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The N-terminal domain of N^{pro} of classical swine fever virus determines its stability and regulates type I interferon production

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23 **Fig. S1. Phylogenetic analysis of CSFVs isolated in Thailand on the basis of the nucleotide**
24 **sequence of E2**

25 Phylogenetic tree of E2 (1119 bp) of CSFVs were constructed using the maximum-likelihood method,
26 and genotypes of four CSFVs isolated in Thailand were characterised. Gene accession numbers are
27 as follows: Shimen-HVRI, AY775178; JL1-06, EU497410; SWH, AY805221; GPE⁻, D49533; ALD,
28 D49532; Alfort/187, X87939; CAP, X96550; Eystrup, AF326963; Koslov, HM237795; India,
29 EU857642; China/2004, AY805221; Riems, AY259122; Brescia, AF091661; CS, AF099102,
30 Malaysia/1986, JQ411570; 0406/CH/01/TWN, AY568569; SXYL2006, GQ122383; Lithuania/2009,
31 JQ411591; SXCDK, GQ923951; Italy/1998, JQ411579; Czech Republic/1994, JQ411587;
32 Germany/1998, JQ411581; Germany/2009, GU233733; Alfort/Tübingen, J04358; Spain/2001,
33 JQ411585; Croatia/2006, JQ411586; Hungary/2007, JQ411589 and Kanagawa/74, JQ411571.
34 Horizontal distances are proportional to the minimum number of nucleotide differences required to
35 join node and sequences. The numbers on the branches indicate the bootstrap values (in percent;
36 1,000 replicates). The grey highlights indicate CSFVs isolated in Thailand.

37 **Fig. S2. Distribution of the amino acid residues responsible for the suppression of type I**
38 **interferon induction**

39 Three of five candidate amino acid residues responsible for the suppression of type I interferon
40 induction were plotted on N^{pro} as yellow spheres with the 3D structure of N^{pro}, (lacking amino acids
41 1-16) as determined by Gottipati *et al.* (2013), with the accession number 4H9J. Amino acid residues
42 at positions 112, 134, 136 and 138 on the TRASH domain of N^{pro} plotted as violet spheres were
43 demonstrated to be responsible for this function in previous studies (Ruggli *et al.*, 2009; Szymanski
44 *et al.*, 2009).

45

46 **Fig. S3. Detection of IRF3 in cells inoculated with CSFV with the proteasome inhibitor**

47 SK-L cells were inoculated with the viruses vA187-1, vA187-N^{pro}(KPP)/L40H and
48 vA187-N^{pro}(KPP)/S17P; N61K with or without the proteasome inhibitor MG-132. The cells were lysed
49 at 60 and 120 hpi. IRF-3 was detected with the monoclonal antibody against porcine IRF3 (34/1).

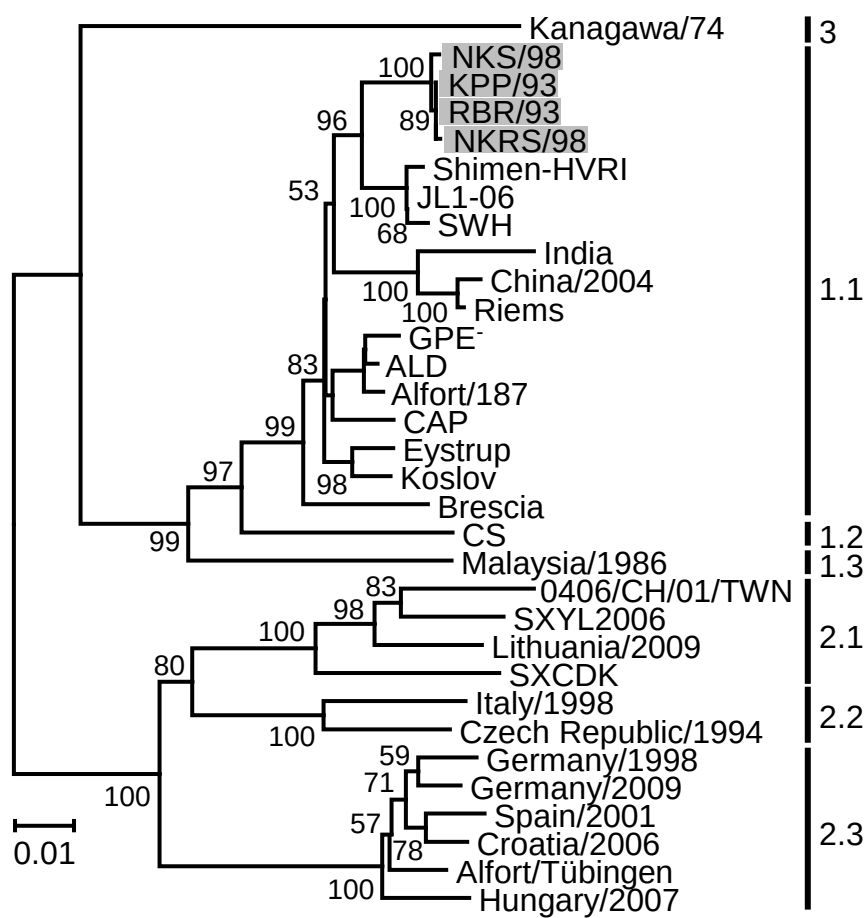


Figure S1, Mine *et al.*

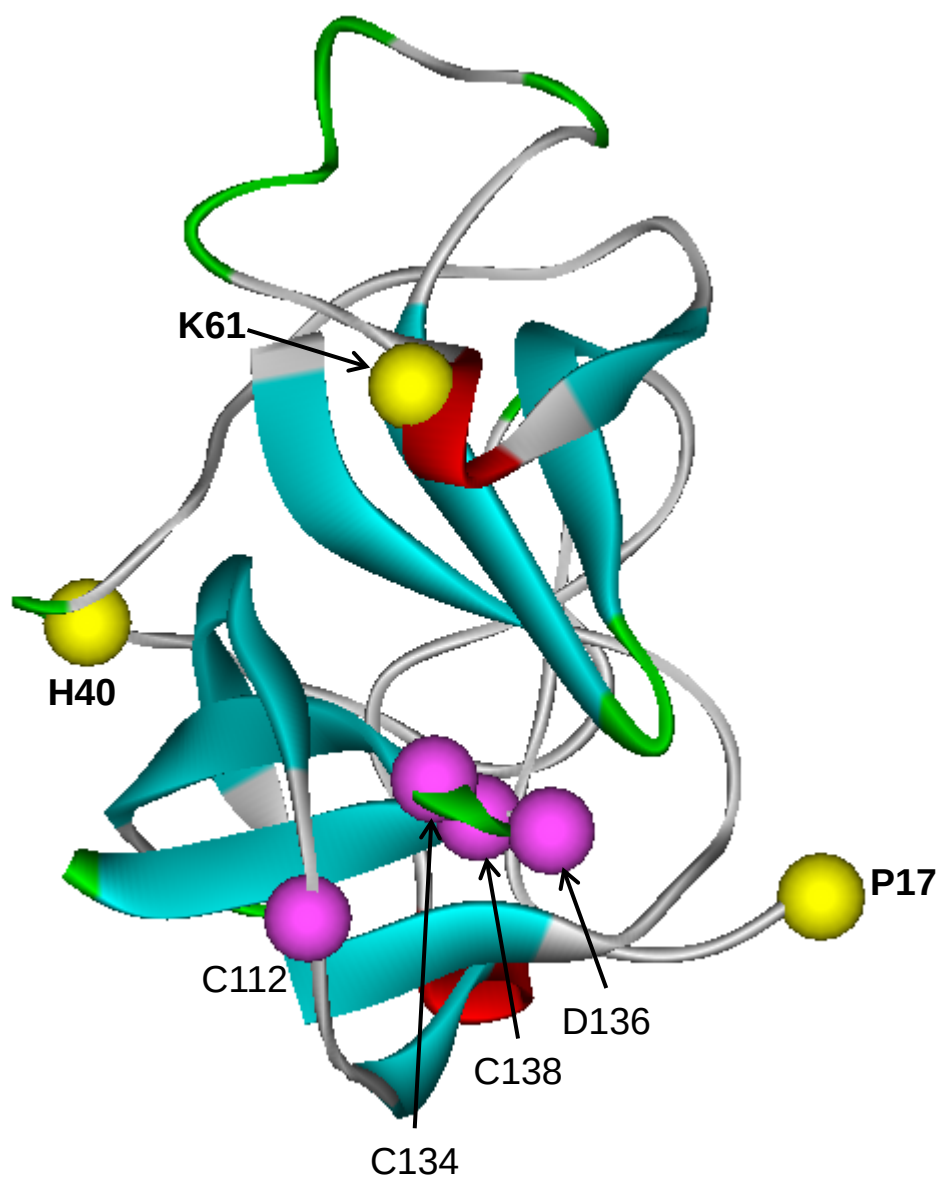


Figure S2, Mine *et al.*

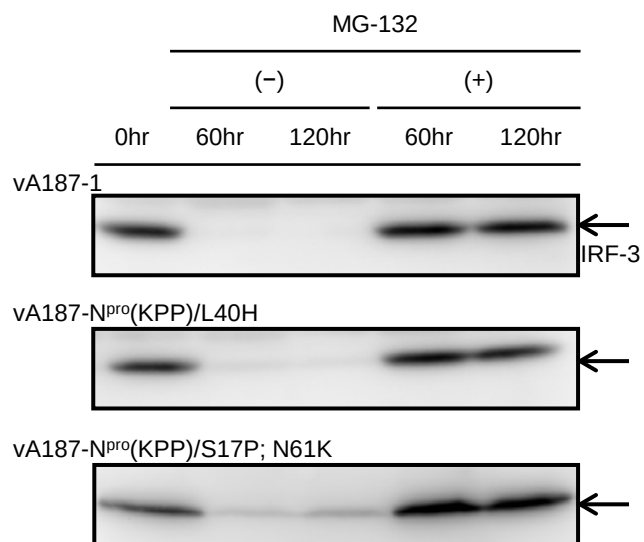


Figure S3, Mine *et al.*