

Resource Summary Report

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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: software resource, software application, data processing software

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

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: 20260731T043016+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 35 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Lin C, et al. (2025) Bifidobacterium species associated with breastfeeding alleviate neonatal hyperbilirubinaemia via the gut microbiota-?-linolenic and linoleic acid metabolism-enterohepatic circulation axis. *Microbiome*, 13(1), 187.

Hartley GA, et al. (2025) Centromeric transposable elements and epigenetic status drive karyotypic variation in the eastern hoolock gibbon. *Cell genomics*, 5(4), 100808.

Dubocanin D, et al. (2025) Conservation of dichromatin organization along regional centromeres. *Cell genomics*, 5(4), 100819.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.

Nebenführ M, et al. (2025) Mediterranean monk seal (*Monachus monachus*) and leopard seal (*Hydrurga leptonyx*) de novo genomes to study the demographic history and genetic diversity of southern seals. *BMC biology*, 23(1), 102.

Winter S, et al. (2025) Chromosome-Level genome assembly and transcriptome analysis of the ural owl, *Strix uralensis* Pallas, 1771. *The Journal of heredity*.

Guang X, et al. (2025) Telomere-to-telomere African wild rice (*Oryza longistaminata*) reference genome reveals segmental and structural variation. *GigaScience*, 14.

Guo Q, et al. (2025) A near-complete genome assembly of the bearded dragon *Pogona vitticeps* provides insights into the origin of *Pogona* sex chromosomes. *GigaScience*, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.

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).

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.

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

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

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.

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.

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.

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