

A. GP2

	20	40	a. (15)	60	80				
KS62	MKWGPCKASL	TKLANFSWML	SRNFWCPLLI	SSYFWPFCCLA	SPSLAGWSS ASDWFAPRYS	VRALPFTLSN	YRRSYEAFLS	80	
NVSLL.....L.....L.....L.....L.....L.....L.....	80	
KS06L.....L.....L.....L.....L.....L.....L.....	80	
VR23FF.....L.....SS.....L.....PV.....F.....H.....	80	
SDSUF.....L.....SS.....L.....PV.....F.....H.....	80	
P129LY.....SS.....L.....L.....S.....L.....S.....PV.....F.....H.....	80	
LVQH.GV--S.SC.TPLSSLLVWLPFSL.Y.GQD.Y.FF.E.....P.....GL.P	77	
	100	120	b. (15)	140	160				
KS62	LCQVDIPTWG	TRHPLGMLWH	HKVSTLIDEM	VSRRMVRTME	KAGQAAWKQV	VSEATLSRIS	GLDVVAHFQH	LAAIEAETCK	160
NVSLQ.....Q.....Q.....Q.....Q.....Q.....Q.....	160	
KS06Q.R.....K.....F.....T.....I.....T.....I.....T.....I.....T.....I.....T.....I.....	160	
VR23Q.....K.....I.....I.....I.....I.....I.....	160	
SDSUQ.....K.....I.....I.....I.....I.....I.....	160	
P129Q.R.....VK.....F.....I.....I.....I.....I.....I.....	160	
LVN.RP.V.QFAVK.....F.....MR.....H.....I.....Q.....HS.....G.....TKLI.....T.....V.....DS.R	157	
	180	200		220	240				
KS62	YLASRLPMLH	NLRMTGSNVT	IVYNSTLNQV	FAIFPTPGSR	PKLHDFQQWL	IAVHSSIFSS	VAASCTLFVV	LWLRIPMLRT	240
NVSLS.....S.....S.....S.....S.....S.....S.....S.....	240
KS06S.....S.....S.....S.....S.....S.....S.....S.....	240
VR23S.....S.....S.....S.....S.....S.....S.....S.....	240
SDSUS.....S.....S.....S.....S.....S.....S.....S.....	240
P129S.....S.....S.....S.....S.....S.....S.....S.....	240
LVF.S.....V.KAV--G.SLQ.T.DREL.....T.....T.....R.....S.....A.....S.....V.....I.....A.....Y	235
KS62	VFGFRWLGA I	FPSNSR * 257							
NVSL							
KS06W. 257							
VR23A.....L.....Q. 257							
SDSUS.....							
P129L.....W. 257							
LVH.PT.TH.S*-- 250							

B. E (2a) protein

	20	40		60				
KS62	MGSMQSLFDK	IGQLFVDAFT	EFLVSIVDII	I FLAILFGFT	IAGWLVVFCI	RLVCSAVLRT	RPTIHPEQLQ	KIL * 74
NVSL
SDSU
P129I.....
VR23Y.....T.....
KS06A.....
LVWS.....S.....V.....A.....V.....L.....LLV.....L.....SSA.....SPE.SV.....	71

C. GP3

	20	40		60	a. (15)	80			
KS62	MANSCALLHI	FLRCGFL-YS	FCCAUVADSN	ATYCFWFPLV	RGNFSFELTV	NYTVCPPCLT	RRAAAEYEP	GRSLWCRIGY	79
NVSL	
P129TF.....C.S.....G.....M.....M.....M.....M.....H.....	
VR23V.....TF.....C.N.....G.....T.....T.....T.....T.....H.....	
SDSUT.....L.C.S.....A.....A.....A.....A.....A.....H.....	
KS06D.....P.....P.....M.....M.....M.....M.....H.....	
LVHQ.RF.FIC.LVHS.LASN.SS.L.....AH.T.....II.M.SSQ.RQRLNM.K.H	
	100	120		140		160			
KS62	DRCSEEDHDD	LGMFVPPG--	-LSSEGLHTS	VYAWLAFLSF	SYTAQFHPEI	FGIGNVSRVY	VDIKHFICA	VHDGKNATLP	156
NVSLD.....D.....S.....S.....S.....S.....S.....S.....	
P129G.D.....EE.....S.....S.....S.....S.....S.....S.....	
VR23E.D.....EE.....S.....S.....S.....S.....S.....S.....	
SDSUG.D.....EE.....S.....S.....S.....S.....S.....S.....	
KS06G.....EE.....A.....A.....A.....A.....A.....A.....	
LVE.R.....ELMSI.S.YDN.KL.Y--A.....LA.....LA.....LA.....LA.....L	
	180	200		220		240			
KS62	RHDNISAVYQ	TYYLHQVDGG	NWFHLEWLRP	FFSSWLVLNV	SWFLRRSPAS	HVSQVFRS	KPTQPQHQAAL	LSSKTSAAALG	236
NVSLF.....Q.....Q.....Q.....Q.....Q.....Q.....Q.....	
P129F.....Q.....Q.....Q.....Q.....Q.....Q.....Q.....	
VR23F.....Q.....Q.....Q.....Q.....Q.....Q.....Q.....	
SDSUF.....Q.....Q.....Q.....Q.....Q.....Q.....Q.....	
KS06H.....T.....Q.....Q.....Q.....Q.....Q.....Q.....Q.....	
LVTGH.....L.AA.H.I.....L.....L.....L.....L.....L.....L.....	
	260								
KS62	MA-----	TRPLRR	FAKALSAARR	* 255					
NVSL					
P129F.....N.....					
VR23I.....S.....V.....					
SDSUI.....S.....V.....					
KS06VN.....					
LVLTGSQQRKRKFPSES..NVVKPSV.PSTS	266				

a. (14)

b. (13)

c. (12)

D. GP4

	20	40	60	80
KS62	MVAPLLFLLV	GFKCFLVSQA	FACKPCFSSS	LSDIKTNTTA
NVSL	.A.	.	.	.
P129	.A.S.	.V.	.	.
KS06	.ATS.	.EH.	.	T
VR23	.ASS.	.V.	.A.	.AS.A.
SDSU	.A.S.	.M.	.L.	.A.
LV	.A.AT.F.A	.AQHIM.E	.TH	.E.
	100	120	140	160
KS62	VYITVTANVT	DENYLHSSDL	LMLSSCLFYA	SEMSEKGFKV
NVSL
P129	.I.	.	.	.
KS06	.I.	.	.	.
VR23	.V.I.	.	.	.
SDSU	.I.	.	.	.
LV	Q.I.	S.YNA.	A.	I.V.S
	180			
KS62	FMPETMRWA	TVLACFLAIL	LAI * 179	
NVSL	.	.F.	.	179
P129	.	.LF.	.	179
KS06	.	.LF.	.	179
VR23	.	.LF.	.	179
SDSU	.	.LF.	.	179
LV	.L.SA.	.TI.LF.	.	184

E. 5a protein

	20	40	
KS62	MFKYVGEMLD	RGLLLAIAFF	VVYRAVLFCC
NVSL	.	.	.I.
VR23	.	.	.R.
SDSU	.	.	.H.
P129	.	.	.
KS06	.	.	.S.
LV	.SQI.AF.	SA.LV.	A.L.VL.

b. (17)

F. GP5

	20	40	60	80
KS62	M-----LGRC	LTAGCCSRLL	SLWCI-VPFC	FAVLVNASSN
NVSLA.N.
P129	.K.	.	.GS.N.S	.F.
VR23	.EK.	.Y.Q.	.	.ND.
SDSU	.K.	.	.T.D.NG.	.
KS06	.VK.	.	.F.L.G.A	.NG.
LV	.RCSHK.F	.PHS.FWW	.F.L.TGLSWS	.DNGND
	100	120	140	160
KS62	HIVSYGALTT	SHFLDTVGLV	TVSTAGFYHG	RYVLSSIIYAV
NVSL
P129
VR23	.	.A.	.V.	.
SDSU	.	.IA.	.L.	.
KS06	.	.F.	.F.	.FA.G
LV	.L.L.F.	.F.AL.G	.A.VG.	.C.V.GA
	180	200		
KS62	WRSPVIEKG	GKVEVEGHLI	DLKRVVLDGS	VATPLTRVSA
NVSL
P129
VR23	.R	.	.	.P
SDSU	.R	.	.	.P
KS06	.	.	.A.	.
LV	.K.IVV.L	.A.D.N.V	.TI.H.E.V	.K.Q.T.

G. M protein

	20	40	60	80
KS62	MGSLLDDFCY	DSTAPQKVLL	AFSITYTPVM	IYALKVSRGR
NVSLLLGLLHLLIF
VR23	.H	.	.	.A.
SDSU	.H	.A.	.	.A.
P129	.H	.	.	.A.
KS06	.N	.	.	.A.
LV	.G.N	.PIA.LV	.	.I.
	100	120	140	160
KS62	LLWGVYSAIE	TWKFITSRCR	LCLLGRKYIL	APAHHVESAA
NVSL
VR23
SDSU
P129
KS06	.	.	.R.	.
LV	.FT	S.	.C.R.	.L.S.S.SG.

KS62	AVKQGVNVLV	KYAK * 175
NVSL	.	175
VR23	.	175
SDSU	.	175
P129	.	175
KS06	.	175
LV	.R.	.GR. 174

Supplementary Figure 1. Peptide sequence alignment of PRRSV isolates incorporated in this study. The alignment of (A) GP2, (B) E protein, (C) GP3, (D) GP4, (E) GP5, (F) 5a protein, and M protein (F) are shown for the seven viruses listed in Table 1. Peptide sequences were aligned using CLC Main Workbench version 6.6.2 (CLC bio). Previously characterized neutralizing epitopes are over-lined and identified by lower case letters with the corresponding reference(s) in parenthesis. Epitopes are shown for both Type 1 and Type 2 genotype viruses.