

1. Pathomic Fusion (in IEEE-TMI)

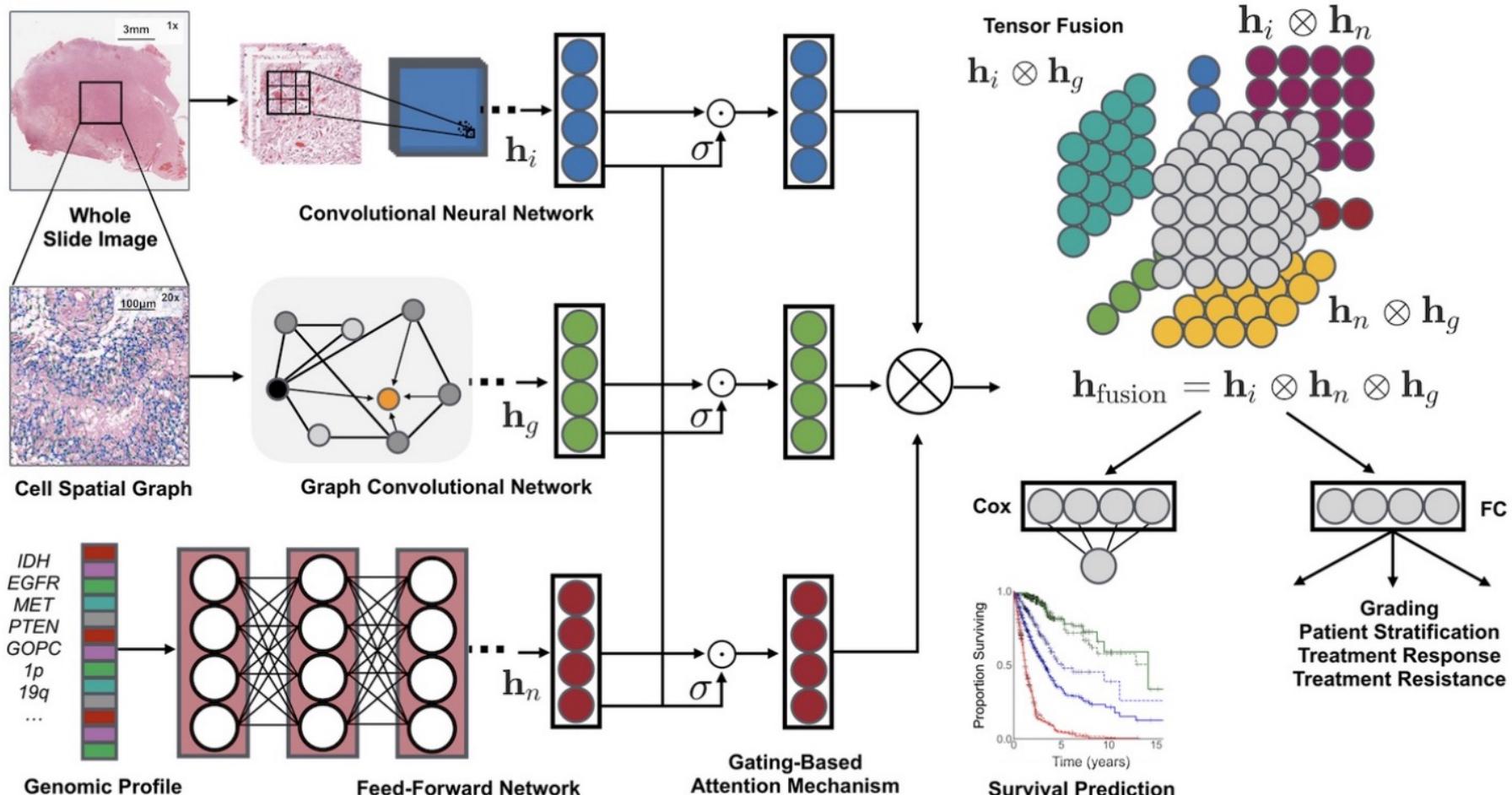
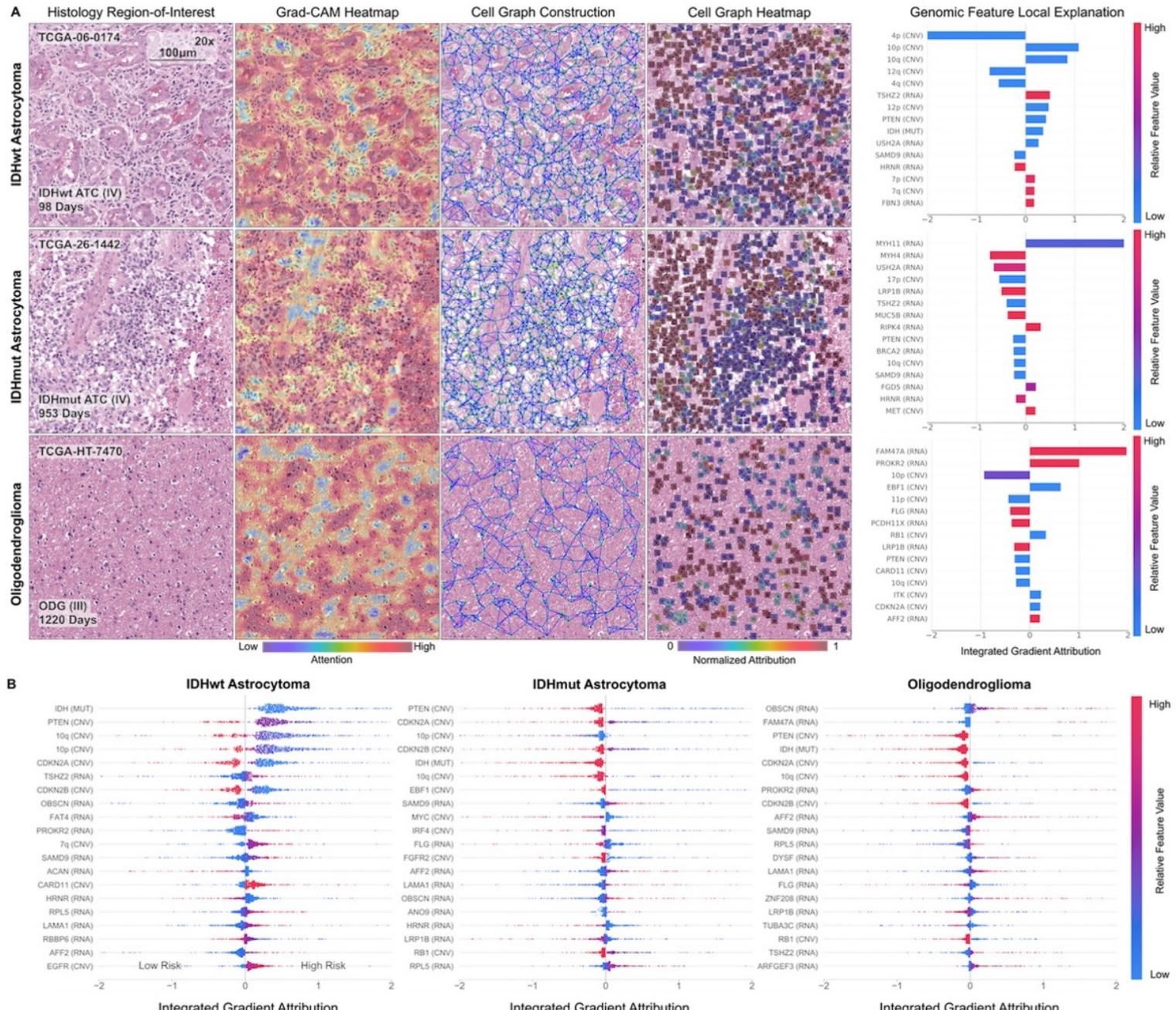


Fig. 1: *Pathomic Fusion*: An integrated framework for multimodal fusion of histology and genomic features for survival outcome prediction and classification. Histology features may be extracted using CNNs, parameter efficient GCNs or a combination of the two. Unimodal networks for the respective image and genomic features are first trained individually for the corresponding supervised learning task, and then used as feature extractors for multimodal fusion. Multimodal fusion is performed by applying an gating-based attention mechanism to first control the expressiveness of each modality, followed by the Kronecker product to model pairwise feature interactions across modalities.

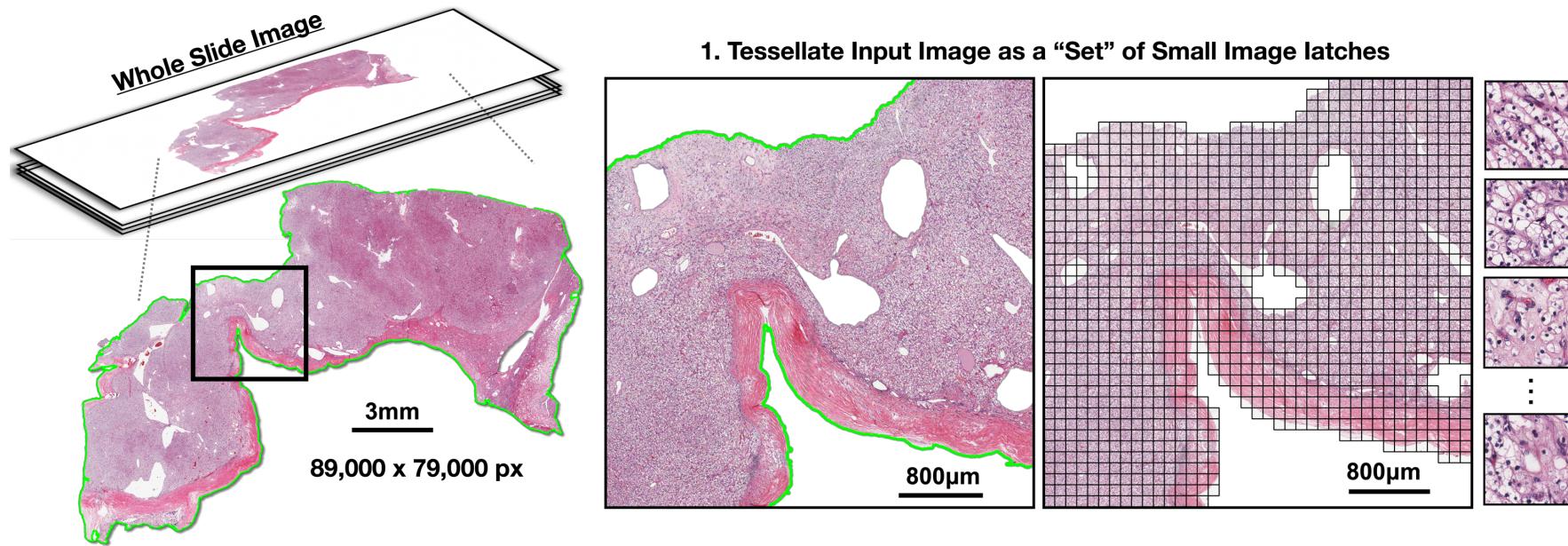
1. Pathomic Fusion (in IEEE-TMI)

- Interpretability of image + graph + genomic modalities
 - Image interpretability performed using GradCAM
 - Graph + genomic interpretability performed using Integrated Gradients
- Histology Interpretability
 - IDHwt ATC: Endothelial cells of the microvascular proliferation
 - ODG: Fried-egg cells
- Genomic Interpretability
 - Canonical biomarkers such as IDH< PTEN, MYC, CDKN2A

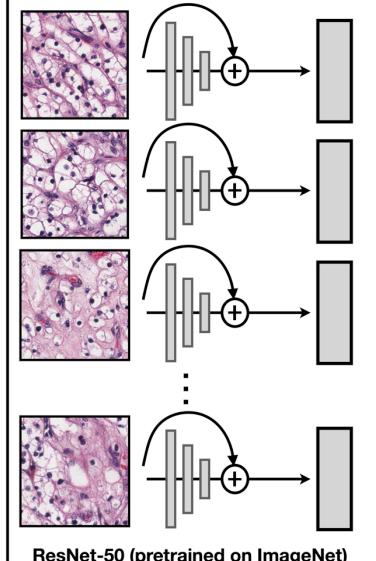


2. CLAM (Nature BME)

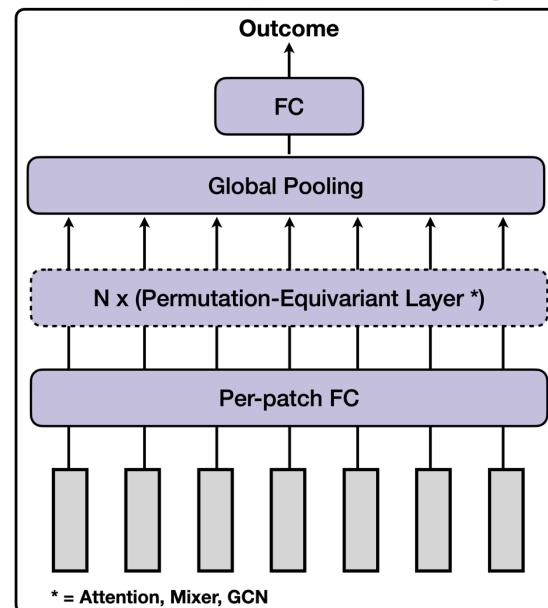
- Formulate gigapixel image as a "bag / sequence" of non-overlapping 256 x 256 patches
- Average sequence length is 15,234 patches
- Use **ResNet-50 encoder pretrained on ImageNet** to extract 1024-dim embeddings per patch
- Weak supervision via Attention MIL [Ilse *et al.* ICML18] to aggregate embeddings



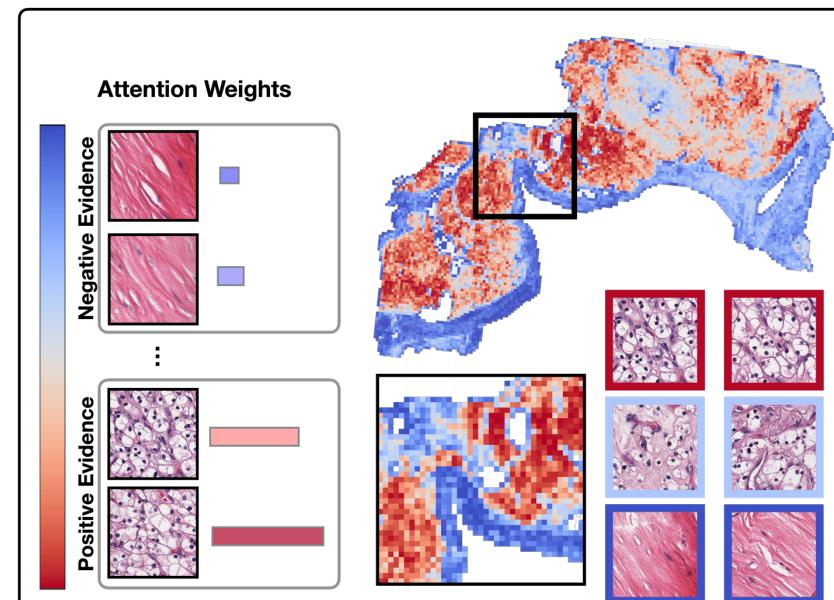
2. Feature Extraction



3. Weakly Supervised Learning

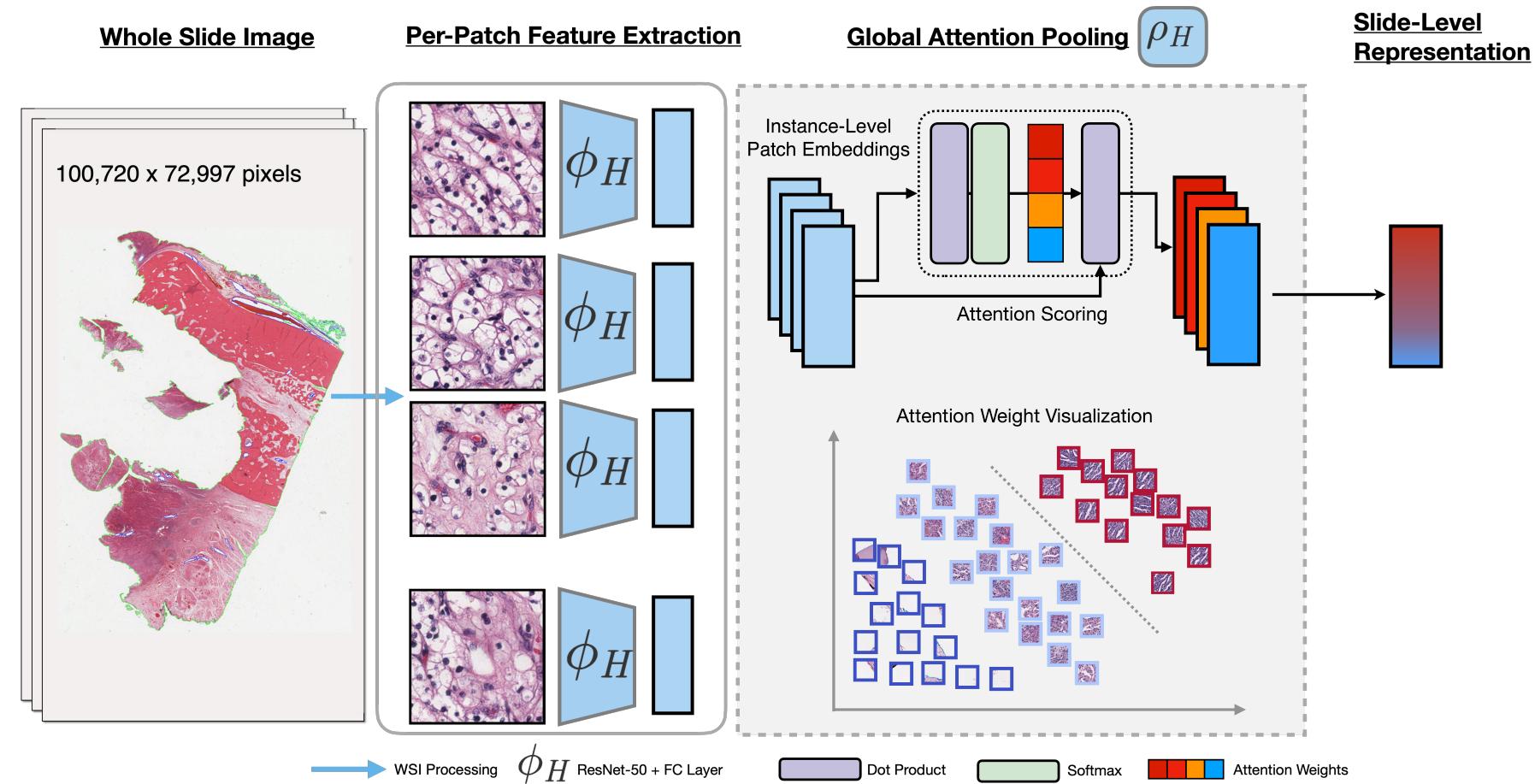


4. Interpretability

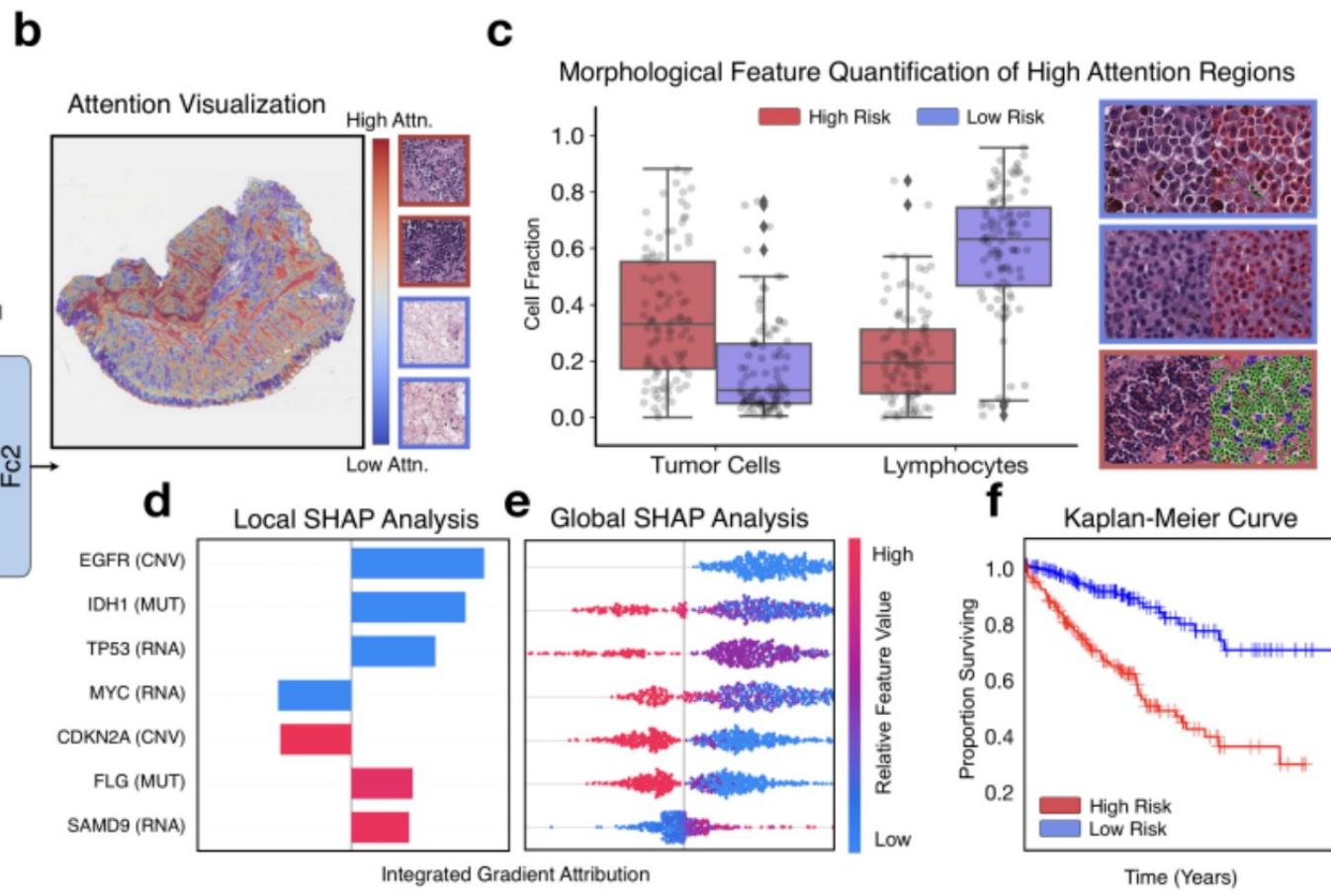
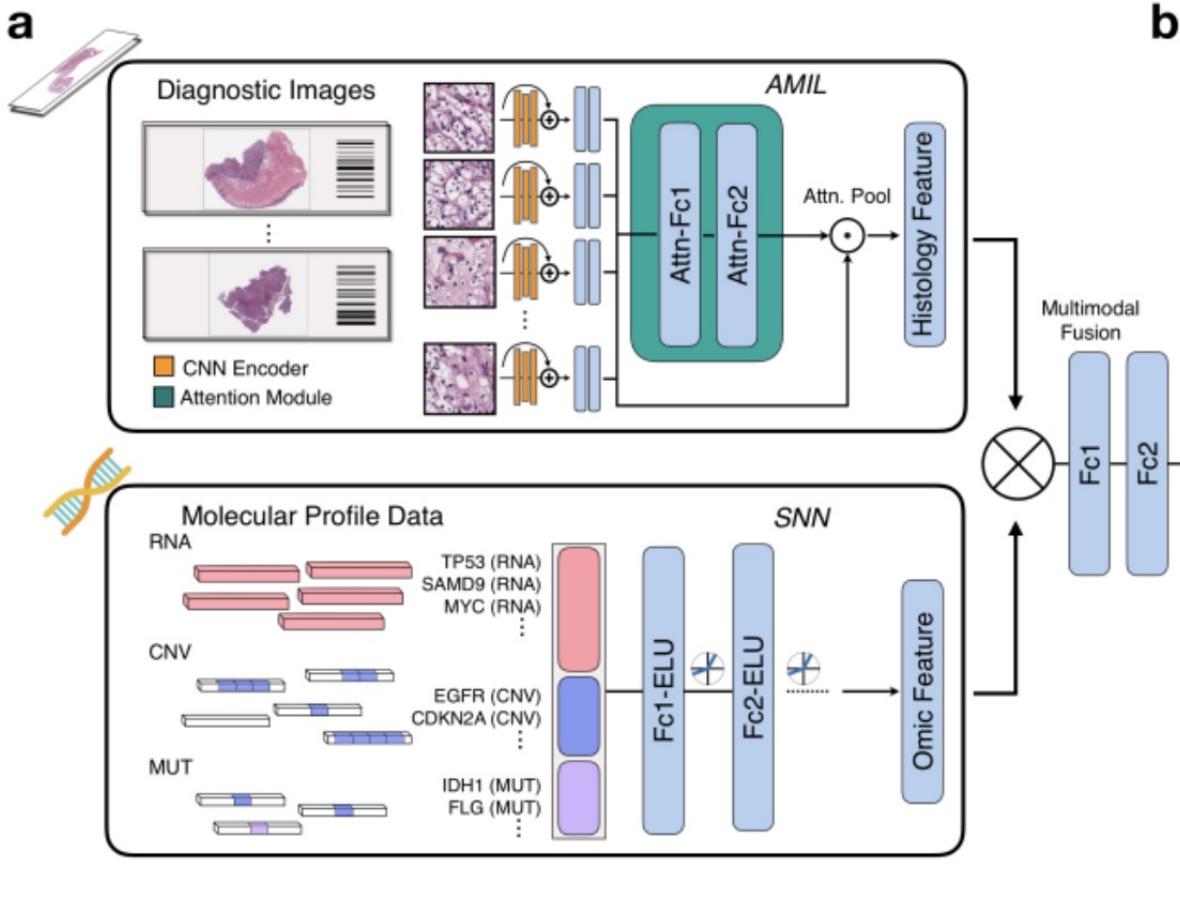


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3. PORPOISE (Submitted to Cancer Cell)



Weakly Supervised Multimodal Training + Validation

Interpretability Analysis + Knowledge Discovery

<http://pancancer.mahmoodlab.org>

4. HistoFL (Submitted to Medical Image Analysis)

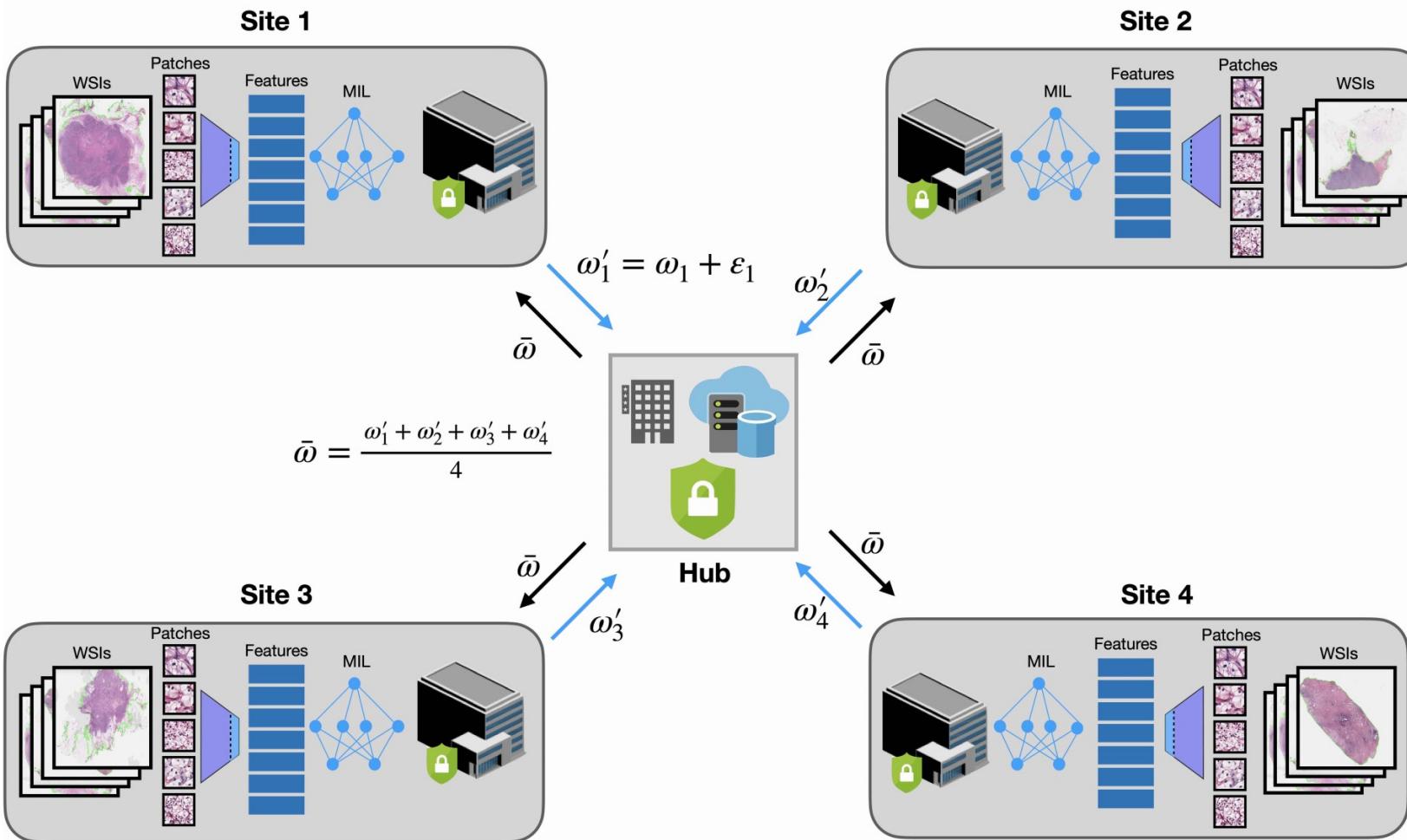
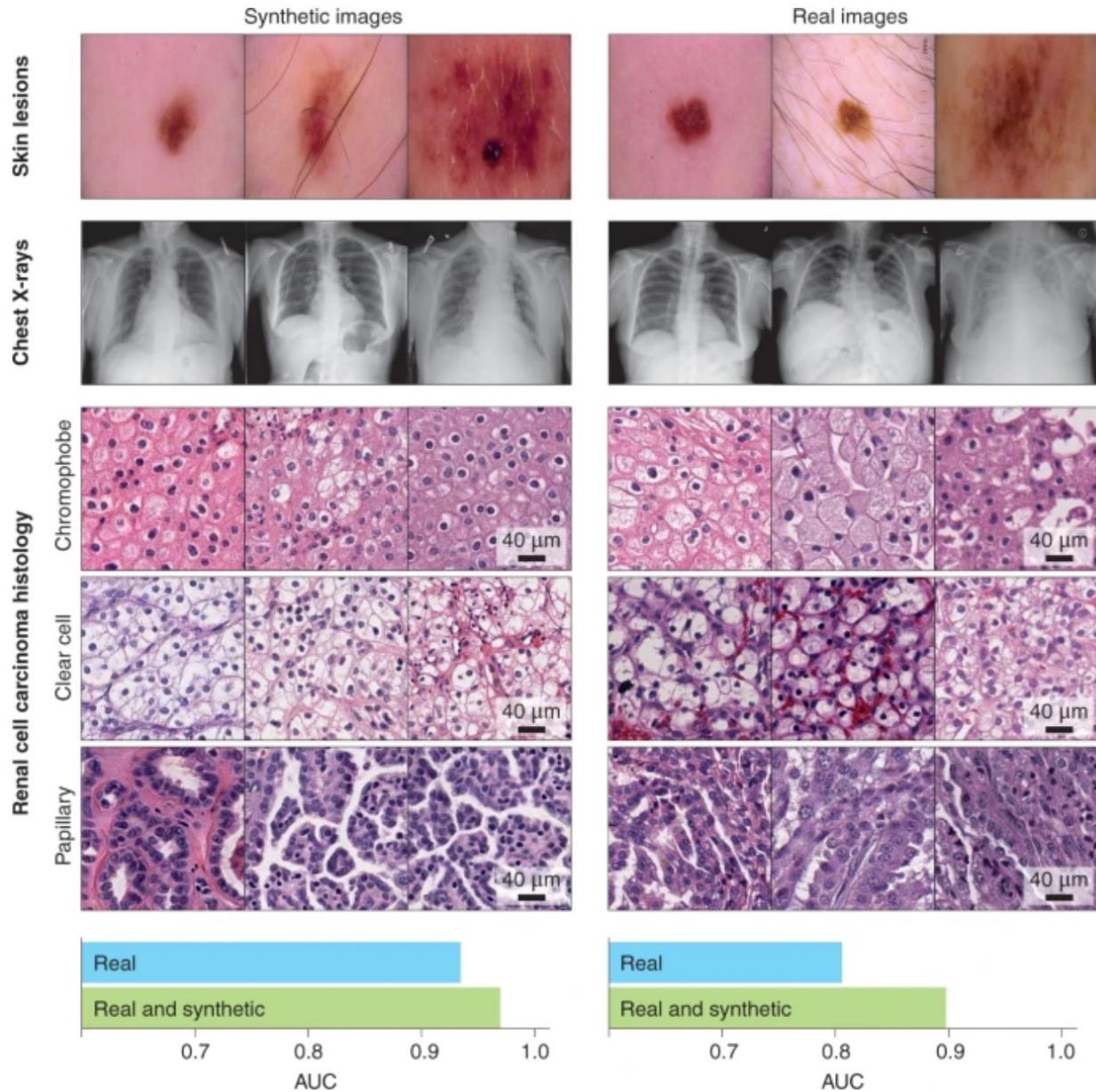


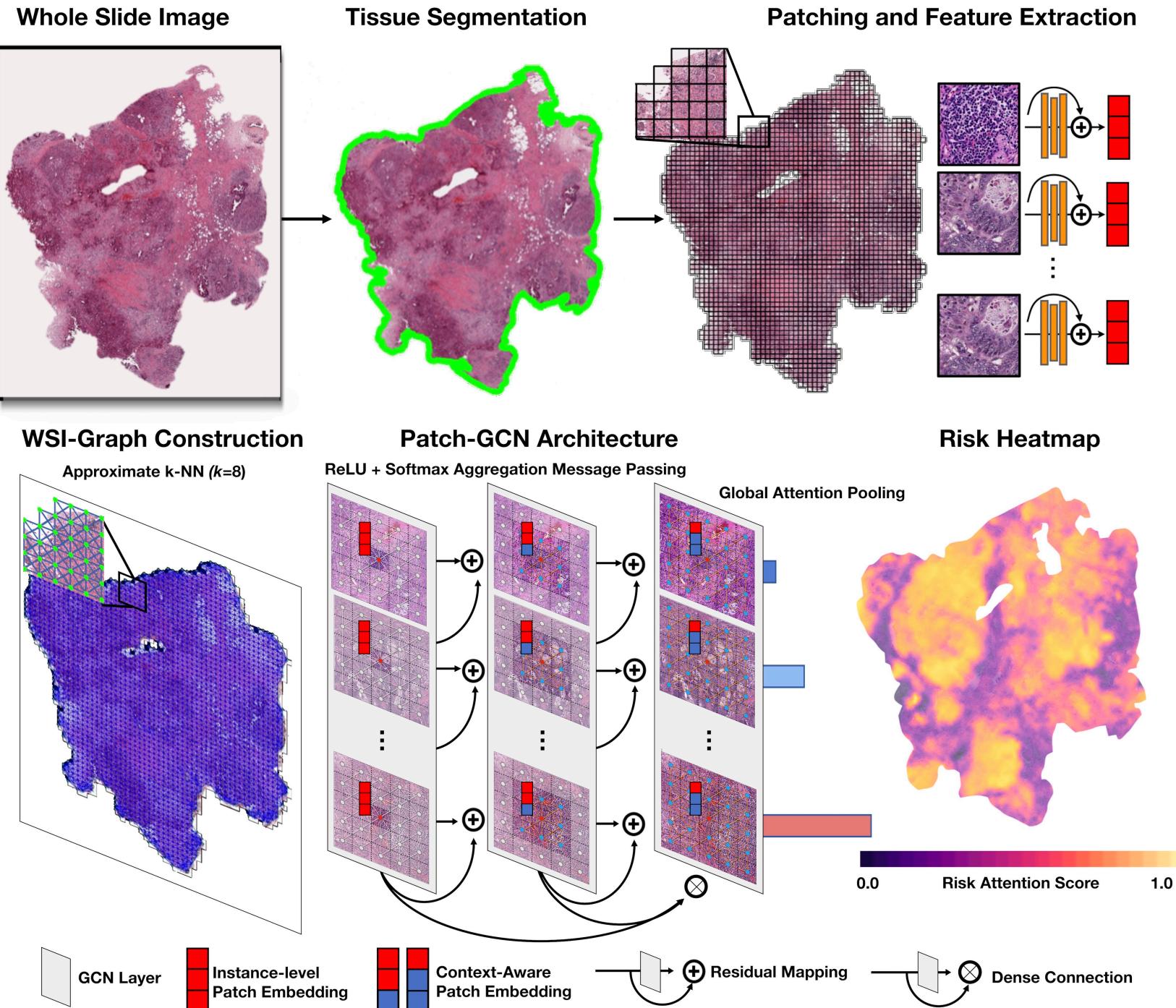
Figure 1: **Overview of the weakly supervised multiple instance learning in a federated learning framework.** At each client site, for each WSI, the tissue regions are first automatically segmented and image patches are extracted from the segmented foreground regions. Then all patches are embedded into a low-dimension feature representation using a pretrained CNN as the encoder. Each client site trains a model using weakly-supervised learning on local data (requires only the slide-level or patient-level labels) and sends the model weights each epoch to a central server. Random noise can be added to the weight parameters before communicating with the central hub for differential privacy preservation. On the central server, the global model is updated by averaging the model weights retrieved from all client sites. After the federated averaging, the updated weights of the global model is then sent to each client model for synchronization prior to starting the next federated round.

5. Synthetic data in machine learning for medicine and healthcare (Nature BME)



6. Patch-GCN (MICCAI 2021)

- Treat extracted ResNet-50 feature embeddings as nodes in a 2D point cloud
- Nodes connected via K-NN spatially adjacent to other nodes by (x,y)-coord
- Use GCN as backbone for feature aggregation, followed by global pooling for weak supervision



7. MCAT (ICCV 2021)

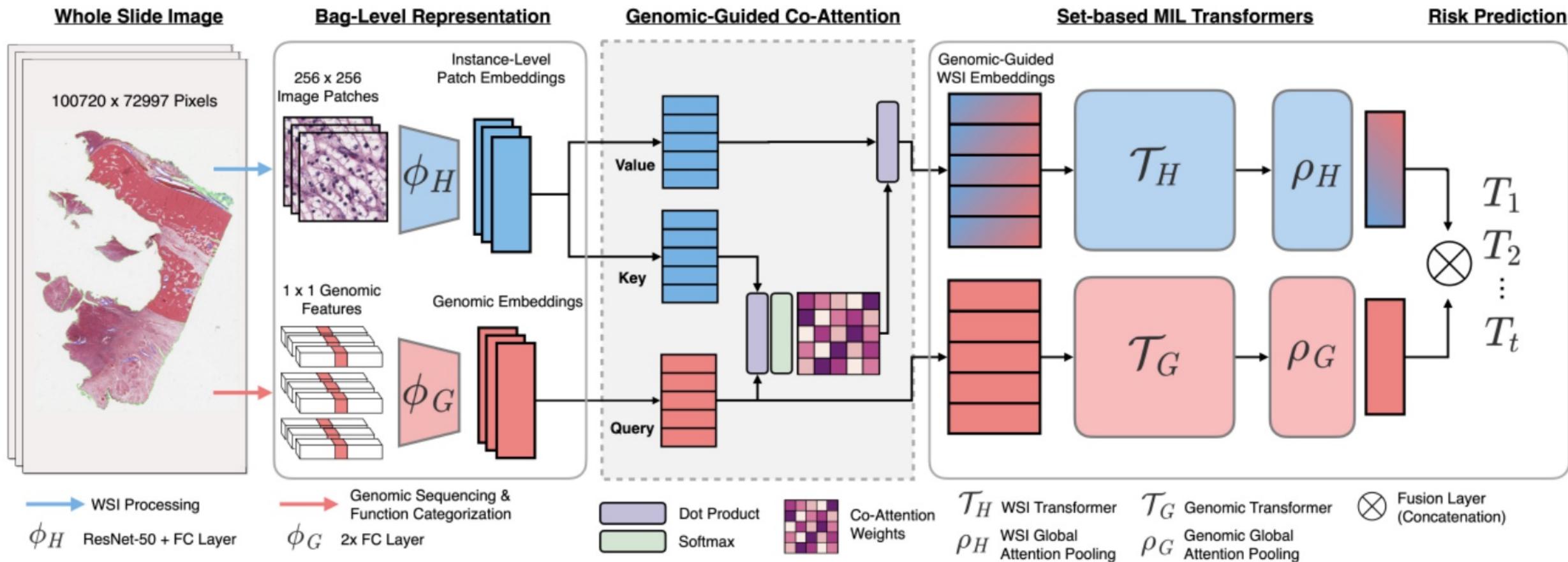
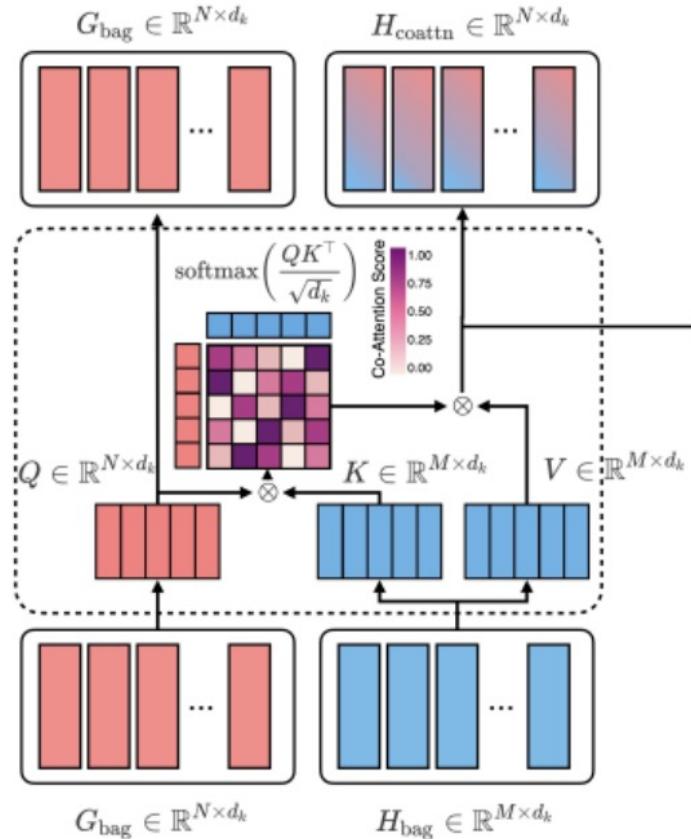


Figure 1: Overview of the Multimodal Co-Attention Transformer (MCAT) architecture. From gigapixel WSIs and genomic features, we formulate both modalities as bags representations, from which we use: 1) Genomic-Guided Co-Attention to capture multimodal interactions, and 2) set-based MIL Transformers as feature aggregation for survival outcome prediction.

7. MCAT (ICCV 2021)

Genomic-Guided Co-Attention Layer



Co-Attention Visualization

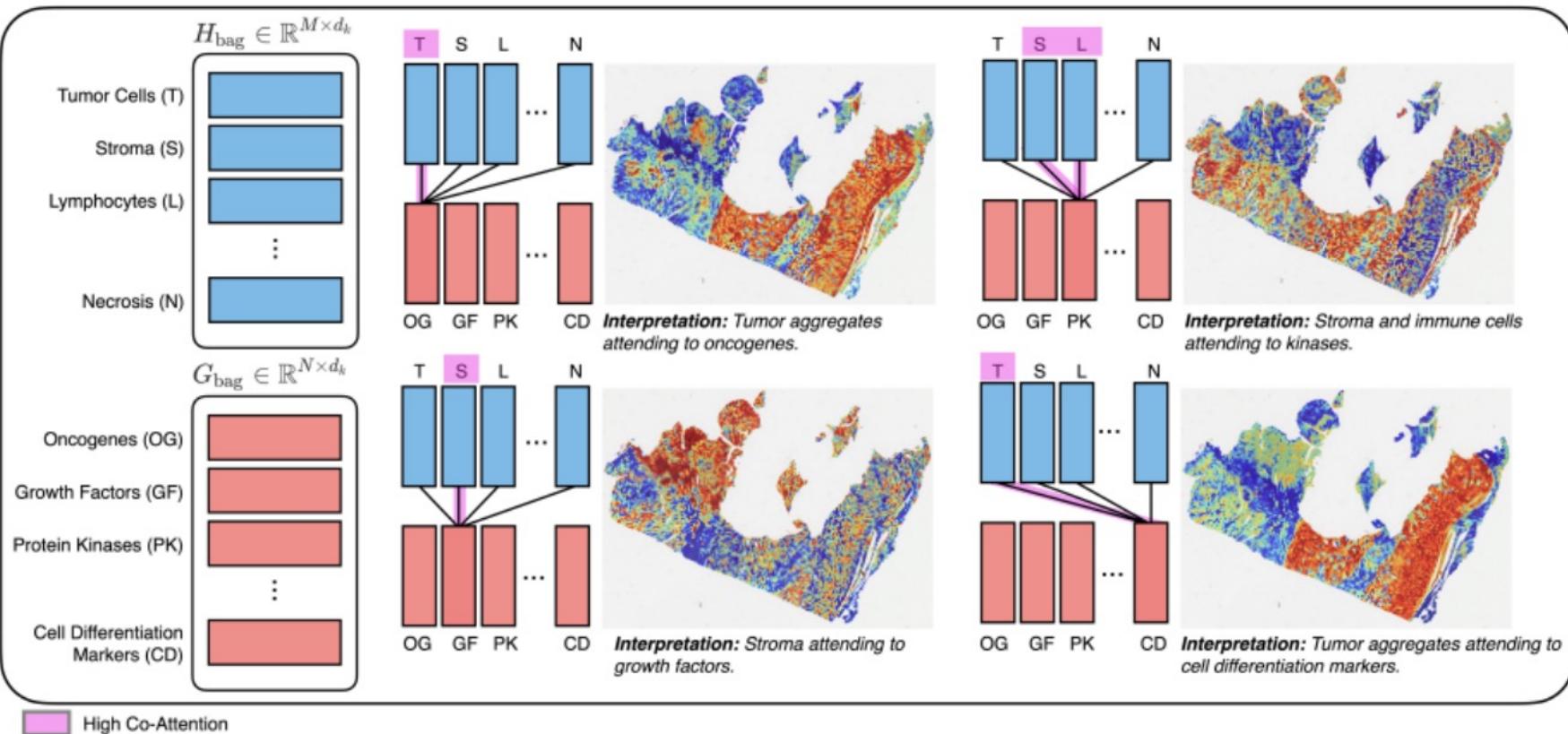
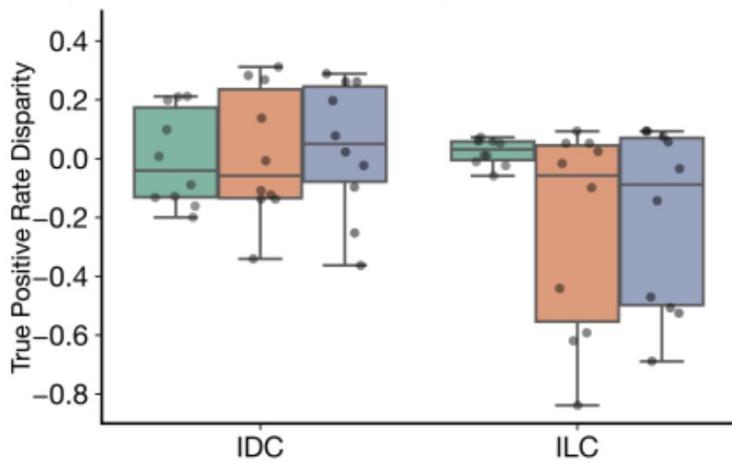
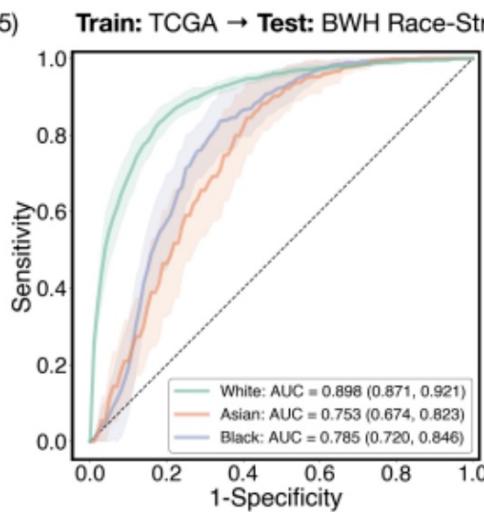
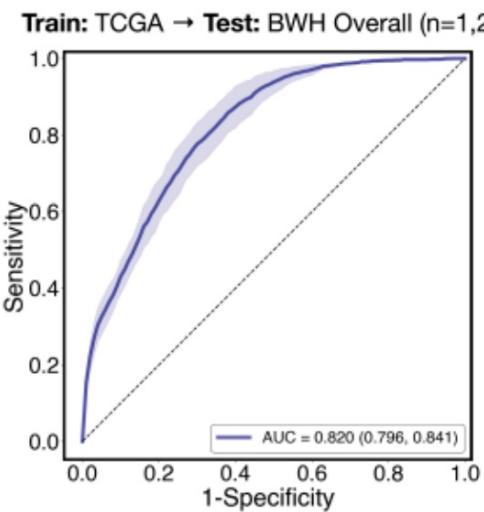
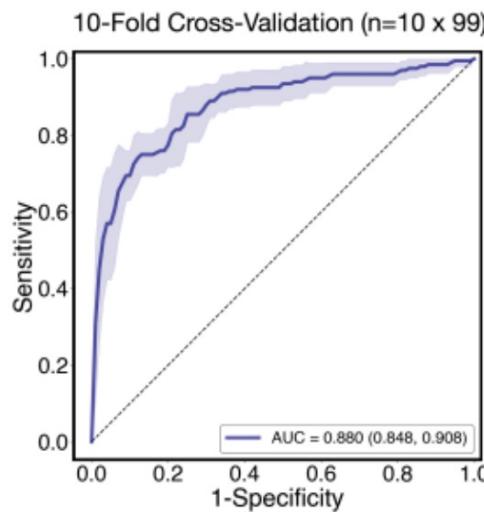


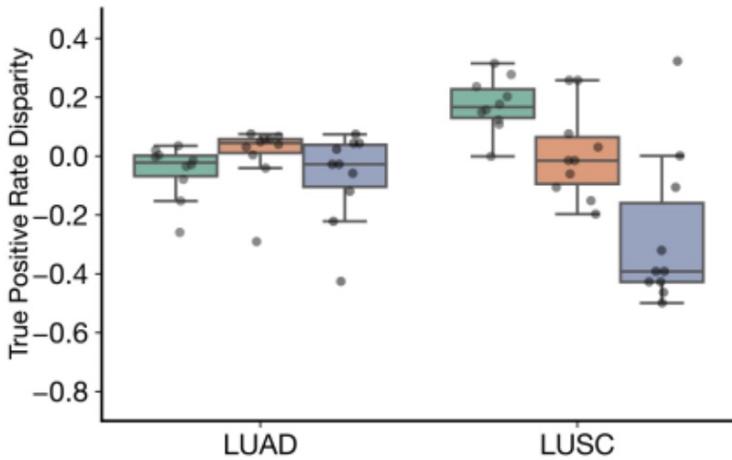
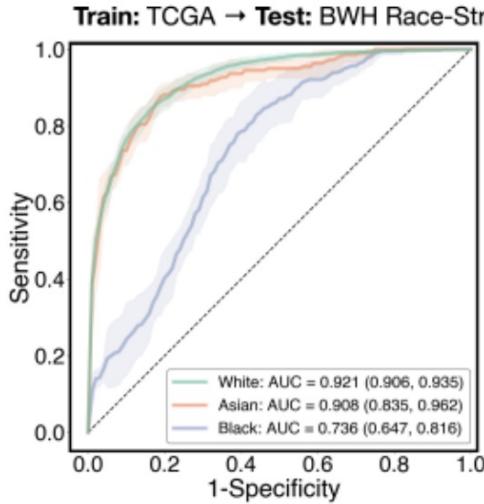
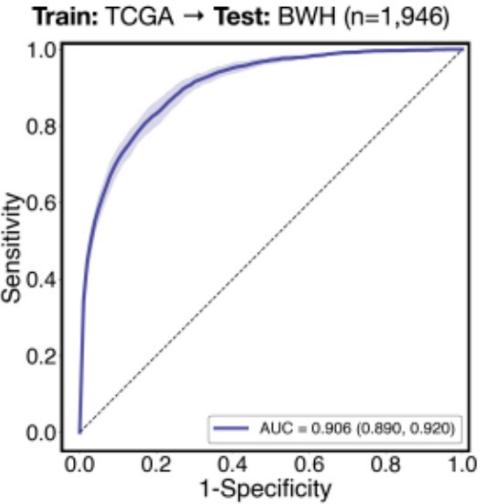
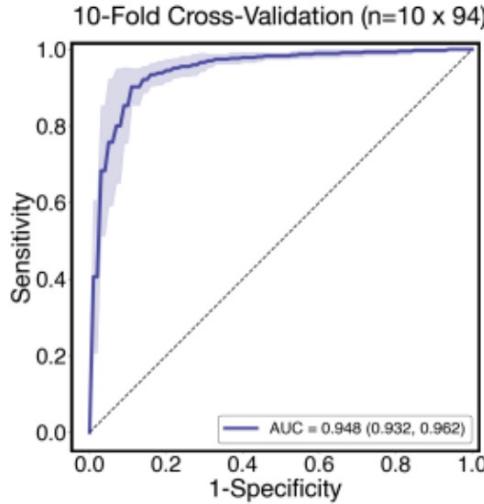
Figure 2: Overview of the Genomic-Guided Co-Attention (GCA) layer with co-attention visualization. The GCA layer uses G_{bag} (red) as queries to guide the aggregation of H_{bag} (blue) into \hat{H}_{coattn} (red/blue) using computed co-attention weights A_{coattn} . From A_{coattn} , we can visualize how each image patch in the gigapixel WSI attends to each genomic embedding.

8. Race Disparities in AI Models (Submitted to JAMA)

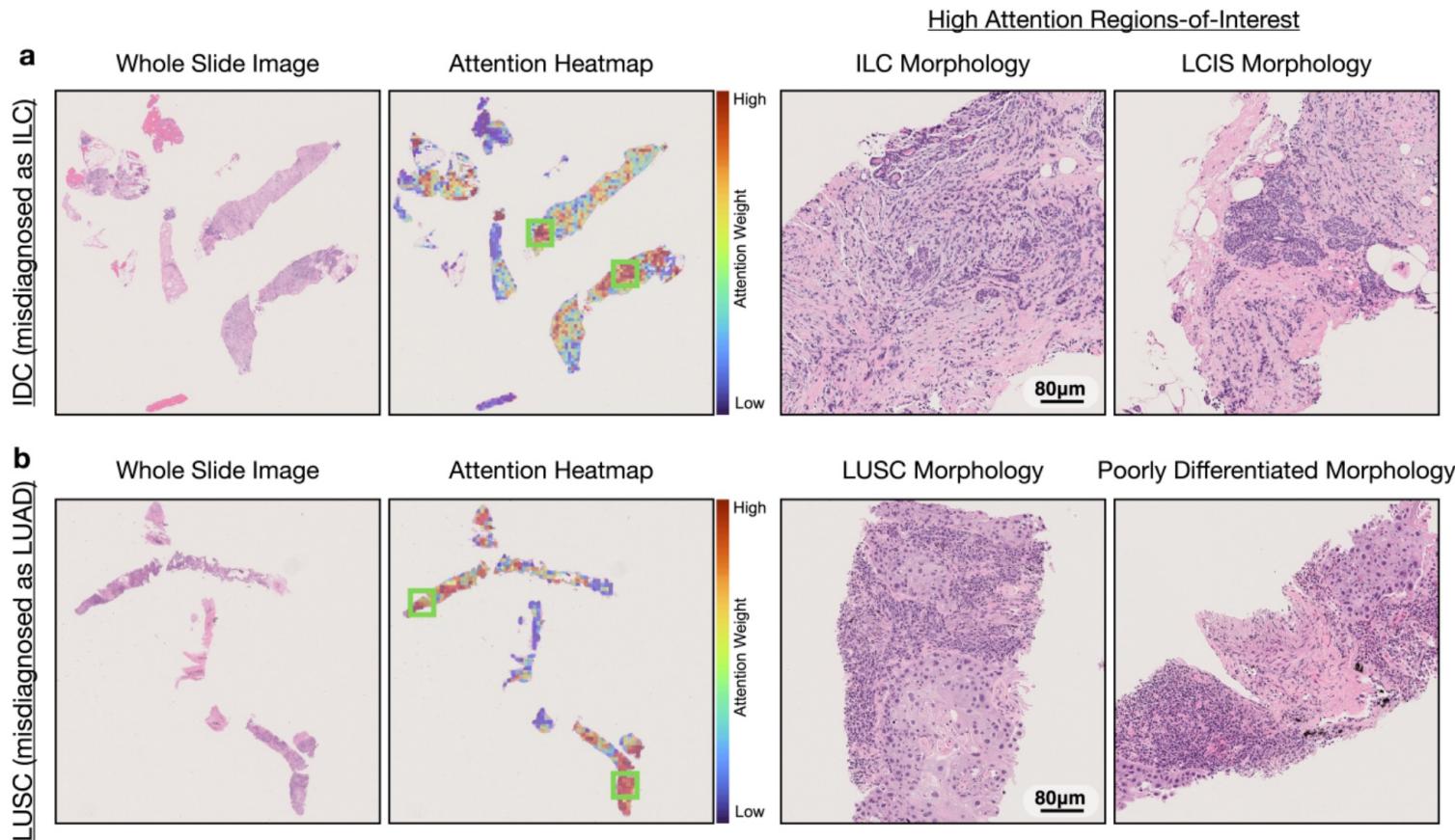
BRCA Subtyping



NSCLC Subtyping



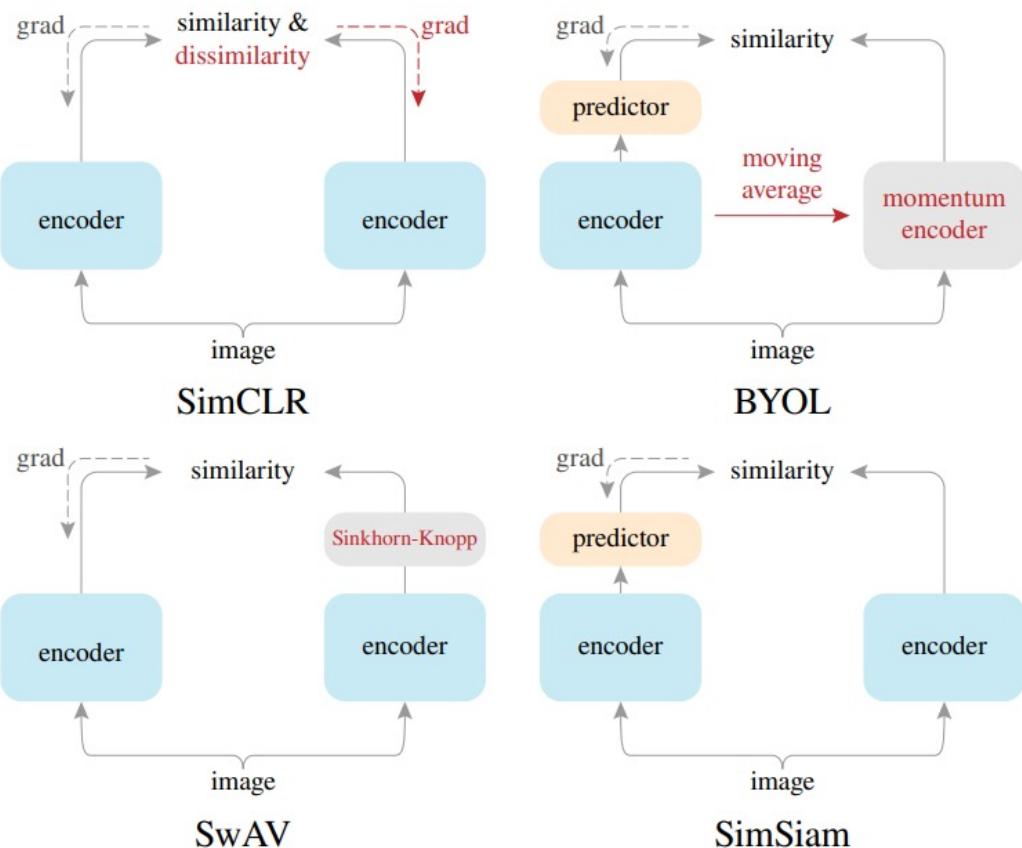
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Extended Data Figure 1: Exemplars of model misdiagnosis in ILC and LUSC subtyping. For both subtypes, misclassification in minority subpopulations resulted from histopathological evidence for both classes being present in the tissue slides, which leads to ambiguity in model diagnosis. **a.** In addition to ILC, tumor microenvironments of Black and Asian patients frequently exhibited Lobular Carcinoma in Situ (LCIS), which shares histopathological similarity with IDC, which biases the model to misclassify slides as IDC. **b.** In LUSC subtyping, tumor microenvironments of Black and Asian patients frequently exhibited poorly differentiated LUSC morphology, which can be indistinguishable from LUAD biases the model to misclassify slides as LUAD.

9. Self-Supervision in Pathology (at MSR)

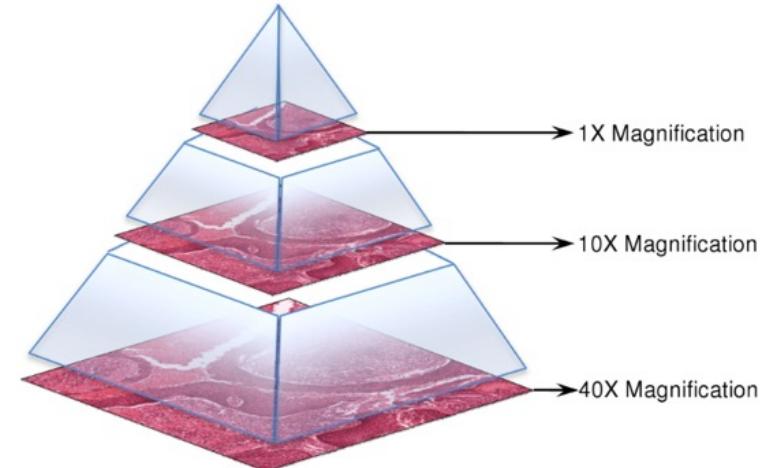
- Establishing benchmarks for common SSL methods on TCGA (organ-specific and pan-cancer)



- Exploring proxy objectives for self-supervision in image pyramids

- e.g. - Learning a **Hierarchical Vision Transformer** that learns:

1. Local representations of 256×256 image patches (with 16×16 subpatches as embeddings)
2. Global representations of $150K \times 150K$ image slides (with the previous 256×256 patches as embeddings)



CAMELYON17 Grand Challenge