Resource Summary Report

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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

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: 20260904T001201+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 kravitz2 .

Dusthackeer 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.

Jurynec 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).

Güne? 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.