

Additional file 10: Table S3. Analysis of *SIEpk1* silencing in *N. benthamiana*. The length of perfect-match stretches of ≥ 17 nucleotides is shown. Possible target genes in *N. benthamiana* are shown in bold font. N.C., not considered due to low/no expression or short sequence encoding a likely non-functional protein.

Gene	Nb-35S:Pto DC3000 $\Delta hopQ1-1$ expression (RPKM)	Length (bp) of perfect match stretches ≥ 17 bp
NbS00051202g0009.1	79.83	43, 28, 29
NbS00020954g0005.1	83.95	32, 28, 29
NbC23305057g0001.1	66.97	N.C.
NbS00014536g0001.1	4.71	26
NbS00023433g0102.1	41.29	N.C.
NbS00003176g0019.1	53.86	20, 26
NbS00029573g0002.1	67.68	N.C.
NbS00029791g0013.1	51.34	20, 23
NbS00042373g0002.1	5.33	23
NbS00000863g0005.1	0	N.C.
NbS00014032g0110.1	0.72	N.C.
NbS00039241g0001.1	0	N.C.