

Resource Summary Report

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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 application, software resource

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: 20260805T044221+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 [RRID](#) .

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.