> NM_001278959.3 Solanum lycopersicum auxin-responsive protein IAA9 (IAA9), mRNA

TGAGCCTAGAGTTTCACATAGGACAGCAAATAAGCTTTTGTTACTGTCTGCCAAATGGAGGGTCCTTAGTTTTTTTCCTCTCTCTCTTTCTGCTACCA
AAAAAAATAGCCTCACTACTCCACCATCATCTTCTTCTTCCTTCTTCCTTCTTCTCTTACTGCTGCTAATAAGCTTTTTCTTACTTGGGTTTTCTCTTACAA
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CTACCTGGATCTCAGTCTCCCGAAAGAGGTGAGGAGACTTGCCCTGTGAGCTCGACAAAGGTTGATGAGAAGCTGCTCTTCCCCTTGCACCCTTCC
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GATGGTGCTCCCTATTTGAGGAAAGTGGACCTCAGAACCTGTTCTGCATACCAGGAGCTATCTTCTGCTCTTGAAAAAATGTTCAGCTGTTTTACAA
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TTGCTTGTTTAAGTTCCCTTAAGTGTGTACTTTAGACCCAACGTTTGTCGTTTGATTAAGTATGCGTGTGCACTTCAGAAATTGTTATTACTGTATGA
ATAAATGTGTCCTCCACATTTTTCATCGGGTTGTAGTTATCGAAATAACTAACCTCTTACCTCA

> NM_001361530.1 Solanum lycopersicum AGAMOUS-like MADS-box protein AGL6 (AGL6), mRNA

TGTTGCAAGAAGAGATATCCAAGATTGAACCTTTTTTTTTCTTATAAGGAAGAAGGGGAATTATGTAGTACACTTTTACACTTATTGCTAACCCCAC
CTCCCCTATTCATTACTGATCATAACATAAATAATCTTTTTGATAGAATTAGCTAGCTCTAGGAATAGAAGAAGAAAAAAATGGGGAGAGGGAGA
GTGGAACTAAAGAGAATAGAGAACAAAATCAACCGTCAAGTGACATTTTCTAAGAGGAGGAATGGTTTGTTGAAGAAAGCTTATGAATTATCAG
TGCTTTGTGAGGCTGAAGTTGCTCTCATCATCTTCTCTAGTCGTGGAAAGCTCTATGAGTTTGGTAGTGCAGGTATCACTAAAACCCTTGAGAGGT
ACCAACGTTGTTGCCTTAATCCTCAAGACAATTGTGGTGAAAGAGAAACACAGAGCTGGTACCAAGAGGTCTCTAAATTAAAGGCCAAGTTTGAA
GCACTTCAACGAACTCAAAGGCACTTGCTTGGTGAAGATCTTGGAGCACTAAGTGTGAAGGAGTTGCAAAATCTTGAAAAACAACTTGAAGGTGC
ACTTGCACAAGCTAGACAAAGAAAGACACAAATAATGATGGAACAGATGGAGGAGCTTCGTAGAAAGGAGCGTCATCTTGGTGATGTGAACAA
GCAGTTGAAGATTAAGGTTTCTCTTGAACTATCATCGTTTGAGGGTGAAGGACAAGGTGTTCCTTTTCCATGGAGTAATTGTAATGCATCTTTAGA
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TATATGGCTGCAGATGGAGCCTCAGGGTCAAGGAACATGGCTGTTGAGAGTAACATTATCCATGGTTGGGGTCTTTAATTTCTAATTCTAATTAT
GGATTATACTAGTACAAGTTTTTTGCTTTTAAGTTTTTCAGATTAAAAAAACTCAAGTGACATATAATTATGATTTGAAATGCATGTTATATAGTAATG
TATAATTTTAGCAAGTGTC

Supplementary file 1. *SlIAA9* and *SlAGL6* mRNA sequences. ATG initiation codons and stop codons are boxed; the portion of the *SlIAA9* sequence used by Wang et al.,(2005) to produce the antisense construct and the genomic target site of the guide sequence used by Klap et al., (2017) to generate the Cas9/sgRNA binary vector are highlighted in yellow (7,42). Regions selected for dsRNA production are in blue with primers used for amplification of RNA *in vitro* transcription template in bold; primers employed for qRT-PCR analysis are designed outside the dsRNA region and are highlighted in green.
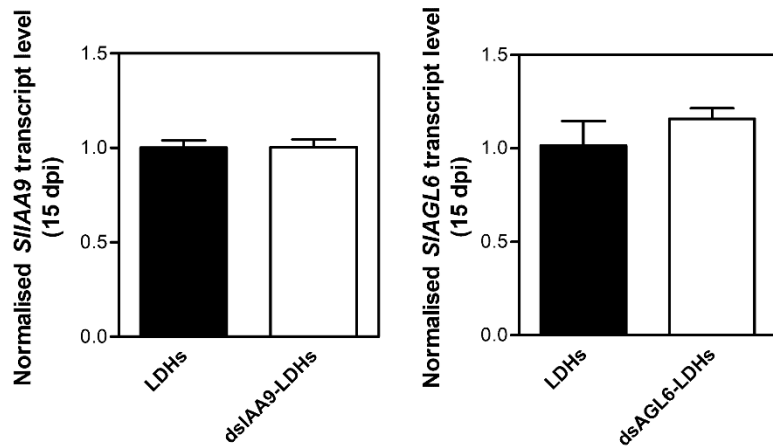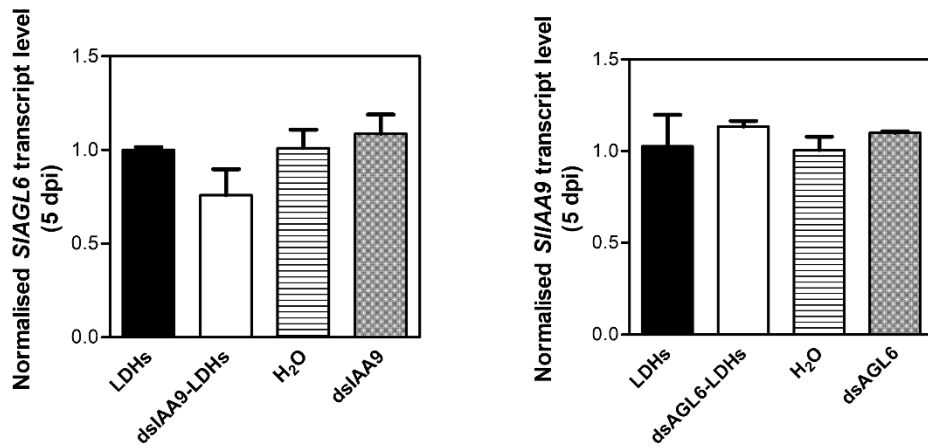
A

B

Supplementary file 2. Evaluation of *SlIAA9* and *SlAGL6* expression levels. (A) qRT-PCR analyses of *SlIAA9* and *SlAGL6* conducted in ovaries at 15 dpi. (B) Expression level of *SlAGL6* in ds*IAA9* and ds*IAA9*-LDHs treated flower buds at 5 dpi compared to the level in the respective control samples (on the left). Expression level of *SlIAA9* in ds*AGL6* and ds*AGL6*-LDHs treated flower buds at 5 dpi compared to the level in the respective control samples (on the right). Values reported are Means ± SE (n=3).
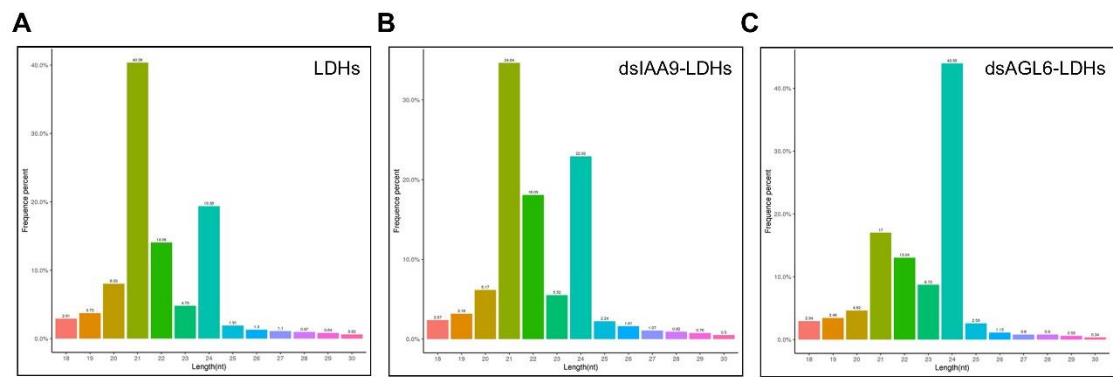
Supplementary file 3. Length distribution of total small RNA obtained from small RNA-seq. The abscissa is the length of sRNA reads; the ordinate is the percentage of one length read accounted for total sRNA.

Supplementary file 4. Small RNA-Seq Data available at this link Supplementary file 4