

# Resource Summary Report

Generated by [NIF](#) on Aug 24, 2026

## MafFilter

RRID:SCR\_024105

Type: Tool

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### Proper Citation

MafFilter (RRID:SCR\_024105)

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### Resource Information

**URL:** <https://jydu.github.io/maffilter/>

**Proper Citation:** MafFilter (RRID:SCR\_024105)

**Description:** Software tool for analysis of genome alignments. It parses and manipulates MAF files as well as more simple fasta files. Despite various filtering options and format conversion tools, MafFilter can compute a wide range of statistics including phylogenetic trees, nucleotide diversity, inference of selection, etc.

**Synonyms:** MafFilter a genome alignment processor, maffilter

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

**Defining Citation:** [PMID:24447531](#)

**Keywords:** genome alignments analysis, parse and manipulate MAF files, genome alignment processor,

**Availability:** Free, Available for download, Freely available,

**Resource Name:** MafFilter

**Resource ID:** SCR\_024105

**Alternate IDs:** OMICS\_06743

**Alternate URLs:** <https://sources.debian.org/src/maffilter/>, <https://github.com/jydu/maffilter>

**License:** GPL-3.0 license

**Record Creation Time:** 20230824T050212+0000

**Record Last Update:** 20260821T194248+0000

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## Ratings and Alerts

No rating or validation information has been found for MafFilter.

No alerts have been found for MafFilter.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Salve BG, et al. (2026) Chromosomal rearrangements and segmental deletions contribute to gene loss in squamates. BMC biology, 24(1).

Lv Y, et al. (2025) Genomic insights into evolution of parthenogenesis and triploidy in the flowerpot snake. Science advances, 11(14), eadt6477.

Bai ??? F, et al. (2025) LCORL and STC2 Variants Increase Body Size and Growth Rate in Cattle and Other Animals. Genomics, proteomics & bioinformatics, 23(3).

Hu C, et al. (2024) Genetic linkage disequilibrium of deleterious mutations in threatened mammals. EMBO reports, 25(12), 5620.

Eastment RV, et al. (2024) Convergent genomic signatures associated with vertebrate viviparity. BMC biology, 22(1), 34.

Borstein SR, et al. (2024) The macroevolutionary dynamics of pharyngognath in fishes fail to support the key innovation hypothesis. Nature communications, 15(1), 10325.

Mathers TC, et al. (2023) Hybridisation has shaped a recent radiation of grass-feeding aphids. BMC biology, 21(1), 157.

Zhang MJ, et al. (2023) Pervasive correlations between causal disease effects of proximal SNPs vary with functional annotations and implicate stabilizing selection. Research square.

Zhang MJ, et al. (2023) Pervasive correlations between causal disease effects of proximal SNPs vary with functional annotations and implicate stabilizing selection. medRxiv : the preprint server for health sciences.

Chiou KL, et al. (2022) Genomic signatures of high-altitude adaptation and chromosomal polymorphism in geladas. Nature ecology & evolution, 6(5), 630.

Libisch MG, et al. (2020) Host-pathogen transcriptomics: Trypanosoma cruzi as a model for studying RNA contamination. Journal of proteomics, 223, 103804.

Humble E, et al. (2018) RAD Sequencing and a Hybrid Antarctic Fur Seal Genome Assembly Reveal Rapidly Decaying Linkage Disequilibrium, Global Population Structure and Evidence for Inbreeding. *G3* (Bethesda, Md.), 8(8), 2709.