

	84	86	88	90	92	
VR-2332_PRRSV	RPP	DD	WAT	DED	LV	Type II
Ingelvac_PRRSV	RPS	DD	WAT	DED	LV	
SP_PRRSV	RPP	DD	WAT	DED	LV	
HB-2_PRRSV	RPS	DD	WAT	DED	LV	
P129_PRRSV	RPS	DD	WAT	DED	LV	
CH-1a_PRRSV	RPL	DD	WAT	DED	LV	
Ja142_PRRSV	RPS	DD	WAT	DED	LV	
MN184A_PRRSV	RSP	ED	WAT	DED	LV	
NADC30_PRRSV	RSP	DD	WAT	DED	LA	
NADC31_PRRSV	RPP	ED	WAT	DED	LV	
Jxwn06_PRRSV	RPS	DD	WAT	DED	LV	
HuN4_PRRSV	RPS	DD	WAT	DED	LV	Type I
Lelystad_PRRSV	RPED	DD	WA	SDY	DLA	
EuroPRRSV_PRRSV	RPED	DD	WA	SDY	DLV	
Belgium_PRRSV	RPED	DD	WA	SDY	DLA	Other arteriviruses
RPOA-SHFV	WAYE	AWTT	NED	IG		
RPOA-LDV	RDS	SE	WLS	DQD	LY	
CAC42775_EAV	CSS	DL	WC	DE	LAY	

Figure. S1. The sequence alignment of the PLP2 acidic cluster. The amino acids sequences of various PRRSV acidic clusters are presented. The residues investigated in our study are highlighted in red or blue. The accession numbers of viruses are as follows: AY150564 (VR-2332), EF532801 (Ingelvac), AF184212 (SP), AY262352 (HB-2), AF494042 (P192), AY032626 (CH-1a), AY424271 (JA142), DQ176019 (MN184A), JN654459 (NADC30), JN660150 (NADC31), EF641008 (JXwn06), EF635006 (HuN4), M96262 (Lelystad), AY366525 (EuroPRRSV), KT159248 (Belgium), Q68722 (RPOA-SHFV), Q06562 (RPOA-LDV), CAC42775 (EAV).