Resource Summary Report

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QualiMap

RRID:SCR_001209
Type: Tool

Proper Citation

QualiMap (RRID:SCR_001209)

Resource Information

URL: http://qualimap.bioinfo.cipf.es/

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Description: Software application written in Java and R that provides both a Graphical User Inteface (GUI) and a command-line interface to facilitate the quality control of alignment sequencing data. It examines sequencing alignment data in SAM / BAM files according to the features of the mapped reads and provides an overall view of the data that helps to the detect biases in the sequencing and/or mapping of the data and eases decision-making for further analysis.

Abbreviations: QualiMap

Synonyms: QualiMap - Evaluating next generation sequencing alignment data

Resource Type: software resource

Defining Citation: PMID:22914218, DOI:10.1093/bioinformatics/bts503

Keywords: next-generation sequencing, alignment, linux, macos, windows, quality control, sam, bam, bio.tools

Funding: Spanish Ministry of Economy and Competitiveness BIO2009-10799;
EU funded program ERA-NET PathoGenoMics BIO2008-05266-E

Availability: Free, Freely available

Resource Name: QualiMap

Resource ID: SCR_001209

Alternate IDs: OMICS_02133, biotools:qualimap

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

Old URLs: https://sources.debian.org/src/qualimap/

License: GNU General Public License v2

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250214T182935+0000

Ratings and Alerts

No rating or validation information has been found for QualiMap.

No alerts have been found for QualiMap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Lehle JD, et al. (2024) An in vitro approach reveals molecular mechanisms underlying endocrine disruptor-induced epimutagenesis. eLife, 13.

Liau Y, et al. (2024) Low-pass nanopore sequencing for measurement of global methylation levels in plants. BMC genomics, 25(1), 1235.

Nebenführ M, et al. (2024) High-speed whole-genome sequencing of a Whippet: Rapid chromosome-level assembly and annotation of an extremely fast dog's genome. GigaByte (Hong Kong, China), 2024, gigabyte134.

Wolf M, et al. (2024) Near chromosome-level and highly repetitive genome assembly of the snake pipefish Entelurus aequoreus (Syngnathiformes: Syngnathidae). GigaByte (Hong Kong, China), 2024, gigabyte105.

Alcala N, et al. (2024) Multi-omic dataset of patient-derived tumor organoids of neuroendocrine neoplasms. GigaScience, 13.

González-Medina A, et al. (2024) Clinical Value of Liquid Biopsy in Patients with FGFR2 Fusion-Positive Cholangiocarcinoma During Targeted Therapy. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(19), 4491.

Nebenführ M, et al. (2024) Whole-genome re-sequencing of the Baikal seal and other phocid seals for a glimpse into their genetic diversity, demographic history, and phylogeny. GigaByte (Hong Kong, China), 2024, gigabyte142.

Winter S, et al. (2023) A chromosome-scale reference genome assembly of the great sand eel, Hyperoplus lanceolatus. The Journal of heredity, 114(2), 189.

Winter S, et al. (2023) A chromosome-scale high-contiguity genome assembly of the cheetah (Acinonyx jubatus). The Journal of heredity.

Barbosa CFC, et al. (2023) Genome-Wide SNP and Indel Discovery in Abaca (Musa textilis Née) and among Other Musa spp. for Abaca Genetic Resources Management. Current issues in molecular biology, 45(7), 5776.

Goodstal SM, et al. (2023) Preclinical evidence for the effective use of TL-895, a highly selective and potent second-generation BTK inhibitor, for the treatment of B-cell malignancies. Scientific reports, 13(1), 20412.

Ziff OJ, et al. (2023) Nucleocytoplasmic mRNA redistribution accompanies RNA binding protein mislocalization in ALS motor neurons and is restored by VCP ATPase inhibition. Neuron, 111(19), 3011.

Çilingir FG, et al. (2022) Chromosome-level genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population. GigaScience, 11.

Di Genova A, et al. (2022) A molecular phenotypic map of malignant pleural mesothelioma. GigaScience, 12.

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. GigaScience, 12.

Winter S, et al. (2022) A Chromosome-Scale Genome Assembly of the Okapi (Okapia johnstoni). The Journal of heredity, 113(5), 568.

Coimbra RTF, et al. (2021) Whole-genome analysis of giraffe supports four distinct species. Current biology : CB, 31(13), 2929.

Vuaroqueaux V, et al. (2021) Pharmacogenomics characterization of the MDM2 inhibitor MI-773 reveals candidate tumours and predictive biomarkers. NPJ precision oncology, 5(1), 96.

Gabriel AAG, et al. (2020) A molecular map of lung neuroendocrine neoplasms.

GigaScience, 9(11).

Brykczynska U, et al. (2020) Distinct Transcriptional Responses across Tissue-Resident Macrophages to Short-Term and Long-Term Metabolic Challenge. Cell reports, 30(5), 1627.