

Table S1. Comparison of the full-length genome of KNU-1907 to the Korean G2b prototype KNU-141112 strain.

Genome Region (Nucleotide Length)	KNU-1907	
	% Identity (No. of nt or aa Differences) to KNU-141112	
5'-UTR (292)	99.6 (1)	
ORF1ab (20,345)	99.7 (19)	
nsp1 (363)	99.1 (1)	
nsp2 (2,322)	99.8 (1)	
nsp3 (4,863)	99.6 (6)	
nsp4 (1,443)	99.3 (3)	
nsp5 (906)	99.6 (1)	
nsp6 (840)	100 (0)	
nsp7 (249)	100 (0)	
nsp8 (585)	100 (0)	
nsp9 (324)	100 (0)	
nsp10 (405)	100 (0)	
nsp11 (54)	100 (0)	
nsp12 (2,781)	99.6 (3)	
nsp13 (1,791)	99.8 (1)	
nsp14 (1,551)	99.6 (2)	
nsp15 (1,017)	100 (0)	
nsp16 (906)	99.6 (1)	
Spike (4,161)	99.2 (11)	
ORF3 (675)	99.5 (1)	
E (231)	100 (0)	
M (681)	100 (0)	
N (1,326)	98.8 (5)	
3'-UTR (334)	99.4 (2)	
Total	99.5 (1/36/2) ^a	

^a The number of individual differences in the 5'-UTR, protein-coding region, and 3'-UTR, respectively.

Table S2. Comparison of the full-length genome among KNU-1907 strains.

Genome Region (Nucleotide Length)	KNU-1907-3	KNU-1907-8
	% Identity (No. of nt or aa Differences) to KNU-1907	
5'-UTR (292)	100 (0)	99.6 (1)
ORF1ab (20,345)	99.8 (10)	99.8 (11)
nsp1 (363)	100 (0)	100 (0)
nsp2 (2,322)	99.8 (1)	99.7 (2)
nsp3 (4,863)	99.9 (1)	99.9 (1)
nsp4 (1,443)	99.5 (2)	99.5 (2)
nsp5 (906)	99.6 (1)	99.6 (1)
nsp6 (840)	100 (0)	100 (0)
nsp7 (249)	100 (0)	100 (0)
nsp8 (585)	100 (0)	100 (0)
nsp9 (324)	100 (0)	100 (0)
nsp10 (405)	100 (0)	100 (0)
nsp11 (54)	100 (0)	100 (0)
nsp12 (2,781)	99.6 (3)	99.6 (3)
nsp13 (1,791)	100 (0)	100 (0)
nsp14 (1,551)	100 (0)	100 (0)
nsp15 (1,017)	99.4 (2)	99.4 (2)
nsp16 (906)	100 (0)	100 (0)
Spike (4,161)	99.7 (4)	99.3 (8)
ORF3 (675)	99.5 (1)	99.5 (1)
E (231)	100 (0)	100 (0)
M (681)	100 (0)	100 (0)
N (1,326)	99.7 (1)	99.3 (3)
3'-UTR (334)	100 (0)	99.7 (1)

Total	99.9 (0/16/0) ^a	99.8 (1/23/1) ^a
^a The number of individual differences in the 5'-UTR, protein-coding region, and 3'-UTR, respectively.		

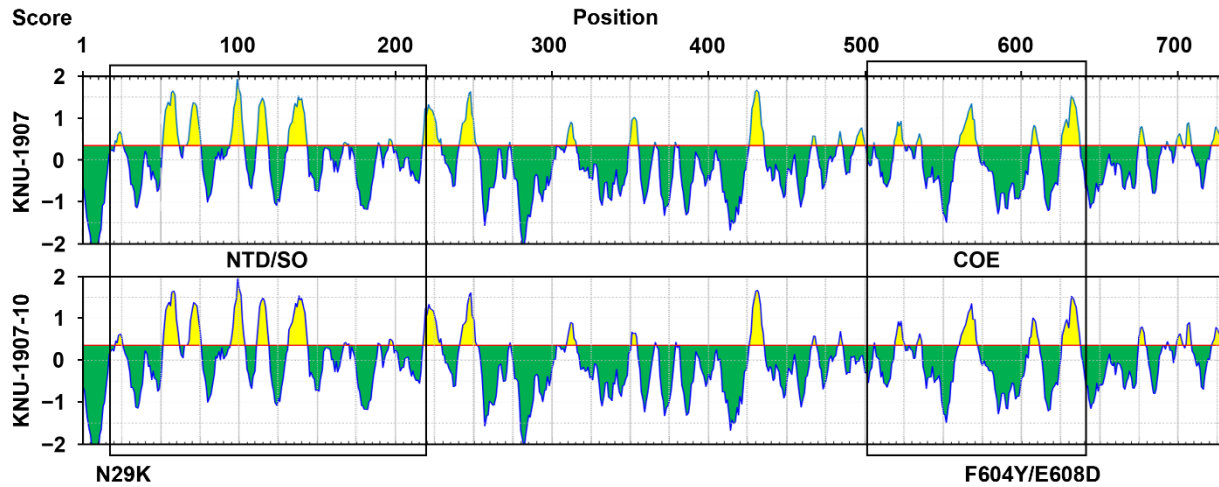


Figure S1. Comparison of Bepipred linear epitope prediction of the S proteins between the KNU-1907 (top) and KNU-1907-10 (bottom) strains. The regions with predicted epitopes on the protein are shown in yellow. Two NTD/SO and COE neutralizing epitope regions at positions 19-220 and 502-641, including one (N29K) and two (F604Y and E608D) amino acid changes between KNU-1907-10, respectively, are indicated by a solid box.

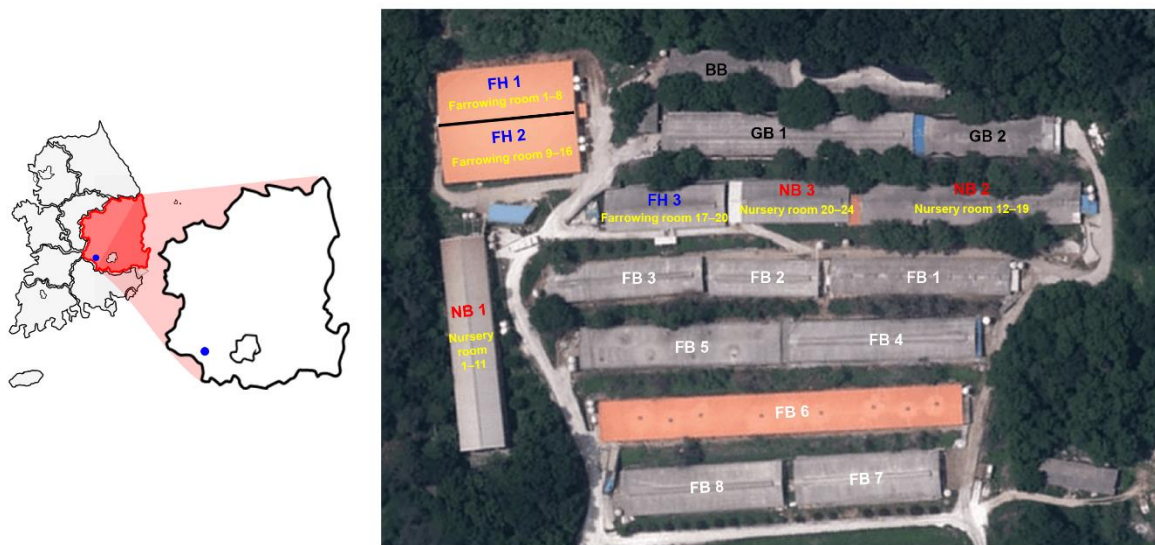


Figure S2. Geographic location and facility layout plan of the PEDV-infected farm analyzed in this study. A map of eight provinces in South Korea is shown on the left. The right is a magnified version of the Gyeongbuk Province in the picture on the left, and the location of the farm in this study is marked with a blue dot. The facility layout plan of the swine farm was drawn using the Google Map service (<http://www.google.co.kr>, accessed on 16 January 2021). The facility layout plan of the swine farm was drawn using the breeding barn (BB: black), two gestation barns (GB: black), three farrowing houses (FH: blue), three nursery barns (NB: red), and eight finisher barns (FB: white), FH 1, 2, and 3 containing farrowing room 1-8, 9-16, and 17-20, respectively, whereas NB 1, 2, and 3 contain nursery rooms 1-11, 12-19, and 20-24, respectively.