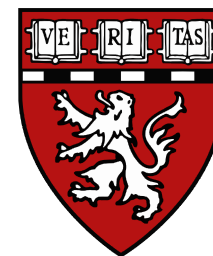


Act Like a Pathologist: Tissue-Aware Whole Slide Image Reasoning

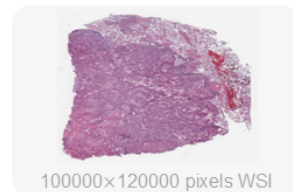
Wentao Huang, Weimin Lyu, Peiliang Lou, Qingqiao Hu, Xiaoling Hu,
Shahira Abousamra, Wenchao Han, Ruifeng Guo, Jiawei Zhou, Chao Chen, Chen Wang



Pathology Visual Question Answering

- **Goal: answer clinical questions about a whole-slide image (WSI).**
 - Diagnostic reasoning, report generation.
- **Why it matters:**
 - Scale pathologist expertise.
 - Clinically trustworthy, interpretable answers.

A



Summarize the key pathological findings from the whole slide image clearly.

The final pathological examination reveals a diagnosis of high-grade urothelial carcinoma with deep invasion into the detrusor muscle but without penetration through it. The carcinoma exhibits papillary ...

What is the pathological stage (pT) of the transitional cell carcinoma? A. pT1 B. pT2 C. pT3 D. pT4

B. pT2

What type of differentiation is observed in this whole slide image?

Squamous differentiation

B

Microscopy

- ◆ Tissue Architecture
- ◆ Tumor Characteristics
- ◆ Histopathological Changes
- ◆ Cytomorphological Characteristics

Diagnosis

- ◆ Disease Detection
- ◆ Staging
- ◆ Grading
- ◆ Disease Classification
- ◆ Differential Diagnosis

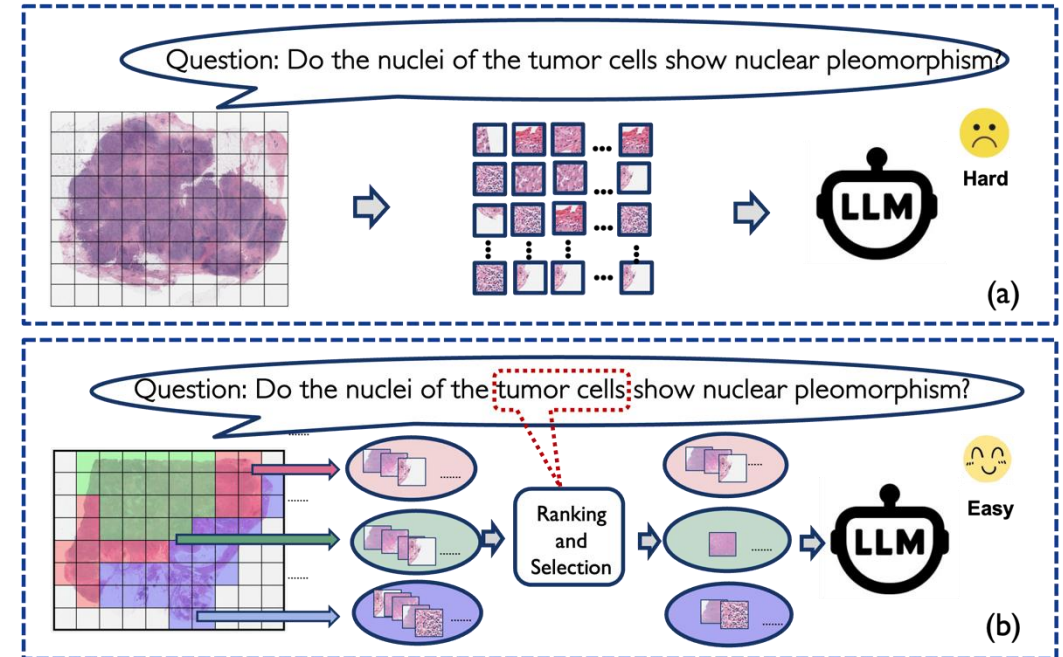
Clinical

- ◆ Treatment Guidance
- ◆ Risk Factors
- ◆ Prognostic Assessment
- ◆ Biomarker Analysis

From Problem to Motivation

The Problem

- **A gigapixel slide contains far more information than necessary for a given question.**
 - A single WSI yields tens of thousands of patches.
 - Only a small subset carries the answer.
- **Current WSI-MLLMs treat every patch equally.**
 - Strict LLM token limits force uniform sampling or pooling.
 - Redundant + question-irrelevant tokens overwhelm the LLM.
- **Predictions are black-box and unverifiable.**
 - No patch-level attribution → pathologists can't verify the reasoning.

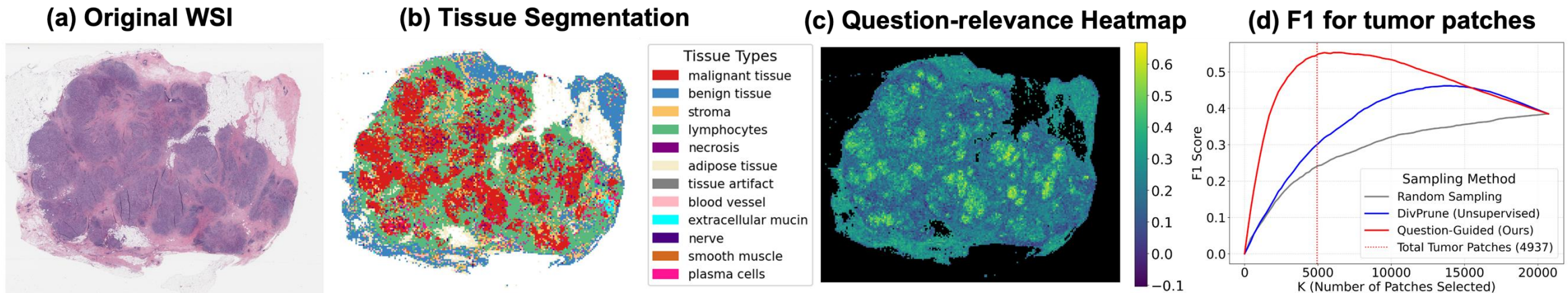


Our Motivation

- Pathologists scan broadly, then zoom in based on the clinical question.

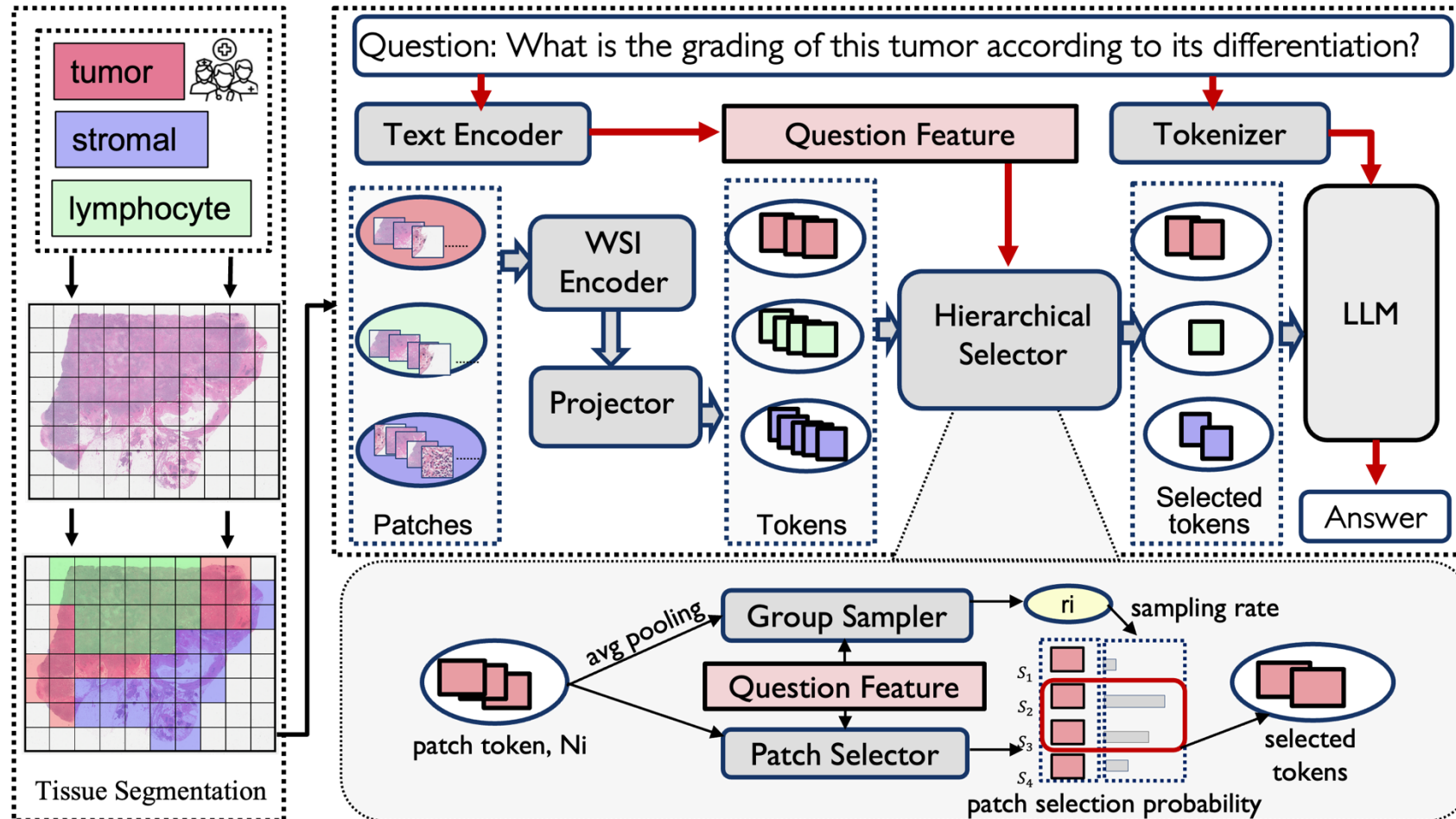
Pre-analysis

- Pathologists scan broadly, then zoom in selectively, guided by the question.
- Pre-analysis on TCGA-BRCA for patch retrieval:
 - Patch-question similarity heatmap overlaps the tumor mask.
 - Question-guided \gg diversity \gg random in F1 score for retrieving tumor patches.
 - Diversity is not enough — patch selection must be driven by the question.



Our Approach: HistoSelect

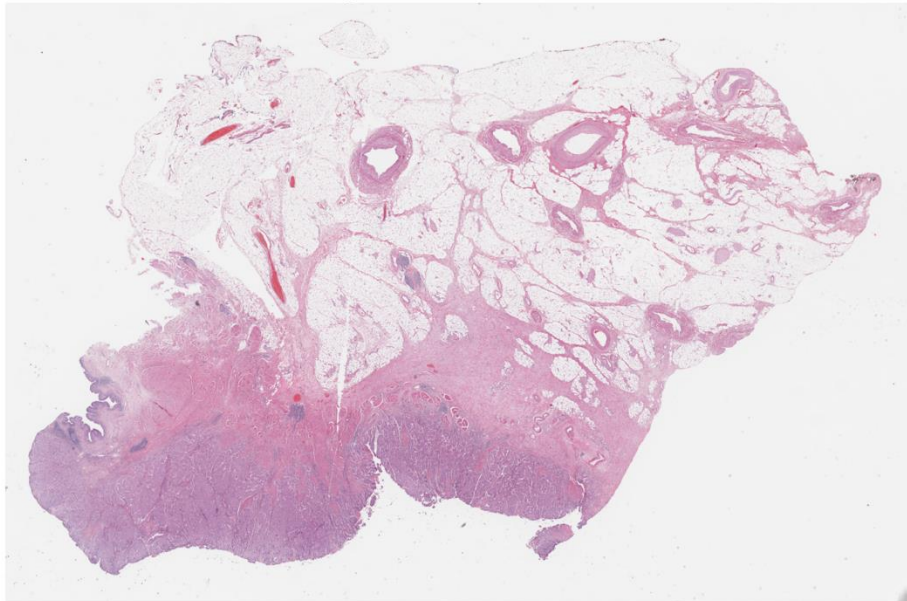
A question-guided, tissue-aware, coarse-to-fine patch selector grounded in the Information Bottleneck (IB).



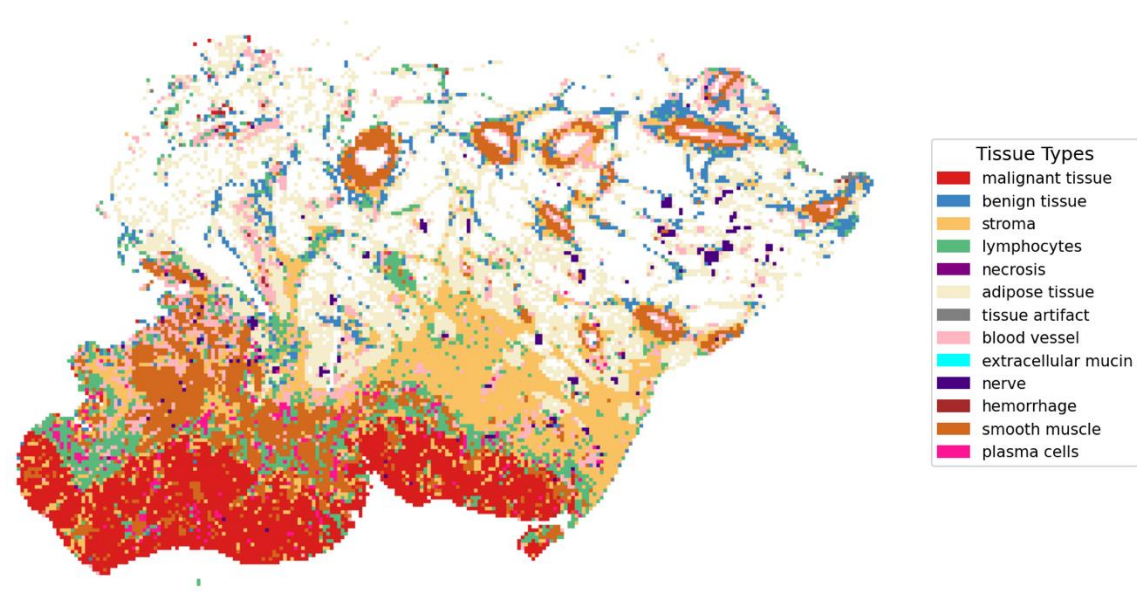
Tissue Segmentation

- **M** pathologist-designed tissue prompts: tumor / stroma / lymphocyte / necrosis / ...
- Match each patch to a prompt by visual–text cosine similarity (CONCH encoders).
 - Patch i is assigned to the tissue group with the highest similarity.
- Yields a partition of the WSI into **M** semantically coherent regions — the tissue segmentation map.

Original WSI (Thumbnail)



Predicted Tissue Class Visualization



Hierarchical Selector + IB

➤ **Group Sampler**

- predicts a question-aware sampling rate per tissue group.

➤ **Patch Selector**

- scores each patch by relevance to the question; top- k_j kept per group.

➤ **Hierarchical Information Bottleneck**

- regularizes selection toward question-aligned tokens.

➤ **Straight-Through Estimator** makes top- k differentiable for end-to-end VQA training.

$$r_j = \sigma(\mathcal{F}_{\text{group}}([\mathbf{g}_j; \mathbf{q}])) \quad s_i = \sigma(\mathcal{F}_{\text{patch}}([\mathbf{x}_i; \mathbf{q}]))$$

$$\mathcal{L}_{\text{final}} = \mathcal{L}_{\text{VQA}} + \beta_g \mathcal{L}_{\text{group}} + \beta_p \mathcal{L}_{\text{patch}}$$

Quantitative Results

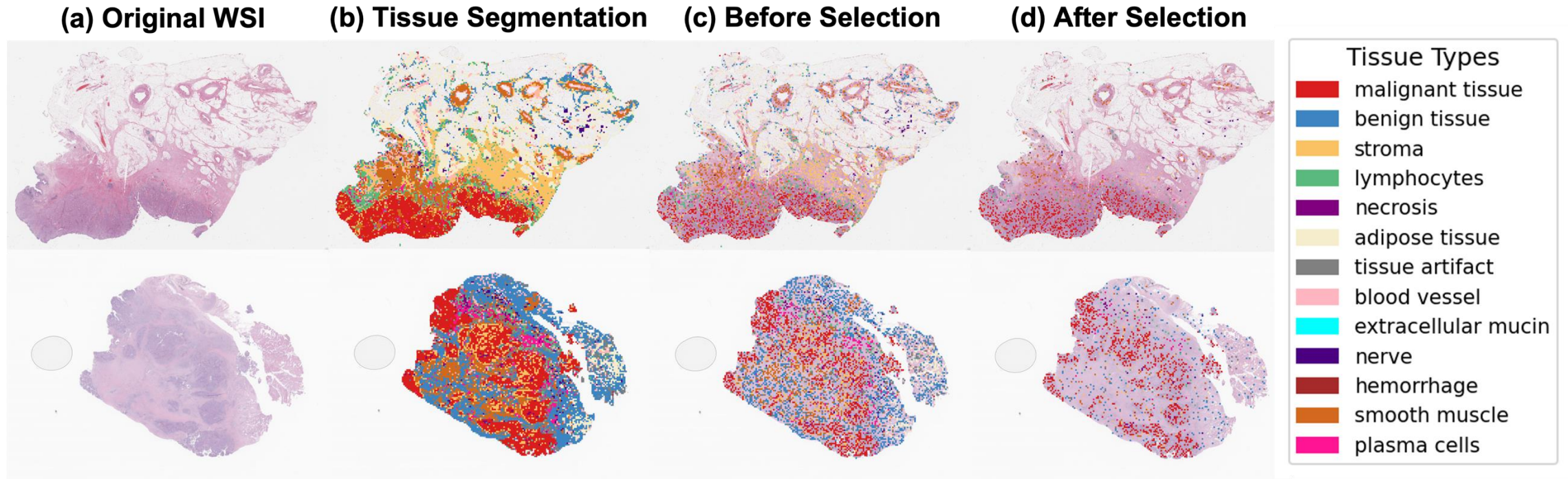
➤ Close Ended

Method	Input	SlideBench-VQA (TCGA)			WSI-Bench (Close)			In-house Ovarian	Average
		Microscopy	Diagnosis	Clinical	Morphology	Diagnosis	Treatment	Diagnosis	
GPT-4o	Thumbnail	39.24	24.12	44.67	47.07	53.06	87.50	—	49.28
Quilt-LLaVA[32]	Thumbnail	52.39	30.19	49.33	94.13	84.13	97.92	70.67	68.39
LLaVA-Med [20]	Thumbnail	52.15	29.97	47.33	91.04	81.32	95.83	70.67	66.90
SlideChat [9]	WSI	83.15	71.36	75.33	91.34	82.15	93.75	69.33	80.88
HistoSelect	WSI	84.62	73.09	77.30	94.57	85.79	97.92	73.33	83.80

➤ Open Ended

Method	WSI-Bench										
	Report Generation					Morphology		Diagnosis		Treatment	
	BLEU-1	BLEU-2	BLEU-3	BLEU-4	ROUGE-L	WSI-P	WSI-R	WSI-P	WSI-R	WSI-P	WSI-R
GPT-4o	0.202	0.069	0.030	0.016	0.132	0.220	0.204	0.472	0.457	0.513	0.704
WSI-VQA [7]	0.301	0.225	0.181	0.155	0.343	0.395	0.462	0.436	0.525	0.591	0.595
MI-Gen [6]	0.403	0.306	0.248	0.209	0.446	—	—	—	—	—	—
Histo-Gen [13]	0.406	0.307	0.248	0.208	0.448	—	—	—	—	—	—
Quilt-LLaVA [32]	0.421	0.316	0.257	0.216	0.455	0.453	0.484	0.521	0.552	0.751	0.807
SlideChat [9]	0.413	0.312	0.254	0.215	0.450	0.512	0.541	0.501	0.522	0.745	0.712
HistoSelect	0.431	0.324	0.262	0.221	0.463	0.538	0.589	0.542	0.587	0.766	0.801

Qualitative Result



Conclusion

- HistoSelect brings a pathologist-style coarse-to-fine, question-guided selection mechanism into WSI-VQA.
- Cuts visual tokens by $\sim 70\%$ while reaching SOTA performance on 3 different datasets.
- Delivers clinically attributable evidence — every prediction is backed by selected patches.

Thank You!

Code: <https://github.com/winston52/HistoSelect>

Contact: wentaohuang@cs.stonybrook.edu

