

# Using Deep Learning to Predict and Visualize STK11 Mutation in LUAD with Histopathological Slides from CPTAC

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## Method

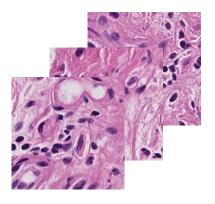
- Maximum image resolution is 20X; 324 slides from 110 patients
- Cutting each slide into 299x299 pixel tiles, excluding background and contaminants
- 80% slides for training; 10% slides for validation; 10% slides for testing. (patient-level separation)

Original image



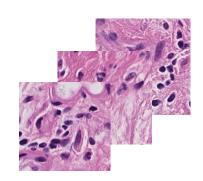
80000x90750 7.26 Billion Pixels

Tile



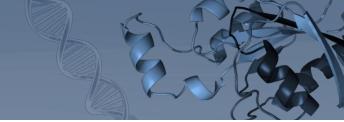
299x299 89400 Pixels 1/81208 of original image

Unique area of each tile

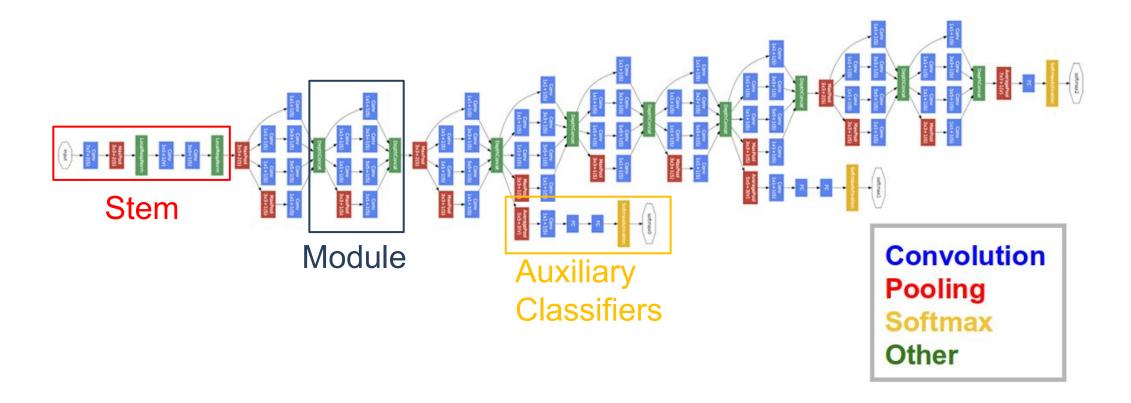


250x250 62500 Pixels 1/116160 of original image

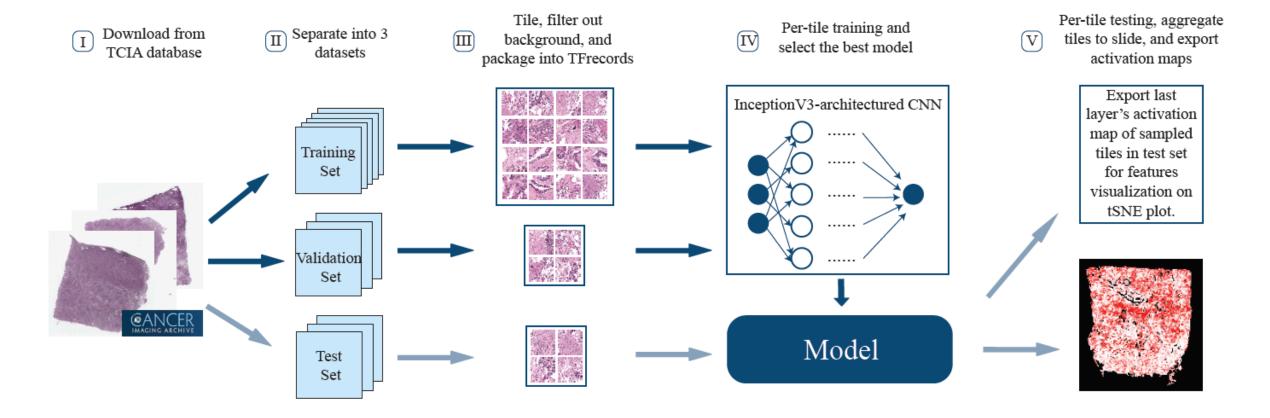
## **Inception Architecture**



InceptionV3

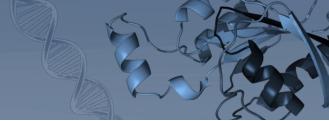


## Workflow

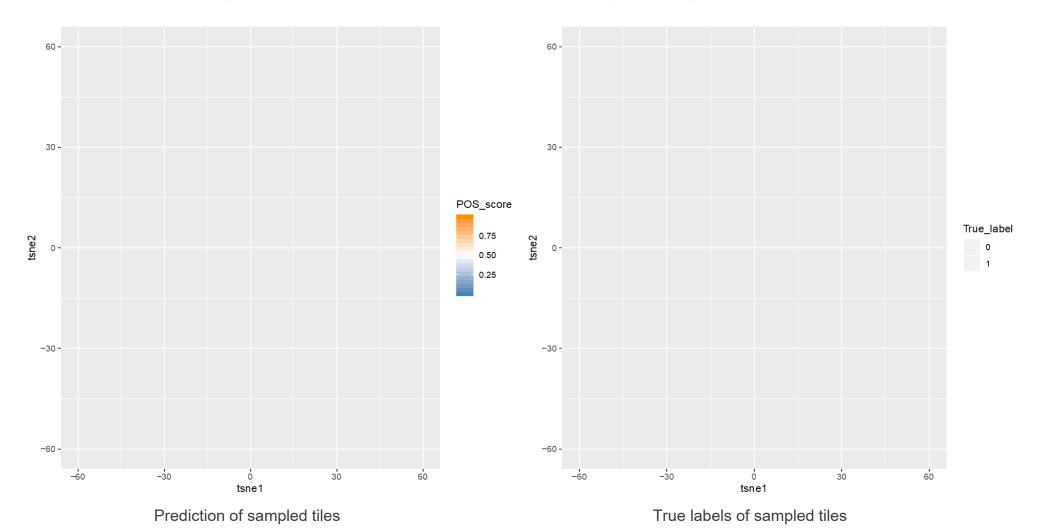


VI Metrics of test set	STK11-mutated count	WT count	AUROC	AUPRC	Accuracy
Per-slide level	5	31	0.961 (0.891-1.000)	0.860	0.944 (0.813-0.993)
Per-tile level	21507	116483	0.892 (0.890-0.894)	0.667	0.873 (0.871-0.875)

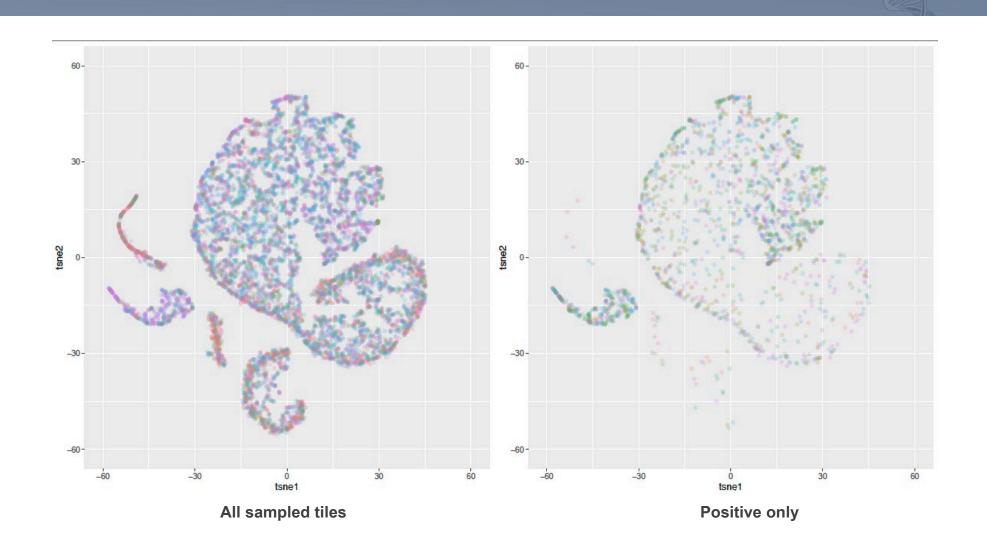
## tSNE of Last CONV layer activation



## Sampled 10000 tiles (2000 positive and 8000 negative) from test set of 36 slides

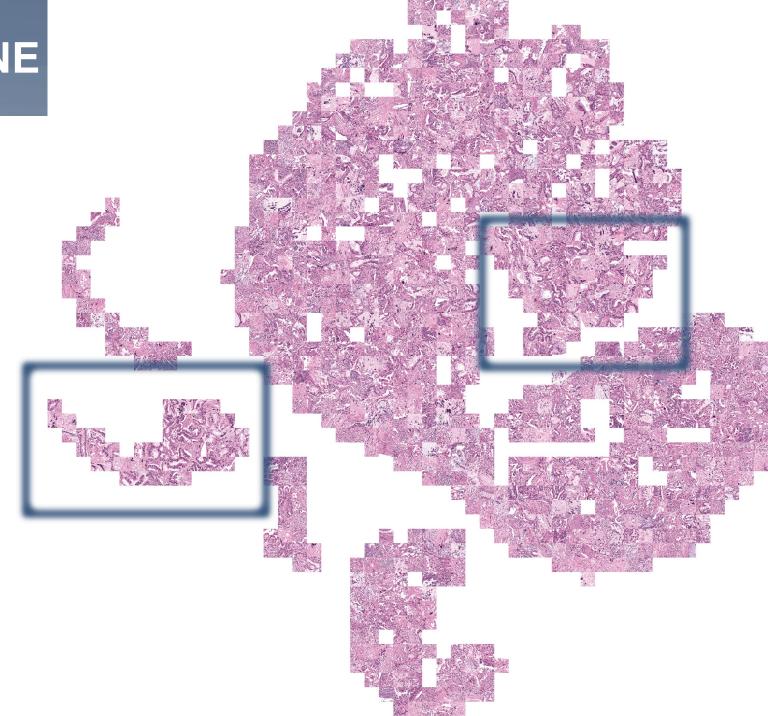


## Tiles labeled by corresponding slides that they belong to



## Tile visualization on tSNE

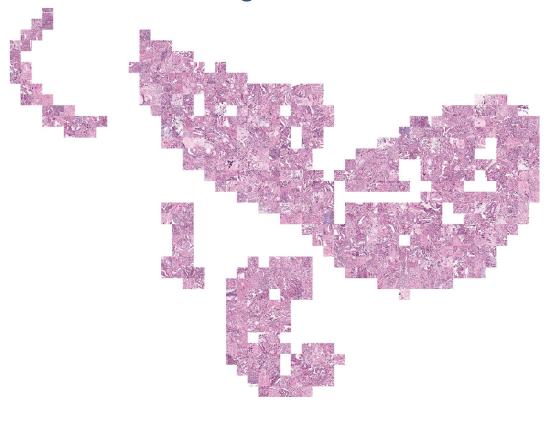
- Binned on tSNE space and sample 1 tile in each bin to represent their relative position on tSNE plot.
- 2 STK11 positive areas are boxed.



# Positive clusters

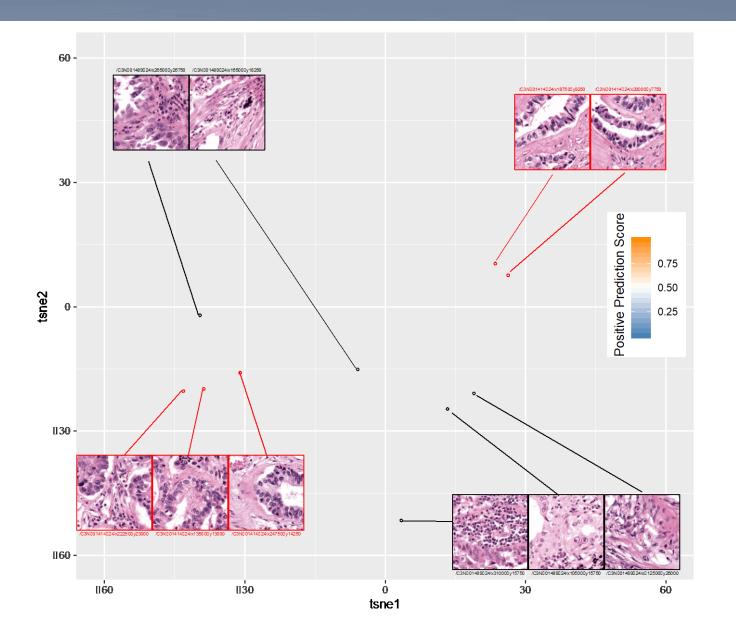
## "Cancer cells, with no inflammatory cells"

## Negative clusters

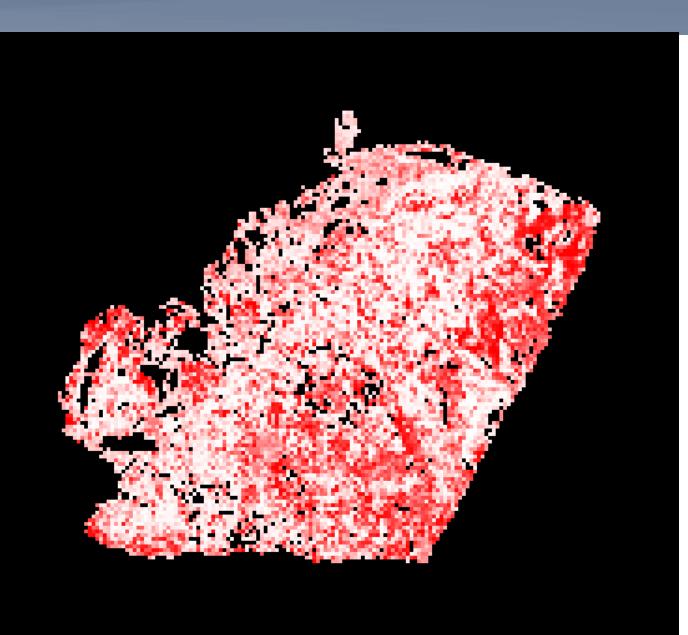


"Inflammatory cells, with some cancer cells nearby"

Corresponds to the findings of STK11 mutation in immune responses of LUAD patients



## Visualization



Each "pixel" represents 1 tile; The more red the more likely to be STK11 mutated

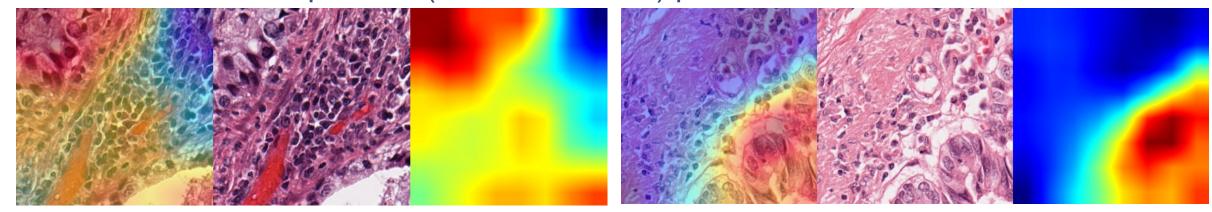




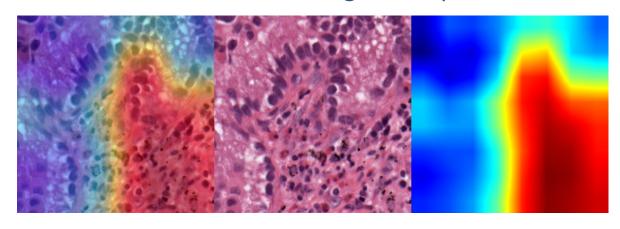
## Class Activation Mapping: Open the "Black Box"

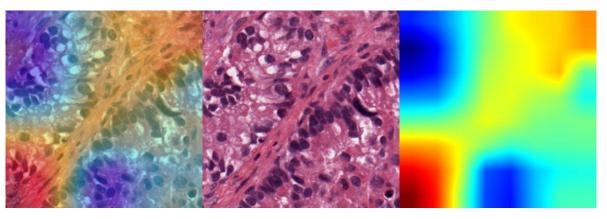


Some tiles with >0.8 positive (STK11 Mutated) prediction score.

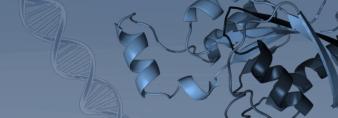


Some tiles with >0.8 negative (**NOT** STK11 Mutated) prediction score.





## Acknowledgement



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