Supplementary Materials

1 The details of the discriminator and classifier

Table.1 and Table.2 demonstrate the structures of the discriminator and classifiers.

Table 1: CNN Discriminator for HU Images

Layer	Kernel	Strides	Channel
conv1	5×5	2	64
conv2	5×5	2	128
conv3	5×5	2	256
conv4	5×5	2	512
FC	—	—	—
sigmoid	—	—	—

Table 2: CNN Classifier for Features

Layer	Kernel	Strides	Channel
conv1	3×3	1	64
pooling1	2×2	2	64
conv2	3×3	1	128
pooling2	2×2	2	128
conv3	3×3	1	256
pooling3	2×2	2	256
FC	—	—	100
FC	—	—	5
sigmoid	—	—	—

2 The details of experiments for malignancy prediction

Table.3 shows the details of experiments for malignancy prediction. As can be seen, we use two data augmentation methods for the prediction task: (1) data resampling; (2) data synthesis. We use 1608 nodule images extracted from LIDC-IDRI. We randomly select 1126 nodules (70%) as the training set and 482 nodules (30%) as the testing set. We use two data augmentation methods to adjust the data distributions of the training set. In this table, 'synth' indicates synthesized data, 'resampling' indicates resampled 352 malignant nodules. Meanwhile, the data distribution of the testing set remains unchanged.

Table 3: The breakdown of training, testing sets

Subset	Benign	Malignant	Total
train	774	352	1126
train + resampling	774	352+352	1478
train + synth	774	352+384	1510
test	332	150	482