

Resource Summary Report

Generated by [kravitz2](#) on Sep 1, 2026

quarTeT

RRID:SCR_025258

Type: Tool

Proper Citation

quarTeT (RRID:SCR_025258)

Resource Information

URL: <http://www.atcgn.com:8080/quarTeT/home.html>

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Description: Web toolkit for studies of large scale T2T genomes. Collection of tools designed for T2T genome assembly and characterization, including reference guided genome assembly, ultra long sequence based gap filling, telomere identification, and de novo centromere prediction. Includes four modules: AssemblyMapper, GapFiller, TeloExplorer, and CentroMiner. Modules can be used alone or in combination with each other for T2T genome assembly and characterization.

Synonyms: quar Telomere-To-Telomere Toolkit

Resource Type: software resource, source code, web application

Defining Citation: [PMID:37560017](#)

Keywords: Telomere-To-Telomere genomes studies, guided genome assembly, ultra long sequence based gap filling, telomere identification, de novo centromere prediction, large scale T2T genomes, assemble and analyse multiple high quality genomes, highly repetitive regions in genomes,

Funding: National Natural Science Foundation of China

Availability: Free, Available for download, Freely available

Resource Name: quarTeT

Resource ID: SCR_025258

Alternate URLs: <https://github.com/aaranyue/quarTeT>

Record Creation Time: 20240412T053246+0000

Record Last Update: 20260829T183359+0000

Ratings and Alerts

No rating or validation information has been found for quarTeT.

No alerts have been found for quarTeT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Xu M, et al. (2026) Telomere to telomere level genome assembly of the Yarkand hare (*Lepus yarkandensis*). *Scientific data*, 13(1).

Chen D, et al. (2026) Insights into karyotype evolution and flower color variation from the genome assembly of wallflower (*Erysimum cheiri*). *Plant physiology*, 200(4).

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Wang YY, et al. (2026) A Near Telomere-to-Telomere Genome of *Belamcanda chinensis* Provides Insights Into Genome Evolution and the Biosynthesis of Characteristic Isoflavones. *Plant biotechnology journal*, 24(6), 4285.

Jiu S, et al. (2026) Pangenome and resequencing analyses reveal flowering evolution and genetic control in *Cerasus*. *Nature communications*, 17(1).

Liu S, et al. (2026) The Genetically Homogeneous Population Structure of *Evynnis cardinalis* Along the Chinese Coast Revealed by Whole Genome Sequencing. *Evolutionary applications*, 19(5), e70272.

Franzo G, et al. (2026) Beyond labels: current sequencing data do not support standardized porcine circovirus 3 (PCV3) genotypes. *BMC veterinary research*, 22(1).

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). *GigaScience*, 15.

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

Xing TF, et al. (2025) Extensive Recombination Suppression and Genetic Degeneration of a Young ZW Sex Chromosome System in Halfbeak Fish. *Molecular biology and evolution*, 42(7).

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. 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.

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

Qin H, et al. (2025) The complete genome assembly of *Astragalus membranaceus*: enabling more accurate genetic research. GigaScience, 14.

Yang W, et al. (2025) A haplotype-resolved chromosomal-level genome assembly of *Oxalis articulata*. Scientific data, 12(1), 856.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. GigaScience, 14.

Zhu M, et al. (2025) A chromosomal-level genome assembly of *Kibakoganea sinica*, Bouchard, 2005 (Coleoptera: Scarabaeidae). Scientific data, 12(1), 1012.

Chen S, et al. (2025) Analysis of a near telomere-to-telomere genome of *Phellodendron amurense* reveals insights into berberine biosynthesis. Nature communications, 16(1), 11437.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. GigaScience, 14.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 231 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. GigaScience, 14.