Resource Summary Report

Generated by NIF on Aug 20, 2026

qSNP

RRID:SCR_005105
Type: Tool

Proper Citation

qSNP (RRID:SCR_005105)

Resource Information

URL: http://www.qcmg.org/bioinformatics/tiki-index.php

Proper Citation: qSNP (RRID:SCR_005105)

Description: A single nucleotide variant caller optimised for identifying somatic variants in low cellularity cancer samples.

Abbreviations: qSNP

Resource Type: software resource

Defining Citation: PMID:24250782

Related Condition: Cancer

Resource Name: qSNP

Resource ID: SCR_005105

Alternate IDs: OMICS_00089

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260815T182307+0000

Ratings and Alerts

No rating or validation information has been found for qSNP.

No alerts have been found for qSNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Zhang J, et al. (2026) Cancer genome standards for long-read sequencing using cancer cell line mixtures. GigaScience, 15.

Nones K, et al. (2026) Multi-omics reveals key molecular and cellular features of advanced small cell lung cancers associated with distinct therapeutic opportunities. Genome medicine, 18(1).

Strom NI, et al. (2025) Genome-wide analyses identify 30 loci associated with obsessive-compulsive disorder. Nature genetics, 57(6), 1389.

Foote IF, et al. (2025) Uncovering the multivariate genetic architecture of frailty with genomic structural equation modeling. Nature genetics, 57(8), 1848.

Park S, et al. (2024) Multivariate genomic analysis of 5 million people elucidates the genetic architecture of shared components of the metabolic syndrome. Nature genetics, 56(11), 2380.

Straube J, et al. (2023) Cre recombinase expression cooperates with homozygous FLT3 internal tandem duplication knockin mouse model to induce acute myeloid leukemia. Leukemia, 37(4), 741.

, et al. (2023) GWAS meta-analysis of over 29,000 people with epilepsy identifies 26 risk loci and subtype-specific genetic architecture. Nature genetics, 55(9), 1471.

Kojic M, et al. (2023) Efficient detection and monitoring of pediatric brain malignancies with liquid biopsy based on patient-specific somatic mutation screening. Neuro-oncology, 25(8), 1507.

Davidson AL, et al. (2023) The clinical utility and costs of whole-genome sequencing to detect cancer susceptibility variants-a multi-site prospective cohort study. Genome medicine, 15(1), 74.

Bonazzi VF, et al. (2022) ctDNA as a biomarker of progression in oesophageal adenocarcinoma. ESMO open, 7(3), 100452.

Newell F, et al. (2022) Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer cell, 40(1), 88.

Newell F, et al. (2022) Comparative Genomics Provides Etiologic and Biological Insight into Melanoma Subtypes. Cancer discovery, 12(12), 2856.

Kondrashova O, et al. (2021) Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. Cancers, 13(8).

Newell F, et al. (2020) Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature communications, 11(1), 5259.

Aoude LG, et al. (2020) Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. Scientific reports, 10(1), 17687.

Joshi SK, et al. (2020) A trusted node-free eight-user metropolitan quantum communication network. Science advances, 6(36).

Wang G, et al. (2019) Facile Fabrication of Fluorescent Inorganic Nanoparticles with Diverse Shapes for Cell Imaging. Nanomaterials (Basel, Switzerland), 9(2).

Akgül S, et al. (2019) Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. Cancers, 11(2).

Newell F, et al. (2019) Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature communications, 10(1), 3163.

Newell F, et al. (2019) Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. BMC medical genomics, 12(1), 31.