

Resource Summary Report

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Purge_haplotigs

RRID:SCR_017616

Type: Tool

Proper Citation

Purge_haplotigs (RRID:SCR_017616)

Resource Information

URL: https://bitbucket.org/mroachawri/purge_haplotigs/src

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Description: Pipeline for reassigning primary contigs that should be labelled as haplotigs. Used for third generation sequencing based assemblies to automate reassignment of allelic contigs, and to assist in manual curation of genome assemblies.

Resource Type: software resource, software application, data processing software

Defining Citation: [PMID:30497373](#)

Keywords: Reassigning, primary, contig, label, haplotig, third, generation, sequencing, assembly, allelic, curation, genome, alignment

Availability: Free, Available for download, Freely available

Resource Name: Purge_haplotigs

Resource ID: SCR_017616

License: MIT licence

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260804T043705+0000

Ratings and Alerts

No rating or validation information has been found for Purge_haplotigs.

No alerts have been found for Purge_haplotigs.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

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

Weng YM, et al. (2024) Evolutionary genomics of three agricultural pest moths reveals rapid evolution of host adaptation and immune-related genes. *GigaScience*, 13.

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.

Yin D, et al. (2024) Telomere-to-telomere gap-free genome assembly of the endangered Yangtze finless porpoise and East Asian finless porpoise. *GigaScience*, 13.

Shen X, et al. (2024) Exploring the cobia (*Rachycentron canadum*) genome: unveiling putative male heterogametic regions and identification of sex-specific markers. *GigaScience*, 13.

Peng D, et al. (2024) The telomere-to-telomere (T2T) genome provides insights into the evolution of specialized centromere sequences in sandalwood. *GigaScience*, 13.

Herliana L, et al. (2023) A chromosome-level genome assembly of *Plantago ovata*. *Scientific reports*, 13(1), 1528.

Schall PZ, et al. (2023) Genome-wide methylation patterns from canine nanopore assemblies. *G3 (Bethesda, Md.)*, 13(11).

Patel S, et al. (2023) Genome assembly of the hybrid grapevine *Vitis* 'Chambourcin'. *GigaByte (Hong Kong, China)*, 2023, gigabyte84.

Kim J, et al. (2022) Comparative Genome and Evolution Analyses of an Endangered Stony Coral Species *Dendrophyllia cribrosa* Near Dokdo Islands in the East Sea. *Genome biology and evolution*, 14(9).

Cuello C, et al. (2022) An updated version of the Madagascar periwinkle genome. *F1000Research*, 11, 1541.

Wang W, et al. (2020) The draft nuclear genome assembly of *Eucalyptus pauciflora*: a pipeline for comparing de novo assemblies. *GigaScience*, 9(1).