

Resource Summary Report

Generated by [RRID](#) 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 [RRID](#) .

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*.

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.

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

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.

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

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

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.

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.

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

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.

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*.

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.

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.

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

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.

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

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.

Shi X, et al. (2025) Nanopore sequencing and hybrid assembly: unraveling the genomic landscape of dollar spot with enhanced annotation and drug resistance profiling. *Frontiers in fungal biology*, 6, 1621663.

Li ES, et al. (2025) Molecular subtyping of endometrial carcinoma cell lines uncovers subtype-specific targetable vulnerabilities. *NPJ precision oncology*, 9(1), 254.