

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

[purge dups](#)

RRID:SCR_021173

Type: Tool

Proper Citation

purge dups (RRID:SCR_021173)

Resource Information

URL: https://github.com/dfguan/purge_dups

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Description: Software tool to purge haplotigs and overlaps in assembly based on read depth. Used for haplotypic duplication identification. Designed to remove haplotigs and contig overlaps in a de novo assembly based on read depth.

Synonyms: purge_dups

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

Keywords: haplotypic duplication identification, remove haplotigs overlap, remove contig overlaps, de novo assembly, read depth

Availability: Free, Available for download, Freely available

Resource Name: purge dups

Resource ID: SCR_021173

License: MIT License

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260813T055231+0000

Ratings and Alerts

No rating or validation information has been found for purge dups.

No alerts have been found for purge dups.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 503 mentions in open access literature.

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

Gumpert N, et al. (2026) Recurrent Immunogenic Neoantigens and Their Cognate T-cell Receptors in Treatment-Resistant Metastatic Prostate Cancer. *Cancer discovery*, 16(2), 250.

Zou R, et al. (2026) A chromosome-level genome assembly of *Cistanche deserticola* provides insights into its evolution and molecular mechanisms of parasitism. *Plant communications*, 7(1), 101581.

Chen Y, et al. (2026) Male and female genomes of millipede (*Trigoniulus corallinus*) and identification of sex chromosomes. *iScience*, 29(2), 114525.

Sari E, et al. (2026) Gene duplication, horizontal gene transfer, and trait trade-offs drive evolution of postfire resource acquisition in pyrophilous fungi. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2519152123.

Hu YF, et al. (2026) Chromosome-level genome assembly of *Phoebe chekiangensis*, an endemic and endangered tree in east Asia. *Scientific data*, 13(1).

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Li X, et al. (2026) A chromosome-level genome assembly of two-spotted cricket, *Gryllus bimaculatus* (Orthoptera: Grylloidea). *Scientific data*, 13(1).

Yue Z, et al. (2026) Chromosome-level genome assembly and annotation of the termite *Reticulitermes chinensis* Snyder. *Scientific data*, 13(1).

Fukui T, et al. (2026) Complete transition from chromosomal to cytoplasmic sex determination during prolonged *Wolbachia* symbiosis. *Nature communications*, 17(1), 104.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Zhou C, et al. (2026) Chromosome-level genome assembly of the deep-sea solemyid bivalve *Acharax haimaensis*. *Scientific data*, 13(1).

Zhang D, et al. (2026) The *Microtus fortis* chromosome-level genome: illuminating adaptive evolution and natural parasite immunity. *BMC genomics*, 27(1).

Latrofa MS, et al. (2026) Nuclear, mitochondrial, and Wolbachia endosymbiont genomes of *Onchocerca lupi*, Portugal. *mSphere*, 11(2), e0062525.

Bibi AC, et al. (2026) High-Quality Genome Assembly and Annotation of *Ceratonia siliqua* Provide Insights Into the Secondary Loss of Symbiotic Nitrogen Fixation. *Physiologia plantarum*, 178(1), e70803.

Xin H, et al. (2025) Jan and mini-Jan, a model system for potato functional genomics. *Plant biotechnology journal*, 23(4), 1243.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (*Leuciscidae*: *Phoxinus phoxinus*) provide evidence of haplotype diversity. *GigaScience*, 14.

Chen D, et al. (2025) An improved chromosome-level genome assembly of a deep-sea limpet (*Bathycyma lactea*). *Scientific data*, 12(1), 2039.

Koch TL, et al. (2025) From Neuropeptides to Toxins: Illuminating the Origins of Venom Complexity in Cone Snails. *bioRxiv : the preprint server for biology*.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. *GigaScience*, 14.

Fletcher C, et al. (2025) The genome sequence of the European smelt, *Osmerus eperlanus* (Linnaeus, 1758). *Wellcome open research*, 10, 118.