Resource Summary Report

Generated by ASWG on Aug 20, 2026

qtltools

RRID:SCR_024200
Type: Tool

Proper Citation

qtltools (RRID:SCR_024200)

Resource Information

URL: https://qtltools.github.io/qtltools/

Proper Citation: qtltools (RRID:SCR_024200)

Description: Software tool set for molecular Quantitative Trait Loci discovery and analysis. Allows to go from raw sequence data to collection of molecular Quantitative Trait Loci in few easy-to-perform steps.

Resource Type: software library, software toolkit, software resource

Defining Citation: PMID:28516912

Keywords: molecular Quantitative Trait Loci, QTL discovery and analysis,

Availability: Free, Available for download, Freely available,

Resource Name: qtltools

Resource ID: SCR_024200

Alternate IDs: OMICS_18457

Alternate URLs: https://sources.debian.org/src/qtltools/

License: GPL-3.0 license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260820T055018+0000

Ratings and Alerts

No rating or validation information has been found for qtltools.

No alerts have been found for qtltools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 51 mentions in open access literature.

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

Kong H, et al. (2026) Functional characterization of a multi-cancer risk locus on chromosome band 2q33.1 near CASP8. bioRxiv : the preprint server for biology.

Tian W, et al. (2026) Genetic alternative splicing regulation mapping of cartilage and synovium reveals tissue-specific mechanisms of joint-related traits. Nature communications, 17(1).

Abou Alaiwi S, et al. (2026) Generation of a comprehensive epigenomic atlas in clear cell renal cell carcinoma informs kidney cancer progression and heritability. Cell reports, 45(2), 116968.

Liu R, et al. (2026) Genetic regulation of methylation across East Asian and European populations. Nature communications, 17(1).

Nishiyama NC, et al. (2026) eQTL in diseased colon tissue identifies potential target genes associated with IBD. Nature communications, 17(1).

Bjarnadottir H, et al. (2026) The impact of low-frequency genetic variants on serum protein levels. bioRxiv : the preprint server for biology.

Small AM, et al. (2026) Genomic and transcriptomic analyses of aortic stenosis enhance therapeutic target discovery and disease prediction. Nature genetics, 58(1), 57.

Nanchira Abraham L, et al. (2026) Population-level Variability in Genome-wide Repressive Histone Marks in a Fungal Wheat Pathogen. Genome biology and evolution, 18(5).

Wang W, et al. (2025) Impact of polymorphisms on gene expression and splicing in response to exercise and diet-induced weight loss in human skeletal muscle tissues. Cell genomics, 5(9), 100951.

Li J, et al. (2025) A multi-tissue atlas of allelic-specific expression reveals the characteristics, mechanisms, and relationship with dominant effects in cattle. BMC biology, 23(1), 148.

Ganapathy KR, et al. (2025) Improved Identification of Large-effect Rare Genetic Variants using Haplotype Aggregated Allele-specific Expression Data. medRxiv : the preprint server for health sciences.

Cheng F, et al. (2025) Distinct methylomic signatures of high-altitude acclimatization and adaptation in the Tibetan Plateau. Cell discovery, 11(1), 45.

Chen W, et al. (2025) Enhancer RNA Transcriptome-Wide Association Study Reveals a Distinctive Class of Pan-Cancer Susceptibility eRNAs. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(13), e2411974.

El Garwany O, et al. (2025) Splicing QTL mapping in stimulated macrophages associates low-usage splice junctions with immune-mediated disease risk. Nature communications, 16(1), 7205.

Liang Q, et al. (2025) Impact of common variants on brain gene expression from RNA to protein to schizophrenia risk. Nature communications, 16(1), 10773.

Ueda MT, et al. (2024) Functional and dynamic profiling of transcript isoforms reveals essential roles of alternative splicing in interferon response. Cell genomics, 4(10), 100654.

Chen Y, et al. (2024) Cross-ancestry analysis of brain QTLs enhances interpretation of schizophrenia genome-wide association studies. American journal of human genetics, 111(11), 2444.

Tian C, et al. (2024) Single-cell RNA sequencing of peripheral blood links cell-type-specific regulation of splicing to autoimmune and inflammatory diseases. Nature genetics, 56(12), 2739.

Advani J, et al. (2024) QTL mapping of human retina DNA methylation identifies 87 gene-epigenome interactions in age-related macular degeneration. Nature communications, 15(1), 1972.

Zouache MA, et al. (2024) Levels of complement factor H-related 4 protein do not influence susceptibility to age-related macular degeneration or its course of progression. Nature communications, 15(1), 443.