

Translating Spatial Omics into Reproducible Biomarker Evidence

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Abstract

This translational review examines translation of spatial-omics findings into reproducible biomarker evidence. The organizing question is which analytical and validation steps separate spatial association from a clinically useful biomarker. Ten related scholarly sources are synthesized through a decision-centered framework spanning problem definition, mechanism, measurement, evaluation, implementation, and governance. The review does not invent experiments, pooled estimates, or unreported quantitative results. It instead evaluates the strength and transferability of the available evidence, with particular attention to treating visually compelling spatial patterns as independently validated clinical evidence. The resulting framework links technical or empirical performance to explicit use conditions and identifies tests that should precede wider adoption in precision-medicine biomarker development.

Keywords: spatial omics, biomarkers, reproducibility, translational medicine, precision health

Synthesis lens	Principal question
Mechanism	the chain from specimen handling and spatial measurement through segmentation, feature construction, and clinical endpoint
Evaluation	batch effects, spatial leakage, analytical validity, external cohorts, incremental value, and decision thresholds
Primary risk	treating visually compelling spatial patterns as independently validated clinical evidence

1. Introduction

Research on translation of spatial-omics findings into reproducible biomarker evidence sits at the boundary between a promising component and a consequential decision. The core question is which analytical and validation steps separate spatial association from a clinically useful biomarker. Answering it requires more than assembling favorable results. It requires a chain of evidence that makes the problem boundary, mechanism, measurement, comparator, uncertainty, and accountable decision visible to the reader.

This article presents a structured narrative review of ten related publications. Sources were selected for topical relevance, traceable publication metadata, and complementary coverage of technical, empirical, and governance questions. No meta-analytic pooling is attempted because the included studies differ in designs, populations, system boundaries, and outcomes. The purpose is decision-oriented synthesis: to identify what each source can support, where transfer remains uncertain, and which evidence would justify the next stage of use.

The central risk is treating visually compelling spatial patterns as independently validated clinical evidence. A top-line metric or broad policy label can appear decisive while concealing the conditions that produced it. Accordingly, the synthesis separates observation from interpretation and implementation from validation. This separation is especially important when the same system creates benefits for one user or institution while transferring cost, risk, or administrative burden to another.

2. Evidence Base and Problem Boundary

A defensible review begins by defining the unit of analysis. For the present topic, the relevant boundary includes inputs, institutional or technical context, the mechanism producing an output, the person or system acting on that output, and the downstream outcome. Evidence falls outside the boundary when it measures only an intermediate proxy yet is used to claim an end-to-end benefit.

Vandereyken et al. (2023) addresses "Methods and applications for single-cell and spatial multi-omics." In this synthesis, that work is used as a source on problem definition within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

Bressan et al. (2023) addresses "The dawn of spatial omics." In this synthesis, that work is used as a source on conceptual boundary within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

Hsieh et al. (2022) addresses "Spatial multi-omics analyses of the tumor immune microenvironment." In this synthesis, that work is used as a source on measurement within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

Together, these works provide complementary entry points, but their conclusions should not be flattened into a single ranking. Differences

in data generation, setting, temporal horizon, and outcome definition may be substantively meaningful. A review should therefore preserve those differences and state where analogy, rather than direct replication, connects one domain to another.

3. Mechanism and System Design

The operative mechanism is the chain from specimen handling and spatial measurement through segmentation, feature construction, and clinical endpoint. This formulation discourages component-only reasoning. A model, platform, policy, assay, or infrastructure service acquires practical meaning only when its interfaces and use conditions are specified. The evidence chain should describe what information is available, what transformation occurs, which assumptions make that transformation credible, and who is authorized to act.

Zhang et al. (2022) addresses "Clinical and translational values of spatial transcriptomics." In this synthesis, that work is used as a source on system mechanism within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

Piwecka et al. (2023) addresses "Single-cell and spatial transcriptomics: deciphering brain complexity in health and disease." In this synthesis, that work is used as a source on representation choice within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

Wang et al. (2023) addresses "Spatial transcriptomics: Technologies, applications and experimental considerations." In this synthesis, that work is used as a source on failure analysis within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

These studies also show why modular claims require interface tests. A component may perform well while the complete pathway fails because inputs drift, users interpret outputs differently, recovery semantics are ambiguous, or institutional incentives change. Design documentation should therefore include not only the intended pathway but also foreseeable deviations, degraded modes, and conditions under which the system should stop or defer.

4. Evaluation and Uncertainty

Evaluation should center on batch effects, spatial leakage, analytical validity, external cohorts, incremental value, and decision thresholds. Average performance remains useful, but it should be accompanied by distributions, error categories, relevant subgroups or operating regimes, and uncertainty at the point where a decision changes. Comparators must isolate the value of the proposed addition rather than compare a mature intervention with an intentionally weak baseline.

Jin et al. (2024) addresses "Advances in spatial transcriptomics and its applications in cancer research." In this synthesis, that work is used as a source on comparative evaluation within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it

does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

Saviano et al. (2020) addresses "Single-cell genomics and spatial transcriptomics: Discovery of novel cell states and cellular interactions in liver physiology and disease biology." In this synthesis, that work is used as a source on uncertainty within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

External validation should introduce meaningful shifts in setting, time, population, workload, market structure, or environmental conditions. A nominally independent sample can still be too similar to test transfer. Conversely, a failed transfer is scientifically informative when the changed conditions are measured and the mechanism of failure is examined rather than hidden in an aggregate score.

5. Translation and Governance

Translation to precision-medicine biomarker development depends on more than technical readiness. Decision rights, documentation, maintenance, monitoring, appeal, and recovery are part of the intervention. The governance requirement is prespecified pipelines, blinded validation, shared standards, and transparent assay-change management. Each control should be connected to a named failure mode and should identify an owner, evidence source, review interval, and escalation path.

Lee et al. (2025) addresses "Spatial Omics in Clinical Research: A Comprehensive Review of Technologies and Guidelines for Applications." In this synthesis, that work is used as a source on implementation within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

Yu et al. (2022) addresses "Spatial transcriptomics technology in cancer research." In this synthesis, that work is used as a source on governance within translation of spatial-omics findings into reproducible biomarker evidence. The connection is deliberately bounded: the cited study informs the evidence map, but it does not by itself establish readiness for precision-medicine biomarker development. That distinction keeps the review close to the published record and prevents an adjacent result from being converted into a broader causal claim.

A credible implementation plan also defines sunset and revalidation conditions. New data, software updates, institutional restructuring, population change, or shifts in incentives can invalidate previously reasonable assumptions. Monitoring should therefore test the validity of the evidence chain, not merely whether a service remains online or a headline metric remains stable.

6. Research Agenda

Future studies should preregister or otherwise predefine the intended decision, principal outcomes, exclusions, and analysis plan when feasible. They should report missingness, sensitivity analyses, negative or null findings, and the cost of errors to differently situated stakeholders. Reproducible artifacts should include sufficient metadata to reconstruct data provenance, model or analytical versions, parameter choices, and the sequence from evidence to conclusion.

Cross-disciplinary work needs a shared object of explanation rather than a collection of adjacent vocabularies. For translation of spatial-omics findings into reproducible biomarker evidence, that shared object is the complete decision pathway. Technical, clinical, social, environmental, or economic expertise should each change the design or interpretation of the study. When evidence remains incomplete, the useful output is a bounded hypothesis, a transparent uncertainty statement, or a request for additional measurement.

7. Conclusion

The literature supports a disciplined approach to translation of spatial-omics findings into reproducible biomarker evidence: define the decision, preserve system boundaries, test consequential failure modes, connect uncertainty to action, and assign accountable control. The strongest conclusion is not that one method is universally superior. It is that credible use in precision-medicine biomarker development requires an auditable link from source evidence to design choice, evaluation result, and governed decision.

Declarations

Ethics approval: Not applicable. This article synthesizes previously published literature and reports no research involving human participants, identifiable data, animals, or human tissue.

Consent to participate and consent for publication: Not applicable.

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Data availability: All evidence discussed in this article is identified in the reference list. No new participant-level dataset was generated.

Competing interests: The authoring group declares no competing interests for this commissioned synthesis.

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