

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

Merqury

RRID:SCR_022964

Type: Tool

Proper Citation

Merqury (RRID:SCR_022964)

Resource Information

URL: <https://github.com/marbl/merqury>

Proper Citation: Merqury (RRID:SCR_022964)

Description: Software toolkit for reference free quality, completeness, and phasing assessment for genome assemblies. Genome assembly quality evaluation based on k-mers.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:32928274](https://pubmed.ncbi.nlm.nih.gov/32928274/)

Keywords: reference free quality, completeness, phasing assessment, genome assemblies, quality evaluation based on k-mers

Funding: NHGRI

Availability: Free, Available for download, Freely available

Resource Name: Merqury

Resource ID: SCR_022964

License URLs: <https://github.com/marbl/merqury/blob/master/LICENSE>

Record Creation Time: 20221115T050204+0000

Record Last Update: 20260808T190535+0000

Ratings and Alerts

No rating or validation information has been found for Merqury.

No alerts have been found for Merqury.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 72 mentions in open access literature.

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

Möllmann JS, et al. (2026) A Chromosome-Level Genome Assembly and Resequencing Data Reveal Low DNA Methylation and Reduced Diversity in the Solitary Bee Pollinator *Osmia cornuta*. *Genome biology and evolution*, 18(1).

Xie X, et al. (2026) Chromosome-level genome assembly of mud snail *Bullacta exarata*. *Scientific data*, 13(1).

Doré G, et al. (2026) First draft genome of the decaploid species, *Ludwigia grandiflora* subsp. *hexapetala*, validated through gene expression. *GigaByte* (Hong Kong, China), 2026, gigabyte176.

Chen G, et al. (2026) Draft assemblies for 177 bird species enhance genus-level coverage. *GigaScience*, 15.

Huang Y, et al. (2026) The near-complete genome assembly of allotetraploid *Pennisetum purpureum* 'Purple' reveals the genetic and epigenetic landscape of centromeres. *Horticulture research*, 13(2), uhaf301.

Peng G, et al. (2025) The high-quality telomere-to-telomere genome assembly of the earthworm (*Amyntas aspergillum*). *Scientific data*, 12(1), 931.

Bian C, et al. (2025) A complete telomere-to-telomere chromosome-level genome assembly of X-ray tetra (*Pristella maxillaris*). *Scientific data*, 12(1), 496.

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte* (Hong Kong, China), 2025, gigabyte150.

Xia W, et al. (2025) Chromosome-level genome assembly and annotation of *Pterygoplichthys pardalis*. *Scientific data*, 12(1), 1091.

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

Li Z, et al. (2025) Phased high-quality genome of the gymnosperm Himalayan Yew assists in paclitaxel pathway exploration. *GigaScience*, 14.

Bian C, et al. (2025) A telomere-to-telomere chromosome-scale genome assembly of glass catfish (*Kryptopterus vitreolus*). *Scientific data*, 12(1), 483.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin.

GigaScience, 14.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). GigaScience, 14.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. GigaScience, 14.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. GigaScience, 14.

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. *Frontiers in zoology*, 22(1), 7.

Simmons NB, et al. (2025) The genome sequence of *Glossophaga mutica* (Chiroptera, Phyllostomidae, Glossophaginae; Merriam, 1898). *Wellcome open research*, 10, 174.

Wang F, et al. (2025) Analysis of the *Rehmannia chingii* genome identifies RcCYP72H7 as an epoxidase in iridoid glycoside biosynthesis. *Nature communications*, 16(1), 6035.

Chrysostomakis I, et al. (2025) A high-quality reference genome for the Ural Owl (*Strix uralensis*) enables investigations of cell cultures as a genomic resource for endangered species. GigaScience, 14.