

Resource Summary Report

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Patchwork

RRID:SCR_000072

Type: Tool

Proper Citation

Patchwork (RRID:SCR_000072)

Resource Information

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

Proper Citation: Patchwork (RRID:SCR_000072)

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: 20260808T185711+0000

Ratings and Alerts

No rating or validation information has been found for Patchwork.

No alerts have been found for Patchwork.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

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

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

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.

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.

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.

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

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.