RetroSeq
RRID:SCR_005133
Type: Tool

Proper Citation

RetroSeq (RRID:SCR_005133)

Resource Information

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

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.

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Resource Type: Resource, software resource

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

Resource ID: SCR_005133

Parent Organization: Wellcome Trust Sanger Institute; Hinxton; United Kingdom

References: PMID: 23233656

Availability: Acknowledgement requested, Open unspecified license
Website Status: Last checked up

Alternate IDs: OMICS_00120

Abbreviations: RetroSeq

Mentions Count: 22

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 22 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


