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

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

Funding:

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: 20250416T063805+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 31 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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

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.

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

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.

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.

Zhang R, et al. (2021) Chromosome-level genome assembly of the humpback puffer, Tetraodon palembangensis. GigaByte (Hong Kong, China), 2021, gigabyte17.

Batra SS, et al. (2020) Accurate assembly of the olive baboon (Papio anubis) genome using long-read and Hi-C data. GigaScience, 9(12).