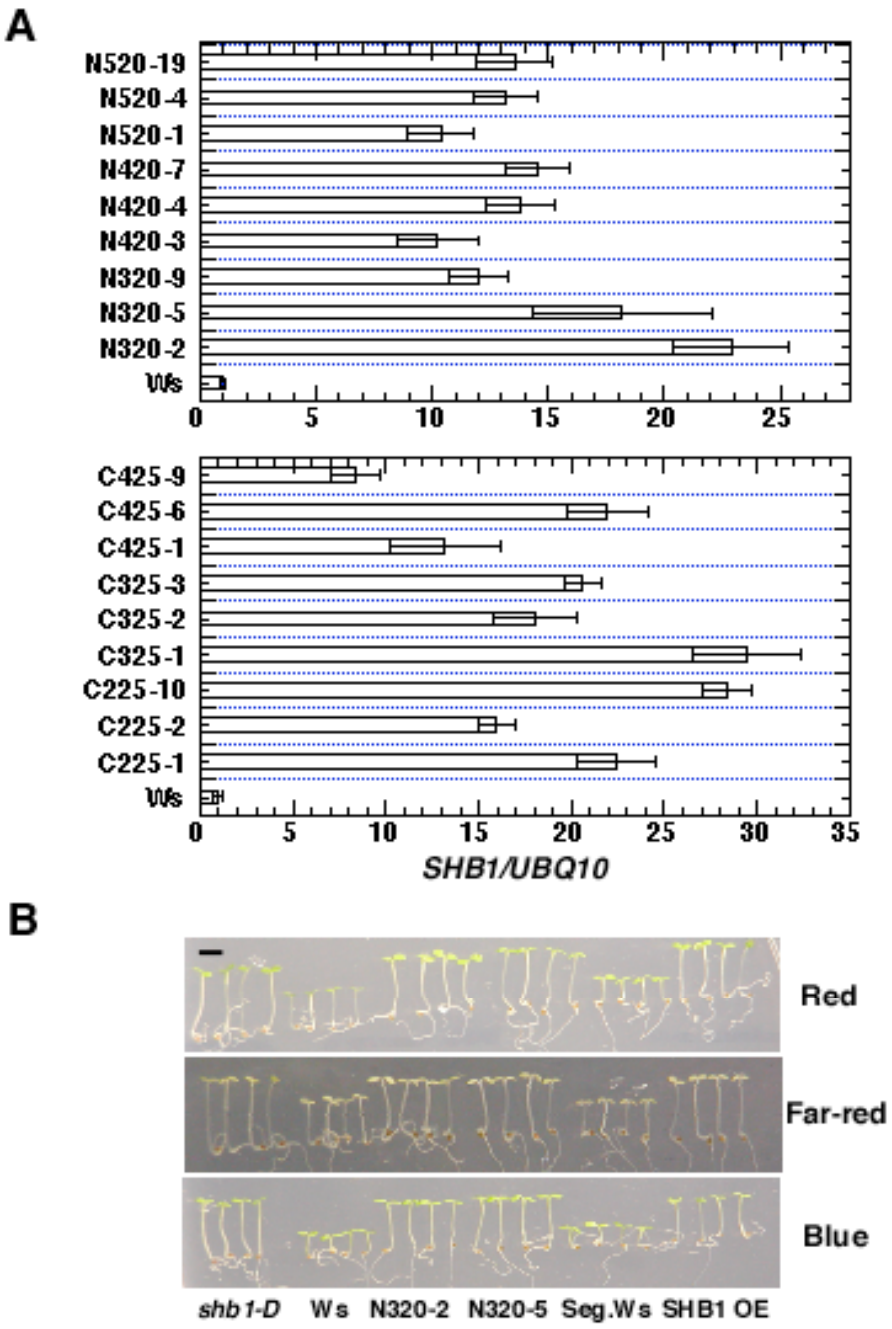
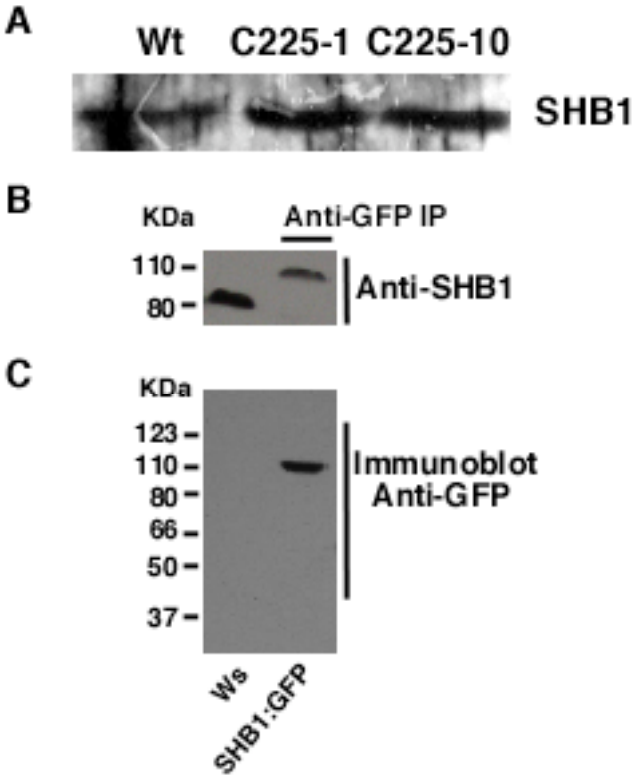
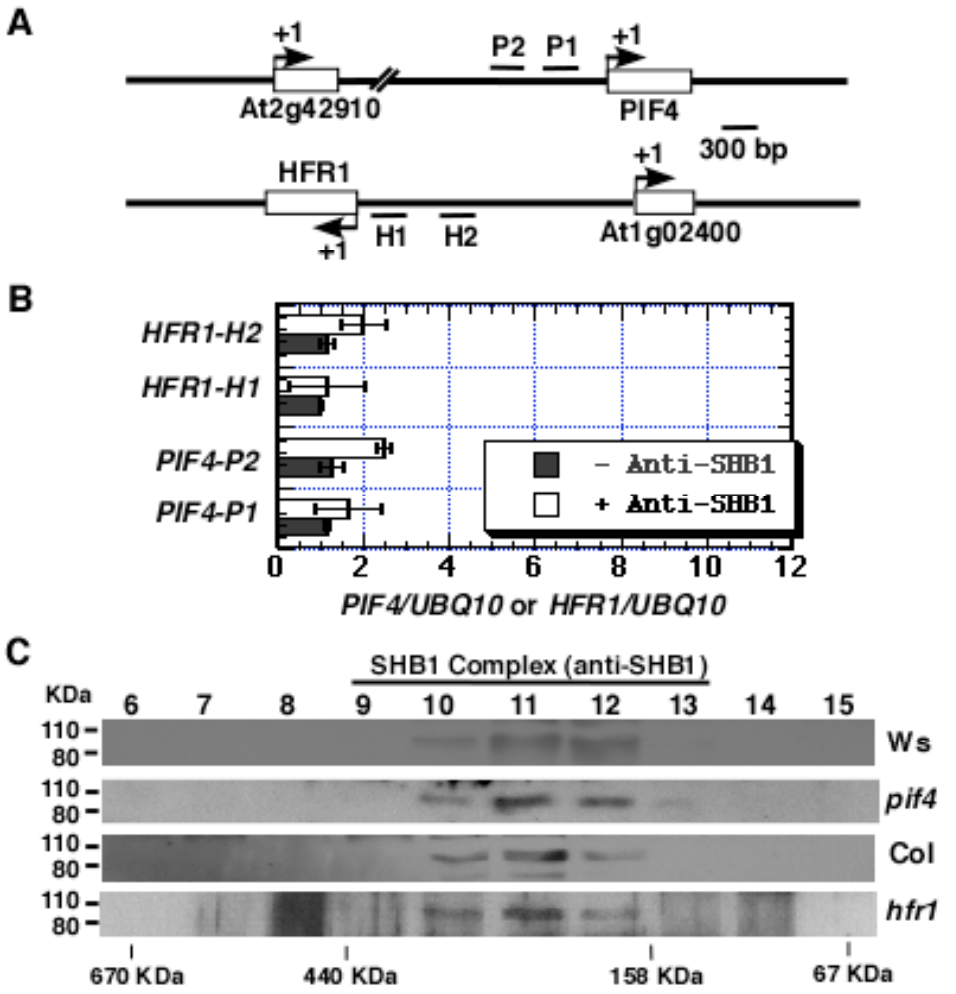


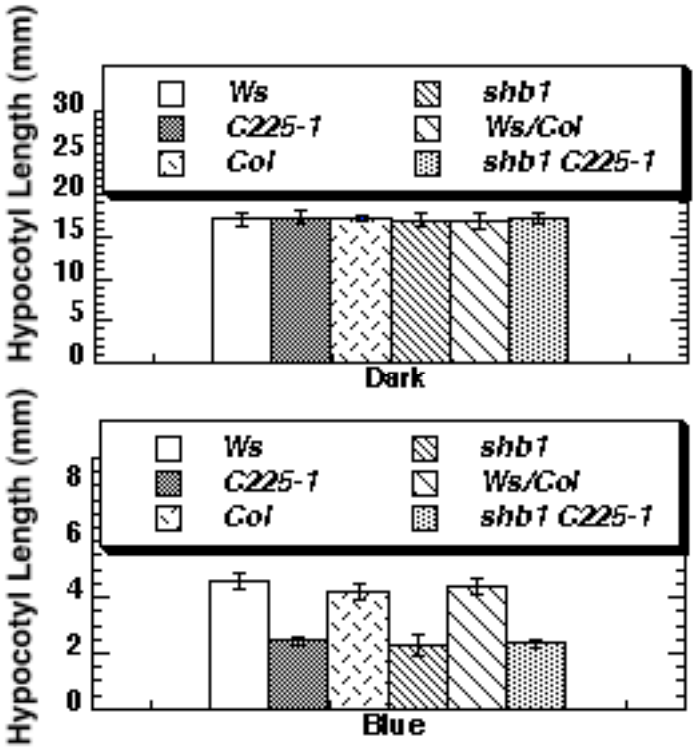
Supplemental figure 1. *SHB1* or truncated *SHB1* transgenes are overexpressed in various transgenic plants. (A) Expression of the truncated transcripts from SHB1 N-terminal deletion series (upper Panel) or C-terminal deletion series (lower panel) compared to Ws wild type through real time RT-PCR analysis. The expression levels of the truncated *SHB1* transgenes were normalized to that of *UBQ10.* Data are presented as means plus or minus the standard errors from three independent biological replicates. (B) Representative images showing the long hypocotyl phenotype of the *N320-GFP* and SHB1 full-length (SHB1 OE) overexpression transgenic lines under red, far-red, or blue light for four days after germination at intensities specified in Figure 1C. Bar = 2 mm.



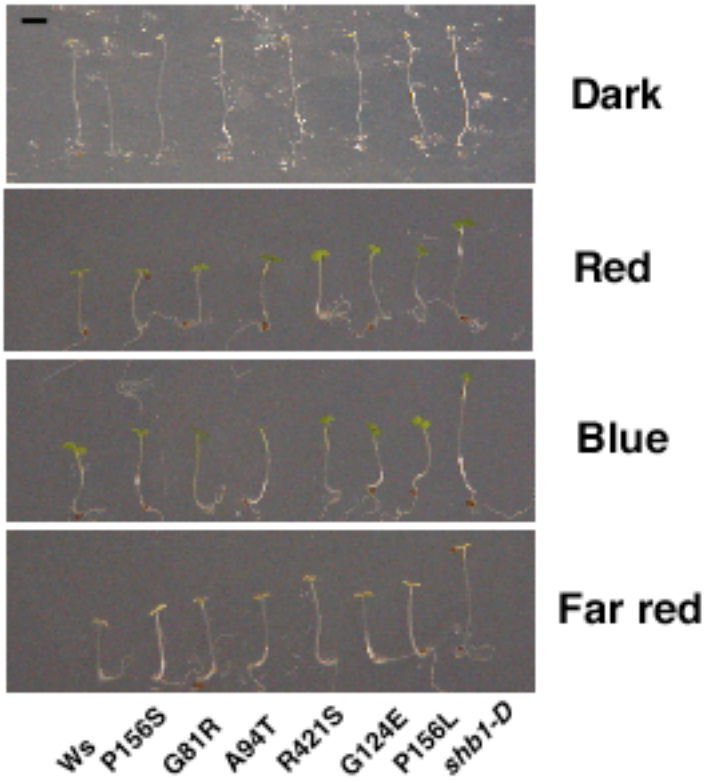
Supplemental figure 2. Over-expression of the EXS domain does not alter the accumulation of endogenous SHB1 protein and SHB1 does not form a homodimer in vivo. (A) Analysis of SHB1 accumulation in protein extracts prepared from Ws or independent transgenic lines that overexpress C225:GFP in the Ws background, separated by SDS-PAGE, and blotted with antisera against SHB1. (B) Plant extract prepared from Ws (left) or immuno-precipitation of plant extract prepared from an *SHB1-GFP* overexpression transgenic line using an anti-GFP antibody (right). Protein blots were probed with antisera against SHB1. (C) Plant extracts prepared from Ws (left) and the *SHB1-GFP* overexpression transgenic line (right). Protein blots were probed with anti-GFP antibody.



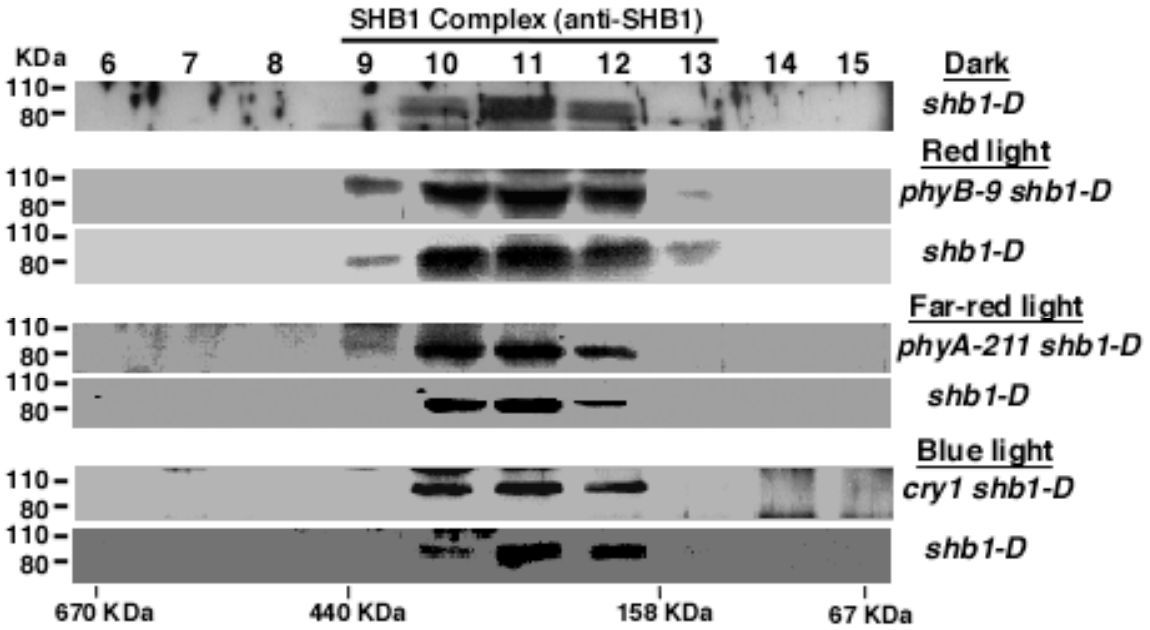
Supplemental figure 3. ChIP analysis over either *PIF4* or *HFR1* promoter using anti-SHB1 antibody and SHB1 complex formation in either *pif4* or *hrf*. (A) Schematic diagram of the *PIF4* and *HFR1* loci and four amplicons in their promoters used for ChIP analysis. (B) ChIP analysis over the *PIF4* and *HFR1* chromatin regions using anti-SHB1 antibody in wild type. The enrichment of particular chromatin regions was detected by real-time PCR analysis. Preimmune serum was used as mock control and the fold-enrichment of the specific chromatin fragment was normalized to the *UBQ10* amplicon and calculated for each amplicon using the following equation: 2(Ct PIF4/P1 MOCK-Ct PIF4/P1 ChIP)/ 2(Ct UBQ10 MOCK-Ct UBQ10 ChIP). Data are means of two independent ChIP experiments with different biological samples and four PCR technical replicates per biological sample plus or minus the standard errors. (C) Gel filtration profiles of SHB1 in Ws, *pif4,* Col, and *hfr1*. Plant extracts from seven-day-old seedlings grown in red, blue, or white light were fractionated on a Superdex-200 gel-filtration column. The various fractions were collected, separated by SDS-PAGE, and blotted with antisera against SHB1. Data are presented for the white light experiment. The molecular mass standards of the gel filtration fractions were labeled at the bottom, and the molecular mass markers of the SDS-PAGE gel were labeled on the left.



Supplemental figure 4. Over-expression of the *SHB1* C-terminal EXS domain in *shb1* shows a short hypocotyl phenotype similar to *shb1* under blue light. Hypocotyl lengths of Ws, transgenic plants that overexpress *C225:GFP* (*C225-1*), Col, *shb1*, Ws Col, and *shb1 C225-1* in Ws Col background in the dark (upper panel) or under blue light (lower panel). Light intensities were specified in Figure 1C. The means plus or minus the standard errors were calculated from at least 25 seedlings per replicate and three replicates total.



Supplemental figure 5. Six mis-sense mutations in the SPX domain revert the hypocotyl phenotype of *shb1-D* to wild type. Visual presentation of the hypocotyl growth responses of Ws, *shb1-D*, and six mis-sense SHB1 mutants in the dark or under red, far-red, or blue light at intensities as specified in the legend to Figure 1C.



Supplemental figure 6. The size and abundance of SHB1 protein complex is not altered by different wavelengths of light. (A) Gel filtration profiles of SHB1 in *shb1-D*, *phyB-9 shb1-D*, *phyA-211 shb1-D*, and *cry 1 shb1-D*, all in mixed Ws/Col genetic background. Plant extracts were prepared from 7-day-old seedlings grown in dark, red light, far-red light, or blue light as indicated. Light intensities were specified in Figure 1C. Equal amount of total proteins were loaded and fractionated on a Superdex-200 gel-filtration column. The various fractions were collected, separated on SDS-PAGE, and blotted with antisera against SHB1. The ÄKTA™ FPLC™ system has a very consistent protein recovery in each fraction, and we also measured the protein content in each fraction, especially the peak fractions, to ensure a consistent recovery of the loaded protein in each fraction between single *shb1-D* mutant and double *shb1-D* photoreceptor mutant. The Molecular mass standards of the gel filtration fractions were labeled at the bottom, and the molecular mass markers of the SDS-PAGE gel were labeled on the left.

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