Artificial-intelligence-based molecular classification of diffuse gliomas using rapid, label-free optical imaging

Hollon, T., et al. Nat Med 29, 828–832 (2023)

Presented by

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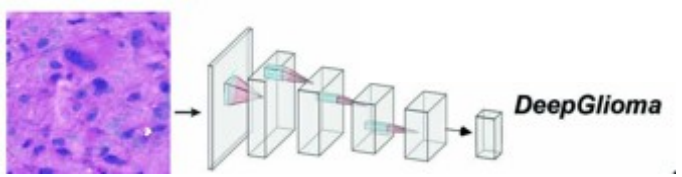
What did the authors do?

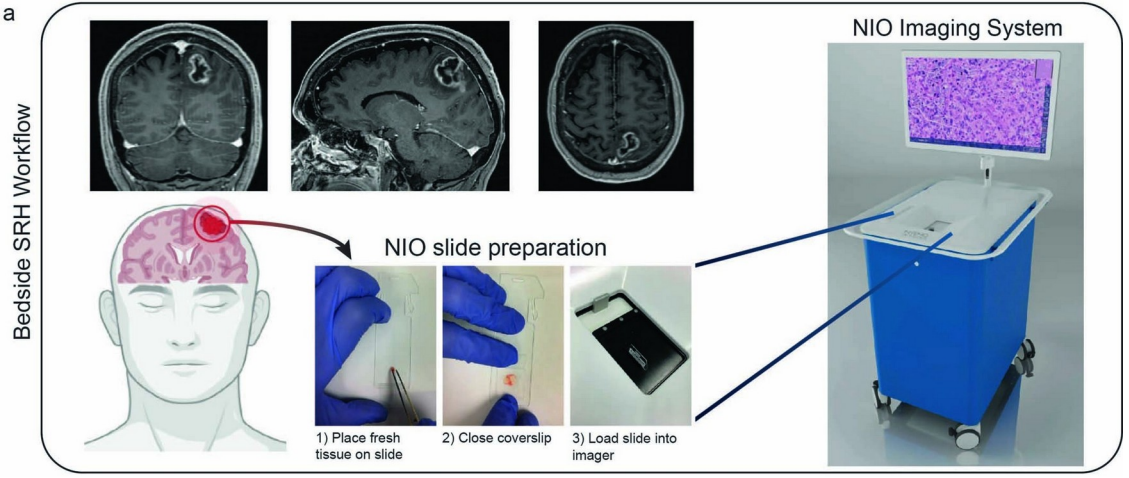


a transformer model (DeepGlioma) designed to evolve

a novel optical imaging method (Stimulated Raman histology)

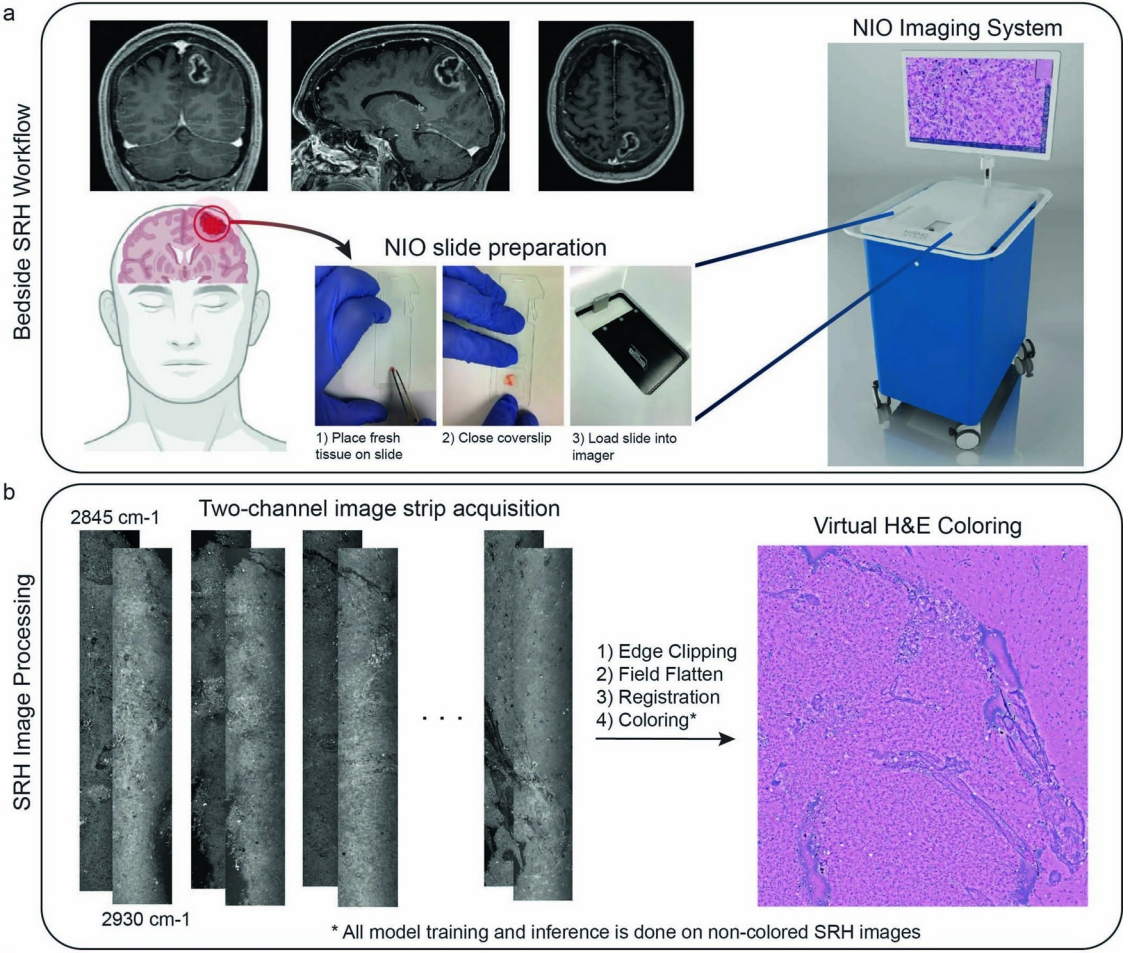
from a tissue level diagnostic tool

into a molecular level diagnostic tool.



Stimulated Raman Histology (SRH):

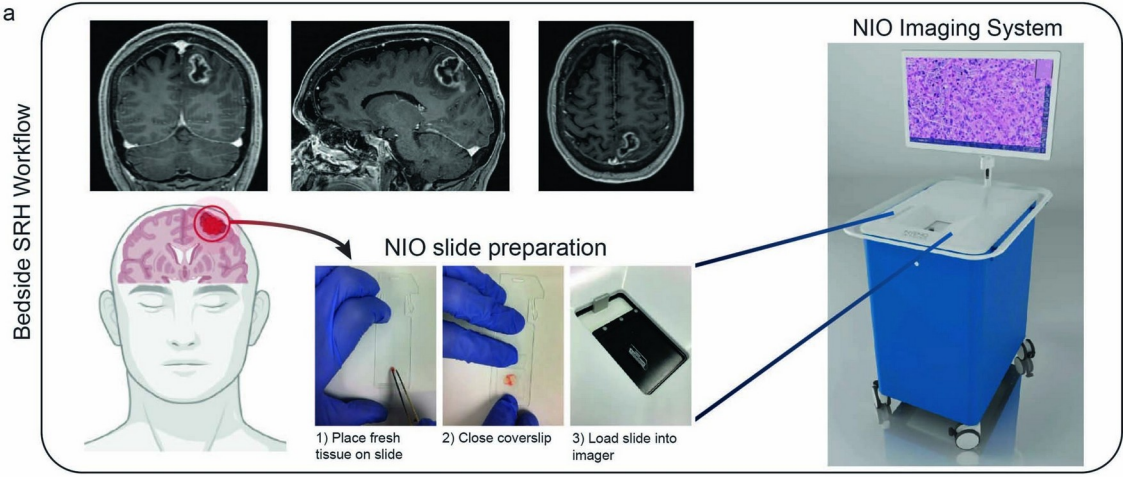
a rapid,
label-free,
and non-consumptive
imaging technique.

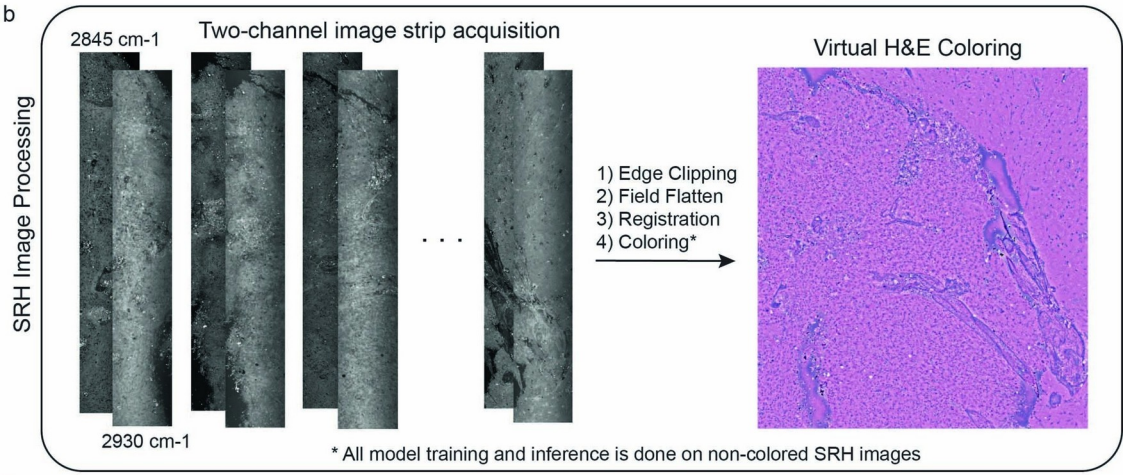


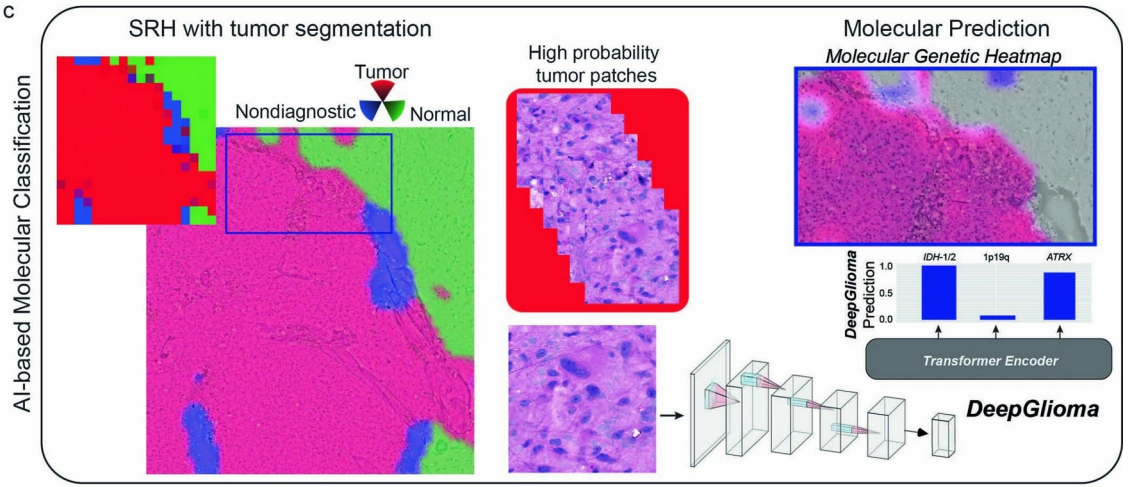
Two Raman shift windows:

(1) 2,845 cm^{-1} is the CH2 stretch vibration.
signal intensity in this channel ~ lipid molecule density

(2) 2,930 cm^{-1} is the CH3 symmetric stretch vibration.
signal intensity in this channel ~ protein and nucleic acid density







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DeepGlioma Model:

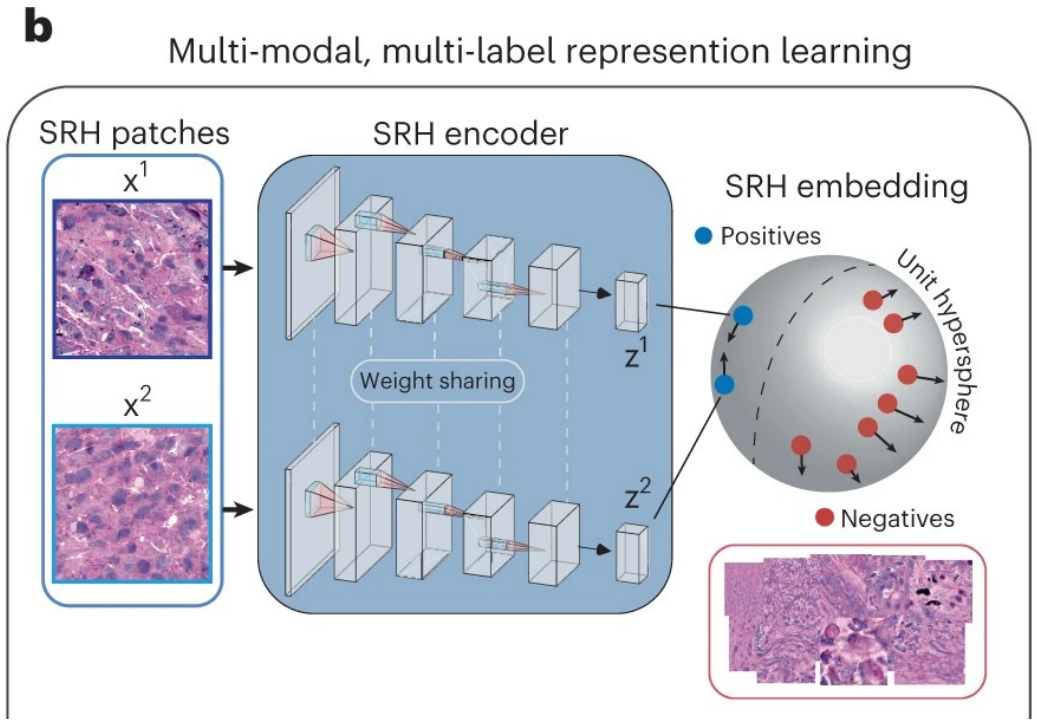
Inputs:

Training: SRH images and genetic mutation of the tumor

Inference: SRH images only

Outputs:

Probability map of molecular subgroup(based on mutation information)



The DeepGlioma Model includes:

(1)A CNN encoder that uses

weakly supervised (label of whole slide image)

multi-label (tumor gene mutation information from patient)

contrastive learning for feature embedding

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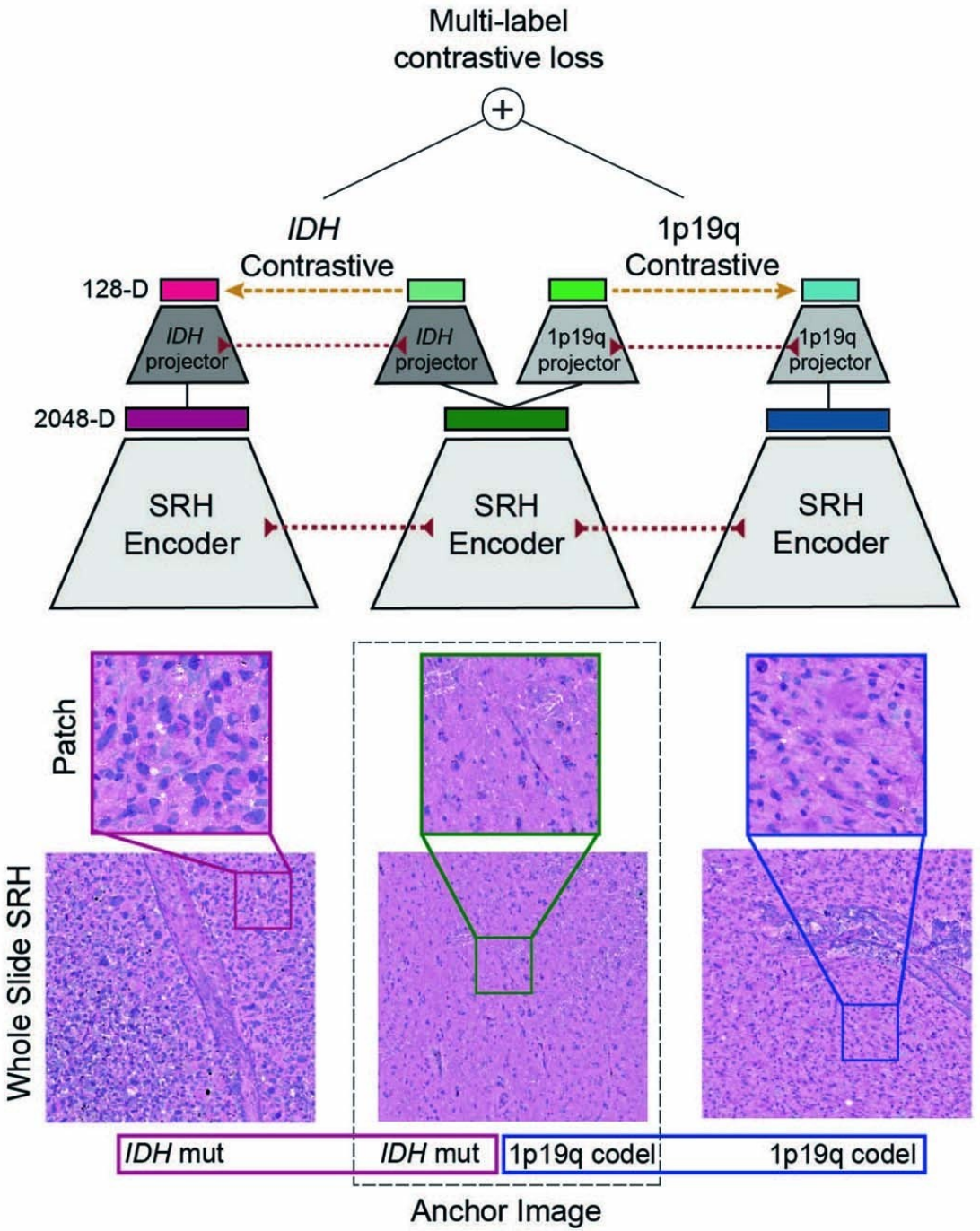
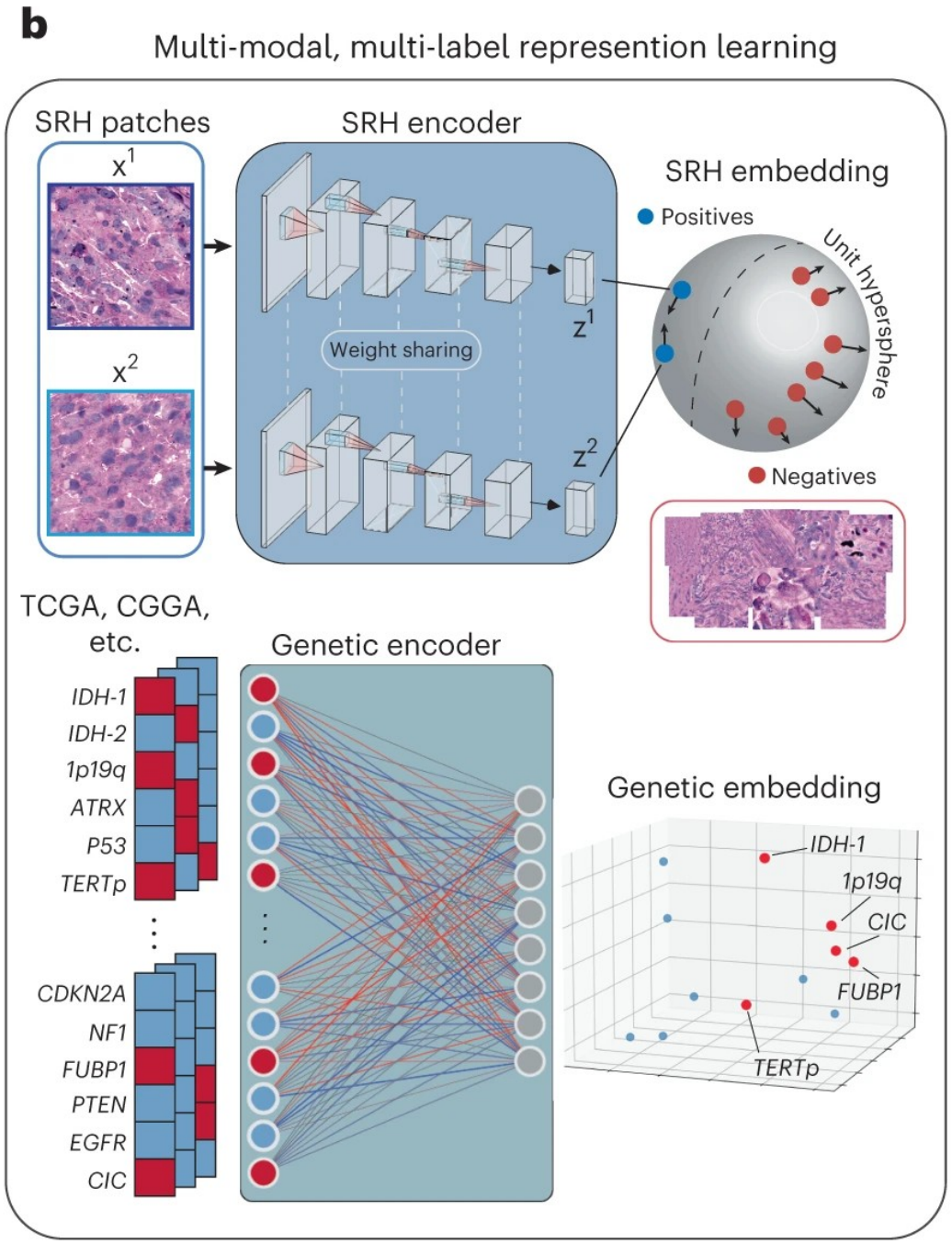


the CNN encoder

(3) Yellow dashed lines indicates computing contrast loss

(2) Red dashed lines indicates weight sharing.

(1) Patches from positive gene mutation patient samples are used as anchor images



The DeepGlioma Model includes:

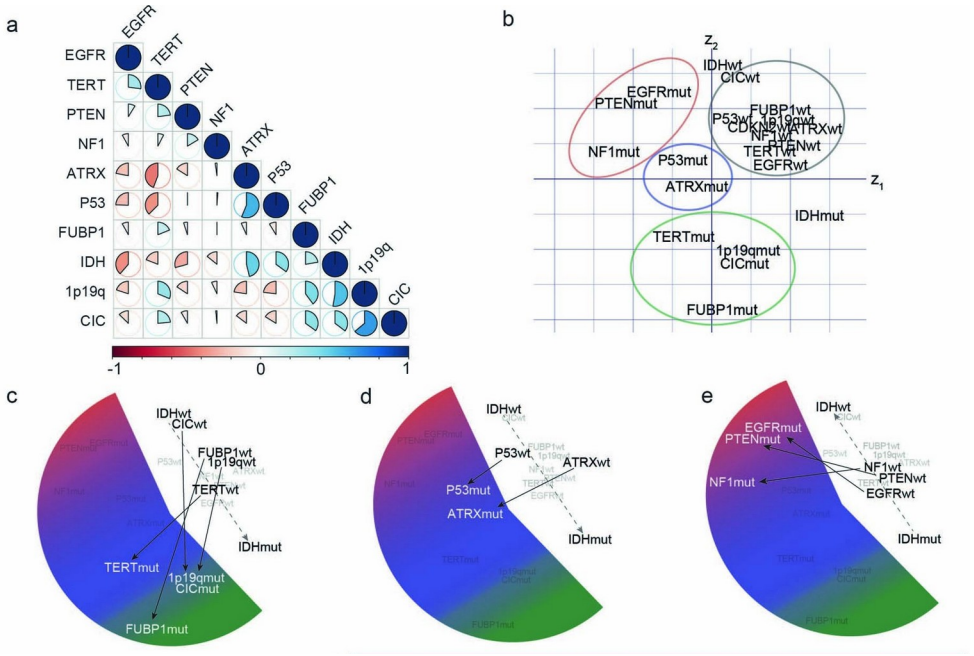
(1) A CNN encoder that uses

weakly supervised (label of whole slide image)

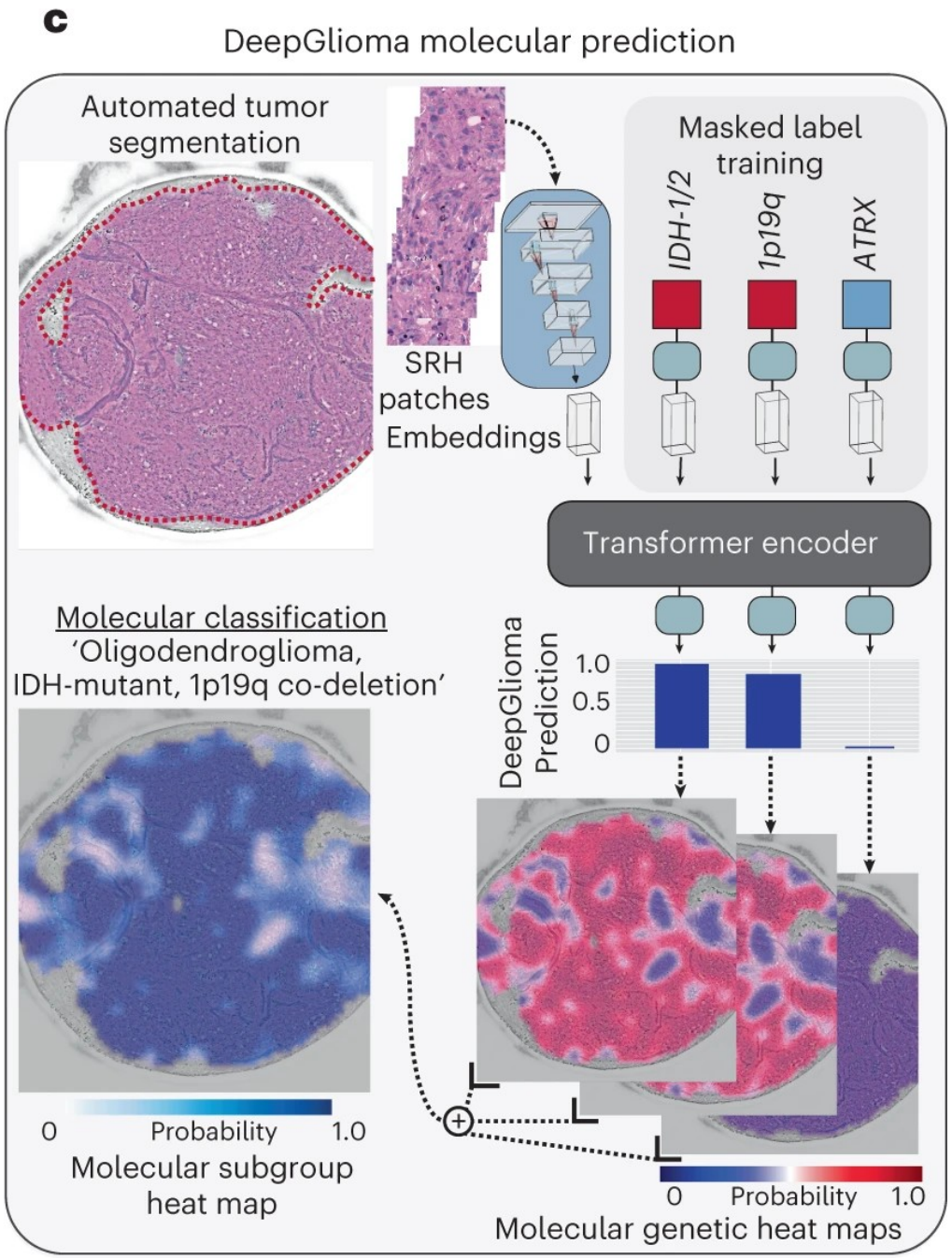
multi-label (tumor gene mutation information from patient)

contrastive learning for feature embedding

(2) A genetic encoder was trained using data from a publicly available dataset.



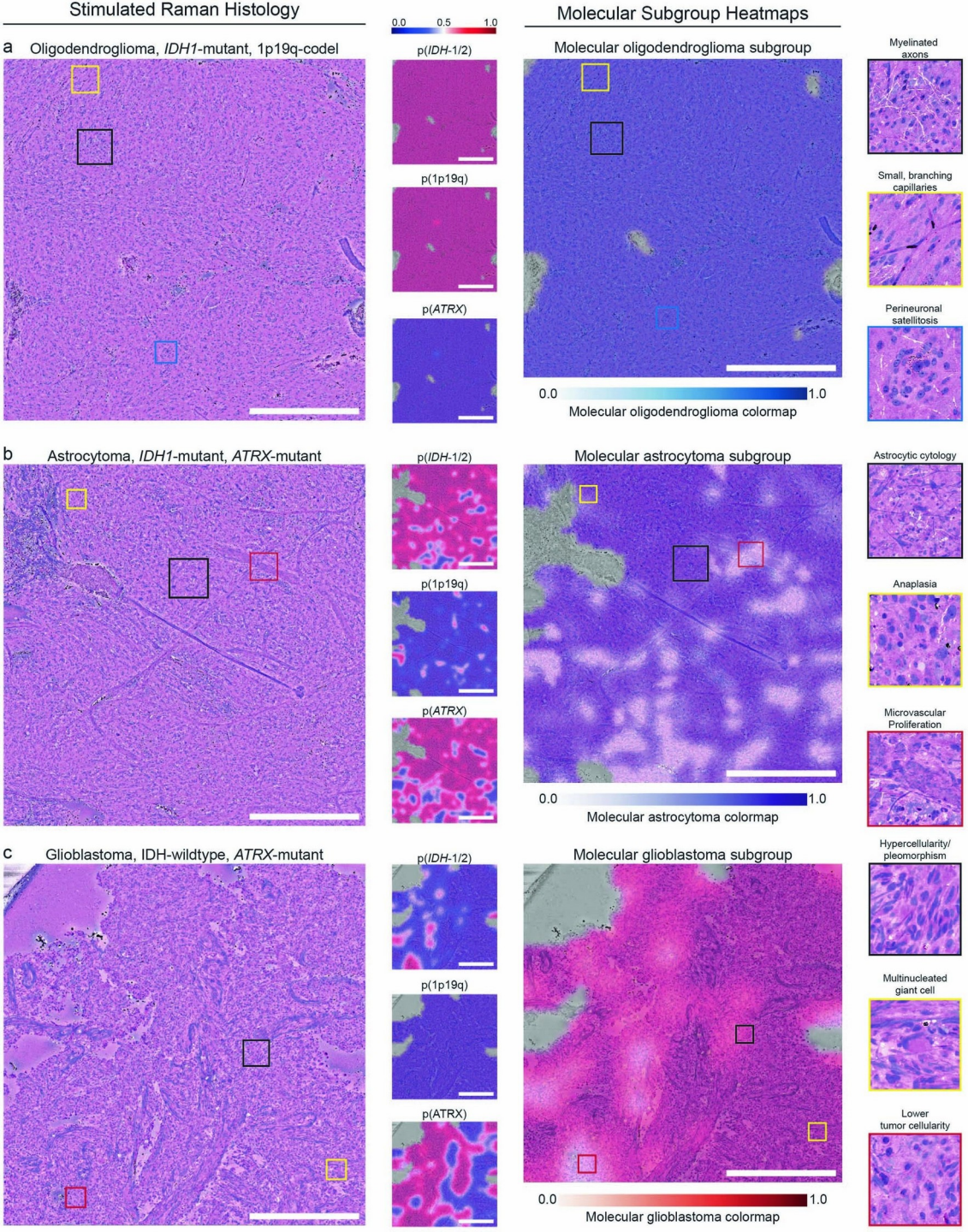
DeepGlioma can be trained using the known genomic landscape of diffuse gliomas, allowing for efficient multi-label molecular classification using SRH image features.



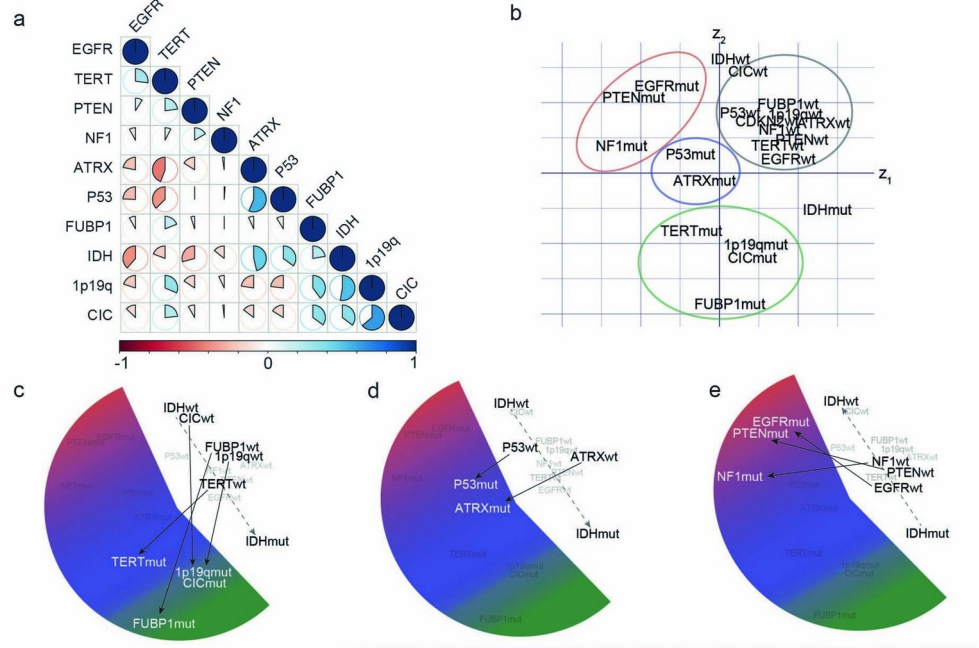
Integration of the two encoders into a transformer for multi-label prediction.

Masked label training is used to train the transformer encoder.

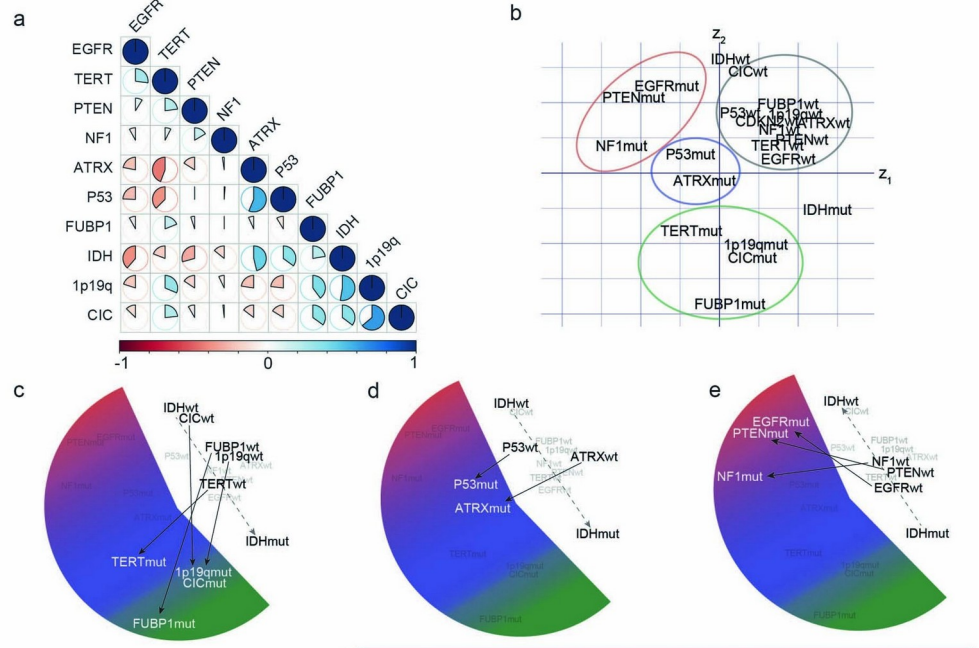
During inference, the model only takes in SGH embeddings to produce probability map for molecular classification.



Molecular subgroup heatmaps of the DeepGlioma model. For a testing patch image, it generates heatmap for tumor type probability heatmap.



Question 1:
In work, the authors trained the genetic encoder on a large dataset but only focused on three mutations, why is that?



The three mutations, isocitrate dehydrogenase-1/2 (IDH) mutations, 1p19q chromosome co-deletion and ATRX loss, are used by the World Health Organization Classification of Tumors of the Central Nervous System (WHO CNS5) to define the diffuse glioma.

Question 2:
In this work, how did the authors create image patches that only contains tumor-positive regions?

Answer:
In their previous work (ref 6) the authors actually showed that their imaging method includes all the information that H&E has, which means that they can used SRH images to perform tumor segmentation.