

Resource Summary Report

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R/QTL

RRID:SCR_009085

Type: Tool

Proper Citation

R/QTL (RRID:SCR_009085)

Resource Information

URL: <http://www.rqtl.org>

Proper Citation: R/QTL (RRID:SCR_009085)

Description: Software program for mapping quantitative trait loci in experimental crosses.
(entry from Genetic Analysis Software)

Abbreviations: R/QTL

Resource Type: software resource, software application

Defining Citation: [DOI:10.1093/bioinformatics/btg112](https://doi.org/10.1093/bioinformatics/btg112)

Keywords: gene, genetic, genomic, c and r, unix, ms-windows, macos

Resource Name: R/QTL

Resource ID: SCR_009085

Alternate IDs: OMICS_07093, nlx_154097

Alternate URLs: <https://sources.debian.org/src/r-cran-qtl/>

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260801T191055+0000

Ratings and Alerts

No rating or validation information has been found for R/QTL.

No alerts have been found for R/QTL.

Data and Source Information

Usage and Citation Metrics

We found 987 mentions in open access literature.

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

Pan K, et al. (2026) Lysine methylation-mediated SMYD2 degradation by casticin sensitizes non-small-cell lung cancer cells to osimertinib therapy. *Biochemical pharmacology*, 243(Pt 2), 117562.

Osuna-Caballero S, et al. (2026) Dissecting Vegetative Period Into Its Phenotypic and Genotypic Components Allows Environment-Specific Breeding in Lentil (*Lens culinaris* Medik). *Physiologia plantarum*, 178(1), e70729.

Dramé D, et al. (2026) Genetic architecture of cowpea domestication: QTL mapping and comparison shed new light on the dual domestication events. *G3 (Bethesda, Md.)*, 16(1).

Goldberg LR, et al. (2025) *Atp1a2* and *Kcnj9* Are Candidate Genes Underlying Sensitivity to Oxycodone-Induced Locomotor Activation and Withdrawal-Induced Anxiety-Like Behaviors in C57BL/6 Substrains. *Genes, brain, and behavior*, 24(1), e70009.

Amado D, et al. (2025) The genetic architecture of resistance to flubendiamide insecticide in *Helicoverpa armigera* (Hübner). *PloS one*, 20(1), e0318154.

Soler-Garzón A, et al. (2025) Mapping resistance to *Sclerotinia* white mold in two pinto bean recombinant inbred line populations. *The plant genome*, 18(1), e20538.

Fang X, et al. (2025) Genome assembly and population genomic analysis reveal the genetic basis of popcorn evolution. *Plant biotechnology journal*, 23(7), 2911.

Duan Y, et al. (2025) Development of recombinant inbred lines and QTL analysis of plant height and fruit shape-related traits in *Cucurbita pepo* L. *Molecular breeding : new strategies in plant improvement*, 45(9), 74.

Wang SS, et al. (2025) Identification and Candidate Gene Analysis of qCTS11-TK9, a Novel Major Quantitative Trait Locus Associated with Chilling Tolerance in Rice Seedlings. *Rice (New York, N.Y.)*, 18(1), 81.

Hasan MM, et al. (2025) *mop1* affects maize recombination landscapes by modulating methylation of MITEs near genes in open chromatin. *Nature communications*, 16(1), 10476.

Floriani TO, et al. (2025) Developing a model to implement marker-assisted selection for root-knot nematode resistance in common bean. *G3 (Bethesda, Md.)*, 15(12).

Rodríguez MV, et al. (2025) Introgression of dwarfing allele *dw1* reduced seed dormancy and increased pre-harvest sprouting susceptibility in grain sorghum converted lines. *Plant biotechnology journal*, 23(5), 1783.

Zhang Y, et al. (2025) Identification of superior haplotypes and candidate gene for seed size-related traits in soybean (*Glycine max* L.). *Molecular breeding : new strategies in plant improvement*, 45(1), 3.

Yamazaki H, et al. (2025) QTL-Based Evidence of Population Genetic Divergence in Male Territorial Aggressiveness of the Japanese Freshwater Threespine Stickleback. *Ecology and evolution*, 15(1), e70795.

Reynard JS, et al. (2025) A divergent haplotype with a large deletion at the berry color locus causes a white-skinned phenotype in grapevine. *Horticulture research*, 12(6), uhaf069.

Teraishi M, et al. (2025) Identification of Novel Candidate Genes Associated With the Symbiotic Compatibility of Soybean With Rhizobia Under Natural Conditions. *Plant direct*, 9(5), e70069.

Eyres I, et al. (2025) The Genetics of Host Plant Acceptance in Pea Aphids. *Molecular ecology*, 34(21), e17795.

Wright D, et al. (2025) Domestication effects on crowing in chickens: variation between wild and captive red junglefowl and domestic white Leghorn and the genetic architecture of crowing vocalizations. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 380(1926), 20240199.

Liu JN, et al. (2025) Pan-genome analyses of 11 *Fraxinus* species provide insights into salt adaptation in ash trees. *Plant communications*, 6(1), 101137.

Warsame AO, et al. (2025) Identification of significant genome-wide associations and QTL underlying variation in seed protein composition in pea (*Pisum sativum* L.). *The plant genome*, 18(2), e70051.