

Table S1. List of oligonucleotides used for the construction of the BMVY-SUL infectious clone, for RT-PCR reactions and northern blot probes.

Primer names	Primer sequences
SUL-pBS_F	TTGATGAGGTTAATCTTTTGGATGACCACTTGGTGGATGTTCTTTTGGATTCTGCACCTTTCCCAATCATCACAGTCAAGCCCG
35S_R	GGTCTTCTGAGACTGTATCTTTG
M13_F	GTAAACGACGGCCAGT
SUL-BMVY_R	ACATCCACCAAGTGGTCATCCAAAAGATTAACTCATCAACATACAGAATTCTTCATCAGAACCTTGGGTCAGGGTTTGTGCC
BMVY_CT_rev2019	ACACCGAAGTGCCGTAGGGAG
BMVY_5300_F	CCCCGGATATTCCAAGGAAGAC
BMVY_CT_rev2021	TTATCCCAGCGTAAAACACTCG
SUL-F	GAGGAATTCTGTATGTTGAT
SUL-R	GCAGAATCCAAAAGAACATC
miR160	TGGCATACAGGGAGCCAGGCA
BMVY_NB_F	AAGACAATCTCGCGGGAAGT
BMVY_NB_R	TGGGAATACCATCGAGAATC

S1

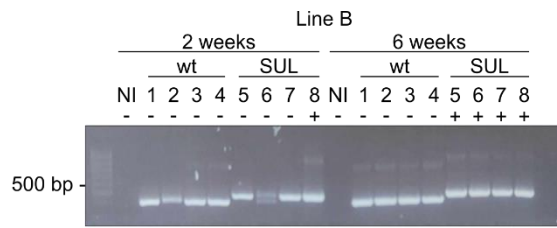


Figure S1. Analysis of viral RNAs produced by BMYV infection over time. RT-PCR analysis of non-agroinoculated (NI), wild-type (wt) or recombinant (SUL) BMYV agroinoculated plants of line B, using oligonucleotides flanking the inserted SUL fragment site. Bands of 402 bp and 472 bp were respectively expected for wild-type BMYV and recombinant BMYV-SUL constructs. Asymptomatic and symptomatic plants are respectively annotated by a minus (-) or a plus (+) sign.

S2

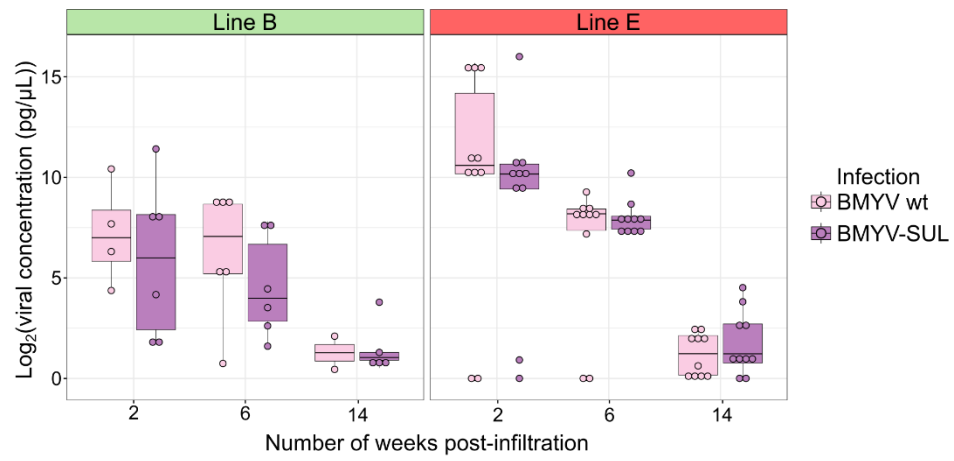


Figure S2. Persistence of BMYV-SUL induced VIGS in sugar beets. Estimated viral load of infected plants, over the 14 weeks is here represented as box plots, pink for wild-type BMYV and purple for recombinant BMYV-SUL.