Resource Summary Report

Generated by ASWG on Sep 18, 2026

variantbenchmarking

RRID:SCR_028995
Type: Tool

Proper Citation

variantbenchmarking (RRID:SCR_028995)

Resource Information

URL: https://github.com/nf-core/variantbenchmarking

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Description: Software pipeline to evaluate and validate the accuracy of variant calling methods in genomic research. The workflow provides benchmarking tools for small variants including SNVs and INDELs, Structural Variants (SVs) and Copy Number Variations (CNVs) for germline and somatic analysis.

Synonyms: nf-core-variantbenchmarking

Resource Type: software resource, software toolkit, source code

Keywords: evaluate and validate accuracy of variant calling methods, genomic research, variant calling, germline and somatic analysis,

Availability: Free, Available for download, Freely available

Resource Name: variantbenchmarking

Resource ID: SCR_028995

Alternate URLs: https://zenodo.org/records/19692596

License: MIT license

Record Creation Time: 20260916T044917+0000

Record Last Update: 20260916T044917+0000

Ratings and Alerts

No rating or validation information has been found for variantbenchmarking.

No alerts have been found for variantbenchmarking.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.