

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

Tombo

RRID:SCR_024388

Type: Tool

Proper Citation

Tombo (RRID:SCR_024388)

Resource Information

URL: <https://github.com/nanoporetech/tombo>

Proper Citation: Tombo (RRID:SCR_024388)

Description: Software suite of tools for identification of modified nucleotides from nanopore sequencing data.Used also for analysis and visualization of raw nanopore signal.

Synonyms: ont-tombo

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

Keywords: identification of modified nucleotides, nanopore sequencing data, analysis and visualization of raw nanopore signal,

Availability: Free, Available for download, Freely available,

Resource Name: Tombo

Resource ID: SCR_024388

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

License: Mozilla Public License Version 2.0

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260728T043707+0000

Ratings and Alerts

No rating or validation information has been found for Tombo.

No alerts have been found for Tombo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Liu C, et al. (2025) Decoding the m6A epitranscriptomic landscape for biotechnological applications using a direct RNA sequencing approach. Nature communications, 16(1), 798.

Jiang C, et al. (2025) Unveiling Tissue-Specific RNA Landscapes in Mouse Organs During Fasting and Feeding Using Nanopore Direct RNA Sequencing. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(5), e2408054.

Fan Q, et al. (2025) De novo non-canonical nanopore basecalling enables private communication using heavily-modified DNA data at single-molecule level. Nature communications, 16(1), 4099.

Zhu Z, et al. (2025) SqueezeCall: nanopore basecalling using a Squeezeformer network. GigaByte (Hong Kong, China), 2025, gigabyte148.

Guo X, et al. (2025) Methylation reference datasets from quartet DNA materials for benchmarking epigenome sequencing. Nature communications, 16(1), 9202.

Ye F, et al. (2025) Characteristics and filtering of low-frequency artificial short deletion variations based on nanopore sequencing. GigaScience, 14.

Zhang Z, et al. (2024) Comprehensive analysis of m6A methylome alterations after azacytidine plus venetoclax treatment for acute myeloid leukemia by nanopore sequencing. Computational and structural biotechnology journal, 23, 1144.

Acera Mateos P, et al. (2024) Prediction of m6A and m5C at single-molecule resolution reveals a transcriptome-wide co-occurrence of RNA modifications. Nature communications, 15(1), 3899.

Furci L, et al. (2024) RNA N6-adenine methylation dynamics impact Hyaloperonospora arabidopsidis resistance in Arabidopsis. Plant physiology, 196(2), 745.

Kawabe H, et al. (2023) Enzymatic synthesis and nanopore sequencing of 12-letter supernumerary DNA. Nature communications, 14(1), 6820.

Yoshida-Tanaka K, et al. (2023) Long-read sequencing reveals the complex structure of extra dic(21;21) chromosome and its biological effects. Human genetics, 142(9), 1375.

Peng L, et al. (2023) New insights into transcriptome variation during cattle adipocyte adipogenesis by direct RNA sequencing. *iScience*, 26(10), 107753.

Zhang S, et al. (2020) New insights into Arabidopsis transcriptome complexity revealed by direct sequencing of native RNAs. *Nucleic acids research*, 48(14), 7700.

Li R, et al. (2020) Direct full-length RNA sequencing reveals unexpected transcriptome complexity during *Caenorhabditis elegans* development. *Genome research*, 30(2), 287.