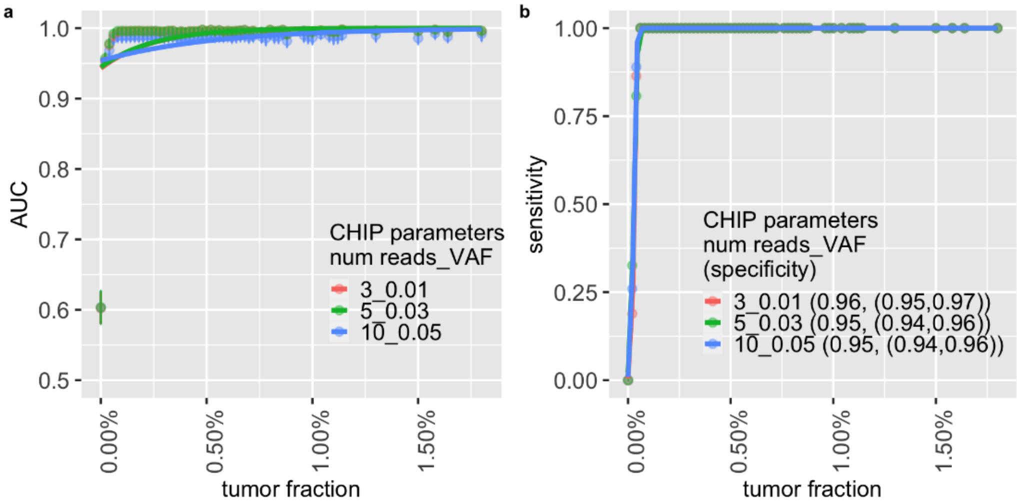

Figure S2. Performance of cancer recurrence and MRD detection using different parameters on the simulation data. (a) The area under the ROC curve (AUC) of the MRD/recurrence detection on the in silico spike-in samples with different tumor fractions and sequencing coverage. **(b)** The sensitivity and specificity of the in silico spike-in samples with different tumor fractions and sequencing depth. In **(a)** the dots indicate the averaged AUC, and the vertical bars indicate average ± SD of the AUC among the 50 rounds of performance evaluation. In **(b)** the dots show the sensitivity using a cutoff p-value = 0.05 of the background noise distribution; the vertical bars indicate average ± SD of the sensitivity; the specificity was shown in the legend in the format of (averaged specificity, (average - SD, average + SD). The curves in both **(a)** and **(b)** were fitted by logit function. The vertical bars are a little obscure, because the range of the metrics are small and the curves under the three sets of parameters are similar.