

Resource Summary Report

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Fastqtl

RRID:SCR_016093

Type: Tool

Proper Citation

Fastqtl (RRID:SCR_016093)

Resource Information

URL: <http://fastqtl.sourceforge.net/>

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Description: Software for mapping of molecular phenotypes that implements a new permutation scheme to accurately and rapidly correct for multiple-testing at both the genotype and phenotype levels in large-scale datasets. It is used to discover quantitative trait loci, multi-dimensional genomic datasets combining DNA-seq and ChIP-/RNA-seq.

Abbreviations: Fastqtl

Synonyms: Fastqtl: Fast quantitative trait loci

Resource Type: software resource, software toolkit

Defining Citation: [PMID:26708335](#)

Keywords: molecular, phenotype, multiply, testing, genotype, correct, genomic dataset, trait, loci, cis, quantitative, multi dimensional

Funding: European Commission SYSCOL FP7;
European Research Council ;
Helse Sør Øst ;
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Swiss National Science Foundation ;
SystemsX

Availability: Free, Available for download

Resource Name: Fastqtl

Resource ID: SCR_016093

Alternate IDs: OMICS_10934

Alternate URLs: <https://sources.debian.org/src/fastqtl/>

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260904T000456+0000

Ratings and Alerts

No rating or validation information has been found for Fastqtl.

No alerts have been found for Fastqtl.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 133 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hu J, et al. (2026) Full-length transcriptome atlas of porcine skeletal muscle reveals isoform-resolved genetic regulatory mechanisms for muscle growth. BMC genomics, 27(1).

Sakaue S, et al. (2026) Early and late RNA eQTL are driven by different genetic mechanisms. Nature communications, 17(1).

Fang X, et al. (2026) Protocol for identifying cell-type-specific genes associated with disease risk using single-cell eQTL data. STAR protocols, 7(2), 104545.

Esmaeili M, et al. (2026) Distinct regulatory elements of SLC6A14 expression contribute to modification of cystic fibrosis phenotypes. Human genetics, 145(1), 8.

Zhao X, et al. (2026) m6AConquer: a consistently quantified and orthogonally validated database for the N6-methyladenosine (m6A) epitranscriptome. Nucleic acids research, 54(D1), D204.

Zhao Y, et al. (2025) The origin and evolution of cultivated rice and genomic signatures of heterosis for yield traits in super-hybrid rice. BMC biology, 23(1), 153.

Zhang ZE, et al. (2025) Efficient count-based models improve power and robustness for large-scale single-cell eQTL mapping. medRxiv : the preprint server for health sciences.

Valencia C, et al. (2025) Modeling heterogeneity in single-cell perturbation states enhances detection of response eQTLs. Nature genetics, 57(11), 2882.

Castel SE, et al. (2025) A map of blood regulatory variation in South Africans enables GWAS interpretation. *Nature genetics*, 57(7), 1628.

Xiao R, et al. (2025) Integrative genomic analysis reveals causal relationships between breast mammary tissue gene expression and breast cancer risk using multi-method Mendelian randomization. *Discover oncology*, 16(1), 2133.

Xu Z, et al. (2025) Impact of HMGA1 on tumorigenesis, prognosis and immune microenvironment in HNSCC: a multi-omics study. *NPJ precision oncology*, 9(1), 269.

Xu H, et al. (2025) Integrating genetic and transcriptomic data to identify genes underlying obesity risk loci. *International journal of obesity* (2005), 49(11), 2346.

Niu ??? Q, et al. (2025) Comprehensive Multi-omics Analysis of Regulatory Variants for Body Weight in Cattle. *Genomics, proteomics & bioinformatics*, 23(4).

Song X, et al. (2025) Systematically identification of survival-associated eQTLs in a Japanese kidney cancer cohort. *PLoS genetics*, 21(7), e1011770.

Zhang T, et al. (2025) Multi-omics dissection of the genetic regulation underlying fatty acid composition in cattle. *Genome biology*, 26(1), 432.

Yu S, et al. (2025) A gene expression atlas of *Nicotiana tabacum* across various tissues at transcript resolution. *Frontiers in plant science*, 16, 1500654.

Tian W, et al. (2025) Genetic transcriptional regulation profiling of cartilage reveals pathogenesis of osteoarthritis. *EBioMedicine*, 117, 105821.

Bian L, et al. (2025) Single-cell eQTL mapping reveals cell-type-specific genes associated with the risk of gastric cancer. *Cell genomics*, 5(4), 100812.

Oliva M, et al. (2025) Integration of GWAS, QTLs and keratinocyte functional assays reveals molecular mechanisms of atopic dermatitis. *Nature communications*, 16(1), 3101.

Li X, et al. (2025) Integrating genetic regulation and schizophrenia-specific splicing quantitative expression with GWAS prioritizes novel risk genes for schizophrenia. *Translational psychiatry*, 15(1), 379.