

Resource Summary Report

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MAPQTL

RRID:SCR_009284

Type: Tool

Proper Citation

MAPQTL (RRID:SCR_009284)

Resource Information

URL: <http://www.mapqtl.nl>

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Description: Software application for mapping of quantitative trait loci (QTLs) for several types of mapping populations: BC1, F2, RILs, (doubled) haploids, full-sib family of outbreeders. Analyses: interval mapping, composite interval mapping, nonparametric mapping, automatic cofactor selection, permutation test for interval mapping. QTL charts. Everything available in an intuitive MS-Windows user interface. (entry from Genetic Analysis Software)

Abbreviations: MAPQTL

Synonyms: Software for the calculation of QTL positions on genetic maps

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, ansi c, delphi, ms-windows, (95/98/me/nt4.0/2000)

Resource Name: MAPQTL

Resource ID: SCR_009284

Alternate IDs: nlx_154468

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260813T054954+0000

Ratings and Alerts

No rating or validation information has been found for MAPQTL.

No alerts have been found for MAPQTL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 403 mentions in open access literature.

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

Pfeifer M, et al. (2026) QTL analysis of *Malus baccata* 'Jackii'-derived offspring reveals a polygenic inheritance pattern of apple blotch resistance. *Frontiers in plant science*, 17, 1854916.

Wu B, et al. (2026) Natural variations in MdBPM2/MdRGLG3-MdNAC83 network controlling the quantitative segregation of apple fruit storability. *Journal of integrative plant biology*, 68(1), 169.

Clevinger EM, et al. (2026) RenSeq-derived SNPs used in mapping resistance to *Phytophthora sojae* and three *Pythium* spp. in multiple soybean RIL populations. *Molecular breeding : new strategies in plant improvement*, 46(6), 64.

Davik J, et al. (2026) Development of a Flex-Seq SNP panel for raspberry (*Rubus idaeus* L.) and validation through linkage map construction and identification of QTL for several traits of agronomic importance to raspberry breeding. *PloS one*, 21(2), e0328606.

Wang Z, et al. (2026) Identification of novel QTL for tiller angle on chromosome 2H and 5H in barley. *BMC plant biology*, 26(1).

Bahmani K, et al. (2026) -Identification of QTL for steviol glycoside biosynthesis using a SNP-based genetic linkage map for *Stevia rebaudiana*. *G3 (Bethesda, Md.)*, 16(3).

Mohanty JK, et al. (2026) Trans-QTL Alliance of HKT1 and PHL7 Modulate Salinity Stress Tolerance and Enhance Crop Yield Endurance. *Plant biotechnology journal*, 24(3), 1166.

Wu Q, et al. (2026) TaKMT-7A Gene Positively Regulates Spike Number in Wheat. *Genes*, 17(6).

Pettenuzzo S, et al. (2025) QTL mapping and underlying genes for heat tolerance in grapevine (Rhine Riesling × Cabernet Sauvignon) under field conditions. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(8), 189.

Zhang C, et al. (2025) Natural allelic variation in SW14 determines seed weight and quality in soybean. *Nature communications*, 16(1), 8070.

Chen X, et al. (2025) Unveiling the genetic architecture of barley embryo: QTL mapping, candidate genes identification and its relationship with kernel size and early vigour. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(1), 32.

Wu Y, et al. (2025) Construction of a High-Density Genetic Linkage Map and QTL Mapping for Stem Rot Resistance in Passion Fruit (*Passiflora edulis* Sims). *Genes*, 16(1).

Kunta S, et al. (2025) Genetic mapping of time-to-maturity trait in hypogaea x fastigiata peanut background reveals a significant effect of pod-related and flowering pattern. BMC plant biology, 26(1), 27.

Liu L, et al. (2025) Natural variation in MdNAC5 contributes to fruit firmness and ripening divergence in apple. Horticulture research, 12(1), uhae284.

Pfeifer M, et al. (2025) Genetic mapping, marker development, and identification of candidate genes for powdery mildew resistance in *Malus baccata* 'Jackii'. Frontiers in plant science, 16, 1716290.

Hong X, et al. (2025) Identification of key candidate genes regulating hundred-grain weight in the maize inbred line Ye107 from Southern China. Plant cell reports, 44(9), 206.

Zhu Y, et al. (2025) Integrative QTL Mapping and Transcriptomic Profiling to Identify Growth-Associated QTL and Candidate Genes in Hong Kong Catfish (*Clarias fuscus*). Animals : an open access journal from MDPI, 15(12).

Goode K, et al. (2025) Candidate genes at the Rmi1 locus for resistance to *Meloidogyne incognita* in soybean. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(11), 286.

Li F, et al. (2025) Fine Mapping and Candidate Gene Identification of ORUFILM03g000096 Gene in Weedy Rice LM8: Insights into Grain Length Regulation. Rice (New York, N.Y.), 18(1), 101.

Zhang P, et al. (2025) Growth-Rate Related Quantitative Trait Locus Analysis of Monokaryotic Isolates of *Grifola albicans* f. *huishuhua* (Maitake). Journal of fungi (Basel, Switzerland), 11(12).