

P2.165: AI-Enabled Automated PD-L1 Tumor Proportion Score Assessment from Whole Slide Images in Non-Small Cell Lung Cancer

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INTRODUCTION

Programmed death-ligand 1 (PD-L1) expression assessed by immunohistochemistry (IHC) is an important biomarker guiding immunotherapy selection in individuals with advanced non-small cell lung cancer (NSCLC). The Tumor Proportion Score (TPS), defined as the percentage of viable tumor cells demonstrating membranous PD-L1 staining, determines eligibility for immune checkpoint inhibitor therapy.

Routine TPS evaluation remains challenging due to subjective interpretation, inter-observer variability, and difficulty distinguishing invasive tumor from surrounding benign tissue, immune infiltrates, necrosis, or control tissue such as placenta or tonsil. Borderline or weakly stained cases further complicate interpretation.

Objective: Develop a multi-stage AI framework to enable automated and reproducible PD-L1 TPS assessment from whole-slide IHC images.

METHODS

A four-stage computational workflow was implemented on 196 PD-L1 IHC slides.

1. Tissue QC & feature extraction — HistoQC-based masking identified diagnostic tissue regions; tile-level 1536-dimensional embeddings were generated using the Optimus-1 foundation model.
2. Control-region detection — an MLP classifier trained on 30 annotated PD-L1 slides (111,156 tiles) distinguished tumor tissue from control regions such as placenta or tonsil.
3. Invasive tumor segmentation — a tumor detector pretrained on H&E histology and fine-tuned on 233 external PD-L1 lung IHC slides enabled cross-stain domain adaptation.
4. Cell-level PD-L1 quantification — a dual-path CellPose approach integrated hematoxylin-driven nuclear detection and DAB-enhanced signal detection. HED color deconvolution was used to derive membrane-associated DAB intensity and classify TPS: Low (<1%), Moderate (1–49%), High (≥50%).

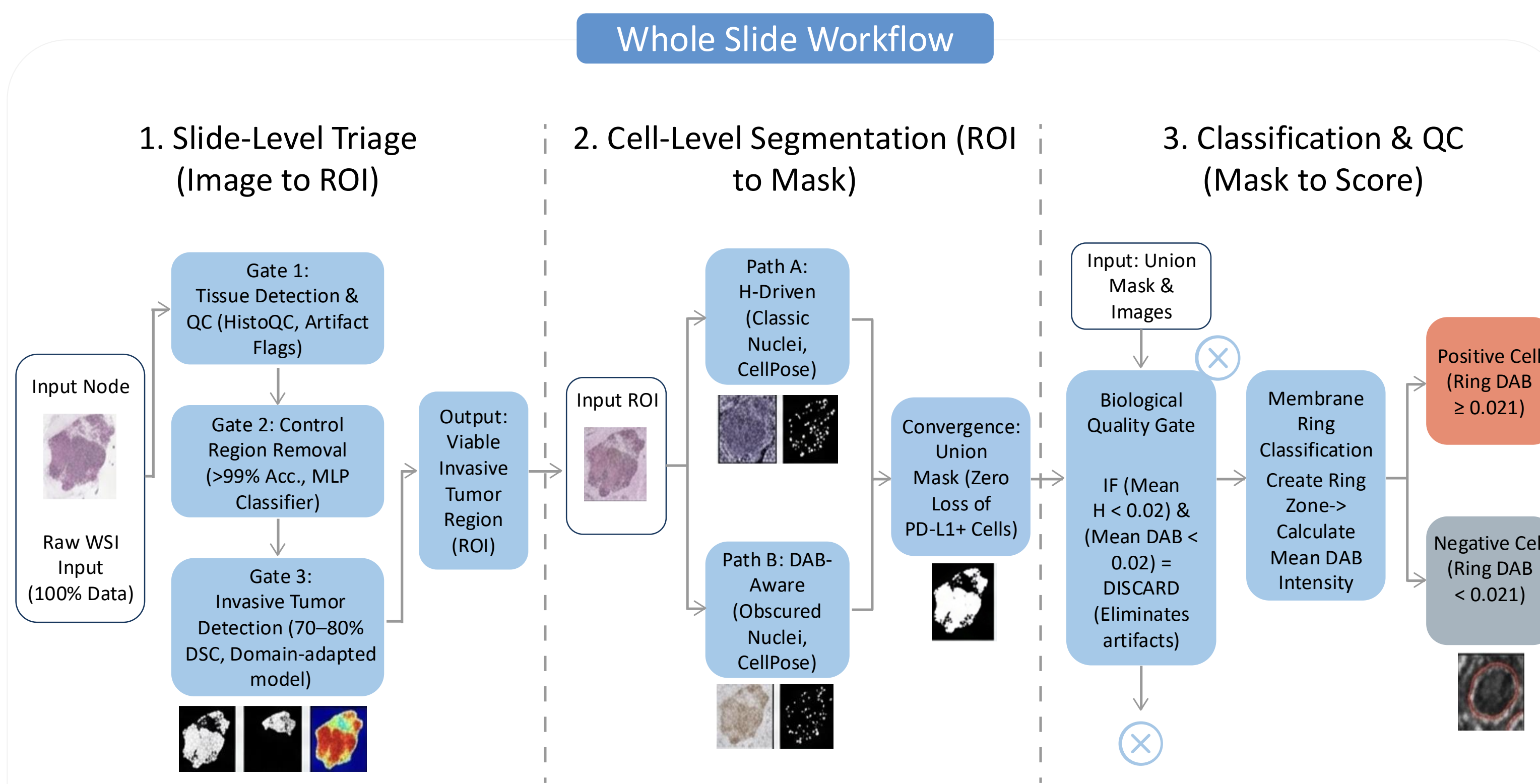


Figure 1. Overview of the AI pipeline for automated PD-L1 TPS assessment from whole-slide images.

DISCUSSION AND CONCLUSION

Actionable Take Away Message

- Automated control-region detection helps prevent non-patient tissue from influencing TPS analysis.
- Tumor segmentation addresses ambiguity between invasive tumor and surrounding tissue.
- Cell-level PD-L1 quantification provides a standardized basis for TPS categorization.
- The framework is designed to reduce analytical burden while supporting reproducible biomarker assessment.

Conclusion:

This multi-stage AI framework enables objective and reproducible PD-L1 TPS assessment by addressing control tissue contamination, tumor demarcation ambiguity and observer variability. Automated tumor detection and cell-level PD-L1 quantification support standardized biomarker assessment and integration into digital pathology workflows.

REFERENCES & ACKNOWLEDGEMENTS

Key computational resources: HistoQC; Optimus-1 foundation model; CellPose; HED color deconvolution.

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RESULTS

Control-region detection: 99.5% accuracy on 30 training slides and 99.1% accuracy on 170 validation slides, effectively excluding non-patient control tissue.

Tumor segmentation: evaluated on 74 slides; mean Dice similarity coefficient 0.80 (range 0.65–0.84) with PPV 0.79.

TPS categorization on the 196-slide cohort achieved 91.3% accuracy for High TPS (≥50%), 81.6% for Low TPS (<1%), and 75.0% for Moderate TPS (1–49%), with strongest discrimination at clinically relevant thresholds.

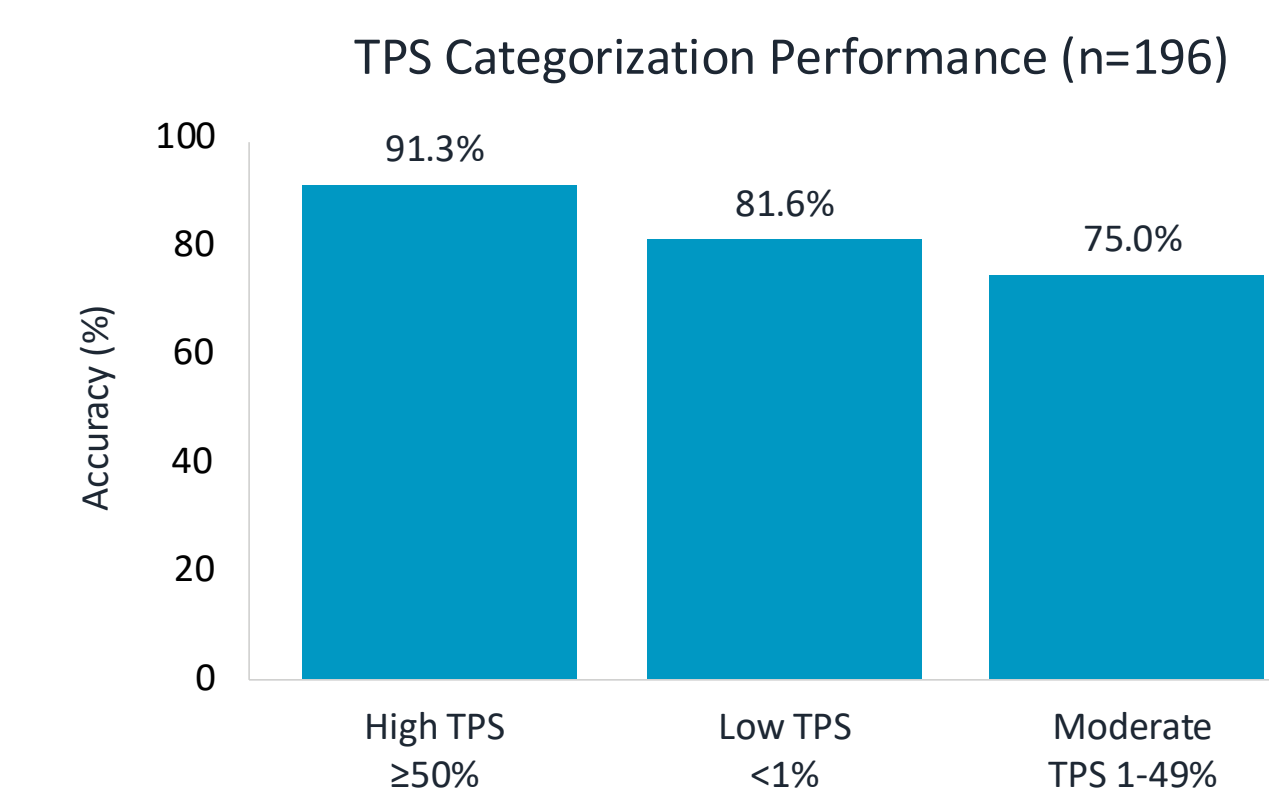


Figure 2. TPS categorization accuracy across clinically relevant score ranges.

High TPS (≥50%): 91.3%
Low TPS (<1%): 81.6%
Moderate TPS (1–49%): 75.0%

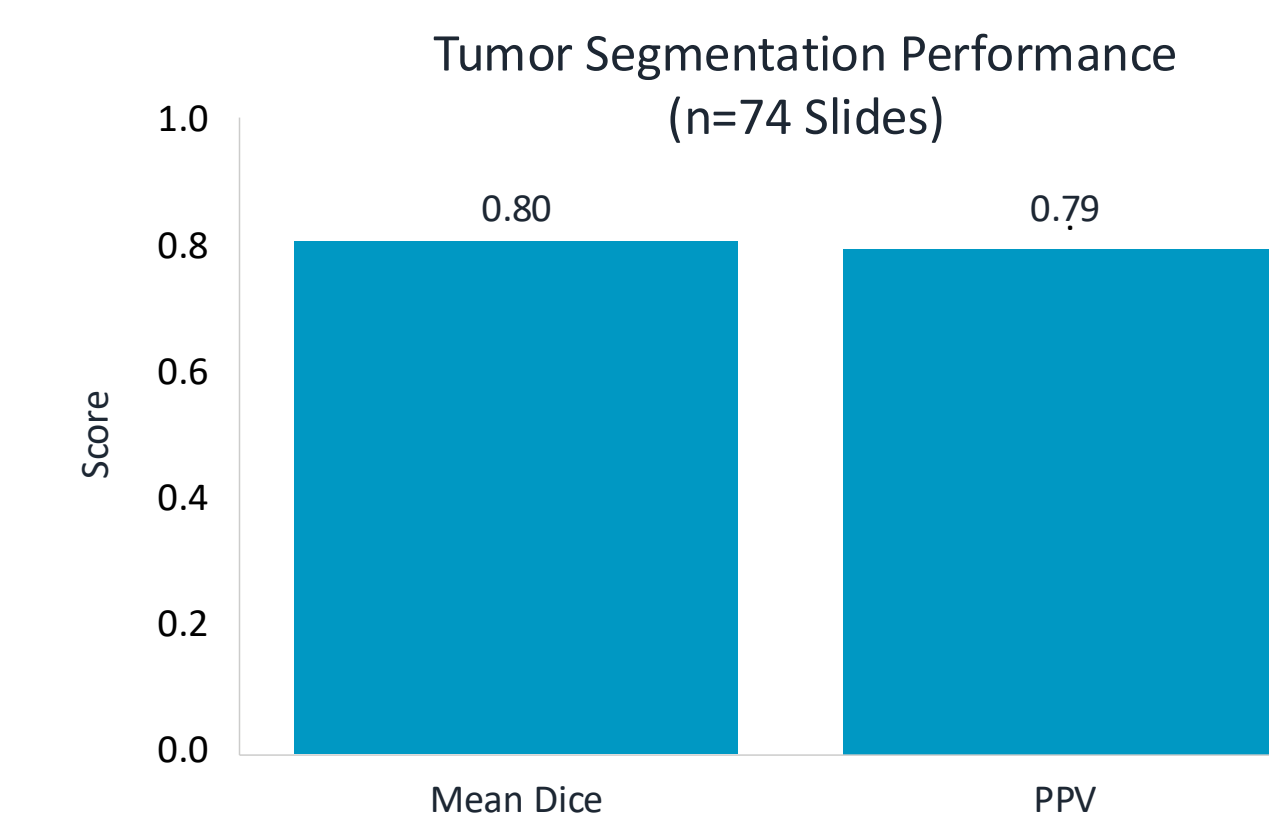


Figure 3. Tumor segmentation performance

Tumor segmentation:
Dice 0.80; PPV 0.79

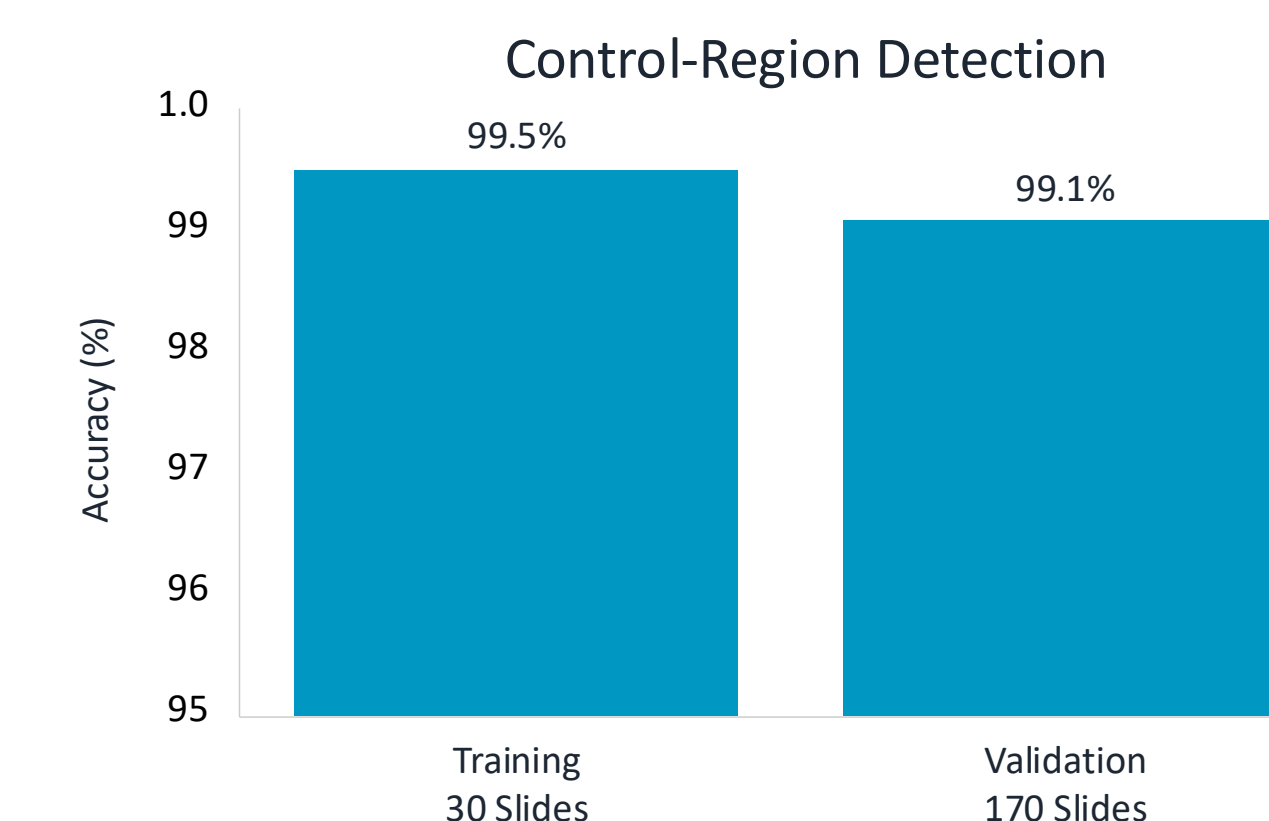


Figure 4. Control-region detection: training vs validation

Control-region detection:
99.5% training accuracy
99.1% validation accuracy

Clinical relevance

Strongest discrimination was observed at clinically relevant TPS thresholds, supporting the potential of automated analysis to improve consistency in PD-L1 biomarker assessment.

Key message: AI can standardize the path from whole-slide PD-L1 IHC images to clinically meaningful TPS categories by combining slide-level QC, control-tissue removal, tumor localization and cell-level signal quantification.