

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## Patchwork

RRID:SCR\_000072

Type: Tool

### Proper Citation

Patchwork (RRID:SCR\_000072)

### Resource Information

**URL:** <http://patchwork.r-forge.r-project.org/>

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**Description:** Software tool for analyzing and visualizing allele-specific copy numbers and loss-of-heterozygosity in cancer genomes. The data input is in the format of whole-genome sequencing data which enables characterization of genomic alterations ranging in size from point mutations to entire chromosomes. High quality results are obtained even if samples have low coverage, ~4x, low tumor cell content or are aneuploid. Patchwork takes BAM files as input whereas PatchworkCG takes input from CompleteGenomics files. TAPS performs the same analysis as Patchwork but for microarray data.

**Abbreviations:** Patchwork

**Resource Type:** software resource

**Defining Citation:** [PMID:23531354](#)

**Keywords:** genome, allele, copy number, bam, unix, r, bio.tools

**Related Condition:** Cancer, Tumor

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

**Resource Name:** Patchwork

**Resource ID:** SCR\_000072

**Alternate IDs:** biotools:patchwork, OMICS\_02118

**Alternate URLs:** <https://bio.tools/patchwork>

**Record Creation Time:** 20220129T080159+0000

**Record Last Update:** 20260905T132411+0000

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## Ratings and Alerts

No rating or validation information has been found for Patchwork.

No alerts have been found for Patchwork.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Meghdadi B, et al. (2026) Digital twins for in vivo metabolic flux estimations in patients with brain cancer. *Cell metabolism*, 38(1), 228.

Hussain U, et al. (2026) Microbial communities in semi-mature oak trees are resilient to drought, nutrient limitation, and pathogen challenge. *Cell host & microbe*, 34(2), 344.

Allen AM, et al. (2026) Differential neuronal survival defines a novel axis of sexual dimorphism in the *Drosophila* brain. *Cell genomics*, 101125.

Vandana JJ, et al. (2025) ChemPerturb-seq screen identifies a small molecule cocktail enhancing human beta cell survival after subcutaneous transplantation. *Cell stem cell*, 32(8), 1299.

Okoye GD, et al. (2025) Single-cell map of innate-like lymphocyte response to *Francisella tularensis* infection reveals interleukin-17-dependent protection by MAIT cells. *iScience*, 28(3), 111810.

Allen AM, et al. (2025) A high-resolution atlas of the brain predicts lineage and birth order underlying neuronal identity. *Cell genomics*, 101103.

Munyoki SK, et al. (2025) The microbiota extends the reproductive lifespan of mice by safeguarding the ovarian reserve. *Cell host & microbe*.

Menozzi E, et al. (2025) Exploring the relationship between GBA1 host genotype and gut microbiome in the GBA1 L444P/WT mouse model: implications for Parkinson's disease pathogenesis. *Frontiers in neuroscience*, 19, 1546203.

Malkani S, et al. (2020) Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. *Cell reports*, 33(10), 108448.

Mayrhofer M, et al. (2013) Patchwork: allele-specific copy number analysis of whole-genome sequenced tumor tissue. *Genome biology*, 14(3), R24.