

Resource Summary Report

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MAREYMAP

RRID:SCR_009066

Type: Tool

Proper Citation

MAREYMAP (RRID:SCR_009066)

Resource Information

URL: <http://pbil.univ-lyon1.fr/software/mareymap/>

Proper Citation: MAREYMAP (RRID:SCR_009066)

Description: Software application that is a meiotic recombination rate estimation program. (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: MAREYMAP

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, r, tcl/tk

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MAREYMAP

Resource ID: SCR_009066

Alternate IDs: nlx_154056

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260731T042806+0000

Ratings and Alerts

No rating or validation information has been found for MAREYMAP.

No alerts have been found for MAREYMAP.

Data and Source Information

Usage and Citation Metrics

We found 41 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Zahid A, et al. (2025) Identifying genetic susceptibility loci associated with human coronary artery disease. PloS one, 20(1), e0315460.

Pushman C, et al. (2025) QTL identification and characterization of the recombination landscape of the mountain pine beetle (*Dendroctonus ponderosae*). G3 (Bethesda, Md.), 15(7).

Crombez E, et al. (2025) The subordinate role of pseudogenization to recombinative deletion following polyploidization in angiosperms. Nature communications, 16(1), 6335.

Leitwein M, et al. (2024) The Fate of a Polygenic Phenotype Within the Genomic Landscapes of Introgression in the European Seabass Hybrid Zone. Molecular biology and evolution, 41(9).

Grattapaglia D, et al. (2024) High-density linkage to physical mapping in a unique Tall × Dwarf coconut (*Cocos nucifera* L.) outbred F2 uncovers a major QTL for flowering time colocalized with the FLOWERING LOCUS T (FT). Frontiers in plant science, 15, 1408239.

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).

Nagasaka K, et al. (2024) A low-cost dpMIG-seq method for elucidating complex inheritance in polysomic crops: a case study in tetraploid blueberry. Horticulture research, 11(11), uhae248.

Ollitrault P, et al. (2024) Comparative genetic mapping and a consensus interspecific genetic map reveal strong synteny and collinearity within the Citrus genus. Frontiers in plant science, 15, 1475965.

Calvez L, et al. (2023) Meiotic Behaviors of Allotetraploid Citrus Drive the Interspecific Recombination Landscape, the Genetic Structures, and Traits Inheritance in Tetrazyg Progenies Aiming to Select New Rootstocks. Plants (Basel, Switzerland), 12(8).

McConaughy S, et al. (2023) Recombination hotspots in soybean [*Glycine max* (L.) Merr.]. G3 (Bethesda, Md.), 13(6).

Ponnikas S, et al. (2022) Extreme variation in recombination rate and genetic diversity along the *Sylvioidea* neo-sex chromosome. Molecular ecology, 31(13), 3566.

Slater GP, et al. (2022) Haploid and Sexual Selection Shape the Rate of Evolution of Genes across the Honey Bee (*Apis mellifera* L.) Genome. Genome biology and evolution, 14(6).

Brazier T, et al. (2022) Diversity and determinants of recombination landscapes in flowering plants. *PLoS genetics*, 18(8), e1010141.

Smith SR, et al. (2022) A chromosome-anchored genome assembly for Lake Trout (*Salvelinus namaycush*). *Molecular ecology resources*, 22(2), 679.

Robledo-Ruiz DA, et al. (2022) Chromosome-length genome assembly and linkage map of a critically endangered Australian bird: the helmeted honeyeater. *GigaScience*, 11.

Mérot C, et al. (2021) Locally Adaptive Inversions Modulate Genetic Variation at Different Geographic Scales in a Seaweed Fly. *Molecular biology and evolution*, 38(9), 3953.

de Blas FJ, et al. (2021) Genetic mapping and QTL analysis for peanut smut resistance. *BMC plant biology*, 21(1), 312.

Leitwein M, et al. (2021) Associative Overdominance and Negative Epistasis Shape Genome-Wide Ancestry Landscape in Supplemented Fish Populations. *Genes*, 12(4).

Liu G, et al. (2021) Identify of Fast-Growing Related Genes Especially in Height Growth by Combining QTL Analysis and Transcriptome in *Salix matsudana* (Koidz). *Frontiers in genetics*, 12, 596749.

Shen C, et al. (2021) *Gossypium tomentosum* genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. *Genomics*, 113(4), 1999.