Resource Summary Report

Generated by T1D on Jul 31, 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 toolkit, software resource, software library

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: 20260731T043145+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 41 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

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.

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.

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.

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.

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

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.

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.

Lykoskoufis NMR, et al. (2024) Transposable elements mediate genetic effects altering the expression of nearby genes in colorectal cancer. Nature communications, 15(1), 749.

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.

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.

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.

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.

Mapel XM, et al. (2024) Molecular quantitative trait loci in reproductive tissues impact male fertility in cattle. Nature communications, 15(1), 674.

Hodonsky CJ, et al. (2024) Multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci. Cell genomics, 4(1), 100465.

Luo J, et al. (2024) Genetic regulation of human brain proteome reveals proteins implicated in psychiatric disorders. Molecular psychiatry, 29(11), 3330.

Leonard AS, et al. (2024) RNA-DNA differences in variant calls from cattle tissues result in erroneous eQTLs. BMC genomics, 25(1), 750.

Nishiyama NC, et al. (2024) eQTL in diseased colon tissue identifies novel target genes associated with IBD. bioRxiv : the preprint server for biology.

Jo Y, et al. (2024) Interpretation of SNP combination effects on schizophrenia etiology based on stepwise deep learning with multi-precision data. Briefings in functional genomics, 23(5), 663.

Th??riault S, et al. (2024) Integrative genomic analyses identify candidate causal genes for calcific aortic valve stenosis involving tissue-specific regulation. Nature communications, 15(1), 2407.