

Resource Summary Report

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QTLNetwork

RRID:SCR_009078

Type: Tool

Proper Citation

QTLNetwork (RRID:SCR_009078)

Resource Information

URL: <http://ibi.zju.edu.cn/software/qtlnetwork>

Proper Citation: QTLNetwork (RRID:SCR_009078)

Description: Software package for mapping and visualizing the genetic architecture underlying complex traits for experimental populations derived from a cross between two inbred lines. (entry from Genetic Analysis Software). QTLNetwork-2.0 for mapping quantitative trait loci (QTL) with epistatic effects and QE interaction effects in DH, RI, BC, F2, IF2 and BxFy populations, and for graphical presentation of QTL mapping results.

Synonyms: , QTLNetwork, QTL network 2, QTLNetwork 2.0

Resource Type: software resource, software application

Defining Citation: [PMID:18202029](#), [PMID:20593516](#)

Keywords: gene, genetic, genomic

Resource Name: QTLNetwork

Resource ID: SCR_009078

Alternate IDs: nlx_154076

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260731T042806+0000

Ratings and Alerts

No rating or validation information has been found for QTLNetwork.

No alerts have been found for QTLNetwork.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 50 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Ullah A, et al. (2025) Integration of QTL mapping and GWAS reveals the complicated genetic architecture of chemical composition traits in tobacco leaves. *Frontiers in plant science*, 16, 1616591.

Li Y, et al. (2024) A novel natural variation in the promoter of GmCHX1 regulates conditional gene expression to improve salt tolerance in soybean. *Journal of experimental botany*, 75(3), 1051.

Xu M, et al. (2024) Dissection of genetic architecture of nine hazardous component traits of mainstream smoke in tobacco (*Nicotiana tabacum* L.). *Frontiers in plant science*, 15, 1358953.

Huang G, et al. (2023) Dynamic QTL mapping revealed primarily the genetic structure of photosynthetic traits in castor (*Ricinus communis* L.). *Scientific reports*, 13(1), 14071.

Yu ZP, et al. (2023) Genetic Dissection of Extreme Seed-Flooding Tolerance in a Wild Soybean PI342618B by Linkage Mapping and Candidate Gene Analysis. *Plants (Basel, Switzerland)*, 12(12).

Guo S, et al. (2023) Mapping of major QTL and candidate gene analysis for hull colour in foxtail millet (*Setaria italica* (L.) P. Beauv.). *BMC genomics*, 24(1), 458.

Bokore FE, et al. (2022) Main effect and epistatic QTL affecting spike shattering and association with plant height revealed in two spring wheat (*Triticum aestivum* L.) populations. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 135(4), 1143.

Sheng C, et al. (2021) QTL-Seq and Transcriptome Analysis Disclose Major QTL and Candidate Genes Controlling Leaf Size in Sesame (*Sesamum indicum* L.). *Frontiers in plant science*, 12, 580846.

Elattar MA, et al. (2021) Identification and Validation of Major QTLs, Epistatic Interactions, and Candidate Genes for Soybean Seed Shape and Weight Using Two Related RIL Populations. *Frontiers in genetics*, 12, 666440.

Xu F, et al. (2021) Fine Mapping of a Major Pleiotropic QTL Associated with Sesamin and Sesamolol Variation in Sesame (*Sesamum indicum* L.). *Plants (Basel, Switzerland)*, 10(7).

Thi KM, et al. (2020) Mapping of QTLs conferring high grain length-breadth relative expansion during cooking in rice cultivar Paw San Hmwe. *Breeding science*, 70(5), 551.

Hina A, et al. (2020) High-Resolution Mapping in Two RIL Populations Refines Major "QTL Hotspot" Regions for Seed Size and Shape in Soybean (*Glycine max* L.). *International journal of molecular sciences*, 21(3).

Prince SJ, et al. (2020) Mapping Quantitative Trait Loci for Soybean Seedling Shoot and Root Architecture Traits in an Inter-Specific Genetic Population. *Frontiers in plant science*, 11, 1284.

Yang J, et al. (2020) Mapping of QTL for Grain Yield Components Based on a DH Population in Maize. *Scientific reports*, 10(1), 7086.

Cao J, et al. (2020) Identification and Validation of New Stable QTLs for Grain Weight and Size by Multiple Mapping Models in Common Wheat. *Frontiers in genetics*, 11, 584859.

Wu X, et al. (2020) QTL mapping and transcriptome analysis identify candidate genes regulating pericarp thickness in sweet corn. *BMC plant biology*, 20(1), 117.

Dhariwal R, et al. (2020) Mapping of Major Fusarium Head Blight Resistance from Canadian Wheat cv. AAC Tenacious. *International journal of molecular sciences*, 21(12).

Li M, et al. (2020) Genetic dissection of stem WSC accumulation and remobilization in wheat (*Triticum aestivum* L.) under terminal drought stress. *BMC genetics*, 21(1), 50.

Wu X, et al. (2019) Construction of High-Density Genetic Map and Identification of QTLs Associated with Seed Vigor after Exposure to Artificial Aging Conditions in Sweet Corn Using SLAF-seq. *Genes*, 11(1).

Patil G, et al. (2018) Dissecting genomic hotspots underlying seed protein, oil, and sucrose content in an interspecific mapping population of soybean using high-density linkage mapping. *Plant biotechnology journal*, 16(11), 1939.