

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 Interface (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 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: 20250420T014023+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 [NIF](#).

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.

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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).

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