Figure S6. Performance of cancer recurrence and MRD detection using the simulation data. **(a-d)** Zoom-in of Figure 3 (a-d). The area under the ROC curve (AUC) of the MRD/recurrence detection on **(a)** the validation dataset and **(c)** the independent dataset with different tumor fractions and sequencing coverage. The sensitivity and specificity with different tumor fractions and sequencing coverage on **(b)** the validation dataset and **(d)** the independent dataset. **(e)** AUCs of MRD/recurrence detection with and without error suppression (ES) on the independent dataset at 200x depth with different tumor fractions. **(f)** The sensitivity and specificity of MRD/recurrence detection with and without error suppression on the independent dataset at 200x depth with different tumor fractions. In **(a)**, **(c)** and **(e)**, the dots indicated the averaged AUC, and the vertical bars indicated average ± SD of the AUC (see Methods). In **(b)**, **(d)** and **(f)**, the dots show the averaged sensitivity using a cutoff p-value = 0.05 of the background noise distribution; the vertical bars indicated average ± SD of the sensitivity; the specificity was shown in the legend in the format of (averaged specificity, (average - SD, average - SD)). The solid lines show the smoothed performance fitted with logit functions.