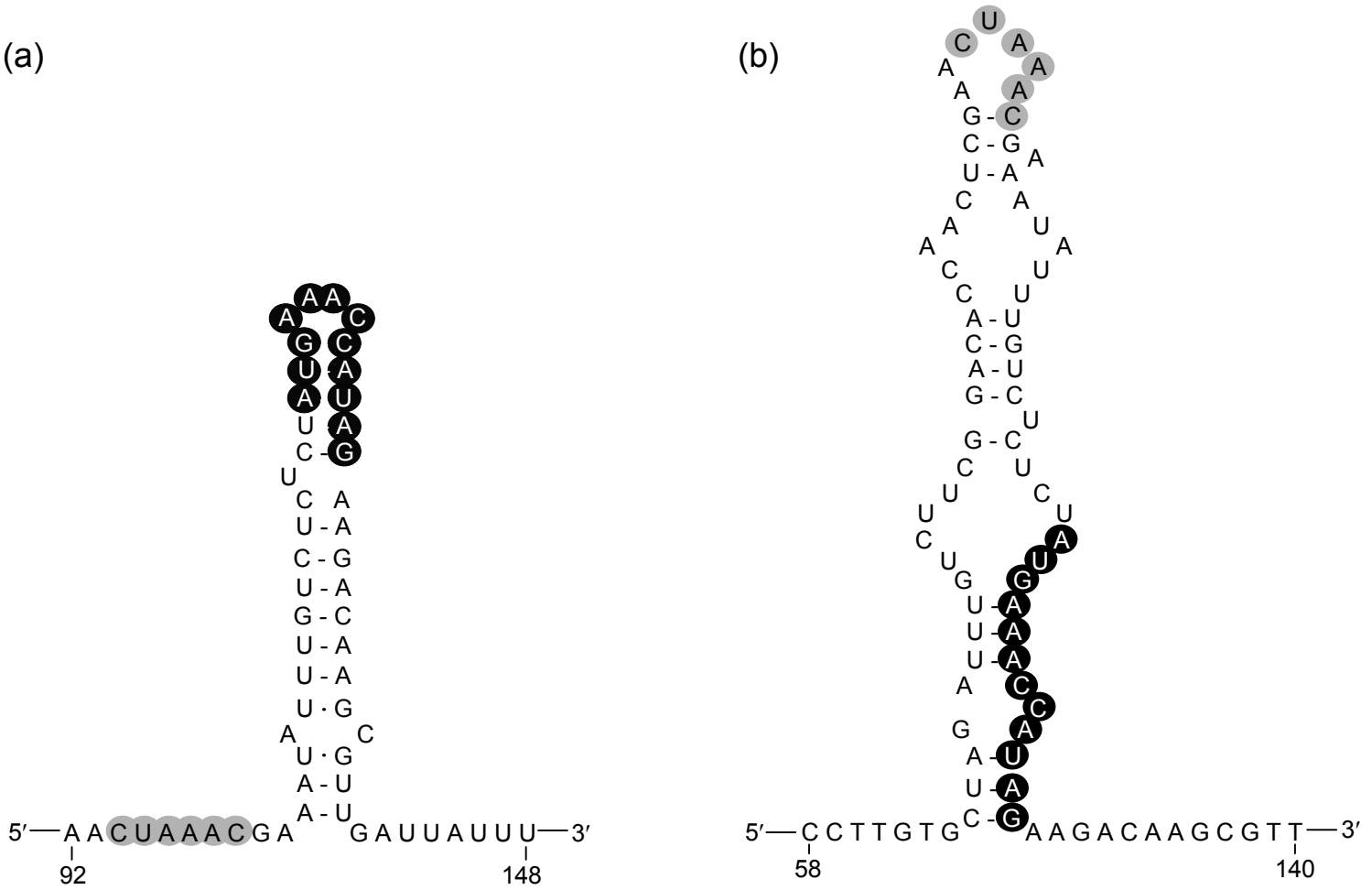
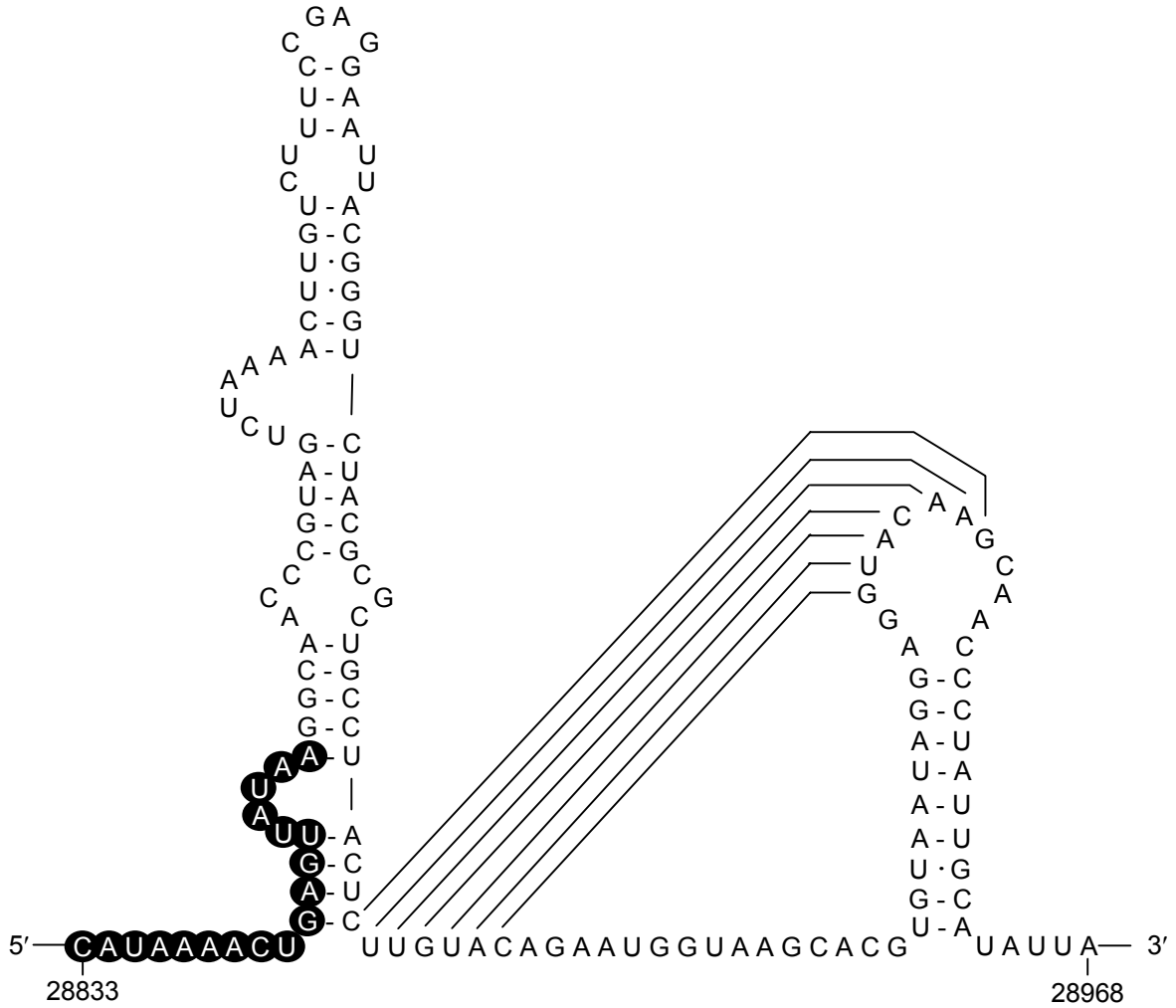
Supplementary Fig. S1. Models of the FIPV WSU-79/1146 RNA 5′ UTR *cis*-acting elements. The putative 5′ UTR stem–loop structure (nt 102–140) (a) and the putative leader–TRS hairpin (nt 65–128) (b) are shown. Nucleotides that comprise the ‘core’ TRS motif (5′-CUAAAC-3′) are highlighted with a grey background and nucleotides that comprise the four-codon ‘mini-ORF’ are highlighted with a black background.



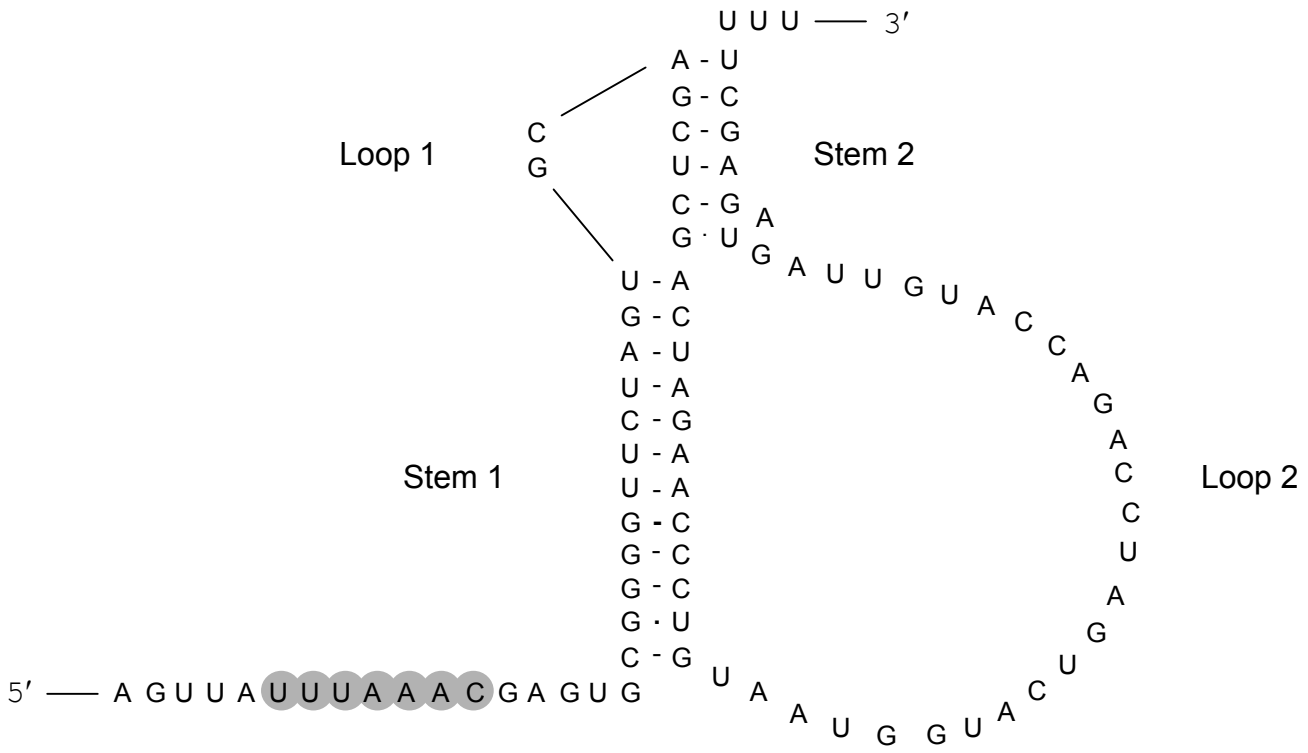
Dye, C. & Siddell, S. G. (2005). Genomic RNA sequence of *Feline coronavirus* strain FIPV WSU-79/1146. *J Gen Virol* **86**, 2249–2253.

Supplementary Fig. S2. Model of the FIPV WSU-79/1146 RNA 3′ UTR *cis*-acting element. The putative 3′ UTR bulged stem–loop–pseudoknot structure (nt 28842–28964) is shown. Nucleotides that comprise the last six codons of the predicted ORF 7b are highlighted with a black background.



Dye, C. & Siddell, S. G. (2005). Genomic RNA sequence of *Feline coronavirus* strain FIPV WSU-79/1146. *J Gen Virol* **86**, 2249–2253.

Supplementary Fig. S3. We are indebted to Dr Ian Brierley (University of Cambridge, UK) for indicating that, as depicted below, the structure of the FIPV WSU-79/1146 frameshifting element is likely to correspond to the proposed structure of the group II and group III coronaviruses. The nucleotides that comprise the 'slip site' are highlighted with a grey background.



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Supplementary Table S1. List of oligonucleotide primers used for RT-PCR amplification of FIPV WSU-79/1146 RNA

Genomic or intracellular poly(A)-containing viral RNA was reverse-transcribed by using Superscript II RNase H^- reverse transcriptase (Invitrogen) and gene-specific priming under standard conditions. PCR amplification of genomic fragments was done by using 2 μl cDNA template from the RT reaction, Platinum PCR Supermix High Fidelity (Invitrogen) and PCR primers that were incubated for 2 min at 94 °C, followed by 35 cycles of 94 °C for 30 s, 55 °C for 30 s and 68 °C for 1 min (kb PCR product)$^{-1}$. PCR amplification of subgenome length mRNA 5′ ends was done by using 2 μl cDNA template from the RT reaction, recombinant *Taq* DNA polymerase and primers that were incubated for 2 min at 94 °C, followed by 35 cycles of 94 °C for 15 s, 56 °C for 30 s and 72 °C for 1 min, with a final incubation for 7 min at 72 °C. The 5′-terminal sequence of genomic viral RNA was determined by 5′-RACE (rapid amplification of cDNA ends). Briefly, a preparation of genomic RNA was dephosphorylated and the RNA cap structure was removed by incubation with tobacco acid pyrophosphatase. The RNA oligonucleotide (5′-CGACUGGAGCACGAGGACACUGACAUGGACUGAAGGAGUAGAAA-3′) was ligated to 5′-phosphorylated RNA, which was then recovered by phenol/chloroform extraction and ethanol precipitation. This RNA was used as a template for RT-PCR with appropriate primers and the conditions described above for genomic RNA. NA, Not applicable; N = A, C, G or T.

Name	Use	Sequence (5′–3′)	Position
CJ01	RT primer for 3′ RACE	TGTTGGAGGGTAATGGGGTTGAAT$_{23}$NN	29124 and 29125 + poly(A) tail
CJ28	RT primer for 5′ RACE	CAAAGAATGCACTATCAAGACC	1827–1848
CJ04	Forward PCR primer for fragment I	TATAAGGCAACCCGATGTCTAAAA	28844–28869
CJ02	Reverse PCR primer for fragment I	TGTTGGAGGGTAATGGGGTTGAA	NA
CJ05	Forward PCR primer for fragment H	AGTCCTGCTTTGATGGTGGTG	26096–26116
CJ03	RT primer and reverse PCR primer for fragment H	TCATAGCGGATCTTTAAACTTCTC	29012–29035
CJ07	Forward PCR primer for fragment G	TACTGGTGGTTACGACATAGC	23166–23186
CJ06	Reverse PCR primer for fragment G	GCCATAATAGCCACATAATAAGC	26135–26157
CJ09	Forward PCR primer for fragment F	TCGGCTTATAGGGATGATGTG	20560–20580
CJ08	Reverse PCR primer for fragment F	TTTAGCAACAGTGGCAAGACC	23488–23508
CJ11	Forward PCR primer for fragment E	ATGCAGGCTGGCTTTACGATA	18203–18223
CJ10	RT primer and reverse PCR primer for fragment E	TTGTCCGTGGGTATGACAGAGAAAGG	20701–20726
CJ13	Forward PCR primer for fragment D	GTAGTAGCAGCATTGATGAAGAATTTG	14337–14363

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Supplementary Table S1. cont.

Name	Use	Sequence (5′–3′)	Position
CJ12	Reverse PCR primer for fragment D	AACGACATTAAAAGCCACATT	18299–18319
CJ15	Forward PCR primer for fragment C	ATGCGTTTTTGGGTGTTGTGTCTG	9001–9024
CJ14	RT primer and reverse PCR primer for fragment C	CAAATTCTTCATCAATGCTGCTACTAC	14337–14363
CJ17	Forward PCR primer for fragment B	GAGGCTAAGTGCTTTGTGCTTGGTTCTAA	1731–1759
CJ16	RT primer and reverse PCR primer for fragment B	CTGGCCTCACGGATTTAAATTTATGTTCTGG	9081–9111
CJ19	Forward PCR primer for fragment A	CGACTGGAGCACGAGGACACTGACAT	NA
CJ18	Reverse PCR primer for fragment A	CACCATCCTTAAGCGCTCTGAAACACAAC	2210–2238
CJ20	Forward PCR primer for mRNA PCR	TGAGGGTGGCGTGGCTATAACTC	16–38
CJ21	RT and reverse primer for mRNA 1 PCR	ACATGACGGAAGGTTCGGTAAGGAGA	536–561
CJ22	RT and reverse primer for mRNA 2 PCR	TAACCACCAACAACTACACTTCCTTCTTC	20353–20381
CJ23	RT and reverse primer for mRNA 3 PCR	AACAACTGTATGACTATTGACTTCTTCA	24816–24843
CJ24	RT and reverse primer for mRNA 4 PCR	TAGTCTTACCCAAATTGCAACATACCA	25852–25878
CJ25	RT and reverse primer for mRNA 5 PCR	AGCCGAACATTACATATCTGGAAACTTG	26302–26329
CJ26	RT and reverse primer for mRNA 6 PCR	CCTTACGCTGGCCTTTTACAATACGATA	27007–27034
CJ27	RT and reverse primer for mRNA 7 PCR	AATCAAGGCAGTCTGGTTTCAA	28088–28109

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Supplementary Table S2. FIPV WSU-79/1146 genomic ORFs and encoded non-structural and structural proteins

ORF (nucleotide positions)	Translation product (aa)	Amino acid identity (%)			
		TGEV	HCoV-229E	MHV	IBV
ORF1a (312–12209)	Polyprotein 1a (3965)	88·1	51·5	34·7	33·2
ORF1ab (312–20209)	Polyprotein 1ab (6632)	91·5	58·1	41·1	39·8
ORF S (20206–24564)	Spike glycoprotein (1452)	94·8	49·8	30·0	33·5
ORF E (25722–25970)	Envelope protein (82)	74·7	28·2	29·2	21·1
ORF M (25981–26769)	Membrane protein (262)	85·5	46·4	37·8	26·8
ORF N (26782–27915)	Nucleocapsid protein (377)	76·2	39·1	26·0	24·5

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Supplementary Table S3. Main features of FIPV WSU-79/1146 structural proteins

N-Glyc, *N*-Glycosylation sites; *O*-Glyc, *O*-glycosylation sites. Potential glycosylation sites were identified with NetNGlyc and NetOGlyc (http://www.cbs.dtu.dk/).

Protein	Glycosylation (predicted sites)	Feature		
		Domain	Position	Reference
Spike protein	Yes	Signal peptide	1Met–Ser19	de Groot *et al.* (1987)
	N-Glyc, 35	Ectodomain	20Thr–Pro1393	de Groot *et al.* (1987)
	O-Glyc 1	Transmembrane domain	1394Trp–Cys1414	de Groot *et al.* (1987)
		Endodomain	1415Cys–His1452	de Groot *et al.* (1987)
		Heptad-repeat region 1	1014Pro–Thr1156	Bosch *et al.* (2004)
		Heptad-repeat region 2	1308Pro–Val1390	Bosch *et al.* (2004)
		Putative fusion peptide	1022Ala–Gln1047	Bosch *et al.* (2004)
Envelope protein	No	Signal anchor sequence	13His–Ile40	This paper
Membrane protein	Yes	Signal peptide	1Met–Gly17	Vennema *et al.* (1991)
	N-Glyc, 3	Ectodomain	18Glu–Ser57	Vennema *et al.* (1991)
		Membrane-spanning domain 1	58Trp–Ser77	Vennema *et al.* (1991)
		Membrane-spanning domain 2	83Ile–Tyr104	Vennema *et al.* (1991)
		Membrane-spanning domain 3	114Met–Val134	Vennema *et al.* (1991)
		Endodomain	135Arg–Val262	Vennema *et al.* (1991)
Nucleocapsid protein	No	Basic domain 1	153Val–Asn183	Laude & Masters (1995)
		Basic domain 2	203Thr–Gly240	Laude & Masters (1995)
		Acidic domain	350Glu–Asn377	Laude & Masters (1995)

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