**Supplementary Materials**

**Table S1.** Primer sequences used in this study.

|  |  |
| --- | --- |
| Name | Sequence |
| HBV qPCR | |
| HBV-qPCR\_Fw | CCGTCTGTGCCTTCTCATCTG |
| HBV-qPCR\_Rv | AGTCCAAGAGTYCTCTTATGYAAGACCTT |
| HBV-qPCR\_Probe | CCGTGTGCACTTCGCTTCACCTCTGC |
| HCV qPCR | |
| HCV-qPCR\_Fw | TGCTAGCCGAGTAGYGTTGG |
| HCV-qPCR\_Rv | ACTCGCAAGCACCCTATCAG |
| HCV-qPCR\_Probe | ACCACAAGGCCTTTCGCRAC |
| HBV genotyping | |
| HBV\_GT\_Fw1 | GGGTCACCATATTCTTGGG |
| HBV\_GT\_Rv1 | CCAAAGACAAAAGAAAATTGGTAAC |
| HBV\_GT\_Fw2 | GAACAAGAGCTACAKCATGGG |
| HBV\_GT\_Rv2 | CGGTAWAAAGGGACTCAAGATG |
| HCV genotyping | |
| HCV\_GT\_Fw | TATGAYACCCGCTGYTTTGACTC |
| HCV\_GT\_Rv | GTAYCTCGTCATAGCYTCCGTGAA |
| HBV whole-genome sequencing | |
| HBV\_WG1\_Fw1 | GTGCACTTCGCTTCACCTCT |
| HBV\_WG1\_Rv | CCACCTTRTGAGTCCAAGGA |
| HBV\_WG1\_Fw2 | CTTGAGGCYTACTTCAAAGACTGTG |
| HBV\_WG2\_Fw1 | GCTCACCTCACCATACAGCA |
| HBV\_WG2\_Rv | GAATGCAGGGTCCAACTGAT |
| HBV\_WG2\_Fw2 | GCTCWCCTCACCATACAGCA |
| HBV\_WG3\_Fw1 | TCCTGTCCTCCAATTTGTCC |
| HBV\_WG3\_Rv | GCCTGAGTGCTGTATGGTGA |
| HBV\_WG3\_Fw2 | TCAGTGGTTCGTAGGGCTTT |

**Table S2.** HBV strains showing high nucleotide identity to HBV-A3, HBV-A1, and HBV-E strains detected in this study.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| HBV-A3: SYMAV-D0231 | | | | | |
| # | Description | E value | Identity % | Country | Accession no. |
| 1 | HBV isolate O64 | 0 | 98.98% | Gabon | AM184125 |
| 2 | HBV isolate N35 | 0 | 98.82% | Gabon | AM184126 |
| 3 | HBV strain FE-929-MO | 0 | 97.98% | Gabon | EU054331 |
| HBV-A1: SYMAV-H0721 | | | | | |
| 1 | HBV isolate A1-SA | 0 | 98.83% | South Africa | KP234050 |
| 2 | HBV isolate 833 | 0 | 98.55% | South Africa | AY233289 |
| 3 | HBV isolate rw14-48 | 0 | 98.51% | Rwanda | MK512473 |
| HBV-E: SYMAV-H0235 | | | | | |
| 1 | HBV isolate Eafr | 0 | 95.16% | Guinea | KX186584 |
| 2 | HBV isolate GU1214 | 0 | 94.91% | Guinea | GQ161816 |
| 3 | HBV isolate CAR039 | 0 | 94.91% | CAR | AM494693 |