




## Correction to: Combined viral quasispecies diversity and hepatitis B core-related antigen predict off-nucleos(t)ide analog durability in HBeAg-negative patients

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Unfortunately, Fig. 3c and d were erroneously labeled in the original publication of the article.

In Fig. 3c, the number of nucleotide diversity at the bottom left corner should be 0.01 instead of 1.00. In Fig. 3d, the group with nucleotide diversity/HBcrAg “<0.01 and  $\geq$

2.00” should be corrected as “<0.01 or  $\geq$  2.00”. Although these two figures were erroneously labeled, all the relevant results in the text were correctly stated. The correct Fig. 3 are given below:

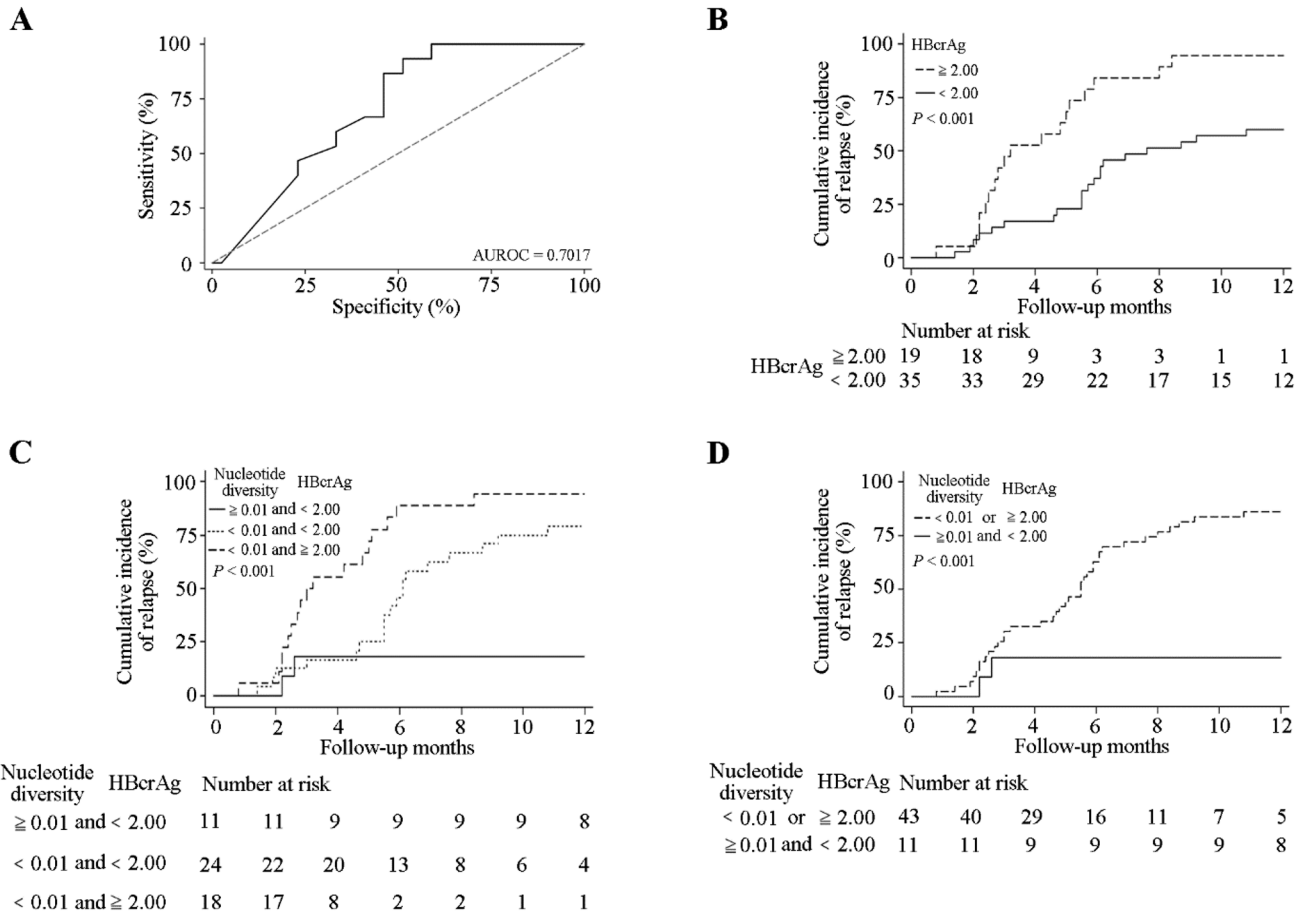
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The original article can be found online at <https://doi.org/10.1007/s12072-021-10186-7>.

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**Fig. 3** Pretreatment viral genetic diversity of the precore/core gene and HBcrAg predicts the risk of virological relapse after discontinuation of NAs. **a** The AUROC analysis of HBcrAg in prediction of virological relapse within 1-year off-therapy. **b** The cumulative incidence of 1-year virological relapse in patients with low ( $< 2$  KU/mL) and high ( $\geq 2$  KU/mL) levels of baseline HBcrAg. **c** The cumulative inci-

dence of 1-year virological relapse in three groups of patients with different levels of baseline the viral nucleotide diversity and HBcrAg. **d** The cumulative incidence of 1-year virological relapse in two groups of patients with different levels of baseline the viral nucleotide diversity and HBcrAg

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