

Resource Summary Report

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HapHiC

RRID:SCR_026284

Type: Tool

Proper Citation

HapHiC (RRID:SCR_026284)

Resource Information

URL: <https://github.com/zengxiaofei/HapHiC>

Proper Citation: HapHiC (RRID:SCR_026284)

Description: Software fast, reference-independent, allele-aware scaffolding tool based on Hi-C data. Allele-aware scaffolding tool that uses Hi-C data to scaffold haplotype-phased genome assemblies into chromosome-scale pseudomolecules.

Resource Type: software application, software resource, source code

Defining Citation: [PMID:39103456](#)

Keywords: reference-independent, allele-aware scaffolding tool, performance on chromosome assignment, contig ordering and orientation, Hi-C data, scaffold haplotype-phased genome assemblies, chromosome-scale pseudomolecules,

Funding: National Natural Science Foundation of China

Availability: Free, Available for download, Freely available

Resource Name: HapHiC

Resource ID: SCR_026284

License: BSD-3-Clause

Record Creation Time: 20250115T053334+0000

Record Last Update: 20260904T001041+0000

Ratings and Alerts

No rating or validation information has been found for HapHiC.

No alerts have been found for HapHiC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Alves MN, et al. (2026) Haplotype-resolved genome of Citrus × sinensis 'Pera IAC', the most widely cultivated sweet orange in Brazil. Scientific data, 13(1).

Guan DL, et al. (2026) A chromosome-level genome assembly for the mulberry thrips Pseudodendrothrips mori (Thysanoptera: Thripidae). Scientific data, 13(1).

Lian Q, et al. (2026) A chromosome-level genome assembly of Hemibarbus maculatus. Scientific data, 13(1).

Wang M, et al. (2026) A near telomere-to-telomere chromosome-level genome assembly of Rhodiola yunnanensis (Crassulaceae). Scientific data, 13(1).

Vu DQ, et al. (2026) A chromosome-scale genome assembly of Tigridiopalma magnifica. Scientific data, 13(1).

Liu P, et al. (2026) Telomere-to-telomere genome of Stylosanthes guianensis uncovers symbiotic adaptation to phosphorus-deficient soils. Genome biology, 27(1).

Lin F, et al. (2026) A chromosome-level genome assembly of the panda loach (Yaoshania pachychilus). Scientific data, 13(1).

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

Zhang Y, et al. (2026) Chromosome-scale genome and lncRNA annotation of the Orange Baboon Tarantula (Pterinochilus murinus). Scientific data, 13(1), 191.

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.

Xiao PX, et al. (2026) Haplotype-resolved and near telomere-to-telomere assembly of the autotetraploid potato genome. Genome biology, 27(1).

Xu K, et al. (2026) Genome evolution and regulatory dynamics underlying salt stress tolerance in the halophyte Halogeton arachnoideus. Communications biology, 9(1).

Xie C, et al. (2026) Chromosomal fusions trigger rediploidization of autopolyploid genomes. Nature, 654(8119), 706.

Guan DL, et al. (2025) Chromosome-level genome assembly and annotation of the predatory stink bug *Eocanthecona furcellata*. *Scientific data*, 12(1), 1920.

Xiao TW, et al. (2025) Chromosome-scale genome assembly of *Sauvagesia rhodoleuca* (Ochnaceae) provides insights into its genome evolution and demographic history. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(5).

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

Hu X, et al. (2025) A Chromosome-scale Genome Assembly for the Broad-leaved Bamboo *Indocalamus tessellatus*. *Scientific data*, 12(1), 1706.

Bing H, et al. (2025) Chromosome-level genome assembly of the obligate cave loach *Troglonectes daqikongensis*. *Scientific data*, 12(1), 1918.

Moon SJ, et al. (2025) Haplotype-resolved chromosome-level genome sequence of *Elsholtzia splendens* (Nakai ex F.Maek.). *Scientific data*, 12(1), 827.

Deng WA, et al. (2025) Chromosome-level genome assembly and annotation of the pygmy grasshopper *Gibbotettix parvipulvillus*. *Scientific data*, 12(1), 1119.