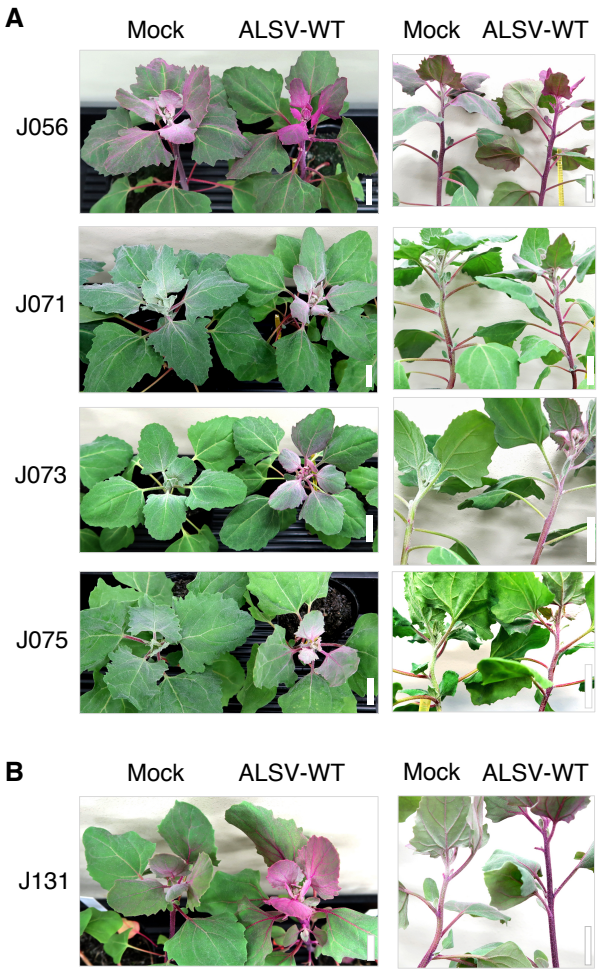

Figure S6 ALSV infection facilitates betalain accumulation in some highland inbred lines. (A–B) Top (left panels) and side (right panels) views of representative plants inoculated with mock buffer and ALSV-WT at 21 dpi for the northern highland lines (J056, J071, J073, and J075) (A) and at 28 dpi for the southern highland line (J131) (B). Scale bars represent 2 cm.

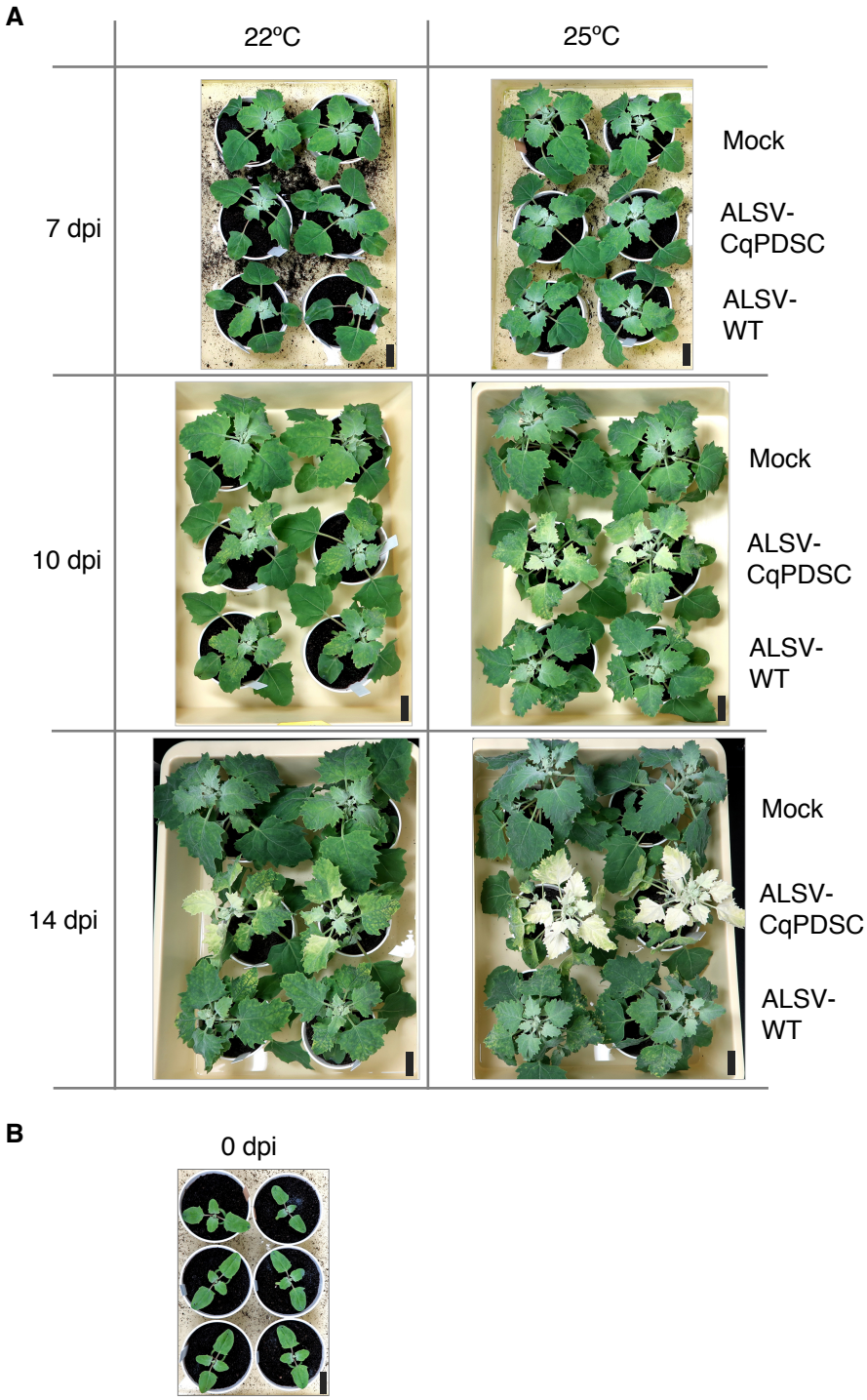

Figure S7 Temperature conditions can alter disease symptoms and VIGS induction in ALSV-infected quinoa plants. (A) Representative images of plants of the inbred Iw line at 7, 10, and 14 dpi with mock buffer, ALSV-CqPDSC, and ALSV-WT. The plants were grown at 22˚C or 25˚C from 0 dpi. (B) A representative image of 18-day-old plants at 0 dpi. Scale bars represent 2 cm.

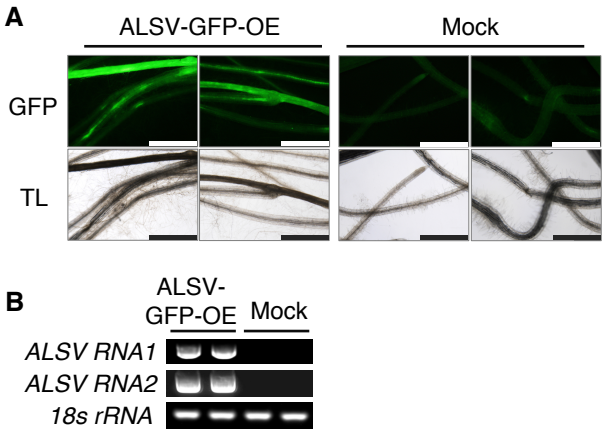

Figure S8 ALSV can be used as a VOX vector in roots. (A) Representative images of GFP fluorescence in quinoa roots at 10 dpi with mock buffer and the packaged virus (ALSV-GFP-OE) derived from recombinant ALSV harboring a full-length *GFP* CDS. Scale bars represent 1 mm. TL indicates transmitted light microscopy images. (B) Semi-quantitative RT-PCR of ALSV RNA1 and RNA2 in roots at 3 wpi with the indicated inocula. *18S rRNA* was used as an internal control.

Figure S9 Alignment of nucleotide sequences of *CqRHT1* homoeolog genes, *CqRHT1A* and *CqRHT1B*. Asterisks indicate conserved bases between the two homoeologs. The VIGS trigger sequence that was inserted into the ALSV-CqRHT1 vector is highlighted in magenta. The positions of primers used for RT-qPCR analysis are indicated with blue arrows.

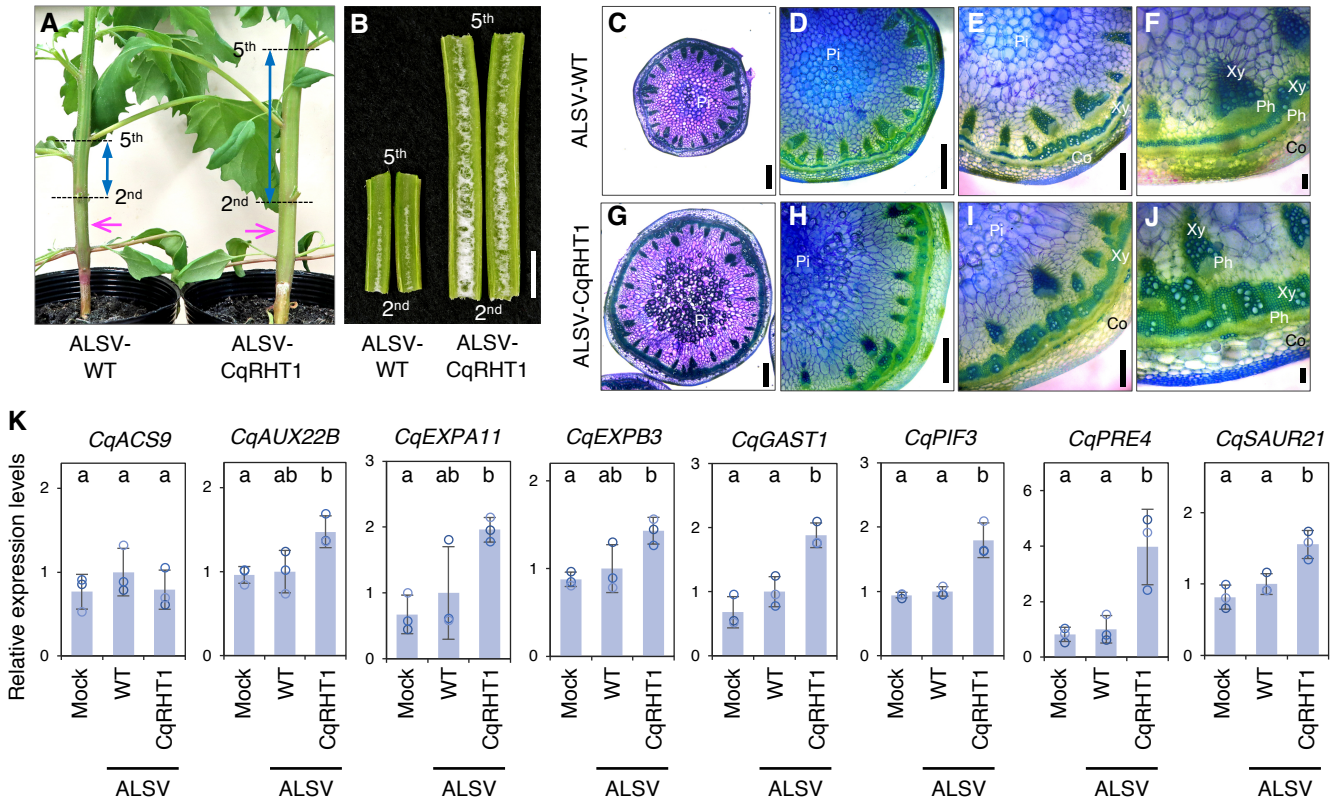

Figure S10 Knockdown of *CqRHT1* results in cell expansion and elongation phenotypes. (A) A representative image of stems of J082 inbred line plants at 25 dpi with ALSV-WT and ALSV-CqRHT1. Blue arrows indicate internode regions between the second and fifth nodes of the quinoa plants, illustrating the location of the longitudinal sections shown in **B**. Magenta arrows indicate the positions of the transverse sections (C–J) of the stems in the quinoa plants. (B) A representative image of longitudinal sections of the internode regions between the second and fifth nodes of the quinoa plants shown in **A**. Scale bar represents 1 cm. (C–J) Representative microscopy images of transverse sections of the stems of the plants shown in **A**, stained with 0.01% toluidine blue before observation. Scale bars represent 1 mm (C,D,G,H), 0.5 mm (E,I), and 0.1 mm (F,J). Pi, pith; Co, collenchyma; Ph, phloem; Xy, xylem. (K) Putative gibberellin-responsive genes were upregulated in the uninoculated upper leaves of J082 inbred line plants inoculated with ALSV-CqRHT1. The relative abundance of transcripts in the uninoculated upper leaves of plants at 15 dpi with mock, ALSV-WT, and ALSV-CqRHT1 was quantified by RT-qPCR analysis. Data were normalized to *CqUBQ10* expression and are shown as means ± SD (n = 3). Different letters indicate significant differences by a Tukey's HSD test ($p < 0.05$). To evaluate the expression of putative gibberellin-responsive genes in quinoa, *CqACS9*, *CqAUX22B*, *CqEXPA11*, *CqEXPB3*, *CqGAST1*, *CqPIF3*, *CqPRE4*, and *CqSAUR21*, primers for real time RT-qPCR were designed using the BLAST program in quinoa genome databases based on the nucleotide sequences of the corresponding *Arabidopsis thaliana* gibberellin-responsive gene homologs obtained from the NCBI database.