Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 2, 2025

FRCbam

RRID:SCR_005189
Type: Tool

Proper Citation

FRCbam (RRID:SCR_005189)

Resource Information

URL: https://github.com/vezzi/FRC_align

Proper Citation: FRCbam (RRID:SCR_005189)

Description: Software package containing tools to process bam files in order to evaluate and analyze de novo assembly / assemblers and identify Structural Variations suspicious genomics regions. The tools have been already successfully applied in several de novo and resequencing projects. This package contains two tools: # FRCbam: tool to compute Feature Response Curves in order to validate and rank assemblies and assemblers # FindTranslocations: tool to identify chromosomal rearrangements using Mate Pairs

Resource Type: software resource

Defining Citation: PMID:23284938

Keywords: standalone software, sam, bam

Funding:

Availability: GNU General Public License, v3

Resource Name: FRCbam

Resource ID: SCR_005189

Alternate IDs: OMICS_04070

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250214T183025+0000

Ratings and Alerts

No rating or validation information has been found for FRCbam.

No alerts have been found for FRCbam.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Papa Y, et al. (2023) Genome assembly and isoform analysis of a highly heterozygous New Zealand fisheries species, the tarakihi (Nemadactylus macropterus). G3 (Bethesda, Md.), 13(2).

Fuller T, et al. (2023) A reference assembly for the legume cover crop hairy vetch (Vicia villosa). GigaByte (Hong Kong, China), 2023, gigabyte98.

Lai S, et al. (2022) metaMIC: reference-free misassembly identification and correction of de novo metagenomic assemblies. Genome biology, 23(1), 242.

Harris RA, et al. (2022) Construction of a new chromosome-scale, long-read reference genome assembly for the Syrian hamster, Mesocricetus auratus. GigaScience, 11.

Urban JM, et al. (2021) High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, Sciara coprophila, using single-molecule sequencing. BMC genomics, 22(1), 643.

Li R, et al. (2021) A near complete genome for goat genetic and genomic research. Genetics, selection, evolution : GSE, 53(1), 74.

Grillová L, et al. (2021) Genetic diversity of Leptospira isolates in Lao PDR and genome analysis of an outbreak strain. PLoS neglected tropical diseases, 15(12), e0010076.

Wang W, et al. (2020) The draft nuclear genome assembly of Eucalyptus pauciflora: a pipeline for comparing de novo assemblies. GigaScience, 9(1).

Í Kongsstovu S, et al. (2019) Using long and linked reads to improve an Atlantic herring (Clupea harengus) genome assembly. Scientific reports, 9(1), 17716.

Morales-Hojas R, et al. (2018) The genome of the biting midge Culicoides sonorensis and gene expression analyses of vector competence for bluetongue virus. BMC genomics, 19(1), 624.

Schneider VA, et al. (2017) Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome research, 27(5), 849.