Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

A Curated Spatial Transcriptomic Dataset of the Human Adrenal Gland Cortex and Medulla

Vedant Srivastava

vedaastha1974@gmail.com

Ulyanovsk State University https://orcid.org/0009-0001-8475-5069

Short Report

Keywords: Spatial transcriptomics, Adrenal gland, 10x Genomics Visium, Data curation, Bioinformatics

Posted Date: August 12th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-10664078/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: The authors declare no competing interests.

Abstract

Background

The adrenal gland is believed to depend on spatial zonation for hormone synthesis. Despite this, high-resolution transcriptomic atlases that preserve this architecture remain relatively scarce. While bulk and single-cell approaches have provided foundational insights, both inherently sacrifice spatial context—a limitation that spatially resolved methods may help address.

Methods

Publicly available data from human adrenal tissues (n = 10 donors; 5 male, 5 female; median age 46 years) were retrieved and curated. Using the 10x Genomics Visium platform, we applied a standardized reprocessing pipeline involving Space Ranger alignment, systematic quality filtering, and spatial coordinate mapping to generate harmonized data objects.

Results

The curated dataset comprises approximately 50,000 tissue-covered spots, with a median of 3,150 genes detected per spot. Notably, canonical marker genes (*CYP11B2, CYP11B1, SULT2A1, CHGA)* demonstrated expected zonal localization across the Zona Glomerulosa, Fasciculata, Reticularis, and Medulla—suggesting accurate spatial registration. However, the spot-level resolution of the Visium platform (55 µm diameter) does not resolve individual cells, which may limit certain downstream applications.

Conclusions

By providing uniformly reprocessed, ready-to-use data objects with comprehensive metadata, this openly accessible resource may accelerate computational modeling, biomarker discovery, and comparative endocrine oncology research. The repository includes raw histology images, processed AnnData objects, and harmonized donor metadata.

1. Introduction

The human adrenal gland is structurally complex, and its functional zonation—Zona Glomerulosa (mineralocorticoids), Zona Fasciculata (glucocorticoids), Zona Reticularis (androgens), and Medulla (catecholamines)—is considered essential for homeostatic regulation[1].

Although bulk transcriptomics has contributed foundational insights, this approach averages layer-specific differences. Consequently, subtle but biologically significant regional variation may be

masked[2]. Single-cell RNA sequencing, by contrast, achieves remarkable cellular resolution. Yet tissue dissociation inevitably discards spatial context, thereby losing information about cellular microenvironments[3]. Spatially resolved transcriptomics offers a promising bridge: it preserves anatomical architecture while maintaining transcriptome-wide data[4]. However, accessible, high-quality reference datasets for the human adrenal gland remain surprisingly scarce.

To help address this gap, we present a curated, open-access spatial transcriptomic and histological dataset derived from human adrenal tissues, accompanied by uniformly processed data objects and comprehensive metadata.

2. Methods

2.1 Data Source

Spatial transcriptomic data from human adrenal gland specimens (n = 10; 5 male, 5 female; age range 24–62 years; median 46 years) were accessed and reprocessed. Donors had no documented history of adrenal disease, chronic corticosteroid use, or severe endocrine dysfunction. Tissues had been collected post-mortem (PMI < 12 hours), embedded in OCT, flash-frozen, and stored at − 80°C[7].

2.2 Original Laboratory Processing (Summary)

The depositing investigators had sectioned OCT-embedded blocks at 10 µm thickness and placed sections onto 10x Genomics Visium slides (~ 5,000 spots per array; 55 µm spot diameter). On-slide H&E staining, tissue permeabilization (18 minutes), mRNA capture, and cDNA library preparation followed standard Visium protocols[4]. Sequencing was performed on an Illumina NovaSeq 6000.

2.3 Curational Reprocessing

Our contribution focused on systematic reprocessing and harmonization of the public data. Raw FASTQ files were retrieved and processed through Space Ranger (v2.0) for read alignment to GRCh38 and fiducial frame alignment. To ensure batch-free comparability, we applied uniform quality control and normalization using Python with Scanpy (v1.9.1) and Squidpy (v1.2.0)[5,6]. Spots falling outside the tissue mask, exhibiting extreme UMI variance (> 3 SD), or overlapping artifacts were computationally flagged and excluded. Expert pathological annotations of the four zones—originally performed on digitized H&E images—were retrieved and mapped to the reprocessed coordinates.

3. Results

3.1 Dataset Overview

The curated repository contains three directories:

· /histology: Raw H&E whole-slide images (.svs, ~ 1.5 GB each) and annotation coordinate files (.json)

· /spatial_transcriptomics: Reprocessed AnnData objects (.h5ad) with raw counts, normalized data, spatial coordinates, and scale factors

· /metadata: Harmonized donor demographics and quality metrics (.csv)

Quality metrics confirmed high data integrity: mean RIN = 7.8 ± 0.5, mean PMI = 7.4 hours, mean sequencing depth = 62,400 reads/spot, and median genes/spot = 3,150.

3.2 Spatial Validation

To assess spatial registration fidelity, we plotted expression profiles of canonical marker genes across the mapped anatomical zones[1]. Expression demonstrated expected zonal localization:

· Zona Glomerulosa: CYP11B2 (aldosterone synthase) was restricted to the outer sub-capsular region

· Zona Fasciculata: CYP11B1 (11β-hydroxylase) was enriched in the middle cortical layer

· Zona Reticularis: SULT2A1 and CYP17A1 were localized to the juxtamedullary region

· Medulla: CHGA and TH were restricted to the central core

These findings suggest accurate spatial registration and adequate dataset quality for downstream applications.

4. Discussion

This curated dataset could serve as a healthy reference benchmark for comparative adrenal pathology studies—including adrenocortical carcinomas, aldosterone-producing adenomas, and pheochromocytomas[7,8]. Additionally, the dual-modality structure (paired morphology and transcriptomics) may facilitate computational method development, such as cell-type deconvolution, spatial interaction frameworks, and histopathological segmentation algorithms[5,6].

Limitations

Several considerations warrant attention. First, because tissues were obtained post-mortem, some degree of RNA degradation is unavoidable—even with strict PMI and RIN cutoffs—which could influence detection of highly labile transcripts. Second, the donor cohort is limited to adults aged 24–62 years of mixed ethnicity; whether these findings generalize to pediatric, geriatric, or specific ancestral populations remains an open question. Third, Visium spot-level resolution (55 μm) does not resolve individual cells; integrative deconvolution with scRNA-seq references is recommended when single-cell resolution is required. Finally, because this paper presents secondary curation rather than de novo data generation, annotation quality is contingent upon the original investigators' protocols and pathological reviews.

5. Conclusion

We present a curated, open-access spatial transcriptomic and histological dataset of the human adrenal cortex and medulla. By providing uniformly reprocessed, ready-to-use data objects with comprehensive metadata, this resource may accelerate computational modeling, biomarker discovery, and comparative endocrine oncology research. The dataset is available in an open-access repository for the broader research community.

Declarations

Ethics Approval and Consent to Participate

The human adrenal tissue samples used in this study were originally collected by the depositing investigators under their respective institutional review board approval, with informed written consent obtained from donors' next of kin. For the present study, we accessed fully de-identified and anonymized data from public repositories. In accordance with institutional policy, the secondary analysis of such publicly available, non-identifiable data does not constitute human subjects research and is therefore exempt from additional ethical review. No new human tissue was procured or handled during this work.

Consent for Publication

Not applicable.

Competing Interests

The author declares no competing interests.

Acknowledgments

The author acknowledges the use of Google Gemini for language refinement and structural formatting assistance. All scientific conceptualization, data verification, critical intellectual revisions, and final manuscript approval were conducted solely by the author. The author assumes full accountability for the accuracy and integrity of this work.

Data Availability Statement

The curated datasets generated during this study are currently being deposited in an open-access repository. Stable accession numbers and persistent DOIs will be provided upon formal publication. For the preprint version, data are available from the corresponding author upon reasonable request.

Code Availability

Custom analysis scripts are available at GitHub (https://github.com/adrenal_spatial/analysis_scripts) under an MIT license.

References

1. Xing Y, Gavrilova–Jordan L, Rainey WE, Parker CR (2015) Development and regulation of the human adrenal cortex. Mol Cell Endocrinol 408:108–117
2. Leng S, Rainey WE (2022) Single–cell transcriptomics of the human adrenal cortex. Curr Opin Endocr Metab Res 24:100346
3. Asp M, Bergenstråhle J, Lundeberg J (2020) Spatially resolved transcriptomes—next generation tools for tissue exploration. BioEssays 42(10):1900221
4. Ståhl PL, Salmén F, Vickovic S et al (2016) Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. Science 353(6294):78–82
5. Wolf FA, Angerer P, Theis FJ (2018) SCANPY: large–scale single–cell gene expression data analysis. Genome Biol 19(1):1–5
6. Palla G, Spitzer H, Klein M et al (2022) Squidpy: a scalable framework for spatial omics analysis. Nat Methods 19(2):171–178
7. Sbiera S, Fassnacht M (2021) Multi–omics approach to adrenal tumors. Front Endocrinol 12:654211
8. Else T, Kim AC, Sabolch A et al (2014) Adrenocortical carcinoma. Endocr Rev 35(2):282–326

Figures

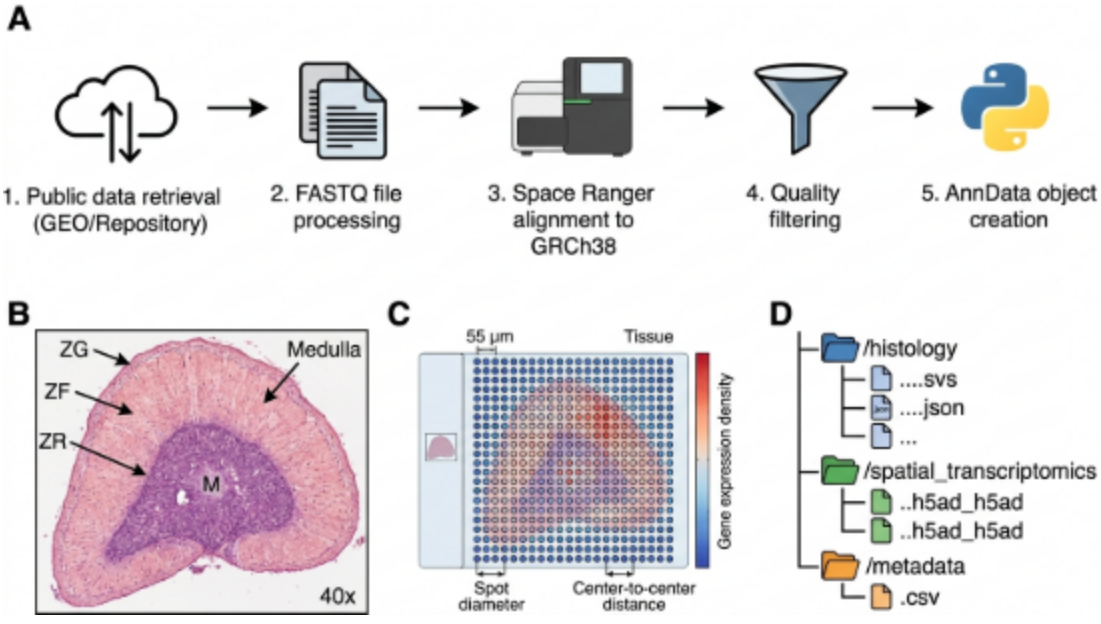


Figure 1

Curational workflow and repository architecture.

(A) Overview of the data reprocessing pipeline: raw public data were retrieved, processed through Space Ranger for alignment, subjected to quality filtering, and formatted into standardized data objects.

(B) Representative 40× H&E pathology image with expert annotations outlining the four anatomical zones: Zona Glomerulosa (ZG), Zona Fasciculata (ZF), Zona Reticularis (ZR), and Medulla (M).

(C) 10x Genomics Visium spatial capture array showing ~5,000 barcoded spots (55 µm diameter) mapped to tissue sections.

(D) Repository structure showing three directories: /histology, /spatial_transcriptomics, and /metadata.

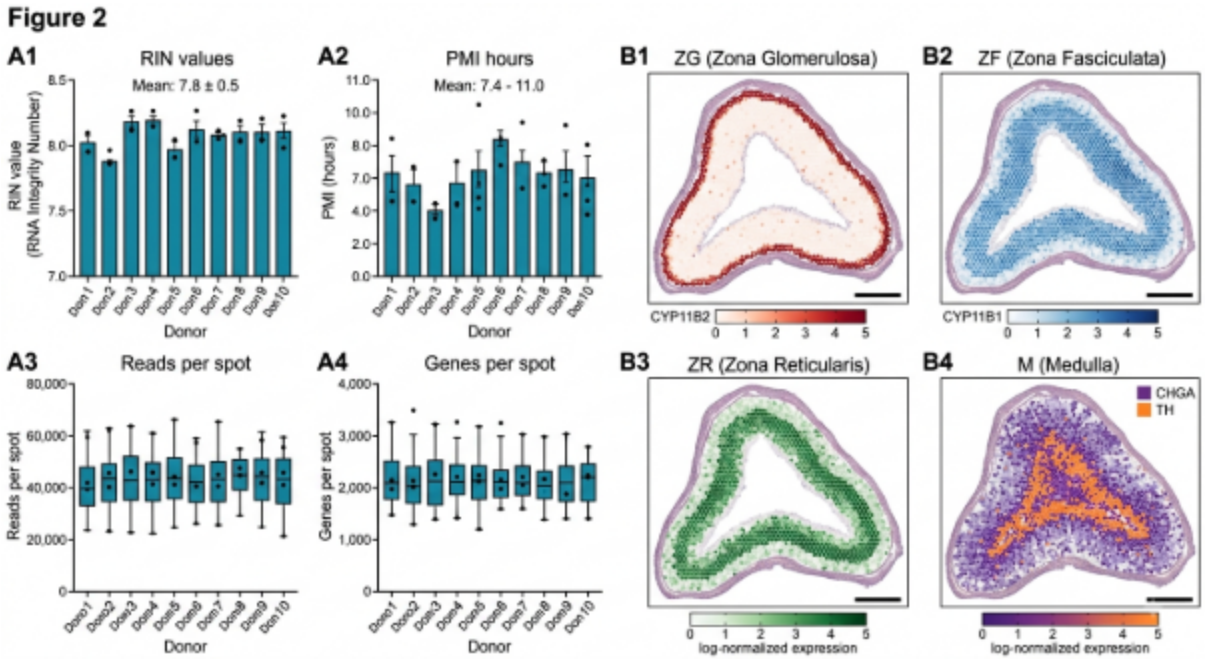


Figure 2

Technical quality control and spatial marker validation.

(A) Quality metrics across all donors (n=10): RNA Integrity Number (mean RIN = 7.8 ± 0.5), post-mortem interval (mean PMI = 7.4 hours), sequencing depth (mean = 62,400 reads/spot), and genes detected per spot (median = 3,150).

(B–E) Spatial expression heatmaps of canonical marker genes:

(B) CYP11B2 restricted to Zona Glomerulosa;

(C) CYP11B1 localized to Zona Fasciculata;

(D) SULT2A1 enriched in Zona Reticularis; and

(E) CHGA and TH co-expression in Medulla. Color scales represent log-transformed, normalized UMIs per spot.