Figure S1. Fluorescent images of epidermal cells of *N. benthamiana* leaves agroinfiltrated with 35S-GFP (left), 35S-GFP:NLS[pTα] (middle) or 35S-GFP:NLS[VirE3] (right), scale bar = 20 μm
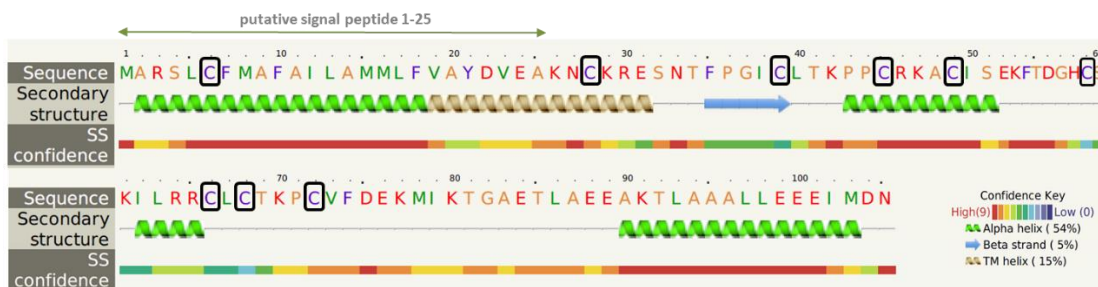

Figure S2. NbγThio secondary structure prediction by Phyre2 service [45] available at http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index. Green helices represent α-helices, blue arrows indicate β-strands. The 'SS confidence' line indicates the confidence in the prediction, with red being high confidence and blue low confidence. The putative signal peptide was predicted by SignalP service (https://services.healthtech.dtu.dk/service.php?SignalP-5.0). Cysteines are outlined with black rectangles.
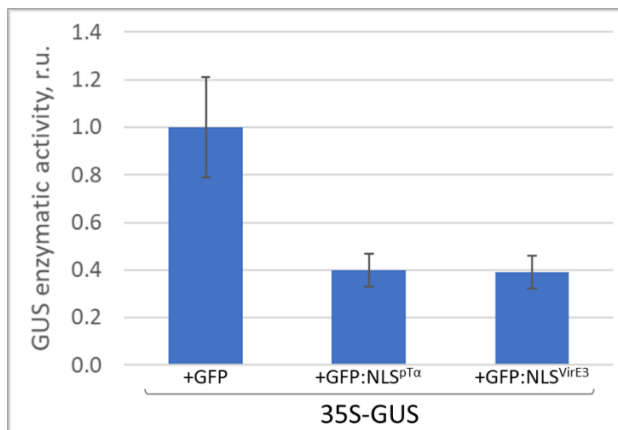

Figure S3. Comparative analysis of GUS activity in arbitrary units (a.u.) in leaves 3 days after co-agroinfiltration with 35S-GUS and 35S-based vectors encoding GFP, GFP:NLS[pTα], and GFP:NLS[VirE3]. The fluorescence detected for the combination of 35S-GUS and 35S-GFP is taken as 1.

Table S2. Oligonucleotides used for cloning and "genome walking"

Name	Nucleotide sequence
mRFP_SacI_d	GAGCTCATGGCCTCCTCCGAGGACGTC
mRFP_SalI_r	GTCGACTTAGGCGCCGGTGGAGTG
mRFP_BamHI_r	GGATCCGGCGCCGGTGGAGTGGC
mRFP_Acc65I_d	GGTACCGCCTCCTCCGAGGACGTC
pTα_NLS_d	GAGCTCGCAATGAGAATCTTTGAATTTG
pTα_NLS_r	GGTACCGTCATCCTCGTCGGTC
VirE3_NLS_d	GGATCCGGTTCTATAAGAACGAAACGGCTTCGAGTAGACAACCCAAAAGAATTAACGCGTG
VirE3_NLS_r	GTCGACTTACGTCTTGGTTTTGCGAAGTCTACCGTGCTCACGCGTTAATTCTTTTGGGTTG
Pr$^{\gamma Thio}$(HindIII+)	AAGCTTACCAGCACCTAAGCTCTCAT
Pr$^{\gamma Thio}$ (NcoI−)	ACAAGGAGCGAGCCATGGAGTTACTTTGAATGAGTAAAAAGG
PrT prom Dir2	TTACCAGCACCTAAGCTCTCA
PrT_ Rev1	ATAGGCAACAAAGAGCATCATT
PrT_ Rev2	GAAGCACAAGGAGCGAGCCAT
PrT_ Rev3	AATAAGTAAAAGGAAATAATTATTGCA
PrT_ Rev10	TAACCTAGAACTCTAATACATGT
PrT_ Rev11	CATGACTTTAAATCGAGATTTCT
PrT_ Rev12	AACTGCACTACAATTCGTGAT