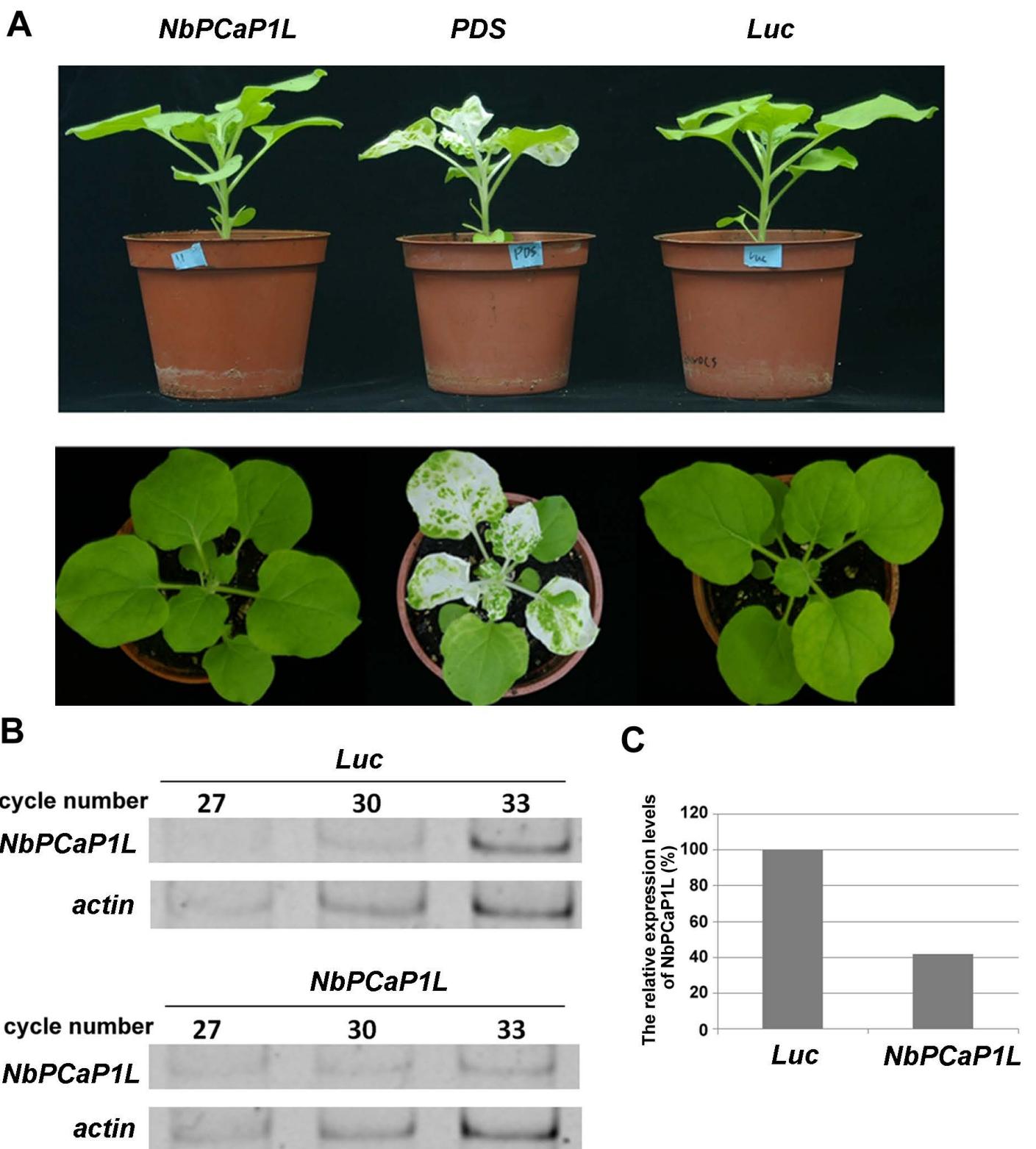
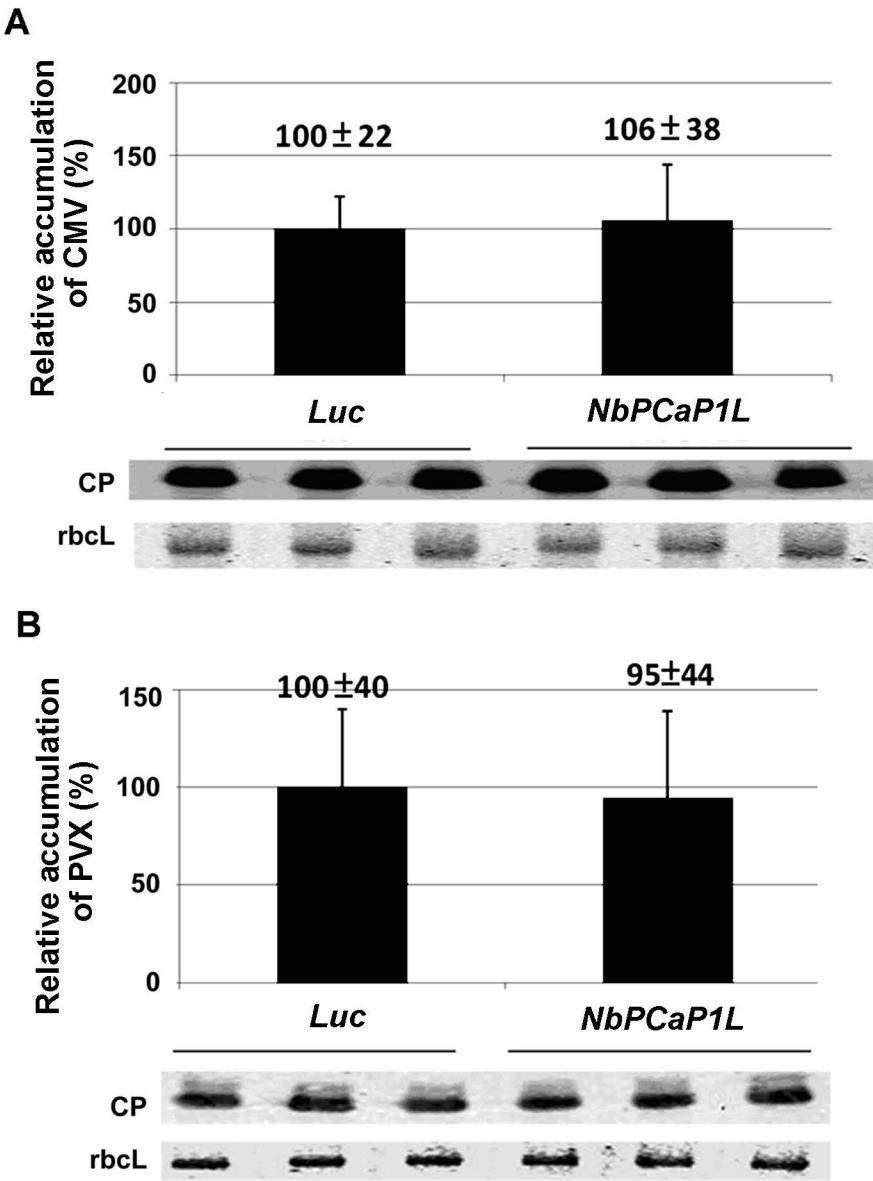


**Supplementary Figure S1.** Amino acid sequence alignment of PCaP1 with related proteins from various plants: PCP1 (*Arabidopsis thaliana*, At4g20260), DREPP1 (*Nicotiana tabacum*, O19910), DREPP4 (*N. tabacum*, O24124), Q9SMK5 (*Cicer arietinum*) and Q0JPA6 (*Oryza sativa*; gene name, Os1g0233000). Phosphorylation sites were predicted by using NetPhos 2.0 (<http://www.cbs.dtu.dk/services/NetPhos/>). The completely conserved residues have no color background, identical residues are yellow, similar residues are cyan and different residues are black.



**Supplementary Figure S2.** The morphology of control and *NbPCaP1L* knockdown plants. (A) Morphology of knockdown plants. The positive control is the phytoene desaturase knockdown plant (PDS), whereas the negative control is the luciferase gene knockdown plant (Luc). (B,C) Semi-quantitative RT-PCR of mRNA level of *NbPCaP1L* in Luc and ACGT11-knockdown plants. The cycling number of the RT-PCR is indicated. The expression of  $\beta$ -actin was an internal control.



**Supplementary Figure S3.** The relative accumulation of viral coat protein (CP) in *NbPCaP1L*-knockdown and control plants. Western blot analysis of CP accumulation in control and *NbPCaP1L*-knockdown plants inoculated with (A) *Cucumber mosaic virus* (CMV) or (B) *Potato virus X* (PVX) at 5 d post-inoculation. Data are mean $\pm$ SD relative accumulation of coat protein from at least 3 independent experiments with at least 3 plants in each experiment. *Luc*: luciferase knockdown control plants; *NbPCaP1L*: *NbPCaP1L*-knockdown plants; CP: coat protein; rbcL: RuBisCO large subunit (the loading control for normalization).