

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

SNPchip

RRID:SCR_001269

Type: Tool

Proper Citation

SNPchip (RRID:SCR_001269)

Resource Information

URL: <http://www.bioconductor.org/packages/2.0/bioc/html/SNPchip.html>

Proper Citation: SNPchip (RRID:SCR_001269)

Description: Software package that contains classes and methods useful for storing, visualizing and analyzing high density SNP data. Originally developed from the SNPscan web-tool, SNPchip utilizes S4 classes and extends other open source R tools available at Bioconductor, including the R packages Biobase and oligo. This has numerous advantages, including the ability to build statistical models for SNP-level data that operate on instances of the class, and to communicate with other R packages that add additional functionality.

Abbreviations: SNPchip

Resource Type: software resource

Defining Citation: [PMID:17204461](#)

Keywords: dna copy number, snp, genetic variability, visualization, high throughput, snp chip, microarray, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: SNPchip

Resource ID: SCR_001269

Alternate IDs: OMICS_02069, biotools:snpchip

Alternate URLs: <https://bio.tools/snpchip>

License: GNU General Public License, v2 or newer

Record Creation Time: 20220129T080206+0000

Ratings and Alerts

No rating or validation information has been found for SNPchip.

No alerts have been found for SNPchip.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Floridia V, et al. (2025) Uncovering the architecture of production-driven introgression in Cinisara cattle breed. BMC genomic data, 26(1), 47.

Lukic B, et al. (2024) Genomic diversity and population structure of Carniolan honey bee in its native habitat. BMC genomics, 25(1), 849.

Klepac CN, et al. (2024) Assessing acute thermal assays as a rapid screening tool for coral restoration. Scientific reports, 14(1), 1898.

Luzarowska U, et al. (2023) Hello darkness, my old friend: 3-KETOACYL-COENZYME A SYNTHASE4 is a branch point in the regulation of triacylglycerol synthesis in Arabidopsis thaliana. The Plant cell, 35(6), 1984.

Taagen E, et al. (2022) If it ain't broke, don't fix it: evaluating the effect of increased recombination on response to selection for wheat breeding. G3 (Bethesda, Md.), 12(12).

Yuan T, et al. (2020) Roles for circulating polyunsaturated fatty acids in ischemic stroke and modifiable factors: a Mendelian randomization study. Nutrition journal, 19(1), 70.

Bianchi M, et al. (2020) Whole-genome genotyping and resequencing reveal the association of a deletion in the complex interferon alpha gene cluster with hypothyroidism in dogs. BMC genomics, 21(1), 307.

Barbato M, et al. (2020) Adaptive introgression from indicine cattle into white cattle breeds from Central Italy. Scientific reports, 10(1), 1279.

Pégard M, et al. (2019) Sequence imputation from low density single nucleotide polymorphism panel in a black poplar breeding population. BMC genomics, 20(1), 302.

Cesar ASM, et al. (2018) Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. BMC genomics, 19(1), 499.

Barroso LMA, et al. (2017) Regularized quantile regression for SNP marker estimation of pig growth curves. *Journal of animal science and biotechnology*, 8, 59.

Farias FHG, et al. (2017) The practical use of genome sequencing data in the management of a feline colony pedigree. *BMC veterinary research*, 13(1), 225.

Berg PR, et al. (2015) Adaptation to Low Salinity Promotes Genomic Divergence in Atlantic Cod (*Gadus morhua* L.). *Genome biology and evolution*, 7(6), 1644.