

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Filtlong

RRID:SCR_024020

Type: Tool

Proper Citation

Filtlong (RRID:SCR_024020)

Resource Information

URL: <https://github.com/rrwick/Filtlong>

Proper Citation: Filtlong (RRID:SCR_024020)

Description: Software tool for filtering long reads by quality. Can take set of long reads and produce smaller, better subset. Uses both read length and read identity when choosing which reads pass the filter.

Synonyms: filtlong

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

Keywords: filtering long reads by quality, read length, read identity, filtering reads,

Availability: Free, Available for download, Freely available

Resource Name: Filtlong

Resource ID: SCR_024020

Alternate URLs: <https://sources.debian.org/src/filtlong/>

License: GPL-3.0 license

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260905T133028+0000

Ratings and Alerts

No rating or validation information has been found for Filtlong.

No alerts have been found for Filtlong.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 474 mentions in open access literature.

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

Rivas L, et al. (2026) *Yersinia fenwicki* sp. nov., isolated from human clinical cases in Aotearoa | New Zealand and Australia. *International journal of systematic and evolutionary microbiology*, 76(1).

Velásquez AC, et al. (2026) Complete genome sequence of *Bradyrhizobium* sp. WCU1 isolated from lager beer. *Microbiology resource announcements*, 15(4), e0110625.

Kawabata Y, et al. (2026) Antimicrobial susceptibility of *Escherichia coli* isolated from wild deer (*Cervus nippon yessoensis*) and fox (*Vulpes vulpes schrencki*) in Hokkaido: a pilot study on sustainable antimicrobial resistance monitoring. *The Journal of veterinary medical science*, 88(4), 642.

van Gorp E, et al. (2026) Ambler class C-type β -lactamases and porin alterations in *Enterobacter cloacae* complex and *Klebsiella aerogenes* in the Netherlands, 2012-2023. *BMC microbiology*, 26(1).

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in *Neisseria gonorrhoeae*. *bioRxiv* : the preprint server for biology.

Leonardo IC, et al. (2026) A novel temperate phage from *Alicyclobacillus*: first evidence in this genus of genomic identity to a sigK-integrated prophage. *Microbiology spectrum*, 14(5), e0374725.

Zhang J, et al. (2026) Cross-kingdom genomic variation in chicken gut microbiomes: insights from China's diverse local breeds. *Microbiome*, 14(1).

Fakoya AO, et al. (2026) HapAsmbl: A reference-aided pipeline for assembling haplotypes in Nanopore amplicon sequence data of polymorphic populations. *Applications in plant sciences*, 14(3), e70062.

Kumar R, et al. (2026) Comparative genomics and molecular insights into smooth and rough clinical isolates of *Mycobacterium abscessus*. *Microbial genomics*, 12(5).

Ivanova M, et al. (2026) Human-associated NDM-5-producing multidrug-resistant *Escherichia coli* detected in retail beef and pork in Hungary, 2021. *Frontiers in bioinformatics*, 6, 1793862.

Huang X, et al. (2026) Pangenome Analysis Reveals Structural Variations Associated With Citric Acid Accumulation in *Prunus mume*. *Plant biotechnology journal*, 24(4), 2623.

Tomita K, et al. (2026) Complete genome sequence of *Fundidesulfovibrio* sp. strain YSD1, an electroactive bacterium isolated from estuarine sediment. *Microbiology resource announcements*, 15(2), e0119325.

Loo EPI, et al. (2026) Removal of Transgenes and Evaluation of Yield Penalties in Genome Edited Bacterial Blight Resistant Rice Varieties. *Plant biotechnology journal*, 24(2), 939.

Bargheet A, et al. (2026) Metabolic reprogramming of the infant gut by bifidobacteria-based probiotics drives exclusion of antibiotic-resistant pathobionts. *Cell reports. Medicine*, 7(5), 102752.

Doi Y, et al. (2026) Draft genome sequence of *Labrys* sp. strain Lb11, an α -glucose-utilizing bacterium isolated from soil. *Microbiology resource announcements*, 15(5), e0009926.

Liu J, et al. (2026) Telomere-to-Telomere Genome Assembly of Two Hemiculter Species Provide Insights into the Genomic and Morphometric Bases of Adaptation to Flow Velocity. *Biomolecules*, 16(1).

Rojas Calderón D, et al. (2026) Genotypic characterization of gut isolates from Atlantic salmon fry reveals beneficial microbes with biotechnological potential. *Applied and environmental microbiology*, 92(3), e0240925.

Möllmann JS, et al. (2026) A Chromosome-Level Genome Assembly and Resequencing Data Reveal Low DNA Methylation and Reduced Diversity in the Solitary Bee Pollinator *Osmia cornuta*. *Genome biology and evolution*, 18(1).

Søndreli KL, et al. (2026) Transcriptomic and functional analyses uncover a conserved effector driving genotype-dependent virulence in the *Sphaerulina musiva*-*Populus trichocarpa* interaction. *mBio*, 17(5), e0312025.

Wang B, et al. (2026) Global genomic diversity of the selfing nematode *Caenorhabditis tropicalis* correlates with geography. *bioRxiv : the preprint server for biology*.