Resource Summary Report

Generated by RRID on Apr 19, 2025

MMAPPR

RRID:SCR_005092
Type: Tool

Proper Citation

MMAPPR (RRID:SCR_005092)

Resource Information

URL: http://yost.genetics.utah.edu/software.php

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Description: A software analysis pipeline for mapping mutations using RNA-seq that works without parental strain information, without the requirement of a pre-existing snp map of the organism, and without erroneous assumptions that recombination occurs at the same frequency across the genome. In addition, it compensates for the considerable amount of noise in RNA-seq datasets and simultaneously identifies the region where the mutation lies and generates a list of putative coding region mutations in the linked genomic segment. MMAPPR can utilize RNA-seq datasets from isolated tissues or whole organisms that are often generated for phenotypic analysis and gene network analysis in novel mutants.

Abbreviations: MMAPPR

Synonyms: Mutation Mapping Analysis Pipeline for Pooled RNA-seq

Resource Type: software resource

Defining Citation: PMID:23299975

Keywords: mutation, rna-seq, bio.tools

Funding:

Availability: Acknowledgement requested

Resource Name: MMAPPR

Resource ID: SCR_005092

Alternate IDs: OMICS_01361, biotools:mmappr

Alternate URLs: https://bio.tools/mmappr

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250410T065227+0000

Ratings and Alerts

No rating or validation information has been found for MMAPPR.

No alerts have been found for MMAPPR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Zhang Q, et al. (2024) Fine mapping and identification of the bright green leaf gene BoBGL in Chinese kale (Brassica oleracea var. alboglabra). Frontiers in plant science, 15, 1507968.

Wu H, et al. (2023) Investigation of SNP markers for the melatonin production trait in the Hu sheep with bulked segregant analysis. BMC genomics, 24(1), 502.

Li C, et al. (2023) Computational Tools and Resources for CRISPR/Cas Genome Editing. Genomics, proteomics & bioinformatics, 21(1), 108.

Casey MA, et al. (2022) Shutdown corner, a large deletion mutant isolated from a haploid mutagenesis screen in zebrafish. G3 (Bethesda, Md.), 12(3).

Ghaffari K, et al. (2021) NCK-associated protein 1 like (nckap1l) minor splice variant regulates intrahepatic biliary network morphogenesis. PLoS genetics, 17(3), e1009402.

Wilson MH, et al. (2020) A point mutation decouples the lipid transfer activities of microsomal triglyceride transfer protein. PLoS genetics, 16(8), e1008941.

Hill JT, et al. (2014) Poly peak parser: Method and software for identification of unknown indels using sanger sequencing of polymerase chain reaction products. Developmental dynamics : an official publication of the American Association of Anatomists, 243(12), 1632.