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CellScape Quality Control (CSQC): A tissue- and protein-agnostic platform for spatial proteomics quality assessment

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Introduction

Spatial proteomics experiments generate rich biological information, but analysis workflows are highly sensitive to variability in tissue integrity and imaging quality. Differences in tissue preparation, antibody performance, and imaging conditions can introduce artifacts that compromise accuracy. Annotation of imaging data is essential, but manual approaches are time-consuming and subjective. To address this, we built a database of CellScape™ images and trained machine-learning models to support QC by automatically distinguishing informative tissue from background and imaging artifacts. A standardized and automated QC framework is essential to enable scalable adoption of spatial proteomic workflows in precision oncology.

CellScape Whole-Slide Multiplex Imaging

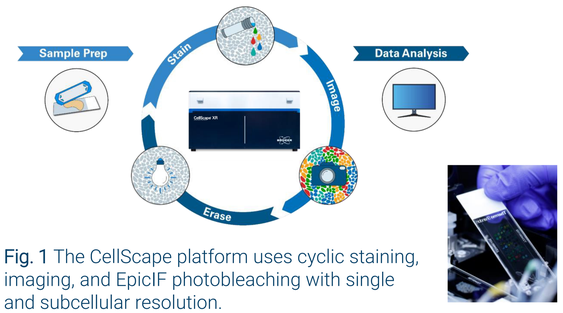

Fig. 1 The CellScape platform uses cyclic staining, imaging, and EpicIF photobleaching with single and subcellular resolution.

Common Imaging Artifacts in Spatial Assays

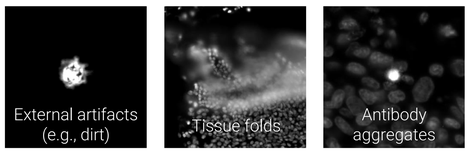

Fig. 2 Representative examples of common artifacts. They can confound quantification and must be excluded prior to analysis.

Annotation and Training Strategy

For each image, a single random position was selected within the valid bounds of each biomarker channel. A 1024x1024 pixel tile was extracted at 1 µm/pixel resolution, combining the target biomarker channel (red) and DNA stain (green). Raw 16-bit grayscale data was converted to 8-bit RGB and rescaled using percentile bounds, excluding fully saturated pixels from the intensity range calculation and mapping them to 255 to preserve saturation information. Tiles were manually annotated in Roboflow and trained with a semantic segmentation model (DeepLabV3+ architecture).

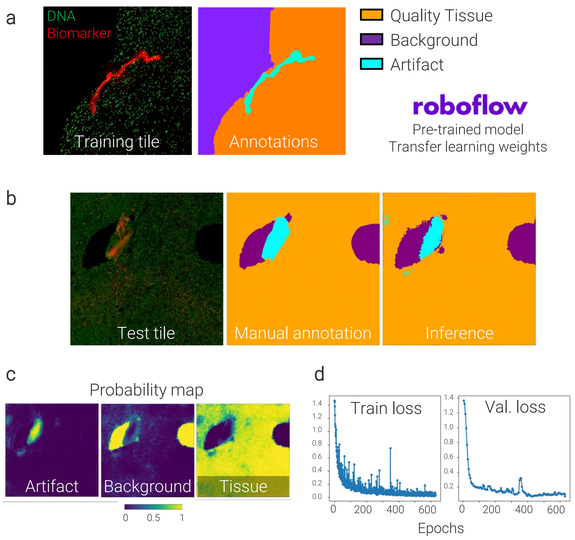

Fig. 4 Model Training, outputs and evaluation. a) Strategy for building the model: Tiles were manually annotated in Roboflow and trained with a semantic segmentation model. b) Tile, manually drawn mask, and auto-labeled output from training split. c) Confidence maps underlying the auto-labeling in b. D) Loss and Intersection over Union (IoU) tracked over 600+ epochs until IoU > 0.7. Checkpoint then served as a starting place for subsequent training rounds improving performance to 0.85. N=578 tiles.

Segmentation Performance across Biomarkers, Organs, and Instruments

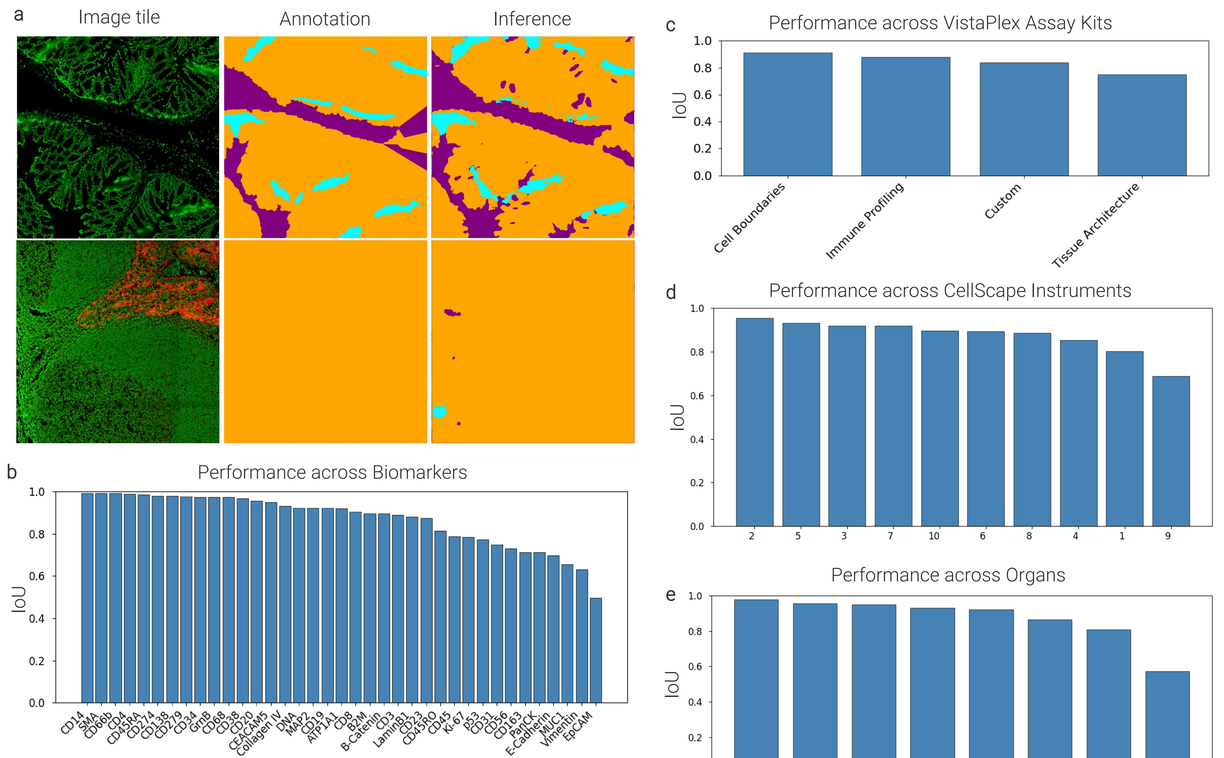

Fig. 5 Model validation: a) Example tiles (not part of training data) shown with manual annotation and model outputs. b-e) IoU metrics broken down across 37 biomarkers (b), 3 VistaPlex Assay kits + custom assays (c), 10 instruments (d) , and 8 organs (e). Micro-IoU is calculated as the total IoU for all pixels across the 3 classes. Mean IoU for full validation set was 0.85, showing strong concordance with expert annotations. The system flags suboptimal staining and artifacts. This reduces manual review time from hours to minutes per sample, enabling rapid scaling of downstream analyses.

CellScape Spatial Proteomics Training Database

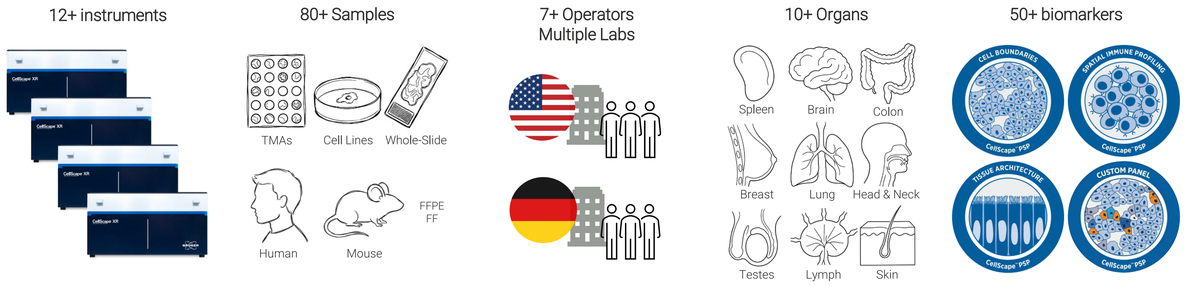

Fig. 3 The CSQC training dataset was compiled over multiple years of CellScape experiments across institutions, capturing the variability of real-world spatial proteomics workflows & data

Automated QC Reporting with Artifact Exclusion

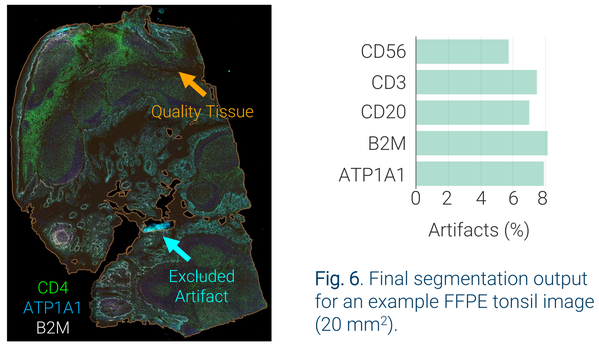

Fig. 6. Final segmentation output for an example FFPE tonsil image (20 mm²).

Conclusion

- Sample review time: From hours to minutes
- Mean IoU = 0.85

- CSQC provides a standardized, quantitative, and scalable approach to stain and tissue quality control, supporting robust multisite spatial proteomics workflows on the CellScape precise spatial phenotyping platform
- This framework facilitates assay harmonization, benchmarked reproducibility, and reliable spatial biomarker discovery for clinical translation.

References:
Andhari et al. Cell. Rep. P. 2024
Baker et al. Nat. Met. 2024

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