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TMEAtlas Maps 15.4 Million Single Cells Across 42 Solid Cancers, Revealing Conserved Tumor Ecosystems Between Mice and Humans

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A landmark pan- cancer single-cell atlas published in Nature on November 18, 2026, integrates 15.4 million individual cells from 3,381 tumor samples across 42 solid cancer types to demonstrate that the cellular ecosystem surrounding solid tumors -- the tumor microenvironment (TME) -- follows deeply conserved organizational rules across anatomical organs and between mice and humans. Led by Michael Januszyk, Jerry M. Lu, Michael Korah, and colleagues in the Longaker Lab at Stanford University, the study introduces the Tumor Microenvironment transcriptomic Atlas (TMEAtlas) alongside an open R software package called scTME to standardize how single-cell oncology datasets are annotated worldwide.

Solid tumors are far more than homogeneous clusters of malignant cells. They operate as complex tissue ecosystems populated by fibroblasts, vascular endothelial cells, pericytes, and diverse infiltrating immune lineages that either restrain or accelerate tumor progression. Until now, fragmented naming conventions and batch effects across hundreds of separate single-cell RNA sequencing (scRNA-seq) studies made it difficult to tell which stromal and immune states are unique to a specific organ -- and which represent universal biological programs shared across species.

Building a 15.4-Million-Cell Cross-Species Atlas

To resolve that cross-study fragmentation, the Stanford team harmonized single-cell transcriptomes from 258 independent datasets into a unified coordinate framework. On the human side, TMEAtlas incorporates approximately 12.8 million cells compiled from 190 studies spanning 42 solid tumor types, including cancers of the breast, lung, brain, and colon. On the preclinical side, it integrates roughly 2.5 million mouse cells across 68 studies.

Harmonizing nearly 15.4 million single-cell profiles required reconciling disparate cell-type labels, sequencing platforms, and tissue-dissociation protocols. By mapping every cell onto a shared, consensus cell-type nomenclature, the researchers could directly quantify whether immune and stromal states observed in mouse models faithfully mirror their human counterparts across distinct tissue microenvironments.

| Atlas Dimension | | Verified TMEAtlas Scale | | Research & Translational Utility |

| Total Harmonized Cells | | 15.4 million single-cell transcriptomes | | Largest cross-species pan-cancer TME reference |

| Human Cohort | | ~12.8 million cells across 190 studies (42 cancers) | | Captures stromal & immune diversity across organs |

| Mouse Cohort | | ~2.5 million cells across 68 studies | | Benchmarks preclinical murine tumor fidelity |

| Open Software & Portal | | TMEAtlas web portal & scTME R package | | Enables standardized annotation of new scRNA-seq data |

Conserved Stromal and Immune Architecture Across Organs

Systematic comparison across the 42 solid tumor types revealed striking evolutionary and organizational conservation within both the stromal and immune compartments of the TME. Rather than reinventing completely separate support networks in every organ, tumors repeatedly recruit and polarize conserved populations of cancer-associated fibroblasts, vascular cells, macrophages, and T-cell states.

Equally significant for translational oncology, those core microenvironmental cell programs are substantially conserved between human tumors and murine cancer models. While important species-specific and organ-specific nuances remain, demonstrating broad conservation validates why mouse models remain informative for dissecting fundamental stromal remodeling and immune-checkpoint biology -- while also giving researchers a quantitative atlas to pinpoint exactly where a given mouse model diverges from human disease.

Standardizing Single-Cell Oncology With scTME

Beyond its biological findings, the Nature resource addresses a practical bottleneck in computational genomics : every new single-cell tumor study previously had to re-cluster and manually re-label stromal and immune subpopulations from scratch, often inventing incompatible names for the same cell state. Through the interactive TMEAtlas portal and the accompanying scTME R package, investigators can project new single-cell RNA-seq datasets directly onto the consensus reference.

Standardizing nomenclature across 15.4 million reference cells accelerates biomarker discovery for immunotherapies and anti-stromal drugs, helping clinical and preclinical teams distinguish universal pan-cancer targets from organ-restricted microenvironmental features.

References & Primary Sources

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