

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: data processing software, software application, software resource

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: 20260821T194122+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 45 mentions in open access literature.

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

Jiang K, et al. (2026) Telomere-to-telomere-level genome assembly and annotation of the Zi goose *Anser cygnoides*. *Scientific data*, 13(1).

Chen H, et al. (2026) A telomere-to-telomere genome assembly of *Nymphaea minima* provides details into the developmental transcriptome atlas and adaptive regulatory mechanisms. *Horticulture research*, 13(6), uhag085.

Duan M, et al. (2026) Genomic Signatures Underlying Environmental Adaptation and Reproductive Traits in the Tibetan Pig. *Animals : an open access journal from MDPI*, 16(3).

Liu J, et al. (2026) Telomere-to-Telomere Genome Assembly of Two Hemicultur Species Provide Insights into the Genomic and Morphometric Bases of Adaptation to Flow Velocity. *Biomolecules*, 16(1).

Kou Y, et al. (2026) Haplotype-resolved T2T genome and population resequencing provide insights into the domestication and mogrosin biosynthesis of *Siraitia grosvenorii* (Cucurbitaceae). *Horticulture research*, 13(7), uhag103.

Zhang X, et al. (2026) A telomere-to-telomere gap-free genome assembly of the protandrous maroon clownfish (*Premnas biaculeatus*). *Scientific data*, 13(1), 220.

Plasil M, et al. (2026) A chromosome-level genome assembly of the snow leopard, *Panthera uncia*. *The Journal of heredity*, 117(2), 272.

Ragosta MC, et al. (2026) The modulation of AUF1 regulates the R-loop resolution activating the immune response in DDR. *iScience*, 29(6), 115900.

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.

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

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

Zhao B, et al. (2025) Chromosome-level genome assembly of the coral grouper, *Epinephelus corallicola* and its evolutionary insights into Eupercaria. BMC genomics, 26(1), 832.

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

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

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.

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.

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

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.