

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 application, software resource

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: 20260727T040447+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 392 mentions in open access literature.

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

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).

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.

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

Somnicka R, et al. (2025) Identification of quantitative trait loci for in vitro plant regeneration from leaf microexplants in cucumber (*Cucumis sativus* L.). Journal of applied genetics, 66(3), 545.

Vervalle JA, et al. (2025) Metabolic and genetic analysis links TRITERPENE SYNTHASE 12 to oleanolic acid biosynthesis in grape berry wax. Journal of experimental botany, 76(11), 3186.

Huang YQ, et al. (2025) Allelic variation and duplication of the dmrt1 were associated with sex chromosome turnover in three representative Scatophagidae fish species. Communications biology, 8(1), 627.

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).

Lee D, et al. (2025) QTL mapping and whole-genome sequencing analysis for novel genetic resources associated with sucrose content in soybean [*Glycine max* (L.) Merr.]. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(2), 43.

Ruud AK, et al. (2025) Quantitative trait loci mapping of resistance to pre-harvest sprouting in the Norwegian spring wheat breeding line T7347. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(7), 159.

Ji X, et al. (2025) Mapping and identification of QTLs for low light tolerance traits in grapevine. *BMC plant biology*, 25(1), 927.

Behling W, et al. (2025) Genetic basis for broad interspecific compatibility in *Solanum verrucosum*. *The Plant journal : for cell and molecular biology*, 123(4), e70426.

Yang G, et al. (2024) Allelic variation of *BBX24* is a dominant determinant controlling red coloration and dwarfism in pear. *Plant biotechnology journal*, 22(6), 1468.

Williams OR, et al. (2024) Physical seed dormancy in pea is genetically separable from seed coat thickness and roughness. *Frontiers in plant science*, 15, 1359226.

Guo L, et al. (2024) Turnovers of Sex-Determining Mutation in the Golden Pompano and Related Species Provide Insights into Microevolution of Undifferentiated Sex Chromosome. *Genome biology and evolution*, 16(3).