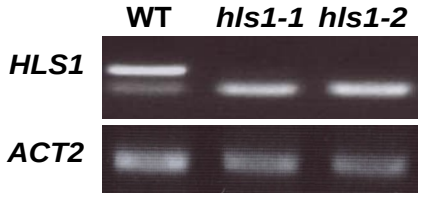
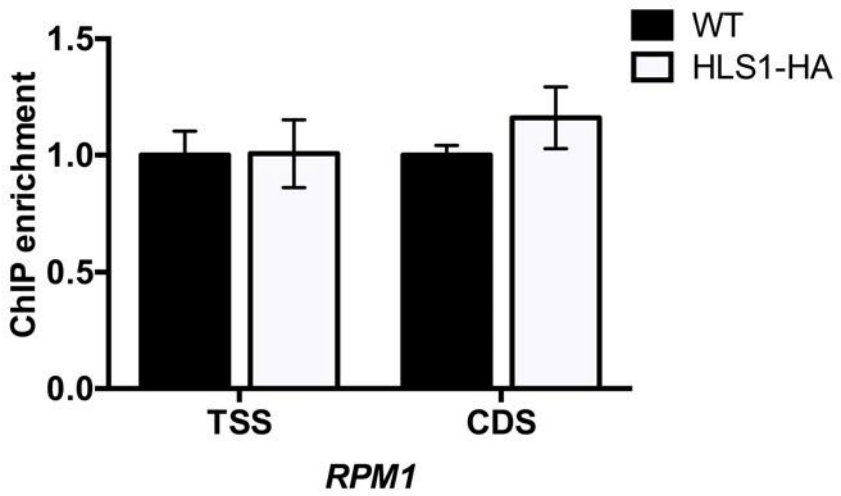
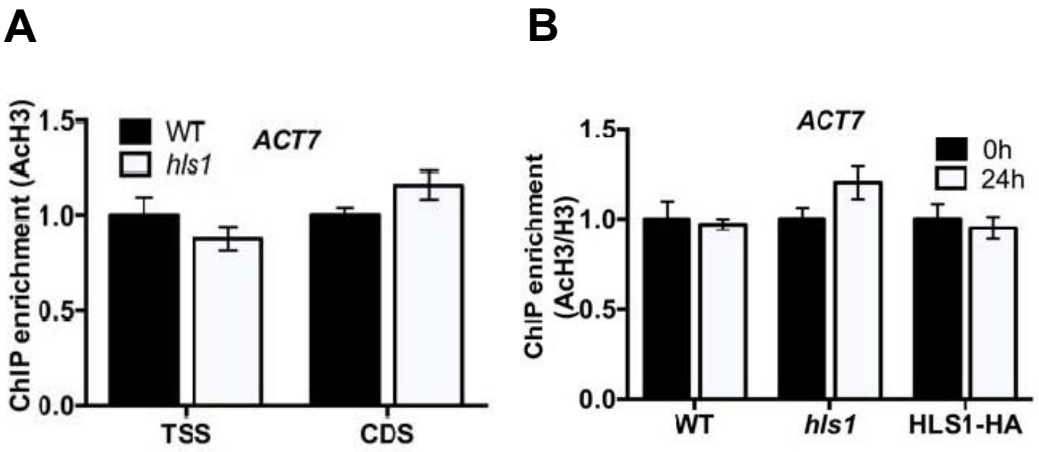



**Supplemental Figure 1. The *hls1* mutants lack *HLS1* expression.** The 3-day-old *hls1* mutant seedlings grown on 1/2 MS medium were collected and RNA was extracted for reverse transcription (RT)-PCR. Results displayed that *hls1* mutants are unable to produce *HLS1* RNA . The amplification of *ACT2* PCR products was used as a control.

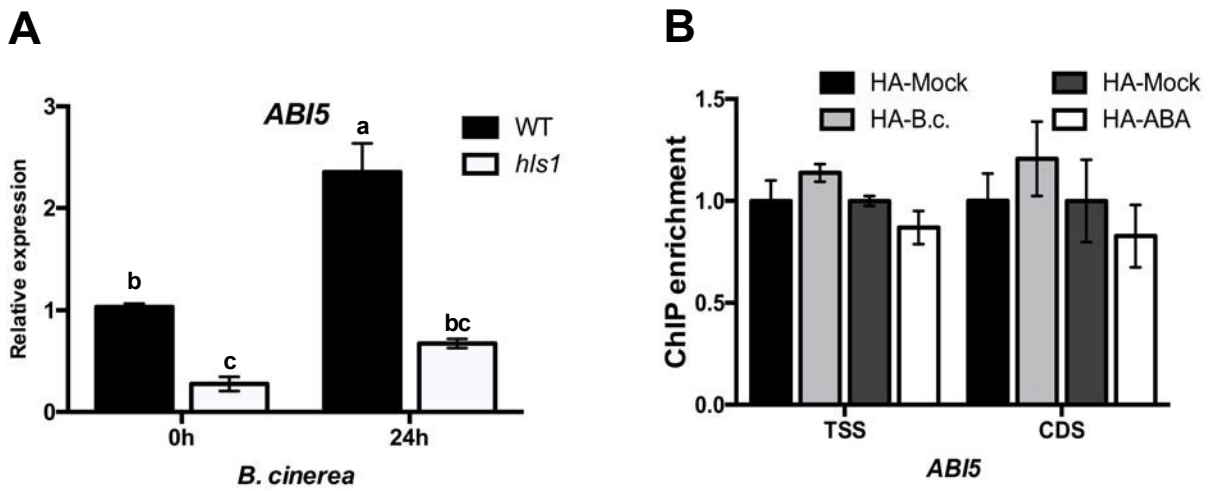



**Supplemental Figure 2. HLS1 protein is not associated with resistance gene *RPM1*.** Samples were collected from wild type (WT) and plants overexpressing *HLS1* for ChIP-qPCR assays. The TSS and CDS regions of *RPM1* were tested and the association of protein from wild type with *RPM1* is set to 1 as a background control. The experiment was repeated two times with similar results. The data represent mean values ± SE (n=3). TSS: transcriptional start site; CDS: 3'-coding DNA sequence region.




**Supplemental Figure 3. The histone H3 acetylation at *ACTIN7* chromatin shows no difference between wild-type and *hls1* plants.**

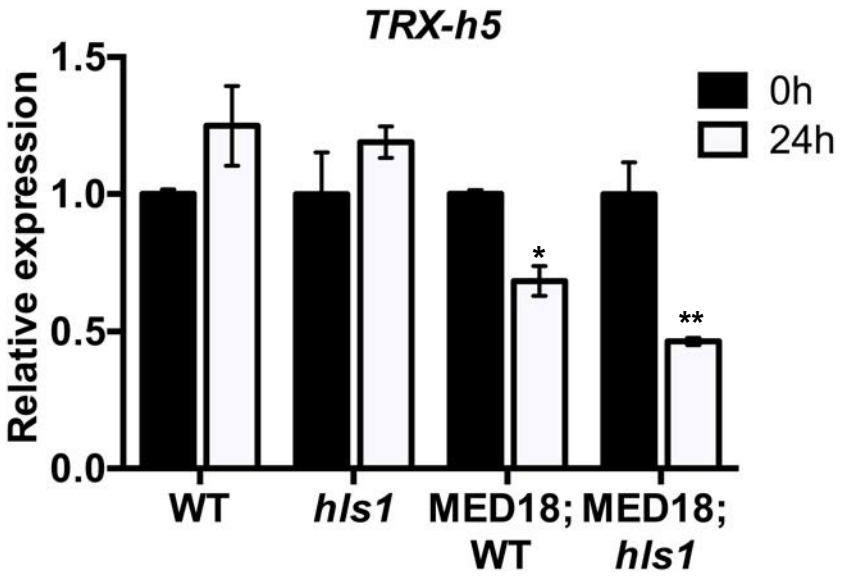
ChIP-qPCR assay was performed using antibodies that recognize acetylated histone H3 and histone H3. (A) Two different regions of *ACTIN7* were amplified by qPCR. The enrichment of *ACTIN7* in wild-type plants was set to 1 as a background control in ChIP-qPCR assay. (B) The TSS region of *ACTIN7* was selected and the H3 acetylation status is normalized with histone H3 from each sample. The enrichment of *ACTIN7* in wild type at 0 hour is set to 1 as a background control in the assay. The data represent mean values ± SE (n=3). Wild type (WT); Transcription start site (TSS); 3'-coding DNA sequence (CDS); *ACTIN7* (*ACT7*).




**Supplemental Figure 4. The recruitment of HLS1 protein to the *ABI5* locus is not enhanced by *B. cinerea* inoculation.**

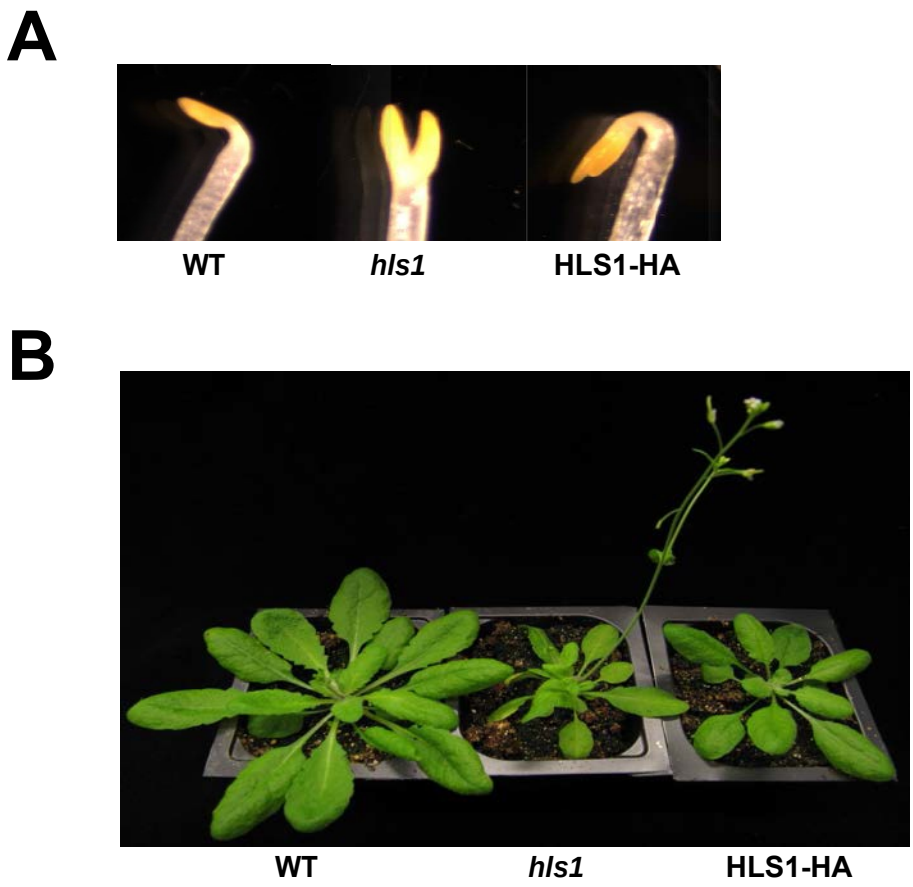
(A) *ABI5* induction is modulated in *hls1* mutants after inoculation with *B. cinerea*. The expression of *ABI5* in WT is set to 1. The statistically significant differences are indicated by different letters (least squares means post hoc test: $P<0.05$).

(B) HLS1 is unable to enhance the association of *ABI5* gene after inoculation with *B. cinerea* or treatment with ABA. The association of 35S:HLS1-HA with *ABI5* under mock treatment is set to 1 as a background control in ChIP-qPCR assay. The data represent mean values ± SE (n=3). TSS: transcription start site; CDS: 3'-coding DNA sequence region.




**Supplemental Figure 5. MED18-mediated plant resistance through *TRX-h5* regulation is HLS1-independent.**

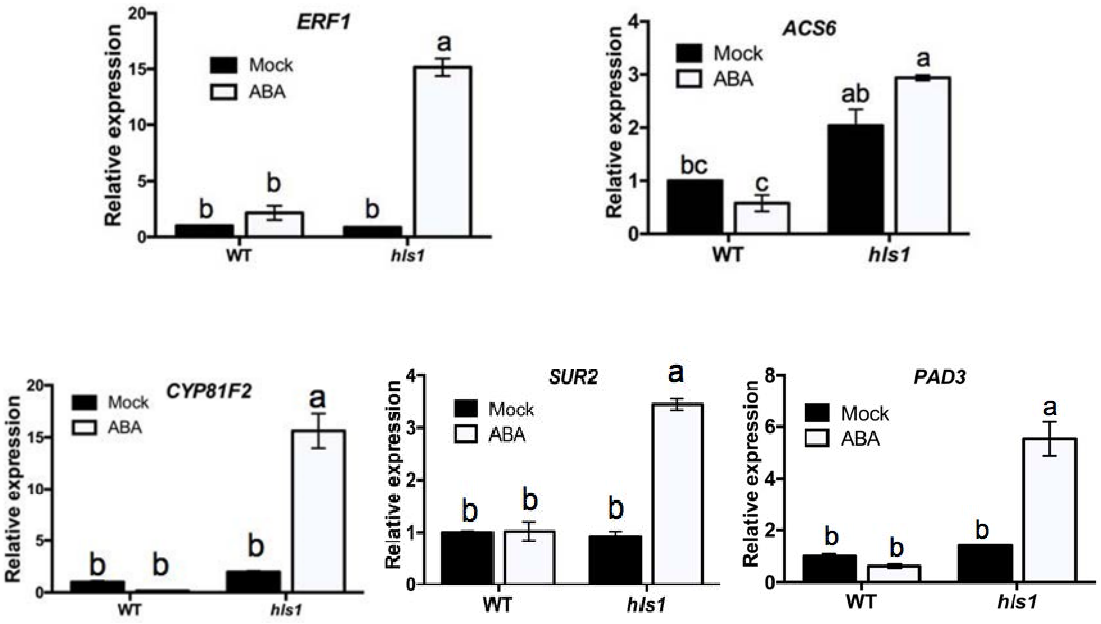
*TRX-h5* is regulated in response to *B. cinerea* inoculation. The expression is reduced and the pattern is similar between transgenic plants overexpressing MED18 in a wild type or *hls1* mutant background. Gene expression at 0 hour is set to 1. The data represent mean values ± SE (n=3) and the statistically significant differences are indicated by asterisks (Student's *t*-test: *P<0.05, **P<0.01).



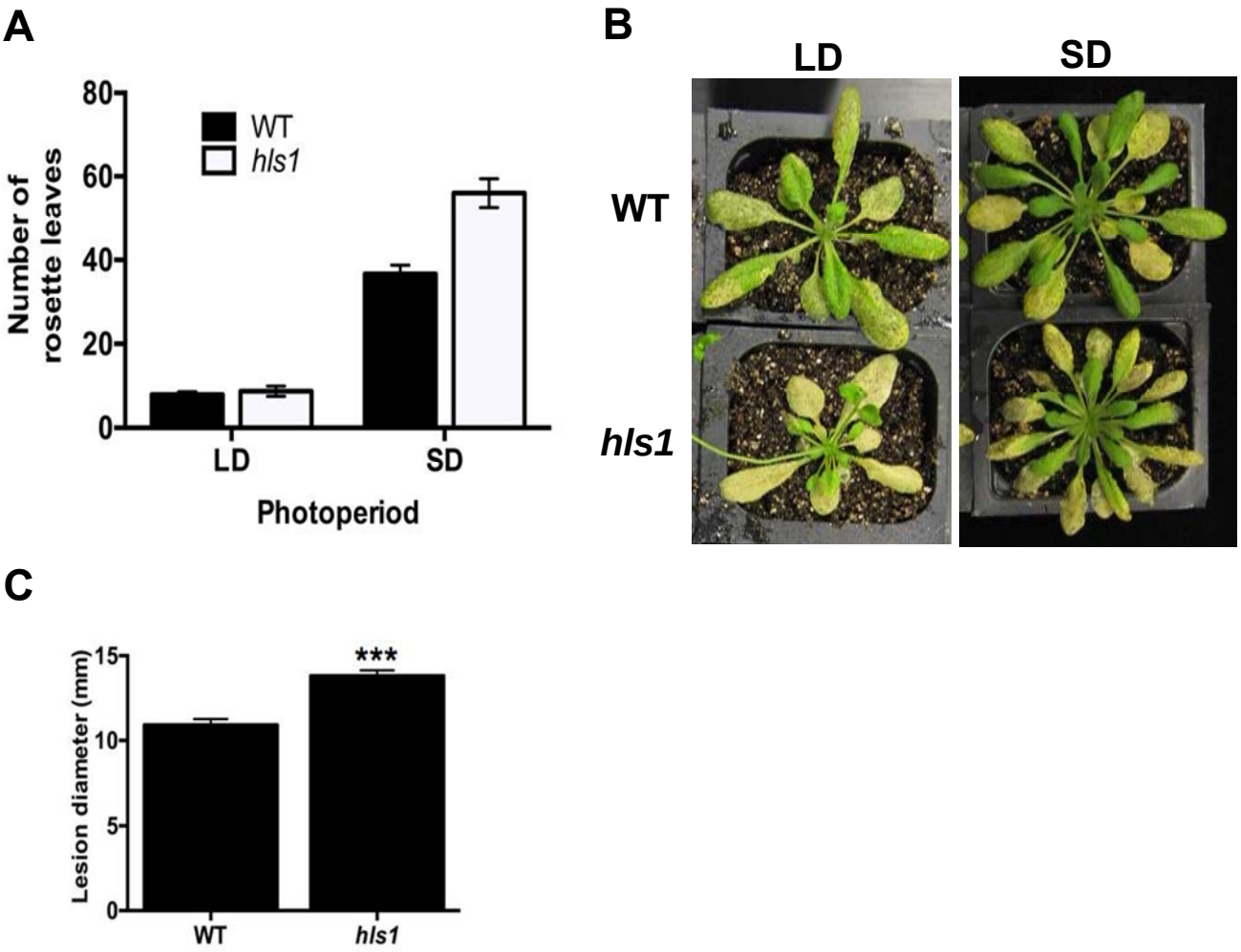

**Supplemental Figure 6. Overexpressing *HLS1-HA* in Arabidopsis shows developmental phenotypes opposite to the *hls1* mutant.**

(A) The hook phenotype in wild-type, *hls1,* and *35S:HLS1HA* (HLS1-HA) plants 5 days after germination.

(B) HLS1 regulates flowering time in Arabidopsis. The photo was taken of 5-week-old plants, demonstrating early flowering of the *hls1* mutant but delayed flowering of the *HLS1-HA* plants. WT: wild type.




**Supplemental Figure 7. Expression of defense-related genes is induced in the *hls1* mutant in response to ABA.** The expression of genes in the wild type after mock inoculation is set to 1. The data represent mean values ± SE (n=3) from two independent experiments and statistically significant differences are indicated by different letters (least squares means post hoc test: $P<0.05$).




**Supplemental Figure 8. Leaf number, but not disease phenotype, is affected by HLS1 under short day conditions.**

(A) Plants were grown under a long day (LD; 12 h light : 12 h dark) or short day (SD; 8 h light : 16 h dark) photoperiod. Leaf number was counted before blotting. The data represent mean values ± SD (n=15) and the experiment was repeated two times with similar results. The statistically significant difference is indicated by asterisks (Student's *t*-test, ***P<0.001).

(B) Plants were spray-inoculated with *B. cinerea* conidia and photos were taken at 5 dai and

(C) The enhanced lesion development in *hls1* mutant plants was measured at 3 dai.

Supplemental Table 1. Primers used in this study.

| Gene Name | Sequence (5' to 3') |
|---|---|
| **Molecular Cloning** | |
| HLS1-HA FP | GCTCTAGAATGACGGTGGTTAGAGAGTAC |
| HLS1-HA RP | TCCCCCGGGAAATTCTCTAGGGTCTACAA |
| HLS1-GFP FP | GAAGATCTATGGCGAGTTCGGAGGTTTCA |
| HLS1-GFP RP | GGGGTACCTTAAAATTCTCTAGGGTC |
| GST-HLS1 FP | CCGGAATTCATGACGGTGGTTAGAGAGTAC |
| GST-HLS1 RP | ATAGTTTAGCGGCCGCTTAAAATTCTCTAGGGTCTACA |
| HLS1-HA TM1 FP | GGGGTACCATGACGGTGGTTAGAGAGTA |
| HLS1-HA TM1 RP | CGACGTCGACAAATTCTCTAGGGTCTACAA |
| pWRKY33-GUS FP | GATCGCCGGCTTAACTATTAATGATTCTGG |
| pWRKY33-GUS RP | CCGGAATTCGTTTTATAAAAG ACCAATTTC |
| pABI5p-GUS FP | TCCTGACCCAAACCGTACTC |
| pABI5p-GUS RP | AGGCAACAAGGAACACACGA |
| **RT-qPCR** | |
| Bc ACTIN A qFP | ACTCATATGTTGGAGATGAAGCGCA |
| Bc ACTIN A qRP | AATGTTACCATACAAATCCTTACGGA |
| At ACTIN 2 qFP | GACCTTTAACTCTCCCGCTATG |
| At ACTIN 2 qRP | AAACCCTCGTAGATTGGCAC |
| PR1 qFP | TTCTTCCCTCGAAAGCTCAA |
| PR1 qRP | ACTTTGGCACATCCGAGTCT |
| RPM1 qFP | AGGGATTGATGCACCCAAGG |
| RPM1 qRP | CCTCCGCACACTTTGAGACT |
| RIN4 qFP | GGACGAGAACAACCCGTCAT |
| RIN4 qRP | TGTTGTTCGGGTTACGGGAG |
| ERF1 qFP | GAGACGGAGAATGACCAATAAG |
| ERF1 qRP | CTGTTCTCCCAAATCCTCAAA |
| PDF1.2 qFP | TGCTTCCATCATCACCCTTA |
| PDF1.2 qRP | CACTTGTGTGCTGGGAAGAC |
| CYP81F2 qFP | CGTGTCCTGGTGCGACTTTA |
| CYP81F2 qRP | TGGCAAACGGCTCGTAATTG |
| CYP79B3 qFP | GGCACTCTCTGATACGACCG |
| CYP79B3 qRP | TTATCGCCGTACCTAACGCC |
| PAD3 qFP | AGAAGCAAGAGAACGATGGAG |
| PAD3 qRP | GGGAATGACCGAGCTGATC |
| SUR2 qFP | TTGTACGAGACGCAAGCACT |
| SUR2 qRP | TTGAGACGTGCACTGAGACC |
| WRKY33 qFP | AATGGTGGTGGAAGCAAGAC |
| WRKY33 qRP | CAGATGCTGCACAACAACA |
| ACS2 qFP | TCATGTTCTGCCTTGCGGAT |
| ACS2 qRP | CTTCCTCGTGACAAACCGGA |
| ACS6 qFP | AAGCTCAACGTGTCTCCAGG |
| ACS6 qRP | GTTGTTGCAGCCATCGGTTT |

| | |
|---|---|
| ABI3 qFP | GTAAGACAACCGAGCGGACA |
| ABI3 qRP | TAACTCTCCGTCGGCGAATG |
| RD29a qFP | TCGCCACATTCTGTTGAAGAGGCT |
| RD29a qRP | TGGAGCCAAGTGATTGTGGAGACT |
| KAT2 qFP | TGCACA AGCGCAGAATTGTC |
| KAT2 qRP | TTGCTCCTGCCTTGAGACAC |
| WRKY40 qFP | AACCGCCACATCTCTCATGG |
| WRKY40 qRP | TCGATTCTTGACGTTGGGCT |
| HY5 qFP | CTGAAGAACACAACAGGAAACAAG |
| HY5 qRP | TTGCAATATTAGCTCTCACATCCC |
| HLS1 qFP | CACGGTTATCAAGTTAGAGC |
| HLS1 qRP | GAAAGTCCCAAGCGAGA |
| **ChIP-qPCR** | |
| WRKY33 Pro FP | TTTTTGAGCAAGAGCCAAGAAT |
| WRKY33 Pro RP | GGCTCAATGCTTTCATCATCTT |
| WRKY33 TATA FP | TTTTCTTCTTCTCCAAGCCCCC |
| WRKY33 TATA RP | TGGTCACAACAATCCGGAAGAA |
| WRKY33 3'CDS FP | GAGCACCACAGGATTCGTCT |
| WRKY33 3'CDS RP | GGGCCTTTTGGTTACGCCAT |
| RPM1 TATA FP | GTGGCAGGCATGTAAGGTGT |
| RPM1 TATA RP | AGTAGCCGAAGCCATCTTCC |
| RPM1 3'CDS FP | TGTCAGGGCTTGTAGAGGGT |
| RPM1 3'CDS RP | TTCTCCGCGAATGCGTTCTA |
| ABI5 ABS FP | CTCCGGCGGCTTTTAAACTATGT |
| ABI5 ABS RP | TTATTTAACAGTCTTCTAATCCAAGATC |
| ABI5 TATA FP | TGTTGACCTTCACGCCTCTC |
| ABI5 TATA RP | AAAGCCGCCGGAGAATTTTG |
| ABI5 3'CDS FP | TCGGAGACAGAACGAGGGAA |
| ABI5 3'CDS RP | GGTGTTCCTCCTACCAACACA |
| ACT2 TATA FP | TGTAACACGCGGATCGAGCA |
| ACT2 TATA RP | AACGTGACCTGGCTGTCAGA |
| ACT7 TATA FP | CGGCTCCCGGGCTAATTCAT |
| ACT7 TATA RP | ACCGACGCGTCTATGTTGCC |
| ACT7 3'CDS FP | TGGTTGTGTCAAGAAGTCTTGTGT |
| ACT7 3'CDS RP | CAGCATCATCACAAGCATCCTAAAG |
| **Genomic DNA PCR** | |
| SALK T-DNA | TTGATTTGGGTGATGGTTCA |
| SAIL T-DNA | TAGCATCTGAATTTCATAACCAATCTCGATACAC |
| hls1-1 LP | GGTTTGGCCACAAAGAAAAAG |
| hls1-1 RP | TATTCGGAGTTTCGTACACCG |
| hls1-2 LP | CATGAACTACTCGCCTTCTCC |
| hls1-2 RP | GAGCTTAAACCCAATCCCTTG |