

Table S1. Primer sets and PCR information for EqPV-CSF/EqCoPV detection.

PCR	Primer Sets	Sequences (5' → 3')	Product Size, bp	Tm	No. PCR Cycles	References	
EqPV-CSF detection (partial NS gene)	Forward	CAAATGGACCAATGCAAGCAG	996	50°C	40	[16]	
	Reverse	ATGGTCCATAGTGACCAGTGTC					
EqCoPV detection (partial VP gene)	Forward	GTGGACAGCCGAAGAGTGGA	522	50°C	40	[1]	
	Reverse	AGTCACTCGGCCATGGTGT					
EqPV-CSF (complete CDS)	EqPV 1F	ATACCCCCAACAGAAACAAGG	1145	56°C	40	MZ100069.1	
	EqPV 1145R	TGTCCTTCATCCCACCATCC					
	EqPV 940F	GGAATGCTATTCTGGCTATGGTC	1153	56°C	40		
	EqPV 2092R	GTCTCTGGTGCTTCTGTGC					
	EqPV 1922F	ACCAGGACCAGACGCATATT	1148	56°C	40		
	EqPV 3069R	ACGCATCCTGTGAAGGTACA					
	EqPV 2724F	AGTTGTGAGAACGCCCTGCT	1551	56°C	40		
	EqPV 4274R	TGCTGTGCTTGGGTTCTG					
	EqPV 3939F	GACAATCCATGGGCCAAACAA	1111	56°C	40		
EqCoPV (complete CDS)	EqPV 5049R	CGGAGGTGAGGCTACATTCC					
	EqCo 26F	GCGTTGCAACAACCACAAAA	1236	56°C	40	MN181468.1	
	EqCo 1261R	TAGTGCTCCTTCATCCCACC					
	EqCo 617F	CTTCGATCCTGGACAACCAT	1637	56°C	40		
	EqCo 2253R	TAGCAGCCCTCCCAATGTAG					
	EqCo 2027F	GGTCACAAAAAGGCACTGGT	1262	56°C	40		
	EqCo 3288R	GCTAAGCCTCCAAGTTCAGC					
	EqCo 2910F	CAACGATAACCGTGTGGACAG	1311	56°C	40		
	EqCo 4220R	AGTAGTCCCCGTCCCTATGT					
	EqCo 3981F	TACCAATGGAACCCCTCACAA	1101	56°C	40		
	EqCo 5081R	GTCTGTCTCATGGGCCAT					
	EqCo 4810F	AATGGTACCAACACCAGGAC	289	60°C	40		
	EqCo 5098F	TTATCTCATTCTCTGGGTCTG					

Abbreviations: bp, base pair; CDS, coding sequences; PCR, polymerase chain reaction; NS, non-structural; Tm, melting temperature.

Table S2. Detailed information on clinical signs of horses in this study.

Clinical Signs	Number of Horses
Colic	41
Osteochondrosis	8
Diarrhea	4
Dystocia	3
Pneumonia	3
Wound	3
Anorexia	2
Cachexia	2
Cellulitis	2
Equine Neonatal Maladjustment Syndrome	2
Hyperthermia	2
Limb deformity	2
Respiratory noise	2
Sesamoid bone fracture	2
Arthritis	1
Castration	1
Corneal ulcer	1
Dermatitis	1
Esophageal stricture	1
Guttural pouch empyema	1
Lameness	1
Laminitis	1
Strangles	1
Suspensory ligament rupture	1

Figure S1. Phylogenetic analysis based on a partial NS gene (872 bp) of EqPV-CSF. Newly identified Korean isolates are indicated by black diamonds. The Korean isolates were analyzed together with other members of genus *Copiparvovirus*.

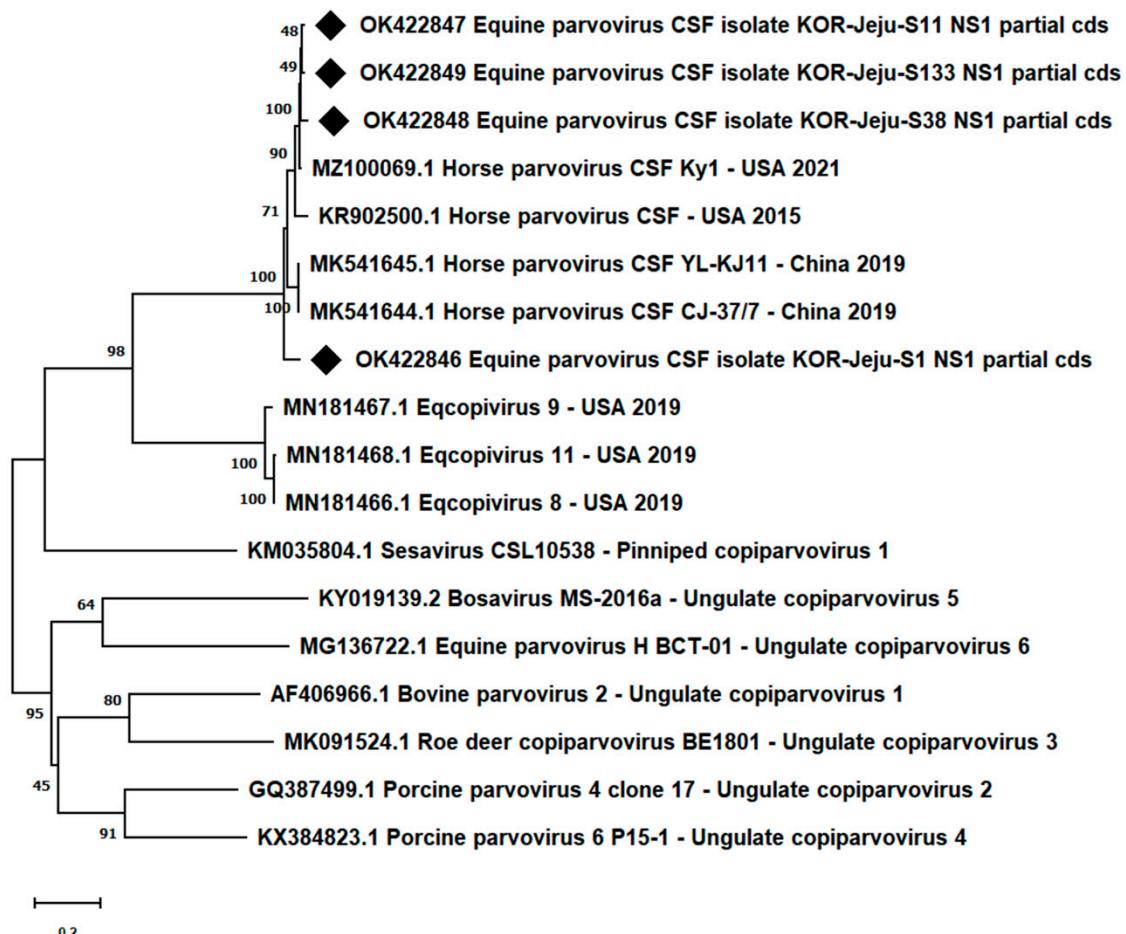


Figure S2. Phylogenetic analysis based on a partial VP gene (479 bp) of EqCoPV. Newly identified Korean isolates are indicated by black circles. The Korean isolates were analyzed together with other members of genus *Copiparvovirus*.

