

Resource Summary Report

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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.