S1 File: List of reference and HBV isolates from the present study

The 103 HBV reference genome sequence including all genotype and at least two sequence for each subgenotype used for phylogenetic analysis: A1\_KJ533385\_India; A1\_KJ533386\_India; A2\_HE576989\_France; A2\_HE974376\_Martinique; A3\_AB194951\_Cameroon; A3\_AM184125\_Gabon; A4\_AY934764\_Gambia; A4\_AM180623\_Mali; A5\_FJ692613\_Haiti; A5\_KP234053\_Haiti; A6\_GQ331047\_Belgium; A6\_GQ331048\_Belgium; A7\_FN545829\_Cameroon; A7\_FN545833\_Cameroon; B1\_AB642091\_Japan; B1\_D00329\_Japan; B2\_FJ899779\_China; B2\_JQ801485\_Thailand; B3\_GQ924617\_Malaysia; B3\_AP011085\_Indonesia; B4\_GQ924626\_Malaysia; B4\_AB115551\_Cambodia; B5\_GQ924640\_Malaysia; B5\_AB219427\_Philippines; B6\_JN792893\_Canada; B6\_DQ463787\_Canada; B7\_GQ358137\_Indonesia; B7\_AP011091\_Indonesia; B8\_GQ358147\_Indonesia; B8\_AP011093\_Indonesia; B9\_GQ358146\_Indonesia; B9\_GQ358149\_Indonesia; C1\_KP017266\_India; C1\_GQ377605\_China; C2\_GQ358158\_Indonesia; C2\_FJ899761\_China; C3\_DQ089801\_Hong Kong; C3\_EU939536\_China; C4\_HM011493\_Malaysia; C4\_Y18855\_China; C5\_EU410080\_Philippines; C5\_Y18856\_China; C6\_EU670263\_Philippines; C6\_AB493838\_Indonesia; C7\_GU721029\_South Korea; C7\_Y18858\_China; C8\_AP011104\_Indonesia; C8\_AP011105\_Indonesia; C9\_AP011108\_Indonesia; C9\_V00867\_Japan; C10\_AB540583\_Indonesia; C10\_KY670782\_China; C11\_AB554019\_Indonesia; C11\_AB554020\_Indonesia; C12\_AB554018\_Indonesia; C12\_AB560662\_Indonesia; C13\_AB644280\_Indonesia; C13\_AB644281\_Indonesia; C14\_AB644283\_Indonesia; C14\_AB644284\_Indonesia; C15\_AB644286\_Indonesia; C15\_D50489\_Japan; C16\_AB644287\_Indonesia; C16\_D23682\_Japan; D1\_GU456636\_Iran; D1\_JN642165\_Lebanon; D2\_GQ477452\_Poland; D2\_KF679995\_India; D3\_EU594434\_Estonia; D3\_X65257\_Italy; D4\_GQ922003\_Canada; D4\_KF192838\_India; D5\_GQ205377\_India; D5\_GQ205384\_India; D6\_KF170740\_Sudan; D6\_AB493845\_Indonesia; D7\_FJ904442\_Tunisia; D7\_FJ904425\_Tunisia; D8\_FN594770\_Niger; D8\_FN594771\_Niger; D9\_JN664942\_India; D9\_X59795\_Italy; D10\_KX357625\_Ethiopia; D10\_KX357629\_Ethiopia; E\_FN594748\_Niger; E\_HM363610\_Nigeria; F1a\_AY090459\_Costa Rica; F1b\_FJ709464\_Chile; F2a\_DQ899142\_Venezuela; F2b\_DQ899146\_Venezuela; F3\_AB036920\_Venezuela; F3\_AB036905\_Venezuela; F4\_AF223965\_Argentina; F4\_DQ823090\_Argentina; G\_GU563556\_Belgium; G\_KP274926\_Belgium; H\_AB516393\_Mexico; H\_AB516395\_Mexico; I1\_FJ023659\_Laos; I1\_FJ023660\_Laos; I2\_FJ023664\_Laos; I2\_FJ023672\_Laos; J\_AB486012\_Japan.

HBV whole genome sequences and genotype of 53 isolates from current study:

C1\_BD\_HBV57; C3\_BD\_HBV19; C1\_BD-HBV55; C3\_BD\_HBV53; C1\_BD\_HBV21; C1\_BD\_HBV09; C1\_BD\_HBV52; C1\_BD\_HBV13; C1\_BD\_HBV44; C1\_BD\_HBV31; C1\_BD\_HBV18; C1\_BD\_HBV02; C1\_BD\_HBV25; C1\_BD\_HBV14; C1\_BD\_HBV45; C1\_BD\_HBV26; C1\_BD\_HBV49; D2\_BD\_HBV24; D2\_BD\_HBV03; D2\_BD\_HBV48; D1\_BD\_HBV35; D1\_BD\_HBV28; D1\_BD\_HBV43; D2\_BD\_HBV27; D2\_BD\_HBV07; D2\_BD\_HBV38; D2\_BD\_HBV08; D2\_BD\_HBV34; D2\_BD\_HBV01; D2\_BD\_HBV37; D2\_BD\_HBV23; D2\_BD\_HBV47; D2\_BD\_HBV32; D2\_BD\_HBV15; D2\_BD\_HBV42; D5\_BD\_HBV10; A1\_BD\_HBV50; A1\_BD\_HBV05; A1\_BD\_HBV16; A1\_BD\_HBV04; A1\_BD\_HBV54; A1\_BD\_HBV29; A1\_BD\_HBV17; A1\_BD\_HBV46; A1\_BD\_HBV12; A2\_BD\_HBV30; C1\_BD\_HBV33; C3\_BD\_HBV20; C1\_BD\_HBV41; 1\_BD\_HBV11; C1\_BD\_HBV56; C1\_BD\_HBV39; C1\_BD\_HBV22. 1a

The accession number for the sequences in GenBank is MF925358 to MF925410.