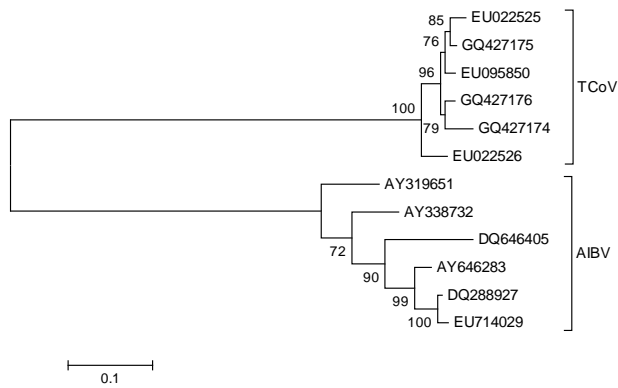


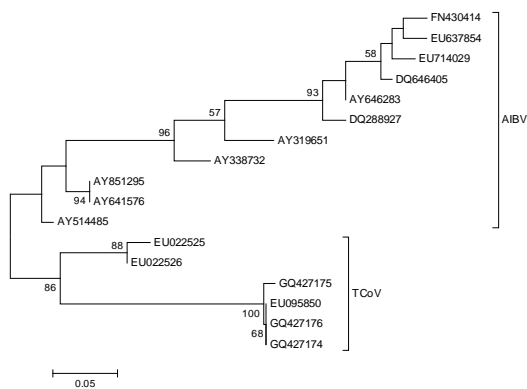
## Supplementary Figures

Supplementary Figure S1. (A) Maximum-likelihood tree of non-overlapping portions of the *S* gene based on MCL distance at 3310 aligned nucleotide sites. (B) Maximum-likelihood tree of the 3' end of the *b* portion of the *Iab* gene based on MCL distance at 114 aligned nucleotide sites. Numbers on the branches represent the percentage of 1000 bootstrap samples supporting the branch; only values  $\geq 50\%$  are shown.

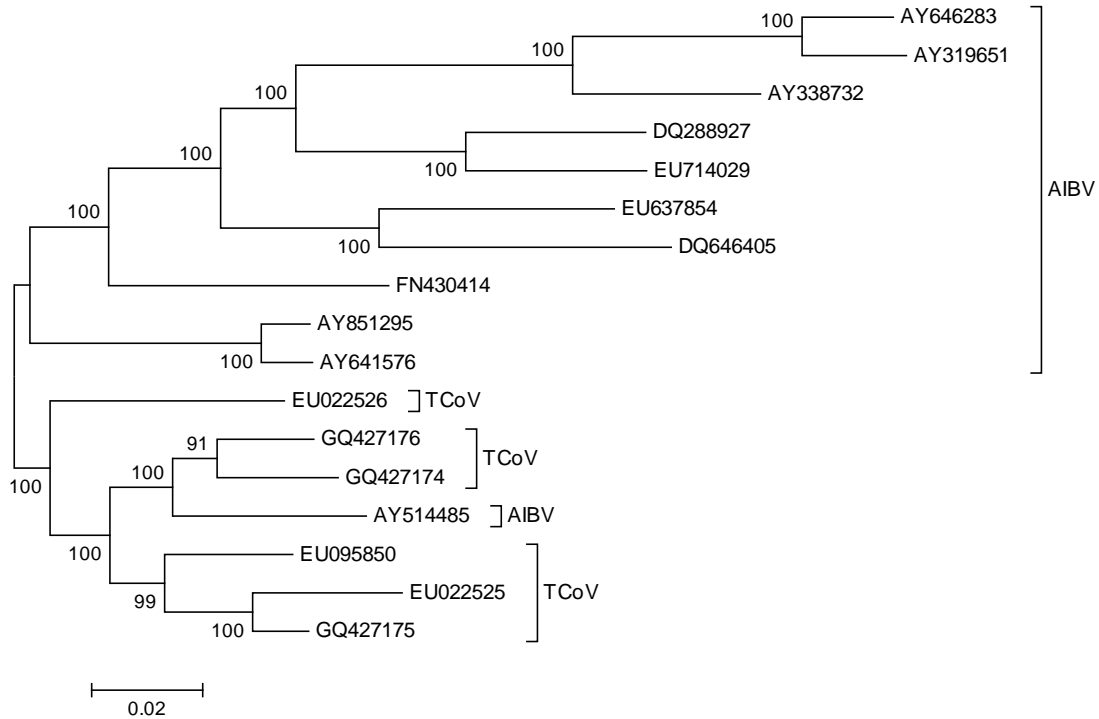
A)



B)

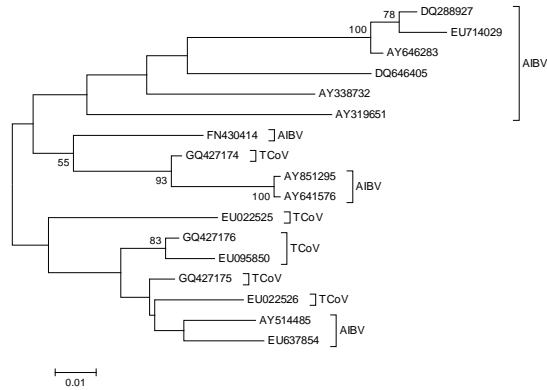


Supplementary Figure S2. Maximum-likelihood tree of non-overlapping portions of *Ia*, the *b* portion of *1ab* (excluding the 3' end; Figure 2A), *3a*, *3b*, and *Env* sequences, based on MCL distance at 20,031 aligned sites. Numbers on the branches represent the percentage of 1000 bootstrap samples supporting the branch; only values  $\geq 50\%$  are shown.

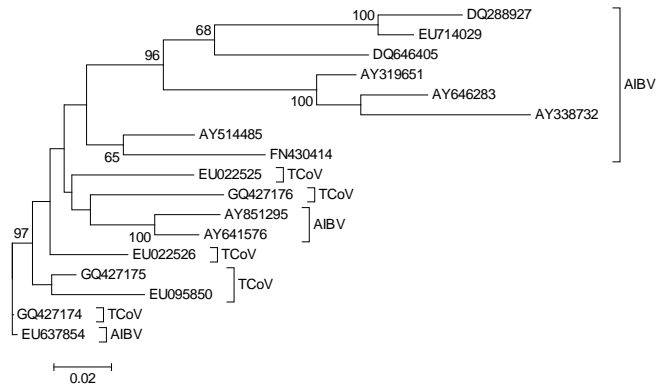


Supplementary Figure S3. (A) Maximum-likelihood tree of non-overlapping portion of the *M* gene based on MCL distance at 668 aligned nucleotide sites. (B) Maximum-likelihood tree of non-overlapping portion of the *N* gene sequences based on MCL distance at 1170 aligned nucleotide sites. Numbers on the branches represent the percentage of 1000 bootstrap samples supporting the branch; only values  $\geq 50\%$  are shown.

A)

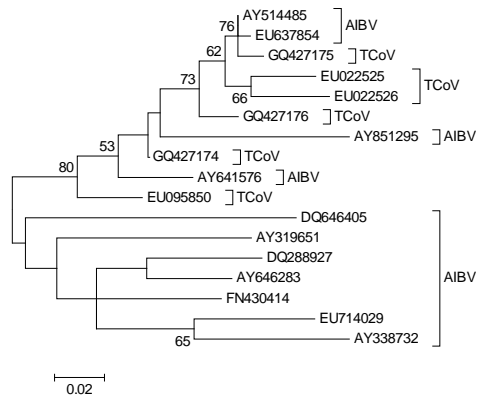


B)

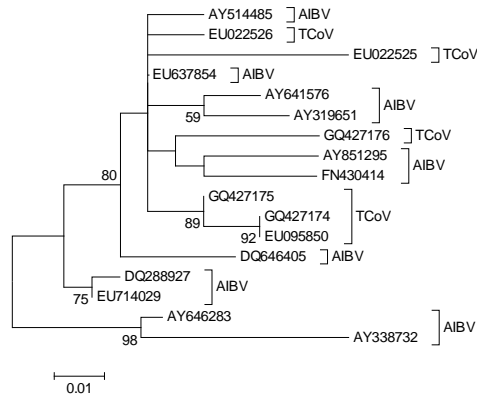


Supplementary Figure S4. (A) Maximum-likelihood tree of non-overlapping portion of the *5a* gene based on MCL distance at 198 aligned nucleotide sites. (B) Maximum-likelihood tree of non-overlapping portion of the *5b* gene based on MCL distance at 180 aligned nucleotide sites. Numbers on the branches represent the percentage of 1000 bootstrap samples supporting the branch; only values  $\geq 50\%$  are shown.

A)



B)



Supplementary Figure S5. Maximum-likelihood tree of S protein sequences of coronaviruses from avian and mammalian hosts based on the JTT model at 796 aligned amino acid sites. Sequences are identified by accession number and host. Numbers on the branches represent the percentage of 1000 bootstrap samples supporting the branch; only values  $\geq 50\%$  are shown.

