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**Supplementary Data**

***In vitro* investigation of HBV clinical isolates from Chinese patients reveals that genotype C isolates possess higher infectivity than genotype B isolates**

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**Supplementary Table S1** Sequences of primers used.

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| **qRT-PCR analysis:** | | |
| HBV DNA | Sense primer | 5’-GAGTGTGGATTCGCACTCC-3’ |
|  | Anti-sense primer | 5’-GAGGCGAGGGAGTTCTTCT-3’ |
|  |  |  |
| Vector | Sense primer | 5’-gatgcttttctgtgactggtgag-3’ |
|  | Anti-sense primer | 5’-cgttttccaatgatgagcactt-3’ |
|  |  |  |
| HBV cccDNA | Sense primer | 5’-TGCACTTCGCTTCACCT-3’ |
| Anti-sense primer | 5’-AGGGGCATTTGGTGGTC-3’ |
|  | Sense primer of isolate C-7 | 5’-TGCACTTCGCGTCACCT-3’ |
|  | Anti-sense primer of isolate B-7 and B-10 | 5’-AGGGGCATTTTGTGGTC-3’ |
|  |  |  |
| **Cloning of 1.1-fold HBV genome:** | | |
| CMV | Sense primer | 5’-GTATGAAAGCTTGTTGACATTGATTATTGA-3’ |
|  | Anti-sense primer | 5’-TTGCATGGTGCTGGTGCTCGACGCTTATATAGACCTCCCA-3’ |
|  |  |  |
| HBV1804-3215-262 | Sense primer | 5’-TCTATATAAGCGTCGAGCACCAGCACCATGCAACTT-3’ |
|  | Anti-sense primer | 5’-CCACCACGAGTCTAGACTCTGT-3’ |
|  |  |  |
| CMV-1804-3215-262 | Sense primer | 5’-GTATGAAAGCTTGTTGACATTGATTATTGA-3’ |
| Anti-sense primer | 5’-CCACCACGAGTCTAGACTCTGT-3’ |
|  |  |  |
| HBV 247-1841 | Sense primer | 5’-ATCTAGTCTAGACTCGTGGTGG-3’ |
|  | Anti-sense prime | 5’-TGATTAGGCAGAGGTGAAAAAGTTGCATGGTGCTGGT-3’ |
| HBV 1805-1986 | Sense primer | 5’-ACCAGCACCATGCAACTTTTTCACCTCTGCCTAATCA-3’ |
|  | Anti-sense prime | 5’-AGTTGCGGCCGCTCTCGAATAGAAGGAAAG-3’ |
|  |  |  |
| HBV 247-1986 | Sense primer | 5’-ATCTAGTCTAGACTCGTGGTGG-3’ |
|  | Anti-sense prime | 5’-AGTTGCGGCCGCTCTCGAATAGAAGGAAAG-3’ |
|  |  |  |
| BGH | Sense primer | 5’-CTTTCCTTCTATTCGAGAGCGGCCGCCAGCCTCGACTGTGCCTTCT-3’ |
|  | Anti-sense primer | 5’-ATCGATGATATCCCATGGGCGGCCGTCTCAGAAGCCATAGAGCCCA-3’ |



**Supplementary Fig. S1** Construction procedures of the plasmids containing 1.1-mer HBV genome.

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**Supplementary Fig. S2** CMV and BGH sequences used in the plasmids containing 1.1-mer HBV genome. **A** The green sequence is the restriction site of *Hin*dIII. The red sequence is the sequence of the CMV promoter, followed by the HBV genomic sequence cloned from HepG2.2.15 cells. **B** The green sequence is the restriction site of *Not* I, and the following red sequence is the sequence of BGH polyadenylation signal. CMV, cytomegalovirus; BGH, bovine growth hormone.

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**Supplementary Fig. S3** Effects of different cell culture conditions on virion DNA production. **A** Addition of DMSO to the culture medium. **B** Different concentrations of FBS in the culture medium. Statistical analysis was performed by the Student's *t*-test (two-tailed). \**P* < 0.05. FBS, fetal bovine serum.

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**Supplementary Fig. S4** Infection of HepG2-NTCP cells by HBV particles derived from the cells transfected with 1.3-mer HBV-expression constructs. **A** HepG2 cells were transiently transfected with 1.3-mer HBV-expression constructs containing indicated HBV isolates. The culture medium was collected at days 5–7 post-transfection. Secreted HBeAg and virion DNA in the supernatants were measured by ELISA and qPCR, respectively. **B** HepG2-NTCP cells were infected with indicated HBV particles concentrated from the culture supernatants of transfected HepG2 cells at 100 MOI. On day 8 post-infection, HBeAg and HBV DNA in the supernatants of infected cells were measured. Results are shown as mean values ± standard deviation. HBeAg, hepatitis B e antigen; HBcAg, hepatitis B core antigen; HBsAg, hepatitis B surface antigen.