SUPPLEMENTARY MATERIAL

FIGURES

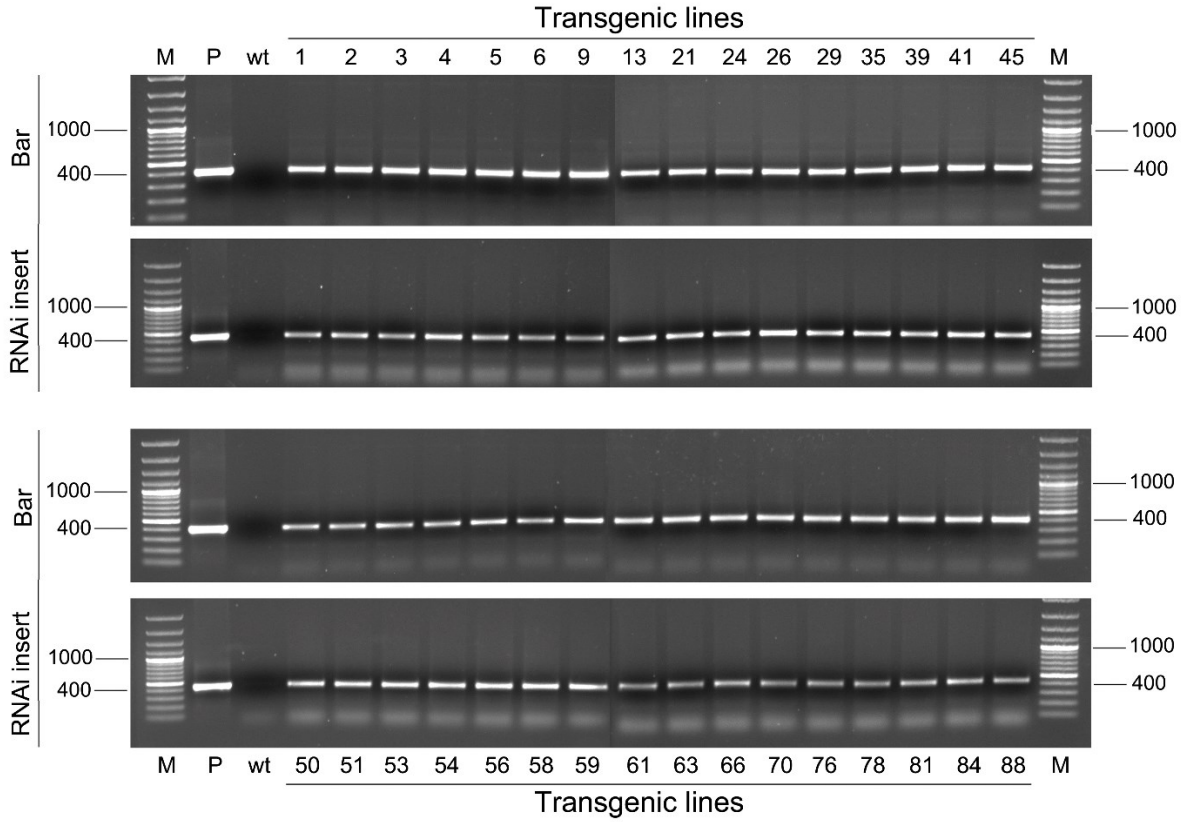


Figure S1. Verification of pLH-*35S-SABP2-INT-SABP2 N. benthamiana* plants by PCR analysis. Genomic DNA from PPT resistant primary regenerants (1, 2, 3, 4, 5, 6, 13, 21, 24, 26, 29, 35,39, 41, 45 50, 51, 53, 64, 56, 58, 59, 61, 63, 66, 70, 76, 78, 81, 84 and 88) was subjected to PCR analysis using the bar-forw/bar-rev and Nb-SABP2-forw/ST-LS1-INT-rev primers that amplify the *bar* and *RNAi* insertion sequences, respectively. The *bar* primers amplify a 401 bp fragment of the corresponding gene, whereas the Nb-SABP2-forw/ST-LS1-INT-rev primers produce a 440 bp fragment. DNAs of non-transgenic *N. benthamiana* plant (wt) and plasmid pLH-*35S-SABP2-INT-SABP2* (P) were included as negative and positive controls, respectively. Molecular marker (M).

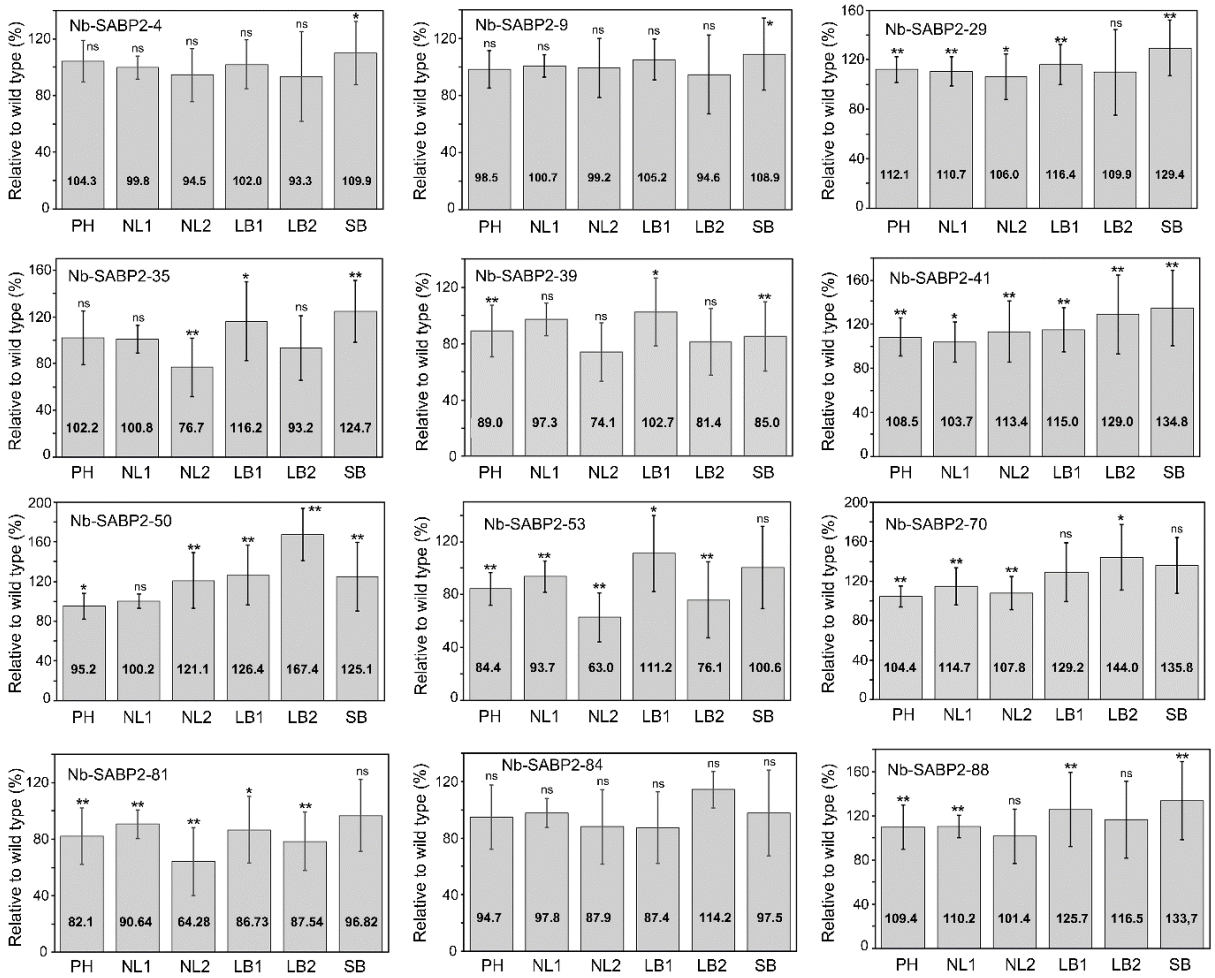


Figure S2. Phenotypic characterization of transgenic *N. benthamiana* lines containing *Nb-SABP2* dsRNA. Wild type and T1 progeny of Nb-SABP2-4, Nb-SABP2-9, Nb-SABP2-29, Nb-SABP2-35, Nb-SABP2-39, Nb-SABP2-41, Nb-SABP2-50, Nb-SABP2-53, Nb-SABP2-70, Nb-SABP2-81, Nb-SABP2-84 and Nb-SABP2-88 transgenic plants were grown in greenhouse for 4 weeks and assayed for plant height (PH), number of primary leaves (NL1), number of secondary leaves (NL2), biomass of primary leaves (LB1) biomass of secondary leaves (LB2) and stem biomass (SB). The phenotypic parameters are expressed as a percent relative to wild type. Values represent the means with standard deviation (n=45). Asterisks indicate significance as determined by unpaired T-test, with * and ** denoting $p<0.05$ and $p<0.01$, respectively. Not significant values are determined as ns.

TABLES

Table S1. Primers used in this study

Primer	Sequence (5'-3')	Application
Bar-forw	GACAAGCACGGTCAACTTCC	PCR
Bar-rev	AGAAACCCACGTCATGCCAG	PCR
Nb-SABP2-forw	GCATGAATTCGGTACCGTTCCCCTGAAGAGC	PCR
ST-LS1-INT-rev	GGATGTCGACCTGCACATCAACAAA	PCR
Cyp-forw	CCGACGAGAACTTCAAGAGG	qPCR
Cyp-rev	CCACAGTCAGCAACCACAAC	qPCR
Nb-SABP2-forw	GCTAGAAGGTGCAGGCCATA	qPCR
Nb-SABP2-rev	CAAGACTATGCCCCACCAAT	qPCR
TMV-forw	AGATCCTGTGCAGCTGATCA	qPCR

TMV-rev	TAGTATTCGGTGCGGGTTGA	qPCR
PVX-forw	CCAGAGACTACGGCAGTGAT	qPCR
PVX-rev	GTCGGCAGGACTACAGTGAT	qPCR
gfp-forw	GAAGCAGCACGACTTCTTCA	qPCR
gfp-rev	CGGCCATGATATAGACGTTG	qPCR
βNGF-forw	AGGTGATGGTGTTGGGAGAG	qPCR
βNGF-rev	GACGCACACACAGGCAGTAT	qPCR

Table S2. Phenotypic evaluation of Nb-SABP2 transgenic lines
The morphological parameters are expressed as precent relative to non-transgenic control *N. benthamiana* plants

Genotype	Phenotypic characteristic	Mean with SD, %	P value
Nb-SABP-16	Plant height	120.9±14.2	< 0,00001
Nb-SABP-19		116.2±25.9	0,00002
Nb-SABP-49		95.5±13.0	0,04741
Nb-SABP-79		104.4±10.5	0,04796
Nb-SABP-16	Number of primary leaves	105.5±9.7	0,00277
Nb-SABP-19		111.4±19.4	0,00029
Nb-SABP-49		104.6±7.9	0,00494
Nb-SABP-79		114.7±18.8	0,00038
Nb-SABP-16	Number of secondary leaves	123.0±22.9	< 0,00001
Nb-SABP-19		113.6±34.9	0,00693
Nb-SABP-49		116.4±23.5	0,00078
Nb-SABP-79		107.8±16.6	0,02238
Nb-SABP-16	Primary leaf biomass	126.2±25.0	< 0,00001
Nb-SABP-19		130.3±31.7	0,00005
Nb-SABP-49		124.9±27.6	0,00001
Nb-SABP-79		129.2±29.9	<0,00001
Nb-SABP-16	Secondary leaf biomass	133.1±30.9	0,00005
Nb-SABP-19		133.8±11.5	0,01978
Nb-SABP-49		142.5±33.8	0,00034
Nb-SABP-79		143.9±33.4	0,00006
Nb-SABP-16	Stem biomass	151.3±32.4	<0,00001.
Nb-SABP-19		135.3±30.1	0,00003
Nb-SABP-49		120.3±31.1	0,00108
Nb-SABP-79		135.8±38.2	< 0,00001