

GENOME SEQUENCING

The Complete Genome Sequence of *Colaptes auratus*, the Northern Flicker

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Biodiversity Genomes

We present the complete genome sequence of *Colaptes auratus*, the Northern Flicker.

Methods

Feather shaft pulp from a naturally molted primary wing feather from a wild individual was used for this study. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard protocol. A paired-end sequencing library was constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The library was sequenced on an Illumina HiSeq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic v0.33 (Bolger et al. 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras et al. 2021).

Data Availability

taxname	accession
<i>Colaptes auratus</i>	JBXGFY000000000

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