

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

RetroSeq

RRID:SCR_005133

Type: Tool

Proper Citation

RetroSeq (RRID:SCR_005133)

Resource Information

URL: <https://github.com/tk2/RetroSeq>

Proper Citation: RetroSeq (RRID:SCR_005133)

Description: A tool for discovery and genotyping of transposable element variants (TEVs) (also known as mobile element insertions) from next-gen sequencing reads aligned to a reference genome in BAM format. The goal is to call TEVs that are not present in the reference genome but present in the sample that has been sequenced. It should be noted that RetroSeq can be used to locate any class of viral insertion in any species where whole-genome sequencing data with a suitable reference genome is available. RetroSeq is a two phase process, the first being the read pair discovery phase where discorandant mate pairs are detected and assigned to a TE class (Alu, SINE, LINE, etc.) by using either the annotated TE elements in the reference and/or aligned with Exonerate to the supplied library of viral sequences.

Abbreviations: RetroSeq

Resource Type: software resource

Defining Citation: [PMID:23233656](#)

Keywords: mobile element insertion, next-gen sequencing, bam, transposable element, genome, sequence

Availability: Acknowledgement requested, Open unspecified license

Resource Name: RetroSeq

Resource ID: SCR_005133

Alternate IDs: OMICS_11232, OMICS_00120

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260815T182259+0000

Ratings and Alerts

No rating or validation information has been found for RetroSeq.

No alerts have been found for RetroSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Daigle A, et al. (2025) Leveraging long-read assemblies and machine learning to enhance short-read transposable element detection and genotyping. bioRxiv : the preprint server for biology.

Tan M, et al. (2025) Image-based DNA sequencing encoding for detecting low-mosaicism somatic mobile element insertions. Nature communications, 16(1), 9195.

Ishihara S, et al. (2025) Endogenous retrovirus loci and induced changes in gene expression in Japanese indigenous chickens. Scientific reports, 15(1), 12290.

Bojang P, et al. (2025) LINE1 insertion into the NACC2 locus disrupts the HDM2 axis and activates lung oncogenic signaling. NPJ precision oncology, 9(1), 255.

Bilgrav Saether K, et al. (2024) Detecting transposable elements in long-read genomes using sTELLeR. Bioinformatics (Oxford, England), 40(11).

Lillie M, et al. (2024) Contrasting segregation patterns among endogenous retroviruses across the koala population. Communications biology, 7(1), 350.

Zhao P, et al. (2023) Young SINEs in pig genomes impact gene regulation, genetic diversity, and complex traits. Communications biology, 6(1), 894.

Ishihara S, et al. (2023) Detection of long terminal repeat loci derived from endogenous retrovirus in junglefowl using whole-genome sequencing. Scientific reports, 13(1), 7380.

Bilgrav Saether K, et al. (2023) Transposable element insertions in 1000 Swedish individuals. PloS one, 18(7), e0289346.

Rajaby R, et al. (2023) INSuVeyor: improving insertion calling from short read sequencing data. Nature communications, 14(1), 3243.

Serra O, et al. (2022) Genome-wide clonal variability in European pear "Rocha" using high-throughput sequencing. Horticulture research, 9, uhac111.

Lillie M, et al. (2022) Expansion of a retrovirus lineage in the koala genome. *Proceedings of the National Academy of Sciences of the United States of America*, 119(25), e2201844119.

Daigle AT, et al. (2022) Bergerac strains of *Caenorhabditis elegans* revisited: expansion of Tc1 elements imposes a significant genomic and fitness cost. *G3 (Bethesda, Md.)*, 12(11).

Navarro-Dominguez B, et al. (2022) Epistatic selection on a selfish Segregation Distorter supergene - drive, recombination, and genetic load. *eLife*, 11.

Yan H, et al. (2022) Exploring transposable element-based markers to identify allelic variations underlying agronomic traits in rice. *Plant communications*, 3(3), 100270.

Vaishnavi A, et al. (2022) Transposon Mutagenesis Reveals RBMS3 Silencing as a Promoter of Malignant Progression of BRAFV600E-Driven Lung Tumorigenesis. *Cancer research*, 82(22), 4261.

Hill J, et al. (2022) Spatiotemporal variations in retrovirus-host interactions among Darwin's finches. *Nature communications*, 13(1), 6033.

Dong R, et al. (2022) svaRetro and svaNUMT: modular packages for annotating retrotransposed transcripts and nuclear integration of mitochondrial DNA in genome sequencing data. *GigaByte (Hong Kong, China)*, 2022, gigabyte70.

Yu T, et al. (2021) A benchmark and an algorithm for detecting germline transposon insertions and measuring de novo transposon insertion frequencies. *Nucleic acids research*, 49(8), e44.

Smukowski Heil C, et al. (2021) Transposable Element Mobilization in Interspecific Yeast Hybrids. *Genome biology and evolution*, 13(3).