

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 9, 2026

ALLMAPS

RRID:SCR_021171

Type: Tool

Proper Citation

ALLMAPS (RRID:SCR_021171)

Resource Information

URL: <https://github.com/tanghaibao/jcvi/wiki/ALLMAPS>

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Description: Software tool for computing scaffold ordering that maximizes colinearity to collection of maps, including genetic, physical or comparative maps into final chromosome build. Robust scaffold ordering based on multiple maps.

Resource Type: software resource

Defining Citation: [PMID:25583564](#)

Keywords: Scaffold ordering, maps collection, genetic maps, physical maps, comparative maps, chromosome build

Funding: Fujian 100 Talent Plan award ;
Gordon and Betty Moore Foundation ;
National Science Foundation DBI 0735191;
National Science Foundation DBI 1265383

Availability: Free, Available for download, Freely available

Resource Name: ALLMAPS

Resource ID: SCR_021171

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260808T190202+0000

Ratings and Alerts

No rating or validation information has been found for ALLMAPS.

No alerts have been found for ALLMAPS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Lötter A, et al. (2022) Haplogenome assembly reveals structural variation in *Eucalyptus* interspecific hybrids. *GigaScience*, 12.

Qi W, et al. (2022) The haplotype-resolved chromosome pairs of a heterozygous diploid African cassava cultivar reveal novel pan-genome and allele-specific transcriptome features. *GigaScience*, 11.

Si Z, et al. (2022) Construction of a high-density genetic map and identification of QTLs related to agronomic and physiological traits in an interspecific (*Gossypium hirsutum* × *Gossypium barbadense*) F2 population. *BMC genomics*, 23(1), 307.

Ma A, et al. (2021) Identification of quantitative trait loci associated with upper temperature tolerance in turbot, *Scophthalmus maximus*. *Scientific reports*, 11(1), 21920.

Jin S, et al. (2020) Rationally Designed APOBEC3B Cytosine Base Editors with Improved Specificity. *Molecular cell*, 79(5), 728.