Supplementary Information for: SpatialMamba: a graph-based model for spatial transcriptomics with feature- and degree-informed spot prioritization for spatial domain annotation

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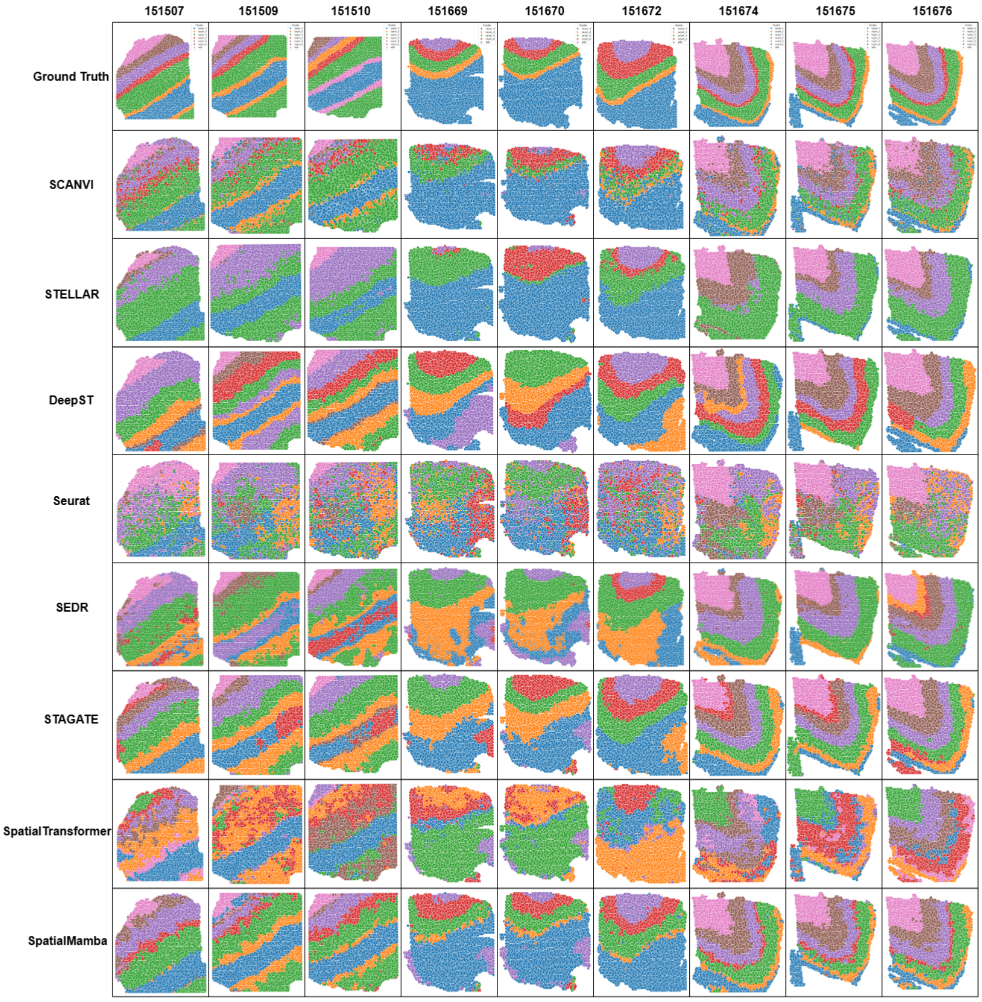
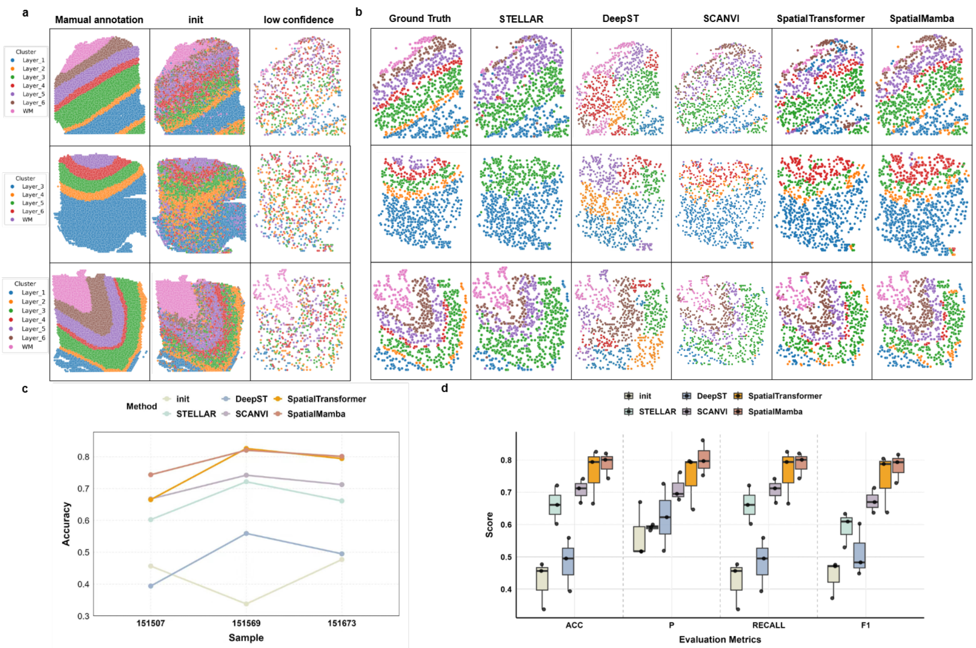
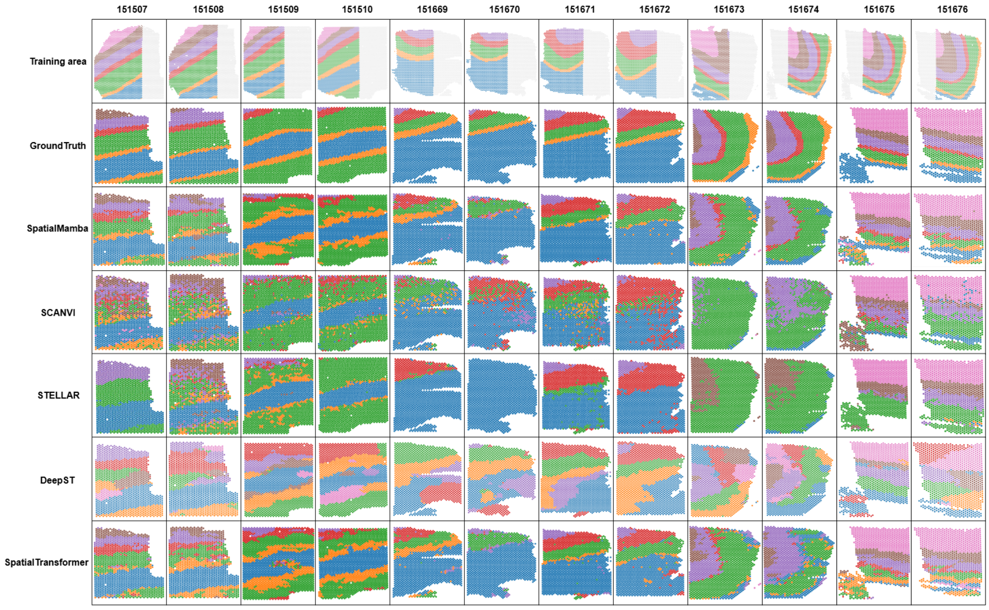


Supplementary Fig. S1 Comprehensive visualization of spatial domain annotation on the Human DLPFC dataset. This figure displays the comparison between the manual ground truth (top row) and the spatial domains predicted by SpatialMamba (bottom row) across multiple tissue slices. Our model consistently reconstructs the fine-grained laminar structures and preserves topological continuity across different donor sections.



Supplementary Fig. S2 Robustness analysis on the Human DLPFC dataset under high-confidence supervision. We trained the model using the top 80% high-confidence spots and evaluated it on the bottom 20% ambiguous (low-confidence) spots. The visualization highlights SpatialMamba's capability to correctly infer the identities of hard spots (e.g., boundary regions) by leveraging global structural context and PPI priors, effectively resolving ambiguities that baseline methods fail to capture.



Supplementary Fig. S3 Visualization of the Spatial Extrapolation experiment. To evaluate generalization capability, the tissue slide was cropped into disjoint training (observed) and testing (unobserved) regions. The figure compares the Ground Truth with SpatialMamba's predictions on the held-out regions. The results demonstrate that our Dual-Branch encoder successfully learns global morphological patterns, allowing accurate extrapolation to unseen tissue areas.