Resource Summary Report

Generated by NIF on Sep 10, 2026

CHISEL

RRID:SCR_023220
Type: Tool

Proper Citation

CHISEL (RRID:SCR_023220)

Resource Information

URL: https://github.com/raphael-group/chisel

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Description: Software tool to infer allele and haplotype specific copy numbers in individual cells from low coverage single cell DNA sequencing data. Integrates weak allelic signals across individual cells, powering strength of single cell sequencing technologies to overcome weakness. Includes global clustering of RDRs and BAFs, and rigorous model selection procedure for inferring genome ploidy that improves both inference of allele specific and total copy numbers.

Abbreviations: CHISEL

Synonyms: Copy-number Haplotype Inference in Single-cell by Evolutionary Links

Resource Type: software application, software resource

Defining Citation: DOI:10.1038/s41587-020-0661-6

Keywords: infer allele and haplotype specific copy numbers, individual cells, low coverage single cell DNA sequencing data, weak allelic signals, weak signals integration,

Funding: Chan Zuckerberg Initiative DAF grants ;
NCI P30CA072720;
NCI U24CA211000;
NHGRI R01HG007069;
NSF CCF 1053753;
O'Brien Family Fund for Health Research ;
Wilke Family Fund for Innovation

Availability: Free, Available for download, Freely available

Resource Name: CHISEL

Resource ID: SCR_023220

Record Creation Time: 20230202T050240+0000

Record Last Update: 20260905T133313+0000

Ratings and Alerts

No rating or validation information has been found for CHISEL.

No alerts have been found for CHISEL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Bassiouni R, et al. (2026) Integrated Single-Cell Whole-Genome Sequencing and Spatial Transcriptomics Reveal Intratumoral Heterogeneity in Ovarian Cancer. Cancer research communications, 6(5), 1020.

Zhao Y, et al. (2025) High-resolution detection of copy number alterations in single cells with HiScanner. Nature communications, 16(1), 5477.

Kuzmin E, et al. (2024) Evolution of chromosome-arm aberrations in breast cancer through genetic network rewiring. Cell reports, 43(4), 113988.