Genome Assemblies

Genome assemblies are not expected to satisfy all of these areas, but rather it is necessary to generally demonstrate high quality genomes that will be strong resources for broader studies for the community.

It is now policy at Molecular Ecology Resources for genome assemblies and all data associated with an assembly to be made available for the editor and reviewers at time of submission. This includes FASTA assembly files and raw read data such as RNAseq data. Please detail how editors and reviewers can access this data in the Cover Letter.

* Were whole genome shotgun libraries sequenced at high coverage for the target species (provide in terms of "X coverage ")?

Yes. 128X

* Did the study generate a pan-genome assembly from several individual samples?

NO

* Were 'long-read' libraries sequenced and included in the genome assembly (specify type and coverage)?

Yes. Nanopore (10X)

* What are the basic assembly statistics: genome size, percent assembled, # contigs, contig N50, #scaffolds, scaffold N50?

genome size: 1.22 Gbp

#scaffolds: 4,149

N50: 2.1 Mb

* Was mapping of some form (genetic, physical, optical) incorporated to order scaffolds?

NO

* Were scaffolds anchored to chromosome positions, and if so, what proportion of the genome is anchored to chromosomes?

No

* Were analyses included that asses the quality of the genome assembly (genomescope, or busco)?

BUSCO

* Were RNAseq libraries sequenced to assemble transcriptomes and annotate genes?

Yes

* Is the genome assembly publicly available through a web-based genome browser?

From NCBI

* How is the genome assembly in this manuscript useful for broader research in the field of molecular ecology?
* Please specify the research community that would use this genome resource. Feel free to include names of laboratories.

Our reference genome will be of a great interest to researchers working on the development of genetic tools and strategies for conservation efforts in critically endangered species, as well as to molecular ecology researchers interested in avian diversification and evolution. For instance, our present analyses resolve current uncertainties into the Procellariiformes order phylogenetic relationships, and uncover a set of candidate genes that may have played an important role into the adaptation to a pelagic lifestyle of Procellariiformes.