

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

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 toolkit, software resource

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: 20260803T040915+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 65 mentions in open access literature.

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

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.

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

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

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.

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.

Martin-Martin N, et al. (2025) Transcriptional analysis of metastatic hormone-naïve prostate cancer primary tumor biopsies reveals a relevant role for SOX11 in prostate cancer cell dissemination. Genome biology, 26(1), 154.

Jia T, et al. (2025) Multi-omics profiling identifies TNFRSF18 as a novel marker of exhausted CD8 $^{+}$ T cells and reveals tumour-immune dynamics in colorectal cancer. Clinical and translational medicine, 15(8), e70425.

Chan PY, et al. (2025) The synthetic lethal interaction between CDS1 and CDS2 is a vulnerability in uveal melanoma and across multiple tumor types. Nature genetics, 57(7), 1672.

Jiang X, et al. (2025) Depletion of Effector Regulatory T Cells Associates with Major Response to Induction Dual Immune Checkpoint Blockade. Cancer discovery, 15(8), 1569.

Wang Y, et al. (2025) Therapeutic implications of cancer-associated fibroblast heterogeneity: insights from single-cell and multi-omics analysis. Frontiers in immunology, 16, 1580315.

Wang L, et al. (2025) CD70-targeted iPSC-derived CAR-NK cells display potent function against tumors and alloreactive T cells. Cell reports. Medicine, 6(1), 101889.

Shi J, et al. (2025) Single-Cell RNA-Seq Recognized Key Genes for Metastasis and Macrophage Infiltration in Colorectal Cancer. *Human mutation*, 2025, 9488531.

Wu Z, et al. (2025) A dual-targeting strategy to inhibit colorectal cancer liver metastasis via tumor cell ferroptosis and cancer-associated fibroblast reprogramming. *Bioactive materials*, 52, 73.

Lu X, et al. (2025) NKX2-1 drives neuroendocrine transdifferentiation of prostate cancer via epigenetic and 3D chromatin remodeling. *Nature genetics*, 57(8), 1966.

Rymuza J, et al. (2025) PIT-1/SF-1-positive pituitary tumors in patients with acromegaly: transcriptomic perspective. *Acta neuropathologica communications*, 13(1), 174.

Sriramareddy SN, et al. (2025) GDF15 reprograms the microenvironment to drive the development of uveal melanoma liver metastases. *bioRxiv : the preprint server for biology*.

Wang G, et al. (2025) Analysis of the associations between DNA methylation and clinical features reveals the potential oncogenic effect of CFAP52 in esophageal squamous cell cancer. *Cancer cell international*, 25(1), 394.

Lei K, et al. (2025) Integrative spatial and single-cell transcriptomics elucidate programmed cell death-driven tumor microenvironment dynamics in hepatocellular carcinoma. *Frontiers in immunology*, 16, 1589563.

Ma H, et al. (2025) Spatially Resolved Tumor Ecosystems and Cell States in Gastric Adenocarcinoma Progression and Evolution. *Cancer discovery*, 15(4), 767.

Song M, et al. (2025) Benchmarking copy number aberrations inference tools using single-cell multi-omics datasets. *Briefings in bioinformatics*, 26(2).