

Resource Summary Report

Generated by [dkNET](#) on Sep 3, 2026

[purge dups](#)

RRID:SCR_021173

Type: Tool

Proper Citation

purge dups (RRID:SCR_021173)

Resource Information

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

Proper Citation: purge dups (RRID:SCR_021173)

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 analysis software, data processing software, software application, software resource

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: 20260829T182749+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 [dkNET](#).

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.

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.

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

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.

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

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.

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

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.

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

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.

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

Crowley LM, et al. (2025) The genome sequence of the lesser earwig, *Labia minor* (Linnaeus, 1758). *Wellcome open research*, 10, 90.

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

Hutchinson F, et al. (2025) The genome sequence of the Maple Pug moth, *Eupithecia inturbata* (Hübner, 1817). *Wellcome open research*, 10, 141.

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

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).

Zhang C, et al. (2025) Chromosome-level genome assembly and annotation of *Gypsophila vaccaria*. *Scientific data*, 12(1), 818.