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GENOME SEQUENCING

The complete genome sequence of Mnemiopsis leidyi (Bolinopsidae, Lobata)

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Biodiversity Genomes

The complete genome sequence of Mnemiopsis leidyi (Bolinopsidae, Lobata)

Methods

Tissue from a single, wild-collected individual was used for this study. DNA extraction was performed using the Qiagen DNEasy genomic extraction kit using the standard process. Paired-end sequencing libraries were constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger et al. 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras et al. 2021).

Results and Data Availability

taxname	accession	specimen
Mnemiopsis leidyi	JAPFFN000000000	EE04

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