Resource Summary Report

Generated by RRID on Apr 28, 2025

TGS-GapCloser

RRID:SCR_017633
Type: Tool

Proper Citation

TGS-GapCloser (RRID:SCR_017633)

Resource Information

URL: https://github.com/BGI-Qingdao/TGS-GapCloser

Proper Citation: TGS-GapCloser (RRID:SCR_017633)

Description: Software tool that uses long reads to enhance genome assembly. Fast and accurate gap closing software tool that uses low coverage of error-prone long reads generated by third generation sequence techniques (Pacbio, Oxford Nanopore, etc.) or preassembled contigs for large genomes.

Resource Type: data processing software, software application, software resource

Keywords: Error, prone, third, generation, sequencing, long, read, gap, closing, genome, assembly, contig, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: TGS-GapCloser

Resource ID: SCR_017633

Alternate IDs: biotools:tGS-GapCloser

Alternate URLs: https://bio.tools/TGS-GapCloser

License: GNU General Public License v3.0

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250428T054057+0000

Ratings and Alerts

No rating or validation information has been found for TGS-GapCloser.

No alerts have been found for TGS-GapCloser.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Wolf M, et al. (2024) Near chromosome-level and highly repetitive genome assembly of the snake pipefish Entelurus aequoreus (Syngnathiformes: Syngnathidae). GigaByte (Hong Kong, China), 2024, gigabyte105.

McEvoy SL, et al. (2024) The reference genome of an endangered Asteraceae, Deinandra increscens subsp. villosa, endemic to the Central Coast of California. G3 (Bethesda, Md.), 14(8).

Wang X, et al. (2024) Telomere-to-telomere and gap-free genome assembly of a susceptible grapevine species (Thompson Seedless) to facilitate grape functional genomics. Horticulture research, 11(1), uhad260.

Hong L, et al. (2024) Construction and analysis of telomere-to-telomere genomes for 2 sweet oranges: Longhuihong and Newhall (Citrus sinensis). GigaScience, 13.

Nebenführ M, et al. (2024) High-speed whole-genome sequencing of a Whippet: Rapid chromosome-level assembly and annotation of an extremely fast dog's genome. GigaByte (Hong Kong, China), 2024, gigabyte134.

Wang YS, et al. (2024) Chromosome-level genome assemblies of two littorinid marine snails indicate genetic basis of intertidal adaptation and ancient karyotype evolved from bilaterian ancestors. GigaScience, 13.

Flack N, et al. (2024) The genome of Przewalski's horse (Equus ferus przewalskii). bioRxiv : the preprint server for biology.

Bisht MS, et al. (2024) Genome of the most noxious weed water hyacinth (Eichhornia crassipes) provides insights into plant invasiveness and its translational potential. iScience,

27(9), 110698.

Bai M, et al. (2024) The telomere-to-telomere (T2T) genome of Peucedanum praeruptorum Dunn provides insights into the genome evolution and coumarin biosynthesis. GigaScience, 13.

Li Q, et al. (2024) The Cissus quadrangularis genome reveals its adaptive features in an arid habitat. Horticulture research, 11(4), uhae038.

Cao S, et al. (2024) Gapless genome assembly and epigenetic profiles reveal gene regulation of whole-genome triplication in lettuce. GigaScience, 13.

Winter S, et al. (2023) A chromosome-scale high-contiguity genome assembly of the cheetah (Acinonyx jubatus). The Journal of heredity.

Winter S, et al. (2023) A chromosome-scale reference genome assembly of the great sand eel, Hyperoplus lanceolatus. The Journal of heredity, 114(2), 189.

Guo X, et al. (2023) The genome of Acorus deciphers insights into early monocot evolution. Nature communications, 14(1), 3662.

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

Schall PZ, et al. (2023) Genome-wide methylation patterns from canine nanopore assemblies. G3 (Bethesda, Md.), 13(11).

Young ND, et al. (2022) Nuclear genome of Bulinus truncatus, an intermediate host of the carcinogenic human blood fluke Schistosoma haematobium. Nature communications, 13(1), 977.

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

Wang ZF, et al. (2022) Genome assembly of Musa beccarii shows extensive chromosomal rearrangements and genome expansion during evolution of Musaceae genomes. GigaScience, 12.

Natarajan P, et al. (2021) A reference-grade genome identifies salt-tolerance genes from the salt-secreting mangrove species Avicennia marina. Communications biology, 4(1), 851.