

GENOME SEQUENCING

# The Complete Genome Sequence of *Haemulon aurolineatum* (Haemulidae, Lutjaniformes), the Tomtate Grunt

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## Biodiversity Genomes

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We present the whole genome sequence of *Haemulon aurolineatum*. Illumina paired-end reads were assembled by a de novo method followed by a finishing step. The raw and assembled data are publicly available via GenBank: Sequence Read Archive (SRR28478403) and assembled genome (JBCAUF000000000).

## Methods

A single wild-collected specimen was used for sequencing. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. 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 Hi-Seq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich, Nurk, Antipov, et al. 2012) followed by a finishing step using Zanfona v1.0 (Kieras 2021) to make additional contig joins based on conserved regions in related species.

## Data availability

Raw and assembled data are publicly available via GenBank.

Raw genome data: SRR28478403

Assembled genome: JBCAUF000000000

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