

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

Tangram

RRID:SCR_006152

Type: Tool

Proper Citation

Tangram (RRID:SCR_006152)

Resource Information

URL: <https://github.com/jiantao/Tangram>

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Description: A C / C++ command line toolbox for structural variation (SV) detection that reports mobile element insertions (MEI). It takes advantage of both read-pair and split-read algorithms and is extremely fast and memory-efficient. Powered by the Bamtools API, it can call SV events on multiple BAM files (a population) simultaneously to increase the sensitivity on low-coverage dataset.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:25228379](#)

Keywords: standalone software, c, c++

Availability: MIT License

Resource Name: Tangram

Resource ID: SCR_006152

Alternate IDs: OMICS_05785

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260821T193758+0000

Ratings and Alerts

No rating or validation information has been found for Tangram.

No alerts have been found for Tangram.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

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

Wang C, et al. (2026) Single-cell and spatial transcriptomics in *Phragmites australis* reveal the association of B chromosomes with plant invasiveness. *Genome biology*, 27(1).

Li H, et al. (2026) *Helicobacter pylori*-linked gene CFAP73 rewires epithelial programs and shapes the gastric cancer microenvironment. *Discover oncology*, 17(1).

Sloan NX, et al. (2026) Uncovering the signatures of aging and senescence in the human dorsolateral prefrontal cortex. *Cell genomics*, 6(2), 101127.

Yang X, et al. (2026) Integrated multi-omic atlas reveals the hierarchy of spatiotemporal regulatory networks of mouse gastrulation. *Nature communications*, 17(1), 1572.

Collot R, et al. (2026) IGSF11-VISTA is a critical and targetable immune checkpoint axis in diffuse midline glioma. *Cancer cell*, 44(3), 641.

Yuan L, et al. (2026) SpaLSTF: Diffusion-based generative model with BiLSTM and XCA-Transformer for spatial transcriptomics imputation. *PLoS computational biology*, 22(2), e1013954.

Zhen P, et al. (2026) DisConST: Distribution-aware Contrastive Learning for Spatial Domain Identification. *Genomics, proteomics & bioinformatics*, 24(1).

Zhang L, et al. (2026) Retinoic Acid Reprograms Mast Cells Toward a Proinflammatory State to Enhance Antitumor Immunity. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(6), e09340.

Giraud-Sauveur F, et al. (2026) STHELAR, a multi-tissue dataset linking spatial transcriptomics and histology for cell type annotation. *Scientific data*, 13(1).

Restrepo P, et al. (2026) Single-cell spatial transcriptomic analysis of human skin anatomy. *Nature genetics*, 58(4), 903.

Ye Y, et al. (2026) CellLoop: Identifying single-cell 3D genome chromatin loops. *Nature communications*, 17(1).

Bourgain-Chang E, et al. (2026) Reconstructing single-cell resolution from spatial transcriptomics with CellRefiner. *Nature communications*, 17(1).

Bi H, et al. (2026) Binary-SPA: A Reference-Free Method for Cell Annotation in High-Resolution Spatial Transcriptomics. *bioRxiv : the preprint server for biology*.

Xue Y, et al. (2026) Integrated Single-Cell and Spatial Transcriptomic Analysis Identifies Putative Metabolic Crosstalk Between SPP1+ TAMs and SLC6A20+ Epithelial Cells in Colorectal Cancer. *Cancers*, 18(11).

Wang R, et al. (2026) Constructing the spatiotemporal atlas of single-cell lineage trajectories in stereotypic biological structures. *iScience*, 29(1), 114307.

Aggarwal B, et al. (2025) CellSP: Module discovery and visualization for subcellular spatial transcriptomics data. *bioRxiv* : the preprint server for biology.

Pareja-Lorente E, et al. (2025) Systematic assessment of microenvironment-dependent transcriptional patterns and intercellular communication. *Genome biology*, 26(1), 193.

Sunil HS, et al. (2025) TMPRSS11B promotes an acidified microenvironment and immune suppression in squamous lung cancer. *EMBO reports*, 26(24), 6346.

Li T, et al. (2025) Computational pathology annotation enhances the resolution and interpretation of breast cancer spatial transcriptomics data. *NPJ precision oncology*, 9(1), 310.

Noor H, et al. (2025) Response to Antiangiogenic Therapy Is Associated with AIMP Protein Family Expression in Glioblastoma and Lower-Grade Gliomas. *Cancer research communications*, 5(9), 1651.