# Resource Summary Report

Generated by NIF on Sep 14, 2026

## NovoBreak

RRID:SCR_026032
Type: Tool

### Proper Citation

NovoBreak (RRID:SCR_026032)

### Resource Information

**URL:** https://github.com/czc/nb_distribution

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**Description:** Software tool to discover somatic and germline structural variation breakpoints in whole genome sequencing data. Can report accurate breakpoints of Deletions, Duplications, Inversions and Translocations. Designed for Illumina paired-end data. Local assembly for breakpoint detection in cancer genomes.

**Resource Type:** software application, software resource, source code

**Defining Citation:** PMID:27892959

**Keywords:** discover somatic and germline structural variation, structural variation breakpoints, whole-genome sequencing data, local assembly, breakpoint detection, cancer genomes,

**Funding:** NCI P30 CA016672;
NCI R01 CA172652;
NHGRI U41 HG007497

**Availability:** Free, Available for download, Freely available,

**Resource Name:** NovoBreak

**Resource ID:** SCR_026032

**License:** MIT license

**Record Creation Time:** 20241113T053248+0000

**Record Last Update:** 20260912T200456+0000

### Ratings and Alerts

No rating or validation information has been found for NovoBreak.

No alerts have been found for NovoBreak.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Lee Y, et al. (2024) Prediction of the 3D cancer genome from whole-genome sequencing using InfoHiC. Molecular systems biology, 20(11), 1156.

Talsania K, et al. (2022) Structural variant analysis of a cancer reference cell line sample using multiple sequencing technologies. Genome biology, 23(1), 255.