

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

QualiMap

RRID:SCR_001209

Type: Tool

Proper Citation

QualiMap (RRID:SCR_001209)

Resource Information

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

Proper Citation: QualiMap (RRID:SCR_001209)

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, Available for download, 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: 20260801T190134+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 47 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Muppirala AN, et al. (2026) Tachykinin signaling defines distinct populations of glia in the enteric nervous system. *Neuron*.

Winter S, et al. (2025) Chromosome-Level genome assembly and transcriptome analysis of the ural owl, *Strix uralensis* Pallas, 1771. *The Journal of heredity*.

Ni A, et al. (2025) Identifying candidate genetic variants for egg number by analyzing over 1,000 fully sequenced layers. *GigaScience*, 14.

Kennard AS, et al. (2025) Tubulin sequence divergence is associated with the use of distinct microtubule regulators. *Current biology : CB*, 35(2), 233.

Sawant A, et al. (2025) Immune Checkpoint Blockade Delays Cancer Development and Extends Survival in DNA Polymerase Mutator Syndromes. *Cancer research*, 85(6), 1130.

Siu LL, et al. (2025) AZD8701, an Antisense Oligonucleotide Targeting FOXP3 mRNA, as Monotherapy and in Combination with Durvalumab: A Phase I Trial in Patients with Advanced Solid Tumors. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(8), 1449.

Light-Maka I, et al. (2025) Bronze Age *Yersinia pestis* genome from sheep sheds light on hosts and evolution of a prehistoric plague lineage. *Cell*.

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.

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.

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.

Starrett GJ, et al. (2024) Multiomics Profiling Distinguishes Sebaceous Carcinoma from Benign Sebaceous Neoplasms and Provides Insight into the Genetic Evolution of Sebaceous Carcinogenesis. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(21), 4887.

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

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.

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.

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.

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.