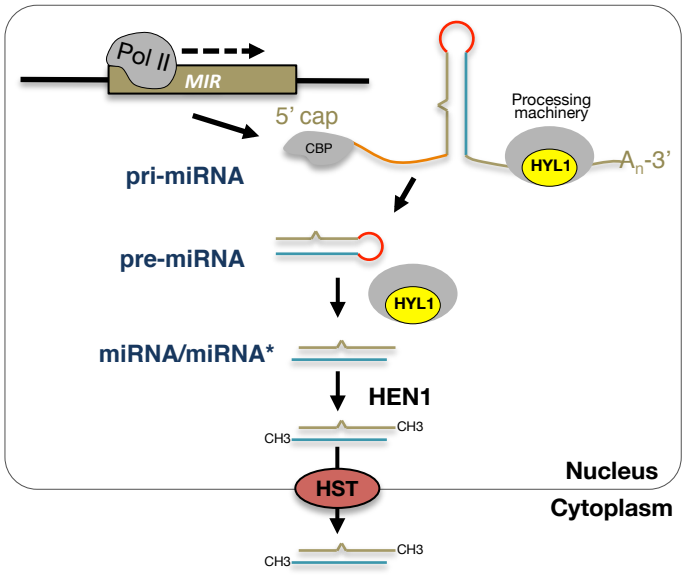
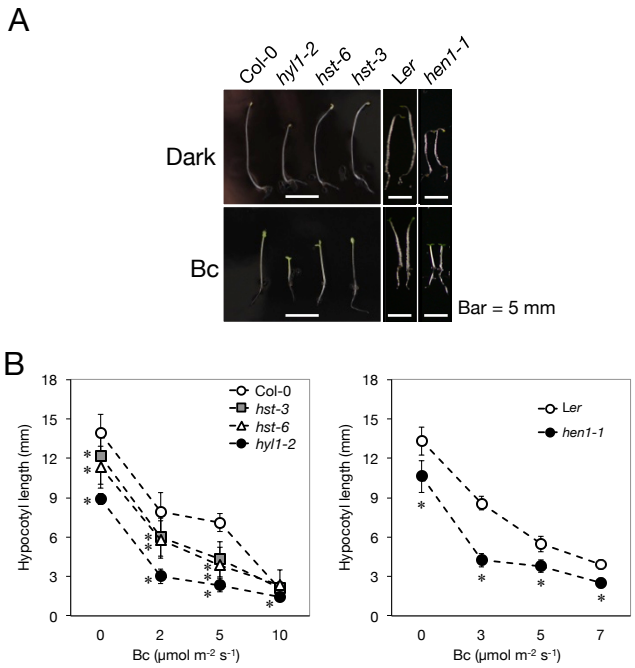
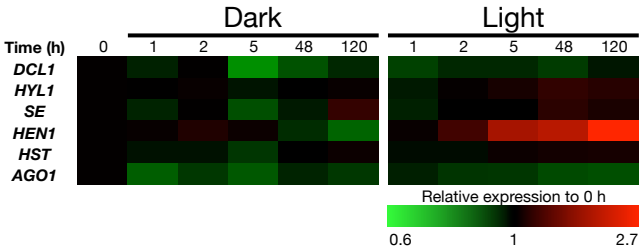



Supplemental Figure 1. **Schematic overview of canonical miRNA biosynthesis (modified from Rogers and Chen, 2013).**



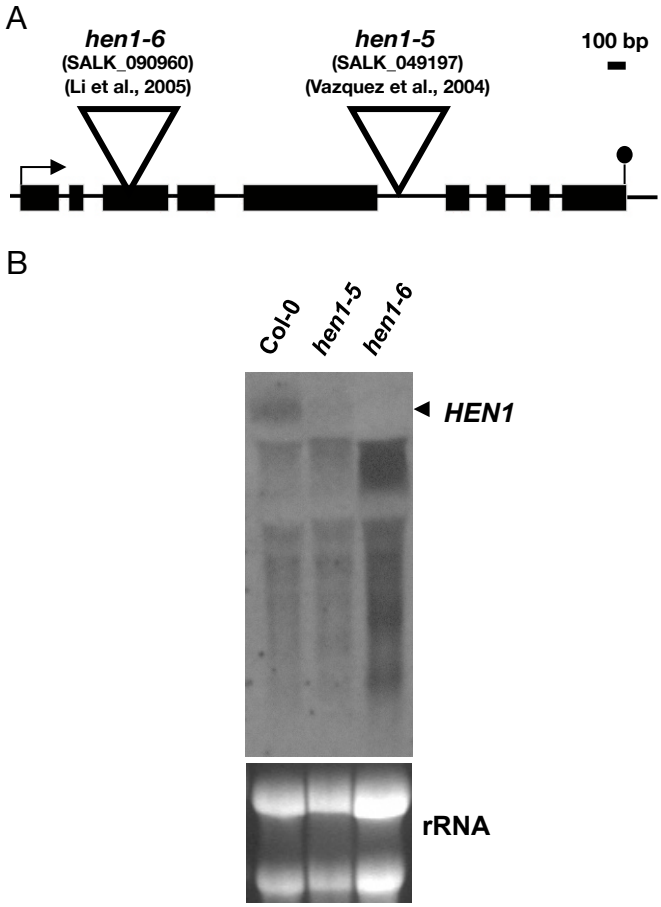

Supplemental Figure 2. **Skotomorphogenesis and photomorphogenesis are defective in miRNA biogenesis mutants**

The *hyl1-2*, *hen1-1*, *hst-3* and *hst-6* mutants show defects in hypocotyl elongation in the dark and light (A). However, the mutants are hypersensitive to continuous blue light (Bc)(B). Data are mean ± SD. *, significantly different from the corresponding wild type (Col-0 and L*er*)($p < 0.05$, Student's *t* test; n = 16-32).



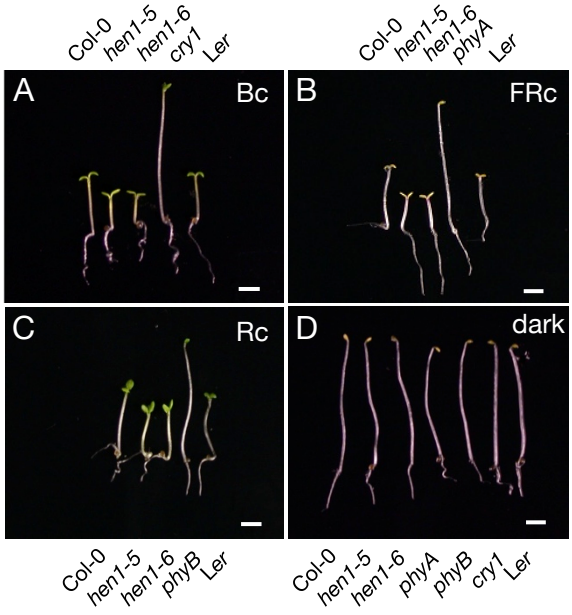

Supplemental Figure 3. **The transcript level of *HEN1* is light-upregulated**

Expression of miRNA biosyntheic genes *HEN1*, *DCL1*, *HYL1*, *SE*, *HST* and *AGO1* in etiolated seedlings under dark and light treatments at the indicated times from Genevestigator sample AT-00003 (repository name: PZ051203_02). Gene expression for the times indicated was normalized to time 0.

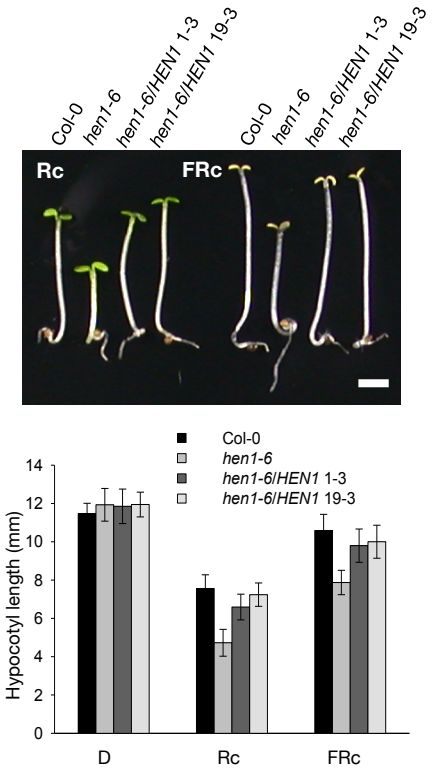



Supplemental Figure 4. **Molecular characterization of *hen1-5* and *hen1-6* mutants**

(A) SALK_049197 (*hen1-5*) and SALK_090960 (*hen1-6*) lines carried the T-DNA insertion in intron 5 and exon 3, respectively, of *HEN1*. The locations of the T-DNA and transcription start/end are marked on the *HEN1* gene model. (B) RNA gel blot analysis with a DNA probe spanning 1 to 500 bp of the *HEN1* coding region for profiling *HEN1* expression in the wild type (Col-0), *hen1-5* and *hen1-6*. Ethidium-bromide–stained rRNA is shown as a loading control.

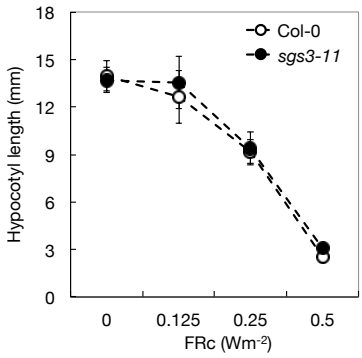



Supplemental Figure 5. **The *hen1* mutants are hypersensitive to blue (B), far-red (FR), and red (R) light**
Representative seedlings of 4-d-old seedlings of Col-0, L*er*, *hen1-5*, *hen1-6*, *phyA*, *phyB* and *cry1* seedlings grown under continuous blue light (Bc) (A), FRc (B), Rc (C) or dark (D). Bar = 2 mm.

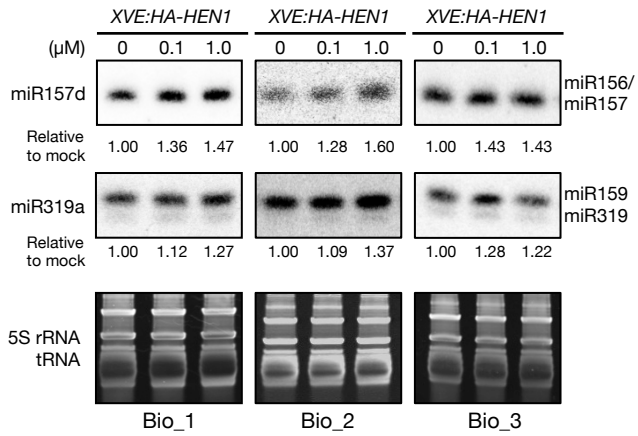



Supplemental Figure 6. **Functional complementation of *hen1* light-hypersensitive phenotype**

A genomic fragment harboring *HEN1* (-2,135 to +4,492 of *HEN1* locus) was generated by PCR with specific primers (Supplemental Table 1 online) and subcloned into the *Sal*I-*Pml*I sites of the binary vector pCAMBIA1390 and introduced into *hen1-6*. Hypocotyl lengths of Col-0, *hen1-6*, and 2 representative complementation lines, *hen1-6/HEN1* 1-3 and *hen1-6/HEN1* 19-3, grown under dark (D), Rc (5 μmol $m^{-2}$ $s^{-1}$) or FRc (0.125 $Wm^{-2}$). Data are mean ± SD. Bar = 2 mm.

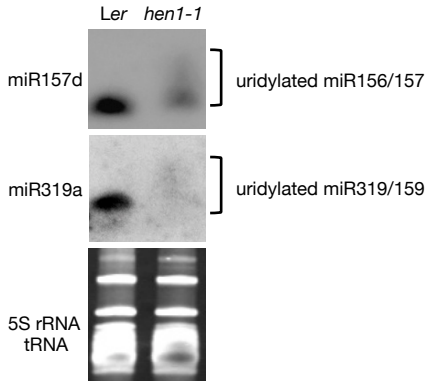



Supplemental Figure 7. **Effect of FR fluence rate on hypocotyl extension in wild-type and *sgs3-11* mutant seedlings**
Hypocotyl lengths of wild-type and *sgs3-11* seedlings grown under different FRc fluence rates for 4 days. Data are mean ± SD.

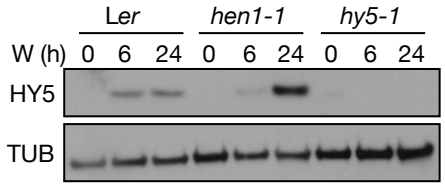



Supplemental Figure 8. **The levels of miR157 and miR159/319 are increased accompanied with increased level of HA-HEN1 protein.**

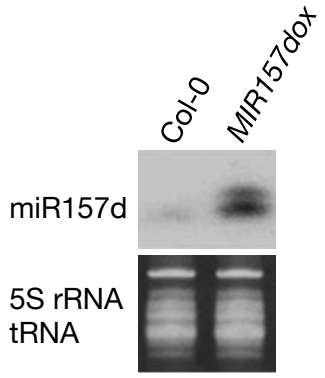
Three biological replicates of small RNA analyses of miR157 and miR159/319 expression levels. The replicate Bio_1 was shown in Figure 5C. The numbers below the blots showed 5S rRNA- and tRNA-normalized miRNA fold increase in HA-HEN1-induced seedlings.



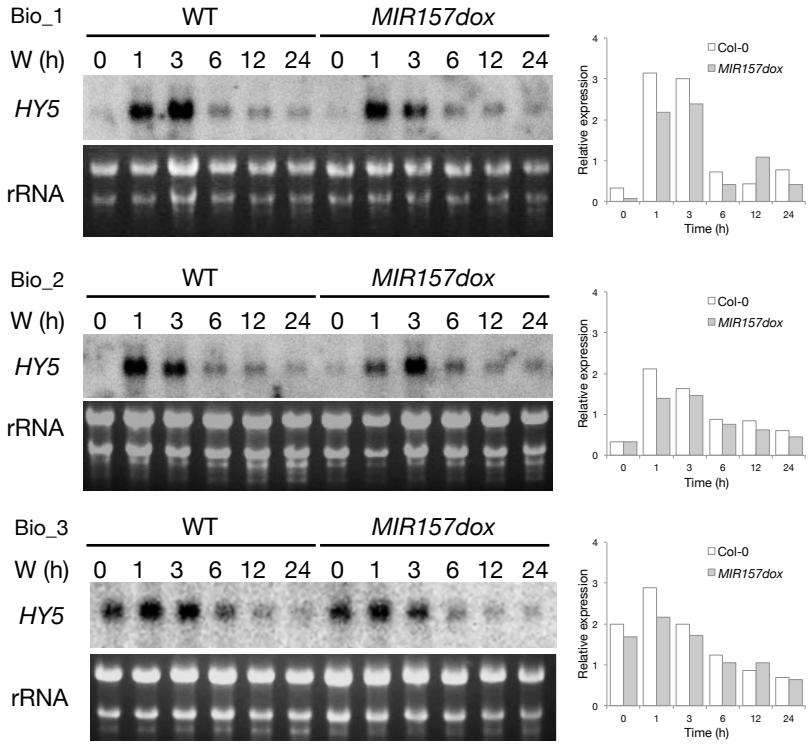

Supplemental Figure 9. **The expressions of miR157d and miR319 are compromised in *hen1-1* mutant**
Four-day-old etiolated wild-type (L*er*) and *hen1-1* seedlings were treated with W (50 μmol $m^{-2}$ $s^{-1}$) for 24 h, and then RNA gel blot analysis was carried out with 1 μg total RNA. DNA oligos used for each blot are indicated to the left of each blot. Despite the clear detection of miR156/157 and miR319/159 in L*er*, only traces of uridylated miR156/157 and miR319/159 were detected in *hen1-1*. Ethidium-bromide-stained rRNA/tRNA is shown as loading control.




Supplemental Figure 10. **HY5 is increased in the *hen1-1* mutant during photomorphogenesis**
Protein levels of HY5 in 4-d-old de-etiolating seedlings of wild type (L*er*) and *hen1-1* under W (100 μmol $m^{-2}$ $s^{-1}$) at the indicated times. HY5 was not detected in the *hy5-1* mutant. TUB was used as a loading control.




Supplemental Figure 11. **Over-accumulation of miR157d detected in the *MIR157dox* line**
RNA gel blot analysis of the miR157d levels in 4-d-old Wc (100 μmol $m^{-2}$ $s^{-1}$)-grown seedlings of the wild type (Col-0) and *MIR157d* overexpression line (*MIR157dox*). DNA oligos used for each blot are indicated to the left of each blot. Each sample contained 1 μg total RNA.




Supplemental Figure 12. **The *HY5* transcript levels are decreased in the *MIR157dox* transgenic line**

Three biological replicates of RNA gel blot analyses on *HY5* transcript levels in *MIR157dox* transgenic line during the de-etiolation. The replicate Bio_1 was shown in Figure 8A. The etiolated seedlings on the time 0 point were collected in the dark except those on Bio_3 time 0, which were collected under the light. The bar graphs show the *HY5* signals normalized to ribosomal RNA using Image J on each biological replicate.

Supplemental Table 1. **Primers and oligos used in this study**

| Primer | Sequence (5' to 3') |
|---|---|
| Quantitative RT-PCR analysis | |
| *HEN1*-F | CAACGTCAAATCTGCTACACTTT |
| *HEN1*-R | AAGTGCCGATGTCAACGTCAT |
| *HY5*-F | ATGTTAAAATTATATGGGATGTGAGAGCTAA |
| *HY5*-R | TTCAATTAAGAGAAATCTAAGACTACAATAAGAGA |
| *TCP2*-F | GGTGGCTTCAGTGGTTTCAAC |
| *TCP2*-R | CCTCTGTAGATTAGCGAGGAATGAC |
| *TCP3*-F | CCGGAGGATTTGTGTTTGCT |
| *TCP3*-R | CCCCTCTGTGATAAAAGCTGACTT |
| *TCP4*-F | CAAAGCCAACAGCTTTATTCTCAGA |
| *TCP4*-R | GATGATGGTGAGGATCAAACCA |
| *TCP10*-F | TGTTTCTTGGTGGCCAACAA |
| *TCP10*-R | TGATCCCAAGAACGAAACGAAT |
| *TCP24*-F | ACCCATTCTCCTTTGTACCTGATT |
| *TCP24*-R | AAGAGAGATTGTGAATTGGACTGAAG |
| *UBQ10*-F (Col-0) | AGAAGTTCAATGTTTCGTTTCATGTAA |
| *UBQ10*-R (Col-0) | GAACGGAAACATAGTAGAACACTTATTCA |
| *UBQ10*-F (Ler) | ACAGCTAGAGGATGGCCGTA |
| *UBQ10*-R (Ler) | GTTGGTCTGGCGGGATAC |
| *GFP*-F | GATGGCCCTGTCCTTTTACCA |
| *GFP*-R | GGCAGATTGTGTGGACAGGTAAT |
| *UBI3*-F (N.b.) | GCCGACTACAACATCCAGAAGG |
| *UBI3*-R (N.b.) | TGCAACACAGCGAGCTTAACC |
| | |
| Northern blot probe | |
| *HEN1*-F | TCTCCATGGATTTCAGGGGTATGCACATTT |
| *HEN1*-R | CGCTCTAAGGTGAGCTCCCA |
| *HY5*-F | GTAGTCGACCAGAGATCTGACGGCGGTAG |
| *HY5*-R | GTAGGATCCCCTCCGCCGGTGTCCTCCCT |
| miR157d-probe | GAGTGCTCTCTATCTTCTGTCATCAAAGAGAATCAATGA |
| miR156a-probe | GTGCTCACTCTCTTCTGTCA |
| miR319a-probe | AGGGAGCTCCCTTCAGTCCAA |
| | |
| *MIR* gene amplification | |
| *MIR156a*-F | GTATCTAGACTCTTATCTTCTTCTCATCAG |
| *MIR156a*-R | GTACCCGGGAACAAGAACAAGCCAGAGTT |
| *MIR157d*-F | GTATCTAGACCATTTACTCTTCACCGCCC |
| *MIR157d*-R | GTACCCGGGTATAACATGAACTGATGAACCT |
| | |
| *HEN1* gene amplification | |
| *HEN1genomic*-F | CGAGGTACCATGGCCGGTGGTGGGAAGCA |
| *HEN1genomic*-R | TGTCCTAGGTCAAAGATCAGTCTTTTTC |
| | |
| *HEN1* complementation | |
| *HEN1*-gDNA-SalI-S1 | AGCGTCGACTGTTATGTGGTATGTATA |
| *HEN1*-gDNA-S1642 | CATGAAAGTCCGCTGAACTCTTTAGGTTCGTTGTCG |
| *HEN1*-gDNA-S3266 | GATGTTTGGCAAAGCTTCCTGTGGCTCTGAGTGTAG |
| *HEN1*-gDNA-S4862 | CAAAGTTATGTAAGAACCTCACGTAAAGTCTTCTGG |
| *HEN1*-gDNA-AS1678 | TCGACAACGAACCTAAAGAGTTCAGCGGACTTTCAT |
| *HEN1*-gDNA-AS3302 | TCTACACTCAGAGCCACAGGAAGCTTTGCCAAACAT |
| *HEN1*-gDNA-AS4897 | CAGAAGACTTTACGTGAGGTTCTTACATAACTTTGC |
| *HEN1*-gDNA-PmlI-AS6627 | AGCACGTGTTAAACTTCAACGGACCA |

| | |
|---|---|
| *HY5* 5'UTR amplification | |
| *HY5-5'UTR*-F | TCTAGAGTCCCGCTCTTTTCCTCTTTATC |
| *HY5-5'UTR*-R | CTCGAGTTTTCTTACTCTTTGAAGATCGAT |
| *HY5-5'UTRm*-F | TTCCTCCAATACCTTTTCACCAG |
| *HY5-5'UTRm*-R | GCTGGTGAAAAGGTATTGGA |
| | |
| *mHY5* cDNA | |
| *HY5*-5'UTRm-*Xba*I-F | GACTCTAGATCCCGCTCTTTTCCTCCAATACCTTTTCACCA |
| *HY5stop-Eco*RI-R | TCGGAATTCTCAAAGGCTTGCATCAGCAT |
| | |
| 5'-RACE | |
| *HY5*-R | TCCTCCCTCGCTTCCTTTGACTTTC |
| *TCP24*-R | TCTCCTTTCCTTTGCCTTGTCAT |