

Table 1 Suppl. Primers used in this study. In the sequence of oligonucleotides used for the site directed mutagenesis mutations are highlighted in bold. Restriction sites (SacI and BamHI) are typed in bold in the oligonucleotide sequences (for - forward, rev - reverse).

Name of the oligomer	Nucleotide sequence (5' - 3')
TSWV NSs BiFC for	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGTCTTCAAGTGTTCATGAGTCGA
TSWV NSs BiFC rev	GGGGACCACTTTGTACAAGAAAGCTGGGTCGTGATGGTGATGGTGATGTTTTGATCCTGA
TSWV R337A for	ATGATCCTTCATATCCTCAGGCGATTGTTTCATGCTCTGCTTGA
TSWV R337A rev	TCAAGCAGAGCATGAACAATCGCCTGAGGATATGAAGGATCAT
TSWV H340A for	CATATCCTCAGAGGATTGTTGCTGCTCTGCTTGAAACTCACAC
TSWV H340A rev	TTGTGAGTTTCAAGCAGAGCAGCAACAATCCTCTGAGGATATG
TSWV E344A for	GGATTGTTTCATGCTCTGCTTGCAACTCACACATCTTTGCACA
TSWV E344A rev	TGTGCAAAAGATGTGTGAGTTGCAAGCAGAGCATGAACAATCC
TSWV NSs SacI for	GGGAGCTCAGAGCAATTGTGTCATAATTTTATTCTTAATCAAACCT
TSWV NSs BamHI rev	GGGGATCCGGACATAGCAAGAATTATTTGATCCTGAAGCATATG
GFP real-time for	AGTGGAGAGGGTGAAGGTGATG
GFP real-time rev	TGATCTGGGTATCTTGAAAAGC
BiFC real-time for	GCTGTTGTAGATTCTTACTGGATT
BiFC real-time rev	TCACAGGGAAGATTCCCTACC
EF1 α for	TGGTGTCTCAAGCCTGGTATGGTTG
EF1 α rev	ACGCTTGAGATCCTTAACCGCAACATTCTT

A

ANOVA					
VAR00002					
	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	2,462	4	,615	3,647	,012
Within Groups	7,594	45	,169		
Total	10,055	49			

Multiple Comparisons							
Dependent Variable: VAR00002							
	(I) VAR00001	(J) VAR00001	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
Lower Bound							
Upper Bound							
Tukey HSD	P14	NSS	-.55280 [*]	,18371	,033	-1,0748	-.0308
		NSSR337A	-.34330	,18371	,349	-.8653	,1787
		NSSH340A	-.43750	,18371	,139	-.9595	,0845
		E344A	-.64150 [*]	,18371	,009	-1,1635	-.1195
	NSS	P14	,55280 [*]	,18371	,033	,0308	1,0748
		NSSR337A	,20950	,18371	,784	-.3125	,7315
		NSSH340A	,11530	,18371	,970	-.4067	,6373
		E344A	-.08870	,18371	,989	-.6107	,4333
	NSSR337A	P14	,34330	,18371	,349	-.1787	,8653
		NSS	-.20950	,18371	,784	-.7315	,3125
		NSSH340A	-.09420	,18371	,986	-.6162	,4278
		E344A	-.29820	,18371	,491	-.8202	,2238
	NSSH340A	P14	,43750	,18371	,139	-.0845	,9595
		NSS	-.11530	,18371	,970	-.6373	,4067
		NSSR337A	,09420	,18371	,986	-.4278	,6162
		E344A	-.20400	,18371	,800	-.7260	,3180
	E344A	P14	,64150 [*]	,18371	,009	,11635	1,1635
		NSS	,08870	,18371	,989	-.4333	,6107
		NSSR337A	,29820	,18371	,491	-.2238	,8202
		NSSH340A	,20400	,18371	,800	-.3180	,7260
Games-Howell	P14	NSS	-.55280 [*]	,16279	,039	-1,0818	-.0238
		NSSR337A	-.34330 [*]	,09971	,027	-.6539	-.0327
		NSSH340A	-.43750 [*]	,12055	,023	-.8203	-.0547
		E344A	-.64150	,20090	,058	-1,3015	,0185
	NSS	P14	,55280 [*]	,16279	,039	,0238	1,0818
		NSSR337A	,20950	,17833	,765	-.3453	,7643
		NSSH340A	,11530	,19077	,972	-.4681	,6987
		E344A	-.08870	,24944	,996	-.8469	,6695
	NSSR337A	P14	,34330 [*]	,09971	,027	,0327	,6539
		NSS	-.20950	,17833	,765	-.7643	,3453
		NSSH340A	-.09420	,14083	,961	-.5224	,3340
		E344A	-.29820	,21369	,641	-.9753	,3789
	NSSH340A	P14	,43750 [*]	,12055	,023	,0547	,8203
		NSS	-.11530	,19077	,972	-.6987	,4681
		NSSR337A	,09420	,14083	,961	-.3340	,5224
		E344A	-.20400	,22417	,888	-.9009	,4929
	E344A	P14	,64150	,20090	,058	-.0185	1,3015
		NSS	,08870	,24944	,996	-.6695	,8469
		NSSR337A	,29820	,21369	,641	-.3789	,9753
		NSSH340A	,20400	,22417	,888	-.4929	,9009

*. The mean difference is significant at the 0.05 level.

B

ANOVA					
VAR00002					
	Sum of Squares	df	Mean Square	F	Sig.
Between Groups	398,595	4	99,649	60,551	,000
Within Groups	41,143	25	1,646		
Total	439,738	29			

Multiple Comparisons							
Dependent Variable: Games-Howell							
	(I) VAR00001	(J) VAR00001	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
Lower Bound							
Upper Bound							
Games-Howell	P14	NSS	-.9167 [*]	0,23883	0,023	0,1248	1,7086
		NSSR337A	1,7883 [*]	0,34601	0,005	0,6080	2,9686
		NSSH340A	-2,2617 [*]	0,50155	0,019	-4,0929	-0,4304
		E344A	3,3883 [*]	0,37976	0,000	2,0693	4,7074
	NSS	P14	-.9167 [*]	0,23883	0,023	-1,7086	-0,1248
		NSSR337A	0,8717	0,32943	0,156	-0,2852	2,0286
		NSSH340A	-3,1783 [*]	0,49026	0,004	-5,0130	-1,3436
		E344A	2,4717 [*]	0,36472	0,002	1,1665	3,7769
	NSSR337A	P14	-1,7883 [*]	0,34601	0,005	-2,9686	-0,6080
		NSS	-0,8717	0,32943	0,156	-2,0286	0,2852
		NSSH340A	-4,0500 [*]	0,55049	0,000	-5,9294	-2,1706
		E344A	1,6000 [*]	0,44238	0,031	0,1397	3,0603
	NSSH340A	P14	2,2617 [*]	0,50155	0,019	0,4304	4,0929
		NSS	3,1783 [*]	0,49026	0,004	1,3436	5,0130
		NSSR337A	4,0500 [*]	0,55049	0,000	2,1706	5,9294
		E344A	5,6500 [*]	0,57230	0,000	3,7270	7,5730
	E344A	P14	-3,3883 [*]	0,37976	0,000	-4,7074	-2,0693
		NSS	-2,4717 [*]	0,36472	0,002	-3,7769	-1,1665
		NSSR337A	-1,6000 [*]	0,44238	0,031	-3,0603	-0,1397
		NSSH340A	-5,6500 [*]	0,57230	0,000	-7,5730	-3,7270

Based on observed means

*. The mean difference is significant at the 0.05 level.

Fig. 1 Suppl. A: Data of the statistical analysis of the electrolyte leakage experiment depicted in Fig. 3. B: Statistical analysis of the GFP mRNA accumulation depicted in Fig. 4.