

Resource Summary Report

Generated by [RRID](#) on Aug 11, 2026

Qualimap 2

RRID:SCR_026258

Type: Tool

Proper Citation

Qualimap 2 (RRID:SCR_026258)

Resource Information

URL: <http://qualimap.conesalab.org/>

Proper Citation: Qualimap 2 (RRID:SCR_026258)

Description: Software platform-independent application written in Java and R that provides both Graphical User Interface and command-line interface to facilitate quality control of alignment sequencing data and its derivatives like feature counts. Used for advanced multi-sample quality control for high-throughput sequencing data.

Resource Type: software application, software resource

Defining Citation: [DOI:10.1093/bioinformatics/btv566](https://doi.org/10.1093/bioinformatics/btv566)

Keywords: ChIP-seq, RNA-seq, quality control of alignment, advanced multi-sample quality control, high-throughput sequencing data,

Availability: Free, Available for download, Freely available

Resource Name: Qualimap 2

Resource ID: SCR_026258

Record Creation Time: 20250110T053324+0000

Record Last Update: 20260810T040924+0000

Ratings and Alerts

No rating or validation information has been found for Qualimap 2.

No alerts have been found for Qualimap 2.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Al Smadi MA, et al. (2026) Genetic alterations in poor-quality individually selected sperm highlight candidate biomarkers for male subfertility. *Scientific reports*, 16(1).

El Daous H, et al. (2026) Integrated fetal testicular transcriptomic and epigenomic profiles during maternal nutrient restriction with dietary melatonin intervention. *Journal of animal science*, 104.

Li X, et al. (2025) One-for-all gene inactivation via PAM-independent base editing in bacteria. *The Journal of biological chemistry*, 301(1), 108113.

Khan MR, et al. (2025) Identifying potential genetic biomarkers for sperm dysfunction through whole-genome sequencing. *Scientific reports*, 15(1), 36476.

Guo X, et al. (2025) Methylation reference datasets from quartet DNA materials for benchmarking epigenome sequencing. *Nature communications*, 16(1), 9202.

Aliu E, et al. (2025) Chromosome architecture affects virulence and competitiveness in *Agrobacterium tumefaciens* C58. *Science advances*, 11(40), eadx7408.

Seid G, et al. (2025) Exploring transmission dynamics in epidemiologically linked pulmonary tuberculosis cases and household contacts: a WGS-based investigation. *BMC genomics*, 27(1), 82.

Ribeiro AAF, et al. (2025) Molecular characterization of hereditary breast and ovarian cancer patients from a public precision medicine service in the Southeast Brazilian population. *Scientific reports*, 15(1), 33495.

Bryushkova EA, et al. (2025) FCRLs and atypical transcriptional pattern in tumor infiltrating B cells from lung and renal cancer. *Frontiers in immunology*, 16, 1587088.

Malhotra N, et al. (2024) Environmental sphagnum-associated fungi target thiol homeostasis to compete with *Mycobacterium tuberculosis*. *bioRxiv : the preprint server for biology*.

Zhang S, et al. (2024) Genome-wide investigation of VNTR motif polymorphisms in 8,222 genomes: Implications for biological regulation and human traits. *Cell genomics*, 4(12), 100699.

Cherkasova V, et al. (2023) Transcriptome Analysis of Cisplatin, Cannabidiol, and Intermittent Serum Starvation Alone and in Various Combinations on Colorectal Cancer Cells. *International journal of molecular sciences*, 24(19).

De Bortoli M, et al. (2023) Modeling incomplete penetrance in arrhythmogenic cardiomyopathy by human induced pluripotent stem cell derived cardiomyocytes. Computational and structural biotechnology journal, 21, 1759.

Cabrera-Rodríguez R, et al. (2022) Transactive Response DNA-Binding Protein (TARDBP/TDP-43) Regulates Cell Permissivity to HIV-1 Infection by Acting on HDAC6. International journal of molecular sciences, 23(11).