

Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

htsfilter

RRID:SCR_024242

Type: Tool

Proper Citation

htsfilter (RRID:SCR_024242)

Resource Information

URL: <https://bioconductor.org/packages/HTSFilter/>

Proper Citation: htsfilter (RRID:SCR_024242)

Description: Software R package implements filtering procedure for replicated transcriptome sequencing data based on global Jaccard similarity index in order to identify genes with low, constant levels of expression across one or more experimental conditions.

Resource Type: software toolkit, software resource

Keywords: filtering procedure, replicated transcriptome sequencing data, global Jaccard similarity index, identify genes with low, constant levels of expression,

Availability: Free, Available for download, Freely available,

Resource Name: htsfilter

Resource ID: SCR_024242

Alternate URLs: <https://sources.debian.org/src/r-bioc-htsfilter/>

Record Creation Time: 20230830T050216+0000

Record Last Update: 20260803T040912+0000

Ratings and Alerts

No rating or validation information has been found for htsfilter.

No alerts have been found for htsfilter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Pirone R, et al. (2025) A comprehensive evaluation of metabolically engineered *Cynara cardunculus* calli as platform for valuable fatty acid derivatives production. *Scientific reports*, 15(1), 40951.

Lin J, et al. (2023) MCP-1-Mediated Immunosuppression of Neutrophils Exacerbates Acute Bacterial Peritonitis and Liver Injury. *Journal of innate immunity*, 15(1), 262.

Mobuchon L, et al. (2015) Food Deprivation Affects the miRNome in the Lactating Goat Mammary Gland. *PloS one*, 10(10), e0140111.

Le Guillou S, et al. (2014) Characterisation and comparison of lactating mouse and bovine mammary gland miRNomes. *PloS one*, 9(3), e91938.

Rau A, et al. (2014) Differential meta-analysis of RNA-seq data from multiple studies. *BMC bioinformatics*, 15, 91.