

## GENOME SEQUENCING

# The Complete Genome Sequence of *Verbascum thapsus* (Scrophulariaceae, Lamiales), the Common Mullein

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## Biodiversity Genomes

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*Verbascum thapsus* is a biennial plant native to Europe, northern Africa, and Asia and introduced in the Americas and Australia. We present the whole genome sequence of this species. 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 (SRR18183247) and assembled genome (JAOXOC000000000).

## Introduction

*Verbascum thapsus*, or the Common Mullein, is a biennial plant that can grow to 2 m tall or more. Its small, yellow flowers are densely grouped on a tall stem, which grows from a large rosette of leaves. It grows in a wide variety of habitats but prefers well-lit areas and can grow from long-lived seeds that persist in the soil. It is a common weedy plant that spreads by prolifically producing seeds and has become invasive in temperate world regions.

## 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 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.

## Results

The genome assembly yielded a total sequence length of 560,917,718 bp.

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## Data availability

Raw and assembled data are publicly available via GenBank.

## **RAW GENOME DATA**

<https://www.ncbi.nlm.nih.gov/sra/?term=SRR18183247>

## **ASSEMBLED GENOME**

<https://www.ncbi.nlm.nih.gov/nucore/JAOXOC000000000>

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