



Figure S1. Phylogenetic analysis based on the PLCP genes of EV-Gs and nidoviruses, including toroviruses (ToVs), coronaviruses (CoVs), and arteriviruses (a) and full-length genomic sequences, excluding the insertion PLCP sequences of EV-G strains (b). Multiple sequence alignments were performed using the ClustalX 2.0 program, and the phylogenetic trees were constructed from the aligned nucleotide sequences using the neighbor-joining method. Numbers at each branch represent bootstrap values greater than 50% of 1000 replicates. Hosts of origin, geographical origins, names of the strains, years of isolation, genotypes, and GenBank accession numbers are shown. The genotypes are indicated on the right-hand side. A solid circle denotes the Korean recombinant EV-G1-PLCP strain identified in this study; solid diamonds indicate global EV-G PLCP strains reported in previous studies. Scale bars indicate nucleotide substitutions per site.

Table S1 Comparison of the full-length genomes of reference EV-G strains with the Korean EV-G1-PLPC KNU-1811 strain

KNU-1811	GBR/UKG/G1	USA/Texas1/G1	BEL/15V010/G1	JPN/MoI2-2-1/G1	JPN/HgYa2-1/G2	USA/08_NC/G17
% nt/aa identity to KOR/KNU-1811/G1						
Genome regions (nt length)						
5' UTR (813)	89.0/– [†]	86.5/–	92.2/–	93.3/–	93.2/–	94.7/–
VP4 (207)	82.6/92.7	74.8/79.7	78.7/89.8	89.8/98.5	72.4/81.1	79.2/92.7
VP2 (738)	80.7/95.1	83.8/96.7	79.9/95.5	87.5/97.9	68.6/81.7	71.0/84.1
VP3 (831)	80.3/92.4	85.9/95.3	81.6/95.7	90.0/97.8	68.0/72.9	69.0/75.8
VP1 (729)	79.0/85.1	85.2/94.6	79.9/93.6	87.9/94.6	61.4/62.5	59.4/61.4
2A (450)	81.3/93.3	85.7/94.6	83.5/96.0	83.1/94.6	80.4/92.6	87.3/95.3
2B (297)	75.4/81.8	82.4/94.9	86.5/100	85.8/96.9	87.2/97.9	89.5/97.9
2C (987)	77.0/86.3	86.2/97.5	86.5/97.2	87.5/99.0	88.6/99.0	87.6/96.6
PLCP (594)	–/–	71.5/75.0	77.3/76.8	77.8/80.1	77.0/79.2	82.6/89.3
3A (267)	74.1/85.3	84.2/96.6	84.2/93.2	82.7/98.8	82.7/96.6	82.3/96.6
3B (66)	81.8/95.4	86.3/100	84.8/100	87.8/100	86.3/100	87.8/100
3C (549)	71.9/84.6	87.6/100	86.5/97.8	83.9/95.6	86.3/100	86.5/97.8
3D (1,386)	78.8/88.0	90.2/98.0	85.4/97.8	86.5/98.0	86.8/97.3	85.8/97.1
3' UTR (71)	82.4/–	35.2/–	80.0/–	73.2/–	70.4/–	98.5/–

[†] Not applicable.