

Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 11, 2025

MAPMAKER/QTL

RRID:SCR_009283

Type: Tool

Proper Citation

MAPMAKER/QTL (RRID:SCR_009283)

Resource Information

URL: http://www-genome.wi.mit.edu/genome_software

Proper Citation: MAPMAKER/QTL (RRID:SCR_009283)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 23,2022. Software application (entry from Genetic Analysis Software)

Abbreviations: MAPMAKER/QTL

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, unix, vms, ms-dos, macos

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MAPMAKER/QTL

Resource ID: SCR_009283

Alternate IDs: nlx_154464

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250411T055311+0000

Ratings and Alerts

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

No alerts have been found for MAPMAKER/QTL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Wang C, et al. (2023) Upgrading the genome of an elite japonica rice variety Kongyu 131 for lodging resistance improvement. *Plant biotechnology journal*, 21(2), 419.

Redina OE, et al. (2021) Hypothalamic Norepinephrine Concentration and Heart Mass in Hypertensive ISIAH Rats Are Associated with a Genetic Locus on Chromosome 18. *Journal of personalized medicine*, 11(2).

Singh CK, et al. (2021) Mechanistic Association of Quantitative Trait Locus with Malate Secretion in Lentil (*Lens culinaris Medikus*) Seedlings under Aluminium Stress. *Plants (Basel, Switzerland)*, 10(8).

Zhang YM, et al. (2021) A rice QTL GS3.1 regulates grain size through metabolic-flux distribution between flavonoid and lignin metabolons without affecting stress tolerance. *Communications biology*, 4(1), 1171.

Dong NQ, et al. (2020) UDP-glucosyltransferase regulates grain size and abiotic stress tolerance associated with metabolic flux redirection in rice. *Nature communications*, 11(1), 2629.

Wang R, et al. (2019) Updating the Genome of the Elite Rice Variety Kongyu131 to Expand Its Ecological Adaptation Region. *Frontiers in plant science*, 10, 288.

Feng X, et al. (2019) Improving the blast resistance of the elite rice variety Kongyu-131 by updating the pi21 locus. *BMC plant biology*, 19(1), 249.

Feng X, et al. (2017) Updating the elite rice variety Kongyu 131 by improving the Gn1a locus. *Rice (New York, N.Y.)*, 10(1), 35.

Yamaguchi M, et al. (2016) Sorghum Dw1, an agronomically important gene for lodging resistance, encodes a novel protein involved in cell proliferation. *Scientific reports*, 6, 28366.

Ren D, et al. (2016) Fine Mapping Identifies a New QTL for Brown Rice Rate in Rice (*Oryza Sativa* L.). *Rice* (New York, N.Y.), 9(1), 4.

Iwata H, et al. (2016) Genomics-assisted breeding in fruit trees. *Breeding science*, 66(1), 100.

Redina OE, et al. (2015) Candidate genes in quantitative trait loci associated with absolute and relative kidney weight in rats with Inherited Stress Induced Arterial Hypertension. *BMC genetics*, 16 Suppl 1(Suppl 1), S1.

Kim CK, et al. (2014) RiceQTLPro: an integrated database for quantitative trait loci marker mapping in rice plant. *Bioinformatics*, 10(10), 664.

Chen J, et al. (2014) Characterization of epistatic interaction of QTLs LH8 and EH3 controlling heading date in rice. *Scientific reports*, 4, 4263.

Honma Y, et al. (2014) Molecular mapping of restorer-of-fertility 2 gene identified from a sugar beet (*Beta vulgaris* L. ssp. *vulgaris*) homozygous for the non-restoring restorer-of-fertility 1 allele. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 127(12), 2567.

Yang Y, et al. (2014) Quantitative trait loci identification, fine mapping and gene expression profiling for ovicidal response to whitebacked planthopper (*Sogatella furcifera* Horvath) in rice (*Oryza sativa* L.). *BMC plant biology*, 14, 145.

Pinto RM, et al. (2013) Mismatch repair genes Mlh1 and Mlh3 modify CAG instability in Huntington's disease mice: genome-wide and candidate approaches. *PLoS genetics*, 9(10), e1003930.

Korbolina EE, et al. (2012) Quantitative trait loci on chromosome 1 for cataract and AMD-like retinopathy in senescence-accelerated OXYS rats. *Aging*, 4(1), 49.

Bai X, et al. (2010) Genetic dissection of rice grain shape using a recombinant inbred line population derived from two contrasting parents and fine mapping a pleiotropic quantitative trait locus qGL7. *BMC genetics*, 11, 16.

Nganga JK, et al. (2010) High resolution mapping of trypanosomosis resistance loci Tir2 and Tir3 using F12 advanced intercross lines with major locus Tir1 fixed for the susceptible allele. *BMC genomics*, 11, 394.