



P1.169: G-MAPS: A Gene-Guided Multi-Scale AI Pathology Signature for Tri-Level Pathological Response Prediction to Neoadjuvant Immunotherapy in NSCLC

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INTRODUCTION

Clinical need

- Neoadjuvant immunotherapy-based regimens are reshaping treatment for resectable NSCLC
- Target task: distinguish non-MPR, MPR, and pCR before/around surgical assessment using routine H&E WSI plus gene-guided signals.

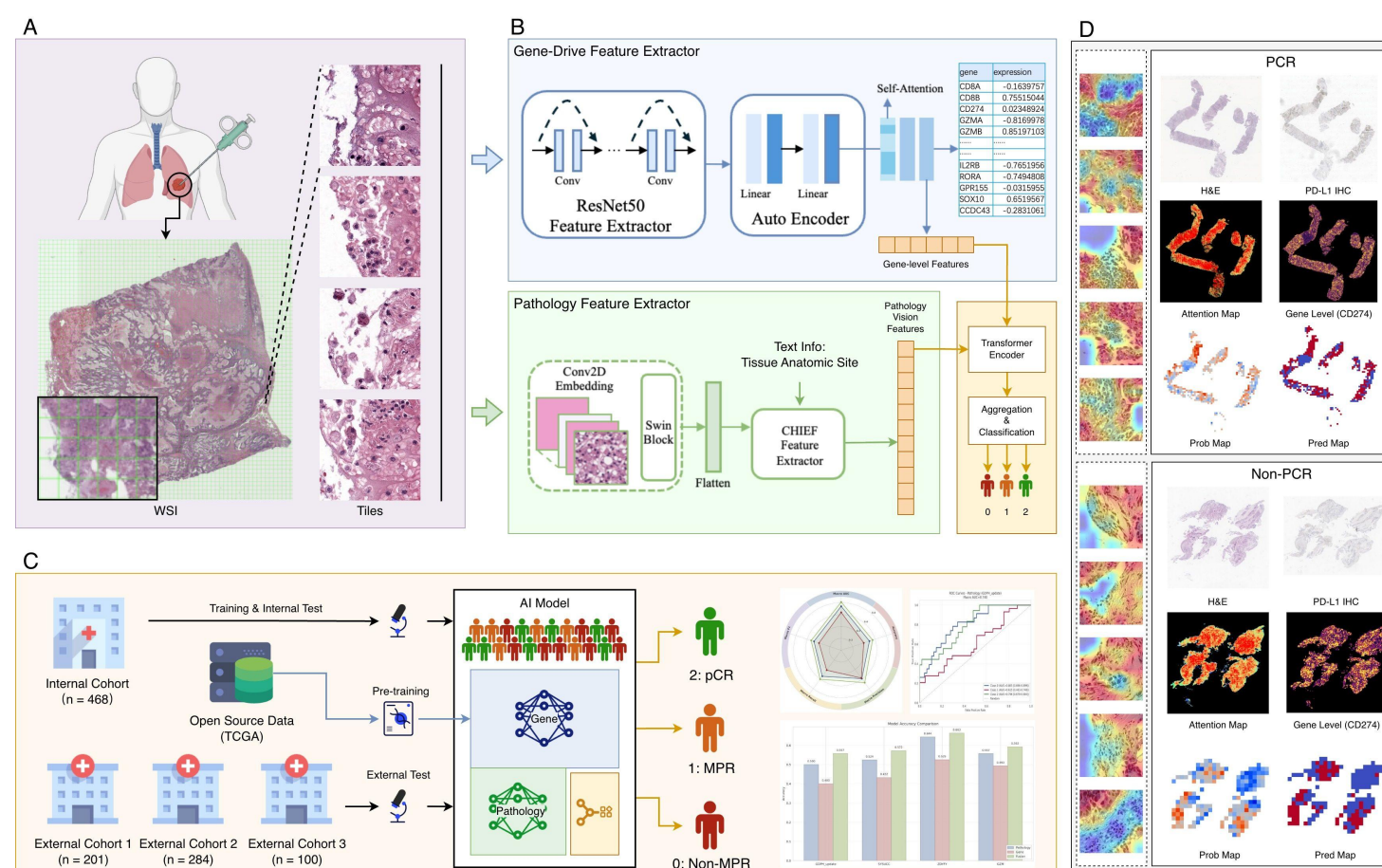
Proposed solution: G-MAPS

- Gene-guided Multi-scale AI Pathology Signature integrating tissue architecture and immune-related transcriptomic programs.
- Designed for tri-level pathological response prediction in stage I-III NSCLC after neoadjuvant ICI-based treatment.

METHODS

Study design and inputs

- Patients: stage I-III NSCLC treated from 2019-2025 with neoadjuvant immunotherapy-based regimens followed by resection.
- Training input: high-definition H&E WSI from GPDH retrospective cohort; gene guidance: TCGA-LUAD/LUSC bulk RNA-seq.
- Model: Swin Transformer pathomic features + ResNet50-autoencoder gene-expression prediction + gated/transformer fusion.



G-MAPS workflow, model architecture, validation design, and model interpretability.

DISCUSSION AND CONCLUSION

Actionable Take Away Message

- G-MAPS provides a single tri-level prediction framework for non-MPR, MPR, and pCR, aligned with clinically meaningful response categories.
- The fusion approach consistently improved performance over pathomic-only and gene-guided models across multiple centers.
- The model links multi-scale H&E morphology with immune-related gene programs, supporting more interpretable AI pathology.

Future Direction for Research

- Prospective workflow validation with locked thresholds and turnaround-time assessment.
- Integration with clinical, radiologic, and treatment-regimen variables.
- Decision-impact evaluation for adjuvant and surveillance strategies.

REFERENCES & ACKNOWLEDGEMENTS

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Reference List



Personal Profile



RESULTS

1,053

patients across cohorts

5

independent cohorts

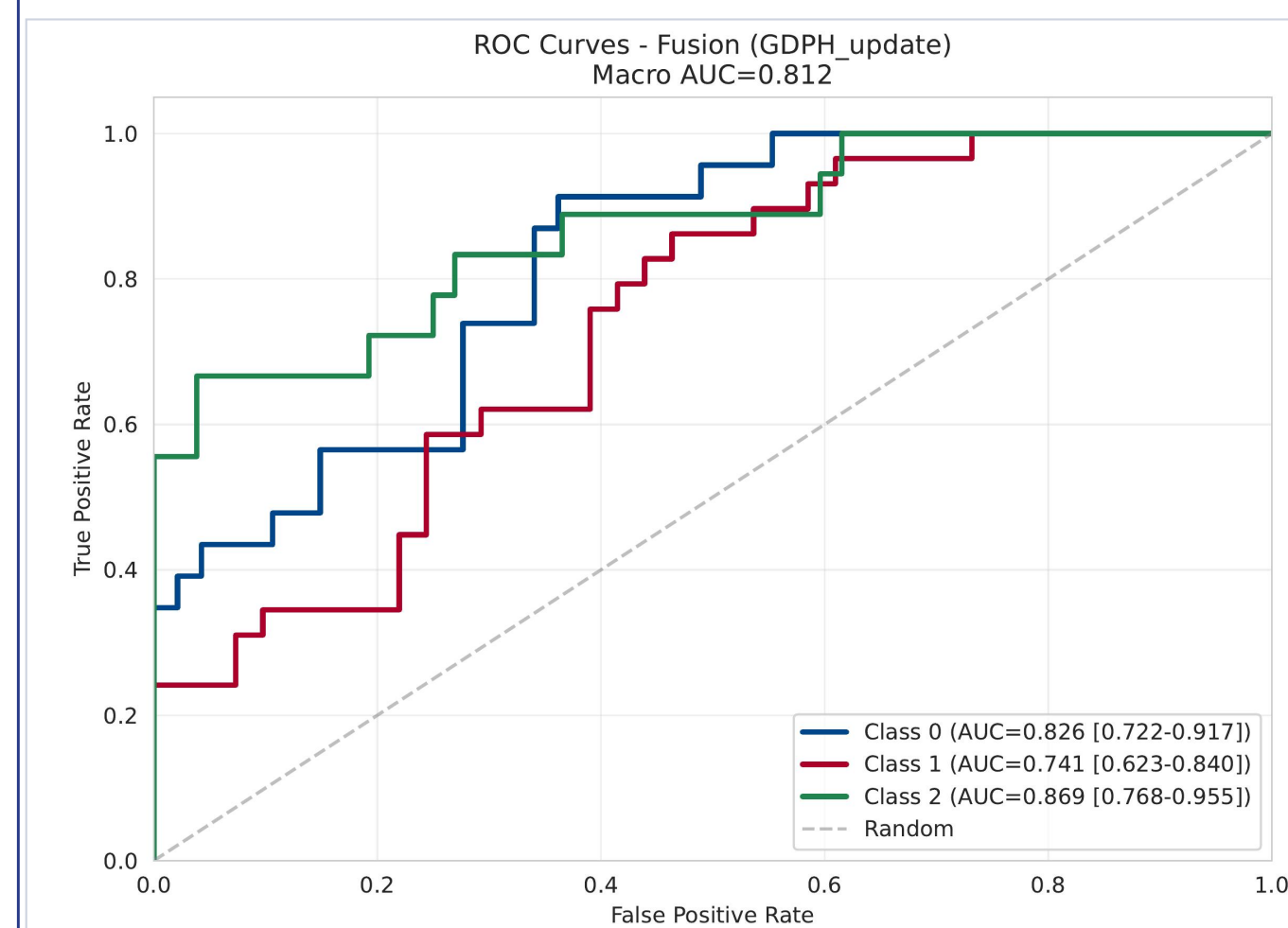
0.812

internal macro AUC

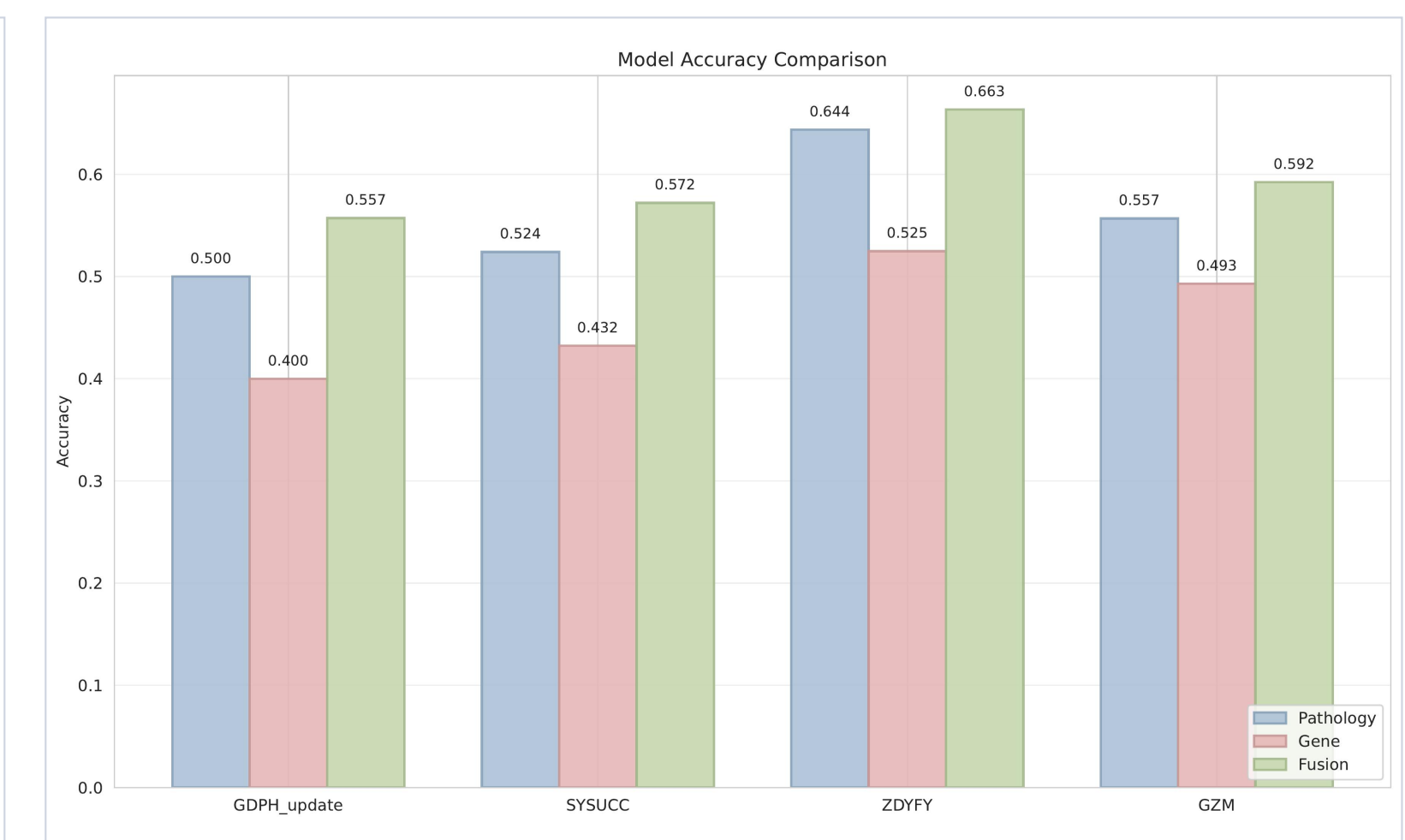
0.869

internal pCR AUC

Performance highlights: multi-class ROC curves and fusion accuracy across internal and external cohorts

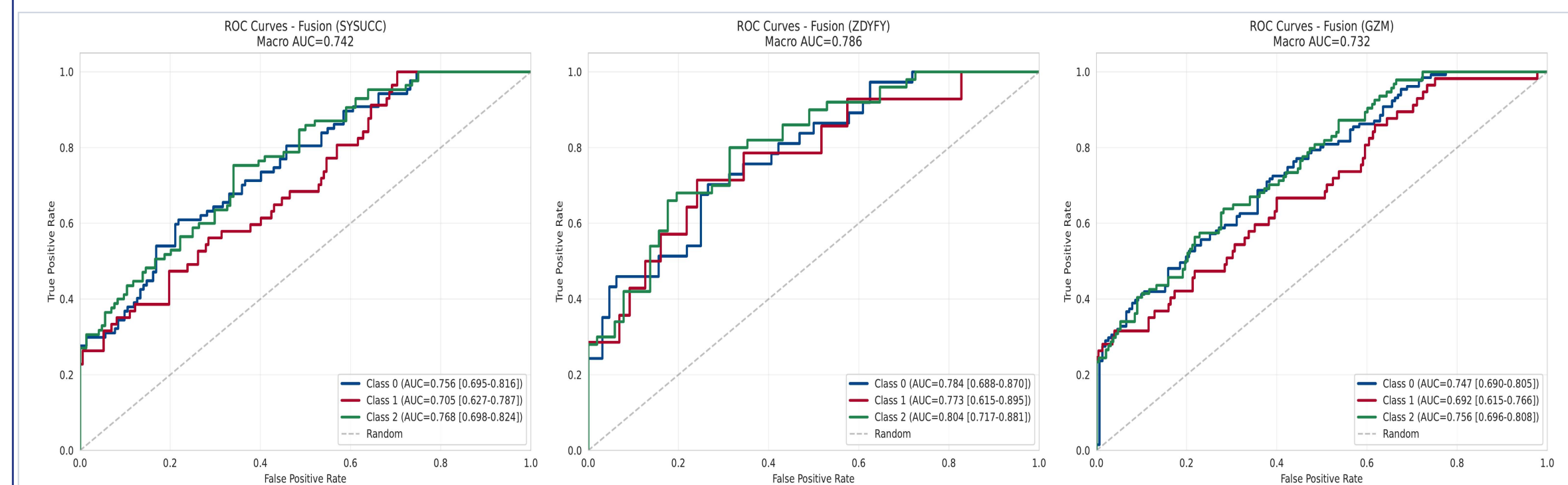


Internal prospective cohort: macro AUC 0.812;
pCR AUC 0.869.



Fusion/G-MAPS improves accuracy versus pathomic-only and gene-guided models.

External validation ROC curves



External macro AUCs: SYSUCC 0.742, ZDYFY/FAHZU 0.786, GZM 0.732.

G-MAPS multi-center performance summary

Cohort	n	Macro AUC	Accuracy	pCR AUC
GDPH prospective	65	0.812	55.7%	0.869
SYSUCC	201	0.742	57.2%	0.768
ZDYFY / FAHZU	100	0.786	66.3%	0.804
GZM	284	0.732	59.2%	0.756

- Large research cohort: training set n=403, internal prospective n=65, external validation n=585.
- Class-specific ROC analysis supports tri-level discrimination for non-MPR, MPR, and pCR.
- Interpretability maps highlight model attention and predicted immune gene-level patterns, including CD274/PD-L1-related signals.

Class 0: non-MPR

Class 1: MPR

Class 2: pCR

Fusion = G-MAPS model