

Resource Summary Report

Generated by T1D on Aug 1, 2026

R/ONEMAP

RRID:SCR_009371

Type: Tool

Proper Citation

R/ONEMAP (RRID:SCR_009371)

Resource Information

URL: <https://cran.r-project.org/web/packages/onemap/index.html>

Proper Citation: R/ONEMAP (RRID:SCR_009371)

Description: Software environment for constructing linkage maps in outcrossing plant species, using full-sib families derived from two outbreed (non-inbreeding) parent plants. (entry from Genetic Analysis Software)

Synonyms: ONEMAP

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, r

Resource Name: R/ONEMAP

Resource ID: SCR_009371

Alternate IDs: nlx_154502, SCR_009312, nlx_154593

Old URLs: <http://www.ciagri.usp.br/~aafgarci/OneMap/>

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260731T042821+0000

Ratings and Alerts

No rating or validation information has been found for R/ONEMAP.

No alerts have been found for R/ONEMAP.

Data and Source Information

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Ouellet-Fagg CL, et al. (2025) Complex and Dynamic Gene-by-Age and Gene-by-Environment Interactions Underlie Functional Morphological Variation in Adaptive Divergence in Arctic Charr (*Salvelinus alpinus*). *Evolution & development*, 27(1), e70000.

Chen R, et al. (2023) XY sex determination in a cnidarian. *BMC biology*, 21(1), 32.

Liu T, et al. (2022) Genome-wide identification of quantitative trait loci for morpho-agronomic and yield-related traits in foxtail millet (*Setaria italica*) across multi-environments. *Molecular genetics and genomics : MGG*, 297(3), 873.

Bartaula R, et al. (2019) Mapping non-host resistance to the stem rust pathogen in an interspecific barberry hybrid. *BMC plant biology*, 19(1), 319.

Hardigan MA, et al. (2019) Genome Synteny Has Been Conserved Among the Octoploid Progenitors of Cultivated Strawberry Over Millions of Years of Evolution. *Frontiers in plant science*, 10, 1789.

Miller JT, et al. (2019) Developing a High-Quality Linkage Map for the Atlantic Killifish *Fundulus heteroclitus*. *G3 (Bethesda, Md.)*, 9(9), 2851.

Smith HM, et al. (2018) Genetic identification of SNP markers linked to a new grape phylloxera resistant locus in *Vitis cinerea* for marker-assisted selection. *BMC plant biology*, 18(1), 360.

Kodama M, et al. (2018) Influence of a growth hormone transgene on the genetic architecture of growth-related traits: A comparative analysis between transgenic and wild-type coho salmon. *Evolutionary applications*, 11(10), 1886.

Smith HM, et al. (2018) SNP markers tightly linked to root knot nematode resistance in grapevine (*Vitis cinerea*) identified by a genotyping-by-sequencing approach followed by Sequenom MassARRAY validation. *PloS one*, 13(2), e0193121.

Oral M, et al. (2017) Gene-centromere mapping in meiotic gynogenetic European seabass. *BMC genomics*, 18(1), 449.

Nunes JR, et al. (2017) Large-scale SNP discovery and construction of a high-density genetic map of *Colossoma macropomum* through genotyping-by-sequencing. *Scientific reports*, 7, 46112.

Niedzicka M, et al. (2017) Linkage Map of Lissotriton Newts Provides Insight into the Genetic Basis of Reproductive Isolation. *G3 (Bethesda, Md.)*, 7(7), 2115.

Schiffthaler B, et al. (2017) BatchMap: A parallel implementation of the OneMap R package for fast computation of F1 linkage maps in outcrossing species. PloS one, 12(12), e0189256.

Brown JK, et al. (2016) Mapping the sex determination locus in the h?puku (Polyprion oxygeneios) using ddRAD sequencing. BMC genomics, 17, 448.

Pértille F, et al. (2016) High-throughput and Cost-effective Chicken Genotyping Using Next-Generation Sequencing. Scientific reports, 6, 26929.

Palaiokostas C, et al. (2015) A novel sex-determining QTL in Nile tilapia (Oreochromis niloticus). BMC genomics, 16(1), 171.

Zhou Z, et al. (2015) High-Density Genetic Mapping with Interspecific Hybrids of Two Sea Urchins, Strongylocentrotus nudus and S. intermedius, by RAD Sequencing. PloS one, 10(9), e0138585.

Kodama M, et al. (2014) Comparative mapping between Coho Salmon (Oncorhynchus kisutch) and three other salmonids suggests a role for chromosomal rearrangements in the retention of duplicated regions following a whole genome duplication event. G3 (Bethesda, Md.), 4(9), 1717.

Palaiokostas C, et al. (2013) Mapping and validation of the major sex-determining region in Nile tilapia (Oreochromis niloticus L.) Using RAD sequencing. PloS one, 8(7), e68389.

Palaiokostas C, et al. (2013) Mapping the sex determination locus in the Atlantic halibut (Hippoglossus hippoglossus) using RAD sequencing. BMC genomics, 14, 566.