Plasmid	TOSV genomic segment end	Sequence (5' -> 3')
pUC57-L	T7 promotor – 3'UTR – ATG	TAATACGACTCACTATAGACACAAAGAGGCCCAAATATG
	TAA – 5′UTR – HδV ribozyme	TAA CAACTTTGACACTTAGAGAAACTAAGAAGGATAAAG GGTTAGGGGGGGTGTTCCTTTGTTATGTCTATAAATTATT TAAGAATTGGGCGGTCTTTGTGTGGGGTCGGCATGGCAT
pCC1-M	T7 promotor – 3'UTR – ATG	TAATACGACTCACTATAGACACAAAGAAGGTGCTT ATG
	TAA – 5′UTR – HδV ribozyme	TAA AATAATCCATCTTCTTTCTATTATTCTCATGTATCTTTCACTCAGGGTTTAGGGGGGGGGGGGGGGGGGGGGGGG
pUC57-S	T7 promotor – 3'UTR – ATG	TAATACGACTCACTATAGACACAGAGATTCCCGTGTATT AATCAAAAGCTATCAAC ATG
	TAA – 5′UTR – HδV ribozyme	CAT GGCTGTCTAGAAGTCTATTATTAGTTCTGGTTTAGC GATACGGGAGGTCTTTGTGTGGGGTCGGCATGGCAT

Figure S1. Sequences of the 3' and 5' ends of the TOSV genomic segments, flanked by the T7 polymerase promotor (T7 promotor) and the H δ V ribozyme respectively. T7 polymerase promotor and H δ V ribozyme appear in black and TOSV genome sequences in blue. The authentic ATG (or CAT) start codons and the UAA stop codons appear in blue bold. UTR, untranslated terminal region.

	1	
NSs	ATG CAATCCAGAGCTGTCATTCTGAAGCACAAGTCTGGTTCAAGCCATAAGAGGTCTTTG	60
b NSs	TAGCAATCCAGAGCTGTCATTCTGAAGCACAAGTCTGGTTCAAGCCATAAGAGGTCTTTG	60
NSG	ჇჇႥჾჇႺႥჾჇჾჾჇჾჇჾჇႦჇႦჇႦჇႦჇႦჇႦჇႦჇႦჇႦჇႦჇႦႦႦႦႦႦႦႦႦႦ	120
		120
φnss	CCIAGGIICIACAIAGACIGIGACCIGGACACCIIIGAIIIIGAAAAAGGACIGCICIIIA	ΤΖU
	2 3	
NSs	ATCGAGA ATG AGTTCCCTATTTACATAAAAAATT ATG AGGTAGTATACAAGTCAAGACCA	180
¢NSs	ATCGAGA TAG AGTTCCCTATTTACATAAAAAATT TAG AGGTAGTATACAAGTCAAGACCA	180
	4 5	
NSs	ACTCTTTCACACTTCCTCATAA ATG GAGAATTCCCTGCAGTTCTGGGACCAGGT ATG ATC	240
¢ NSs	ACTCTTTCACACTTCCTCATAA TAG GAGAATTCCCTGCAGTTCTGGGACCAGGT TAG ATC	240
•		
NSs	₀ AGTGCTGTTCGAACTAGACTTT <mark>ATG</mark> AGCCAACAATAAGGGAGCTTTACCAGGAATCTATT	300
ANG a		300
φιιδε	AGIGCIGIICGAACIAGACIIIIAGAGCCAACAAIAAGGGAGCIIIACCAGGAAICIAII	300
110		200
NSS	CATCAGCTAAAAAGGAGCAATAAGAAATATCTCTTGTCTGCCCTCAG ATG GCCAACAGGA	360
¢NSs	CATCAGCTAAAAAGGAGCAATAAGAAATATCTCTTGTCTGCCCTCAG TAG GCCAACAGGA	360
NSs	ATCCCCTCTTTGAGTTCATAGATTACTATTTCGAGGAGCTCCTGTTCTTGTCCGAGTTT	420
¢NSs	ATCCCCTCTCTTGAGTTCATAGATTACTATTTCGAGGAGCTCCTGTTCTTGTCCGAGTTT	420
NSs	GATCCAGGATCTATTCAGAGATATCTCAAATTACTGGTCAAGGCTTCTGGACTCTACTGT	480
μN23	ϲͽͲϲϲͽϲϲͻͲϲͲͽͲϲͽϲͽϲͽͲͽͲϲͲϲͽͽͽͲͲͽϲͲϲϲͲϲͽͽδϲϲϲͲͲϲͲϲϲͽϲͲϲͲ	480
Ψισσ		100
NCa		E10
		540
φNSS	TCAACCATTGAGGAGCAAATAGTGGAAATTCATAGGAGGGTTCTCCTAGAAGGCAAGAAG	540
	8 9 10	
NSs	C ATG GATTAACTGCTTTTGACCTCCCAGGAA ATG ACATCCTCGGAGACAT ATG TGTGGTT	600
¢ NSs	CTAGGATTAACTGCTTTTGACCTCCCAGGAATAGACATCCTCGGAGACATTAGTGTGGTT	600
	11	
NSs	CAAGCAGCACGGGTGACTAAATTGGTTGCAAAGGCATTTTCTAGA ATG ACCAGAGACTCC	660
¢ NSs	CAAGCAGCACGGGTGACTAAATTGGTTGCAAAGGCATTTTCTAGA TA GACCAGAGACTCC	660
	12	
NSs		720
μN23	ĊͽͽĊͲĊ ͲͽĊ ͽͲͽͲͽĊͲͲͲϔĊͽͽͲͽͽĊĊĊĊͽĊͲϲϨͽͽͲͲͽĊͲϔĊͽĊĊͽͽĊĊͲϔĊͽͲͽĊĊ	720
φιιδδ		120
NC~		700
NSS	AAAGATGACAAGAAGGCIAAGGCAAAGGGIIIACTAICAATGAGIGCIGCCAAGICIIAT	780
φNSs	AAAG TA GACAAGAAGGC'I'AAGGCAAAGGG'I''I''I'AC'I'AI'CA TAG AG'I'GC'I'GCCAAG'I'C'I''I 'TA	780
	16	
NSs	GACTACTTCATGAAAACAGACCTGAGATTTAGAGAAACTGCTCTTTCCACCTTCTGGGCT	840
¢NSs	G ACTACTTC TAG AAAACAGACCTGAGATTTAGAGAAACTGCTCTTTCCACCTTCTGGGCT	840
	17 18	
NSs	AAAGATTGGCCCACAATACATGAGTCTGTGCTGTCTAATAGACGATGCCCTAAGGAAGAC	900
d NSs	AAAGATTGGCCCACAATAC TAG AGTCTGTGCTGTCTAATAGACG TAG CCCTAAGGAAGAC	900
1		
NSG	ΔΑGAGAGTGACAAAGTGGCTGCCTAGTCCCCCCCCCCCCCC	
$\varphi_{IV} \supset \Box$	ATUAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU	

Figure S2. Nucleotide sequence alignment of TOSV NSs (H4906) strain and the derived mutant ϕ NSs, the 18 first ATG codons of which were replaced by TAG stop codons. The blue numbers indicate the ATG codons that have been mutated in the ϕ NSs sequence. ATG codons appear in bold red in the wild type NSs sequence when they have been replaced by TAG stop codons, which appear in bold green in the ϕ NSs sequence.



