

Resource Summary Report

Generated by [T1D](#) on Aug 9, 2026

Pindel

RRID:SCR_000560

Type: Tool

Proper Citation

Pindel (RRID:SCR_000560)

Resource Information

URL: <http://gmt.genome.wustl.edu/pindel/0.2.4/>

Proper Citation: Pindel (RRID:SCR_000560)

Description: Software to detect breakpoints of large deletions, medium sized insertions, inversions, tandem duplications and other structural variants at single-based resolution from next-gen sequence data. It uses a pattern growth approach to identify the breakpoints of these variants from paired-end short reads., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Pindel

Resource Type: software resource

Defining Citation: [PMID:19561018](#)

Keywords: deletion, insertion, nucleotide, genome, read, inversion, tandem duplication, structural variant, next-generation sequencing, pattern growth, indel, breakpoint, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Pindel

Resource ID: SCR_000560

Alternate IDs: biotools:pindel, OMICS_00321

Alternate URLs: <https://bio.tools/pindel>

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260808T185725+0000

Ratings and Alerts

No rating or validation information has been found for Pindel.

No alerts have been found for Pindel.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Tang C, et al. (2026) Investigating the determinants of immunotherapy response in the primary tumour of clear cell renal cell carcinoma (RCC). *BMJ oncology*, 5(2), e001031.

Chen J, et al. (2026) A Genomically Tailored Multiagent Precision Medicine Clinical Trial for Adults with Recurrent Glioblastoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1652.

Chang HY, et al. (2026) Uniform Processing of Diverse Sequencing Data: A Cross-Population Comparison of Colon Cancer Genomic Landscapes from The Cancer Genome Atlas and a Chinese Cohort. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(5), 762.

Li YR, et al. (2025) Long-Term Latency of Highly Mutated Cells in Normal Mouse Skin Is Reversed by Exposure to Tumor Promoters and Chronic Tissue Damage. *Cancer discovery*, 15(6), 1115.

Lee LH, et al. (2025) Defining Non-small Cell Lung Cancer Tumor Microenvironment Changes at Primary and Acquired Immune Checkpoint Inhibitor Resistance Using Clinical and Real-World Data. *Cancer research communications*, 5(6), 1049.

Wisniewski DJ, et al. (2025) Dual inhibition of EGFR and PI3Kinase signaling in EGFR amplified triple negative breast cancer cells induces apoptosis and reduces tumor growth. *bioRxiv : the preprint server for biology*.

Ghani H, et al. (2025) GPSai: A Clinically Validated AI Tool for Tissue of Origin Prediction during Routine Tumor Profiling. *Cancer research communications*, 5(9), 1477.

Varadarajan K, et al. (2025) Efficacy of ATR Kinase Inhibitor Elimusertib Monotherapy or Combination in Tumors with DNA Damage Response Pathway and Other Genomic Alterations. *Molecular cancer therapeutics*, 24(9), 1402.

DiPeri TP, et al. (2024) Utilizing Patient-derived Xenografts to Model Precision Oncology for Biliary Tract Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*.

Lheureux S, et al. (2023) Identifying Mechanisms of Resistance by Circulating Tumor DNA in EVOLVE, a Phase II Trial of Cediranib Plus Olaparib for Ovarian Cancer at Time of PARP Inhibitor Progression. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(18), 3706.

Louw N, et al. (2023) Incorporating CNV analysis improves the yield of exome sequencing for rare monogenic disorders-an important consideration for resource-constrained settings. *Frontiers in genetics*, 14, 1277784.

Spitzer B, et al. (2022) Bone Marrow Surveillance of Pediatric Cancer Survivors Identifies Clones that Predict Therapy-Related Leukemia. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 28(8), 1614.

Cao Q, et al. (2021) Dynamics of the Auditory Continuity Illusion. *Frontiers in computational neuroscience*, 15, 676637.

Kolara SRR, et al. (2019) Divergent evolution in the genomes of closely related lacertids, *Lacerta viridis* and *L. bilineata*, and implications for speciation. *GigaScience*, 8(2).

Lee B, et al. (2018) Clinical Relevance of Genomic Changes in Recurrent Pediatric Solid Tumors. *Translational oncology*, 11(6), 1390.

Maes T, et al. (2018) ORY-1001, a Potent and Selective Covalent KDM1A Inhibitor, for the Treatment of Acute Leukemia. *Cancer cell*, 33(3), 495.

Radovich M, et al. (2018) The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer cell*, 33(2), 244.

Goryca K, et al. (2018) Exome scale map of genetic alterations promoting metastasis in colorectal cancer. *BMC genetics*, 19(1), 85.

Booth CAG, et al. (2018) Ezh2 and Runx1 Mutations Collaborate to Initiate Lympho-Myeloid Leukemia in Early Thymic Progenitors. *Cancer cell*, 33(2), 274.

Jing D, et al. (2018) Lymphocyte-Specific Chromatin Accessibility Pre-determines Glucocorticoid Resistance in Acute Lymphoblastic Leukemia. *Cancer cell*, 34(6), 906.