Resource Summary Report

Generated by ASWG on Aug 2, 2026

Control-FREEC

RRID:SCR_010822
Type: Tool

Proper Citation

Control-FREEC (RRID:SCR_010822)

Resource Information

URL: http://bioinfo-out.curie.fr/projects/freec/tutorial.html

Proper Citation: Control-FREEC (RRID:SCR_010822)

Description: Prediction of copy number alterations and loss of heterozygosity using deep-sequencing data.

Abbreviations: Control-FREEC

Resource Type: software resource

Resource Name: Control-FREEC

Resource ID: SCR_010822

Alternate IDs: OMICS_00344

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190416+0000

Ratings and Alerts

No rating or validation information has been found for Control-FREEC.

No alerts have been found for Control-FREEC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 327 mentions in open access literature.

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

Morrissey RL, et al. (2026) Elucidating cooperative genetic events in DCIS progression in mutant p53-driven breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 123(2), e2526544123.

Mohammadi M, et al. (2025) Cyclin-dependent kinase 9 inhibitors as oncogene signaling modulators in combination with targeted therapy for the treatment of colorectal cancer. bioRxiv : the preprint server for biology.

Zheng C, et al. (2025) A novel organoid model retaining the glioma microenvironment for personalized drug screening and therapeutic evaluation. Bioactive materials, 53, 205.

Suzuki K, et al. (2025) Bidirectional anti-tumor and immunological strategies by targeting GARP-TGF-?? axis in adult T-cell leukemia/lymphoma. Leukemia, 39(10), 2465.

Du R, et al. (2025) Comparative study of tools for copy number variation detection using next-generation sequencing data. Scientific reports, 15(1), 22145.

Loegler V, et al. (2025) Whole-genome sequencing of 1,060 Brettanomyces bruxellensis isolates reveals significant phenotypic impact of acquired subgenomes in allopolyploids. Nature communications, 16(1), 5500.

Geng Z, et al. (2025) The Open Pediatric Cancer Project. GigaScience, 14.

Cui Q, et al. (2025) Genomic profiling and pathological assessment of malignant peripheral nerve sheath tumors. Journal of cancer research and clinical oncology, 151(5), 165.

Kyung SM, et al. (2025) Delineating molecular mechanisms on the acquisition of in vitro-adapted colistin-resistant Klebsiella pneumoniae by transcriptomic analysis. Microbiology spectrum, 13(12), e0342824.

Tian Y, et al. (2025) Comprehensive characterization of early-onset lung cancer, in Chinese young adults. Nature communications, 16(1), 1976.

Lee JJY, et al. (2025) ZIC1 is a context-dependent medulloblastoma driver in the rhombic lip. Nature genetics, 57(1), 88.

Zamuner FT, et al. (2025) Molecular patterns and mechanisms of tumorigenesis in HPV-associated and HPV-independent sinonasal squamous cell carcinoma. Nature communications, 16(1), 5285.

Hakim JMC, et al. (2025) Clinical Trypanosoma cruzi isolates share a common antigen repertoire that is absent from culture adapted strains. bioRxiv : the preprint server for biology.

Gao J, et al. (2025) Comprehensive genomic and transcriptomic analyses reveal prognostic stratification for esophageal squamous cell carcinoma. Signal transduction and targeted therapy, 10(1), 223.

Xie B, et al. (2025) Clinicopathological and molecular features of so-called low-grade oncocytic fumarate hydratase-deficient renal cell carcinoma: a study of 5 cases. Virchows Archiv : an international journal of pathology, 487(2), 377.

Wang N, et al. (2025) Benchmarking copy number variation detection with low-coverage whole-genome sequencing. Briefings in bioinformatics, 26(5).

Chen F, et al. (2025) Germline structural variations involving the pediatric brain tumor transcriptome include disease-relevant and ancestry-related genes. Acta neuropathologica communications, 13(1), 179.

Yin X, et al. (2025) Pathogenic germline variants in Chinese pancreatic adenocarcinoma patients. Nature communications, 16(1), 2214.

Sollier E, et al. (2025) Enhancer Hijacking Discovery in Acute Myeloid Leukemia by Pyjacker Identifies MNX1 Activation via Deletion 7q. Blood cancer discovery, 6(4), 343.

Zhang L, et al. (2025) Functional screening of somatic mutant events in extranodal natural killer/T-cell lymphoma with adrenal involvement. Frontiers in immunology, 16, 1566794.