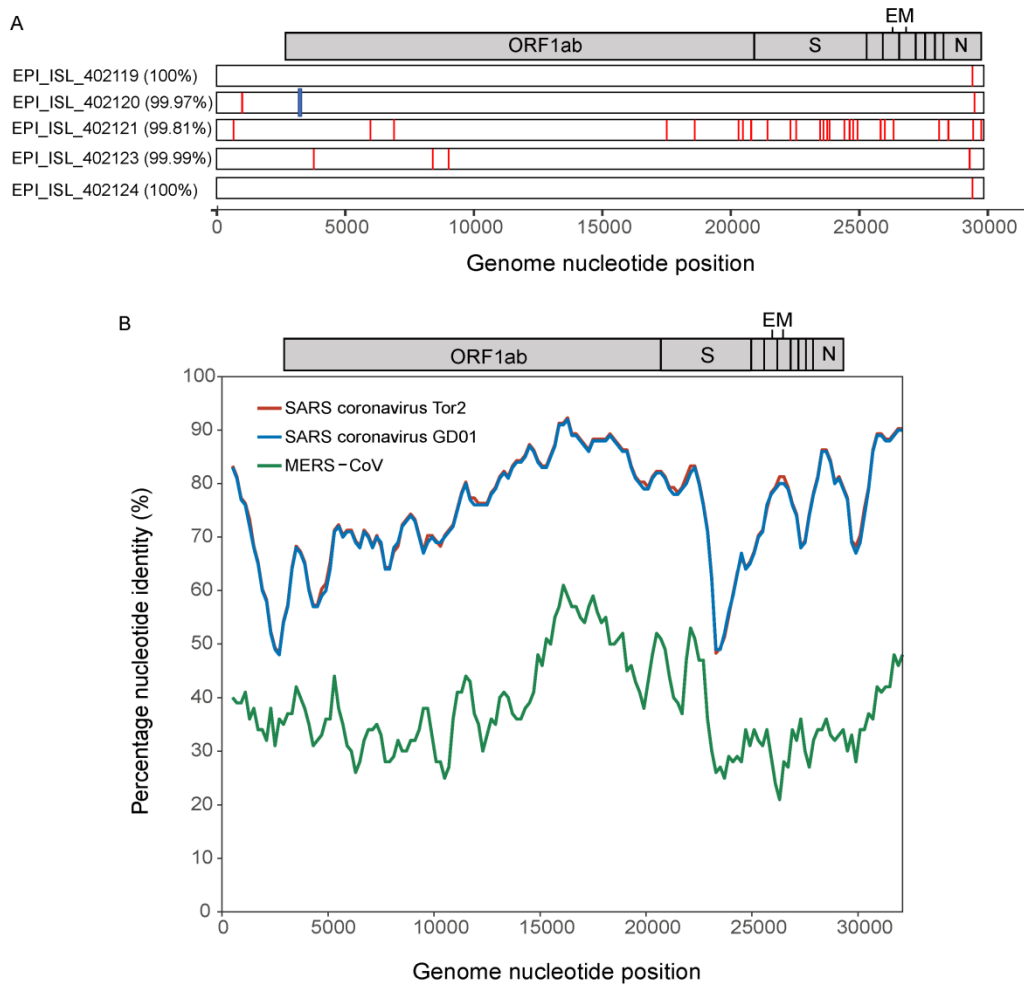**Supporting Information:**

Figure S1 Sequence similarity analysis among six Wuhan CoV genomes and between Wuhan CoV and the human-infecting coronaviruses, SARS-CoV and MERS-CoV. A) Sequence comparison of five Wuhan CoV genomes against WH-Human_1 genome, respectively. Regions of open read frames (ORF) are represented with gray box on the top. Single nucleotide variations (SNVs) were identified by comparing to the WH-human_1 genome using the NCBI Blast tool. SNVs are marked with red lines, and indels marked with blue bars. The more frequent SNVs in the genome of Wuhan/IVDCHB05/2019_EPI_ISL_402121 are likely the result of poor quality sequence data. B) Similarity plot of the Wuhan CoV genome (WH-human_1 used as representative) compared to those of SARS-CoV and MERS-CoV. The analysis was performed using the Kimura model with a window size of 1000 bp and a step size of 200 bp.