

Resource Summary Report

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SyRI

RRID:SCR_023008

Type: Tool

Proper Citation

SyRI (RRID:SCR_023008)

Resource Information

URL: <https://github.com/schneebergerlab/syri>

Proper Citation: SyRI (RRID:SCR_023008)

Description: SyRI compares alignments between two chromosome level assemblies and identifies synteny and structural rearrangements.

Abbreviations: SyRI

Synonyms: Synteny and Rearrangement Identifier

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

Defining Citation: [DOI:10.1186/s13059-019-1911-0](https://doi.org/10.1186/s13059-019-1911-0)

Keywords: Synteny identifier, rearrangement identifier, compare alignments, two chromosome level assemblies, structural rearrangements

Funding: German Federal Ministry of Education and Research

Availability: Free, Available for download, Freely available

Resource Name: SyRI

Resource ID: SCR_023008

License: MIT license

Record Creation Time: 20221129T050146+0000

Record Last Update: 20260903T235902+0000

Ratings and Alerts

No rating or validation information has been found for SyRI.

No alerts have been found for SyRI.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 43 mentions in open access literature.

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

Sedaghatkish A, et al. (2026) A contamination-reduced genome of *Plasmodiophora brassicae* with comprehensive functional annotation. *BMC microbiology*, 26(1), 118.

Li R, et al. (2026) The chromosome-scale genome assembly and annotation of *Rosa bracteata* (Macartney Rose). *Scientific data*, 13(1).

Hoff SNK, et al. (2026) Rapid genome modifications including chromosomal fusions and large-scale inversions are key features in Arctic codfish species. *Genome biology*, 27(1).

Han D, et al. (2026) Pan-genome assembly of vine tea (*Nekemias grossedentata*) reveals structural variation in its dihydromyricetin biosynthesis diversity. *Horticulture research*, 13(2), uhaf307.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Zhao G, et al. (2026) Improved Longan Genome Assembly Reveals Insights Into Flowering Mechanisms. *Plant biotechnology journal*, 24(3), 1678.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 231 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

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.

Guang X, et al. (2025) Telomere-to-telomere African wild rice (*Oryza longistaminata*) reference genome reveals segmental and structural variation. *GigaScience*, 14.

Volpe E, et al. (2025) The reference genome of the human diploid cell line RPE-1. *Nature communications*, 16(1), 7751.

Ahmad B, et al. (2025) Mango pangenome reveals dramatic impacts of reference bias on population genomic analyses. *Horticulture research*, 12(9), uhaf166.

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

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. *GigaScience*, 14.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Wang Y, et al. (2024) Graph-Based Pangenome of *Actinidia chinensis* Reveals Structural Variations Mediating Fruit Degreening. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 11(28), e2400322.

Li K, et al. (2024) Haplotype-resolved T2T reference genomes for wild and domesticated accessions shed new insights into the domestication of jujube. *Horticulture research*, 11(5), uhae071.

Chen X, et al. (2024) Telomere-to-Telomere Haplotype-Resolved Genomes of *Agrocybe chaxingu* Reveals Unique Genetic Features and Developmental Insights. *Journal of fungi* (Basel, Switzerland), 10(9).

Chen XY, et al. (2024) Evolution of the Correlated Genomic Variation Landscape Across a Divergence Continuum in the Genus *Castanopsis*. *Molecular biology and evolution*, 41(9).

Talbot SC, et al. (2024) A first look at the genome structure of hexaploid "Mitcham" peppermint (*Mentha × piperita* L.). *G3* (Bethesda, Md.), 14(12).