

Resource Summary Report

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JupiterPlot

RRID:SCR_022961

Type: Tool

Proper Citation

JupiterPlot (RRID:SCR_022961)

Resource Information

URL: <https://github.com/JustinChu/JupiterPlot>

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Description: Software pipeline for generating Circos based genome assembly consistency plot given set of contigs relative to reference genome. Intended to visualize large scale translocations or missassemblies in draft assemblies, but it can also be useful when trying to show synteny between whole genomes. Circos based tool to visualize genome assembly consistency

Resource Type: software resource, software toolkit

Keywords: visualize large scale translocations, visualize large scale missassemblies in draft assemblies, visualize genome assembly consistency, consistency plot, set of contigs relative to reference genome,

Availability: Free, Available for download, Freely available

Resource Name: JupiterPlot

Resource ID: SCR_022961

License: GNU GPL v3

Record Creation Time: 20221115T050204+0000

Record Last Update: 20260725T191310+0000

Ratings and Alerts

No rating or validation information has been found for JupiterPlot.

No alerts have been found for JupiterPlot.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Bekavac M, et al. (2026) De novo genome assembly of Ansell's mole-rat (*Fukomys anelli*). *G3* (Bethesda, Md.), 16(1).

Canitz J, et al. (2025) Reference genome of the leopard seal (*Hydrurga leptonyx*), a Southern Ocean apex predator. *Frontiers in genetics*, 16, 1561273.

Manko E, et al. (2025) Novel zoonotic cases of *Plasmodium simium* from São Paulo with a reference genome of the Brazilian strain. *Scientific reports*, 15(1), 43703.

Deng Q, et al. (2025) Genetic Adaptation to Brackish Water and Spawning Season in European Cisco. *Molecular ecology*, 34(20), e70094.

Veith AC, et al. (2025) The draft genome of the Wisconsin Miniature SwineTM, a valuable biomedical research tool. *G3* (Bethesda, Md.), 15(6).

Winter S, et al. (2025) Chromosome-Level genome assembly and transcriptome analysis of the ural owl, *Strix uralensis* Pallas, 1771. *The Journal of heredity*.

Fuhrmann N, et al. (2024) Chromosome-Level Genome Assembly of the Viviparous Eelpout *Zoarces viviparus*. *Genome biology and evolution*, 16(8).

Benham PM, et al. (2024) Remarkably High Repeat Content in the Genomes of Sparrows: The Importance of Genome Assembly Completeness for Transposable Element Discovery. *Genome biology and evolution*, 16(4).

Ferrette BLDS, et al. (2023) Seascape Genomics and Phylogeography of the Sailfish (*Istiophorus platypterus*). *Genome biology and evolution*, 15(4).

Winter S, et al. (2023) A chromosome-scale high-contiguity genome assembly of the cheetah (*Acinonyx jubatus*). *The Journal of heredity*.

Sinha A, et al. (2023) Multiple lineages of nematode-Wolbachia symbiosis in supergroup F and convergent loss of bacterioferritin in filarial Wolbachia. *Genome biology and evolution*, 15(5).

Benham PM, et al. (2023) A highly contiguous genome assembly for the California quail (*Callipepla californica*). *The Journal of heredity*, 114(4), 418.

Benham PM, et al. (2023) A highly contiguous reference genome for the Steller's jay (*Cyanocitta stelleri*). *The Journal of heredity*, 114(5), 549.

Cho CH, et al. (2023) Genome-wide signatures of adaptation to extreme environments in red algae. *Nature communications*, 14(1), 10.

Eliason CM, et al. (2022) Genomic novelty within a "great speciator" revealed by a high-quality reference genome of the collared kingfisher (*Todiramphus chloris collaris*). *G3* (Bethesda, Md.), 12(11).

Louha S, et al. (2020) A High-Quality Genome Assembly of the North American Song Sparrow, *Melospiza melodia*. *G3* (Bethesda, Md.), 10(4), 1159.