

Resource Summary Report

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Supernova assembler

RRID:SCR_016756

Type: Tool

Proper Citation

Supernova assembler (RRID:SCR_016756)

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, software application, software resource, sequence analysis software, data processing software

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: 20260801T190541+0000

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 33 mentions in open access literature.

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

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.

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

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

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).

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

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

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 Oriental rat snake *Ptyas mucosa*. *GigaByte (Hong Kong, China)*, 2023, gigabyte92.

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

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.

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).

Coimbra RTF, et al. (2021) Whole-genome analysis of giraffe supports four distinct species. *Current biology : CB*, 31(13), 2929.

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

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

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.