

Figure S1. Serum viral markers distribution across CHB phases in untreated patients. (A) serum HBV DNA (B) HBcrAg (C) HBsAg. Boxes span the  $25^{th}$ - $75^{th}$  percentile, whiskers span the range, and horizontal bar in the box represents the median. CH: chronic hepatitis. CI: chronic infection. \* p < 0.05; \*\*\*\* p < 0.0001; ns: not significant

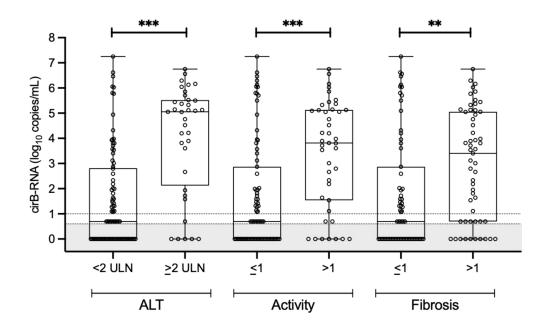
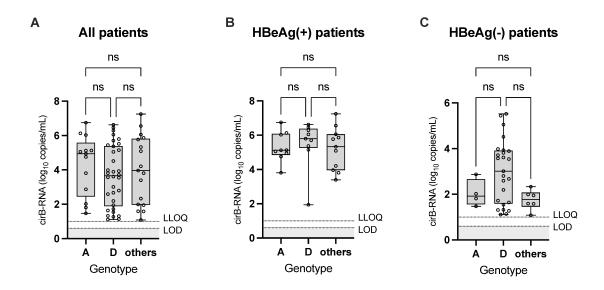


Figure S2. cirB-RNA values according to markers of liver damage in untreated patients. Boxes span the  $25^{th}$ - $75^{th}$  percentile, whiskers span the range, and horizontal bar in the box represents the median. \*\* p < 0.01; \*\*\* p < 0.001; ns: not significant; ULN: upper limit of normal



**Figure S3. cirB-RNA values according to HBV genotypes in untreated patients.** Boxes span the 25<sup>th</sup>-75<sup>th</sup> percentile, whiskers span the range, and horizontal bar in the box represents the median. ns: not significant.

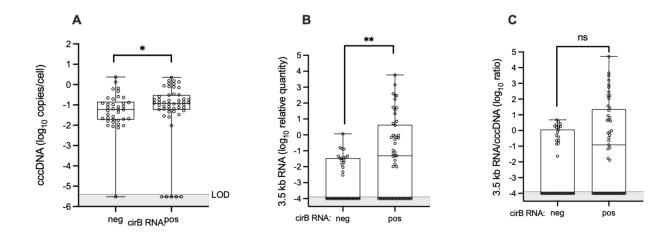


Figure S4. Intrahepatic viral markers vs. cirB-RNA (untreated HBeAg- patients only). (A) cccDNA (B) 3.5 kb RNA (C) 3.5 kb RNA/cccDNA ratio. Intrahepatic HBV markers quantification was available for 88/90 HBeAg(-) patients. cccDNA was negative in 6 patients [5 cirB-RNA(+) and 1 cirB-RNA(-)], while 3.5kb RNA was negative in 41 patients [22 cirB-RNA(+) and 19 cirB-RNA(-)]. 3.5Kb RNA/cccDNA ratio could be calculated for 82 patients and different from zero in 46 patients [29 cirB-RNA(+) and 17 cirB-RNA (-) patients]. \* p < 0.05; \*\* p < 0.01.

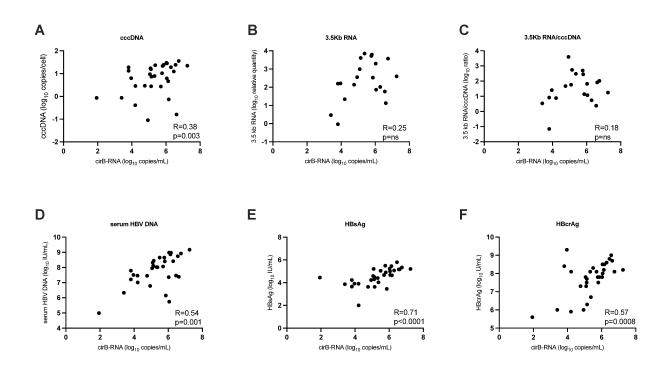


Figure S5. Correlations between cirB-RNA and intrahepatic viral markers in HBeAg (+) untreated patients. (A) cccDNA (B) 3.5 kb RNA (C) 3.5 kb RNA/cccDNA ratio (D) serum HBV DNA (E) HBsAg (F) HBcrAg. Intrahepatic HBV markers and serum HBcrAg quantifications were available for 32 patients. 3.5Kb RNA/cccDNA ratio could be calculated for 20 patients. Only samples having quantifiable values for both intrahepatic HBV markers, serum HBV DNA, HBsAg or HBcrAg and cirB-RNA (n=31 for cccDNA, n=20 for 3.5kb RNA, n=20 for 3.5kb RNA/cccDNA, n=32 for serum HBV DNA, n=32 for HBsAg, n=31 for HBcrAg) were included in the analysis.

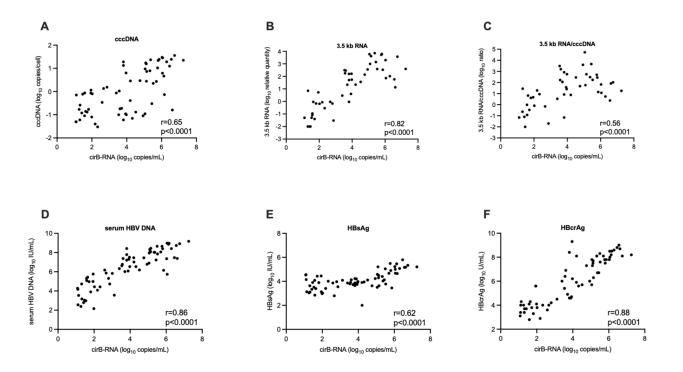


Figure S6. Correlations between cirB-RNA and intrahepatic viral markers (untreated patients). (A) cccDNA (B) 3.5 kb RNA (C) 3.5 kb RNA/cccDNA ratio (D) serum HBV DNA (E) HBsAg (F) HBcrAg. Intrahepatic HBV markers and serum HBcrAg quantifications were available for 120/122 patients. 3.5Kb RNA/cccDNA ratio could be calculated for 113 patients. Only samples having quantifiable values for both intrahepatic HBV markers, serum HBV DNA, HBsAg or HBcrAg and cirB-RNA (n=64 for cccDNA, n=50 for 3.5kb RNA, n=48 for 3.5kb RNA/cccDNA, n=71 for serum HBV DNA, n=70 for HBsAg, n=66 for HBcrAg) were included in the analysis.

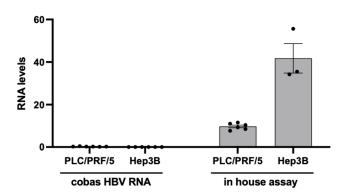
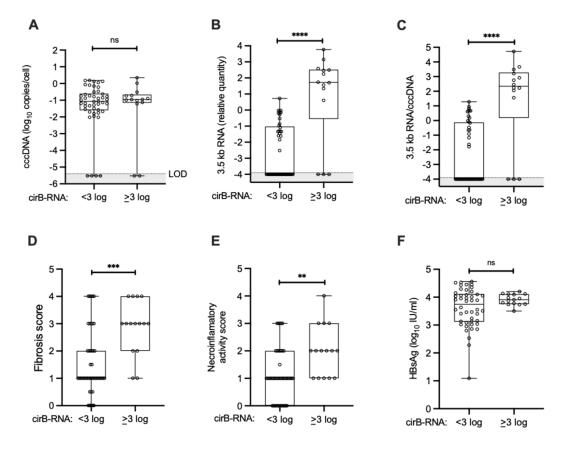


Figure S7. cobas® HBV RNA assay preferentially recognizes RNA derived from cccDNA in cell culture. Total RNA was extracted from cell lysates using the Manual Workflow for cobas HBV RNA or Trizol reagent for the in-house protocol and then quantified by ddPCR (Scholtes et al. J Clin Virol 2022;150-151:105150). The in-house assay uses primers and a TaqMan probe located in the HBx open reading frame (Pa03453406\_s1, ThermoFisher Scientific), and is thus capable of recognizing viral RNA produced both by cccDNA and integrated sequences. β-glucuronidase (GUSB) RNA quantification served as internal references for RNA relative quantity expression.



**Figure S8.** Intrahepatic viral markers in HBeAg(-) CH patients with high or low cirB RNA levels. Boxes span the  $25^{th}$ - $75^{th}$  percentile, whiskers span the range, and the horizontal bar in the box represents the median. Assay detection limits are marked with dotted lines; the shaded area represents undetectability. Intrahepatic cccDNA (A) and 3.5 kb RNA (B) results were available for 60 of 61 HBeAg(-) CH patients. 3.5 kb RNA/cccDNA ratio (C) could be calculated for 56 patients and was different from zero in 25 patients (14 cirB-RNA <3  $\log_{10}$  and 11 cirB-RNA >3  $\log_{10}$  patients). cccDNA was negative in 4 patients (2 cirB-RNA <3  $\log_{10}$  and 2 cirB-RNA >3  $\log_{10}$ ), while 3.5 kb RNA was negative in 18 patients (14 cirB-RNA <3  $\log_{10}$  and 4 cirB-RNA >3  $\log_{10}$ ). (D) Fibrosis score; (E) necroinflamatory activity score; (F) HBsAg levels. \*\*\*\* p<0.0001; \*\*\* p<0.001; \*\*\* p<0.001.