



Figure S1 of the Supplementary File. Comparison of ORF 5 sequences between the DV vaccine strain and the wild-type PRRSV strain of the trial farm: 90.7% sequence identity.

Maximum Likelihood Analysis (MLA) based on ORF 5 (Gp5) sequences.
 Nucleotide substitution model: Kimura 2 with gamma distributed rates (K2+Γ).
 Comparison of ORF 5 sequences between the DV vaccine strain (●) and the wild type virus circulating in the farm (▲): 90.7% sequence identity.

Table S1 of the Supplementary File. Results of qRT-PCR in blood serum samples of the sampled animals at ages of 4, 7 and 10 weeks.

Group	Blood Sampling/Age		
	4 Weeks	7 Weeks	10 Weeks
	Number of PRRSV Positive Samples/Total Samples Average Ct Value (Min–Max)		
Group A (Porcilis PRRS ID)	0/6	0/6	6/6
	N/A	N/A	33.3 (30.5–36.5)
Group B (Porcilis PRRS IM)	0/6	2/6	6/6
	N/A	35.2 (32.3–38)	34.6 (29.5–39.7)
Group C (Diluvac ID)	0/6	5/6	6/6
	N/A	34.7 (25.5–40.8)	29.4 (25.4–32.9)
Group D (Diluvac IM)	0/6	5/6	6/6
	N/A	29.2 (24.2–32.2)	34.4 (25.6–39.0)

N/A: not applicable.