

# Resource Summary Report

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## Supernova assembler

RRID:SCR\_016756

Type: Tool

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### Proper Citation

Supernova assembler (RRID:SCR\_016756)

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### Resource Information

**URL:** <https://support.10xgenomics.com/de-novo-assembly/software/overview/latest/welcome>

**Proper Citation:** Supernova assembler (RRID:SCR\_016756)

**Description:** Software to generate phased, whole genome de novo assemblies from a Chromium prepared library. Used to create true diploid de novo assemblies and can separate homologous chromosomes over long distances.

**Resource Type:** data analysis software, data processing software, sequence analysis software, software application, software resource

**Keywords:** generate, phased, whole, genome, de novo, assembly, Chromium, prepared, library

**Availability:** Free, Available for download, Freely available

**Resource Name:** Supernova assembler

**Resource ID:** SCR\_016756

**Alternate URLs:** <https://support.10xgenomics.com/de-novo-assembly/software/pipelines/latest/installation>

**Record Creation Time:** 20220129T080332+0000

**Record Last Update:** 20260912T195844+0000

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### Ratings and Alerts

No rating or validation information has been found for Supernova assembler.

No alerts have been found for Supernova assembler.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 34 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Chen G, et al. (2026) Draft assemblies for 177 bird species enhance genus-level coverage. *GigaScience*, 15.

Azam S, et al. (2025) Advancing the Indian cattle pangenome: characterizing non-reference sequences in *Bos indicus*. *Journal of animal science and biotechnology*, 16(1), 21.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia ?? blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Silver LW, et al. (2024) A reference genome for the eastern bettong ( *Bettongia gaimardi*). *F1000Research*, 13, 1544.

Jiang L, et al. (2024) The Bioinformatic Applications of Hi-C and Linked Reads. *Genomics, proteomics & bioinformatics*, 22(4).

Niu X, et al. (2024) The genome assembly and annotation of the white-lipped tree pit viper *Trimeresurus albolabris*. *GigaByte (Hong Kong, China)*, 2024, gigabyte106.

Lu L, et al. (2023) Comparative genomics revealed drastic gene difference in two small Chinese perches, *Siniperca undulata* and *S. obscura*. *G3 (Bethesda, Md.)*, 13(7).

Wang J, et al. (2023) The genome assembly and annotation of the Oriental rat snake *Ptyas mucosa*. *GigaByte (Hong Kong, China)*, 2023, gigabyte92.

Niu X, et al. (2023) Genome assembly and annotation of the Brown-Spotted Pit viper *Protobothrops mucrosquamatus*. *GigaByte (Hong Kong, China)*, 2023, gigabyte97.

Wang J, et al. (2023) The genome assembly and annotation of the Chinese cobra, *Naja atra*. *GigaByte (Hong Kong, China)*, 2023, gigabyte99.

Liu B, et al. (2023) The genome assembly and annotation of the many-banded krait, *Bungarus multicinctus*. *GigaByte (Hong Kong, China)*, 2023, gigabyte82.

Fan J, et al. (2023) Genome assembly and annotation of the king ratsnake, *Elaphe carinata*. *GigaByte (Hong Kong, China)*, 2023, gigabyte101.

Wang X, et al. (2023) Genome assembly and annotation of the Sharp-nosed Pit Viper *Deinagkistrodon acutus* based on next-generation sequencing data. *GigaByte (Hong Kong, China)*, 2023, gigabyte88.

Wang H, et al. (2022) Chromosome-level assembly and annotation of the blue catfish *Ictalurus furcatus*, an aquaculture species for hybrid catfish reproduction, epigenetics, and heterosis studies. *GigaScience*, 11.

Winter S, et al. (2022) A Chromosome-Scale Genome Assembly of the Okapi (*Okapia johnstoni*). *The Journal of heredity*, 113(5), 568.

De Silva NP, et al. (2022) Genome assembly of an Australian native grass species reveals a recent whole-genome duplication and biased gene retention of genes involved in stress response. *GigaScience*, 12.

Li C, et al. (2021) Bicolor angelfish (*Centropyge bicolor*) provides the first chromosome-level genome of the Pomacanthidae family. *GigaByte* (Hong Kong, China), 2021, gigabyte32.

Pavese V, et al. (2021) Whole-genome assembly of *Corylus avellana* cv "Tonda Gentile delle Langhe" using linked-reads (10X Genomics). *G3* (Bethesda, Md.), 11(7).

Cai L, et al. (2021) Deeply Altered Genome Architecture in the Endoparasitic Flowering Plant *Sapria himalayana* Griff. (Rafflesiaceae). *Current biology : CB*, 31(5), 1002.

Xu M, et al. (2021) Accurate haplotype-resolved assembly reveals the origin of structural variants for human trios. *Bioinformatics* (Oxford, England), 37(15), 2095.