## **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)

Abbreviations: MAREYMAP

Resource Type: software application, software resource

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

Funding:

Resource Name: MAREYMAP

Resource ID: SCR\_009066

Alternate IDs: nlx\_154056

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250419T055154+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

Source: SciCrunch Registry

#### **Usage and Citation Metrics**

We found 39 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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.

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

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).

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

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).

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.

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

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.

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

Correa M, et al. (2021) The Transposable Element Environment of Human Genes Differs According to Their Duplication Status and Essentiality. Genome biology and evolution, 13(5).

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.

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.

Chen ZJ, et al. (2020) Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement. Nature genetics, 52(5), 525.