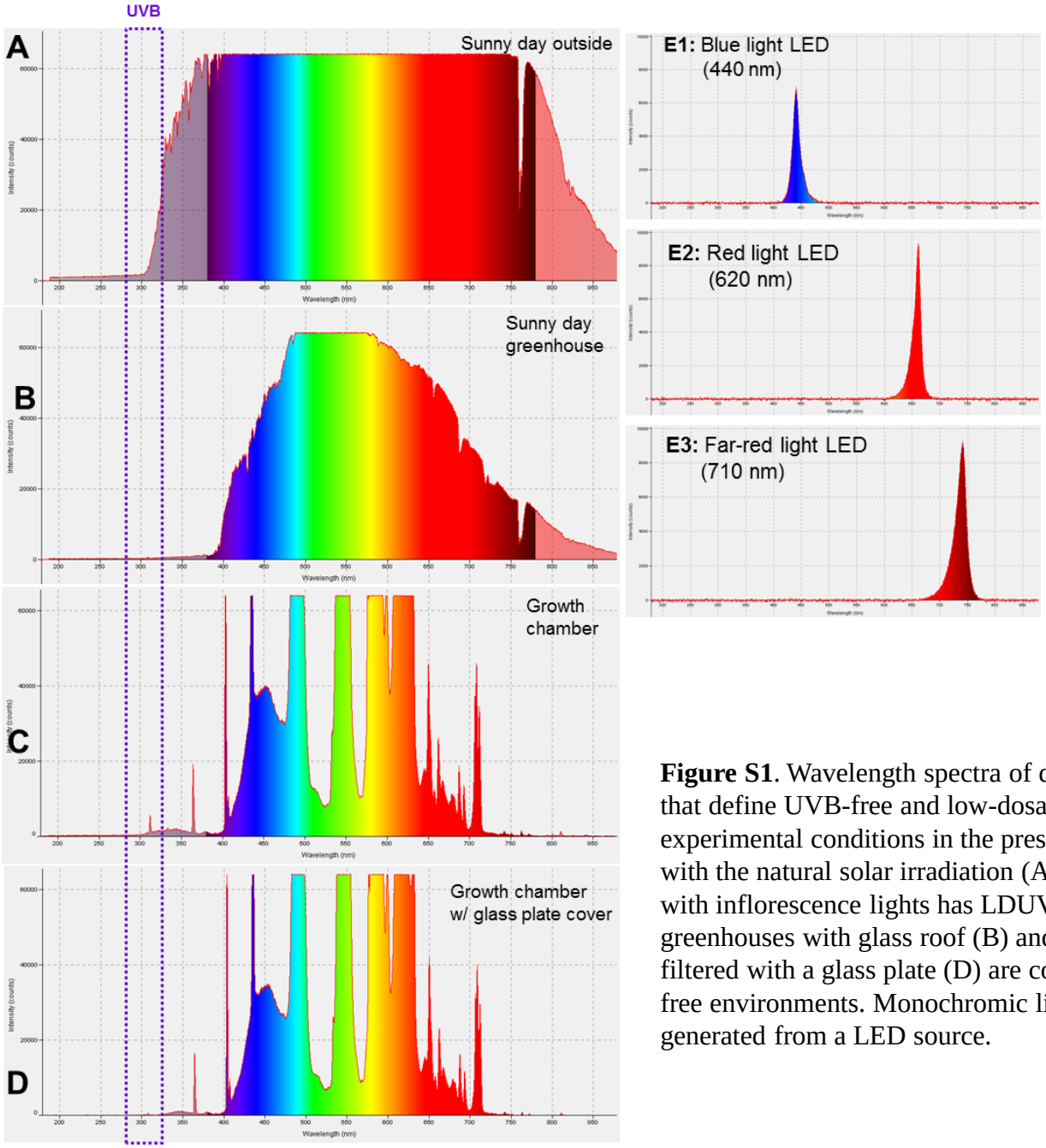


Figure S1. Wavelength spectra of different light sources that define UVB-free and low-dosage UVB (LDUVB) experimental conditions in the present study. Compared with the natural solar irradiation (A), a growth chamber with inflorescence lights has LDUVB (C). The greenhouses with glass roof (B) and growth chambers filtered with a glass plate (D) are considered as UVB-free environments. Monochromic lights (E) are generated from a LED source.

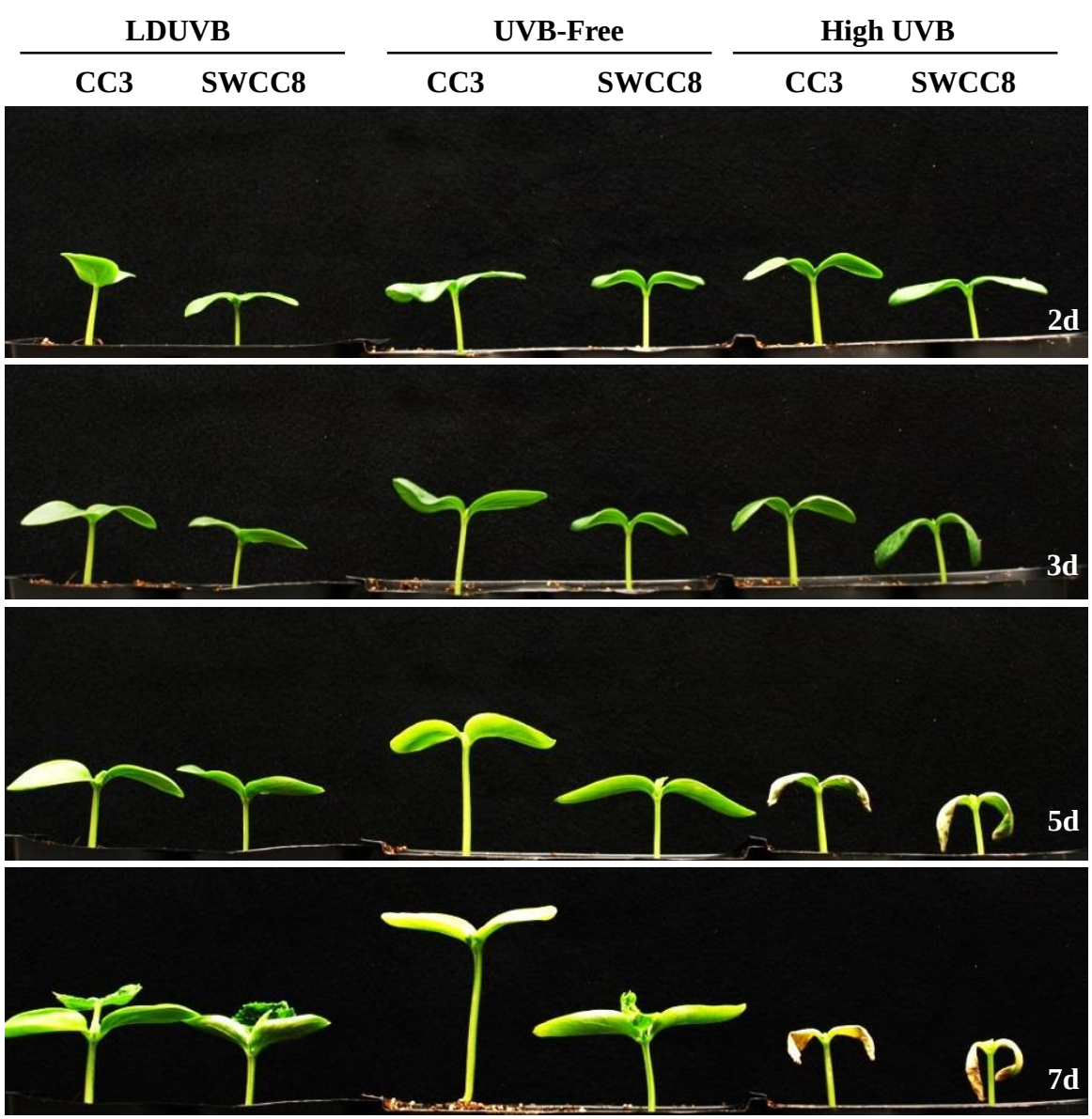


Figure S2. Hypocotyl elongation of SWCC8 and CC3 under LDUVB (left), high dosage UV (right) and UVB-free (center) conditions. Germinated seeds of CC3 and SWCC8 were grown under three light conditions for one week, and hypocotyl length was measured at every other day. LDUVB inhibits CC3 hypocotyl elongation, but high dosage UV results in inhibition of seedling growth, stunting and death in both lines.

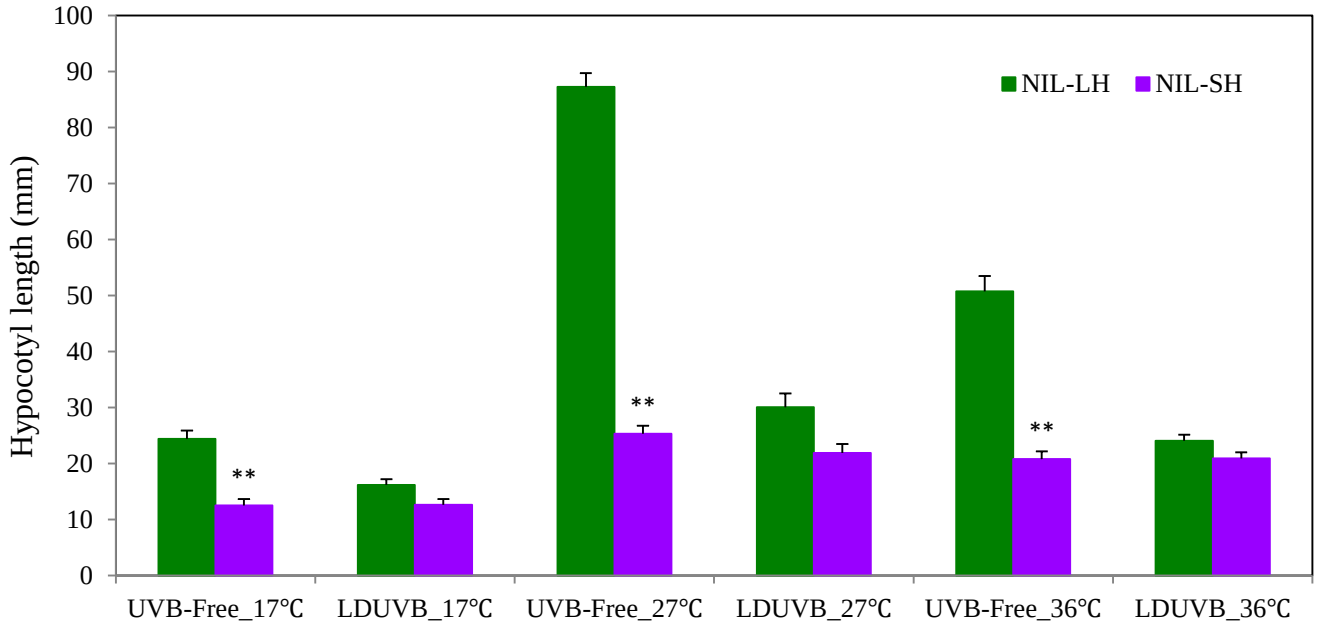


Figure S3. Effect of temperature on hypocotyl elongation in two near isogenic lines of the *Sh1* gene under LDUVB and UVB-free conditions. Under UVB-free light, hypocotyl elongation is faster at optimal temperature (27 °C) than under either low (17 °C) or high (36 °C) temperature, but there seems no interactions of temperature and LDUVB on hypocotyl elongation in both NILs. NIL-SH and NIL-LH are near isogenic lines carrying the homozygous short (*sh1*) and long hypocotyl (*Sh1*) allele, respectively. ** indicates statistically significant differences of hypocotyl length based on *t*-tests ($P < 0.01$).

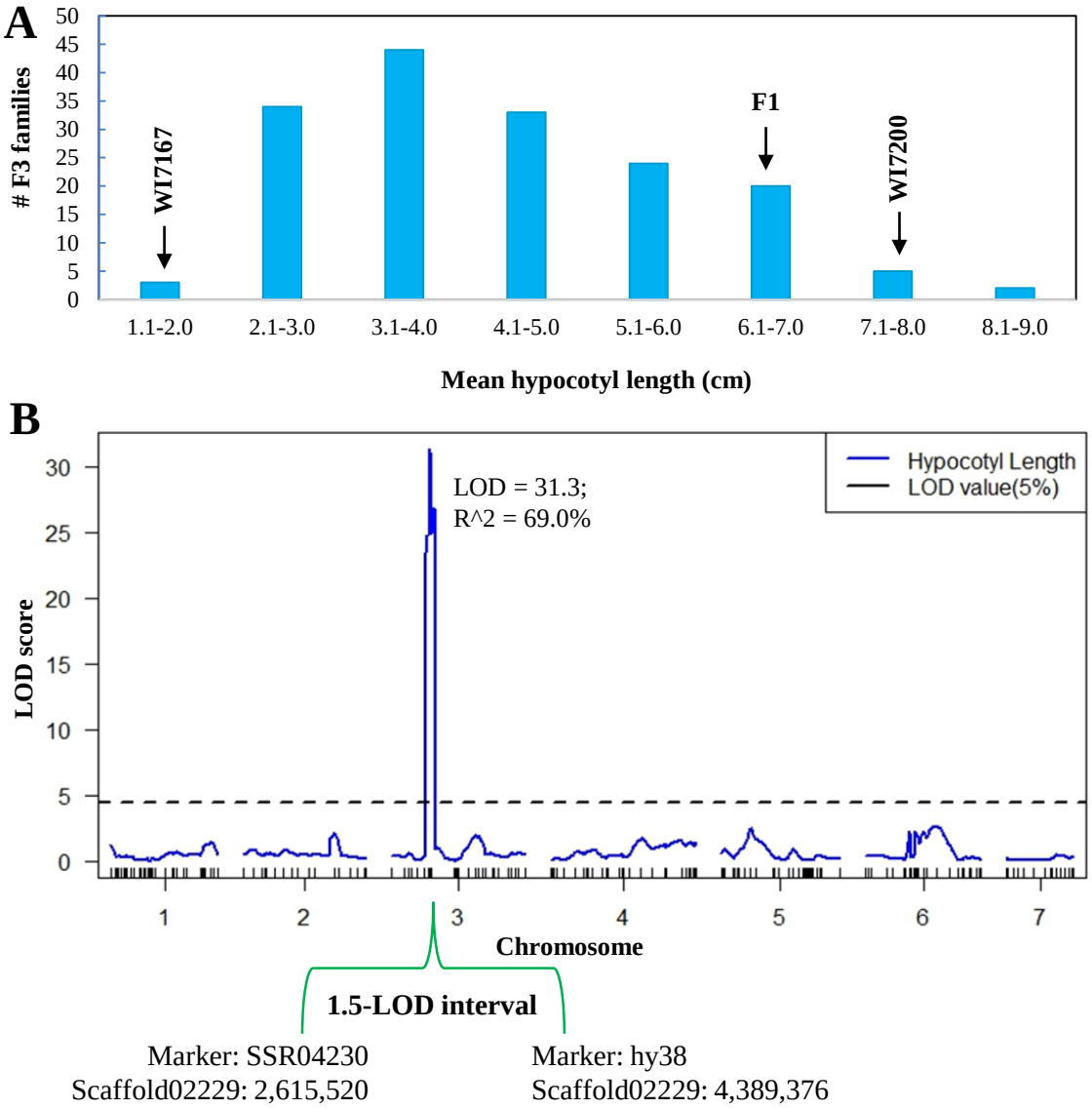


Figure S4. QTL analysis in the WI7167 × WI7200 F2:3 population identifies a major-effect QTL for hypocotyl length that co-localizes with the *Sh1* locus. **A.** Frequency distribution of hypocotyl length among 164 F3 families, which is largely normal. **B.** LOD profile of hypocotyl length QTL based on F3 phenotypic data and genotypic data with 225 SSR markers. One major-effect QTL with high LOD support (LOD = 31.3) is identified that can explain 69% observed phenotypic variations. Based on scaffold location of this QTL, it is co-localized with the *Sh1* locus.

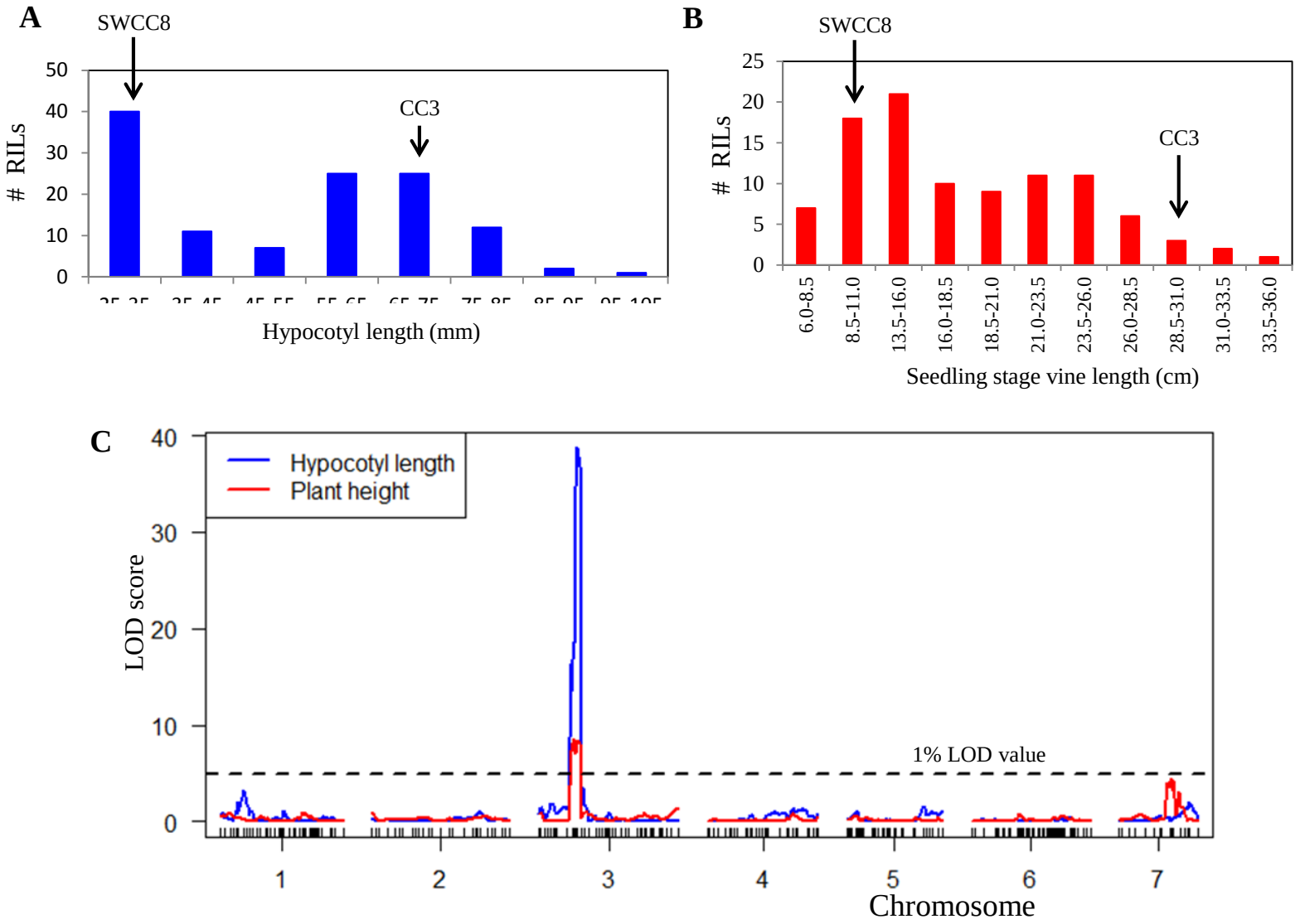


Figure S5. QTL analysis in SWCC8 × CC3 RIL population suggests that the slow vine growth in seedling stage in SWCC8 is a pleiotropic effect of the *sh1* locus. **A.** Frequency distribution of hypocotyl length among 148 RILs. **B.** A. Frequency distribution of seedling vine length at 5-true-leaf stage among 148 RILs. **C.** LOD profiles of hypocotyl length and seedling height QTL indicate co-localization of vine length QTL with the *Sh1* locus. That is, the two traits are under the control of the same gene.

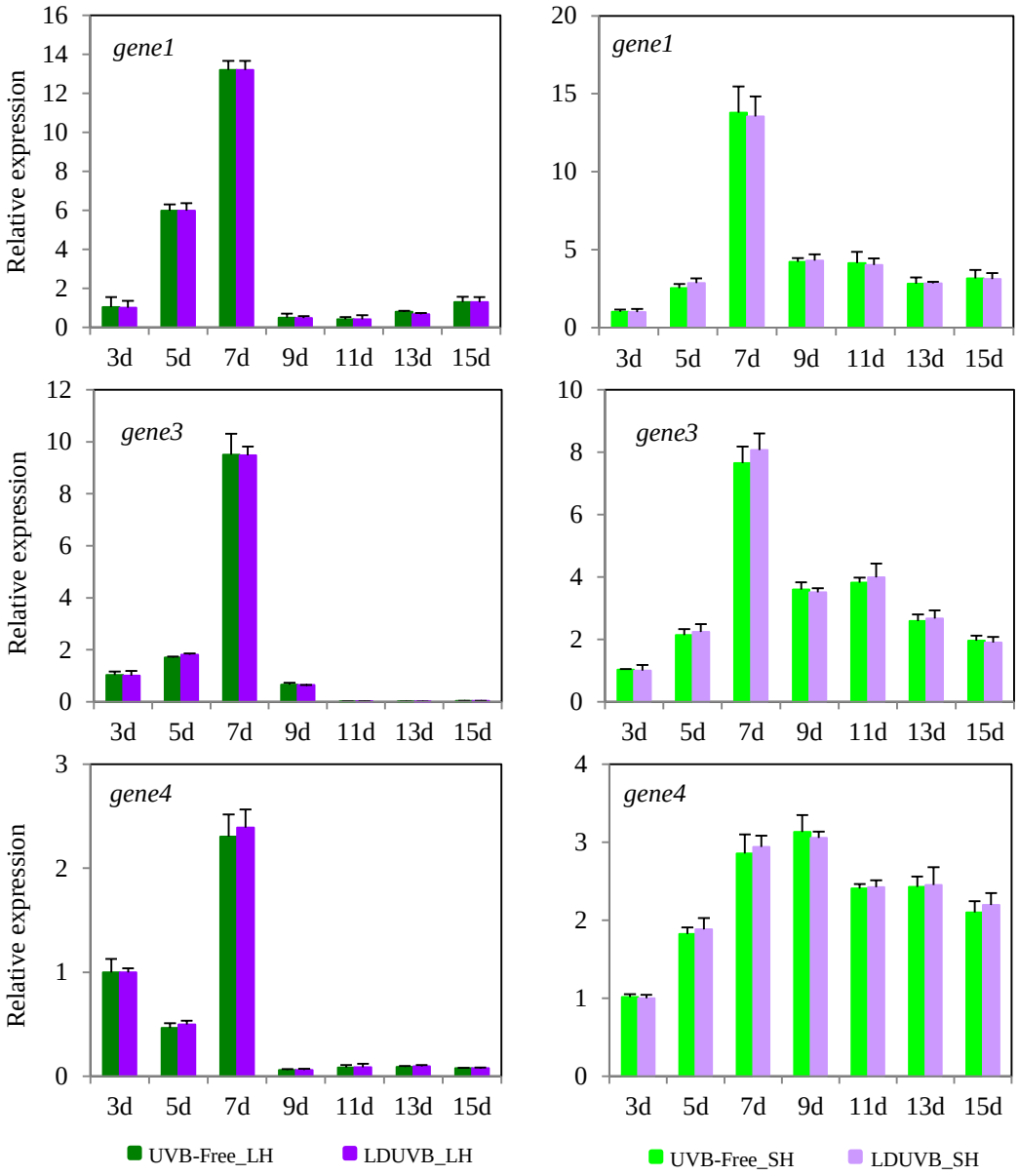


Figure S6. Expression patterns of Gene 1, Gene 3 and Gene 4 in the 42-kb region in NILs (SH and LH) of *Sh1* under UVB-free and LDUVB light conditions exclude the three genes as the candidate of the *Sh1* locus. No significant difference of expression level is found between NIL-LH (left panel) and NIL-SH (right panel) under the two light conditions in any of the three genes. NIL-SH and NIL-LH are near isogenic lines carrying the homozygous short (*sh1*) and long hypocotyl (*Sh1*) allele, respectively.

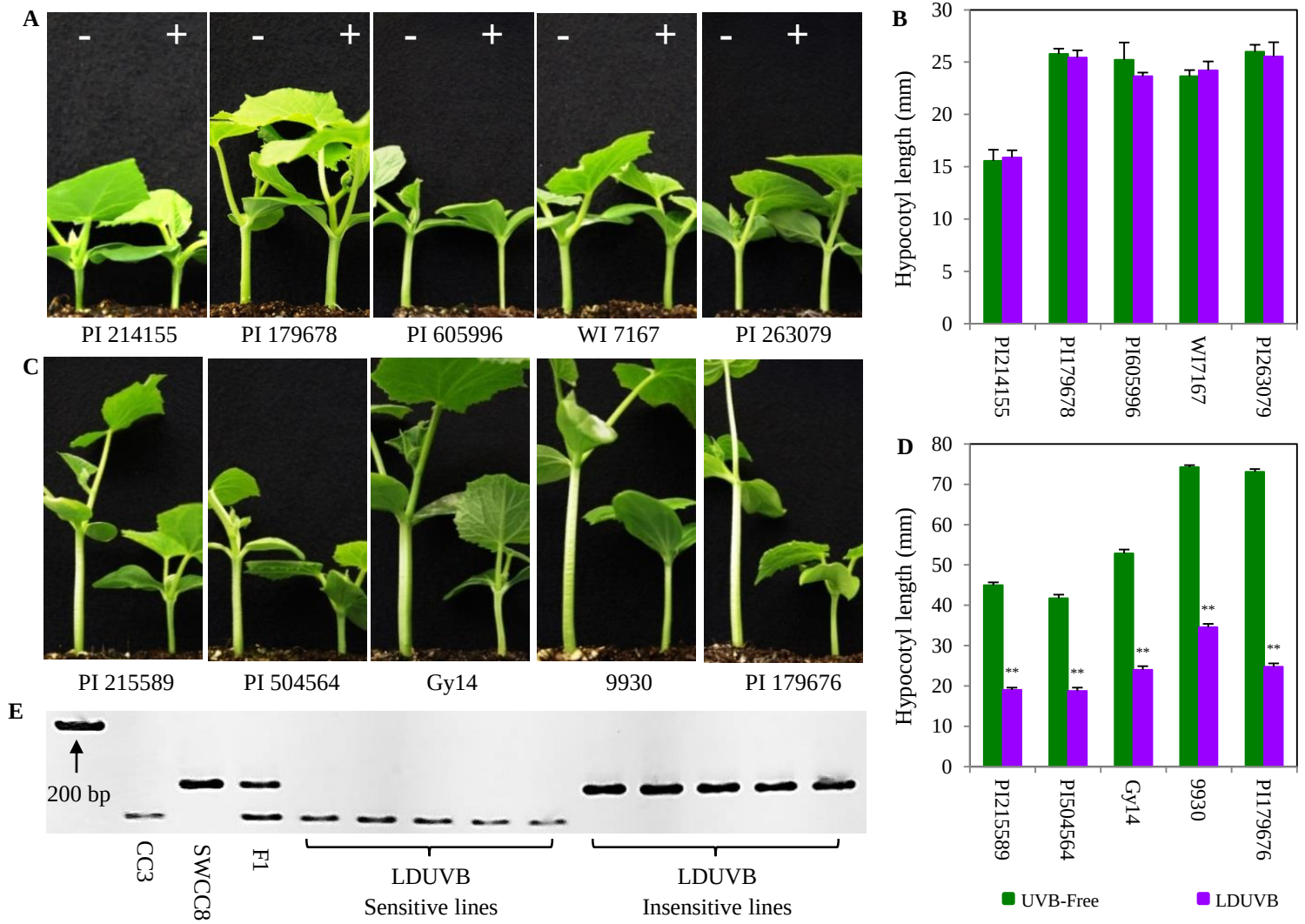


Figure S7. Association of LDUVB-dependent hypocotyl elongation with the *Sh1* locus in cucumber natural populations. **A** and **C** are representative images of LDUVB insensitive or sensitive lines, respectively. Hypocotyl length at 10d after germination of these lines are graphed in **B** and **D**, respectively. **E.** Polyacrylamide gel profile of selected lines genotyped with dCAPS-51 marker derived from the SNP within the *Sh1* candidate gene showing complete association of alternate alleles with LDUVB sensitivity of hypocotyl elongation. ** indicates statistically significant differences of hypocotyl length based on *t*-tests ($P < 0.01$).

Figure S8. Hypocotyl elongation dynamics of SWCC8 and CC3 under LDUVB and UVB-free conditions within 15d after germination. Seedling images under investigation at different time points are shown in **A**, and hypocotyl length dynamics are graphed in **B**.

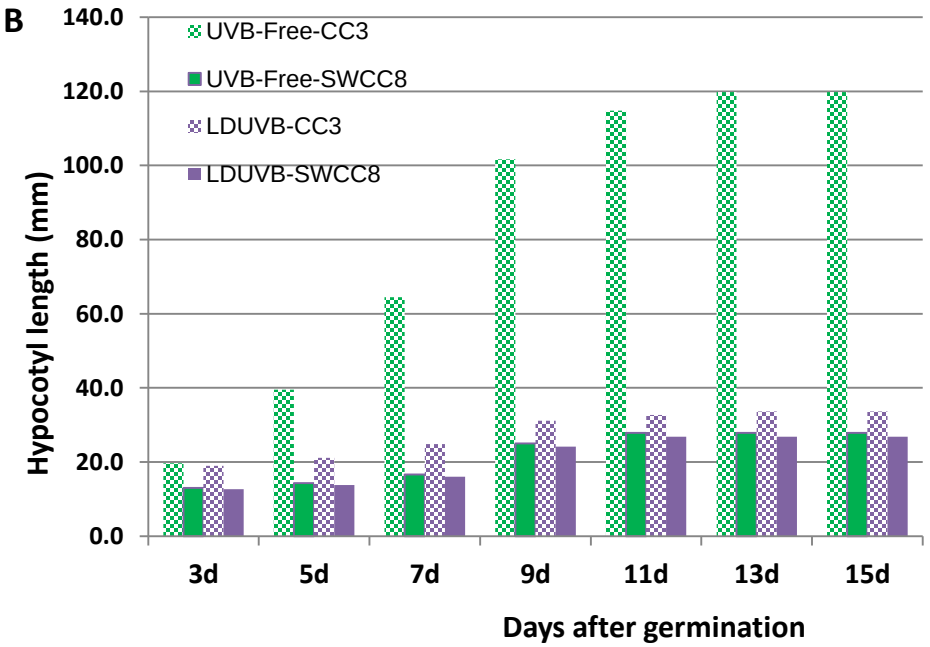
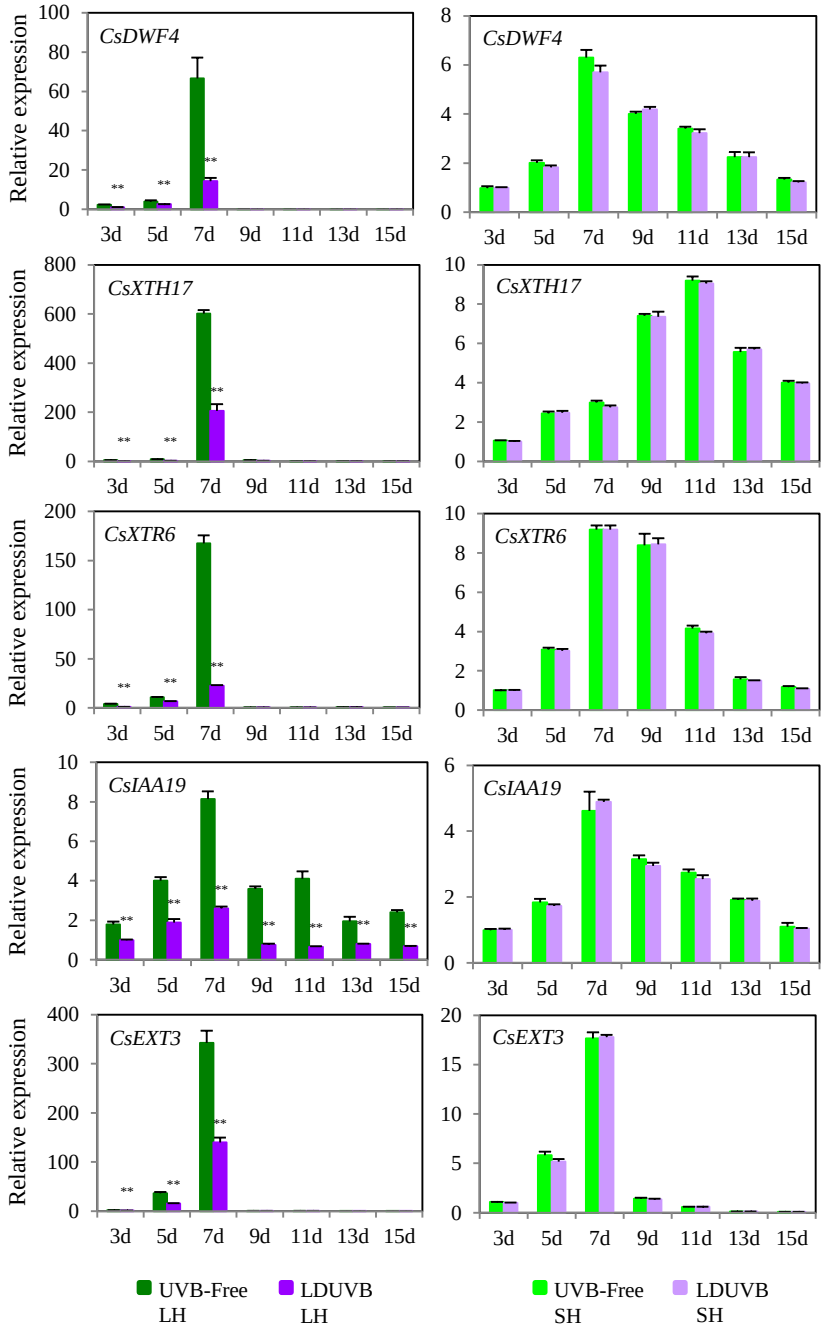


Figure S9. Expression dynamics of 5 cell-elongation related genes in two NILs of the *Sh1* gene under UVB-free and LDUVB light conditions in 15d after germination. The Y-axis of each graph is relative expression level of the gene. NIL-LH and NIL-SH are in the left and right panels respectively. For all five genes, the expression level is significantly upregulated in NIL-LH which is consistent with increased hypocotyl elongation under UVB-free light. No difference in expression is found in NIL-SH between two light conditions. NIL-SH and NIL-LH are near isogenic lines carrying the homozygous short (*sh1*) and long hypocotyl (*Sh1*) allele, respectively.



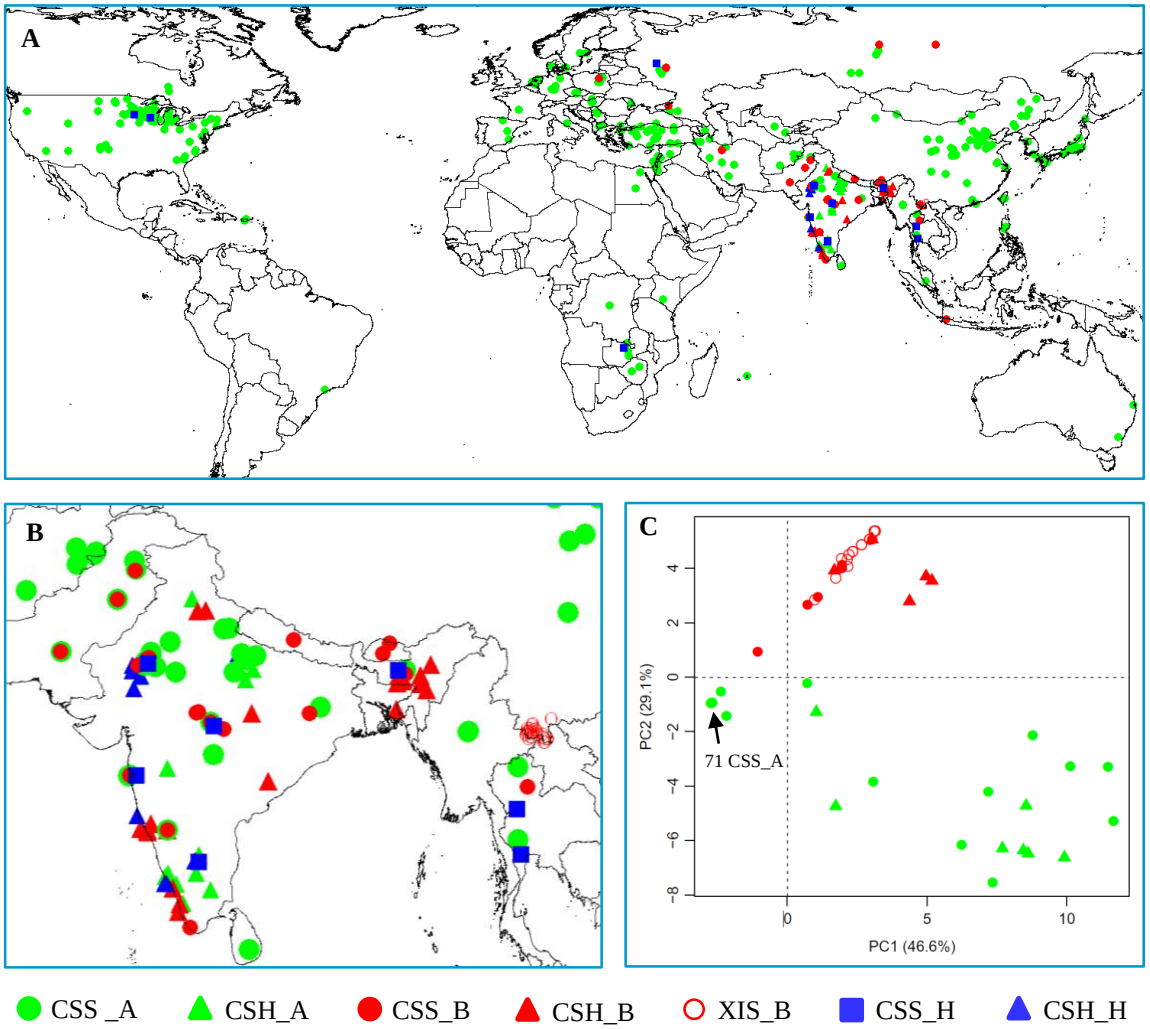


Figure S10. Worldwide geographic distribution of the *Sh1* and *sh1* alleles among natural populations of the cultivated CSS, wild CSH and semi-wild XIS cucumbers. **A.** Distribution of 502 cucumber lines in different continents based on genotypic data at the *Sh1* locus. **B.** Distribution of the two alleles in cucumber accessions originated from or close to the genetic diversity center (India and surrounding regions). **C.** Groupings of 120 *C. sativus* accessions with principal component analysis (PCA) based on 67 SNPs within 15kb region of the *Sh1* locus. Allele A = *Sh1* from CC3, B = *sh1* from SWCC8, and H = heterozygotes (*Sh1sh1*).