

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: 20260905T133054+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 [Kravitz](#) .

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 Hemicultured 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.

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.

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.

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.

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.

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.