

Resource Summary Report

Generated by [NIF](#) on Aug 26, 2026

GATK HaplotypeCaller

RRID:SCR_028440

Type: Tool

Proper Citation

GATK HaplotypeCaller (RRID:SCR_028440)

Resource Information

URL: <https://gatk.broadinstitute.org/hc/en-us/articles/360042913231-HaplotypeCaller>

Proper Citation: GATK HaplotypeCaller (RRID:SCR_028440)

Description: Software tool for identifying single nucleotide polymorphisms (SNPs) and insertion/deletion (indels) variants, offering high accuracy via local de-novo assembly of reads. It works by identifying "active regions" with potential variation, reassembling those reads, and calculating genotype likelihoods, making it superior for complex variant detection.

Resource Type: software application, software resource

Defining Citation: [DOI:10.1101/201178](https://doi.org/10.1101/201178)

Keywords: identifying single nucleotide polymorphisms, insertion, deletion, indels, variants, local de-novo assembly of reads,

Availability: Free, Freely available

Resource Name: GATK HaplotypeCaller

Resource ID: SCR_028440

Alternate URLs: <https://gatk.broadinstitute.org/hc/en-us>,
<https://gatk.broadinstitute.org/hc/en-us/articles/360035531412-HaplotypeCaller-in-a-nutshell>

Record Creation Time: 20260514T062433+0000

Record Last Update: 20260821T043158+0000

Ratings and Alerts

No rating or validation information has been found for GATK HaplotypeCaller.

No alerts have been found for GATK HaplotypeCaller.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 104 mentions in open access literature.

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

Dusthacker A, et al. (2026) Wild-type MIC distribution and evaluation of epidemiological cut-offs of second-line TB-drugs in susceptible and MDR-TB clinical isolates from Chennai, India. *Frontiers in microbiology*, 17, 1739149.

Jurynek MJ, et al. (2026) PIEZO1 variants that reduce open channel probability are associated with familial osteoarthritis. *The Journal of biological chemistry*, 302(5), 111426.

Moloto K, et al. (2026) Carbapenem resistant *Klebsiella pneumoniae* isolates at a tertiary hospital in Cape Town, South Africa, are dominated by specific local clones rather than previously described international lineages. *PLoS pathogens*, 22(1), e1013859.

Fu L, et al. (2026) Completely resolved structural variants by optical genome mapping with adaptive sampling from CNV discovery. *NPJ genomic medicine*, 11(1).

Ahoty ESS, et al. (2026) Whole-Genome Sequencing and Analysis Reveals Plant Growth-Promoting Properties and Biocontrol Potential of the *Crotalaria retusa* Endophytic *Bacillus velezensis* Strain G2T39. *Microorganisms*, 14(1).

Hinson S, et al. (2026) Non-uniform chromosomal SNP density biases sites of meiotic crossovers in *Drosophila melanogaster*. *G3 (Bethesda, Md.)*, 16(6).

Güneş N, et al. (2026) Acromelic dysplasias: similarities and differences in clinical and molecular findings in 12 Turkish patients. *European journal of pediatrics*, 185(6).

Härkönen J, et al. (2026) Clinicopathological characteristics of patients with inoperable non-small cell lung cancer harboring circulating NRF2 pathway mutations. *The Journal of pathology*, 269(2), 164.

Chao MC, et al. (2026) Population-level genome sequencing reveals distinct *Mycobacterium tuberculosis* intrahost mutational trajectories in simian immunodeficiency virus co-infected and antiretroviral treated non-human primates. *bioRxiv : the preprint server for biology*.

Shen Y, et al. (2026) HSD17B7 is required for the function of sensory hair cells by regulating cholesterol synthesis. *eLife*, 14.

Peabody I, et al. (2026) An NT5E loss-of-function variant permits tissue inflammation and hypertension in systemic lupus erythematosus. *iScience*, 29(6), 116017.

Eržen M, et al. (2026) Population Structure of Genotypes and Genome-Wide Association Studies of Cannabinoids and Terpenes Synthesis in Hemp (*Cannabis sativa* L.). *Plants* (Basel, Switzerland), 15(2).

Kim N, et al. (2026) Performance Evaluation of Whole-Genome Amplification Platforms for Clinical Next-Generation Sequencing with Minimal Nucleic Acid Input. *Annals of laboratory medicine*, 46(4), 476.

Zhu Y, et al. (2026) Primary pulmonary angiosarcoma: A case study with genetic insights and potential therapeutic targets. *Oncology letters*, 31(1), 15.

Gao W, et al. (2025) Screening for Resistant Germplasms and Quantitative Trait Locus Mapping of Resistance to Tomato Chlorosis Virus. *International journal of molecular sciences*, 26(5).

Murdock DR, et al. (2025) Non-canonical splice variants in thoracic aortic dissection cases and Marfan syndrome with negative genetic testing. *NPJ genomic medicine*, 10(1), 25.

Klangjorhor J, et al. (2025) Compound Heterozygous Null Variants in *ITGB4* Gene Causing Severe Phenotype of Junctional Epidermolysis Bullosa With Pyloric Atresia in Thai Newborn: Genotype-Phenotype Correlation From a Case Report and Review of the Literature. *International journal of genomics*, 2025, 2680052.

Ebrahimi Z, et al. (2025) Evaluation of Germline Pathogenic Variant of *TP53* Gene in an Iranian Pedigree with Familial Sarcoma: A Case Report. *Advanced biomedical research*, 14, 160.

Zheng K, et al. (2025) A *FANCD2* gene mutation case analysis providing potential insights into the molecular mechanisms of gastric adenocarcinoma: A case report. *Oncology letters*, 30(3), 422.

Sina M, et al. (2025) Germline testing of Iranian families suspected of Lynch syndrome: molecular characterization and current surveillance of families with pathogenic variants in *MSH2*, *MSH6*, and *PMS2*. *European journal of cancer prevention : the official journal of the European Cancer Prevention Organisation (ECP)*, 34(4), 349.