

Resource Summary Report

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CopyKAT

RRID:SCR_024512

Type: Tool

Proper Citation

CopyKAT (RRID:SCR_024512)

Resource Information

URL: <https://github.com/navinlabcode/copykat>

Proper Citation: CopyKAT (RRID:SCR_024512)

Description: Software R package to estimate genomic copy number profiles at average genomic resolution of 5 Mb from read depth in high throughput single cell RNA sequencing data. Used for inference of genomic copy number and subclonal structure of human tumors from high-throughput single cell RNAseq data.

Synonyms: , Copynumber Karyotyping of Aneuploid Tumors

Resource Type: software resource, software toolkit

Defining Citation: [PMID:33462507](#)

Keywords: Inference of genomic copy number and subclonal structure of human tumors, high throughput single cell RNAseq data,

Availability: Free, Available for download, Freely available

Resource Name: CopyKAT

Resource ID: SCR_024512

Record Creation Time: 20231002T161337+0000

Record Last Update: 20260905T133108+0000

Ratings and Alerts

No rating or validation information has been found for CopyKAT.

No alerts have been found for CopyKAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Xiong Z, et al. (2026) C/EBP β -induced alternative splicing of RCAN1 generates a potent TCR-T target in mesenchymal glioblastoma. Cellular & molecular immunology, 23(1), 94.

Jiménez-Sánchez A, et al. (2026) Transcriptomic Plasticity Is a Hallmark of Metastatic Pancreatic Cancer. Cancer research, 86(7), 1769.

George J, et al. (2026) Single-cell transcriptomics reveals FXR1 as an actionable target for siRNA therapy in ovarian cancer. Nature communications, 17(1).

Huang L, et al. (2026) Multi-cohort and single-cell profiling of aging genes reveals prognostic and therapeutic targets in breast cancer. iScience, 29(3), 114847.

Gu L, et al. (2026) PD-1 blockade plus tyrosine kinase inhibitor remodels the tumor microenvironment in advanced renal cell carcinoma. Nature communications, 17(1).

Banerjee S, et al. (2026) Tumor-infiltrating lymphocytes display prognostic signatures associated with chemotherapy response in TNBC patients. iScience, 29(6), 116295.

Nie RC, et al. (2026) Spatial single-cell landscape of tumor-associated macrophages and their crosstalk with the tumor microenvironment. Cell discovery, 12(1).

Guo Y, et al. (2026) Characterization of natural killer (NK) cells in lung adenocarcinoma and construction of an NK risk signature based on single-cell and macromolecular RNA-seq data. Discover oncology, 17(1).

Jin M, et al. (2026) Single-cell transcriptomic landscape highlights epithelial-fibroblast interactions and CD44-mediated malignant traits in laryngeal squamous cell carcinoma. NPJ precision oncology, 10(1).

Tang D, et al. (2026) Poly-L-lactic acid electrospun membrane with specific morphology promotes bone regeneration through macrophage reprogramming. Journal of nanobiotechnology, 24(1).

Subhash S, et al. (2026) A Single-Cell Atlas of Uterine Carcinosarcoma from Diverse Ancestries. bioRxiv : the preprint server for biology.

Van Khanh N, et al. (2026) Single-cell fixed RNA profiling of the osteosarcoma clinical Spectrum identifies ADAMTS12 and RNASE1 as key drivers of the metastatic niche. Journal of bone oncology, 59, 100781.

Wang J, et al. (2026) The phosphatase DUSP2 constrains lymphoid remodeling and immunotherapy response in lung squamous carcinoma. *Molecular therapy : the journal of the American Society of Gene Therapy*, 34(7), 4279.

Li S, et al. (2026) PRECISE: A Prognostic Thyrocyte-Derived Gene Signature for Papillary Thyroid Carcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(13), 2667.

Apostolov E, et al. (2026) Single-Cell and Spatial Transcriptomic Profiling Reveals Epithelial Functional States and Fibroblast Phenotypes in Hormone Therapy-Naïve Localized Prostate Cancer. *Cancer research*, 86(8), 1836.

Pan R, et al. (2025) BestopCloud: an integrated one-stop solution for single-cell RNA sequencing data analysis. *BMC genomics*, 26(1), 905.

Song X, et al. (2025) A Single-Cell Atlas of RNA Alternative Splicing in the Glioma-Immune Ecosystem. *bioRxiv : the preprint server for biology*.

Liu Y, et al. (2025) Proteogenomic characterisation of primary oral cancer unveils extracellular matrix remodelling and immunosuppressive microenvironment linked to lymph node metastasis. *Clinical and translational medicine*, 15(3), e70261.

Zhao L, et al. (2025) Unraveling tumoral heterogeneity and angiogenesis-associated mechanisms of PD-1 and LAG-3 dual inhibition in lung cancers by single-cell RNA sequencing. *Chinese medical journal pulmonary and critical care medicine*, 3(1), 41.

Ying L, et al. (2025) Cancer-associated fibroblasts expressing FSTL3 promote vasculogenic mimicry formation and drive colon cancer malignancy. *Cell death & disease*, 16(1), 706.