from DQ385297.1 to MN356420.1, ATP6: changed from DQ385246.1 to MN356420.1, ATP8: changed from DQ385263.1 to MN356420.1, Cox1: changed from DQ385178.1 to MN356420.1, Cox2: changed from DQ385195.1 to MN356420.1, Cox3: changed from DQ385212.1 to MN356420.1, CytB: changed from DQ385229.1 to MN356420.1, ND1: changed from DQ385076.1 to MN356420.1, ND2: changed from AY590389.1 to MN356420.1, ND3: changed from DQ385110.1 to MN356420.1, ND4: changed from DQ385144.1 to MN356420.1, ND4L: changed from DQ385127.1 to MN356420.1, ND5: changed from AY590409.1 to MN356420.1)
- *Rissa tridactyla*: sequence data added (ND6: MN356420.1, from whole-genome shotgun sequence: ADNH: VZUC01000089.1, ALDOB: VZUC01000125.1, BDNF: VZUC01051744.1, c-mos: VZUC01000016.1, FGB7: VZUC01000089.1, GAPDH: VZUC01000277.1, Myo2: VZUC01000028.1, NTF3: VZUC01000060.1)
- *Rostratula australis* **[added species]**: sequence data added (ATP6, ATP8: EF632100.1, Cox1: BROM695-07 from BOLD, Cox3: EF632100.1, c-mos: JX533082.1, CytB: EF632085.1, ND2: JQ963037.1, ND5: EF632082.1, NTF3: JX533273.1)
- *Rostratula benghalensis*: sequence data replaced (12S: changed from DQ674583.1 to MN356297.1, 16S: changed from DQ674621.1 to MN356297.1, ADNH: changed from DQ674657.1 to VXAI01000024.1 from whole-genome shotgun sequence, ATP6 and ATP8: changed from EF632099.1 to MN356297.1, Cox1: changed from EF632098.1 to MN356297.1, CytB: changed from FJ205692.1 to MN356297.1, FGB7: changed from AY695177.1 to EU739483.1, GAPDH: changed from DQ674691.1 to VXAI01000119.1 from whole-genome shotgun sequence, ND2: changed from EF373265.1 to MN356297.1, ND5: changed from EF632082.1 to MN356297.1, RAG1: changed from AY228801.1 to VXAI01000240.1 from whole-genome shotgun sequence). The original nuclear sequences were published by Paton et al. (2003; RAG1) and Fain & Houde (2007; ADNH, GAPDH) and have been replaced because after the separation of *Rostratula australis* from *Rostratula benghalensis sensu stricto*, they were no longer identifiable to the species level. No additional information (geographic provenance or subspecies identity) is available for the RAG1 sequence. For the ADNH and GAPDH sequences, GenBank shows that they were obtained from specimen LSUMZ B-26286; unfortunately, this is the only specimen of *R. benghalensis* at the Louisiana State University Museum of Natural Science for which the museum website does not show provenance data (<http://portal.vertnet.org/o/lsuzm/birdstissues?id=urn-catalog-lsumz-birdstissues-26286>), making it impossible to establish its identity. In contrast, the ALDOB, BDNF, FGB7, Myo2, and NTF3 sequences were obtained from specimen FMNH 358283 that was collected in the Philippines (Hackett et al. 2008: Supplementary Table 1), which lie within the geographic range of *R. benghalensis* but outside that of *R. australis*. Similarly, the mitogenome MN356297.1 and the corresponding nuclear genome scaffolds come from a specimen (USNM 613014) collected in Luzon, Cagayan, Philippines (Feng et al. 2020: Supplementary Table 1), again establishing their identity as *R. benghalensis*.
- *Rostratula benghalensis*: sequence data added (Cox2, Cox3, ND1, ND3, ND4, ND4L: MN356297.1, from whole-genome shotgun sequence: c-mos: VXAI01000132.1). Note that the mitogenome does not include an ND6 sequence.
- *Rostratula semicollaris*: sequence data replaced (12S: changed from DQ385274.1 to MN356246.1, 16S: changed from DQ385291.1 to MN356246.1, ATP6: changed from DQ385240.1 to MN356246.1, ATP8: changed from DQ385257.1 to MN356246.1, Cox1:



- changed from DQ385172.1 to MN356246.1, Cox2: changed from DQ385189.1 – misrecorded as “DQ385189.1” – to MN356246.1, Cox3: changed from DQ385206.1 to MN356246.1, CytB: changed from DQ385223.1 to MN356246.1, ND1: changed from DQ385070.1 to MN356246.1, ND2: changed from DQ385087.1 to MN356246.1, ND3: changed from DQ385104.1 to MN356246.1, ND4: changed from DQ385138.1 to MN356246.1, ND4L: changed from DQ385121.1 to MN356246.1, ND5: changed from DQ385155.1 to MN356246.1)
- *Rostratula semicollaris*: sequence data added (ND6: MN356246.1, from whole-genome shotgun sequence: ADN: VXB01001575.1, ALDO: VXB01004260.1, BDNF: VXB01006938.1, c-mos: VXB01000836.1, FGB7: VXB01002084.1, GAPDH: VXB01006300.1, Myo2: VXB01000704.1, NTF3: VXB01005699.1)
  - *Rynchops niger*: sequence data replaced (12S: changed from DQ674567.1 to MN356248.1, 16S: changed from DQ674605.1 to MN356248.1, ATP6: changed from DQ385247.1 to MN356248.1, ATP8: changed from DQ385264.1 to MN356248.1, Cox1: changed from DQ385179.1 to MN356248.1, Cox2: changed from DQ385196.1 to MN356248.1, Cox3: changed from DQ385213.1 to MN356248.1, CytB: changed from DQ385230.1 to MN356248.1, FGB7: changed from AY695191.1 to VXBH01006810.1 from whole-genome shotgun sequence, ND1: changed from DQ385077.1 to MN356248.1, ND2: changed from DQ385094.1 to MN356248.1, ND3: changed from DQ385111.1 to MN356248.1, ND4: changed from DQ385145.1 to MN356248.1, ND4L: changed from DQ385128.1 to MN356248.1, ND5: changed from DQ385162.1 to MN356248.1). The new FGB7 sequence is substantially longer.
  - *Rynchops niger*: sequence data added (ND6: MN356248.1, from whole-genome shotgun sequence: ALDO: VXBH01000823.1, BDNF: VXBH01000788.1, c-mos: VXBH01000327.1, NTF3: VXBH01007348.1)
  - *Saundersilarus saundersi*: sequence data replaced (Cox2: changed from JQ071443.1 to KJ631624.1)
  - *Scolopax minor*: incorrect accession numbers fixed (12S: from SMU83744.1 to U83744.1, ND5: from AF082068.1 to AF082068.2)
  - *Scolopax mira*: sequence data replaced (Cox1: changed from AB843747.1 to LC541431.1)
  - *Scolopax mira*: sequence data added (12S, 16S, ATP6, ATP8, Cox2, Cox3, CytB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: LC541431.1, from whole-genome shotgun sequence: ADN: BJBW01002710.1, ALDO: BJBW01006919.1, BDNF: BJBW01008310.1, c-mos: BJBW01010380.1, FGB7: BJBW01001235.1, GAPDH: BJBW01010148.1, Myo2: BJBW01003289.1, NTF3: BJBW01009050.1, RAG1: BJBW01016199.1)
  - *Steganopus tricolor*: sequence data removed (CytB: AY894240.1). This appears to be a misidentified *Gallinago gallinago* sequence. This problem has first been pointed out by Laurent Raty at <https://www.birdforum.net/threads/scolopaci.171100/page-2>, and it is confirmed by our own CytB tree.
  - *Stercorarius longicaudus*: incorrect accession number fixed (CytB: from SLU76822.1 to U76822.1)
  - *Stercorarius parasiticus*: sequence data replaced (12S: changed from U76766.1 – misrecorded as “SPU76766.1” to MN356186.1, Cox1: changed from GU571623.1 to MN356186.1, CytB: changed from AJ004228.1 to MN356186.1)
  - *Stercorarius parasiticus*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: MN356186.1, from whole-genome shotgun sequence: ADN: VWZL01000556.1, ALDO: VWZL01001669.1, BDNF: VWZL01000846.1, c-mos: VWZL01004825.1, FGB7: VWZL01004535.1, GAPDH: VWZL01000898.1, Myo2: VWZL01003680.1, NTF3: VWZL01002554.1, RAG1: VWZL01001426.1)
  - *Sterna albifrons*: sequence data replaced (ND2: changed from AY631366.1 to KT350612.1)
  - *Sterna albobriata*: sequence data added (Cox1: MK262173.1)
  - *Sterna aleutica*: sequence data added (12S: AY631355.1)
  - *Sterna anaethetus*: sequence data added (12S: AY631332.1)
  - *Sterna bengalensis*: sequence data added (12S: AY631334.1, FGB7: KU577489.1, Myo2: KU577501.1, from BOLD: Cox1: BROM017-06)
  - *Sterna bergii*: sequence data replaced (12S: changed from MH006899.1 to AY631335.1). The new sequence is slightly longer.
  - *Sterna bergii*: sequence data added from BOLD (Cox1: BROM038-06)
  - *Sterna dougallii*: sequence data added (12S: AY631337.1)
  - *Sterna elegans*: sequence data added (12S: AY631338.1, FGB7: KU577475.1, Myo2: KU577496.1)

- *Sterna eurygnatha*: sequence data removed (RAG1: AY228786.1). The sequence comes from Paton et al. (2003), who, however, only list *Sterna hirundinacea* among their sampled species (with the vernacular name – “South American tern” – also corresponding to *S. hirundinacea* rather than *S. eurygnatha*). There is no GenBank annotation clarifying whether this sequence was originally misidentified. As such, we do not consider it identifiable to the species level, and do not use it for either of the two species.
- *Sterna eurygnatha*: sequence data replaced (ND5: changed from AY590408.1 to DQ385163.1). The new sequence is slightly longer.
- *Sterna eurygnatha*: sequence data added (FGB7: FJ356204.1, Myo2: FJ356216.1). The taxonomy of this species is extremely problematic. Our original table distinguished only *Sterna sandvicensis* and *Sterna eurygnatha*; Boyd (2019) distinguishes *Thalasseus* (formerly *Sterna*) *sandvicensis* and *Thalasseus acuflavidus*, considering *eurygnathus* to be a mere subspecies of *T. acuflavidus*; and Clements et al. (2021) treat both *acuflavidus* and *eurygnathus* as a subspecies of *T. sandvicensis*. Since we follow Boyd’s (2019) treatment, we can afford to combine *acuflavidus* and *eurygnathus* sequence data; as a result, most of our *acuflavidus* sequences come from *eurygnathus*. This is the case for all the mitochondrial sequences, whose identity is further complicated by the fact that in the original paper (Paton & Baker 2006), they were attributed to *Sterna bengalensis* instead. However, the GenBank annotation clarifies that this identification was mistaken and the data really belongs to *S. eurygnatha*. For Cox1, CytB, and ND2, alternative sequences are available directly from *acuflavidus*; (FJ356193.1, AY631313.1, and AY631385.1, respectively); however, these are generally shorter, and were therefore not used. In contrast, the newly added sequences come specifically from *acuflavidus*.
- *Sterna fuscata*: sequence data added (12S: AY631341.1)
- *Sterna hirundinacea*: sequence data added (12S: AY631343.1, Cox1: JQ176282.1)
- *Sterna hirundo*: sequence data replaced (ND2: changed from AY631378.1 to MF582632.1, RAG1: changed from EF373209.1 to WNMW01000007.1 from whole-genome shotgun sequence). The new RAG1 sequence is slightly longer.
- *Sterna hirundo*: sequence data added from whole-genome shotgun sequence (ADNH: WNMW01000006.1, ALDOB: WNMW01000004.1, BDNF: WNMW01000007.1, c-mos: WNMW01000003.1, FGB7: WNMW01000006.1, GAPDH: WNMW01000001.1, NTF3: WNMW01000001.1)
- *Sterna lunata*: sequence data added (12S: AY631344.1, Cox1: JQ175611.1)
- *Sterna maxima*: sequence data removed (12S: DQ674571.1, 16S: DQ674609.1, ADNH: DQ674647.1, GAPDH: DQ674682.1). These were sequenced by Fain & Houde (2007) and have been removed because after the separation of *Thalasseus albididorsalis* from *Thalasseus maximus* (formerly *Sterna maxima*) *sensu stricto*, they are no longer identifiable to the species level. The identity of the Cox1 sequence (FJ028399.1) as *T. m. maximus* (rather than *T. m. albididorsalis*) is confirmed by Collinson et al. (2017; doi:10.1093/biolinnean/blw049; Figure 1). The identity of the CytB (AY631309.1) and ND2 (AY631381.1) sequences as *T. m. maximus* is indirectly confirmed by Bridge et al. (2005: Table 2) based on provenance information. Finally, the identity of the FGB7 sequence (AY695189.1) as *T. m. maximus* is confirmed by Dufour et al. (2016; doi:10.1007/s10336-016-1380-0; Table S1). Note that since *T. maximus* occurs in North America, while *T. albididorsalis* is restricted to Africa, it is almost certain that specimen NMSU 1620X used by Faine & Houde (2007), housed at the New Mexico State University, actually belongs to the former species – in fact, it might be the very same specimen whose tissues were sampled several years earlier by Fain & Houde (2004) for the FGB7 sequence. However, this is a mere conjecture.
- *Sterna maxima*: sequence data added (12S: AY631345.1). This sequence was published by Bridge et al. (2005), who report in their Table 2 that the sequence was extracted from a specimen collected in Rio Grande do Sul, Brazil; as such, it could only represent *Thalasseus maximus* (formerly *Sterna maxima*) *sensu stricto* rather than *Thalasseus albididorsalis*, as the distribution of the latter species is exclusively African.
- *Sterna nereis*: sequence data added (12S: AY631346.1, Cox1: MK262186.1)
- *Sterna nilotica*: sequence data replaced (ND2: changed from AY631383.1 to MF582631.1)
- *Sterna paradisaea*: sequence data replaced (ND2: changed from AY631384.1 to MK946458.1)
- *Sterna sandvicensis*: sequence data replaced (Cox1: changed from DQ434170.1 to FJ356195.1, CytB: changed from FM209938.1 to FJ356184.1, FGB7: changed from

FJ356204.1 to FJ356206.1, ND2: changed from AY631385.1 to FJ356227.1). GenBank shows that the FGB7 and ND2 sequences actually belong to *Thalasseus* (formerly *Sterna*) *sandvicensis acutiflavus*, which we treat as a separate species (see above). Similarly, the Cox1 sequence comes from a study titled “Comprehensive DNA barcode coverage of North American birds”, and can therefore only refer to *T. acutiflavus* (since *T. sandvicensis sensu stricto* only occurs in Europe, Africa, and India). The CytB sequence has been removed because after the separation of *T. acutiflavus* from *T. sandvicensis sensu stricto*, it is no longer identifiable to the species level. In contrast, the new sequences are specifically listed as belonging to *T. sandvicensis sandvicensis* on GenBank.

- *Sterna sandvicensis*: sequence data added (Myo2: FJ356219.1)
- *Sterna striata*: sequence data added (12S: AY631350.1, Cox1: MK262418.1)
- *Sterna sumatrana*: sequence data added (12S: AY631351.1)
- *Sterna superciliaris*: sequence data added (12S: AY631352.1)
- *Sterna trudeaui*: sequence data added (12S: AY631353.1)
- *Sterna vittata*: sequence data added (12S: AY631354.1, Cox1: BROM087-06 from BOLD)
- *Stiltia isabella*: sequence data replaced (12S: changed from EF373110.1 to EF373110.2)
- *Stiltia isabella*: sequence data added from BOLD (Cox1: BROM460-06)
- *Synthliboramphus antiquus*: sequence data replaced (12S: changed from EF373111.1 to AP009042.1, Cox1: changed from EF380331.1 to AP009042.1, ND6: changed from X73920.1 to AP009042.1)
- *Synthliboramphus craveri*: incorrect accession number fixed (CytB: from SCU37304.1 to U37304.1)
- *Synthliboramphus hypoleucus* **[removed species]**: sequence data removed (Cox1: DQ434184.1, CytB: U37305.1 – misrecorded as “SHU37305.1”, ND6: X73921.1). The Cox1 and CytB sequences have been removed because they belong to *S. scrippsi* rather than *S. hypoleucus* (see below). The ND6 sequence has been removed because after the separation of *S. scrippsi* from *S. hypoleucus sensu stricto*, it is no longer identifiable to the species level. Corresponding row not deleted (the species is valid, only unsampled).
- *Synthliboramphus scrippsi* **[added species]**: sequence data added (Cox1: DQ434184.1, CytB: U37305.1). GenBank classifies the Cox1 sequence as *S. hypoleucus*, but it also provides the catalogue number of the voucher specimen: UWBM (University of Washington Burke Museum) 54879. The museum website shows that this specimen has been reclassified as *S. scrippsi* (<https://tinyurl.com/3fet3zzj>). The CytB sequence is also classified as *S. hypoleucus* by GenBank, but the original paper of Friesen et al. (1996; doi:10.1093/oxfordjournals.molbev.a025595; see Table 1) clarifies that it comes from *S. scrippsi* (then classified as *S. hypoleucus scrippsi*).
- *Synthliboramphus wumizusume*: sequence data replaced (12S: changed from EF380312.1 to KT592378.1, 16S: changed from EF380296.1 to KT592378.1, Cox1: changed from EF380333.1 to KT592378.1, ND6: changed from X73919.1 to KT592378.1)
- *Thalasseus albididorsalis* **[added species]**: sequence data added (Cox1: LT717640.1, CytB: LT717644.1, FGB7: LT717670.1, ND2: LT717642.1)
- *Thinocorus orbignyianus*: sequence data replaced (12S: changed from DQ674585.1 to MN356267.1, 16S: changed from DQ674623.1 to MN356267.1, Cox1: changed from FJ028423.1 – misrecorded as “JF028423.1” – to MN356267.1)
- *Thinocorus orbignyianus*: sequence data added (ATP6, ATP8, Cox2, Cox3, CytB. ND1, ND2, ND3, ND4, ND4L, ND5, ND6: MN356267.1, BDNF: EU738093.1, from whole-genome shotgun sequence: c-mos: VXBW01005499.1)
- *Tringa erythropus*: sequence data replaced (ND1: changed from AY894277.1 to KX230491.1, ND5: changed from AY894243.1 to KX230491.1)
- *Tringa flavipes*: sequence data added (Cox3: AY894261.1)
- *Tringa glareola*: sequence data replaced (CytB: changed from AF417923.1 to KY128485.1, ND1: changed from AY894279.1 to KY128485.1, ND5: changed from AY894245.1 to KY128485.1, ND6: changed from AF411395.1 to KY128485.1)
- *Tringa guttifer*: sequence data added (12S: MK905885.1)
- *Tringa inornata* **[added species]**: sequence data added (12S, 16S, ATP6, ATP8, Cox1, Cox2, Cox3, CytB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: MF036175.1). See Bi (2017) for the

confirmation that the mitogenome MF036175.1 belongs to *T. inornata* rather than *T. semipalmata*.

- *Tringa melanoleuca*: sequence data added (Cox3: AY894266.1)
- *Tringa nebularia*: sequence data replaced (ND1: changed from AY894284.1 to MK460251.1, ND5: changed from AY894250.1 to MK460251.1, ND6: changed from AF411406.1 to MK460251.1)
- *Tringa ochropus*: sequence data replaced (ND5: changed from AY894251.1 to KX668223.1)
- *Tringa solitaria*: sequence data added (Cox3: AY894269.1)
- *Tringa stagnatilis*: sequence data removed (RAG1: KC969148.1). The sequence may be a chimera or suffer from other unidentified problems based on its position in our RAG1 tree. See also the comment by Laurent Raty regarding AY894219.1 at <https://www.birdforum.net/threads/scolopaci.171100/page-2>.
- *Tringa stagnatilis*: sequence data replaced (12S: changed from AY894151.1 to MT572847.1, 16S: changed from AY894168.1 to MT572847.1, ATP6, ATP8: changed from AY894270.1 to MT572847.1, Cox1: changed from KF147204.1 to MT572847.1, CytB: changed from AY894236.1 to MT572847.1, ND1: changed from AY894287.1 to MT572847.1, ND2: changed from AY894185.1 to MT572847.1, ND5: changed from AY894253.1 to MT572847.1)
- *Tringa stagnatilis*: sequence data added (Cox2, Cox3, ND3, ND4, ND4L, ND6: MT572847.1)
- *Tringa totanus*: sequence data replaced (Cox1, Cox2: changed from NC\_044648.1 to MT410861.1 from which most of the other mitochondrial loci were drawn, ND1: changed from AY894288.1 to MT410861.1, ND5: changed from AY894254.1 to MT410861.1). The mitogenome MK922124.1 (= RefSeq NC\_044648.1) suffers from sequencing errors / numts (Sangster & Luksenburg 2021). Note that MT410861.1 does not include CytB and ND6.
- *Tringa totanus*: sequence data added (12S, 16S, ATP6, ATP8, Cox3, ND2, ND3, ND4, ND4L: MT410861.1)
- *Turnix sylvaticus*: sequence data added (FGB7: EU739503.1)
- *Turnix tanki*: sequence data replaced (12S: changed from AY447959.1 to MW307919.1, Cox1: changed from JQ342133.1 to MW307919.1, CytB: changed from JQ342155.1 to MW307919.1)
- *Turnix tanki*: sequence data added (16S, ATP6, ATP8, Cox2, Cox3, ND1, ND2, ND3, ND4, ND4L, ND5, ND6: MW307919.1)
- *Turnix velox*: sequence data added from whole-genome shotgun sequence (ADNH: VZTY01017687.1, ALDOB: VZTY01014799.1, BDNF: VZTY01030276.1, c-mos: VZTY01014397.1, FGB7: VZTY01014327.1, GAPDH: VZTY01021477.1, Myo2: VZTY01030238.1, NTF3: VZTY01024752.1, RAG1: VZTY01021834.1)
- *Uria aalge*: sequence data replaced (12S: changed from EF380314.1 to MN356418.1, 16S: changed from DQ485832.1 to MN356418.1, Cox1: changed from EF380335.1 to MN356418.1, CytB: changed from DQ485892.1 to MN356418.1, FGB7: changed from AY695194.1 to VZUE01000006.1 from whole-genome shotgun sequence, ND2: changed from JQ434924.1 to MN356418.1, ND5: changed from AJ242686.1 to MN356418.1, ND6: changed from AJ242686.1 to MN356418.1). The new FGB7 sequence is substantially longer.
- *Uria aalge*: sequence data added (ATP6, ATP8, Cox2, Cox3, ND1, ND3, ND4, ND4L: MN356418.1, from whole-genome shotgun sequence: ALDOB: VZUE01000214.1, BDNF: VZUE01000101.1, c-mos: VZUE01000005.1, Myo2: VZUE01000070.1, NTF3: VZUE01000197.1)
- *Uria lomvia*: sequence data added from whole-genome shotgun sequence (ADNH: NOXD01000001.1, ALDOB: NOXD01000087.1, BDNF: NOXD01000126.1, c-mos: NOXD01000059.1, FGB7: NOXD01000001.1, GAPDH: NOXD01000311.1, Myo2: NOXD01000012.1, NTF3: NOXD01000034.1)
- *Vanellus armatus*: sequence data added (Cox1: KM001328.1)
- *Vanellus cinereus*: sequence data replaced (12S: changed from AY447955.1 to KM404175.1 from which the rest of mitochondrial loci were drawn, ND5: changed from KM873665.1 to KM404175.1). Note that KM873665.1 is a chimera of *Vanellus cinereus* and *Motacilla alba* (Sangster & Luksenburg 2021).
- *Vanellus coronatus*: sequence data added from BOLD (Cox1: BROM705-07)
- *Vanellus miles*: sequence data added (Cox1: MK262456.1)
- *Vanellus resplendens*: sequence data added (Cox1: JQ176606.2)
- *Vanellus senegallus*: sequence data added from BOLD (Cox1: BROM872-07)
- *Vanellus tricolor*: sequence data added from BOLD (Cox1: BROM593-07)

- *Xenus cinereus*: sequence data replaced (Cox1: changed from GQ482914.1 to KX644890.1, CytB: changed from AF417922.1 to KX644890.1, ND1: changed from AY894289.1 to KX644890.1, ND5: changed from AY894255.1 to KX644890.1, ND6: changed from AF411394.1 to KX644890.1)
- Deleted the "CONTROVERSIAL" category containing *Larus vegae*
- *Balearica regulorum*: sequence data replaced (CytB: changed from U27543.1 to FJ769841.1, FGB7: changed from AY695251.1 to JJRR01064175.1 from whole-genome shotgun sequence). The new FGB7 sequence is substantially longer.
- *Actophilornis albinucha*: vernacular name added ("Madagascan Jacana")
- *Anous tenuirostris*: vernacular name added ("Lesser Noddy")
- *Aphriza virgata*: renamed to *Calidris virgata*
- *Brachyramphus perdix*: vernacular name added ("Long-billed Murrelet")
- *Burhinus grallarius*: vernacular name changed from "Bush Thick-knee" to "Bush Stone-Curlew"
- *Burhinus indicus*: row added (vernacular name: "Indian Stone-Curlew")
- *Burhinus oediconemus*: vernacular name changed from "Eurasian Thick-knee" to "Eurasian Stone-Curlew"
- *Calidris falcinellus*: vernacular name added ("Broad-billed Sandpiper")
- *Calidris subminuta*: vernacular name added ("Long-toed Stint")
- *Calidris temminckii* [sic]: name corrected to *Calidris temminckii*, vernacular name added ("Temminck's Stint")
- *Catharacta antarctica*: renamed to *Stercorarius antarcticus*
- *Catharacta chilensis*: renamed to *Stercorarius chilensis*, vernacular name added ("Chilean Skua")
- *Catharacta maccormicki*: renamed to *Stercorarius maccormicki*
- *Catharacta skua*: renamed to *Stercorarius skua*
- *Catoptrophorus semipalmatus*: renamed to *Tringa semipalmata*, vernacular name changed from "Willet" to "Eastern Willet"
- *Cerorhinca monocerata*: vernacular name corrected from "Rhinoceros [sic] Auklet" to "Rhinoceros Auklet"
- *Charadrius alexandrinus*: renamed to *Ochthodromus alexandrinus*
- *Charadrius alticola*: renamed to *Ochthodromus alticola*, vernacular name added ("Puna Plover")
- *Charadrius asiaticus*: renamed to *Eupoda asiatica*
- *Charadrius australis*: renamed to *Peltohyas australis*
- *Charadrius bicinctus*: renamed to *Anarhynchus bicinctus*
- *Charadrius collaris*: renamed to *Ochthodromus collaris*
- *Charadrius dealbatus*: renamed to *Ochthodromus dealbatus*, vernacular name added ("White-faced Plover")
- *Charadrius dubius*: renamed to *Thinornis dubius*
- *Charadrius falklandicus*: renamed to *Ochthodromus falklandicus*
- *Charadrius forbesi*: renamed to *Thinornis forbesi*, vernacular name added ("Forbes's Plover")
- *Charadrius javanicus*: renamed to *Ochthodromus javanicus*, vernacular name added ("Javan Plover")
- *Charadrius leschenaultii*: renamed to *Eupoda leschenaultii*, vernacular name changed from "Greater Sandplover" to "Greater Sand-Plover"
- *Charadrius marginatus*: renamed to *Ochthodromus marginatus*
- *Charadrius modestus*: renamed to *Zonibyx modestus*
- *Charadrius mongolus*: renamed to *Eupoda mongola*, vernacular name added ("Lesser Sand-Plover")
- *Charadrius montanus*: renamed to *Ochthodromus montanus*
- *Charadrius nivosus*: renamed to *Ochthodromus nivosus*, vernacular name added ("Snowy Plover")
- *Charadrius obscurus*: renamed to *Anarhynchus obscurus*, vernacular name added ("New Zealand Plover")
- *Charadrius pallidus*: renamed to *Ochthodromus pallidus*
- *Charadrius pecuarius*: renamed to *Ochthodromus pecuarius*
- *Charadrius peronii*: renamed to *Ochthodromus peronii*, vernacular name added ("Malaysian Plover")

- *Charadrius placidus*: renamed to *Thinornis placidus*, vernacular name added ("Long-billed Plover")
- *Charadrius ruficapillus*: renamed to *Ochthodromus ruficapillus*
- *Charadrius sanctaehelenae*: renamed to *Ochthodromus sanctaehelenae*, vernacular name added ("St. Helena Plover")
- *Charadrius thoracicus*: renamed to *Ochthodromus thoracicus*, vernacular name added ("Madagascan Plover")
- *Charadrius tricollaris*: renamed to *Afroxyechus tricollaris*, vernacular name changed from "African Three-banded Plover" to "Three-banded Plover"
- *Charadrius veredus*: renamed to *Eupoda veredus*, vernacular name added ("Oriental Plover")
- *Charadrius wilsonia*: renamed to *Ochthodromus wilsonia*
- *Chionis minor*: vernacular name added ("Black-faced Sheathbill")
- *Chroicocephalus poiocephalus*: vernacular name added ("Gray-headed Gull")
- *Cladorhynchus leucocephalus*: vernacular name added ("Banded Stilt")
- *Coenocorypha aucklandica*: vernacular name added ("Subantarctic Snipe")
- *Coenocorypha huegeli*: vernacular name added ("Snares Snipe")
- *Cursorius coromandelicus*: vernacular name added ("Indian Courser")
- *Cursorius rufus*: vernacular name added ("Burchell's Courser")
- *Cursorius somalensis*: vernacular name added ("Somali Courser")
- *Elseyaornis melanops*: renamed to *Thinornis melanops*
- *Erythrogonyx cinctus*: vernacular name added ("Red-kneed Dotterel")
- *Esacus giganteus*: renamed to *Esacus magnirostris*, vernacular name added ("Beach Stone-Curlew")
- *Esacus recurvirostris*: vernacular name added ("Great Stone-Curlew")
- *Eurynorhynchus pygmeus*: renamed to *Calidris pygmaea*, vernacular name added ("Spoon-billed Sandpiper")
- *Gabianus scoresbii*: renamed to *Leucophaeus scoresbii*
- *Gallinago andina*: row added
- *Gallinago delicata*: vernacular name added ("Wilson's Snipe")
- *Gallinago imperialis*: renamed to *Chubbia imperialis*, vernacular name added ("Imperial Snipe")
- *Gallinago jamesoni*: renamed to *Chubbia jamesoni*
- *Gallinago macrodactyla*: vernacular name added ("Madagascan Snipe")
- *Gallinago magellanica*: row added
- *Gallinago nemoricola*: vernacular name added ("Wood Snipe")
- *Gallinago solitaria*: vernacular name added ("Solitary Snipe")
- *Gallinago stricklandii*: renamed to *Chubbia stricklandii*, vernacular name added ("Fuegian Snipe")
- *Gallinago undulata*: vernacular name added ("Giant Snipe")
- *Glareola cinerea*: vernacular name added ("Gray Pratincole")
- *Glareola lactea*: vernacular name added ("Small Pratincole")
- *Glareola nuchalis*: vernacular name added ("Rock Pratincole")
- *Glareola ocularis*: vernacular name added ("Madagascan Pratincole")
- *Heteroscelus brevipes*: renamed to *Tringa brevipes*
- *Heteroscelus incanus*: renamed to *Tringa incana*
- *Himantopus himantopus*: vernacular name added ("Black-winged Stilt")
- *Himantopus leucocephalus*: vernacular name added ("White-headed Stilt")
- *Himantopus novaeseelandiae*: vernacular name added ("Black Stilt")
- *Hydrophasianus chirurgus*: vernacular name changed from "Pheasant Tailed Jacana" to "Pheasant-tailed Jacana"
- *Larosterna inca*: vernacular name changed from "Incan Tern" to "Inca Tern"
- *Larus argentatus*: vernacular name changed from "Herring Gull" to "European Herring Gull"
- *Larus armenicus*: vernacular name added ("Armenian Gull")
- *Larus atlanticus*: vernacular name added ("Olrog's Gull")
- *Larus atricilla*: renamed to *Leucophaeus atricilla*
- *Larus audouini* [sic]: renamed to *Ichthyæetus audouinii*, vernacular name added ("Audouin's Gull")
- *Larus brachyrhynchus*: vernacular name added ("Short-billed Gull")

- *Larus brunnicephalus*: renamed to *Chroicocephalus brunnicephalus*, vernacular name added ("Brown-headed Gull")
- *Larus bulleri*: renamed to *Chroicocephalus bulleri*, vernacular name added ("Black-billed Gull")
- *Larus cachhinans* [sic]: name corrected to *Larus cachinnans*
- *Larus cirrocephalus*: renamed to *Chroicocephalus cirrocephalus*, vernacular name changed from "Grey-headed Gull" to "Gray-hooded Gull"
- *Larus fuliginosus*: renamed to *Leucophaeus fuliginosus*, vernacular name added ("Lava Gull")
- *Larus genei*: renamed to *Chroicocephalus genei*
- *Larus hartlaubi* [sic]: renamed to *Chroicocephalus hartlaubii*
- *Larus hemprichi* [sic]: renamed to *Ichthyaelus hemprichii*, vernacular name added ("Sooty Gull")
- *Larus heuglini*: vernacular name added ("Heuglin's Gull")
- *Larus ichthyaelus*: renamed to *Ichthyaelus ichthyaelus*, vernacular name added ("Pallas's Gull")
- *Larus maculipennis*: renamed to *Chroicocephalus maculipennis*, vernacular name added ("Brown-hooded Gull")
- *Larus melanocephalus*: renamed to *Ichthyaelus melanocephalus*, vernacular name added ("Mediterranean Gull")
- *Larus michahellis*: vernacular name added ("Yellow-legged Gull")
- *Larus minutus*: renamed to *Hydrocoloeus minutus*, vernacular name added ("Little Gull")
- *Larus modestus*: renamed to *Leucophaeus modestus*, vernacular name added ("Gray Gull")
- *Larus mongolicus*: vernacular name added ("Mongolian Gull")
- *Larus novaehollandiae*: renamed to *Chroicocephalus novaehollandiae*
- *Larus philadelphia*: renamed to *Chroicocephalus philadelphia*
- *Larus pipixcan*: renamed to *Leucophaeus pipixcan*
- *Larus relictus*: renamed to *Ichthyaelus relictus*, vernacular name added ("Relict Gull")
- *Larus ridibundus*: renamed to *Chroicocephalus ridibundus*, vernacular name added ("Black-headed Gull")
- *Larus scolopinus* [sic]: renamed to *Chroicocephalus scopulinus*, vernacular name added ("Red-billed Gull")
- *Larus serranus*: renamed to *Chroicocephalus serranus*
- *Larus smithsonianus*: vernacular name added ("American Herring Gull")
- *Larus vegae*: vernacular name added ("Vega Gull")
- *Limnodromus semipalmatus*: vernacular name added ("Asian Dowitcher")
- *Numenius borealis*: vernacular name added ("Eskimo Curlew")
- *Numenius tenuirostris*: vernacular name added ("Slender-billed Curlew")
- *Ortyxelos meiffrenii*: row added
- *Pedionomus torquatus*: vernacular name added ("Plains-wanderer")
- *Phegornis mitchellii*: vernacular name added ("Diademed Sandpiper-Plover")
- *Philomachus pugnax*: renamed to *Calidris pugnax*
- *Pluvianellus socialis*: vernacular name added ("Magellanic Plover")
- *Procelsterna albivitta*: renamed to *Anous albivitta*
- *Procelsterna cerulea*: renamed to *Anous ceruleus*
- *Recurvirostra novaehollandiae*: vernacular name added ("Red-necked Avocet")
- *Rhinoptilus bitorquatus*: vernacular name added ("Jerdon's Courser")
- *Rostratula australis*: vernacular name added ("Australian Painted-snipe")
- *Rostratula semicollaris*: renamed to *Nycticryphes semicollaris*
- *Rynchops albicollis*: vernacular name added ("Indian Skimmer")
- *Scolopax bukidnonensis*: vernacular name added ("Bukidnon Woodcock")
- *Scolopax celebensis*: vernacular name added ("Sulawesi Woodcock")
- *Scolopax mira*: vernacular name added ("Amami Woodcock")
- *Scolopax rosenbergii*: vernacular name added ("New Guinea Woodcock")
- *Scolopax saturata*: vernacular name added ("Javan Woodcock")
- *Steganopus tricolor*: renamed to *Phalaropus tricolor*
- *Sterna acuticauda*: vernacular name added ("Black-bellied Tern")
- *Sterna albifrons*: renamed to *Sternula albifrons*
- *Sterna albobristata*: renamed to *Chlidonias albobristatus*, vernacular name added ("Black-fronted Tern")



- *Sterna aleutica*: renamed to *Onychoprion aleuticus*
- *Sterna anaethetus*: renamed to *Onychoprion anaethetus*
- *Sterna antillarum*: renamed to *Sternula antillarum*
- *Sterna aurantia*: vernacular name added ("River Tern")
- *Sterna balaenarum*: renamed to *Sternula balaenarum*, vernacular name added ("Damara Tern")
- *Sterna bengalensis*: renamed to *Thalasseus bengalensis*
- *Sterna bergii*: renamed to *Thalasseus bergii*
- *Sterna bernsteini*: renamed to *Thalasseus bernsteini*, vernacular name added ("Chinese Crested Tern")
- *Sterna caspia*: renamed to *Hydroprogne caspia*
- *Sterna elegans*: renamed to *Thalasseus elegans*
- *Sterna eurygnatha*: renamed to *Thalasseus acuflavidus*, vernacular name added ("Cabot's Tern")
- *Sterna fuscata*: renamed to *Onychoprion fuscatus*
- *Sterna lorata*: renamed to *Sternula lorata*, vernacular name added ("Peruvian Tern")
- *Sterna lunata*: renamed to *Onychoprion lunatus*
- *Sterna maxima*: renamed to *Thalasseus maximus*
- *Sterna nereis*: renamed to *Sternula nereis*, vernacular name added ("Fairy Tern")
- *Sterna nilotica*: renamed to *Gelochelidon nilotica*, vernacular name changed from "Gull-bellied Tern" to "Gull-billed Tern"
- *Sterna sandvicensis*: renamed to *Thalasseus sandvicensis*
- *Sterna superciliaris*: renamed to *Sternula superciliaris*
- *Sterna virgata*: vernacular name added ("Kerguelen Tern")
- *Sternula saundersi*: row added
- *Stiltia isabella*: renamed to *Glareola isabella*
- *Synthliboramphus hypoleucus*: vernacular name added ("Guadalupe Murrelet")
- *Synthliboramphus scrippsi*: vernacular name added ("Scripps's Murrelet")
- *Synthliboramphus wumizusume*: vernacular name added ("Japanese Murrelet")
- *Thinornis novaeseelandiae*: vernacular name added ("Shore Dotterel")
- *Thinornis rubricollis*: renamed to *Thinornis cucullatus*, vernacular name changed from "Hooded Plover" to "Hooded Dotterel"
- *Tringa erythropus*: vernacular name added ("Spotted Redshank")
- *Tringa guttifer*: vernacular name added ("Nordmann's Greenshank")
- *Tryngites subruficollis*: renamed to *Calidris subruficollis*
- *Turnix castanotus*: vernacular name added ("Chestnut-backed Buttonquail")
- *Turnix everetti*: vernacular name added ("Sumba Buttonquail")
- *Turnix hottentottus*: vernacular name added ("Hottentot Buttonquail")
- *Turnix maculosus*: vernacular name added ("Red-backed Buttonquail")
- *Turnix melanogaster*: vernacular name added ("Black-breasted Buttonquail")
- *Turnix nanus*: vernacular name added ("Black-rumped Buttonquail")
- *Turnix nigricollis*: vernacular name added ("Madagascan Buttonquail")
- *Turnix ocellatus*: vernacular name added ("Spotted Buttonquail")
- *Turnix olivii*: vernacular name added ("Buff-breasted Buttonquail")
- *Turnix pyrrhothorax*: vernacular name added ("Red-chested Buttonquail")
- *Turnix siciator* [sic]: name corrected to *Turnix suscitator*, vernacular name added ("Barred Buttonquail")
- *Turnix sylvaticus*: vernacular name added ("Common Buttonquail")
- *Turnix tanki*: vernacular name added ("Yellow-legged Buttonquail")
- *Turnix varius*: vernacular name added ("Painted Buttonquail")
- *Turnix velox*: vernacular name added ("Little Buttonquail")
- *Turnix worcesteri*: vernacular name added ("Worcester's Buttonquail")
- *Vanellus albiceps*: vernacular name added ("White-crowned Lapwing")
- *Vanellus cayanus*: vernacular name added ("Pied Lapwing")
- *Vanellus chilensis*: vernacular name added ("Southern Lapwing")
- *Vanellus cinereus*: vernacular name added ("Gray-headed Lapwing")
- *Vanellus gregarius*: vernacular name added ("Sociable Lapwing")
- *Vanellus indicus*: vernacular name added ("Red-wattled Lapwing")

- *Vanellus leucurus*: vernacular name added (“White-tailed Lapwing”)
- *Vanellus lugubris*: vernacular name added (“Senegal Lapwing”)
- *Vanellus malarbaricus* [sic]: named corrected to *Vanellus malabaricus*, vernacular name added (“Yellow-wattled Lapwing”)
- *Vanellus melanocephalus*: vernacular name added (“Spot-breasted Lapwing”)
- *Vanellus melanopterus*: vernacular name added (“Black-winged Lapwing”)
- *Vanellus resplendens*: vernacular name added (“Andean Lapwing”)
- *Vanellus senegallus*: vernacular name added (“African Wattled Lapwing”)
- *Vanellus superciliosus*: vernacular name added (“Brown-chested Lapwing”)
- *Xenus cinereus*: vernacular name added (“Terek Sandpiper”)
- Added the “RECENTLY EXTINCT” category and moved *Pinguinus impennis* and *Prosobonia leucoptera* into it
- *Coenocorypha barrierensis*: row added
- *Coenocorypha iredalei*: row added
- *Prosobonia cancellata*: row added
- *Vanellus macropterus*: row added
- *Balearica regulorum*: vernacular name added (“Gray Crowned-Crane”)
- Across the table: RefSeq accession numbers (prefixed with “NC\_”) replaced with the corresponding GenBank accession numbers
- New column “GAPDH11” added for glyceraldehyde-3-phosphate dehydrogenase intron 11. Note that while GenBank classifies sequences JQ708871.1 and JQ708878.1 as *Larus argentatus* and *Larus canus*, respectively, Appendix S1 to the paper in which these sequences were published (Sonsthagen et al. 2012; doi:10.1002/ece3.240) confirms that they specifically belong to the subspecies *L. argentatus vegae* and *L. canus brachyrhynchus*, which we treat as full species here. Conversely, Appendix S1 also shows that sequences JQ708809.1 and JQ708916.1 belong to *L. argentatus argentatus* and *L. canus canus*, respectively, i.e., to *Larus argentatus* and *Larus canus* in the narrow sense in which they are used here.
- New column “MUSK” added for muscle skeletal receptor tyrosine kinase (exons 4 and 5 + intron 4). Note that no BLAST hit was found for *Phaetusa simplex*.
- New column “ODC” added for ornithine decarboxylase (introns 6 and 7 + exon 7). Note that while GenBank classifies sequences JQ710098.1 and JQ710104.1 as *Larus argentatus* and *Larus canus*, respectively, Sonsthagen et al. (2012; Appendix S1) confirm that they specifically belong to subspecies *L. argentatus vegae* and *L. canus brachyrhynchus*, which we treat as full species here. They also show that sequences JQ710008.1 and JQ710156.1 belong to *L. argentatus argentatus* and *L. canus canus*, respectively, i.e., to *Larus argentatus* and *Larus canus* in the narrow sense in which they are used here.
- Column “Myo2” renamed to “MB2”
- Column “ADNH” renamed to “ADH5”
- Column “c-mos” renamed to “CMOS”
- Column “Complete Mitogenome” renamed to “Mitogenome”
- Column “FGB7 (intron 7?)” renamed to “FGB7”
- Column “GPDH” renamed to “GAPDH3–5”
- Columns reordered first by genome (mitochondrial first, nuclear second), then alphabetically, with the loci that were eventually not used going last: 12S, 16S, ATP6, ATP8, Cox1, Cox2, Cox3, CytB, ND1, ND2, ND3, ND4, ND4L, ND5, ND6, complete mitogenome, ADH5, ALDOB, BDNF, CMOS, FGB7, GAPDH3–5, GAPDH11, MB2, MUSK, NTF3, ODC, RAG1, BMP2, DNAH3, PRLR, PTPN12, TRAF6.

#### **./Coverage.csv**

- ADH5 sequences dropped after initial tree inference (*Burhinus oedicnemus*: [VFFE01007878.1], *Balearica regulorum*: [JJRR01094557.1]) marked with square brackets to indicate their removal.
- BDNF sequences dropped after initial tree inference (*Balearica regulorum*: [JJRR01026322.1], *Burhinus bistriatus*: [EU737971.1], *Calidris pygmaea*: [QJSC01026553.1], *Turnix sylvaticus*: [EU738099.1], *Turnix velox*: [VZTY01030276.1]) marked with square brackets to indicate their removal.

- CMOS sequence dropped after initial tree inference (*Balearica regulorum*: [JJRR01077102.1]) marked with square brackets to indicate its removal.
- FGB7 sequences dropped after initial tree inference (*Balearica regulorum*: [JJRR01064175.1], *Ochthodromus peronii*: [FGB7\_peroni001a], *Pluvialis squatarola*: [KM001471.1], *Vanellus armatus*: [KM001494.1]) marked with square brackets to indicate their removal.
- GAPDH3-5 sequence dropped after initial tree inference (*Chroicocephalus maculipennis*: [VYZF01000064.1]) marked with square brackets to indicate its removal.
- MUSK sequence dropped after initial tree inference (*Balearica regulorum*: [JJRR01056355.1]) marked with square brackets to indicate its removal.
- ODC sequence dropped after initial tree inference (*Balearica regulorum*: [JJRR01048851.1]) marked with square brackets to indicate its removal.
- RAG1 sequence dropped after initial tree inference (*Balearica regulorum*: [JJRR01094532.1]) marked with square brackets to indicate its removal.
- 12S sequences dropped after initial tree inference (*Anarhynchus obscurus*: [KF357995.1], *Tringa guttifer*: [MK905885.1]) marked with square brackets to indicate their removal.
- ATP6 sequences dropped after initial tree inference (*Numenius arquata*: [EU826408.1], *Phalaropus tricolor*: [AY894274.1]) marked with square brackets to indicate their removal.
- Cox1 sequence dropped after initial tree inference (*Pluvianus aegyptius*: [BROM444-06]) marked with square brackets to indicate its removal.
- Cox2 sequences dropped after initial tree inference (*Rissa tridactyla*: [MN356420.1], *Sternula albifrons*: [KT350612.1]) marked with square brackets to indicate their removal.
- Cox3 sequences dropped after initial tree inference (*Balearica regulorum*: [FJ769841.1], *Pedionomus torquatus*: [DQ385208.1]) marked with square brackets to indicate their removal.
- CytB sequence dropped after initial tree inference (*Pluvialis fulva*: [KX639757.1]) marked with square brackets to indicate its removal.
- ND2 sequence dropped after initial tree inference (*Sterna trudeaui*: [AY631389.1]) marked with square brackets to indicate its removal.
- ND3 sequence dropped after initial tree inference (*Rynchops niger*: [MN356248.1]) marked with square brackets to indicate its removal.
- ND4L sequences dropped after initial tree inference (*Balearica regulorum*: [FJ769841.1], *Metopidius indicus*: [MW482963.1]) marked with square brackets to indicate their removal.
- ND5 sequences dropped after initial tree inference (*Actitis macularius*: [AY894248.1], *Alle alle*: [AJ242684.1]) marked with square brackets to indicate their removal.
- ND6 sequences dropped after initial tree inference (*Calidris tenuirostris*: [MK992912.1], *Tringa guttifer*: [MK905885.1]) marked with square brackets to indicate their removal.

#### **./Coverage.csv**

- Inserted a new column stating what family a given species belongs to; gave names to the first three columns (Vernacular name, Family, Scientific name); inserted a new Morphology column (after RAG1 and before BMP2) indicating which species were sampled for the morphological characters from Strauch (1978).

#### **./coverage\_check.R**

- Added an R script used to check the taxon sample of the manually renamed but otherwise unmodified alignments (expected ending: “\_renamed.fasta”) against Coverage.csv.

#### **./Family-level\_coverage.txt**

- This file compared the total number of shorebird species recognized by three major checklists (Howard & Moore, Clements, Boyd) to the number of taxa included in concatenated alignment and total-evidence dataset, with all counts broken down by family. It was largely used as input for Figure 2, and was deleted as redundant w.r.t. ./TaxonomyInFlux\_v3.05\_2019-12-18.csv, which is more detailed (as it does not just give numbers, but actually maps our taxonomy onto Boyd’s and Clements’ checklists).

### **./Genbank\_searches/**

- Deleted a folder containing some (but not all) Geneious data files storing the results of GenBank searches for specific loci. Redundant with respect to ./Coverage.csv, which is complete and up-to-date.

### **./README.md**

- Added a file describing the contents of the Dryad repository, which is organized in the same manner as the local project directory.

### **./table1\_info\_grabber.R**

- Deleted; the script no longer grabbed the right path names after the new gene trees have been generated using RAxML-NG rather than RAxML, and there was little point to it given that the relevant information was easy to extract manually.

### **./TaxonomyInFlux\_v3.05\_2019-12-18.csv**

- A spreadsheet that maps the 391 extant or recently extinct species recognized by our taxonomy onto the taxonomies employed by the Clements checklist (August 2021 version) and Taxonomy in Flux (v3.05).

## Data assembly – checking taxon/locus coverage against Burleigh et al. (2015) (section 2.1)

[./Coverage\\_check.Rmd](#)

[./Coverage\\_check.html](#)

[./Burleigh\\_et\\_al\\_data/Burleigh\\_coverage\\_check.Rmd](#)

[./Burleigh\\_et\\_al\\_data/Burleigh\\_coverage\\_check.html](#)

- Changed and moved the R Markdown notebook used to check the locus coverage of our dataset against the supermatrix of Burleigh et al. (2014). This time around, we were able to use the “rentrez” package to translate sequence IDs given in Burleigh et al.’s (2015) accession table into actual accession numbers, which allowed us to check their identity.

# Gene tree alignments and analyses (sections 2.1, 2.2, 3.1, 3.2)

## [./Individual\\_loci/BLAST\\_searches.txt](#)

- Added a text file recording which sequences were blasted against the NCBI WGS database to obtain the corresponding sequences from the B10K and other whole-genome contigs.

## [./Individual\\_loci/gene\\_regions.csv](#)

## [./Individual\\_loci/missing\\_sequence\\_decisiveness.csv](#)

## [./Individual\\_loci/sumac\\_log](#)

- Replaced after rerunning SUMAC on the new supermatrix. The gene\_regions.csv file produced by SUMAC was manually edited by inserting an "Avg. Pairwise Identity (%)" column.

## [./Individual\\_loci/gene-tree-analysis.sh](#)

## [./Individual\\_loci/muscle-refinement.sh](#)

## [./Individual\\_loci/nucl\\_bootstrap.sh](#)

## [./Individual\\_loci/pruned-gene-trees.sh](#)

- Now handled by locus-specific scripts in the corresponding directories.

## [./Individual\\_loci/intron\\_exon\\_boundaries.csv](#)

- Added a file recording the positions of intron/exon boundaries for the original and final alignments, used to define the initial scheme in the IQ-TREE 2 partitioning analysis.

## [./Individual\\_loci/locus\\_table.csv](#)

- Replaced after rerunning Supermatrix\_statistics.Rmd on the new supermatrix.

## [./Individual\\_loci/Renaming.Rmd](#)

## [./Individual\\_loci/Renaming.html](#)

- Deleted, since the step of renaming the sequences downloaded from GenBank is now handled manually to avoid taxonomic reconciliation errors.

## [./Individual\\_loci/sequence\\_data\\_plot.pdf](#)

## [./Individual\\_loci/sequence\\_decisiveness\\_scores\\_plot.pdf](#)

- Deleted old figures produced using SUMAC, as these are redundant with respect to the information contained in Supermatrix\_Statistics.html.

## [./Individual\\_loci/Supermatrix\\_Statistics.Rmd](#)

## [./Individual\\_loci/Supermatrix\\_Statistics.html](#)

- Replaced after rerunning SUMAC on the new supermatrix

## [./Individual\\_loci/Taxonomy\\_FINAL.csv](#)

- Deleted; synonym lookup dictionary no longer needed now that taxonomic reconciliation is handled manually.

## **./Individual\_loci/alignments/**

- Deleted; a temporary folder with copies of the final versions of the individual gene alignments, created specifically for SUMAC (which needed all of these in a single place).

## **./Individual\_loci/ADNH5/**

**./Individual\_loci/ADNH5/ADNH5\_aligned.fasta**  
**./Individual\_loci/ADNH5/ADNH5\_aligned\_renamed.fasta**  
**./Individual\_loci/ADNH5/ADNH5\_aligned\_renamed.fasta.reduced**  
**./Individual\_loci/ADNH5/ADNH5\_MUSCLE\_alignment.log**  
**./Individual\_loci/ADNH5/ADNH5\_to\_align.fasta**  
**./Individual\_loci/ADNH5/RAxML\_bestTree.ADNH5**  
**./Individual\_loci/ADNH5/RAxML\_bipartitions.ADNH5\_biparts**  
**./Individual\_loci/ADNH5/RAxML\_bipartitionsBranchLabels.ADNH5\_biparts**  
**./Individual\_loci/ADNH5/RAxML\_bootstrap.ADNH5-bs**  
**./Individual\_loci/ADNH5/RAxML\_info.ADNH5**  
**./Individual\_loci/ADNH5/RAxML\_info.ADNH5-bs**  
**./Individual\_loci/ADNH5/RAxML\_info.ADNH5\_biparts**

## **./Individual\_loci/ADH5/**

**./Individual\_loci/ADH5/RAxML-NG\_output/**  
**./Individual\_loci/ADH5/RAxML-NG\_output/ADH5.raxml.bestModel**  
**./Individual\_loci/ADH5/RAxML-NG\_output/ADH5.raxml.bestTreeCollapsed**  
**./Individual\_loci/ADH5/RAxML-NG\_output/ADH5.raxml.log**  
**./Individual\_loci/ADH5/RAxML-NG\_output/ADH5.raxml.mlTrees**  
**./Individual\_loci/ADH5/RAxML-NG\_output/ADH5.raxml.rba**  
**./Individual\_loci/ADH5/RAxML-NG\_output/ADH5.raxml.reduced.phy**  
**./Individual\_loci/ADH5/RAxML-NG\_output/ADH5.raxml.startTree**  
**./Individual\_loci/ADH5/RAxML-NG\_FINAL\_output/**  
**./Individual\_loci/ADH5/RAxML-NG\_FINAL\_output/ADH5\_FINAL.raxml.bestModel**  
**./Individual\_loci/ADH5/RAxML-NG\_FINAL\_output/ADH5\_FINAL.raxml.bestTreeCollapsed**  
**./Individual\_loci/ADH5/RAxML-NG\_FINAL\_output/ADH5\_FINAL.raxml.log**  
**./Individual\_loci/ADH5/RAxML-NG\_FINAL\_output/ADH5\_FINAL.raxml.mlTrees**  
**./Individual\_loci/ADH5/RAxML-NG\_FINAL\_output/ADH5\_FINAL.raxml.rba**  
**./Individual\_loci/ADH5/RAxML-NG\_FINAL\_output/ADH5\_FINAL.raxml.reduced.phy**  
**./Individual\_loci/ADH5/RAxML-NG\_FINAL\_output/ADH5\_FINAL.raxml.startTree**  
**./Individual\_loci/ADH5/ADH5\_aligned\_refined\_renamed.fasta**  
**./Individual\_loci/ADH5/ADH5\_FINAL.fasta**  
**./Individual\_loci/ADH5/ADH5\_FINAL.raxml.bestTree**  
**./Individual\_loci/ADH5/ADH5\_MUSCLE\_refinement.log**  
**./Individual\_loci/ADH5/ADH5\_Oct2021\_aligned.fasta**  
**./Individual\_loci/ADH5/ADH5\_pruned.fasta**  
**./Individual\_loci/ADH5/ADH5\_pruned\_MUSCLE\_refinement.log**  
**./Individual\_loci/ADH5/ADH5\_pruned\_refined.fasta**  
**./Individual\_loci/ADH5/ADH5.raxml.bestTree**  
**./Individual\_loci/ADH5/ADH5.sh**

- The original alignment was refined using MUSCLE and analyzed. Based on this initial tree, two sequences were excluded: those of *Burhinus oedicephalus*, which was subtended by an extremely long terminal branch and misplaced as the sister group of *Pedionomus*, and of *Balearica regulorum*, which caused rooting issues (rendering Charadrii paraphyletic, with *Pluvianus* as the earliest-diverging taxon). The pruned alignment was refined again, and the final alignment was created by making small manual edits to this second refined version. This final round of manual edits did not affect tree topology, but helped decrease alignment length (from 922 bp to 916 bp) and increase the likelihood of the best tree (pruned and refined: lnL = -7302.853914, manually realigned/final: lnL = -7285.096150).



./Individual\_loci/ALDOB/  
./Individual\_loci/ALDOB/ALDOB\_aligned.fasta  
./Individual\_loci/ALDOB/ALDOB\_MUSCLE\_alignment.log  
./Individual\_loci/ALDOB/ALDOB\_to\_align.fasta  
./Individual\_loci/ALDOB/ALDOB\_with\_outgroup\_renamed.fasta  
./Individual\_loci/ALDOB/RAxML\_bestTree.ALDOB  
./Individual\_loci/ALDOB/RAxML\_bipartitions.ALDOB\_biparts  
./Individual\_loci/ALDOB/RAxML\_bipartitionsBranchLabels.ALDOB\_biparts  
./Individual\_loci/ALDOB/RAxML\_bootstrap.ALDOB-bs  
./Individual\_loci/ALDOB/RAxML\_info.ALDOB  
./Individual\_loci/ALDOB/RAxML\_info.ALDOB-bs

./Individual\_loci/ALDOB/  
./Individual\_loci/ALDOB/RAxML-NG\_output/  
./Individual\_loci/ALDOB/RAxML-NG\_output/ALDOB.raxml.bestModel  
./Individual\_loci/ALDOB/RAxML-NG\_output/ALDOB.raxml.bestTreeCollapsed  
./Individual\_loci/ALDOB/RAxML-NG\_output/ALDOB.raxml.log  
./Individual\_loci/ALDOB/RAxML-NG\_output/ALDOB.raxml.mlTrees  
./Individual\_loci/ALDOB/RAxML-NG\_output/ALDOB.raxml.rba  
./Individual\_loci/ALDOB/RAxML-NG\_output/ALDOB.raxml.startTree  
./Individual\_loci/ALDOB/ALDOB\_aligned\_renamed.fasta  
./Individual\_loci/ALDOB/ALDOB\_Oct2021\_aligned.fasta  
./Individual\_loci/ALDOB/ALDOB.raxml.bestTree  
./Individual\_loci/ALDOB/ALDOB.sh

- The original alignment was used without any modifications.

./Individual\_loci/BDNF/  
./Individual\_loci/BDNF/BDNF\_with\_outgroup\_renamed.fasta  
./Individual\_loci/BDNF/RAxML\_bestTree.BDNF  
./Individual\_loci/BDNF/RAxML\_bipartitions.BDNF\_biparts  
./Individual\_loci/BDNF/RAxML\_bipartitionsBranchLabels.BDNF\_biparts  
./Individual\_loci/BDNF/RAxML\_bootstrap.BDNF-bs  
./Individual\_loci/BDNF/RAxML\_info.BDNF-bs  
./Individual\_loci/BDNF/RAxML\_info.BDNF\_biparts

./Individual\_loci/BDNF/  
./Individual\_loci/BDNF/RAxML-NG\_output/  
./Individual\_loci/BDNF/RAxML-NG\_output/BDNF.raxml.bestModel  
./Individual\_loci/BDNF/RAxML-NG\_output/BDNF.raxml.bestTreeCollapsed  
./Individual\_loci/BDNF/RAxML-NG\_output/BDNF.raxml.log  
./Individual\_loci/BDNF/RAxML-NG\_output/BDNF.raxml.mlTrees  
./Individual\_loci/BDNF/RAxML-NG\_output/BDNF.raxml.rba  
./Individual\_loci/BDNF/RAxML-NG\_output/BDNF.raxml.reduced.phy  
./Individual\_loci/BDNF/RAxML-NG\_output/BDNF.raxml.startTree  
./Individual\_loci/BDNF/RAxML-NG\_FINAL\_output/  
./Individual\_loci/BDNF/RAxML-NG\_FINAL\_output/BDNF\_FINAL.raxml.bestModel  
./Individual\_loci/BDNF/RAxML-NG\_FINAL\_output/BDNF\_FINAL.raxml.bestTreeCollapsed  
./Individual\_loci/BDNF/RAxML-NG\_FINAL\_output/BDNF\_FINAL.raxml.log  
./Individual\_loci/BDNF/RAxML-NG\_FINAL\_output/BDNF\_FINAL.raxml.mlTrees  
./Individual\_loci/BDNF/RAxML-NG\_FINAL\_output/BDNF\_FINAL.raxml.rba  
./Individual\_loci/BDNF/RAxML-NG\_FINAL\_output/BDNF\_FINAL.raxml.reduced.phy  
./Individual\_loci/BDNF/RAxML-NG\_FINAL\_output/BDNF\_FINAL.raxml.startTree  
./Individual\_loci/BDNF/BDNF\_aligned\_renamed.fasta  
./Individual\_loci/BDNF/BDNF\_FINAL.fasta  
./Individual\_loci/BDNF/BDNF\_FINAL.raxml.bestTree

./Individual\_loci/BDNF/BDNF\_Oct2021\_aligned.fasta  
./Individual\_loci/BDNF/BDNF.raxml.bestTree  
./Individual\_loci/BDNF/BDNF.sh

- Final tree based on the original alignment with five sequences excluded. These belonged to: (1) *Burhinus bistriatus*, which failed to group with the other two burhinids; (2) *Calidris pygmaea*, which grouped with Jacanida rather than *Calidris pugnax*; (3) *Turnix sylvaticus*; (4) *Turnix velox*; and (5) *Balearica regulorum*. The last three sequences were excluded because they were causing rooting issues (Turnicidae sister to a clade comprising Scolopaci on the one hand and Larida nested within a paraphyletic Charadrii on the other).

./Individual\_loci/CMOS/  
./Individual\_loci/CMOS/CMOS\_aligned.fasta  
./Individual\_loci/CMOS/CMOS\_aligned\_renamed.fasta  
./Individual\_loci/CMOS/CMOS\_aligned\_renamed.fasta.reduced  
./Individual\_loci/CMOS/CMOS\_MUSCLE\_alignment.log  
./Individual\_loci/CMOS/CMOS\_to\_align.fasta  
./Individual\_loci/CMOS/RAxML\_bestTree.CMOS  
./Individual\_loci/CMOS/RAxML\_bipartitions.CMOS\_biparts  
./Individual\_loci/CMOS/RAxML\_bipartitionsBranchLabels.CMOS\_biparts  
./Individual\_loci/CMOS/RAxML\_bootstrap.CMOS-bs  
./Individual\_loci/CMOS/RAxML\_info.CMOS  
./Individual\_loci/CMOS/RAxML\_info.CMOS-bs  
./Individual\_loci/CMOS/RAxML\_info.CMOS\_biparts

./Individual\_loci/CMOS/  
./Individual\_loci/CMOS/RAxML-NG\_output/  
./Individual\_loci/CMOS/RAxML-NG\_output/CMOS.raxml.bestModel  
./Individual\_loci/CMOS/RAxML-NG\_output/CMOS.raxml.bestTreeCollapsed  
./Individual\_loci/CMOS/RAxML-NG\_output/CMOS.raxml.log  
./Individual\_loci/CMOS/RAxML-NG\_output/CMOS.raxml.mlTrees  
./Individual\_loci/CMOS/RAxML-NG\_output/CMOS.raxml.rba  
./Individual\_loci/CMOS/RAxML-NG\_output/CMOS.raxml.reduced.phy  
./Individual\_loci/CMOS/RAxML-NG\_output/CMOS.raxml.startTree  
./Individual\_loci/CMOS/RAxML-NG\_FINAL\_output/  
./Individual\_loci/CMOS/RAxML-NG\_FINAL\_output/CMOS\_FINAL.raxml.bestModel  
./Individual\_loci/CMOS/RAxML-NG\_FINAL\_output/CMOS\_FINAL.raxml.bestTreeCollapsed  
./Individual\_loci/CMOS/RAxML-NG\_FINAL\_output/CMOS\_FINAL.raxml.log  
./Individual\_loci/CMOS/RAxML-NG\_FINAL\_output/CMOS\_FINAL.raxml.mlTrees  
./Individual\_loci/CMOS/RAxML-NG\_FINAL\_output/CMOS\_FINAL.raxml.rba  
./Individual\_loci/CMOS/RAxML-NG\_FINAL\_output/CMOS\_FINAL.raxml.reduced.phy  
./Individual\_loci/CMOS/RAxML-NG\_FINAL\_output/CMOS\_FINAL.raxml.startTree  
./Individual\_loci/CMOS/CMOS\_aligned\_renamed.fasta  
./Individual\_loci/CMOS/CMOS\_FINAL.fasta  
./Individual\_loci/CMOS/CMOS\_FINAL.raxml.bestTree  
./Individual\_loci/CMOS/CMOS\_Oct2021\_aligned.fasta  
./Individual\_loci/CMOS/CMOS.raxml.bestTree  
./Individual\_loci/CMOS/CMOS.sh

- Final tree based on the original alignment with a single excluded sequence: that of *Balearica regulorum*, which was causing rooting issues (Charadrii paraphyletic with respect to the rest of the clade).

```

./Individual_loci/FIB7/
./Individual_loci/FIB7/FIB7_aligned.fasta
./Individual_loci/FIB7/FIB7_aligned.fasta.reduced
./Individual_loci/FIB7/FIB7_MUSCLE_alignment.log
./Individual_loci/FIB7/FIB7_to_align.fasta
./Individual_loci/FIB7/FIB7_with_outgroup_renamed.fasta
./Individual_loci/FIB7/RAxML_bestTree.FIB7
./Individual_loci/FIB7/RAxML_bipartitions.FIB7_biparts
./Individual_loci/FIB7/RAxML_bipartitionsBranchLabels.FIB7_biparts
./Individual_loci/FIB7/RAxML_bootstrap.FIB7-bs
./Individual_loci/FIB7/RAxML_info.FIB7
./Individual_loci/FIB7/RAxML_info.FIB7-bs
./Individual_loci/FIB7/RAxML_info.FIB7_biparts

./Individual_loci/FGB7/
./Individual_loci/FGB7/RAxML-NG_output/
./Individual_loci/FGB7/RAxML-NG_output/FGB7.raxml.bestModel
./Individual_loci/FGB7/RAxML-NG_output/FGB7.raxml.bestTreeCollapsed
./Individual_loci/FGB7/RAxML-NG_output/FGB7.raxml.log
./Individual_loci/FGB7/RAxML-NG_output/FGB7.raxml.mlTrees
./Individual_loci/FGB7/RAxML-NG_output/FGB7.raxml.rba
./Individual_loci/FGB7/RAxML-NG_output/FGB7.raxml.reduced.phy
./Individual_loci/FGB7/RAxML-NG_output/FGB7.raxml.startTree
./Individual_loci/FGB7/RAxML-NG_FINAL_output/
./Individual_loci/FGB7/RAxML-NG_FINAL_output/FGB7_FINAL.raxml.bestModel
./Individual_loci/FGB7/RAxML-NG_FINAL_output/FGB7_FINAL.raxml.bestTreeCollapsed
./Individual_loci/FGB7/RAxML-NG_FINAL_output/FGB7_FINAL.raxml.log
./Individual_loci/FGB7/RAxML-NG_FINAL_output/FGB7_FINAL.raxml.mlTrees
./Individual_loci/FGB7/RAxML-NG_FINAL_output/FGB7_FINAL.raxml.rba
./Individual_loci/FGB7/RAxML-NG_FINAL_output/FGB7_FINAL.raxml.reduced.phy
./Individual_loci/FGB7/RAxML-NG_FINAL_output/FGB7_FINAL.raxml.startTree
./Individual_loci/FGB7/FGB7_aligned_renamed.fasta
./Individual_loci/FGB7/FGB7_FINAL.fasta
./Individual_loci/FGB7/FGB7_FINAL.raxml.bestTree
./Individual_loci/FGB7/FGB7_manually_realigned.fasta
./Individual_loci/FGB7/FGB7_Nov2021_aligned.fasta
./Individual_loci/FGB7/FGB7.raxml.bestTree
./Individual_loci/FGB7/FGB7.sh

```

- Final tree based on a manually refined alignment with four sequences excluded. These belonged to (1) *Balearica regulorum*, (2) *Ochthodromus peronii*, (3) *Pluvialis squatarola*, and (4) *Vanellus armatus*. The manual edits had no effect on the tree topology, but helped reduce the length of the branch subtending Thinocoridae and increase the likelihood of the best tree (original:  $\ln L = -17705.222797$ , manually realigned:  $\ln L = -15658.354225$ ). The trees based on both the original and manually refined alignment were misrooted, with Charadriidae (including Pluvianus) branching off first, followed by Chionoidea and finally by Burhinidae as the sister group to (Lari + Scolopaci). In addition, *Ochthodromus peronii* was misplaced, falling within Vanellinae rather than among other species of *Ochthodromus* (likely as a consequence of its short length – just 120 bp – that did not allow it to be accurately placed); similarly, *Vanellus armatus* was sister to a clade comprising *Anarhynchus*, *Eupoda*, and *Ochthodromus* (other than *O. peronii*) instead of grouping with the other two species of *Vanellus*, possibly as a result of its “gappy” and relatively short sequence. Finally, *Pluvialis squatarola*, while grouping correctly with the other two species of *Pluvialis*, was subtended by an extremely long branch indicative of sequencing errors; indeed, a long stretch of its sequence (positions 1712–1795 in the manually edited alignment) aligned poorly against the others. As a result, all the four sequences were excluded from the final alignment, which yielded a more orthodox tree where Chionida formed a

monophyletic sister group to Charadriiida, *Ochthodromus* became monophyletic, and *Vanellus* alone became sister to all charadriids other than *Pluvialis*. Both the original and the final (manually refined and pruned) alignments produced trees that were very nearly orthodox, with the following exceptions: *Pluvialis* was sister to (Charadriidae + Haematopodoidea) rather than nested within Charadriidae; Alcidae was sister to Laridae rather than Stercorariidae; *Calidris* was paraphyletic with respect to *Arenaria*; *Actitis* was more closely related to *Phalaropus* than to *Tringa*; *Larus* and *Chroicocephalus* were not reciprocally monophyletic; and neither were *Charadrius* and *Thinornis*.

**./Individual\_loci/GAPDH/**

**./Individual\_loci/GAPDH/GAPDH\_aligned.fasta**

**./Individual\_loci/GAPDH/GAPDH\_aligned\_renamed.fasta**

**./Individual\_loci/GAPDH/GAPDH\_MUSCLE\_alignment.log**

**./Individual\_loci/GAPDH/GAPDH\_to\_align.fasta**

**./Individual\_loci/GAPDH/RAxML\_bestTree.GAPDH**

**./Individual\_loci/GAPDH/RAxML\_bipartitions.GAPDH\_biparts**

**./Individual\_loci/GAPDH/RAxML\_bipartitionsBranchLabels.GAPDH\_biparts**

**./Individual\_loci/GAPDH/RAxML\_bootstrap.GAPDH-bs**

**./Individual\_loci/GAPDH/RAxML\_info.GAPDH**

**./Individual\_loci/GAPDH/RAxML\_info.GAPDH-bs**

**./Individual\_loci/GAPDH/RAxML\_info.GAPDH\_biparts**

**./Individual\_loci/GAPDH3-5/**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_output/**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_output/GAPDH3-5.raxml.bestModel**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_output/GAPDH3-5.raxml.bestTreeCollapsed**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_output/GAPDH3-5.raxml.log**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_output/GAPDH3-5.raxml.mlTrees**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_output/GAPDH3-5.raxml.rba**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_output/GAPDH3-5.raxml.startTree**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_FINAL\_output/**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_FINAL\_output/GAPDH3-5\_FINAL.raxml.bestModel**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_FINAL\_output/**

**GAPDH3-5\_FINAL.raxml.bestTreeCollapsed**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_FINAL\_output/ GAPDH3-5\_FINAL.raxml.log**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_FINAL\_output/ GAPDH3-5\_FINAL.raxml.mlTrees**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_FINAL\_output/ GAPDH3-5\_FINAL.raxml.rba**

**./Individual\_loci/GAPDH3-5/RAxML-NG\_FINAL\_output/ GAPDH3-5\_FINAL.raxml.startTree**

**./Individual\_loci/GAPDH3-5/GAPDH3-5\_aligned\_refined\_renamed.fasta**

**./Individual\_loci/GAPDH3-5/GAPDH3-5\_aligned\_renamed.fasta**

**./Individual\_loci/GAPDH3-5/GAPDH3-5\_FINAL.fasta**

**./Individual\_loci/GAPDH3-5/GAPDH3-5\_FINAL.raxml.bestTree**

**./Individual\_loci/GAPDH3-5/GAPDH3-5\_manually\_realigned.fasta**

**./Individual\_loci/GAPDH3-5/GAPDH3-5\_MUSCLE\_refinement.log**

**./Individual\_loci/GAPDH3-5/GAPDH3-5\_Oct21\_aligned.fasta**

**./Individual\_loci/GAPDH3-5/GAPDH3-5.raxml.bestTree**

**./Individual\_loci/GAPDH3-5/GAPDH3-5.sh**

- Final tree based on a manually refined alignment with a single excluded sequence: that of *Chroicocephalus maculipennis*, which was correctly placed within Laridae but subtended by an extremely long terminal branch indicative of sequencing errors. The manual edits did not affect tree topology, but helped increase the likelihood of the best tree (original: lnL = -8293.053724, manually realigned: lnL = -7695.105916).

```

./Individual_loci/GAPDH11/
./Individual_loci/GAPDH11/RAxML-NG_output/
./Individual_loci/GAPDH11/RAxML-NG_output/GAPDH11.raxml.bestModel
./Individual_loci/GAPDH11/RAxML-NG_output/GAPDH11.raxml.bestTreeCollapsed
./Individual_loci/GAPDH11/RAxML-NG_output/GAPDH11.raxml.log
./Individual_loci/GAPDH11/RAxML-NG_output/GAPDH11.raxml.mlTrees
./Individual_loci/GAPDH11/RAxML-NG_output/GAPDH11.raxml.rba
./Individual_loci/GAPDH11/RAxML-NG_output/GAPDH11.raxml.reduced.phy
./Individual_loci/GAPDH11/RAxML-NG_output/GAPDH11.raxml.startTree
./Individual_loci/GAPDH11/RAxML-NG_FINAL_output/
./Individual_loci/GAPDH11/RAxML-NG_FINAL_output/GAPDH11_FINAL.raxml.bestModel
./Individual_loci/GAPDH11/RAxML-NG_FINAL_output/
  GAPDH11_FINAL.raxml.bestTreeCollapsed
./Individual_loci/GAPDH11/RAxML-NG_FINAL_output/GAPDH11_FINAL.raxml.log
./Individual_loci/GAPDH11/RAxML-NG_FINAL_output/GAPDH11_FINAL.raxml.mlTrees
./Individual_loci/GAPDH11/RAxML-NG_FINAL_output/GAPDH11_FINAL.raxml.rba
./Individual_loci/GAPDH11/RAxML-NG_FINAL_output/GAPDH11_FINAL.raxml.reduced.phy
./Individual_loci/GAPDH11/RAxML-NG_FINAL_output/GAPDH11_FINAL.raxml.startTree
./Individual_loci/GAPDH11/GAPDH11_aligned_refined_renamed.fasta
./Individual_loci/GAPDH11/GAPDH11_aligned_refined_renamed.fasta
./Individual_loci/GAPDH11/GAPDH11_FINAL.fasta
./Individual_loci/GAPDH11/GAPDH11_FINAL.raxml.bestTree
./Individual_loci/GAPDH11/GAPDH11_MUSCLE_refinement.log
./Individual_loci/GAPDH11/GAPDH11_Oct2021_aligned.fasta
./Individual_loci/GAPDH11/GAPDH11.raxml.bestTree
./Individual_loci/GAPDH11/GAPDH11.sh

```

- Final tree based on a manually refined alignment. The manual edits did not affect tree topology, but helped increase the likelihood of the best tree (original:  $\ln L = -5219.754840$ , manually realigned/final:  $\ln L = -5118.780217$ ).

```

./Individual_loci/Myo2/
./Individual_loci/Myo2/Myo2_aligned.fasta
./Individual_loci/Myo2/Myo2_MUSCLE_alignment.log
./Individual_loci/Myo2/Myo2_to_align.fasta
./Individual_loci/Myo2/Myo2_with_outgroup_renamed.fasta
./Individual_loci/Myo2/RAxML_bestTree.Myo2
./Individual_loci/Myo2/RAxML_bipartitions.Myo2_biparts
./Individual_loci/Myo2/RAxML_bipartitionsBranchLabels.Myo2_biparts
./Individual_loci/Myo2/RAxML_bootstrap.Myo2-bs
./Individual_loci/Myo2/RAxML_info.Myo2
./Individual_loci/Myo2/RAxML_info.Myo2-bs
./Individual_loci/Myo2/RAxML_info.Myo2_biparts

```

```

./Individual_loci/MB2/
./Individual_loci/MB2/RAxML-NG_output/
./Individual_loci/MB2/RAxML-NG_output/MB2.raxml.bestModel
./Individual_loci/MB2/RAxML-NG_output/MB2.raxml.bestTreeCollapsed
./Individual_loci/MB2/RAxML-NG_output/MB2.raxml.log
./Individual_loci/MB2/RAxML-NG_output/MB2.raxml.mlTrees
./Individual_loci/MB2/RAxML-NG_output/MB2.raxml.rba
./Individual_loci/MB2/RAxML-NG_output/MB2.raxml.startTree
./Individual_loci/MB2/RAxML-NG_FINAL_output/
./Individual_loci/MB2/RAxML-NG_FINAL_output/MB2_FINAL.raxml.bestModel
./Individual_loci/MB2/RAxML-NG_FINAL_output/MB2_FINAL.raxml.bestTreeCollapsed
./Individual_loci/MB2/RAxML-NG_FINAL_output/MB2_FINAL.raxml.log

```

./Individual\_loci/MB2/RAXML-NG\_FINAL\_output/MB2\_FINAL.raxml.mlTrees  
 ./Individual\_loci/MB2/RAXML-NG\_FINAL\_output/MB2\_FINAL.raxml.rba  
 ./Individual\_loci/MB2/RAXML-NG\_FINAL\_output/MB2\_FINAL.raxml.startTree  
 ./Individual\_loci/MB2/MB2\_aligned\_renamed.fasta  
 ./Individual\_loci/MB2/MB2\_FINAL.fasta  
 ./Individual\_loci/MB2/MB2\_FINAL.raxml.bestTree  
 ./Individual\_loci/MB2/MB2\_Oct2021\_aligned.fasta  
 ./Individual\_loci/MB2/MB2.raxml.bestTree  
 ./Individual\_loci/MB2/MB2.sh

- Final tree based on a manually refined alignment. The manual edits had only a negligible effect on the tree topology (rendering Tringinae monophyletic), but helped increase the likelihood of the best tree (original:  $\ln L = -6082.272681$ , manually realigned/final:  $\ln L = -5936.054235$ ). Note that although the inclusion of the outgroup (*Balearica regulorum*) causes the tree to be misrooted (with Chionida, rather than Charadrii as a whole, as the sister group to the rest of the clade), its exclusion caused Turnicidae to move from its expected position as the sister group of Larida to a more deeply branching position as the sister group of (Larida + Scolopaci). Accordingly, the outgroup was retained in spite of the rooting issues.

./Individual\_loci/MUSK/  
 ./Individual\_loci/MUSK/RAXML-NG\_output/  
 ./Individual\_loci/MUSK/RAXML-NG\_output/MUSK.raxml.bestModel  
 ./Individual\_loci/MUSK/RAXML-NG\_output/MUSK.raxml.bestTreeCollapsed  
 ./Individual\_loci/MUSK/RAXML-NG\_output/MUSK.raxml.log  
 ./Individual\_loci/MUSK/RAXML-NG\_output/MUSK.raxml.mlTrees  
 ./Individual\_loci/MUSK/RAXML-NG\_output/MUSK.raxml.rba  
 ./Individual\_loci/MUSK/RAXML-NG\_output/MUSK.raxml.reduced.phy  
 ./Individual\_loci/MUSK/RAXML-NG\_output/MUSK.raxml.startTree  
 ./Individual\_loci/MUSK/RAXML-NG\_FINAL\_output/  
 ./Individual\_loci/MUSK/RAXML-NG\_FINAL\_output/MUSK\_FINAL.raxml.bestModel  
 ./Individual\_loci/MUSK/RAXML-NG\_FINAL\_output/MUSK\_FINAL.raxml.bestTreeCollapsed  
 ./Individual\_loci/MUSK/RAXML-NG\_FINAL\_output/MUSK\_FINAL.raxml.log  
 ./Individual\_loci/MUSK/RAXML-NG\_FINAL\_output/MUSK\_FINAL.raxml.mlTrees  
 ./Individual\_loci/MUSK/RAXML-NG\_FINAL\_output/MUSK\_FINAL.raxml.rba  
 ./Individual\_loci/MUSK/RAXML-NG\_FINAL\_output/MUSK\_FINAL.raxml.reduced.phy  
 ./Individual\_loci/MUSK/RAXML-NG\_FINAL\_output/MUSK\_FINAL.raxml.startTree  
 ./Individual\_loci/MUSK/MUSK\_aligned\_renamed.fasta  
 ./Individual\_loci/MUSK/MUSK\_FINAL.fasta  
 ./Individual\_loci/MUSK/MUSK\_FINAL.raxml.bestTree  
 ./Individual\_loci/MUSK/MUSK\_Oct2021\_aligned.fasta  
 ./Individual\_loci/MUSK/MUSK\_pruned.fasta  
 ./Individual\_loci/MUSK/MUSK\_pruned\_MUSCLE\_refinement.log  
 ./Individual\_loci/MUSK/MUSK.raxml.bestTree  
 ./Individual\_loci/MUSK/MUSK.sh

- The original alignment was analyzed and found to produce a misrooted tree (with Charadrii, rather than Charadrii as a whole, as the sister group to the rest of the clade). Accordingly, the outgroup (*Balearica regulorum*) was excluded, and the resulting alignment was refined using MUSCLE. The refinement step did not affect tree topology, but helped increase the likelihood of the best tree (pruned:  $\ln L = -5033.503238$ , pruned and refined/final:  $\ln L = -4951.854393$ ).



./Individual\_loci/NTF3/  
./Individual\_loci/NTF3/NTF3\_with\_outgroup\_renamed.fasta  
./Individual\_loci/NTF3/RAxML\_bestTree.NTF3  
./Individual\_loci/NTF3/RAxML\_bipartitions.NTF3\_biparts  
./Individual\_loci/NTF3/RAxML\_bipartitionsBranchLabels.NTF3\_biparts  
./Individual\_loci/NTF3/RAxML\_bootstrap.NTF3-bs  
./Individual\_loci/NTF3/RAxML\_info.NTF3-bs  
./Individual\_loci/NTF3/RAxML\_info.NTF3\_biparts

./Individual\_loci/NTF3/  
./Individual\_loci/NTF3/RAxML-NG\_output/  
./Individual\_loci/NTF3/RAxML-NG\_output/NTF3.raxml.bestModel  
./Individual\_loci/NTF3/RAxML-NG\_output/NTF3.raxml.bestTreeCollapsed  
./Individual\_loci/NTF3/RAxML-NG\_output/NTF3.raxml.log  
./Individual\_loci/NTF3/RAxML-NG\_output/NTF3.raxml.mlTrees  
./Individual\_loci/NTF3/RAxML-NG\_output/NTF3.raxml.rba  
./Individual\_loci/NTF3/RAxML-NG\_output/NTF3.raxml.reduced.phy  
./Individual\_loci/NTF3/RAxML-NG\_output/NTF3.raxml.startTree  
./Individual\_loci/NTF3/NTF3\_aligned\_renamed.fasta  
./Individual\_loci/NTF3/NTF3\_Oct2021\_aligned.fasta  
./Individual\_loci/NTF3/NTF3.raxml.bestTree  
./Individual\_loci/NTF3/NTF3.sh

- The original alignment was used without any modifications.

./Individual\_loci/ODC/  
./Individual\_loci/ODC/RAxML-NG\_output/  
./Individual\_loci/ODC/RAxML-NG\_output/ODC.raxml.bestModel  
./Individual\_loci/ODC/RAxML-NG\_output/ODC.raxml.bestTreeCollapsed  
./Individual\_loci/ODC/RAxML-NG\_output/ODC.raxml.log  
./Individual\_loci/ODC/RAxML-NG\_output/ODC.raxml.mlTrees  
./Individual\_loci/ODC/RAxML-NG\_output/ODC.raxml.rba  
./Individual\_loci/ODC/RAxML-NG\_output/ODC.raxml.reduced.phy  
./Individual\_loci/ODC/RAxML-NG\_output/ODC.raxml.startTree  
./Individual\_loci/ODC/RAxML-NG\_FINAL\_output/  
./Individual\_loci/ODC/RAxML-NG\_FINAL\_output/ODC\_FINAL.raxml.bestModel  
./Individual\_loci/ODC/RAxML-NG\_FINAL\_output/ODC\_FINAL.raxml.bestTreeCollapsed  
./Individual\_loci/ODC/RAxML-NG\_FINAL\_output/ODC\_FINAL.raxml.log  
./Individual\_loci/ODC/RAxML-NG\_FINAL\_output/ODC\_FINAL.raxml.mlTrees  
./Individual\_loci/ODC/RAxML-NG\_FINAL\_output/ODC\_FINAL.raxml.rba  
./Individual\_loci/ODC/RAxML-NG\_FINAL\_output/ODC\_FINAL.raxml.reduced.phy  
./Individual\_loci/ODC/RAxML-NG\_FINAL\_output/ODC\_FINAL.raxml.startTree  
./Individual\_loci/ODC/ODC\_aligned\_renamed.fasta  
./Individual\_loci/ODC/ODC\_FINAL.fasta  
./Individual\_loci/ODC/ODC\_FINAL.raxml.bestTree  
./Individual\_loci/ODC/ODC\_Oct2021\_aligned.fasta  
./Individual\_loci/ODC/ODC\_pruned.fasta  
./Individual\_loci/ODC/ODC.raxml.bestTree  
./Individual\_loci/ODC/ODC.sh

- The original alignment was analyzed and found to produce a misrooted tree (with Scolopaci rather than Charadrii as the sister group to the rest of the clade). Accordingly, the outgroup (*Balearica regulorum*) was excluded, and the resulting alignment was manually refined. The manual edits had only a negligible effect on the tree topology (rendering Arenariinae paraphyletic), but helped reduce the length of the branch subtending Turnicidae and increase



the likelihood of the best tree (pruned: lnL = -5926.625937, pruned and manually edited/final: lnL = -5633.615278).

./Individual\_loci/RAG1/  
./Individual\_loci/RAG1/RAG1\_aligned.fasta  
./Individual\_loci/RAG1/RAG1\_aligned.fasta.reduced  
./Individual\_loci/RAG1/RAG1\_MUSCLE\_alignment.log  
./Individual\_loci/RAG1/RAG1\_to\_align.fasta  
./Individual\_loci/RAG1/RAxML\_bestTree.RAG1  
./Individual\_loci/RAG1/RAxML\_bipartitions.RAG1\_biparts  
./Individual\_loci/RAG1/RAxML\_bipartitionsBranchLabels.RAG1\_biparts  
./Individual\_loci/RAG1/RAxML\_bootstrap.RAG1-bs  
./Individual\_loci/RAG1/RAxML\_info.RAG1  
./Individual\_loci/RAG1/RAxML\_info.RAG1-bs  
./Individual\_loci/RAG1/RAxML\_info.RAG1\_biparts

./Individual\_loci/RAG1/  
./Individual\_loci/RAG1/RAxML-NG\_output/  
./Individual\_loci/RAG1/RAxML-NG\_output/RAG1.raxml.bestModel  
./Individual\_loci/RAG1/RAxML-NG\_output/RAG1.raxml.bestTreeCollapsed  
./Individual\_loci/RAG1/RAxML-NG\_output/RAG1.raxml.log  
./Individual\_loci/RAG1/RAxML-NG\_output/RAG1.raxml.mlTrees  
./Individual\_loci/RAG1/RAxML-NG\_output/RAG1.raxml.rba  
./Individual\_loci/RAG1/RAxML-NG\_output/RAG1.raxml.reduced.phy  
./Individual\_loci/RAG1/RAxML-NG\_output/RAG1.raxml.startTree  
./Individual\_loci/RAG1/RAxML-NG\_FINAL\_output/  
./Individual\_loci/RAG1/RAxML-NG\_FINAL\_output/RAG1\_FINAL.raxml.bestModel  
./Individual\_loci/RAG1/RAxML-NG\_FINAL\_output/RAG1\_FINAL.raxml.bestTreeCollapsed  
./Individual\_loci/RAG1/RAxML-NG\_FINAL\_output/RAG1\_FINAL.raxml.log  
./Individual\_loci/RAG1/RAxML-NG\_FINAL\_output/RAG1\_FINAL.raxml.mlTrees  
./Individual\_loci/RAG1/RAxML-NG\_FINAL\_output/RAG1\_FINAL.raxml.rba  
./Individual\_loci/RAG1/RAxML-NG\_FINAL\_output/RAG1\_FINAL.raxml.reduced.phy  
./Individual\_loci/RAG1/RAxML-NG\_FINAL\_output/RAG1\_FINAL.raxml.startTree  
./Individual\_loci/RAG1/RAG1\_aligned\_refined\_renamed.fasta  
./Individual\_loci/RAG1/RAG1\_aligned\_renamed.fasta  
./Individual\_loci/RAG1/RAG1\_FINAL.fasta  
./Individual\_loci/RAG1/RAG1\_FINAL.raxml.bestTree  
./Individual\_loci/RAG1/RAG1\_MUSCLE\_refinement.log  
./Individual\_loci/RAG1/RAG1\_Oct2021\_aligned.fasta  
./Individual\_loci/RAG1/RAG1.raxml.bestTree  
./Individual\_loci/RAG1/RAG1.sh

- Final tree based on a refined alignment (using MUSCLE) with a single excluded sequence: that of *Balearica regulorum*, which was causing rooting issues (with Charadrii, rather than Charadrii as a whole, as the sister group to the rest of the clade).

./Individual\_loci/phyluce\_align\_format\_nexus\_files\_for\_raxml.log  
./Individual\_loci/Mitogenome/phyluce\_align\_format\_nexus\_files\_for\_raxml.log

- Replaced after rerunning Phyluce on the new alignments, and moved into the Mitogenome folder.

./Individual\_loci/Mitogenome/Mitogenome.charsets  
./Individual\_loci/Mitogenome/Mitogenome\_concat.charsets

- Replaced after rerunning Phyluce on the new alignments.

./Individual\_loci/Mitogenome/infile.phy  
./Individual\_loci/Mitogenome/Mitogenome\_concat.phy

- Replaced after rerunning Phyluce on the new alignments

./Individual\_loci/Mitogenome/best\_scheme.txt  
./Individual\_loci/Mitogenome/genecodon\_pfindex.txt  
./Individual\_loci/Mitogenome/genecodon\_pfindex.txt.reduced  
./Individual\_loci/Mitogenome/log.txt  
./Individual\_loci/Mitogenome/partition\_finder.cfg

./Individual\_loci/Mitogenome/mito\_pfindex.best\_scheme.nex  
./Individual\_loci/Mitogenome/partitions.nex

- Replaced after the partitioning analysis has been repeated on the mitogenome alignment (this time using IQ-TREE rather than PartiitonFinder).

./Individual\_loci/Mitogenome/RAxML\_bestTree.mitogenome  
./Individual\_loci/Mitogenome/RAxML\_bipartitions.mitogenome\_biparts  
./Individual\_loci/Mitogenome/RAxML\_bipartitionsBranchLabels.mitogenome\_biparts  
./Individual\_loci/Mitogenome/RAxML\_bootstrap.mitogenome-bs  
./Individual\_loci/Mitogenome/RAxML\_info.mitogenome  
./Individual\_loci/Mitogenome/RAxML\_info.mitogenome\_biparts  
./Individual\_loci/Mitogenome/RAxML\_log.mitogenome.RUN.0  
./Individual\_loci/Mitogenome/RAxML\_log.mitogenome.RUN.1  
./Individual\_loci/Mitogenome/RAxML\_log.mitogenome.RUN.2  
./Individual\_loci/Mitogenome/RAxML\_parsimonyTree.mitogenome.RUN.0  
./Individual\_loci/Mitogenome/RAxML\_parsimonyTree.mitogenome.RUN.1  
./Individual\_loci/Mitogenome/RAxML\_parsimonyTree.mitogenome.RUN.2  
./Individual\_loci/Mitogenome/RAxML\_result.mitogenome.RUN.0  
./Individual\_loci/Mitogenome/RAxML\_result.mitogenome.RUN.1  
./Individual\_loci/Mitogenome/RAxML\_result.mitogenome.RUN.2

./Individual\_loci/Mitogenome/Mitogenome.raxml.bestTree  
./Individual\_loci/Mitogenome/Mitogenome.raxml.bootstraps  
./Individual\_loci/Mitogenome/Mitogenome.raxml.log  
./Individual\_loci/Mitogenome/Mitogenome.raxml.support  
./Individual\_loci/Mitogenome/mito\_partitions.txt

- Replaced after the maximum-likelihood analysis has been repeated on the mitogenome alignment (this time using RAxML-NG rather than RAxML).

./Individual\_loci/12S/  
 ./Individual\_loci/12S/12S\_FINAL.fasta  
 ./Individual\_loci/12S/12S\_pruned.fasta  
 ./Individual\_loci/12S/12S\_with\_outgroup\_renamed.fasta  
 ./Individual\_loci/12S/RAxML\_bestTree.12S  
 ./Individual\_loci/12S/RAxML\_bestTree.12S\_FINAL  
 ./Individual\_loci/12S/RAxML\_info.12S\_FINAL

./Individual\_loci/12S/  
 ./Individual\_loci/12S/RAxML-NG\_output/  
 ./Individual\_loci/12S/RAxML-NG\_output/12S.raxml.bestModel  
 ./Individual\_loci/12S/RAxML-NG\_output/12S.raxml.bestTreeCollapsed  
 ./Individual\_loci/12S/RAxML-NG\_output/12S.raxml.log  
 ./Individual\_loci/12S/RAxML-NG\_output/12S.raxml.mlTrees  
 ./Individual\_loci/12S/RAxML-NG\_output/12S.raxml.rba  
 ./Individual\_loci/12S/RAxML-NG\_output/12S.raxml.reduced.phy  
 ./Individual\_loci/12S/RAxML-NG\_output/12S.raxml.startTree  
 ./Individual\_loci/12S/RAxML-NG\_FINAL\_output/  
 ./Individual\_loci/12S/RAxML-NG\_FINAL\_output/12S\_FINAL.raxml.bestModel  
 ./Individual\_loci/12S/RAxML-NG\_FINAL\_output/12S\_FINAL.raxml.bestTreeCollapsed  
 ./Individual\_loci/12S/RAxML-NG\_FINAL\_output/12S\_FINAL.raxml.log  
 ./Individual\_loci/12S/RAxML-NG\_FINAL\_output/12S\_FINAL.raxml.mlTrees  
 ./Individual\_loci/12S/RAxML-NG\_FINAL\_output/12S\_FINAL.raxml.rba  
 ./Individual\_loci/12S/RAxML-NG\_FINAL\_output/12S\_FINAL.raxml.reduced.phy  
 ./Individual\_loci/12S/RAxML-NG\_FINAL\_output/12S\_FINAL.raxml.startTree  
 ./Individual\_loci/12S/12S\_aligned\_refined\_renamed.fasta  
 ./Individual\_loci/12S/12S\_aligned\_renamed.fasta  
 ./Individual\_loci/12S/12S\_FINAL.fasta  
 ./Individual\_loci/12S/12S\_FINAL.raxml.bestTree  
 ./Individual\_loci/12S/12S\_manually\_realigned.fasta  
 ./Individual\_loci/12S/12S\_MUSCLE\_refinement.log  
 ./Individual\_loci/12S/12S\_Oct2021\_aligned.fasta  
 ./Individual\_loci/12S/12S.raxml.bestTree  
 ./Individual\_loci/12S/12S.sh

- Final tree based on a manually refined alignment with two sequences excluded. These belonged to: (1) *Anarhynchus obscurus*, which formed the sister group of Haematopodoidea instead of grouping with other charadriids (likely as a consequence of its short length – just 247 informative residues including partial ambiguities – that did not allow it to be accurately placed); and (2) *Tringa guttifer*, which was misplaced as deeply nested within *Calidris* (indicating that the mitogenome from which the 12S sequence was extracted is probably chimerical, since other loci such as 16S and ND2 correctly place it within *Tringa*). The manual edits made the topology more orthodox in the following ways: Turnicidae moved to a more deeply nested position sister to Larida + Scolopaci (rather than to all other charadriiforms); *Arenaria*, *Calidris*, and *Phalaropus* became monophyletic (except for the inclusion of *T. guttifer* within *Calidris*); and *Phegornis* moved to a deeply nested position within Charadriidae (instead of forming the sister group to the rest of Charadriida). They made the topology less orthodox in the following ways: *Dromas* moved sister to Laridae + Alcoidea (rather than Glareolidae), and *Arenaria* no longer formed the sister group of *Calidris* (in the tree based on the original alignment, *A. interpres* was sister to *Calidris* while *A. melanocephala* was sister to *Chubbia* + *Coenocorypha*). The manual edits increased the likelihood of the best tree (original:  $\ln L = -28215.681849$ , manually realigned:  $\ln L = -25556.075214$ ). Both the original and manually edited alignments produced trees that differed from the orthodox topology as follows: three-way paraphyly of Charadrii (with Chionida, *Pluvianus*, and the rest of Charadriida forming successive outgroups to Lari + Scolopaci); absence of a sister-group relationship between Turnicidae and Laridae; paraphyly of Laridae with respect to Alcidae and Scolopacidae; nonmonophyly of Alcoidea; *Bartramia* forming the

sister group of the rest of Scolopacidae rather than of *Numenius* alone; sister-group relationship between *Numenius* and *Limosa*; and the nonmonophyly of *Gallinago* (with *G. media* within Limosinae in the tree based on the original alignment and the inclusion of *Coenocorypha* and *Chubbia* in the tree based on the manual realignment). The exclusion of *Anarhynchus obscurus* and *Tringa guttifer* further increased the likelihood of the best tree (lnL = -25470.691816) and rendered Alcoidea (= Alcidae + Stercorariidae) monophyletic.

./Individual\_loci/16S/  
 ./Individual\_loci/16S/16S\_FINAL.fasta  
 ./Individual\_loci/16S/16S\_pruned.fasta  
 ./Individual\_loci/16S/16S\_with\_outgroup\_renamed.fasta  
 ./Individual\_loci/16S/RAxML\_bestTree.16S  
 ./Individual\_loci/16S/RAxML\_bestTree.16S\_FINAL  
 ./Individual\_loci/16S/RAxML\_info.16S\_FINAL

./Individual\_loci/16S/  
 ./Individual\_loci/16S/RAxML-NG\_output/  
 ./Individual\_loci/16S/RAxML-NG\_output/16S.raxml.bestModel  
 ./Individual\_loci/16S/RAxML-NG\_output/16S.raxml.bestTreeCollapsed  
 ./Individual\_loci/16S/RAxML-NG\_output/16S.raxml.log  
 ./Individual\_loci/16S/RAxML-NG\_output/16S.raxml.mlTrees  
 ./Individual\_loci/16S/RAxML-NG\_output/16S.raxml.rba  
 ./Individual\_loci/16S/RAxML-NG\_output/16S.raxml.startTree  
 ./Individual\_loci/16S/RAxML-NG\_FINAL\_output/  
 ./Individual\_loci/16S/RAxML-NG\_FINAL\_output/16S\_FINAL.raxml.bestModel  
 ./Individual\_loci/16S/RAxML-NG\_FINAL\_output/16S\_FINAL.raxml.bestTreeCollapsed  
 ./Individual\_loci/16S/RAxML-NG\_FINAL\_output/16S\_FINAL.raxml.log  
 ./Individual\_loci/16S/RAxML-NG\_FINAL\_output/16S\_FINAL.raxml.mlTrees  
 ./Individual\_loci/16S/RAxML-NG\_FINAL\_output/16S\_FINAL.raxml.rba  
 ./Individual\_loci/16S/RAxML-NG\_FINAL\_output/16S\_FINAL.raxml.startTree  
 ./Individual\_loci/16S/16S\_aligned\_refined\_renamed.fasta  
 ./Individual\_loci/16S/16S\_aligned\_renamed.fasta  
 ./Individual\_loci/16S/16S\_FINAL.fasta  
 ./Individual\_loci/16S/16S\_FINAL.raxml.bestTree  
 ./Individual\_loci/16S/16S\_MUSCLE\_refinement.log  
 ./Individual\_loci/16S/16S\_Oct2021\_aligned.fasta  
 ./Individual\_loci/16S/16S.raxml.bestTree  
 ./Individual\_loci/16S/16S.sh

- Final tree based on a manually refined alignment. The manual edits made the topology more orthodox in the following ways: Charadrii became monophyletic; *Pluvianus* became the sister group of the rest of Charadriidae rather than Burhinidae; *Pluvialis* became part of a monophyletic Charadriidae rather than the sister group of Haematopodoidea; Turnicidae moved to a position within Lari (instead of being deeply nested within Scolopacidae); and the topology of Jacanida changed from (Rostratulidae, (Thinocoridae, (*Pedionomus*, Jacanidae))) to the orthodox ((Rostratulidae, Jacanidae), (Thinocoridae, *Pedionomus*)). They also increased the likelihood of the best tree (original: lnL = -41386.868353, manually realigned/final: lnL = -37107.589554). Both the original and the manually edited alignments produced trees that differed from the orthodox topology in the paraphyly of Alcidae with respect to Stercorariidae (although the latter became less deeply nested within the former in the tree based on the manual realignment) and in the position of Turnicidae (within Scolopacidae in the tree based on the original alignment; sister to Glareoloidea in the tree based on the manual realignment).

./Individual\_loci/ATP6/  
./Individual\_loci/ATP6/ATP6\_FINAL.fasta  
./Individual\_loci/ATP6/ATP6\_pruned.fasta  
./Individual\_loci/ATP6/ATP6\_with\_outgroup\_renamed.fasta  
./Individual\_loci/ATP6/RAxML\_bestTree.ATP6  
./Individual\_loci/ATP6/RAxML\_bestTree.ATP6\_FINAL  
./Individual\_loci/ATP6/RAxML\_info.ATP6\_FINAL

./Individual\_loci/ATP6/  
./Individual\_loci/ATP6/RAxML-NG\_output/  
./Individual\_loci/ATP6/RAxML-NG\_output/ATP6.raxml.bestModel  
./Individual\_loci/ATP6/RAxML-NG\_output/ATP6.raxml.bestTreeCollapsed  
./Individual\_loci/ATP6/RAxML-NG\_output/ATP6.raxml.log  
./Individual\_loci/ATP6/RAxML-NG\_output/ATP6.raxml.mlTrees  
./Individual\_loci/ATP6/RAxML-NG\_output/ATP6.raxml.rba  
./Individual\_loci/ATP6/RAxML-NG\_output/ATP6.raxml.reduced.phy  
./Individual\_loci/ATP6/RAxML-NG\_output/ATP6.raxml.startTree  
./Individual\_loci/ATP6/RAxML-NG\_FINAL\_output/  
./Individual\_loci/ATP6/RAxML-NG\_FINAL\_output/ATP6\_FINAL.raxml.bestModel  
./Individual\_loci/ATP6/RAxML-NG\_FINAL\_output/ATP6\_FINAL.raxml.bestTreeCollapsed  
./Individual\_loci/ATP6/RAxML-NG\_FINAL\_output/ATP6\_FINAL.raxml.log  
./Individual\_loci/ATP6/RAxML-NG\_FINAL\_output/ATP6\_FINAL.raxml.mlTrees  
./Individual\_loci/ATP6/RAxML-NG\_FINAL\_output/ATP6\_FINAL.raxml.rba  
./Individual\_loci/ATP6/RAxML-NG\_FINAL\_output/ATP6\_FINAL.raxml.reduced.phy  
./Individual\_loci/ATP6/RAxML-NG\_FINAL\_output/ATP6\_FINAL.raxml.startTree  
./Individual\_loci/ATP6/ATP6\_aligned\_renamed.fasta  
./Individual\_loci/ATP6/ATP6\_FINAL.fasta  
./Individual\_loci/ATP6/ATP6\_FINAL.raxml.bestTree  
./Individual\_loci/ATP6/ATP6\_Nov2021\_aligned.fasta  
./Individual\_loci/ATP6/ATP6.raxml.bestTree  
./Individual\_loci/ATP6/ATP6.sh

- Final tree based on the original alignment with two sequences excluded: those of *Numenius arquata*, which was subtended by an extremely long terminal branch and misplaced within the Charadriidae (possibly because of sequencing error; the fact that the last 81 bp of the sequence are missing may have also contributed), and of *Phalaropus tricolor*, which was deeply nested inside the genus *Tringa* (suggesting the sequence was likely misidentified). The tree topology was only minimally sensitive to the order of the sequences in the alignment, and reordering these according to an accepted phylogeny failed to improve upon the likelihood of the best tree (original:  $\ln L = -18810.918585$ ; reordered:  $\ln L = -18810.921402$ ).

./Individual\_loci/ATP8/  
./Individual\_loci/ATP8/ATP8\_FINAL.fasta  
./Individual\_loci/ATP8/ATP8\_pruned.fasta  
./Individual\_loci/ATP8/ATP8\_with\_outgroup\_renamed.fasta  
./Individual\_loci/ATP8/RAxML\_bestTree.ATP8  
./Individual\_loci/ATP8/RAxML\_bestTree.ATP8\_FINAL  
./Individual\_loci/ATP8/RAxML\_info.ATP8\_FINAL

./Individual\_loci/ATP8/  
./Individual\_loci/ATP8/RAxML-NG\_output/  
./Individual\_loci/ATP8/RAxML-NG\_output/ATP8.raxml.bestModel  
./Individual\_loci/ATP8/RAxML-NG\_output/ATP8.raxml.bestTreeCollapsed  
./Individual\_loci/ATP8/RAxML-NG\_output/ATP8.raxml.log  
./Individual\_loci/ATP8/RAxML-NG\_output/ATP8.raxml.mlTrees  
./Individual\_loci/ATP8/RAxML-NG\_output/ATP8.raxml.rba

```
./Individual_loci/ATP8/RAxML-NG_output/ATP8.raxml.reduced.phy
./Individual_loci/ATP8/RAxML-NG_output/ATP8.raxml.startTree
./Individual_loci/ATP8/ATP8_aligned_renamed.fasta
./Individual_loci/ATP8/ATP8_Nov2021_aligned.fasta
./Individual_loci/ATP8/ATP8.raxml.bestTree
./Individual_loci/ATP8/ATP8.sh
```

- The original alignment was used without any modifications. The locus contains so little data that the resulting phylogeny is mostly noise, with the monophyly of some (but not all) families as the only “reasonable” result; both inter- and intra-familial relationships are drastically different from previous estimates and estimates based on other loci. No attempt was made to identify specific problematic sequences, as generic nonmonophyly was rampant and no taxa showed extremely long branches indicative of sequencing errors. The tree topology was only minimally sensitive to the order of the sequences in the alignment, and reordering these according to an accepted phylogeny failed to improve upon the likelihood of the best tree (original: lnL = -4993.132913; reordered: lnL = -4993.182653).

```
./Individual_loci/Cox1/
./Individual_loci/Cox1/Cox1_FINAL.fasta
./Individual_loci/Cox1/Cox1_FINAL_corr_codon_pos.fasta
./Individual_loci/Cox1/Cox1_pruned.fasta
./Individual_loci/Cox1/Cox1_with_outgroup_renamed.fasta
./Individual_loci/Cox1/RAxML_bestTree.Cox1
./Individual_loci/Cox1/RAxML_bestTree.Cox1_FINAL
./Individual_loci/Cox1/RAxML_info.Cox1_FINAL
```

```
./Individual_loci/Cox1/
./Individual_loci/Cox1/RAxML-NG_output/
./Individual_loci/Cox1/RAxML-NG_output/Cox1.raxml.bestModel
./Individual_loci/Cox1/RAxML-NG_output/Cox1.raxml.bestTreeCollapsed
./Individual_loci/Cox1/RAxML-NG_output/Cox1.raxml.log
./Individual_loci/Cox1/RAxML-NG_output/Cox1.raxml.mlTrees
./Individual_loci/Cox1/RAxML-NG_output/Cox1.raxml.rba
./Individual_loci/Cox1/RAxML-NG_output/Cox1.raxml.startTree
./Individual_loci/Cox1/RAxML-NG_FINAL_output/
./Individual_loci/Cox1/RAxML-NG_FINAL_output/Cox1_FINAL.raxml.bestModel
./Individual_loci/Cox1/RAxML-NG_FINAL_output/Cox1_FINAL.raxml.bestTreeCollapsed
./Individual_loci/Cox1/RAxML-NG_FINAL_output/Cox1_FINAL.raxml.log
./Individual_loci/Cox1/RAxML-NG_FINAL_output/Cox1_FINAL.raxml.mlTrees
./Individual_loci/Cox1/RAxML-NG_FINAL_output/Cox1_FINAL.raxml.rba
./Individual_loci/Cox1/RAxML-NG_FINAL_output/Cox1_FINAL.raxml.startTree
./Individual_loci/Cox1/Cox1_aligned_renamed.fasta
./Individual_loci/Cox1/Cox1_FINAL.fasta
./Individual_loci/Cox1/Cox1_FINAL.raxml.bestTree
./Individual_loci/Cox1/Cox1_manually_realigned.fasta
./Individual_loci/Cox1/Cox1_Nov2021_aligned.fasta
./Individual_loci/Cox1/Cox1.raxml.bestTree
./Individual_loci/Cox1/Cox1.sh
```

- Final tree based on a manually refined alignment with a single excluded sequence: that of *Pluvianus aegyptius*, which was misplaced as the sister group of all other charadriiforms. The manual edits mostly helped reduce the length of the branch subtending *Limnocyrtus*, and caused it to move from a deeply nested position within *Calidris* into a sister-group relationship with a clade formed by *Limnodromus griseus* and *Limnodromus scolopaceus* (but not *Limnodromus semipalmatus*, which instead formed the sister group of *Calidris* + *Arenaria*), in agreement with the results of Baker et al. (2007). They also improved the likelihood of the best tree (original: lnL = -52694.134808, manually realigned: lnL = -52601.536619). The subsequent



removal of *Pluvianus aegyptius* caused cascading changes down the tree: *Limnodromus* became monophyletic, but instead of forming a sister group to Scolopacini, it branched off earlier and became sister to (Scolopacini + Tringinae), while *Lymnocryptes* became sister to Scolopacini alone. Both the original and the final (manually refined and pruned) alignments produced trees that were very nearly orthodox, with the following exceptions: Turnicidae was sister to Jacanida rather than Larida, Stercorariidae was sister to Fraterculinae rather than to Alcidae as a whole, and *Gallinago undulata* emerged as more closely related to *Coenocorypha* than to other species of the same genus.

```
./Individual_loci/Cox2/
./Individual_loci/Cox2/Cox2_FINAL.fasta
./Individual_loci/Cox2/Cox2_pruned.fasta
./Individual_loci/Cox2/Cox2_with_outgroup_renamed.fasta
./Individual_loci/Cox2/RAxML_bestTree.Cox2
./Individual_loci/Cox2/RAxML_bestTree.Cox2_FINAL
./Individual_loci/Cox2/RAxML_info.Cox2_FINAL
```

```
./Individual_loci/Cox2/
./Individual_loci/Cox2/RAxML-NG_output/
./Individual_loci/Cox2/RAxML-NG_output/Cox2.raxml.bestModel
./Individual_loci/Cox2/RAxML-NG_output/Cox2.raxml.bestTreeCollapsed
./Individual_loci/Cox2/RAxML-NG_output/Cox2.raxml.log
./Individual_loci/Cox2/RAxML-NG_output/Cox2.raxml.mlTrees
./Individual_loci/Cox2/RAxML-NG_output/Cox2.raxml.rba
./Individual_loci/Cox2/RAxML-NG_output/Cox2.raxml.startTree
./Individual_loci/Cox2/RAxML-NG_FINAL_output/
./Individual_loci/Cox2/RAxML-NG_FINAL_output/Cox2_FINAL.raxml.bestModel
./Individual_loci/Cox2/RAxML-NG_FINAL_output/Cox2_FINAL.raxml.bestTreeCollapsed
./Individual_loci/Cox2/RAxML-NG_FINAL_output/Cox2_FINAL.raxml.log
./Individual_loci/Cox2/RAxML-NG_FINAL_output/Cox2_FINAL.raxml.mlTrees
./Individual_loci/Cox2/RAxML-NG_FINAL_output/Cox2_FINAL.raxml.rba
./Individual_loci/Cox2/RAxML-NG_FINAL_output/Cox2_FINAL.raxml.startTree
./Individual_loci/Cox2/Cox2_aligned_renamed.fasta
./Individual_loci/Cox2/Cox2_FINAL.fasta
./Individual_loci/Cox2/Cox2_FINAL.raxml.bestTree
./Individual_loci/Cox2/Cox2_Nov2021_aligned.fasta
./Individual_loci/Cox2/Cox2.raxml.bestTree
./Individual_loci/Cox2/Cox2.sh
```

- Final tree based on the original alignment with two sequences excluded: those of *Sternula albifrons*, which formed the sister group of Turnicidae (with the resulting clade nested in a paraphyletic Laridae), and of *Rissa tridactyla*, which was deeply nested within *Larus* (indicating that the mitogenome from which the Cox2 sequence was extracted is probably chimerical, since other loci such as 16S and ND2 correctly place it outside of the *Larus* + *Chroicocephalus* clade). The exclusion of *Sternula albifrons* had a far-reaching impact on the topology, rendering it more orthodox in the following ways: Charadrii and Chionida became monophyletic (instead of Burhinidae, Charadriidae, and Chionoidea forming successive sister group to Scolopaci + Lari); Turnicidae became sister to a monophyletic Lari; and Laridae became monophyletic. It made the topology less orthodox as follows: Jacanida was rendered paraphyletic with respect to Scolopacidae; and Charadriidae became massively paraphyletic with respect to Haematopodoidea (in the tree based on the original alignment, only *Pluvialis* was closer to Haematopodoidea than to other charadriids). The removal of *Sternula albifrons* also increased the likelihood of the best tree (original: lnL = -14245.438418, pruned: lnL = -14096.182003). Both the original and the pruned alignments produced trees that differed from the orthodox topology in the nonmonophyly of Jacanoidea (with Thinocoridae rather than Rostratulidae as the sister group of Jacanidae), the nesting of *Pedionomus* within Rostratulidae, the paraphyly of *Haematopus* with respect to *Ibidorhyncha* and Recurvirostridae, the sister-group relationship

between *Dromas* and Stercorariidae, the paraphyly of *Chroicocephalus* with respect to other Larinae, and the nesting of *Rissa tridactyla* within *Larus*. The further removal of *Rissa tridactyla* rendered *Larus* monophyletic, made the topology of Scolopacidae more orthodox (with *Numenius* sister to the rest of the group), and further improved the likelihood of the best tree (lnL = -13991.936137).

```
./Individual_loci/Cox3/
./Individual_loci/Cox3/Cox3_FINAL.fasta
./Individual_loci/Cox3/Cox3_pruned.fasta
./Individual_loci/Cox3/Cox3_with_outgroup_renamed.fasta
./Individual_loci/Cox3/RAxML_bestTree.Cox3
./Individual_loci/Cox3/RAxML_bestTree.Cox3_FINAL
./Individual_loci/Cox3/RAxML_info.Cox3_FINAL
```

```
./Individual_loci/Cox3/
./Individual_loci/Cox3/RAxML-NG_output/
./Individual_loci/Cox3/RAxML-NG_output/Cox3.raxml.bestModel
./Individual_loci/Cox3/RAxML-NG_output/Cox3.raxml.bestTreeCollapsed
./Individual_loci/Cox3/RAxML-NG_output/Cox3.raxml.log
./Individual_loci/Cox3/RAxML-NG_output/Cox3.raxml.mlTrees
./Individual_loci/Cox3/RAxML-NG_output/Cox3.raxml.rba
./Individual_loci/Cox3/RAxML-NG_output/Cox3.raxml.startTree
./Individual_loci/Cox3/RAxML-NG_FINAL_output/
./Individual_loci/Cox3/RAxML-NG_FINAL_output/Cox3_FINAL.raxml.bestModel
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./Individual_loci/Cox3/RAxML-NG_FINAL_output/Cox3_FINAL.raxml.log
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./Individual_loci/Cox3/RAxML-NG_FINAL_output/Cox3_FINAL.raxml.rba
./Individual_loci/Cox3/Cox3_aligned_renamed.fasta
./Individual_loci/Cox3/Cox3_FINAL.fasta
./Individual_loci/Cox3/Cox3_FINAL.raxml.bestTree
./Individual_loci/Cox3/Cox3_Nov2021_aligned.fasta
./Individual_loci/Cox3/Cox3.raxml.bestTree
./Individual_loci/Cox3/Cox3.sh
```

- Final tree based on the original alignment with two sequences excluded: those of *Balearica regulorum*, which was causing rooting issues (with a clade comprising non-numeniine scolopacids and turnicids sister to the rest of the clade), and of *Pedionomus torquatus*, which was misplaced as the sister group of Turnicidae, with the resulting clade deeply nested within Scolopacidae (and specifically within Scolopacini). The removal of these two sentences did not restore Turnicidae to its usual position, but made it much less deeply nested within Scolopaci (with a spurious clade of *Numenius* + Turnicidae sister to the rest of the group). Both the original and the pruned alignments produced trees that differed from the orthodox topology in the nonmonophyly of Scolopacidae (with *Numenius* widely separated from the rest of the clade) and of Jacanida (with either *Pedionomus* or Thinocoridae separated from the rest of the clade), the paraphyly of Burhinidae with respect to Chionoidea, the paraphyly of Glareolidae with respect to *Dromas*, the paraphyly of Alcidae with respect to Stercorariidae, and the inclusion of the auk *Synthliboramphus* in the Laridae. These likely represent stochastic errors due to the short length of the alignment.



```
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./Individual_loci/CytB/Cytb_FINAL_corr_codon_pos.fasta
./Individual_loci/CytB/Cytb_MUSCLE_alignment.log
./Individual_loci/CytB/Cytb_no_L-atlanticus_L-fuliginosus.fasta
./Individual_loci/CytB/Cytb_pruned.fasta
./Individual_loci/CytB/Cytb_to_align.fasta
./Individual_loci/CytB/Larus_atlanticus_Cytb.fasta
./Individual_loci/CytB/Leucophaeus_fuliginosus_Cytb.fasta
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./Individual_loci/CytB/RAXML_info.Cytb
```

```
./Individual_loci/CytB/
./Individual_loci/CytB/RAXML-NG_output/
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./Individual_loci/CytB/RAXML-NG_output/CytB.raxml.log
./Individual_loci/CytB/RAXML-NG_output/CytB.raxml.mlTrees
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./Individual_loci/CytB/RAXML-NG_output/CytB.raxml.reduced.phy
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./Individual_loci/CytB/RAXML-NG_FINAL_output/CytB_FINAL.raxml.reduced.phy
./Individual_loci/CytB/RAXML-NG_FINAL_output/CytB_FINAL.raxml.startTree
./Individual_loci/CytB/CytB_aligned_refined_renamed.fasta
./Individual_loci/CytB/CytB_aligned_renamed.fasta
./Individual_loci/CytB/CytB_FINAL.fasta
./Individual_loci/CytB/CytB_FINAL.raxml.bestTree
./Individual_loci/CytB/CytB_manually_realigned.fasta
./Individual_loci/CytB/CytB_MUSCLE_refinement.log
./Individual_loci/CytB/CytB_Nov2021_aligned.fasta
./Individual_loci/CytB/CytB.raxml.bestTree
./Individual_loci/CytB/CytB.sh
```

- The original alignment was refined using MUSCLE and analyzed. The resulting tree was misrooted, with *Pluvialis fulva* forming a sister group to all other charadriiforms. A clade comprising Charadriidae (other than *P. fulva*) and Haematopodoidea was sister to (Burhinidae + Turnicidae), while (Chionoidea + *Pluvianus*) formed the sister group of (Lari + Scolopaci). Subsequent manual edits affected the position of *Pluvianus aegyptius*, which moved sister to (Burhinidae + Turnicidae) rather than Chionoidea, and rendered the genera *Rhinoptilus* and *Glareola* reciprocally monophyletic. They also helped increase the likelihood of the best tree (refined/original: lnL = -48593.387979, manually realigned: lnL = -48513.951833). The *Pluvialis fulva* sequence was removed, as it was clearly misplaced (likely due to the fact that a frameshift rendered it nonfunctional – see the GenBank annotation for KX639757.1); this reverted the changes to the topology of Glareolidae, again making *Rhinoptilus* paraphyletic with respect to *Glareola*. Both the MUSCLE-refined and the final (manually edited and pruned) alignments produced trees that were misrooted (see above), and further differed from the orthodox topology as follows: within Scolopacidae, *Bartramia* alone was sister to the rest of the clade, followed by *Limosa*, *Numenius*, and *Phalaropus* as the next three clades to branch off; Scolopacinae was paraphyletic with respect to Arenariinae and Tringini, with *Gallinago*, *Coenocorypha* and *Chubbia* more closely related to Tringini and *Scolopax*, *Limnodromus*, and

*Lymnocyrtes* more closely related to Arenariinae; within Jacanida, Rostratulidae formed the sister group of *Pedionomus* rather than Jacanidae; *Dromas* was sister to the rest of Larida rather than Glareolidae alone; *Cerorhinca* was nested within *Fratercula*; and *Leucophaeus* was paraphyletic with respect to the remaining Larinae, with *Leucophaeus scoresbii* alone forming the sister group to the rest of the clade.

```
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./Individual_loci/ND1/RAxML_bestTree.ND1
./Individual_loci/ND1/RAxML_bestTree.ND1_FINAL
./Individual_loci/ND1/RAxML_info.ND1_FINAL
```

```
./Individual_loci/ND1/
./Individual_loci/ND1/RAxML-NG_output/
./Individual_loci/ND1/RAxML-NG_output/ND1.raxml.bestModel
./Individual_loci/ND1/RAxML-NG_output/ND1.raxml.bestTreeCollapsed
./Individual_loci/ND1/RAxML-NG_output/ND1.raxml.log
./Individual_loci/ND1/RAxML-NG_output/ND1.raxml.miTrees
./Individual_loci/ND1/RAxML-NG_output/ND1.raxml.rba
./Individual_loci/ND1/RAxML-NG_output/ND1.raxml.startTree
./Individual_loci/ND1/RAxML-NG_FINAL_output/
./Individual_loci/ND1/RAxML-NG_FINAL_output/ND1_FINAL.raxml.bestModel
./Individual_loci/ND1/RAxML-NG_FINAL_output/ND1_FINAL.raxml.bestTreeCollapsed
./Individual_loci/ND1/RAxML-NG_FINAL_output/ND1_FINAL.raxml.log
./Individual_loci/ND1/RAxML-NG_FINAL_output/ND1_FINAL.raxml.miTrees
./Individual_loci/ND1/RAxML-NG_FINAL_output/ND1_FINAL.raxml.rba
./Individual_loci/ND1/RAxML-NG_FINAL_output/ND1_FINAL.raxml.startTree
./Individual_loci/ND1/ND1_aligned_refined_renamed.fasta
./Individual_loci/ND1/ND1_aligned_renamed.fasta
./Individual_loci/ND1/ND1_FINAL.fasta
./Individual_loci/ND1/ND1_FINAL.raxml.bestTree
./Individual_loci/ND1/ND1_MUSCLE_refinement.log
./Individual_loci/ND1/ND1_Nov2021_aligned.fasta
./Individual_loci/ND1/ND1.raxml.bestTree
./Individual_loci/ND1/ND1.sh
```

- Final tree based on a manually refined alignment. The manual edits had no effect on the tree topology but helped increase the likelihood of the best tree (original:  $\ln L = -26391.678824$ , manually edited/final:  $\ln L = -26280.146634$ ). Both the original and the pruned alignments produced trees that differed from the orthodox topology in the position of *Dromas* (sister to Laridae + Alcoidea rather than Glareolidae), the internal topology of the Scolopacidae (with *Limosa* branching off before *Numenius*), the position of Alcidae (sister to Laridae rather than Stercorariidae), and the position of *Fratercula arctica*, which grouped with Laridae rather than *Aethia cristatella* as expected. However, the removal of *Fratercula arctica* simply resulted in *Aethia cristatella* moving into this position instead. Only the simultaneous removal of both *Fratercula* and *Aethia* rendered Alcidae monophyletic with respect to Laridae, and additionally reduced the length of the branch separating (Alcidae + Laridae) from Stercorariidae to zero, effectively placing the three taxa in an unresolved trichotomy. However, as neither *Fratercula* nor *Aethia* exhibited any obvious signs of sequencing error (long branches, alignment issues), their failure to group together was interpreted as stochastic error, and both taxa were kept in the final alignment.

```

./Individual_loci/ND2/
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./Individual_loci/ND2/ND2_with_outgroup_renamed.fasta
./Individual_loci/ND2/RAxML_bestTree.ND2
./Individual_loci/ND2/RAxML_bestTree.ND2_FINAL
./Individual_loci/ND2/RAxML_info.ND2_FINAL

```

```

./Individual_loci/ND2/
./Individual_loci/ND2/RAxML-NG_output/
./Individual_loci/ND2/RAxML-NG_output/ND2.raxml.bestModel
./Individual_loci/ND2/RAxML-NG_output/ND2.raxml.bestTreeCollapsed
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./Individual_loci/ND2/RAxML-NG_output/ND2.raxml.rba
./Individual_loci/ND2/RAxML-NG_output/ND2.raxml.reduced.phy
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./Individual_loci/ND2/RAxML-NG_FINAL_output/ND2_FINAL.raxml.bestTreeCollapsed
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./Individual_loci/ND2/RAxML-NG_FINAL_output/ND2_FINAL.raxml.rba
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./Individual_loci/ND2/ND2_FINAL.fasta
./Individual_loci/ND2/ND2_FINAL.raxml.bestTree
./Individual_loci/ND2/ND2_manually_realigned.fasta
./Individual_loci/ND2/ND2_Nov2021_aligned.fasta
./Individual_loci/ND2/ND2.raxml.bestTree
./Individual_loci/ND2/ND2.sh

```

- Final tree based on a manually refined alignment with a single excluded sequence: that of *Sterna trudeaui*, which was found outside of a clade formed by other species of *Sterna* and *Thalasseus*, and which was subtended by a long branch that attracted *Rynchops niger*, causing the latter taxon to become deeply nested within Sterninae. The manual edits made the topology more orthodox with respect to the position of *Prosobonia*, whose long branch was deeply nested within *Calidris* in the original tree (as a sister group to *C. tenuirostris* + *C. virgata*), but which formed the second deepest-branching taxon within Scolopacidae in the tree based on the manually edited alignment (after *Bartramia* + *Numenius*). They made the topology less orthodox with respect to the position of Alcidae, which became sister to Laridae rather than Stercorariidae. The manual edits helped increase the likelihood of the best tree (original:  $\ln L = -52334.589093$ , manually edited:  $\ln L = -52208.038937$ ). The removal of *Sterna trudeaui* reverted the changes to the position of Alcidae (rendering Alcoidea monophyletic again), but caused *Eudromias morinellus* to become sister to (*Ibidorhyncha* + Haematopodoidea) instead of representing a derived charadriid. This further exacerbated the paraphyly of Charadriidae, which was already present in the trees based on the original and manually refined alignments: in all three trees, *Pluvialis* is more closely related to *Ibidorhyncha* and Haematopodoidea than to other charadriids (though not as closely as *Eudromias* in the final tree), while *Oreopholus* forms the sister group of a clade comprising Haematopodoidea, *Ibidorhyncha*, and all remaining charadriids. Both the original and the final (manually edited and pruned) alignments produced trees that differed from the orthodox topology as follows: *Dromas* was sister to (Laridae + Alcoidea) rather than Glareolidae; Tringinae was paraphyletic with respect to all scolopacids other than *Numenius* and *Bartramia* (and *Prosobonia* in the tree based on the final alignment), with (*Tringa* + *Phalaropus*), *Xenus*, and *Actitis* forming progressively more distant outgroups to a

clade consisting of Scolopacinae on the one hand and (Limosinae + Arenariinae) on the other; and Limnodromini was paraphyletic with respect to Scolopacini, as *L. semipalmatus* was more closely related to a clade including *Scolopax*, *Gallinago*, and *Chubbia* than to *Limnocyrtus* and the remaining species of *Limnodromus*.

```
./Individual_loci/ND3/
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./Individual_loci/ND3_FINAL.fasta
./Individual_loci/ND3_pruned.fasta
./Individual_loci/ND3_with_outgroup_renamed.fasta
./Individual_loci/RAxML_bestTree.ND3
./Individual_loci/RAxML_bestTree.ND3_FINAL
./Individual_loci/RAxML_info.ND3_FINAL
```

```
./Individual_loci/ND3/
./Individual_loci/ND3/RAxML-NG_output/
./Individual_loci/ND3/RAxML-NG_output/ND3.raxml.bestModel
./Individual_loci/ND3/RAxML-NG_output/ND3.raxml.bestTreeCollapsed
./Individual_loci/ND3/RAxML-NG_output/ND3.raxml.log
./Individual_loci/ND3/RAxML-NG_output/ND3.raxml.mlTrees
./Individual_loci/ND3/RAxML-NG_output/ND3.raxml.rba
./Individual_loci/ND3/RAxML-NG_output/ND3.raxml.reduced.phy
./Individual_loci/ND3/RAxML-NG_output/ND3.raxml.startTree
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./Individual_loci/ND3/RAxML-NG_FINAL_output/ND3_FINAL.raxml.rba
./Individual_loci/ND3/RAxML-NG_FINAL_output/ND3_FINAL.raxml.reduced.phy
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./Individual_loci/ND3/ND3_manually_realigned.fasta
./Individual_loci/ND3/ND3_Nov2021_aligned.fasta
./Individual_loci/ND3/ND3.raxml.bestTree
./Individual_loci/ND3/ND3.sh
```

- Final tree based on a manually refined alignment with a single excluded sequence: that of *Rynchops niger*, which was misplaced as the sister group to the rest of Larida in a severely misrooted tree. The manual edits made the topology more orthodox in the following ways: *Gallinago* became the first-diverging branch within a monophyletic Scolopacidae (instead of forming a sister group to Jacanidae), and *Thinornis* (including *Afroxyechus*) became monophyletic with respect to *Charadrius*. They also improved the likelihood of the best tree (original:  $\ln L = -9320.396489$ , manually realigned:  $\ln L = -9311.679329$ ). Both the original and manually refined alignments produced trees that were highly unorthodox: Laridae was paraphyletic not only with respect to Alcidae and Stercorariidae, but also with respect to Glareolidae, and Alcidae was itself paraphyletic with respect to *Dromas*. Rostratulidae was sister to the entire rest of Jacanida, rather than to Jacanidae alone. Neither Lari nor Charadrii were monophyletic: Turnicidae was sister either to Scolopaci (in the tree based on the original alignment) or to Chionoidea (in the tree based on the manually edited alignment), and Chionida (in the tree based on the original alignment) or Burhinidae alone (in the tree based on the manually edited alignment) formed the sister group of all other charadriiforms. In addition, Larida and Charadrii were more closely related to each other than either was to Scolopaci. The removal of *Rynchops niger* had far-reaching effects on the topology: a clade close to the traditional Charadrii (including Charadriidae, *Ibidorhyncha*, Haematopodoidea, Chionoidea, but

also Turnicidae and not Burhinidae) became sister to all other non-burhinid charadriiforms (i.e., to Larida + Scolopaci); Glareolidae became sister to the rest of Larida; and Laridae ceased to be paraphyletic with respect to Alcidae (though it still included Stercorariidae as a sister group to Sterninae). As in the trees based on the full original or manually edited alignments, *Dromas* was deeply nested within Alcidae as the sister group of *Aethia* (which failed to group with *Fratercula* as expected). An attempt to remove *Dromas* as well as *Rynchops* rendered Alcidae monophyletic and reunited Burhinidae with Chionoidea into a monophyletic Chionida (sister to all other charadriiforms), but caused *Gallinago* to again become sister to Jacanida and rendered Charadriidae massively paraphyletic with respect to (*Ibidorhyncha* + Haematopodoidea). The further removal of both species of *Gallinago* failed to improve the topology, causing Turnicidae to become deeply nested within Scolopacidae and yielding a sister-group relationship between Alcidae and Glareolidae. In contrast, excluding *Aethia* had no effect on the topology; *Dromas* remained deeply nested within Alcidae, and all other features of the tree remained the same as when *Rynchops* alone was removed. As a result of these experiments, *Aethia*, *Dromas*, and *Gallinago* were all retained in the final alignment, with only *Rynchops* excluded.

```
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./Individual_loci/RAxML_info.ND4_FINAL

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./Individual_loci/ND4/RAxML-NG_output/ND4.raxml.rba
./Individual_loci/ND4/RAxML-NG_output/ND4.raxml.startTree
./Individual_loci/ND4/ND4_aligned_renamed.fasta
./Individual_loci/ND4/ND4_Nov2021_aligned.fasta
./Individual_loci/ND4/ND4.raxml.bestTree
./Individual_loci/ND4/ND4.sh
```

- The original alignment was used without any modifications. The resulting tree was almost perfectly orthodox, with several exceptions: Turnicidae formed the sister group of Scolopaci rather than Larida, Alcidae was sister to Laridae rather than Stercorariidae, and *Numenius* formed the sister group of *Limosa* alone rather than the entire rest of Scolopacidae. *Pluvialis* was found to be more closely related to Haematopodoidea than to the rest of Charadriidae.

```
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./Individual_loci/RAxML_info.ND4L_FINAL

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```



```

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./Individual_loci/ND4L/RAxML-NG_FINAL_output/
./Individual_loci/ND4L/RAxML-NG_FINAL_output/ND4L_FINAL.raxml.bestModel
./Individual_loci/ND4L/RAxML-NG_FINAL_output/ND4L_FINAL.raxml.bestTreeCollapsed
./Individual_loci/ND4L/RAxML-NG_FINAL_output/ND4L_FINAL.raxml.log
./Individual_loci/ND4L/RAxML-NG_FINAL_output/ND4L_FINAL.raxml.mlTrees
./Individual_loci/ND4L/RAxML-NG_FINAL_output/ND4L_FINAL.raxml.rba
./Individual_loci/ND4L/RAxML-NG_FINAL_output/ND4L_FINAL.raxml.reduced.phy
./Individual_loci/ND4L/RAxML-NG_FINAL_output/ND4L_FINAL.raxml.startTree
./Individual_loci/ND4L/ND4L_aligned_renamed.fasta
./Individual_loci/ND4L/ND4L_FINAL.fasta
./Individual_loci/ND4L/ND4L_FINAL.raxml.bestTree
./Individual_loci/ND4L/ND4L_Nov2021_aligned.fasta
./Individual_loci/ND4L/ND4L.raxml.bestTree
./Individual_loci/ND4L/ND4L.sh

```

- Final tree based on the original alignment with two sequences excluded: those of *Balearica regulorum* and *Metopidius indicus*. The tree containing both of these sequences was severely misrooted, with the first-diverging branch subtending a clade that included the thinocorids, jacanids other than *Metopidius*, *Nycticryphes* (but not *Rostratula*), and *Charadrius vociferus* (but no other charadriids). The exclusion of *Balearica* and *Metopidius* allows the tree to be rooted on a clade that closely resembles the conventional Charadrii, except that it also includes Turnicidae (as the sister group of Charadriidae, which is itself paraphyletic with respect to Haematopodoidea). Scolopaci is paraphyletic with respect to Larida: the first clade to branch off includes *Pedionomus* as the sister group of Jacanidae + *Nycticryphes*, and is followed by Thinocoridae and finally by *Rostratula benghalensis* as the sister group of (Scolopacidae + Larida). Within Larida, a monophyletic Glareoloidea forms the sister group to the rest of the clade, which consists of an Alcidae that is massively paraphyletic with respect to both Stercorariidae and Laridae. *Aethia* forms the sister group of *Cephus* rather than *Fratercula* as expected. A further attempt to remove *Rostratula* to eliminate the polyphyly of Rostratulidae made the topology significantly worse, and was therefore reverted, leaving *Rostratula* in the final alignment.

```

./Individual_loci/ND5/
./Individual_loci/ND5_FINAL.fasta
./Individual_loci/ND5_pruned.fasta
./Individual_loci/ND5_with_outgroup_renamed.fasta
./Individual_loci/RAxML_bestTree.ND5
./Individual_loci/RAxML_bestTree.ND5_FINAL
./Individual_loci/RAxML_info.ND5_FINAL

```

```

./Individual_loci/ND5/
./Individual_loci/ND5/RAxML-NG_output/
./Individual_loci/ND5/RAxML-NG_output/ND5.raxml.bestModel
./Individual_loci/ND5/RAxML-NG_output/ND5.raxml.bestTreeCollapsed
./Individual_loci/ND5/RAxML-NG_output/ND5.raxml.log
./Individual_loci/ND5/RAxML-NG_output/ND5.raxml.mlTrees
./Individual_loci/ND5/RAxML-NG_output/ND5.raxml.rba
./Individual_loci/ND5/RAxML-NG_output/ND5.raxml.startTree
./Individual_loci/ND5/RAxML-NG_FINAL_output/
./Individual_loci/ND5/RAxML-NG_FINAL_output/ND5_FINAL.raxml.bestModel
./Individual_loci/ND5/RAxML-NG_FINAL_output/ND5_FINAL.raxml.bestTreeCollapsed
./Individual_loci/ND5/RAxML-NG_FINAL_output/ND5_FINAL.raxml.log
./Individual_loci/ND5/RAxML-NG_FINAL_output/ND5_FINAL.raxml.mlTrees

```

```
./Individual_loci/ND5/RAxML-NG_FINAL_output/ND5_FINAL.raxml.rba
./Individual_loci/ND5/RAxML-NG_FINAL_output/ND5_FINAL.raxml.startTree
./Individual_loci/ND5/ND5_aligned_renamed.fasta
./Individual_loci/ND5/ND5_FINAL.fasta
./Individual_loci/ND5/ND5_FINAL.raxml.bestTree
./Individual_loci/ND5/ND5_Nov2021_aligned.fasta
./Individual_loci/ND5/ND5.raxml.bestTree
./Individual_loci/ND5/ND5.sh
```

- Final tree based on the original alignment with two sequences excluded: those of *Alle alle*, which was deeply nested inside the Laridae (likely as a consequence of its short length – just 114 bp – that did not allow it to be accurately placed), and of *Actitis macularius*, which was deeply nested inside the genus *Tringa* (suggesting the sequence was likely misidentified). Both the original and the pruned alignments produced trees that were very nearly orthodox, with the following exceptions: *Pedionomus* was sister to Rostratulidae rather than Thinocoridae, and *Pluvialis* formed the sister group of a clade consisting of Haematopodoidea and all remaining charadriids.

```
./Individual_loci/ND6/
./Individual_loci/ND6_FINAL.fasta
./Individual_loci/ND6_pruned.fasta
./Individual_loci/ND6_with_outgroup_renamed.fasta
./Individual_loci/RAxML_bestTree.ND6
./Individual_loci/RAxML_bestTree.ND6_FINAL
./Individual_loci/RAxML_info.ND6_FINAL
```

```
./Individual_loci/ND6/
./Individual_loci/ND6/RAxML-NG_output/
./Individual_loci/ND6/RAxML-NG_output/ND6.raxml.bestModel
./Individual_loci/ND6/RAxML-NG_output/ND6.raxml.bestTreeCollapsed
./Individual_loci/ND6/RAxML-NG_output/ND6.raxml.log
./Individual_loci/ND6/RAxML-NG_output/ND6.raxml.mlTrees
./Individual_loci/ND6/RAxML-NG_output/ND6.raxml.rba
./Individual_loci/ND6/RAxML-NG_output/ND6.raxml.reduced.phy
./Individual_loci/ND6/RAxML-NG_output/ND6.raxml.startTree
./Individual_loci/ND6/RAxML-NG_FINAL_output/
./Individual_loci/ND6/RAxML-NG_FINAL_output/ND6_FINAL.raxml.bestModel
./Individual_loci/ND6/RAxML-NG_FINAL_output/ND6_FINAL.raxml.bestTreeCollapsed
./Individual_loci/ND6/RAxML-NG_FINAL_output/ND6_FINAL.raxml.log
./Individual_loci/ND6/RAxML-NG_FINAL_output/ND6_FINAL.raxml.mlTrees
./Individual_loci/ND6/RAxML-NG_FINAL_output/ND6_FINAL.raxml.rba
./Individual_loci/ND6/RAxML-NG_FINAL_output/ND6_FINAL.raxml.startTree
./Individual_loci/ND6/ND6_aligned_renamed.fasta
./Individual_loci/ND6/ND6_FINAL.fasta
./Individual_loci/ND6/ND6_FINAL.raxml.bestTree
./Individual_loci/ND6/ND6_manually_realigned.fasta
./Individual_loci/ND6/ND6_Nov2021_aligned.fasta
./Individual_loci/ND6/ND6.raxml.bestTree
./Individual_loci/ND6/ND6.sh
```

- Final tree based on a manually refined alignment with two sequences excluded: those of *Calidris tenuirostris*, which was nested within the charadriid genus *Pluvialis* (indicating that the mitogenome from which the ND6 sequence was extracted is probably chimerical, since other loci such as 16S and ND2 correctly place it within *Calidris*), and *Tringa guttifer*, which formed the sister group to the rest of Scolopaci. The manual edits moved *T. guttifer* sister to all scolopacids other than *Numenius* and *Limosa*, and changed the internal topology of Larida:

instead of Larinae being sister to a group comprising (*Rynchops* + *Dromas*) on the one hand and a (Sterninae + (Stercorariidae + (Alcidae + Glareolidae))) clade on the other, (Larinae + *Dromas*) became sister to a clade that included *Rynchops* as the sister group of (Alcidae + (Stercorariidae + (Larinae + Glareolidae))). They also increased the likelihood of the best tree (original:  $\ln L = -13679.546712$ , manually realigned:  $\ln L = -13611.848875$ ). Both trees were misrooted in that Turnicidae formed the sister group to a clade uniting all other charadriiforms, which consisted of Larida on the one hand and (Chionida + (Charadriida + Scolopaci)) on the other. The removal of *C. tenuirostris* and *T. guttifer* from the manually edited alignment reverted the changes to the topology of Larida, making it identical to the tree based on the original alignment. Attempts to remove *Dromas*, *Rynchops*, or both in order to eliminate their spurious sister-group relationship failed to make the overall relationships within Larida more orthodox. Because of this, and because neither taxon exhibited any obvious signs of sequencing error, their grouping together was interpreted as stochastic error, and both sequences were kept in the final alignment. The same applies to *Tringa ochropus*, which was subtended by an unusually long branch, but correctly placed among other species of *Tringa*; its branch was comparable in length to those of *Ibidorhyncha* or *Scolopax*, and was not due to obvious sequencing errors.



## Preparing and analyzing Strauch's (1978) morphological character matrix (section 2.1)

**./Morphology/RAxML/  
./Morphology/cform\_part.txt  
./Morphology/RAxML\_bestTree.Strauch  
./Morphology/RAxML\_info.Strauch  
./Morphology/strauch\_final.phy  
./Morphology/strauch\_final.phy.reduced**

**./Morphology/RAxML-NG/  
./Morphology/morph\_part.txt  
./Morphology/Strauch\_FINAL.phy  
./Morphology/strauch\_morph.raxml.bestModel  
./Morphology/strauch\_morph.raxml.bestTree  
./Morphology/strauch\_morph.raxml.bestTreeCollapsed  
./Morphology/strauch\_morph.raxml.log  
./Morphology/strauch\_morph.raxml.mlTrees  
./Morphology/strauch\_morph.raxml.rba  
./Morphology/strauch\_morph.raxml.reduced.partition  
./Morphology/strauch\_morph.raxml.reduced.phy  
./Morphology/strauch\_morph.raxml.startTree**

- Name of the folder changed to reflect the fact that a different program was used to carry out the maximum-likelihood analyses on the newly reconciled matrix.

**./Morphology/Strauch\_data\_final.csv**

- Ordering and names of the taxa changed to correspond exactly to Strauch's (1978) Table I (the original file had partially reconciled names that corresponded neither to our preferred taxonomy nor to Strauch's). In addition, two rows present in Strauch's table but not in the original file were added back: those corresponding to *Prosobonia cancellatus* and *Haematopus frazari*. However, we did not add back the two columns that corresponded to characters 51 and 59, which were deleted following Chu (1995).

**./Morphology/Strauch\_morph\_data.Rmd  
./Morphology/Strauch\_morph\_data.html**

- Changed after rerunning the analyses on the newly reconciled matrix.

**./Morphology/Strauch\_renamed.csv  
./Morphology/Strauch\_reconciled\_pruned.csv**

- Replaced and renamed to emphasize that while the original file (Strauch\_data\_final.csv) included the full taxon sample of Strauch (1978), this one only includes the species that were retained after the taxonomic reconciliation step.

**./Morphology/Strauch\_relabeled.csv  
./Morphology/Strauch\_reconciled\_pruned\_relabeled.csv**

## Species tree analyses (sections 2.2, 3.2 of the original manuscript)

```
./ASTRAL/  
./ASTRAL/ASTRAL_analyses.Rmd  
./ASTRAL/ASTRAL_analyses.html  
./ASTRAL/Charadriiformes_ASTRAL.tre  
./ASTRAL/Charadriiformes_ASTRAL_rerooted.tre  
./ASTRAL/bootstrap.gene.trees  
./ASTRAL/cform.log  
./ASTRAL/cforms_10_gene.trees  
./ASTRAL/treeScored_1.log  
./ASTRAL/treeScored_1.tre  
./ASTRAL/treeScored_2.log  
./ASTRAL/treeScored_2.tre  
./ASTRAL/treeScored_3.log  
./ASTRAL/treeScored_3.tre  
./ASTRAL/treeScored_5.log  
./ASTRAL/treeScored_5.tre  
./ASTRAL/treeScored_6.log  
./ASTRAL/treeScored_6.tre  
./ASTRAL/treeScored_7.log  
./ASTRAL/treeScored_7.tre  
./ASTRAL/treeScored_8.log  
./ASTRAL/treeScored_8.tre  
./ASTRAL/treeScored_9.log  
./ASTRAL/treeScored_9.tre  
./ASTRAL/treeToScore_1.tre  
./ASTRAL/treeToScore_2.tre  
./ASTRAL/treeToScore_3.tre  
./ASTRAL/treeToScore_5.tre  
./ASTRAL/treeToScore_6.tre  
./ASTRAL/treeToScore_7.tre  
./ASTRAL/treeToScore_8.tre  
./ASTRAL/treeToScore_9.tre
```

- Deleted, as we did not repeat the ASTRAL analyses on the new dataset.

# DiscoVista gene tree discordance visualizations (sections 2.2, 3.2)

`./DiscoVista/annotation.txt`  
`./DiscoVista/clade_defs.txt`  
`./DiscoVista/DiscoVista.Rmd`  
`./DiscoVista/DiscoVista.html`

- Replaced after rerunning DiscoVista on the new gene trees.

`./DiscoVista/Gene_trees/ALDOB/`  
`./DiscoVista/Gene_trees/BDNF/`  
`./DiscoVista/Gene_trees/CMOS/`  
`./DiscoVista/Gene_trees/NTF3/`  
`./DiscoVista/Gene_trees/RAG1/`

- Folder contents replaced after rerunning DiscoVista on the new gene trees.

`./DiscoVista/Gene_trees/ADNH5`  
`./DiscoVista/Gene_trees/FIB7`  
`./DiscoVista/Gene_trees/GAPDH/`  
`./DiscoVista/Gene_trees/mitogenome`  
`./DiscoVista/Gene_trees/Myo2`

`./DiscoVista/Gene_trees/ADH5`  
`./DiscoVista/Gene_trees/FGB7`  
`./DiscoVista/Gene_trees/GAPDH3-5/`  
`./DiscoVista/Gene_trees/Mitogenome`  
`./DiscoVista/Gene_trees/MB2`

- Folder contents replaced and folder names changed after rerunning DiscoVista on the new gene trees.

`./DiscoVista/Gene_trees/GAPDH11`  
`./DiscoVista/Gene_trees/MUSK`  
`./DiscoVista/Gene_trees/ODC`

- New folders added for the three previously unsampled genes.

`./DiscoVista/Monophyletic_Bargraph2.pdf`  
`./DiscoVista/Monophyletic_Bargraphs.pdf`  
`./DiscoVista/Monophyletic_Bargraphs_Porportion.pdf`  
`./DiscoVista/Monophyletic_Bootstrap_Support_2.pdf`  
`./DiscoVista/clades.hs.txt`  
`./DiscoVista/clades.hs.txt.res`  
`./DiscoVista/clades.txt`  
`./DiscoVista/clades.txt.res`  
`./DiscoVista/error.log`  
`./DiscoVista/finegrained/`  
`./DiscoVista/nucl123.counts.csv`

`./DiscoVista/results/Monophyletic_Bargraph2.pdf`  
`./DiscoVista/results/Monophyletic_Bargraphs.pdf`

[./DiscoVista/results/Monophyletic\\_Bargraphs\\_Porportion.pdf](#)  
[./DiscoVista/results/Monophyletic\\_Bootstrap\\_Support\\_2.pdf](#)  
[./DiscoVista/results/clades.hs.txt](#)  
[./DiscoVista/results/clades.hs.txt.res](#)  
[./DiscoVista/results/clades.txt](#)  
[./DiscoVista/results/clades.txt.res](#)  
[./DiscoVista/results/error.log](#)  
[./DiscoVista/results/finegrained/](#)  
[./DiscoVista/results/nucl123.counts.csv](#)

- Replaced and moved into a new subfolder after rerunning DiscoVista on the new gene trees.

[./DiscoVista/Taxon\\_tests/](#)  
[./DiscoVista/Taxon\\_tests/Ibidorhyncha/](#)  
[./DiscoVista/Taxon\\_tests/Pluvianus/](#)

- New folders added to repeat the DiscoVista analysis on those nodes of interest whose resolution was not informed by all 27 loci.

## Concatenated analyses (sections 2.3, 3.3)

**./Concatenated/Cform\_concat\_analyses.Rmd**  
**./Concatenated/Cform\_concat\_analyses.html**  
**./Concatenated/Concatenated.charsets**  
**./Concatenated/infile.phy**  
**./Concatenated/RAxML-NG/**

- Replaced after the new concatenated alignment has been assembled from the \*\_FINAL.fasta alignments in ./Individual\_loci/, and after it has been re-analyzed using RAxML-NG.

**./Concatenated/mol\_exp\_unpart.fasta**  
**./Concatenated/354taxon\_alignment.fasta**

- A FASTA version of infile.phy, created to be used with the msaplot() function in ./Individual\_loci/Supermatrix\_Statistics.Rmd. First, the infile.phy alignment was converted from Phylip to Fasta using Geneious; then, the 19 taxa only known from morphology were manually added in as gap-only sequences.

**./Concatenated/phyluce\_align\_format\_nexus\_files\_for\_raxml.log**

- Added the Phyluce log file

**./Concatenated/partition\_finder.cfg**  
**./Concatenated/IQ-TREE\_partitioning/partitions.nex**

- Replaced the initial partitioning scheme (now formatted for IQ-TREE rather than PartitionFinder)

**./Concatenated/best\_scheme.txt**  
**./Concatenated/IQ-TREE\_partitioning/output.best\_scheme.nex**

- Replaced the final partitioning scheme (now produced by IQ-TREE rather than PartitionFinder)

**./Concatenated/ExaBayes/aln.part**

- Replaced to correspond to the best partitioning scheme found using IQ-TREE 2

**./Concatenated/ExaBayes/config.nexus**

- Changed to account for the greater number of partitions

**./Concatenated/ExaBayes/eMRC\_tree\_prunings.trees**  
**./Concatenated/ExaBayes/ExaBayes\_ConsensusExtendedMajorityRuleNewick.tree\_output**  
**./Concatenated/ExaBayes/ExaBayes\_ConsensusExtendedMajorityRuleNexus.tree\_output**  
**./Concatenated/ExaBayes/ExaBayes\_parameterStatistics.paramCons**  
**./Concatenated/ExaBayes/ExaBayes\_per-branch\_locus\_coverage.log**  
**./Concatenated/ExaBayes/ExaBayes\_per-branch\_locus\_coverage.tre**  
**./Concatenated/ExaBayes/STDOUT.txt**

- Replaced after rerunning ExaBayes on the new supermatrix.

**./Concatenated/RAxML/ML\_tree\_prunings.trees**  
**./Concatenated/RAxML/partitions.txt**  
**./Concatenated/RAxML/RAxML\_bestTree.cform\_molecular**  
**./Concatenated/RAxML/RAxML\_bipartitionsBranchLabels.cform\_molecular\_biparts**

./Concatenated/RAxML/RAxML\_bipartitions.cform\_molecular\_biparts  
./Concatenated/RAxML/RAxML\_bootstrap.cform\_molecular-bs  
./Concatenated/RAxML/RAxML\_info.cform\_molecular  
./Concatenated/RAxML/RAxML\_info.cform\_molecular\_biparts  
./Concatenated/RAxML/RAxML\_info.cform\_molecular-bs  
./Concatenated/RAxML/RAxML\_info.internode\_certainty  
./Concatenated/RAxML/RAxML\_IC\_Score\_BranchLabels.internode\_certainty  
./Concatenated/RAxML/RAxML\_IC\_Score\_NodeLabels.internode\_certainty  
./Concatenated/RAxML/RAxML\_per-branch\_locus\_coverage.log  
./Concatenated/RAxML/RAxML\_per-branch\_locus\_coverage.tre

./Concatenated/RAxML-NG/  
./Concatenated/RAxML-NG/concatenated.per-branch\_locus\_coverage.log  
./Concatenated/RAxML-NG/concatenated.per-branch\_locus\_coverage.tre  
./Concatenated/RAxML-NG/concatenated.raxml.bestModel  
./Concatenated/RAxML-NG/concatenated.raxml.bestTree  
./Concatenated/RAxML-NG/concatenated.raxml.bs  
./Concatenated/RAxML-NG/concatenated.raxml.log  
./Concatenated/RAxML-NG/concatenated.raxml.support  
./Concatenated/RAxML-NG/ML\_tree\_prunings.trees  
./Concatenated/RAxML-NG/partitions.txt  
./Concatenated/RAxML-NG/RAxML\_IC\_Score\_BranchLabels.internode\_certainty  
./Concatenated/RAxML-NG/RAxML\_IC\_Score\_NodeLabels.internode\_certainty  
./Concatenated/RAxML-NG/RAxML\_info.internode\_certainty

- Replaced after rerunning the maximum-likelihood analyses (now handled using RAxML-NG rather than RAxML) on the new supermatrix.

# Analyses of combined morphological and molecular data (sections 2.4, 3.4)

**./Total\_evidence/IQ-TREE/dna.phy**

- Replaced by a renamed copy of the concatenated alignment (./Concatenated/infile.phy)

**./Total\_evidence/IQ-TREE/bin.phy**

**./Total\_evidence/IQ-TREE/multi3.phy**

**./Total\_evidence/IQ-TREE/multi4.phy**

**./Total\_evidence/IQ-TREE/multi5.phy**

**./Total\_evidence/IQ-TREE/multi6.phy**

- Recreated from ./Morphology/RAxML-NG/Strauch\_FINAL.phy

**./Total\_evidence/IQ-TREE/test.trees**

- Replaced. The new file includes 3 rather than 2 trees: ./Total\_evidence/RAxML-NG/total-evidence.raxml.bestTree, ./Total\_evidence/EPA/RAxML\_portableTree.EPA\_unresolved.newick (the “unresolved” / group-together evolutionary placement tree), and ./Total\_evidence/EPA/RAxML\_portableTree.EPA\_fullyResolved.newick (the “fully resolved” / split-scaffold-edges evolutionary placement tree). Note that the latter two are actually both strictly bifurcating.

**./Total\_evidence/IQ-TREE/analysis.nex**

**./Total\_evidence/IQ-TREE/analysis.nex.iqtree**

**./Total\_evidence/IQ-TREE/analysis.nex.log**

**./Total\_evidence/IQ-TREE/analysis.nex.parstree**

**./Total\_evidence/IQ-TREE/analysis.nex.treefile**

**./Total\_evidence/IQ-TREE/analysis.nex.trees**

**./Total\_evidence/partitions.nex**

**./Total\_evidence/TE\_EPA\_comparison.best\_model.nex**

**./Total\_evidence/TE\_EPA\_comparison.ckp.gz**

**./Total\_evidence/TE\_EPA\_comparison.iqtree**

**./Total\_evidence/TE\_EPA\_comparison.log**

**./Total\_evidence/TE\_EPA\_comparison.parstree**

**./Total\_evidence/TE\_EPA\_comparison.treefile**

**./Total\_evidence/TE\_EPA\_comparison.trees**

- Replaced after repeating the IQ-TREE 2 analysis (comparing the fit of the total-evidence and evolutionary placement trees) on the new dataset.

**./Total\_evidence/E\_FRP.raxml.bestModel**

**./Total\_evidence/E\_FRP.raxml.bestTree**

**./Total\_evidence/E\_FRP.raxml.log**

**./Total\_evidence/E\_FRP.raxml.rba**

**./Total\_evidence/E\_FRP.raxml.reduced.partition**

**./Total\_evidence/E\_FRP.raxml.reduced.phy**

**./Total\_evidence/E\_FRP.raxml.startTree**

**./Total\_evidence/RAxML\_EPA.fossil-placement.newick**

**./Total\_evidence/RAxML\_classification.fossil-placement**

**./Total\_evidence/RAxML\_classificationLikelihoodWeights.fossil-placement**

./Total\_evidence/RAxML\_entropy.fossil-placement  
./Total\_evidence/RAxML\_fullyResolved.fossil-placement.newick  
./Total\_evidence/RAxML\_info.fossil-placement  
./Total\_evidence/RAxML\_info.morph-weights  
./Total\_evidence/RAxML\_labelledTree.fossil-placement  
./Total\_evidence/RAxML\_molecular\_scaffold.tre  
./Total\_evidence/RAxML\_originalLabelledTree.fossil-placement  
./Total\_evidence/RAxML\_portableTree.fossil-placement.jplace  
./Total\_evidence/RAxML\_weights.morph-weights

./Total\_evidence/EPA/  
./Total\_evidence/EPA/GT-EPA\_evaluation.raxml.bestModel  
./Total\_evidence/EPA/GT-EPA\_evaluation.raxml.bestTree  
./Total\_evidence/EPA/GT-EPA\_evaluation.raxml.log  
./Total\_evidence/EPA/GT-EPA\_evaluation.raxml.rba  
./Total\_evidence/EPA/GT-EPA\_evaluation.raxml.startTree  
./Total\_evidence/EPA/RAxML\_classification.EPA  
./Total\_evidence/EPA/RAxML\_classificationLikelihoodWeights.EPA  
./Total\_evidence/EPA/RAxML\_entropy.EPA  
./Total\_evidence/EPA/RAxML\_info.EPA  
./Total\_evidence/EPA/RAxML\_info.morph-weights  
./Total\_evidence/EPA/RAxML\_labelledTree.EPA  
./Total\_evidence/EPA/RAxML\_originalLabelledTree.EPA  
./Total\_evidence/EPA/RAxML\_portableTree.EPA.jplace  
./Total\_evidence/EPA/RAxML\_portableTree.EPA\_fullyResolved.newick  
./Total\_evidence/EPA/RAxML\_portableTree.EPA\_unresolved.newick  
./Total\_evidence/EPA/RAxML\_weights.morph-weights  
./Total\_evidence/EPA/SSE-EPA\_evaluation.raxml.bestModel  
./Total\_evidence/EPA/SSE-EPA\_evaluation.raxml.bestTree  
./Total\_evidence/EPA/SSE-EPA\_evaluation.raxml.log  
./Total\_evidence/EPA/SSE-EPA\_evaluation.raxml.rba  
./Total\_evidence/EPA/SSE-EPA\_evaluation.raxml.startTree  
./Total\_evidence/EPA/infile.phy  
./Total\_evidence/EPA/molecular\_scaffold.tre  
./Total\_evidence/EPA/morph\_aln.phy  
./Total\_evidence/EPA/partitions.txt

- Replaced after rerunning the evolutionary placement analyses on a (now substantially more complete) concatenated tree.



## Testing the phylogenetic positions of *Ibidorhyncha* and *Pluvialis* (sections 2.5, 3.5)

[./Ibidorhyncha\\_and\\_Pluvialis/](#)

- Added a new folder containing the data, scripts, and results from the analyses performed on the new 100-locus dataset.

# Re-inferring the phylogenetic positions of potential calibration fossils (sections 2.6, 3.6)

**./Musser\_et\_Clarke/**  
**./Heingard\_et\_al/**

- Name of the folder changed to reflect the use of an updated dataset.

**./Heingard\_et\_al/Final\_Constraints\_778.nex**

- Deleted a file containing the original topology constraints used by Musser & Clarke (2020), since we ended up using our own, more stringent ones.

**./Heingard\_et\_al/Musser\_et\_Clarke\_reanalyses.Rmd**  
**./Heingard\_et\_al/Musser\_et\_Clarke\_reanalyses.html**  
**./Heingard\_et\_al/Heingard\_et\_al\_reanalyses.Rmd**  
**./Heingard\_et\_al/Heingard\_et\_al\_reanalyses.html**

- File names changed to reflect the use of an updated dataset

**./Heingard\_et\_al/Kimball\_constraint/kimball\_constraints.nex**  
**./Heingard\_et\_al/Prum\_constraint/prum\_constraints.nex**  
**./Heingard\_et\_al/Reddy\_constraint/kimball\_constraints.nex**

- Changed the Nexus configuration files by keeping the MrBayes block identical but replacing the 693-character matrix of Musser & Clarke (2020) with the 721-character matrix of Heingård et al. (2021). This was made easy by the fact that both matrices have the same set of taxa, listed in the same order (except for "*Porphyrio martinicus*", whose name was corrected to *Porphyryla martinica* in the updated matrix, and *Canirallus oculus batesi*, whose name was misspelled as "*Canirallus oceleus batesi*" in the updated matrix and had to be corrected).

**./Heingard\_et\_al/X26886\_Morphology\_Matrix\_morphobank.nex**  
**./Heingard\_et\_al/X27612\_12-15-2021\_359\_no\_notes.nex**

- Added the new dataset in Nexus format; deleted the old one.

## **Calibration outgroup sequences and upper bounds (section 2.6, Appendix A)**

**./Calibrations/calibration\_locations.png**

- Replaced after the new total-evidence tree has been inferred and changes to the original calibration scheme.

**./Calibrations/Charadriiform calibrations.pdf**

**./Calibrations/Non-charadriiform calibrations.pdf**

- These were brainstorming documents, used first to compile all potential calibrations (and taxa to be included in their outgroup sequences), then to annotate them and, based on these notes, to choose the best candidates for inclusion. They are now redundant with respect to Appendix A, in which all phylogenetic and age justifications are given in much greater detail.

**./Calibrations/cauchy\_cals.png**

**./Calibrations/cform\_cauchy\_estimator.r**

**./Calibrations/Hedman\_dating.Rmd**

**./Calibrations/Hedman\_dating.html**

- Replaced after rerunning the analyses on the new set of calibrations and with updated outgroup sequences

## Divergence time estimation (sections 2.7, 3.7)

### **./Dating/**

- Completely overhauled; no files in common with the original directory. In general, the latter contained the data, configuration files, and results from the four different MCMCTree analyses (strategies 1–4), as well as several files from unsuccessful attempts to perform BEAST 1.10 and BEAST 2.6 analyses. The new directory contains the data, configuration files, and results from the treePL analyses, and from the unsuccessful attempt (described in detail in Appendix A) to perform a partitioned, autocorrelated-rates MCMCTree analysis on the complete revised supermatrix.

# Macroevolutionary rate estimation (sections 2.8, 3.8)

`./BAMM/Cform_BAMM_analyses.Rmd`  
`./BAMM/Cform_BAMM_analyses.html`

- Replaced after rerunning BAMM on the new (treePL-generated) time tree.

`./BAMM/pbdb_data.csv`  
`./BAMM/pbdb_data_no_metadata.csv`

- Replaced with updated fossil occurrence data; the original file was downloaded on 2022-04-22 and contained 388 stratigraphically unique occurrences after filtering; the new one was downloaded on 2022-05-26 and contains stratigraphically unique occurrences after filtering.

`./BAMM/credibleshiftset.pdf`

- Removed after rerunning BAMM on the new time tree. The new 95% credible set contains too many distinct configurations (506 rather than 22) to be visualized in this way, so we did not recreate this figure.

`./BAMM/autocorr_BAMM_priors.txt`  
`./BAMM/autocorr_chain_swap1.txt`  
`./BAMM/autocorr_chain_swap2.txt`  
`./BAMM/autocorr_control.txt`  
`./BAMM/autocorr_event_data_comb.txt`  
`./BAMM/autocorr_event_data1.txt`  
`./BAMM/autocorr_event_data2.txt`  
`./BAMM/autocorr_out_comb.txt`  
`./BAMM/autocorr_out1.txt`  
`./BAMM/autocorr_out2.txt`  
`./BAMM/autocorr_rates.tre`  
`./BAMM/autocorr_runInfo1.txt`  
`./BAMM/autocorr_runInfo2.txt`  
`./BAMM/indep_BAMM_priors.txt`  
`./BAMM/indep_chain_swap1.txt`  
`./BAMM/indep_chain_swap2.txt`  
`./BAMM/indep_control.txt`  
`./BAMM/indep_event_data_comb.txt`  
`./BAMM/indep_event_data1.txt`  
`./BAMM/indep_event_data2.txt`  
`./BAMM/indep_out_comb.txt`  
`./BAMM/indep_out1.txt`  
`./BAMM/indep_out2.txt`  
`./BAMM/indep_rates.tre`  
`./BAMM/indep_runInfo1.txt`  
`./BAMM/indep_runInfo2.txt`

`./BAMM/BAMM_priors.txt`  
`./BAMM/cform_chain_swap1.txt`  
`./BAMM/cform_chain_swap2.txt`  
`./BAMM/cform_control.txt`  
`./BAMM/cform_event_data_comb.txt`  
`./BAMM/cform_event_data1.txt`  
`./BAMM/cform_event_data2.txt`

[./BAMM/cform\\_out\\_comb.txt](#)  
[./BAMM/cform\\_out1.txt](#)  
[./BAMM/cform\\_out2.txt](#)  
[./BAMM/cform\\_runInfo1.txt](#)  
[./BAMM/cform\\_runInfo2.txt](#)  
[./BAMM/ICS\\_colors.csv](#)  
[./BAMM/treepl.tre](#)

- Replaced after rerunning BAMM on the new time tree.

# Topological and divergence time comparisons with the Jetz et al. (2012) pseudoposterior (sections 3.3, 3.4, 4.3)

[./JetzCformTaxonomy.csv](#)

[./Megaphylogenies/JetzCformTaxonomy.csv](#)

- Moved to the appropriate folder.

[./Megaphylogenies/taxon\\_dictionary.csv](#)

- A new synonym dictionary that partially replaces the old ./Individual\_loci/Taxonomy\_FINAL.csv.

[./Megaphylogenies/Topology\\_comparisons.Rmd](#)

[./Megaphylogenies/Topology\\_comparisons.html](#)

[./Megaphylogenies/Tree\\_comparisons.Rmd](#)

[./Megaphylogenies/Tree\\_comparisons.html](#)

- Changed after rerunning the concatenated, total-evidence, and dating analyses, and renamed to better reflect the fact that the comparisons in questions involve not just topologies but also divergence times.



# Figures from the main manuscript (Figures 1–7) and the graphical abstract

[./Figs/](#)

- A new dedicated folder for the data and standalone scripts used to generate several of the figures included in the main manuscript, as well as the figures themselves.

[./Figure\\_1.pdf](#)

[./figure1\\_plotter.R](#)

[./Prev\\_date\\_estimates.csv](#)

[./Figs/Figure\\_1.pdf](#)

[./Figs/figure1\\_plotter.R](#)

[./Figs/Prev\\_date\\_estimates.csv](#)

- Moved to the new folder; the script was modified accordingly to recognize the new path.

[./Figure\\_3.pdf](#)

[./Figs/Figure\\_3.pdf](#)

[./Figure\\_4.pdf](#)

[./Figs/Figure\\_4.pdf](#)

[./Figs/Figure\\_5.pdf](#)

[./Figure\\_5.pdf](#)

[./Figure\\_5pg1.pdf](#)

[./Figure\\_5pg2.pdf](#)

[./Figure\\_5\\_AR.pdf](#)

[./Figs/Figure\\_6\\_base.pdf](#)

- The former Figure 5 corresponds to the new Figure 6, and since the new chronogram it depicts has been produced using treePL rather than MCMCTree, there are no longer two versions of it corresponding to different clock models.

[./Figure\\_6.pdf](#)

[./Figure\\_7.pdf](#)

[./figure6\\_plotter.R](#)

[./figure7\\_plotter.R](#)

- These figures have no counterpart in the revised manuscript.

[./Figure\\_8.pdf](#)

[./Figs/Figure\\_7.pdf](#)

- The former Figure 8 corresponds to the new Figure 7.

[./figure3\\_plotter.R](#)

[./Figs/figure3\\_plotter.R](#)

[./figure4\\_plotter.R](#)

[./Figs/figure4\\_plotter.R](#)

**./figure5\_AR\_plotter.R**  
**./figure5\_plotter.R**  
**./Figs/figure6\_plotter.R**

- The former Figure 5 corresponds to the new Figure 6.

**./Manuscript/graphical\_abstract.R**  
**./Figs/graphical\_abstract.R**

- Changed to use the new treePL rather than the old MCMCTree chronogram, and moved into this folder along with other figure-generating scripts.

## Figures from Appendix A (Figures A.2–A.37)

**[./Supp\\_figs/figs2&3\\_plotter.R](#)**

- No longer needed after dropping the ASTRAL analysis.

**[./Supp\\_figs/figs4&5\\_plotter.R](#)**

**[./Supp\\_figs/SuppFigs31&32\\_plotter.R](#)**

- Changed the script used to plot the maximum-likelihood tree.

**[./Supp\\_figs/figs6&7\\_plotter.R](#)**

**[./Supp\\_figs/SuppFigs33&34\\_plotter.R](#)**

- Changed the script used to plot the ExaBayes tree.

**[./Supp\\_figs/figs11\\_plotter.R](#)**

**[./Supp\\_figs/SuppFig35\\_plotter.R](#)**

**[./Supp\\_figs/SuppFig36\\_plotter.R](#)**

- Changed the script used to compare the total-evidence (TE) and evolutionary placement algorithm (EPA) trees. Now broken into two scripts used to produce two separate figures: one comparing the TE tree against the split-scaffold-edges version of the EPA (SSE-EPA), and the other comparing it against the group-together version (GT-EPA).

**[./Supp\\_figs/figs12\\_plotter.R](#)**

- No longer needed after dropping the MCMCTree analyses.

**[./Supp\\_figs/S1.pdf](#)**

**[./Supp\\_figs/A2.pdf](#)**

- Changed and renamed to what it is actually labeled as in Appendix A.

**[./Supp\\_figs/S2.pdf](#)**

**[./Supp\\_figs/S3.pdf](#)**

- No longer needed after dropping the ASTRAL analysis.

**[./Supp\\_figs/A3.pdf](#)**

**[./Supp\\_figs/A4.pdf](#)**

**[./Supp\\_figs/A5.pdf](#)**

**[./Supp\\_figs/A6.pdf](#)**

**[./Supp\\_figs/A7.pdf](#)**

**[./Supp\\_figs/A8.pdf](#)**

**[./Supp\\_figs/A9.pdf](#)**

**[./Supp\\_figs/A10.pdf](#)**

**[./Supp\\_figs/A11.pdf](#)**

**[./Supp\\_figs/A12.pdf](#)**

**[./Supp\\_figs/A13.pdf](#)**

**[./Supp\\_figs/A14.pdf](#)**

**[./Supp\\_figs/A15.pdf](#)**

**[./Supp\\_figs/A16.pdf](#)**

**[./Supp\\_figs/A17.pdf](#)**

[./Supp\\_figs/A18.pdf](#)  
[./Supp\\_figs/A19.pdf](#)  
[./Supp\\_figs/A20.pdf](#)  
[./Supp\\_figs/A21.pdf](#)  
[./Supp\\_figs/A22.pdf](#)  
[./Supp\\_figs/A23.pdf](#)  
[./Supp\\_figs/A24.pdf](#)  
[./Supp\\_figs/A25.pdf](#)  
[./Supp\\_figs/A26.pdf](#)  
[./Supp\\_figs/A27.pdf](#)  
[./Supp\\_figs/A28.pdf](#)  
[./Supp\\_figs/A29.pdf](#)  
[./Supp\\_figs/A30.pdf](#)

- Newly added figures depicting individual gene trees, as well as the tree inferred from Strauch's (1978) morphological data.

[./Supp\\_figs/S4.pdf](#)  
[./Supp\\_figs/A31.pdf](#)

- Changed and renamed to what it is actually labeled as in Appendix A.

[./Supp\\_figs/S5.pdf](#)  
[./Supp\\_figs/A32.pdf](#)

- Changed and renamed to what it is actually labeled as in Appendix A.

[./Supp\\_figs/S6.pdf](#)  
[./Supp\\_figs/A33.pdf](#)

- Changed and renamed to what it is actually labeled as in Appendix A.

[./Supp\\_figs/S7.pdf](#)  
[./Supp\\_figs/A34.pdf](#)

- Changed and renamed to what it is actually labeled as in Appendix A.

[./Supp\\_figs/S11.pdf](#)  
[./Supp\\_figs/A35.pdf](#)  
[./Supp\\_figs/A36.pdf](#)

- The former total-evidence (TE) vs. evolutionary placement algorithm comparison (EPA) tree comparison now split into two figures with TE vs. SSE-EPA and TE vs. GT-EPA comparisons, respectively.

[./Supp\\_figs/S8.pdf](#)  
[./Supp\\_figs/A37.pdf](#)

- Changed and renamed to what it is actually labeled as in Appendix A.

[./Supp\\_figs/figs12\\_plotter.R](#)  
[./Supp\\_figs/S9.pdf](#)  
[./Supp\\_figs/S10.pdf](#)  
[./Supp\\_figs/S12.pdf](#)

- No longer needed after dropping the MCMCTree analyses.