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CqPDS1B 1699 GGCAATGTATAA 1710

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Figure S1 Alignment of nucleotide sequences of *CqPDS1* homoeolog genes, *CqPDS1A* and *CqPDS1B*. Asterisks indicate conserved bases between the two homoeolog genes. Two 300-bp VIGS trigger sequences inserted into ALSV-CqPDSN and ALSV-CqPDSC vectors are highlighted in magenta and turquoise, respectively. The primer positions designed for RT-qPCR analysis are indicated with blue arrows.

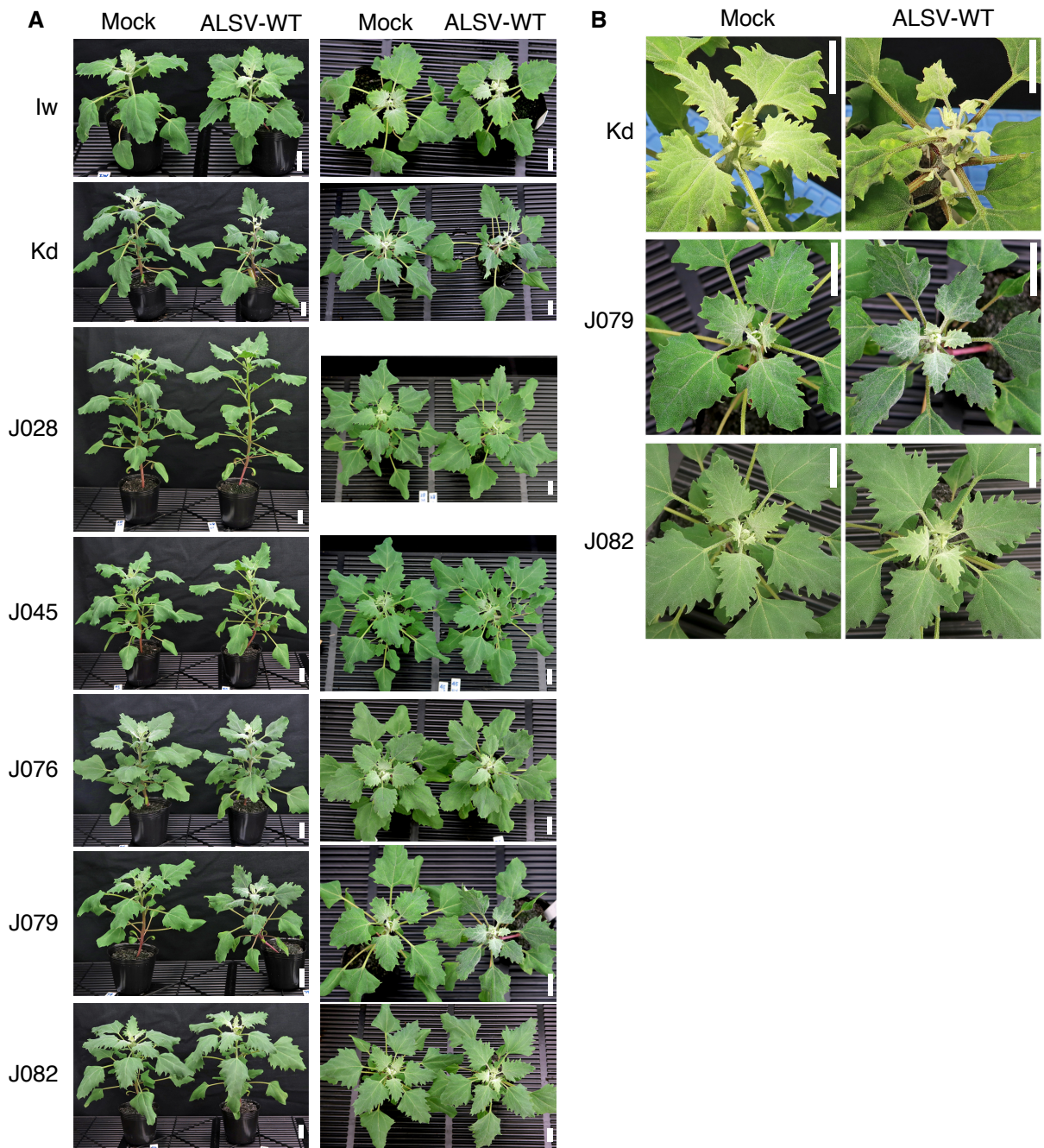


Figure S2 Three lowland inbred lines of quinoa, J028, J045, and J082, display almost no symptoms and show no negative growth effects following ALSV infection. (A) Side (left panels) and top (right panels) views of representative images of lowland line plants at 16 dpi with mock buffer and ALSV-WT. (B) Representative images of enlarged views of the uninoculated upper leaves of Kd, J079, and J082 inbred line plants at 16 dpi with mock and ALSV-WT. Scale bars represent 2 cm.

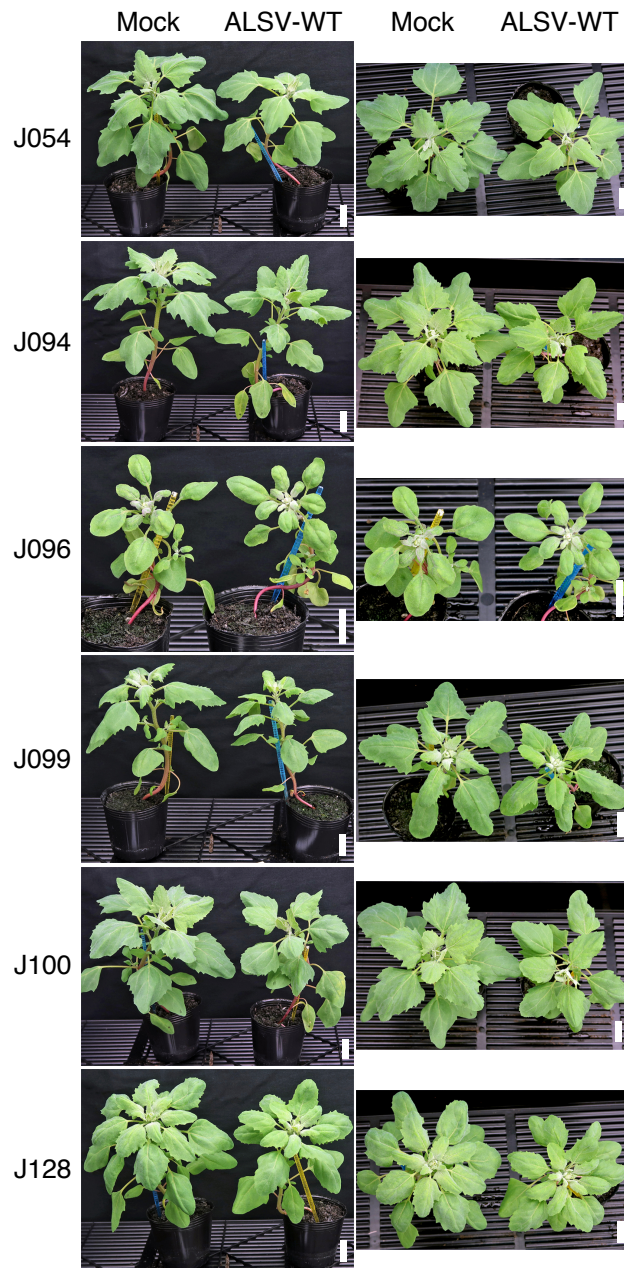


Figure S3 Southern highland inbred lines of quinoa show mild growth retardation following ALSV infection. Side (left panels) and top (right panels) views of representative images of southern highland line plants at 16 dpi with mock buffer and ALSV-WT. Scale bars represent 2 cm.

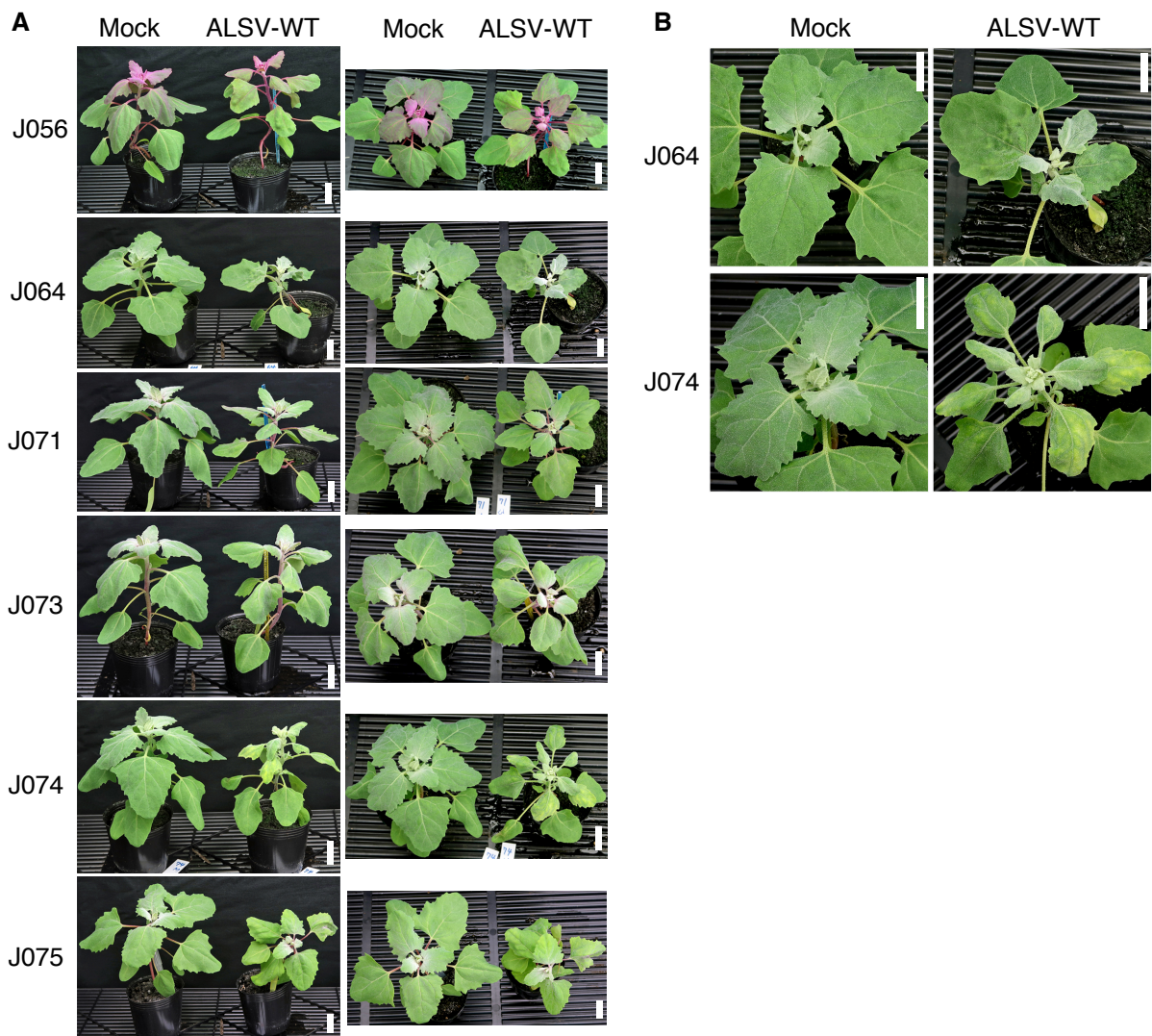


Figure S4 Some northern highland inbred lines exhibit growth retardation and visible symptoms following ALSV infection. (A) Side (left panels) and top (right panels) views of representative northern highland line plants at 16 dpi with mock buffer and ALSV-WT. ALSV-infected plants showed some growth retardation to varying degrees in the northern highland lines used in this study. (B) Enlarged views of representative uninoculated upper leaves of J064 and J074 inbred line plants at 16 dpi with mock and ALSV-WT. Scale bars represent 2 cm.

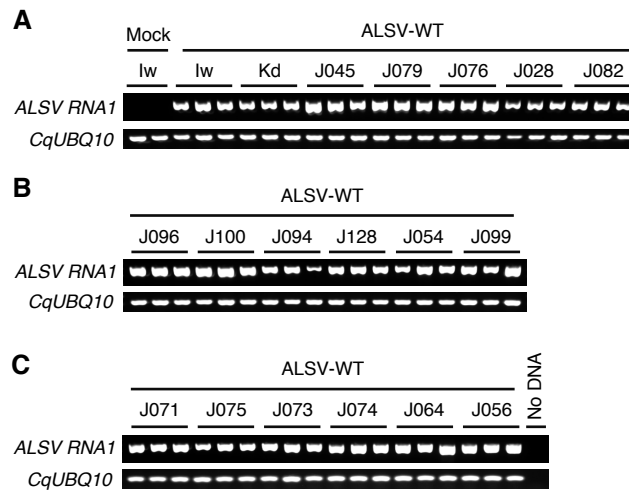


Figure S5 ALSV can infect plants systemically in a variety of quinoa inbred lines. (A–C) Semi-quantitative RT-PCR of ALSV RNA1 in the uninoculated upper leaves of plants at 16 dpi with mock and ALSV-WT in 19 representative lines, including seven lowland (A), six southern (B), and six northern highland lines (C). *CqUBQ10* was used as an internal control. No DNA indicates the absence of DNA template in PCR as a negative control. Two or three independent plants per inbred line were examined.