

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

## BRASS

RRID:SCR\_017091

Type: Tool

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### Proper Citation

BRASS (RRID:SCR\_017091)

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### Resource Information

**URL:** <https://github.com/cancerit/BRASS>

**Proper Citation:** BRASS (RRID:SCR\_017091)

**Description:** Software tool for analysis of one or more related BAM files of paired end sequencing to determine potential rearrangement breakpoints. Identifies breaks and attempts to assemble rearrangements.

**Resource Type:** data analysis software, data processing software, software application, software resource

**Keywords:** analysis, BAM, file, paired, end, sequencing, determine, rearrangement, breakpoint, assemble

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

**Resource Name:** BRASS

**Resource ID:** SCR\_017091

**License:** GNU AGPL v3

**Record Creation Time:** 20220129T080333+0000

**Record Last Update:** 20260903T235420+0000

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### Ratings and Alerts

No rating or validation information has been found for BRASS.

No alerts have been found for BRASS.

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### Data and Source Information

## Usage and Citation Metrics

We found 47 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Davies HR, et al. (2026) Homologous recombination deficiency in primary ER-positive and HER2-negative breast cancer. *Communications medicine*, 6(1), 118.

Leongamornlert D, et al. (2026) Genomic evolution and natural history of myeloproliferative neoplasms on therapy. *Cancer discovery*.

Rekhtman N, et al. (2025) Chromothripsis-Mediated Small Cell Lung Carcinoma. *Cancer discovery*, 15(1), 83.

Yost KE, et al. (2025) Three-dimensional genome landscape of primary human cancers. *Nature genetics*, 57(5), 1189.

Díaz-Gay M, et al. (2025) Geographic and age variations in mutational processes in colorectal cancer. *Nature*, 643(8070), 230.

Díaz-Gay M, et al. (2025) Geographic and age-related variations in mutational processes in colorectal cancer. *medRxiv : the preprint server for health sciences*.

Domenico D, et al. (2025) Enabling whole genome sequencing analysis from FFPE specimens in clinical oncology. *Nature communications*, 16(1), 10649.

Minello A, et al. (2025) A recurrent pathogenic BRCA2 truncating variant reveals a role for BRCA2-PCAF complex in modulating NF- $\kappa$ B-driven transcription. *Nature communications*, 16(1), 10953.

Lee-Six H, et al. (2025) High resolution clonal architecture of hypomutated Wilms tumours. *Nature communications*, 16(1), 4647.

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.

Treger TD, et al. (2025) Predisposition Footprints in the Somatic Genome of Wilms Tumors. *Cancer discovery*, 15(2), 286.

Persaud N, et al. (2025) Clinical Significance of TERT Promoter Mutations in Neuroblastoma. *JCO precision oncology*, 9, e2500074.

Anselmino N, et al. (2024) Integrative Molecular Analyses of the MD Anderson Prostate Cancer Patient-derived Xenograft (MDA PCa PDX) Series. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(10), 2272.

Vergara X, et al. (2024) Widespread chromatin context-dependencies of DNA double-strand break repair proteins. *Nature communications*, 15(1), 5334.

Ijaz J, et al. (2024) Haplotype-specific assembly of shattered chromosomes in esophageal adenocarcinomas. *Cell genomics*, 4(2), 100484.

Wu CC, et al. (2024) Whole genome and reverse protein phase array landscapes of patient derived osteosarcoma xenograft models. *Scientific reports*, 14(1), 19891.

Hu X, et al. (2024) The evolution of lung adenocarcinoma precursors is associated with chromosomal instability and transition from innate to adaptive immune response/evasion. *Research square*.

Keahi DL, et al. (2024) G-quadruplexes are a source of vulnerability in BRCA2 deficient granule cell progenitors and medulloblastoma. *bioRxiv : the preprint server for biology*.

Koh GCC, et al. (2024) The chemotherapeutic drug CX-5461 is a potent mutagen in cultured human cells. *Nature genetics*, 56(1), 23.

Nunes L, et al. (2024) Prognostic genome and transcriptome signatures in colorectal cancers. *Nature*, 633(8028), 137.