

Resource Summary Report

Generated by SPARC SAWG on Sep 12, 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: data analysis software, data processing software, software application, software resource

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: 20260912T200047+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 18 mentions in open access literature.

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

Shao L, et al. (2026) Structural Variation and 3D Genome-Driven DNA/RNA Methylation Divergence Contributing to Cotton Fiber Domestication. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(9), e14381.

Brandt D, et al. (2026) A pentose, as a cytosine nucleobase modification in Shewanella phage Thanatos genomic DNA, mediates enhanced resistance toward host restriction systems. *Applied and environmental microbiology*, 92(1), e0133325.

Cruciani S, et al. (2025) De novo basecalling of RNA modifications at single molecule and nucleotide resolution. *Genome biology*, 26(1), 38.

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

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.

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.

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

Liao Y, et al. (2025) Transcriptome-wide m6A landscape across diverse porcine tissues revealed by nanopore direct RNA sequencing. *Frontiers in genetics*, 16, 1725608.

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.

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.