

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: 20260829T183441+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).

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.

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).

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

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).

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.