

# Resource Summary Report

Generated by T1D on Aug 10, 2026

## ALLMAPS

RRID:SCR\_021171

Type: Tool

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### Proper Citation

ALLMAPS (RRID:SCR\_021171)

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### Resource Information

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

**Proper Citation:** ALLMAPS (RRID:SCR\_021171)

**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

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### Ratings and Alerts

No rating or validation information has been found for ALLMAPS.

No alerts have been found for ALLMAPS.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.