

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 8, 2026

TAGSNP

RRID:SCR_008623

Type: Tool

Proper Citation

TAGSNP (RRID:SCR_008623)

Resource Information

URL: <http://www-rcf.usc.edu/~stram/tagSNPs.html>

Proper Citation: TAGSNP (RRID:SCR_008623)

Description: Software application (entry from Genetic Analysis Software)

Abbreviations: TAGSNP

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, fortran90

Resource Name: TAGSNP

Resource ID: SCR_008623

Alternate IDs: nlx_154671

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260808T190453+0000

Ratings and Alerts

No rating or validation information has been found for TAGSNP.

No alerts have been found for TAGSNP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 71 mentions in open access literature.

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

Yang W, et al. (2026) Research note: Genome-wide association study reveals candidate genes for egg production in Muscovy duck. *Poultry science*, 105(9), 107198.

Choi SH, et al. (2025) AKT1 Functional Polymorphism (rs2494750) Influences Clinical Outcomes in Patients With Advanced Lung Cancer Treated With EGFR Inhibitors. *Journal of Korean medical science*, 40(31), e184.

Zhou YL, et al. (2025) The rs34416841 polymorphism in the Alu element of the circSirt1 flanking intron is associated with an increased risk of myocardial infarction. *BMC medical genomics*, 19(1), 9.

Shilenok I, et al. (2024) C11orf58 (Hero20) Gene Polymorphism: Contribution to Ischemic Stroke Risk and Interactions with Other Heat-Resistant Obscure Chaperones. *Biomedicines*, 12(11).

Adjemout M, et al. (2024) From Genome-wide Association Studies to Functional Variants: ARL14 Cis-regulatory Variants Are Associated With Severe Malaria. *The Journal of infectious diseases*, 230(3), e743.

Cheng S, et al. (2024) Harnessing landrace diversity empowers wheat breeding. *Nature*, 632(8026), 823.

Lee JH, et al. (2023) Genetic variants in key necroptosis regulators predict prognosis of non-small cell lung cancer after surgical resection. *Thoracic cancer*, 14(26), 2678.

Hebbar P, et al. (2023) Linkage analysis using whole exome sequencing data implicates SLC17A1, SLC17A3, TATDN2 and TMEM131L in type 1 diabetes in Kuwaiti families. *Scientific reports*, 13(1), 14978.

Lee S, et al. (2023) Genetic variants of NEUROD1 target genes are associated with clinical outcomes of small-cell lung cancer patients. *Thoracic cancer*, 14(13), 1145.

Warburton ML, et al. (2022) Comparative Analysis of Multiple GWAS Results Identifies Metabolic Pathways Associated with Resistance to *A. flavus* Infection and Aflatoxin Accumulation in Maize. *Toxins*, 14(11).

Lee JH, et al. (2022) Epigenetic readers and lung cancer: the rs2427964C>T variant of the bromodomain and extraterminal domain gene BRD3 is associated with poorer survival outcome in NSCLC. *Molecular oncology*, 16(3), 750.

Choi SH, et al. (2022) Genetic variants in LKB1/AMPK/mTOR pathway are associated with clinical outcomes of chemotherapy in non-small cell lung cancer. *Thoracic cancer*, 13(23), 3322.

Wittenburg D, et al. (2021) Grouping of genomic markers in populations with family structure. *BMC bioinformatics*, 22(1), 79.

Lee JH, et al. (2021) Impact of immune checkpoint gene CD155 Ala67Thr and CD226 Gly307Ser polymorphisms on small cell lung cancer clinical outcome. *Scientific reports*, 11(1), 1794.

Parra-Galindo MA, et al. (2021) Pathway-based analysis of anthocyanin diversity in diploid potato. *PloS one*, 16(4), e0250861.

Benna C, et al. (2021) Gender-specific associations between polymorphisms of the circadian gene RORA and cutaneous melanoma susceptibility. *Journal of translational medicine*, 19(1), 57.

Mohr S, et al. (2021) The alternative serotonin transporter promoter P2 impacts gene function in females with irritable bowel syndrome. *Journal of cellular and molecular medicine*, 25(16), 8047.

Kang MK, et al. (2021) Prognostic significance of genetic variants in GLUT1 in stage III non-small cell lung cancer treated with radiotherapy. *Thoracic cancer*, 12(6), 874.

Zhou W, et al. (2021) A case-control study on correlation between the single nucleotide polymorphism of CLEC4E and the susceptibility to tuberculosis among Han people in Western China. *BMC infectious diseases*, 21(1), 788.

Li Z, et al. (2020) Association of Genetic and Environmental Factors with Non-Alcoholic Fatty Liver Disease in a Chinese Han Population. *International journal of environmental research and public health*, 17(14).