



Supplementary Figure S1. Segmentation performance of nnU-Net models by tumor size across different datasets. **(A)** Tumor segmentation performance of nnU-Net models on baseline (BL), **(B,E)** after two cycles (C2), **(C,F)** and after four cycles (C4) test sets across different tumor sizes. Horizontal bar indicates significant difference in paired Wilcoxon signed rank test ($p < 0.05$). **(D)**, the detailed quantitative results used for the boxplots in **(A)**. **(G)**, the detailed quantitative results used for the boxplots in **(B)** and **(E)**. **(H)**, the detailed quantitative results used for the boxplots in **(C)** and **(F)**.

- nnU-Net model training configuration and procedure

The source code of nnU-Net was downloaded from <https://github.com/MIC-DKFZ/nnUNet>. All trainings used the default set-up³⁶, and important parameters included the following: data augmentation was implemented using the batchgenerators framework that was included in nnU-Net (a series of augmentations involving spatial, color, noise, and crop processes); the training length was fixed at 1000 epochs, with 250 training iterations per epoch; and the learning rate was 0.01 initially and then was gradually reduced using the “polyLR” schedule⁵⁵. All training used the 2D nnU-Net framework and full-resolution 3D nnU-Net framework and then ensembled these frameworks for inferences. A five-fold cross-validation was performed on the development dataset (training + validation, randomly split at 4:1).