Stability of Begomoviral pathogenicity determinant βC1 is modulated by mutually antagonistic SUMOylation and SIM interactions

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This file contains following information:

Additional File 1: Fig.S1-19

A)

Site	AA	Sequence	Type	P.S.
Ss1	**K18**	F I V D V **K** L M Q E D ←	INV. consensus	Low
Ss2	**K24**	K L M Q E D **K** I S V Q I ←	INV. consensus	High
Ss3	**K83**	T I G E F **K** Q E D M I E →	Consensus	Low

B)

Conserved SUMOylation sites

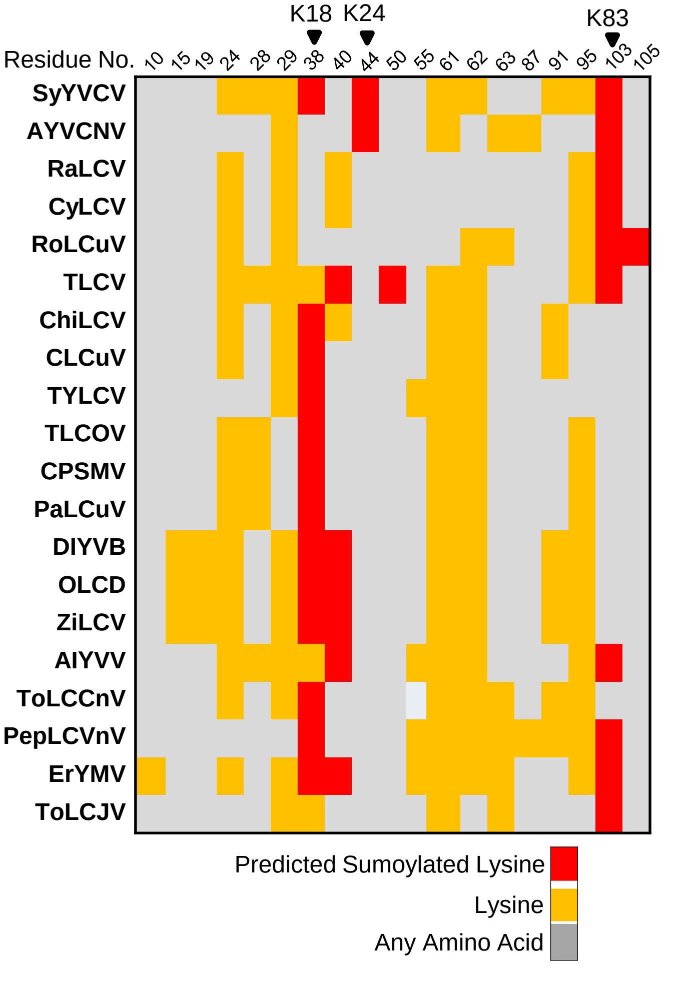


Fig.S1: SyYVCV βC1 has multiple conserved SUMOylation sites.

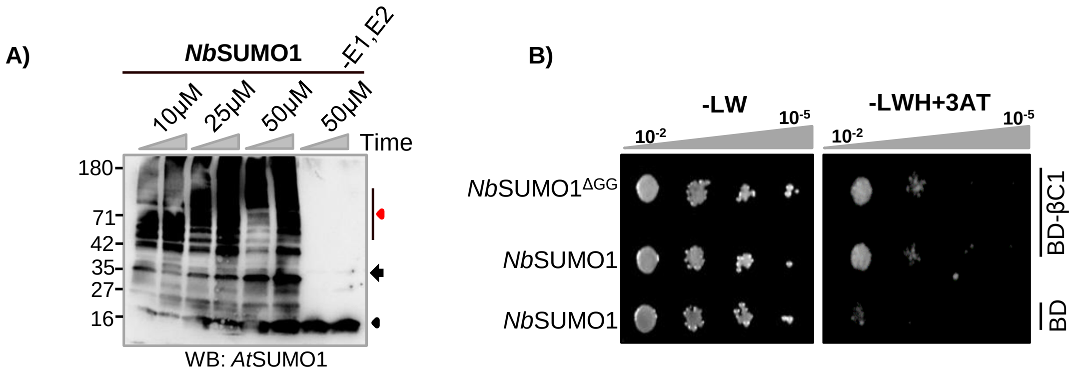


Fig.S2: SyYVCV βC1 can interact with *Nb*SUMO1.

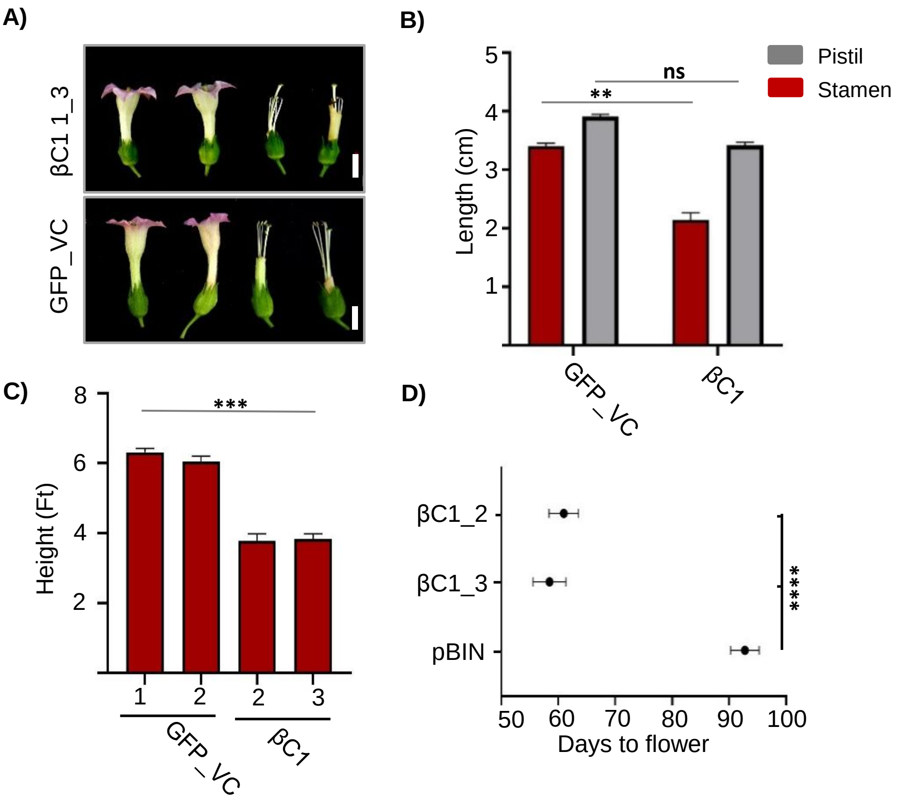


Fig.S3: SyYVCV βC1 induces various developmental defects in transgenic plants.

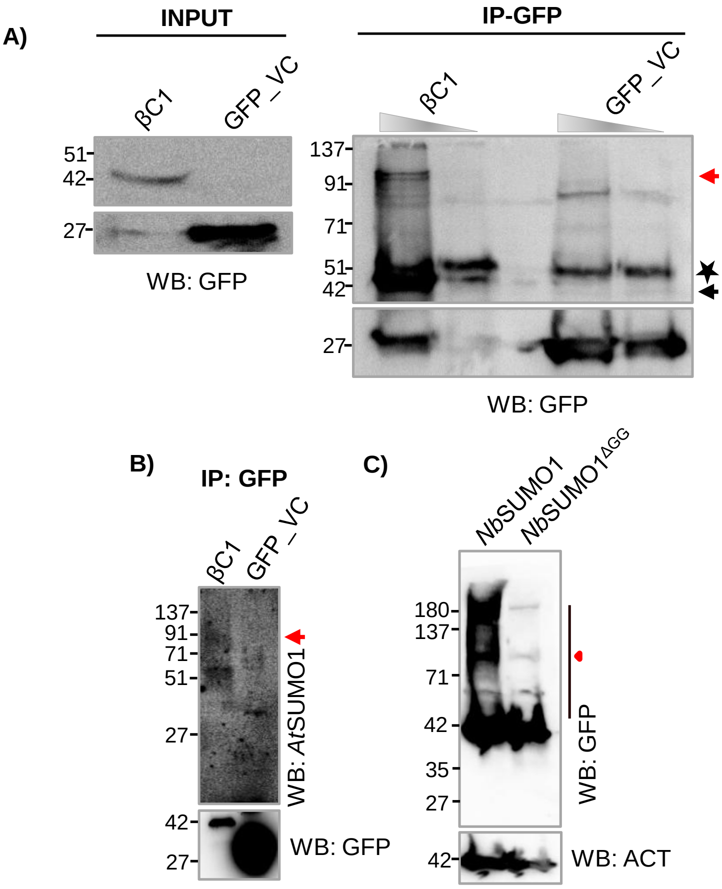


Fig.S4: SyYVCV βC1 undergoes SUMOylation *in planta*.

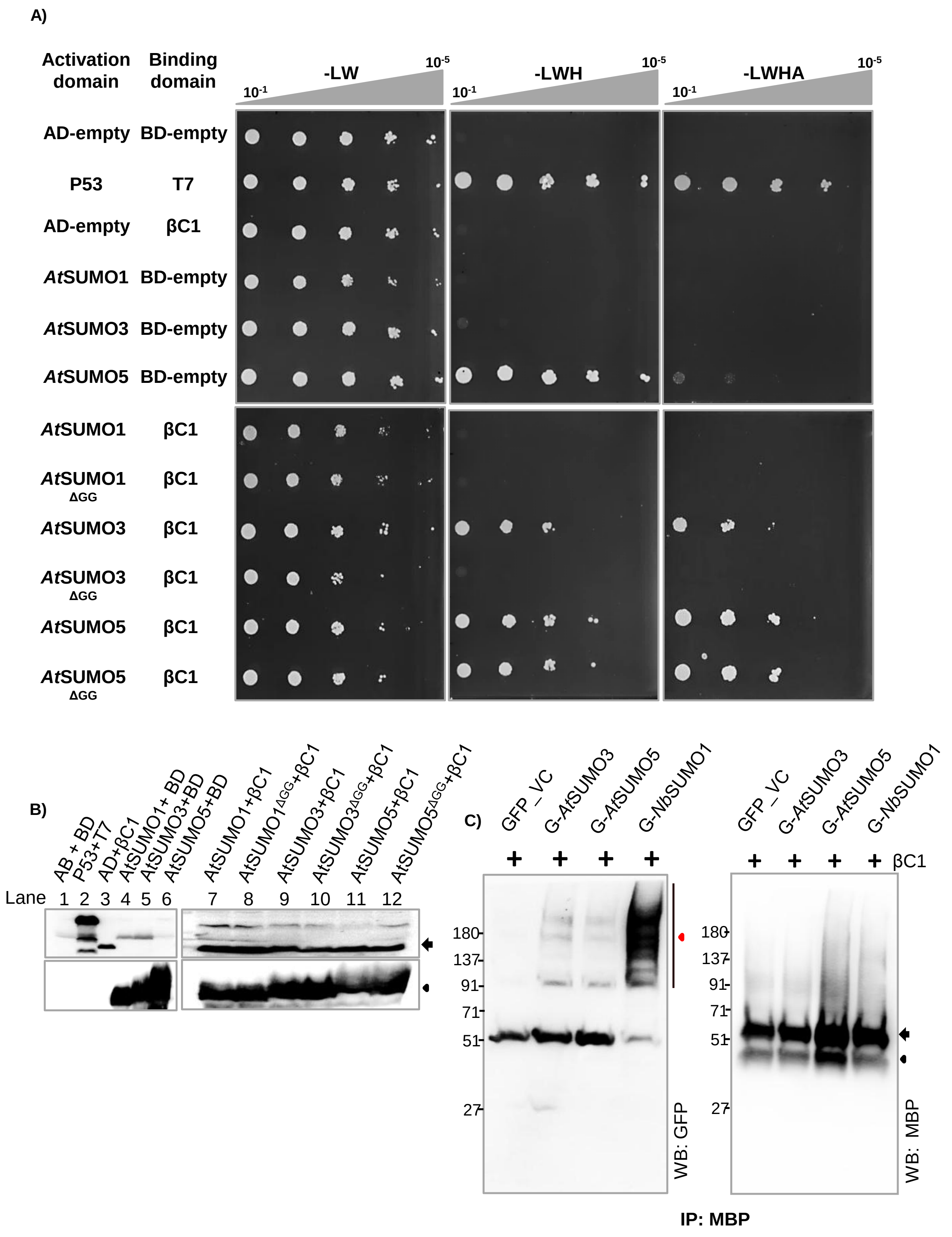


Fig.S5: SyYVCV βC1 weakly interacts with other plant SUMO proteins.

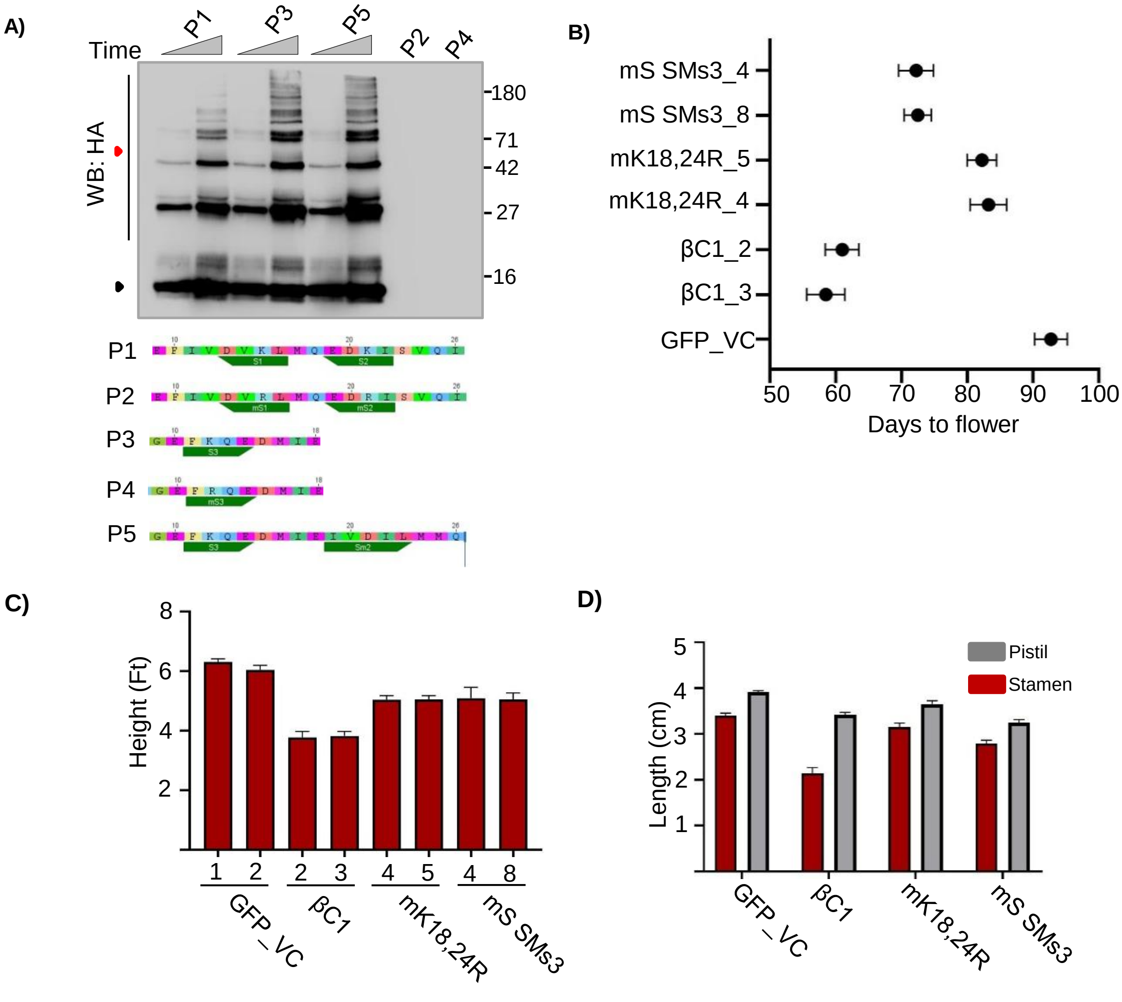


Fig.S6: SUMOylation of βC1 is required for symptom development.

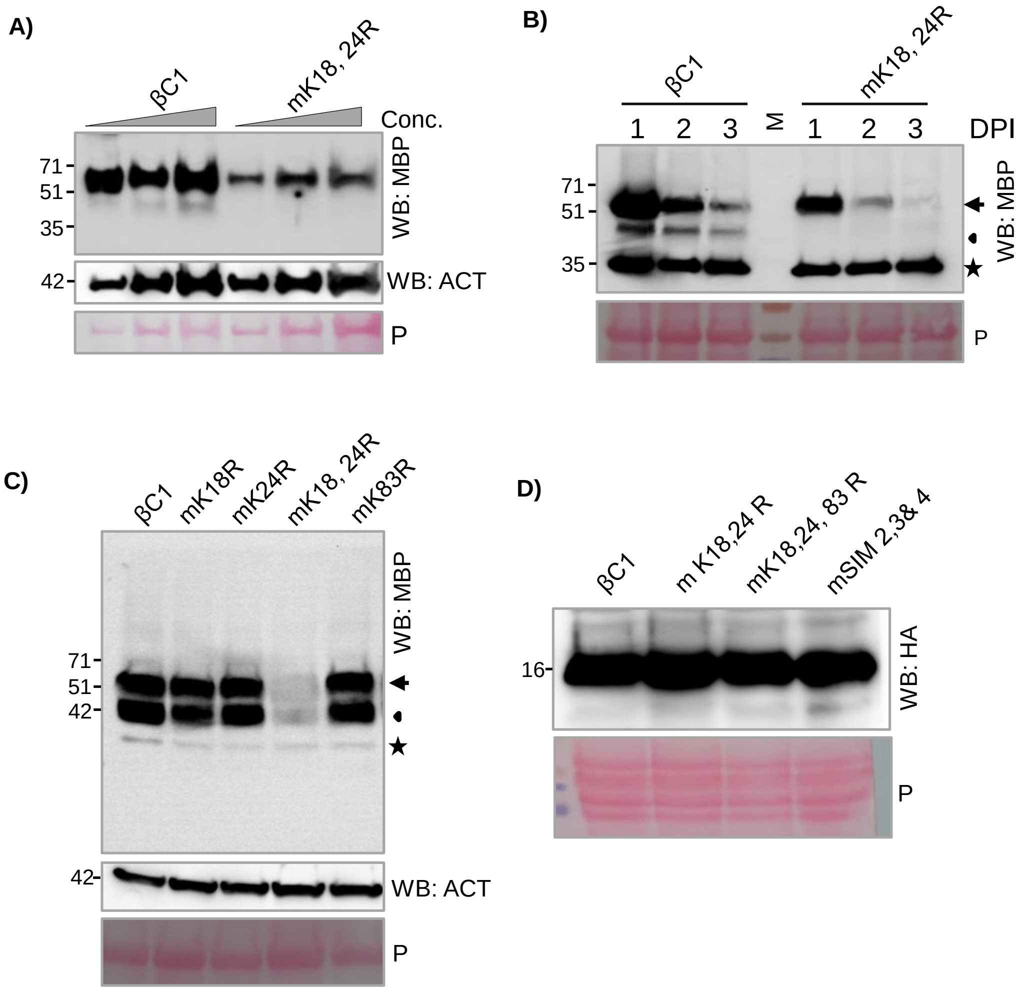


Fig.S7: SUMOylation is required for the stability of βC1 *in planta*.

A)

Domain	Sequence	Type	PS	AA No.
SIM s1	G M E F I V D V K L M Q	SIM β	4.191	**14-17**
SIM s2	D M I E I V D I L M M Q E	SIM β	4.501	**90-93**
SIM s3	M I E I V D I L M M Q E	SIM 2	0.918	**91-94**
SIM s4	Q E A P V I D I N V S D E	SIM β	24.07	**101-104**

B)

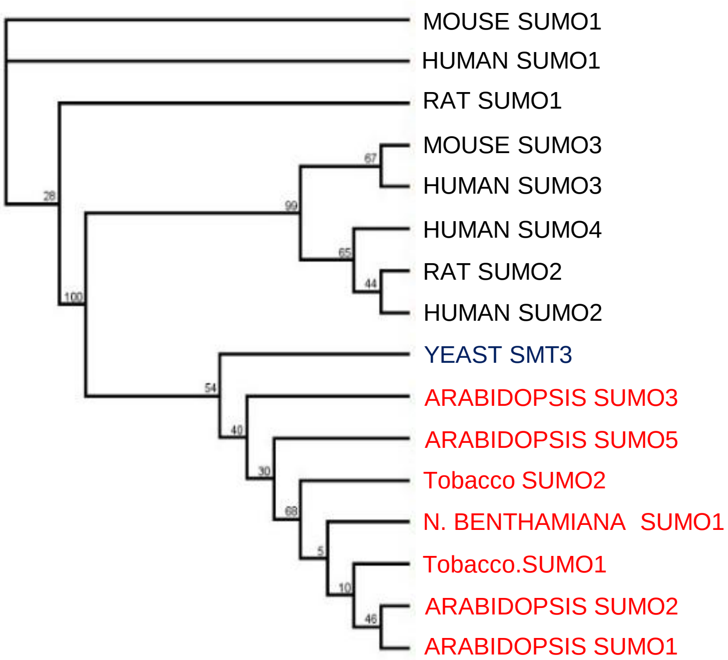


Fig.S8: SIM sites in SyYVCV βC1 and phylogeny of its potential partner SUMO proteins.

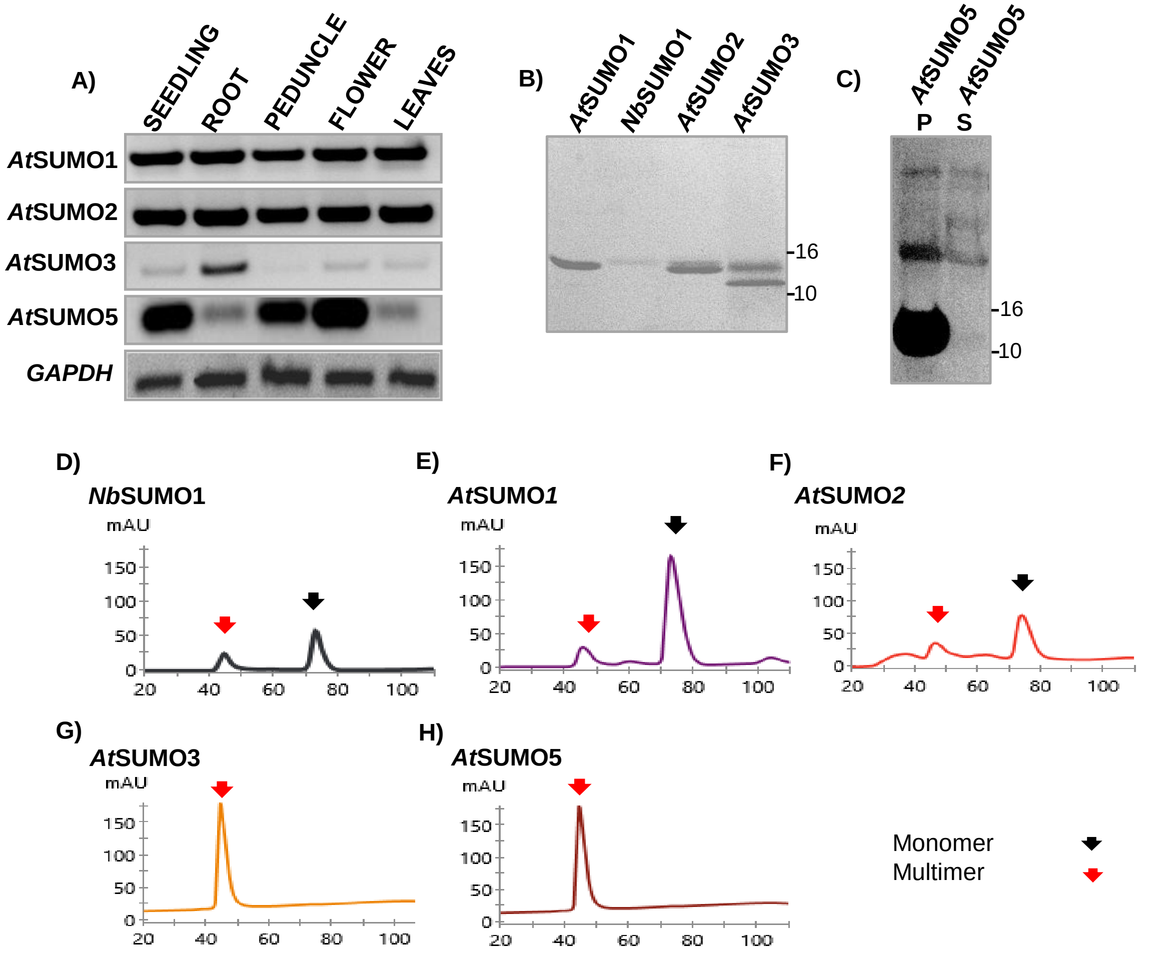


Fig.S9: Expression analysis and purification of plant SUMO proteins.

A)

pSIM1 : KKGMEF**IVDV**KLMQEDKI
pmSIM1 : WKKGMEF**AADA**KLMQEDKI
pSIM 2,3 : KQEDMIE**IVDIL**MMQEAPVI
pmSIM2,3 : WKQEDMIEI**ADAA**MMQEAPVI
pSIM4 : ILMMQEAP**VIDI**NVSDEYEV
pmSIM4 : WILMMQEAP**AADA**NVSDEYEV

B)

Residue No.	14 18	90 95	101 105	118
SyYVCV βC1	M- FI VDVK-	I EI VDI L-	PVI DI N-	V
mSIM 1	M- FAAAAK-	I EI VDI L-	PVI DI N-	V
mSIM 2,3	M- FI VDVK-	I EAAAAL-	PVI DI N-	V
mSIM 4	M- FI VDVK-	I EI VDI L-	PAAAAN-	V
mSIM 2,3,4	M- FI VDVK-	I EAAAAL-	PAAAAN-	V
mS SIM 2,3	M- FI VDVK-	I EI KAI L-	PVI DI N-	V
mS SIM 4	M- FI VDVK-	I EI VDI L-	PVI SGN-	V

Fig.S10: Sequence of SIM mutants.

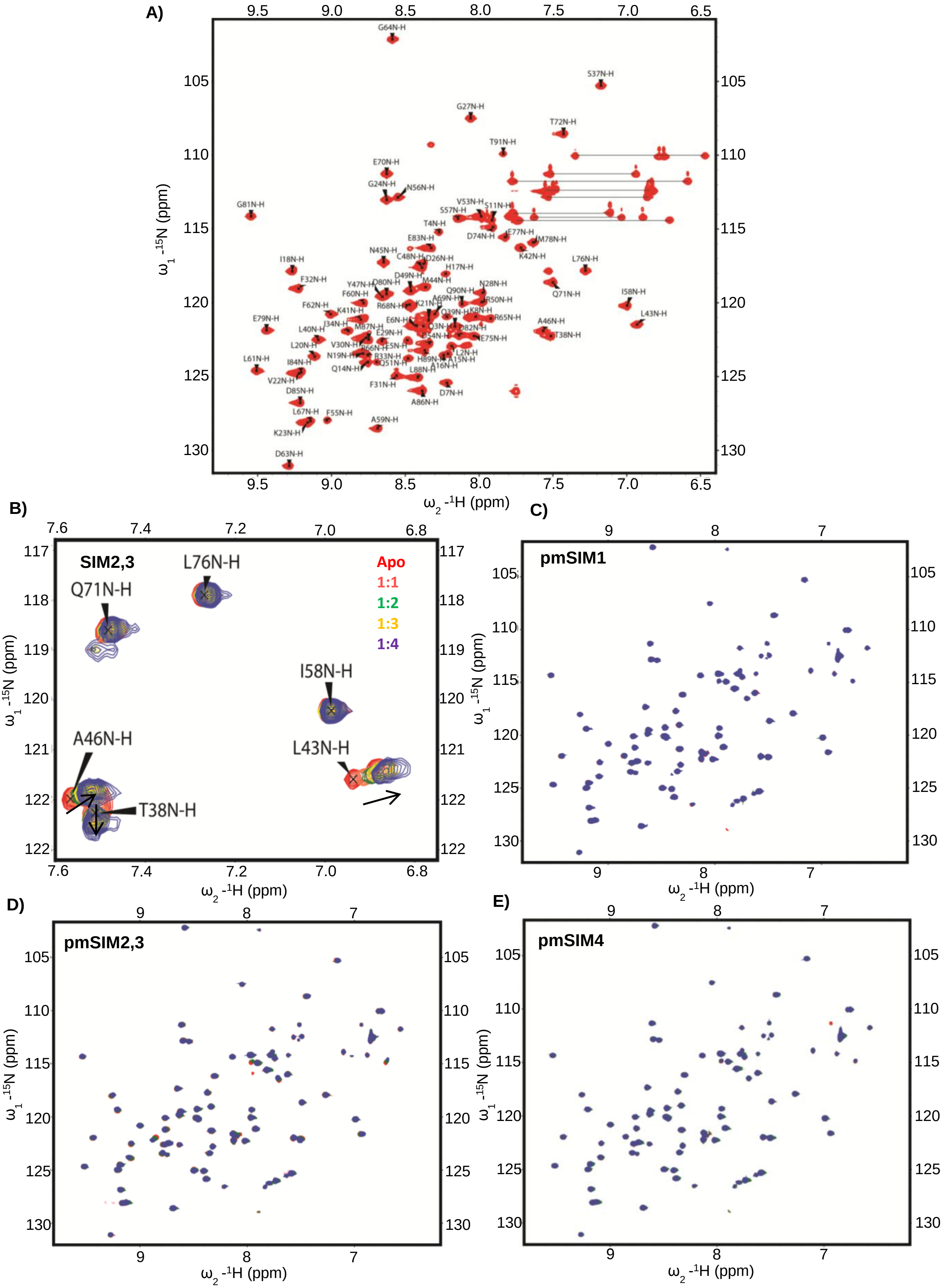


Fig.S11: SIM sites in βC1 C-terminal end interact with *Nb*SUMO1.

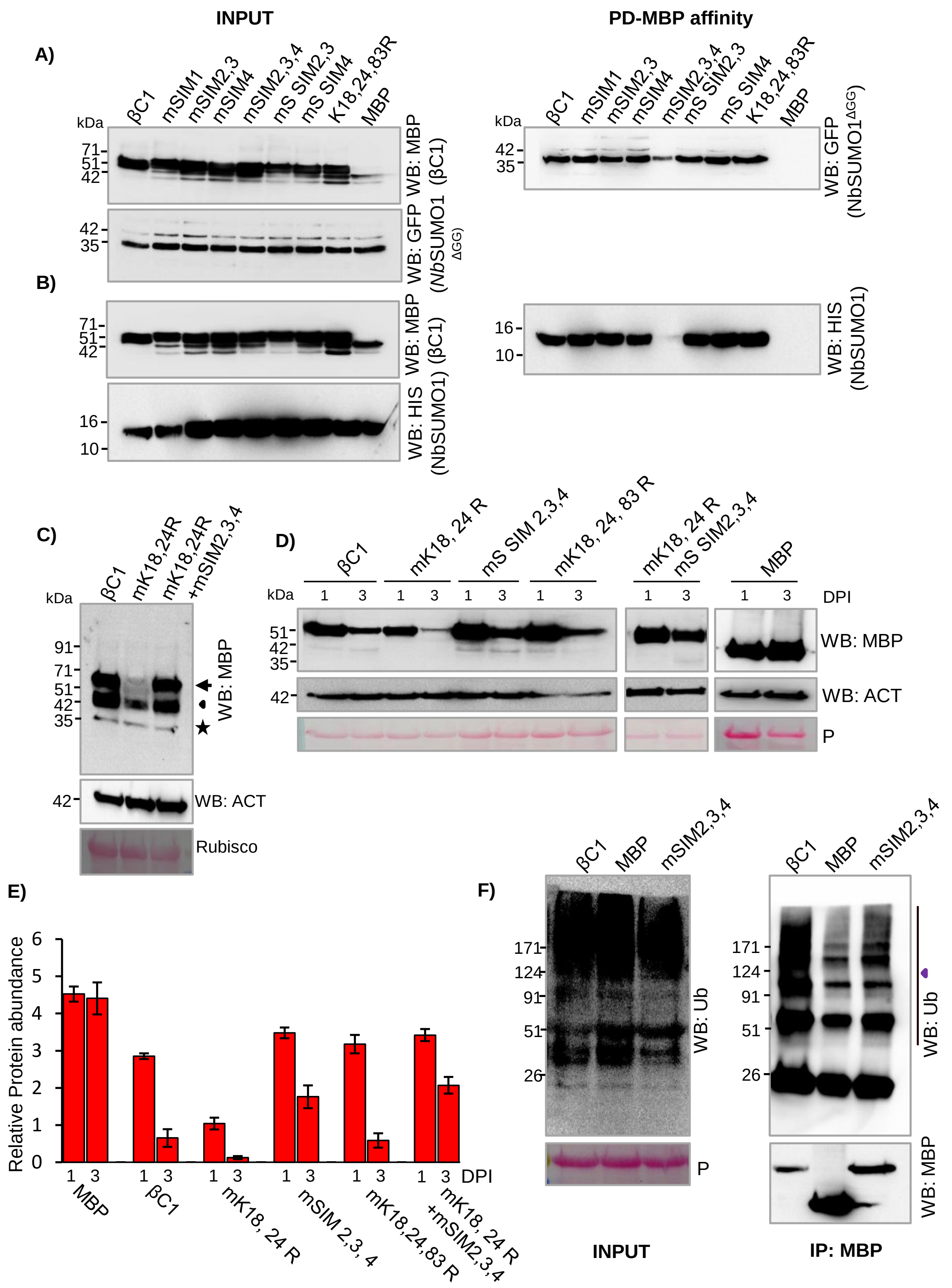


Fig.S12: SIM sites in SyYVCV βC1 regulate its stability.

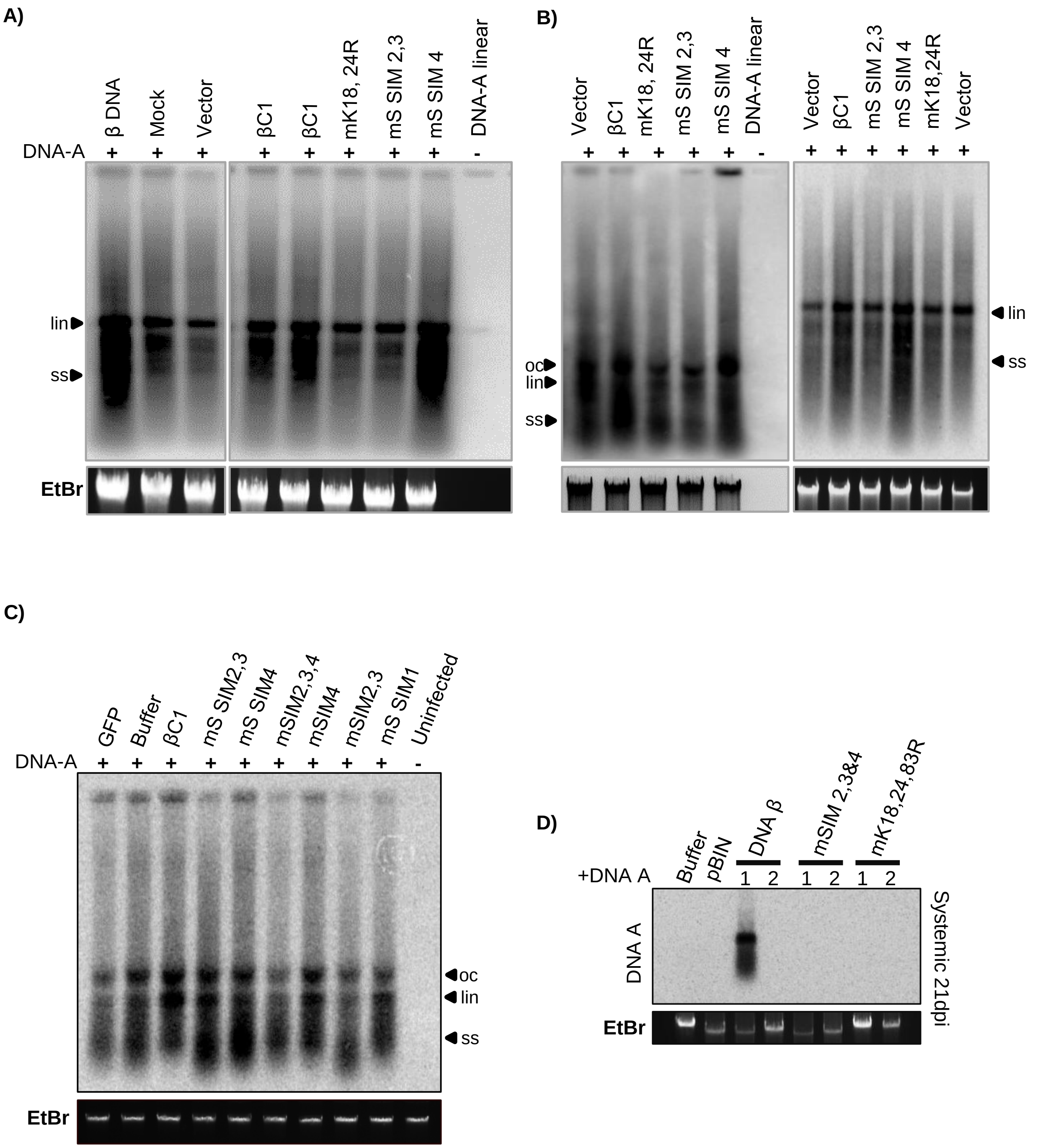


Fig.S13: SIM and SUMOylation motifs of βC1 are necessary for its pathogenicity determinant function.

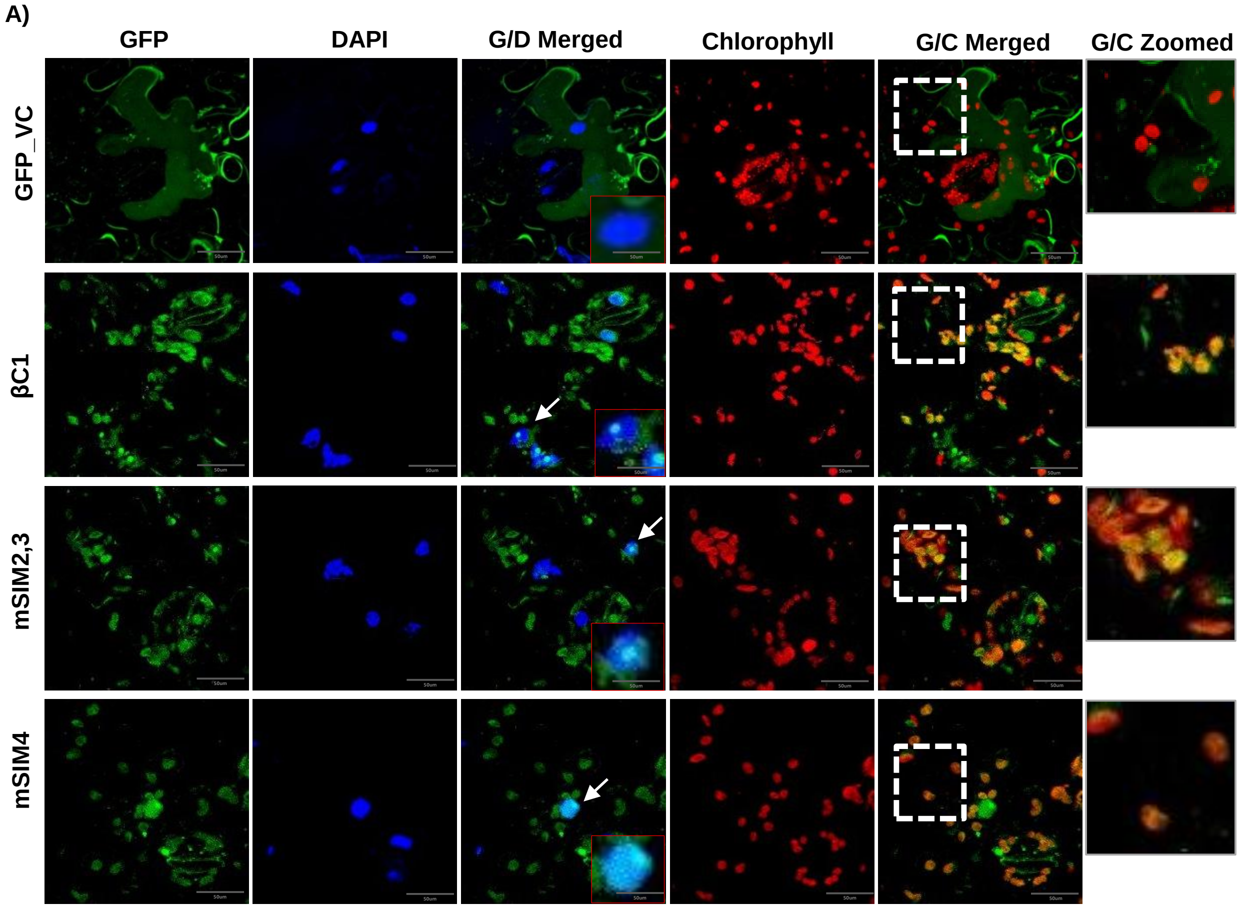


Fig.S14: SUMOylation motif in βC1 is important for its subcellular localization.

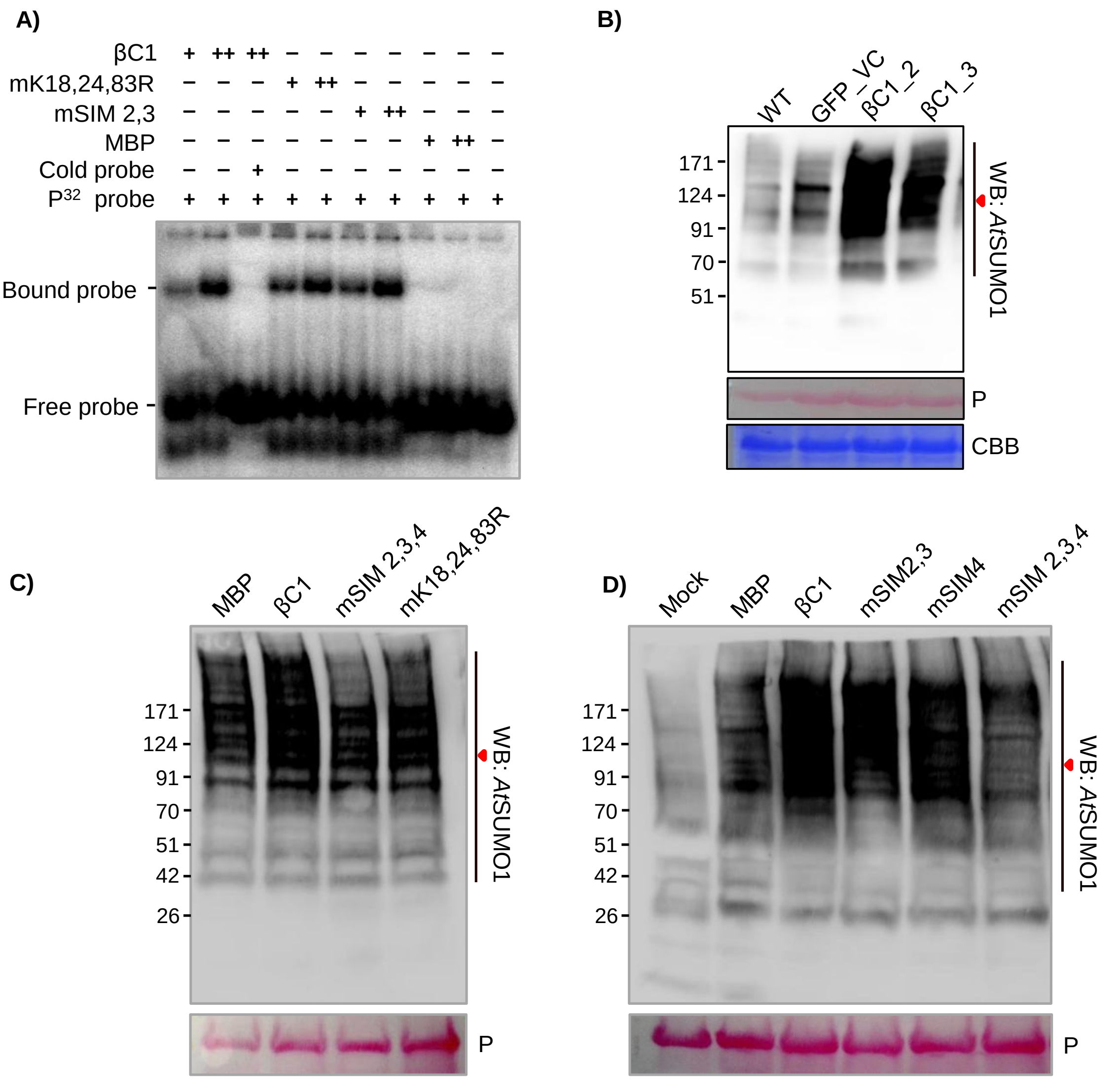
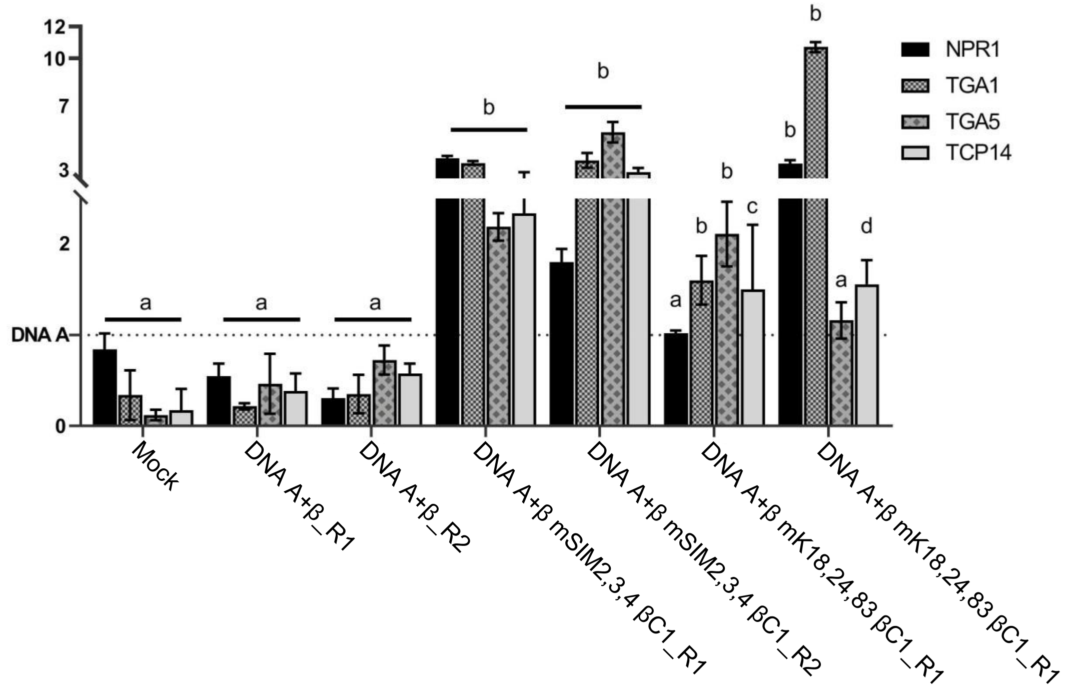


Fig.S15: SyYVCV βC1 induces global SUMOylation.

A



B)

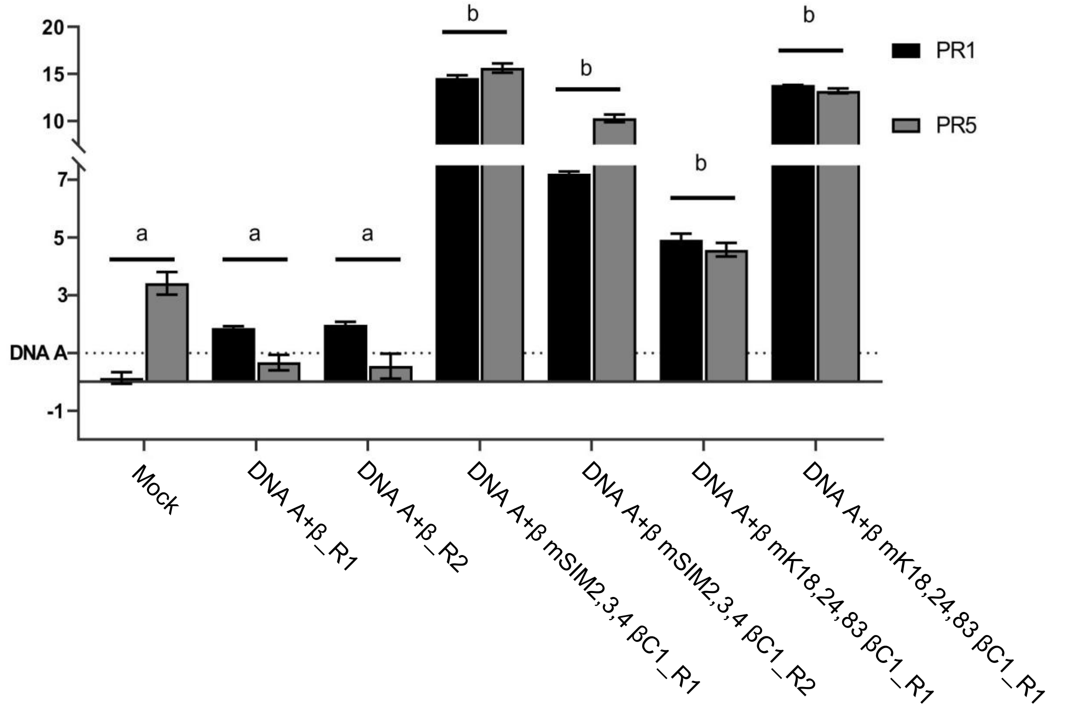


Fig.S16: SIM and SUMOylation motifs of βC1 is essential for host defense suppression.

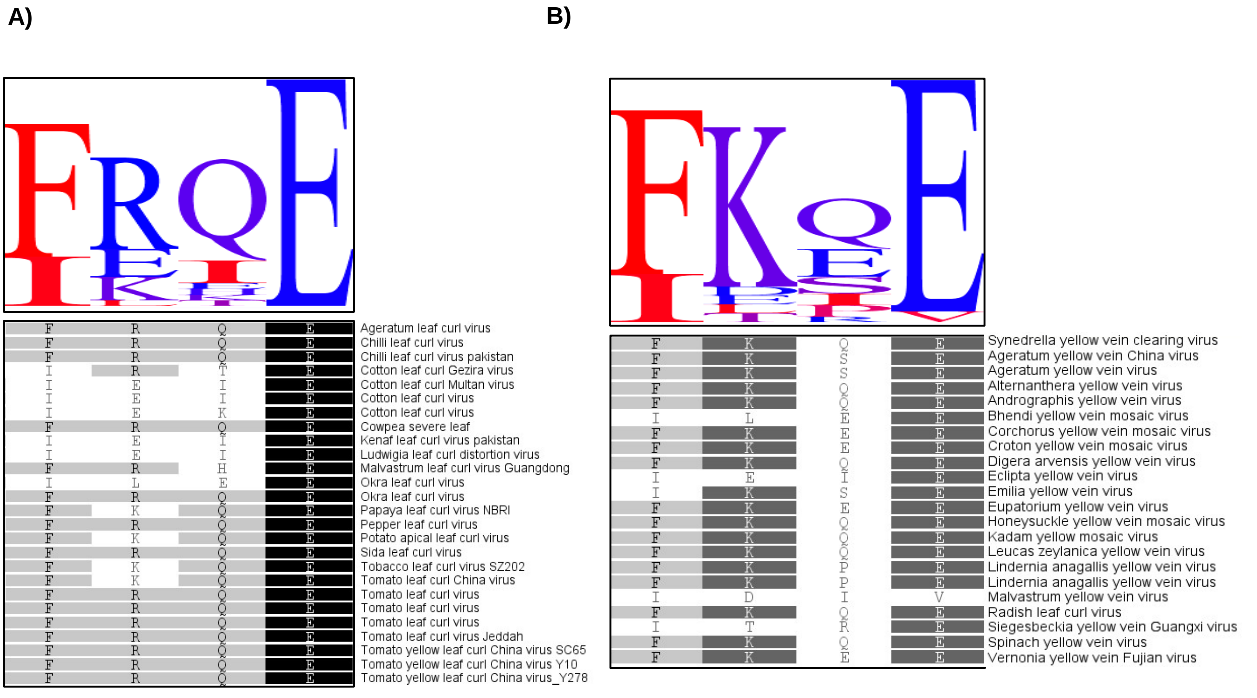


Fig.S17: Conservation of SUMOylation sites among viruses producing similar symptoms..

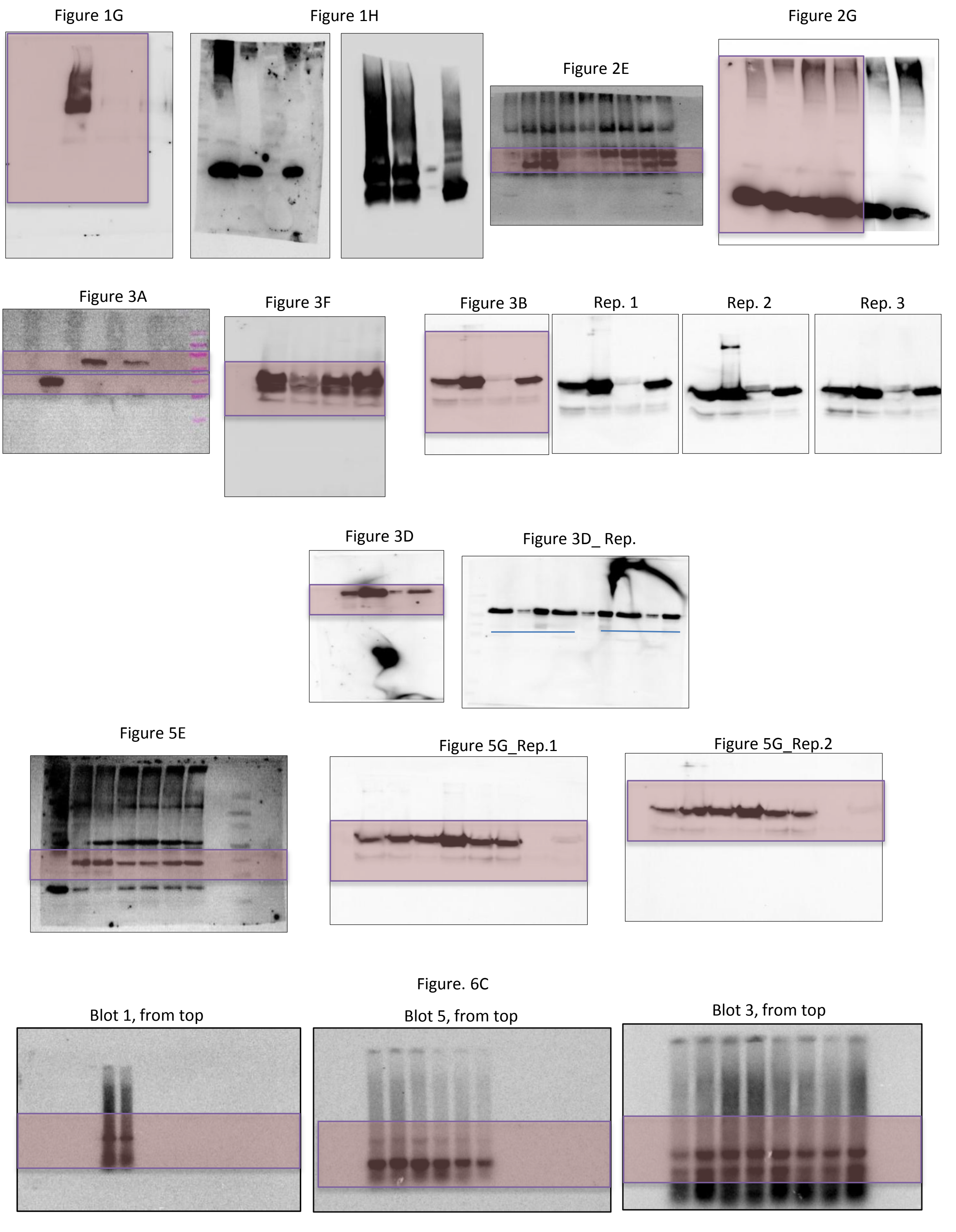
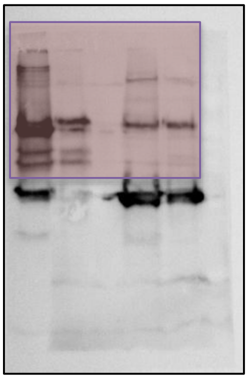


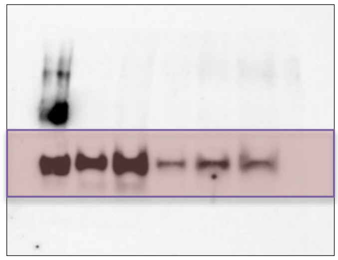
Fig.S18: Uncropped images of blots in main figures 1-7 and replicates of western blots.

S. Figure 4A

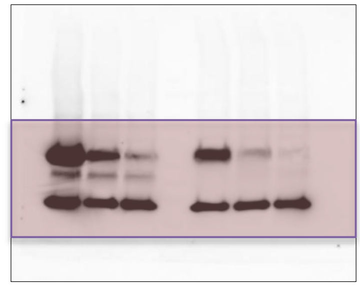


S. Figure 4B

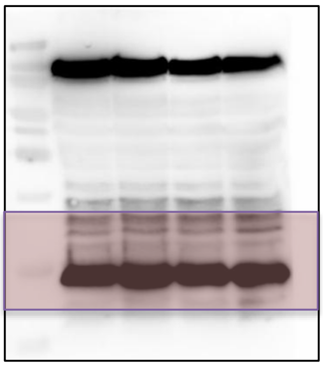
S. Figure 7A



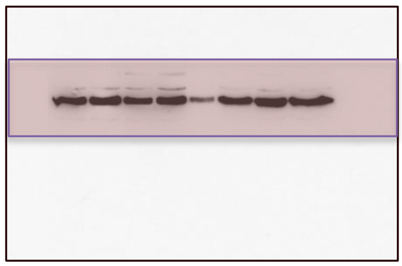
S. Figure 7B



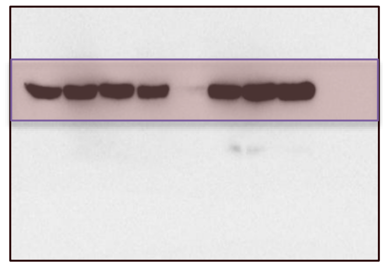
S. Figure 7D



S. Figure 12A



S. Figure 12B



S Figure 12D

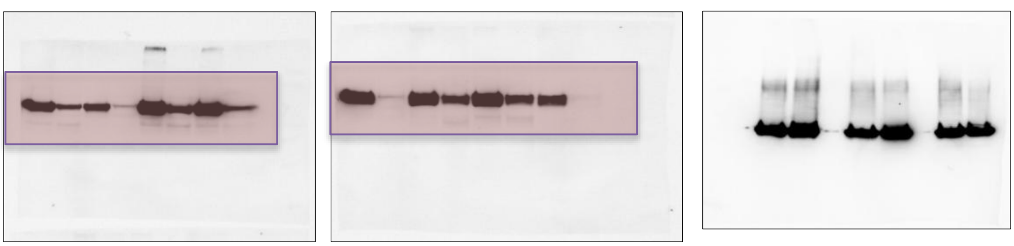


Fig.S19: Uncropped images of blots in Supplemental Figure 1-16.