

Figure S1 Study design and data flow.

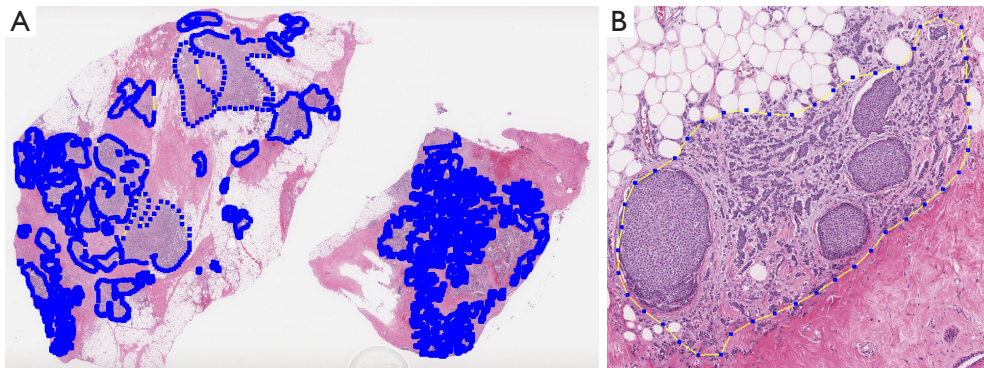


Figure S2 Tumor region labeled on HE-stained WSIs by experienced pathologists under 5× (A) and 20× (B). HE, hematoxylin and eosin; WSIs, whole slide images.

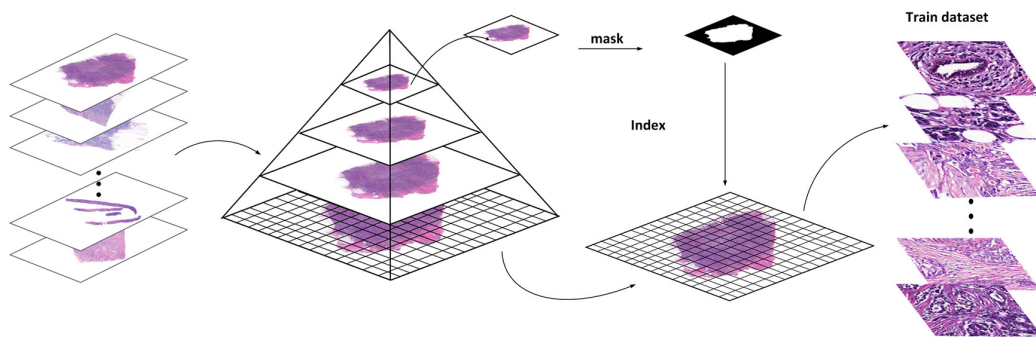


Figure S3 The generation procedure of the training dataset. Each WSI was stored in the format of a pyramid file. The top layer was firstly taken for image segmentation, and the cancerous region was obtained. Successively, the lower tiles of the images were indexed and cut into the training dataset. WSI, whole slide image.

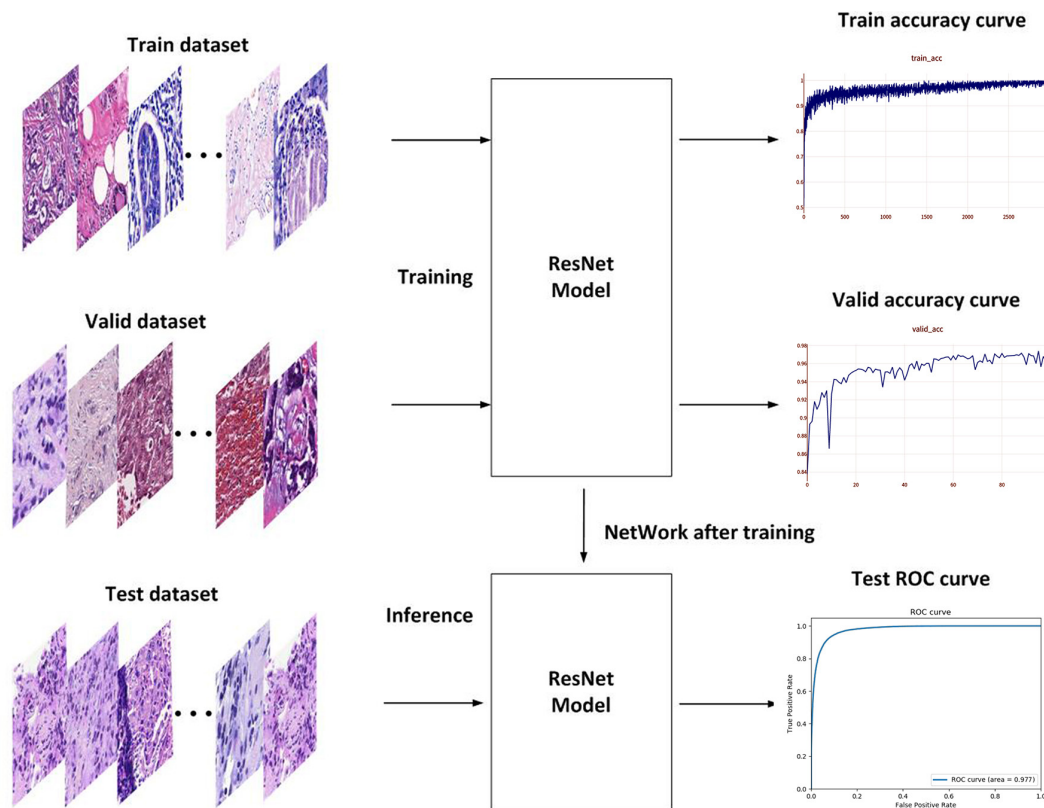


Figure S4 The whole procedure of the network for tumor region recognition. All data was divided into training dataset, validation dataset, and test dataset. The ResNet model was trained using the training dataset and validated using the validation dataset. The training and validation accuracy curves were exhibited in the upper and middle right panels. To test the ResNet model after training, the test dataset was inferred and the test ROC curve was exhibited in the bottom-right panel. ROC, receiver operating characteristic.

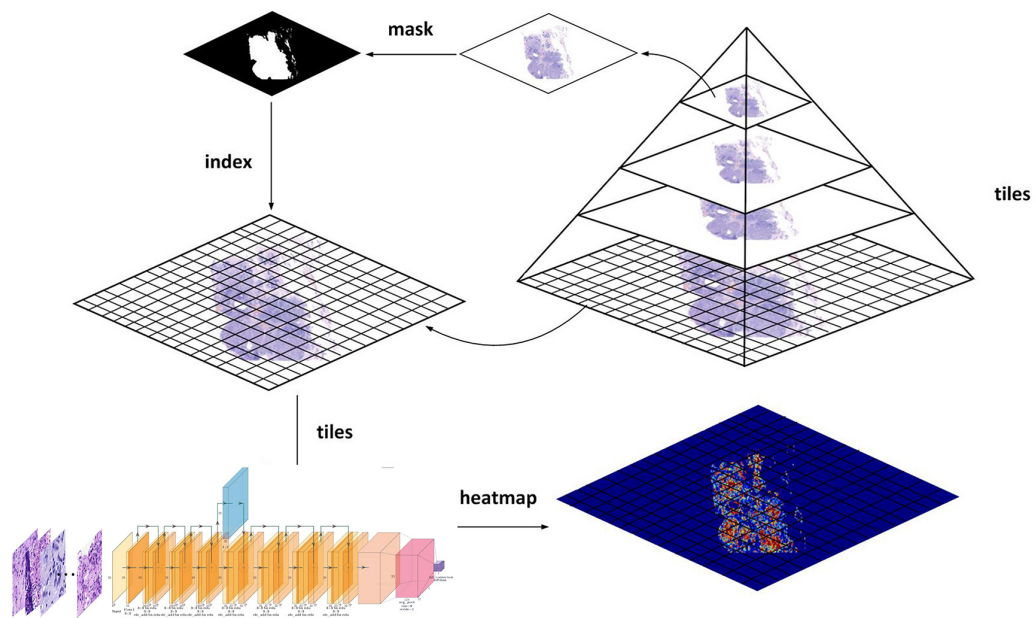


Figure S5 The prediction process for tumor region recognition for a single WSI. The top layer of the pyramid was masked, the bottom layer was divided into tiles, and according to the masked image, the tiles were indexed. Finally, we generated a heatmap according to the probability of whether each tile is a tumor. The darker the color (red), the greater the probability of cancer tissue. WSI, whole slide image.

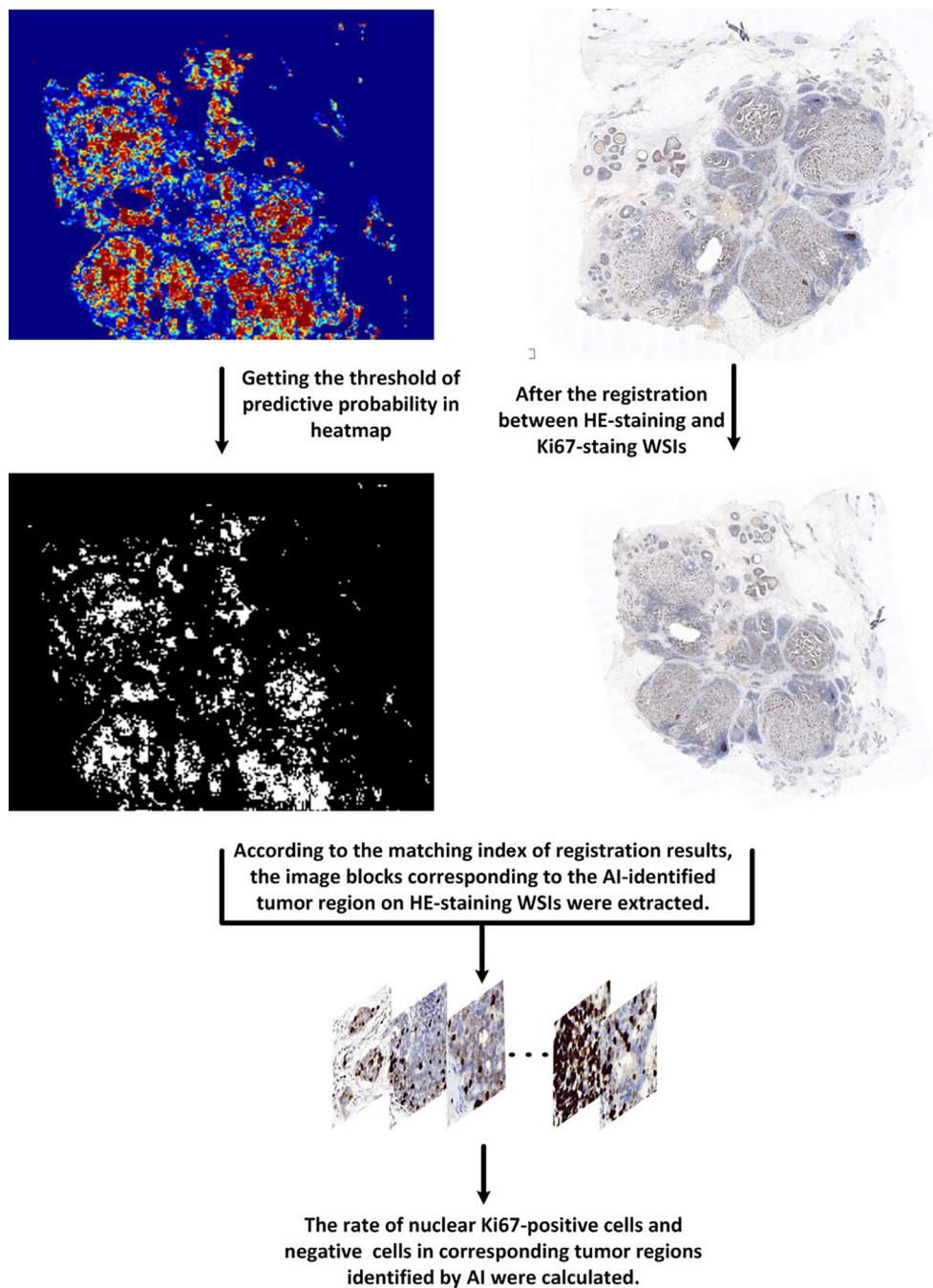


Figure S6 The procedure for the calculation of the Ki-67 nuclear positive index. After tumor tissue recognition by the AI algorithm, a heatmap of the probability of cancer tissue was generated to obtain the threshold of the probability to predict the cancer region (upper- and middle-left panels). According to the matching index of the registration results, Ki-67-stained image blocks corresponding to the HE-stained tumor region were extracted (upper- and middle-right panels). Then, the number of nuclear-positive cells and negative cells in cancer tissues identified by AI were counted (bottom panel). AI, artificial intelligence; HE, hematoxylin and eosin. Magnification, $\times 100$.

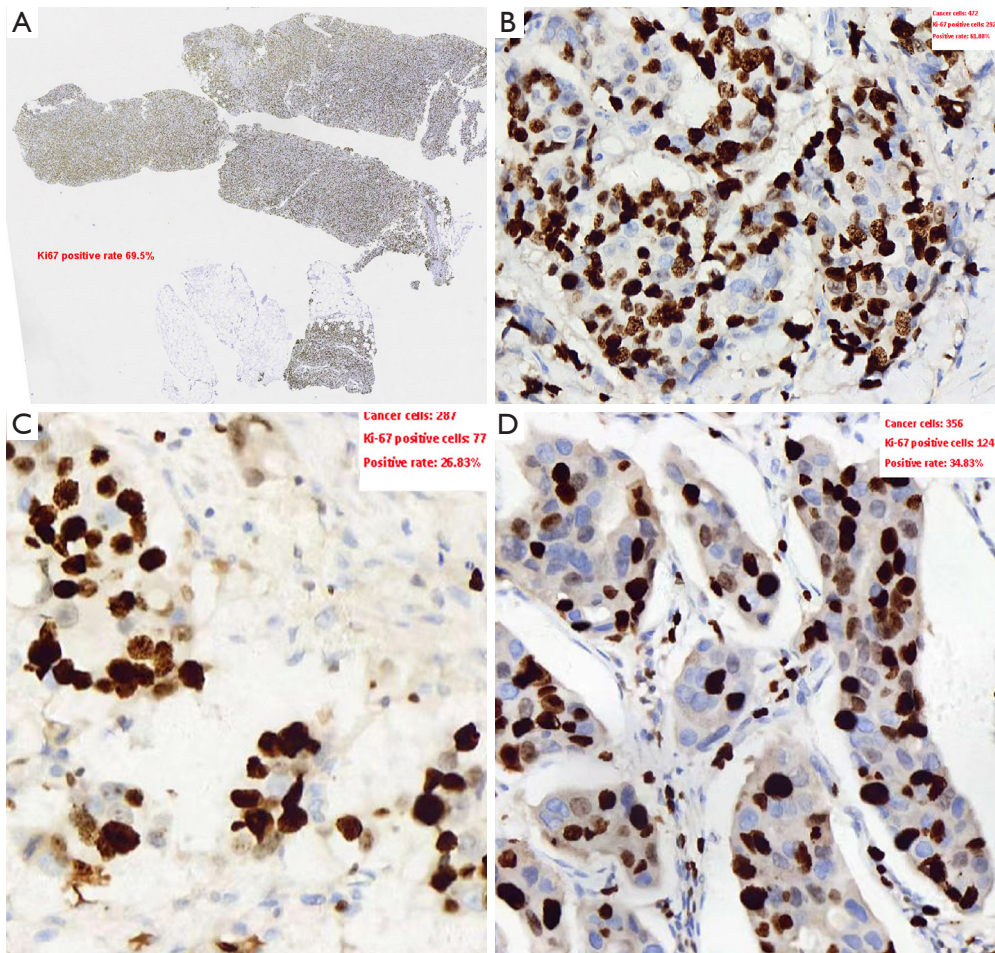


Figure S7 Calculation of Ki-67-positive tumor cells and the Ki-67-positive rate using the SIFT algorithm-based artificial intelligence (AI) model in WSIs of Ki-67-stained slides, magnification ($\times 100$). (A). (B-D) Three high-definition images of Ki-67 count results. SIFT, scale-invariant feature transform; WSIs, whole slide images. Magnification, $\times 400$.