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**Supplementary Data**

**A Novel Bat Coronavirus with a Polybasic Furin-like Cleavage Site**

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**Supplementary Table S1** The primers were used to confirm the genome of Bat CoV CD35 in this study.

|  |  |  |  |
| --- | --- | --- | --- |
| Primer names | Primer sequences | Targeted region | Length of amplified region (bp) |
| CD35-F1  | TTCGTCTTATCTTTTGCCTTCA | NS2 and spike genes | 2090 |
| CD35-R1 | ACCAGTTCCCTTGTAACCATAAA |
| CD35-F2 | TGTCATTGGCTACTCACTAAAAA | ORF4, E, M, ORF7, ORF8, N genes | 2503 |
| CD35-R2 | CCATCGTTTGCTGAGTTTCTA |

**Supplementary Table S2** Coding of potential of the Bat CoV CD35 genome.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Location (nt) | Length (nt) | Length (aa) | Frames(s) |
| ORF1ab | 286–21929 | 21645 |  | +1, +3 |
| ORF1a | 286–13824 | 13539 | 4512 | +1 |
| ORF1b | 13824–21929 | 8106 | 2701 | +3 |
| ORF2 | 21944–23170 | 1227 | 408 | +2 |
| S | 23320–27330 | 4011 | 1336 | +1 |
| ORF4 | 27330–28055 | 726 | 241 | +3 |
| E | 28106–28345 | 240 | 79 | +2 |
| M | 28405–28067 | 663 | 220 | +1 |
| ORF7 | 29083–29298 | 216 | 71 | +1 |
| ORF8 | 29312–29644 | 333 | 110 | +2 |
| N | 29692–30945 | 1254 | 417 | +1 |



**Supplementary Fig. S1** Phylogenetic analysis based on nucleotide sequences of *RdRp* genes within *Bat coronavirus* HKU10 species. The tree (IBV as outgroup) is built by the maximum-likelihood method with the JC model and 1000 bootstrap replicates. Only bootstrap values > 90% are shown. Virus from this study is labeled with a blue star. IBV, infectious bronchitis virus; HKU10, *Bat coronavirus* HKU10. The background colors are labeled with lineages respectively.



**Supplementary Fig. S2** The schematic diagram showing alignment of spike protein cleavage sites between Bat CoV CD35 and other human coronaviruses. Cleavage sites are indicated by arrows. The strictly conserved residues in the column are labeled using white characters on a red background. The red characters on a white background within blue frames are colored when the similarity global score is greater than 0.7.