

## **Supplementary Information**

### **Intermediate hepatitis B virus infection prevalence among 1622 pregnant women in rural Burkina Faso and implications for mother-to-child transmission**

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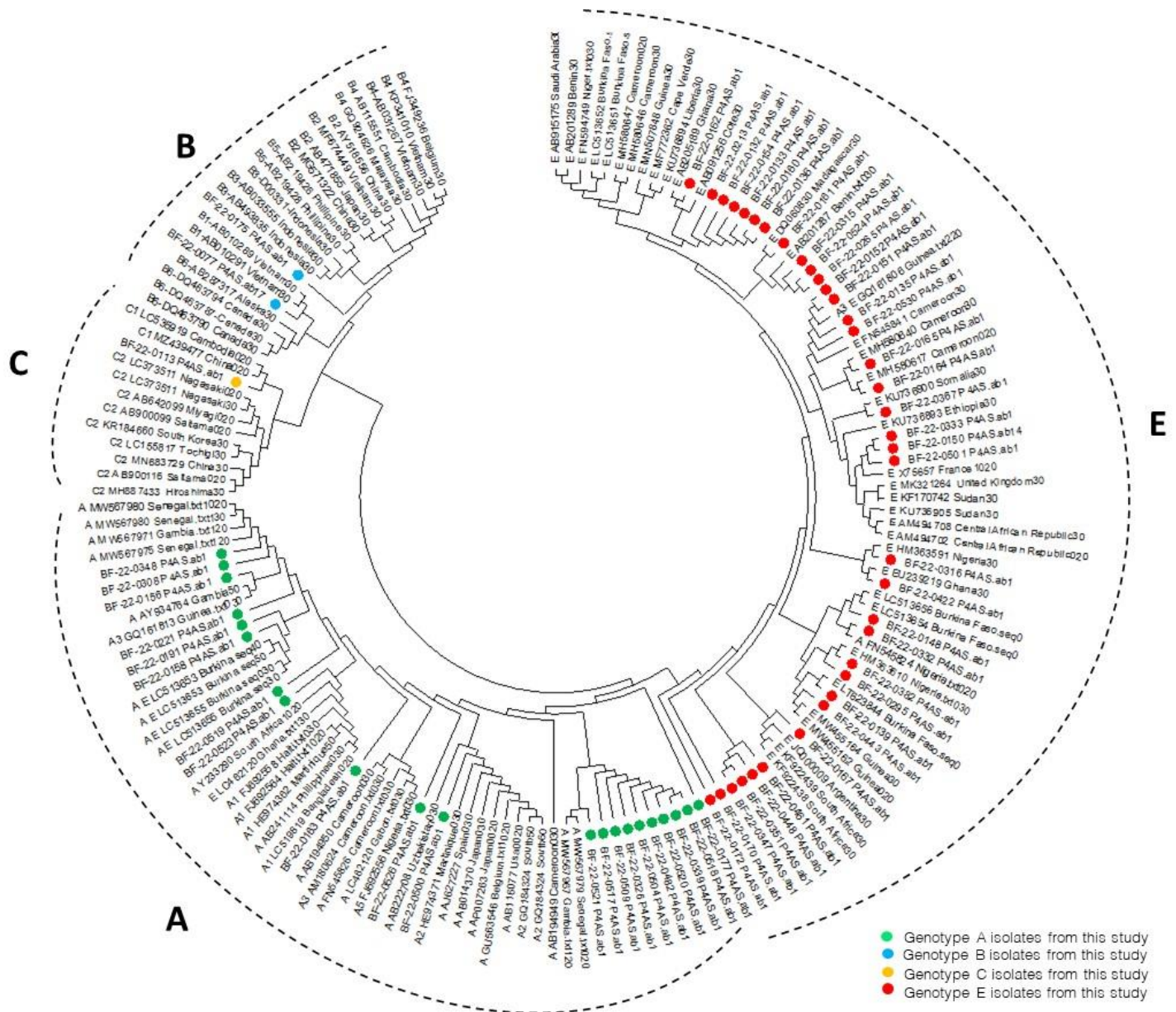
**Supplementary Table S1. Primers used for nested PCR and partial genome sequencing**

**a) Nested PCR**

| <b>Target region</b>                  | <b>Primer name</b> | <b>Stage polarity</b> | <b>Nucleotide position</b> | <b>Nucleotide sequence (5'-3')</b> | <b>Reference</b> |
|---------------------------------------|--------------------|-----------------------|----------------------------|------------------------------------|------------------|
| <b>Surface-polymerase (SP) region</b> | S1                 | PCR 1st Sense         | 1414–1434                  | ACGTCCTTTGTTTACGTCCCG              | 13               |
|                                       | S2                 | PCR 1st Sense         | 1436–1456                  | CGGCGCTGAATCCCGCGGACG              | 13               |
|                                       | AS1                | PCR 2nd Sense         | 2130–2110                  | TCCAAATTACTTCCCACCCAG              | 13               |
|                                       | AS2                | PCR 2nd Sense         | 2160–2140                  | CTGACTACTAATTCCCTGGAT              | 13               |
|                                       | S3                 | PCR 1st Antisense     | 1489–1508                  | CCGCTTCTCCGTCTGCCGTA               | 13               |
|                                       | S4                 | PCR 1st Antisense     | 1527–1547                  | CACCTCTCTTTACGCGGACTC              | 13               |
|                                       | AS3                | PCR 2nd Antisense     | 2185–2165                  | TAGGCCCATATTAACATTGAC              | 13               |
|                                       | AS4                | PCR 2nd Antisense     | 2098–2078                  | CATCAACTCACCCCAACACAG              | 13               |
| <b>Surface (S) region</b>             | S1-1               | PCR 1st Sense         | 192-211                    | TCGTGTTACAGGCGGGGTTT               | 14               |
|                                       | S1-2               | PCR 2nd Sense         | 455-474                    | CGAACCACTGAACAAATGGC               | 14               |
|                                       | S2-1               | PCR 1st Antisense     | 685-704                    | CAAGGTATGTTGCCCGTTTG               | 14               |
|                                       | S2-2               | PCR 2nd Antisense     | 668-687                    | GGCACTAGTAAACTGAGCCA               | 14               |

**b) Genome sequencing**

| <b>Target region</b> | <b>Primer name</b> | <b>Nucleotide sequence (5'-3')</b> | <b>Length</b> | <b>Target nucleotide position</b> | <b>Reference</b> |
|----------------------|--------------------|------------------------------------|---------------|-----------------------------------|------------------|
| <b>SP region</b>     | AS4                | CATCAACTCACCCCAACACAG              | 458 bp        | 475-933                           | 13               |
| <b>S region</b>      | S2-2               | GGCACTAGTAAACTGAGCCA               | 232 bp        | 455-687                           | 14               |



Supplementary Figure S1. Phylogenetic tree of the overlapping surface-polymerase region of HBV genome

