

Sample	Nucleotide polymorphism			Amino acid polymorphism		
	Reference VPg	SNP	Position	Reference VPg	AA substitution	Position
wild-type 1	A	R (A or G)	338	D (GAC)	G (GGC)	113
wild-type 2						
wild-type 3						
wild-type 4						
wild-type 5	A	R (A or G)	358	N (AAU)	D (GAU)	120
wild-type 6	C	Y (C or U)	341	S (UCA)	L (UUA)	114
<i>eif4e1^{KO}</i> 1						
<i>eif4e1^{KO}</i> 2						
<i>eif4e1^{KO}</i> 3						
<i>eif4e1^{KO}</i> 4						
<i>eif4e1^{KO}</i> 5						
<i>eif4e1^{KO}</i> 6	A	R (A or G)	358	N (AAU)	D (GAU)	120
<i>eif4e1^{KO}</i> 7	A	R (A or G)	310	M (AUG)	V (GUG)	104
<i>eif4e1^{KO}</i> 8						
<i>eif4e1^{KO}</i> 9	C	Y (C or U)	341	S (UCA)	L (UUA)	114
<i>eif4e1^{KO}</i> 10	A	M (A or C)	344	N (AAU)	T (ACU)	115

Supplementary table 1. Recapitulative table of detected single nucleotide polymorphisms (SNP) at the TuMV VPg coding sequence and the associated amino acid substitutions at relative to the reference TuMV-GFP UK1 VPg sequence (GenBank ID: EF028235.1) obtained from six wild-type and ten *eif4e1^{KO}* TuMV-GFP UK1-inoculated plants. The identical polymorphisms corresponding to the amino acid substitutions N120G and S114L observed in TuMV VPg sequences obtained from both wild-type and *eif4e1^{KO}* plants are highlighted in green and blue, respectively.