

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

QualitySNPng

RRID:SCR_002479

Type: Tool

Proper Citation

QualitySNPng (RRID:SCR_002479)

Resource Information

URL: <http://www.bioinformatics.nl/QualitySNPng/>

Proper Citation: QualitySNPng (RRID:SCR_002479)

Description: Software for the detection and visualization of single nucleotide polymorphisms (SNPs) from next generation sequencing data that uses a haplotype-based strategy.

Resource Type: data visualization software, software resource, software application, data processing software, standalone software

Defining Citation: [PMID:23632165](#)

Keywords: single nucleotide polymorphism, haplotype strategy, next generation sequencing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: QualitySNPng

Resource ID: SCR_002479

Alternate IDs: biotools:qualitysnpng, OMICS_00070

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

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260728T043133+0000

Ratings and Alerts

No rating or validation information has been found for QualitySNPng.

No alerts have been found for QualitySNPng.

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 [nidm-terms](#) .

Clot CR, et al. (2025) Resolving a century-old enigma: potato 'Bolters' originate from instability of the StCDF1.3 allele. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(10), 245.

van Haperen P, et al. (2021) Fine mapping of a thrips resistance QTL in Capsicum and the role of diterpene glycosides in the underlying mechanism. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 134(5), 1557.

Vilela MM, et al. (2017) Analysis of Three Sugarcane Homo/Homeologous Regions Suggests Independent Polyploidization Events of Saccharum officinarum and Saccharum spontaneum. Genome biology and evolution, 9(2), 266.

Fu Y, et al. (2016) Transcriptome Analysis of Gerbera hybrida Including in silico Confirmation of Defense Genes Found. Frontiers in plant science, 7, 247.

Scholten OE, et al. (2016) SNP-markers in Allium species to facilitate introgression breeding in onion. BMC plant biology, 16(1), 187.

Koning-Boucoiran CF, et al. (2015) Using RNA-Seq to assemble a rose transcriptome with more than 13,000 full-length expressed genes and to develop the WagRhSNP 68k Axiom SNP array for rose (Rosa L.). Frontiers in plant science, 6, 249.