## **Supplementary figures**

## Adaptive evolution of proteins in hepatitis B virus during divergence of genotypes

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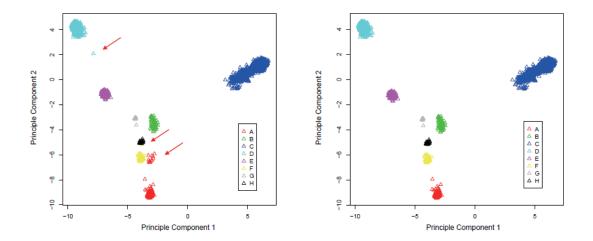
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AB116079: AB113877: C-C-C-C-C-C-C-C-C-C **A-A-A-A-A-A-A-A-A-A** JQ272886: DQ993705: C-B-B-B-B-B-B-B-B-C-C

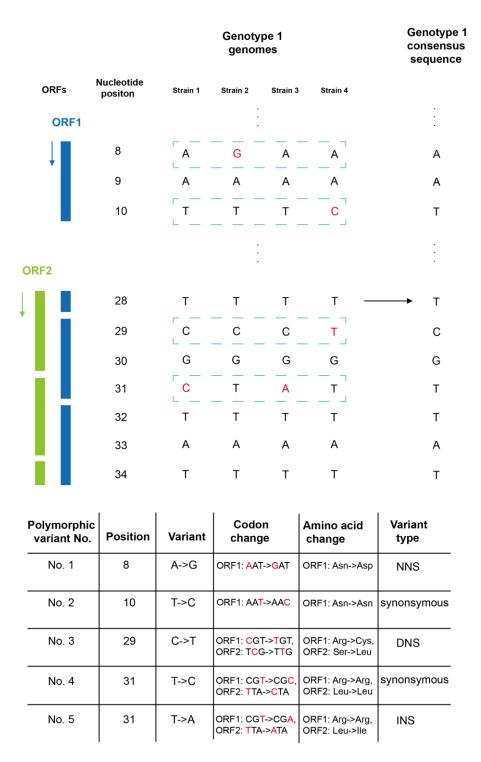
Supplementary figure S1. Visualization of pure-genotypic strains and inter-genotypic recombinants by jpHMM.

The genotype plots of two pure strains (AB116079, AB113877) and two inter-genotypic recombinants (JQ272886, DQ993705) generated by jpHMM. The fragmental genotypes (13 characters) predicted by fragment typing are displayed accordingly.



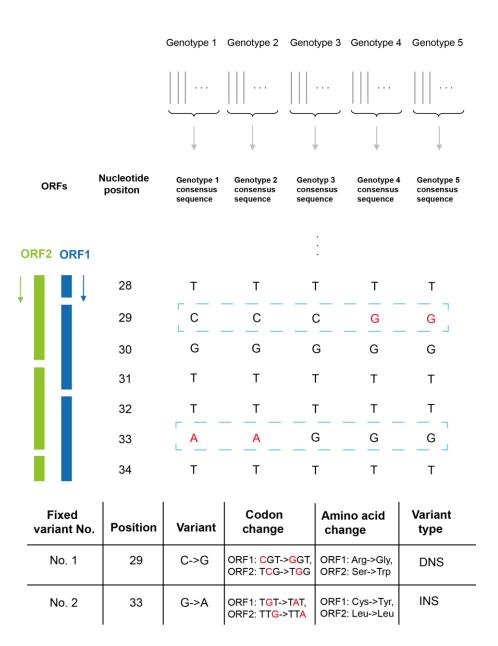
Supplementary figure S2. Removal of population outliers.

The genetic relationship of 3006 genomes before removing outliers (left) and 2992 genomes in final dataset (right) revealed by PCA. Population outliers were indicated by arrows.



## Supplementary figure S3. Example of determining four categories of polymorphic variants.

This is an example on determination of NNS, DNS, INS and synonymous variants. The template dataset contains 4 strains from fictional genotype 1. Polymorphic sites are indicated in dashed boxes and variants distinguished from consensus sequence are marked as red. The codons of two open reading frames (ORF1 and ORF2) are showed as blue and green bars.



## Supplementary figure S4. Example of determining fixed variants.

The consensus sequences of each genotype were first generated and aligned. Fixed variants were then identified similarly as **Supplementary figure S3**.