

Resource Summary Report

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[vcf2maf](#)

RRID:SCR_027063

Type: Tool

Proper Citation

vcf2maf (RRID:SCR_027063)

Resource Information

URL: <https://github.com/mskcc/vcf2maf>

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Description: Software tool to convert Virtual Contact File into Mutation Annotation Format, where each variant is annotated to only one of all possible gene isoforms.

Resource Type: source code, software application, software resource

Keywords: Virtual Contact File, Mutation Annotation Format, convert VCF into MAF, gene isoforms, genomics, aggregate mutation data, storing genetic variation data, variant annotation, one gene isoform,

Availability: Free, Available for download, Freely available

Resource Name: vcf2maf

Resource ID: SCR_027063

License: Apache license

Record Creation Time: 20250614T055057+0000

Record Last Update: 20260815T183254+0000

Ratings and Alerts

No rating or validation information has been found for vcf2maf.

No alerts have been found for vcf2maf.

Data and Source Information

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Yan P, et al. (2026) Aging-associated differences in mammary tumor-initiating populations and immune evasion pathways in breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*, 123(8), e2523254123.

Safonov A, et al. (2026) Homologous recombination deficiency and hemizyosity drive resistance in breast cancer. *Nature*, 652(8110), 752.

Siga H, et al. (2026) Resolving the Haplotype Complexity of Colorectal Cancer Genomes with Droplet Barcode Sequencing. *Life (Basel, Switzerland)*, 16(6).

De Marco L, et al. (2026) NOUS-209 Off-the-shelf Immunotherapy Has the Potential to Hit Primary and Metachronous Colorectal and Urothelial Cancers in Lynch Syndrome. *Molecular cancer therapeutics*, 25(4), 650.

Yoshimoto D, et al. (2026) Downregulation of HLA Class I Expression through HLA-A DNA Methylation Is Associated with Reduced CD8+ T-cell Infiltration in Cervical Cancer. *Cancer immunology research*, 14(1), 77.

Tran T, et al. (2026) Disruption of the structural maintenance of chromosomes 5/6 complex enables tumor mutagenesis. *NAR cancer*, 8(2), zcag012.

Browne IM, et al. (2026) The Prognostic and Predictive Impact of ctDNA Levels in Patients with Advanced Breast Cancer Enrolled on the plasmaMATCH Trial. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(1), 148.

Jiménez-Sánchez A, et al. (2026) Transcriptomic Plasticity Is a Hallmark of Metastatic Pancreatic Cancer. *Cancer research*, 86(7), 1769.

Blas M, et al. (2026) Evaluation of ensilication technology for ambient DNA preservation. *NAR molecular medicine*, 3(1), ugag011.

Feng C, et al. (2026) Spatial tumor evolution panorama of ovarian cancer. *Cell reports. Medicine*, 7(3), 102666.

Sauty SM, et al. (2026) Motif-Centered Analyses Reveal Universal and Tissue-Specific Mutagenic Mechanisms Operating in the Human Body. *bioRxiv : the preprint server for biology*.

Chang HY, et al. (2026) Uniform Processing of Diverse Sequencing Data: A Cross-Population Comparison of Colon Cancer Genomic Landscapes from The Cancer Genome Atlas and a Chinese Cohort. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(5), 762.

Tanaka A, et al. (2025) Proteogenomic profiling of soft tissue leiomyosarcoma reveals distinct molecular subtypes with divergent outcomes and therapeutic vulnerabilities. *bioRxiv : the preprint server for biology*.

Lee YJ, et al. (2025) Oncogenic pathway landscape of ovarian cancer and correlation with clinical prognosis. *Journal of gynecologic oncology*, 36(6), e128.

Wang X, et al. (2025) CaMutQC: An R package for integrative quality control and filtration of cancer somatic mutations. *Computational and structural biotechnology journal*, 27, 3147.

Das S, et al. (2025) Comparative genomic and clinicopathological analysis uncovers contrasting molecular profiles of canine and human thyroid carcinomas. *Communications biology*, 9(1), 4.

Park CK, et al. (2023) Evaluation of Blood Tumor Mutation Burden for the Efficacy of Second-Line Atezolizumab Treatment in Non-Small Cell Lung Cancer: BUDDY Trial. *Cells*, 12(9).

Scheiter A, et al. (2022) Wnt/ β -Catenin-Pathway Alterations and Homologous Recombination Deficiency in Cholangiocarcinoma Cell Lines and Clinical Samples: Towards Specific Vulnerabilities. *Journal of personalized medicine*, 12(8).

Nilsson LM, et al. (2022) Genetics and Therapeutic Responses to Tumor-Infiltrating Lymphocyte Therapy of Pancreatic Cancer Patient-Derived Xenograft Models. *Gastro hep advances*, 1(6), 1037.

Ren F, et al. (2022) Cross Analysis of Genomic-Pathologic Features on Multiple Primary Hepatocellular Carcinoma. *Frontiers in genetics*, 13, 846517.