

1 Supplementary Information

2

3 **Ultraviolet-B enhances the resistance of multiple plant species to lepidopteran**
4 **insect herbivory through the jasmonic acid pathway**

5

6 Jinfeng Qi^a, Mou Zhang^b, Chengkai Lu^a, Christian Hettenhausen^a, Qing Tan^a, Guoyan
7 Cao^a, Xudong Zhu^c, Guoxing Wu^b, and Jianqiang Wu^{a,*}

8

9 ^a Department of Economic Plants and Biotechnology, Yunnan Key Laboratory for
10 Wild Plant Resources, Kunming Institute of Botany, Chinese Academy of Sciences,
11 Kunming 650201, China

12 ^b College of Plant Protection, Yunnan Agriculture University, Kunming 650201,
13 China

14 ^c State Key Laboratory of Rice Biology, China National Rice Research Institute,
15 Hangzhou 31006, China

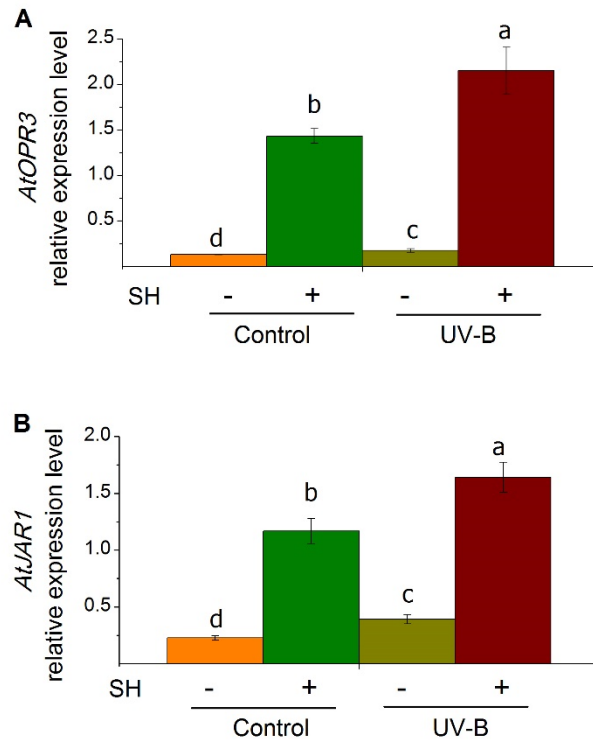
16

17 * Corresponding author: Jianqiang Wu

18 Phone/Fax: +86-871-65229562

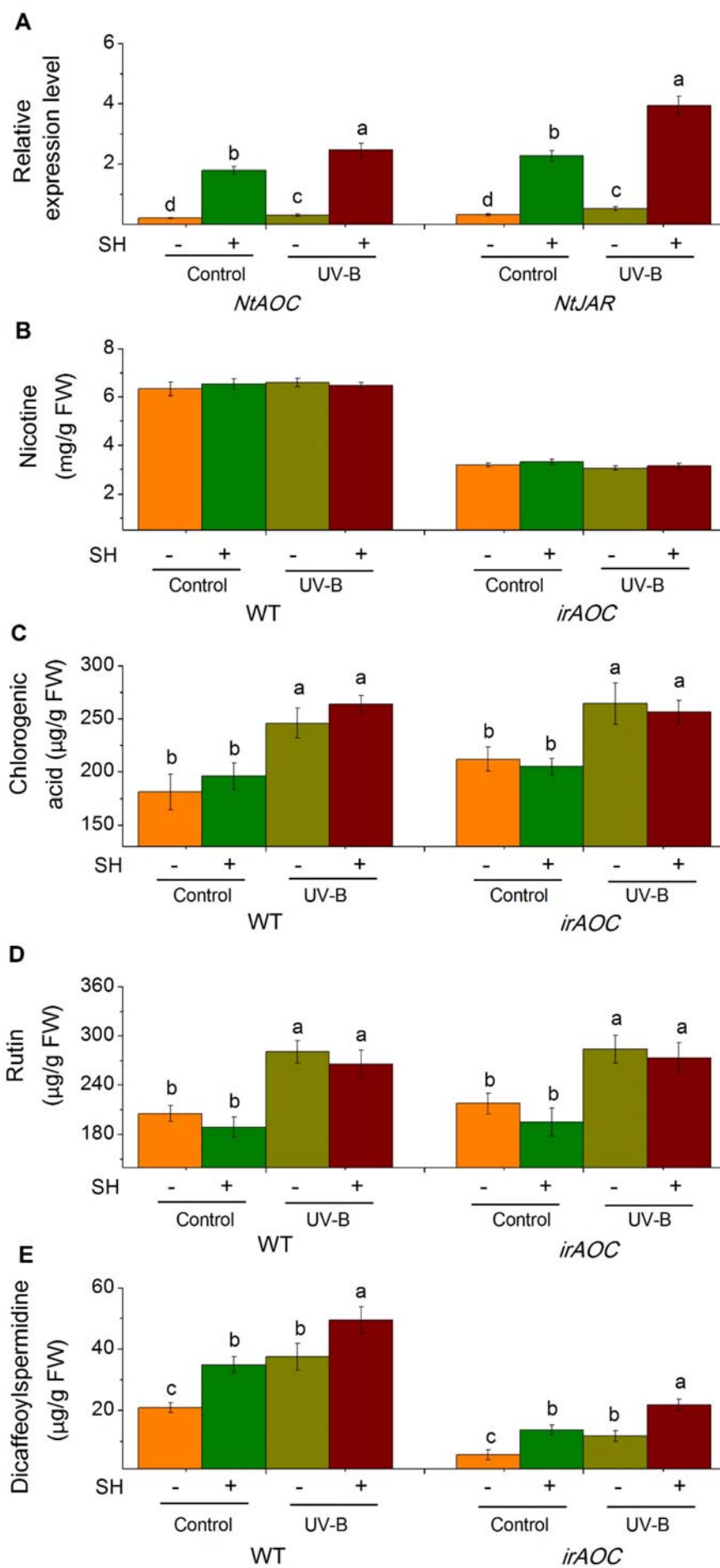
19 Email: wujianqiang@mail.kib.ac.cn

20



Supplementary Figure 1. UV-B treatment elevates the expression levels of *AtOPR3* and *AtJAR1*.

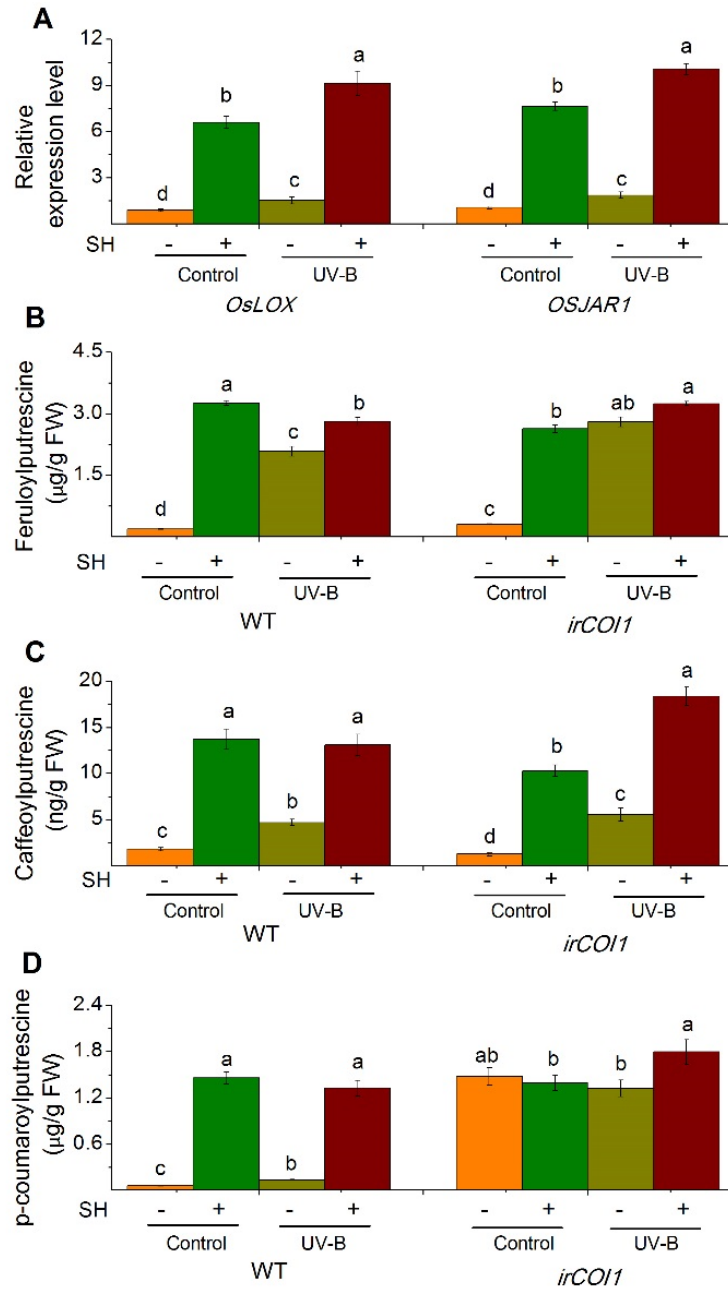
Control and UV-B-pre-exposed Arabidopsis plants were treated with simulated herbivory (SH +) or left untreated (SH -), and the levels (mean $\pm$ SE) of *AtOPR3* (A) and *AtJAR1* (B) were determined in samples collected at 2 h. $n = 6-8$. Different letters ($P < 0.05$, Duncan's multiple range test) indicate significant differences between groups.



Supplementary Figure 2. Gene expression and secondary metabolites of *N. tabacum*

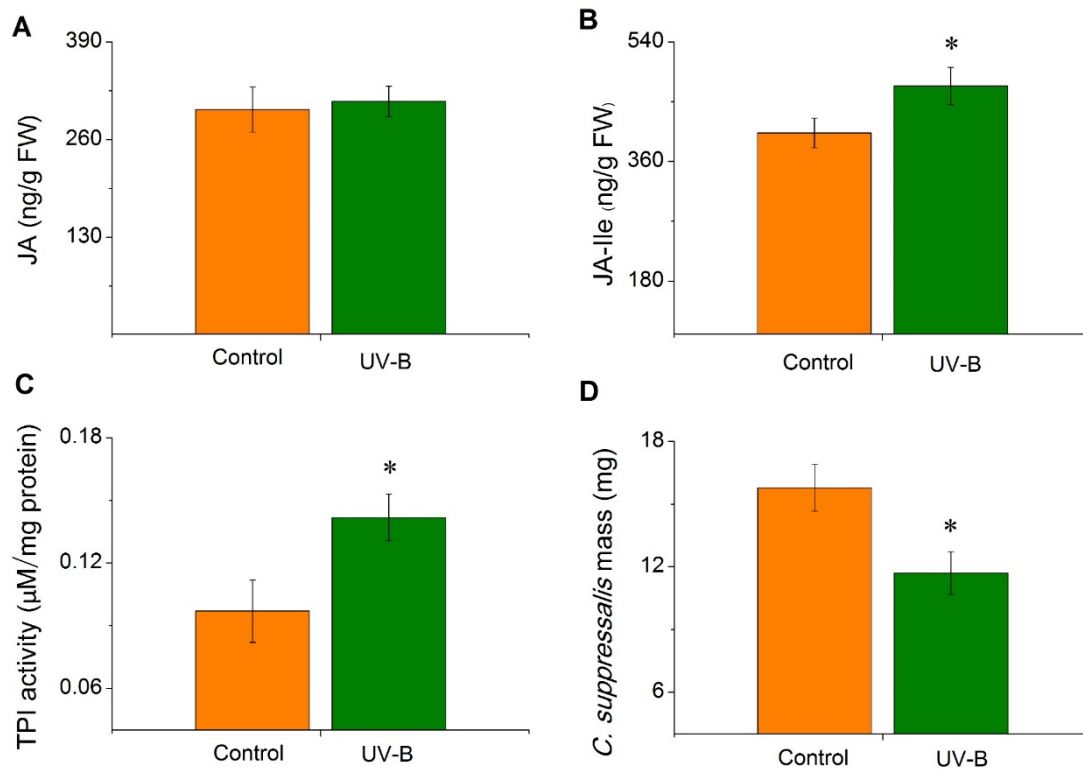
in response to UV-B treatment and simulated herbivory.

Control and UV-B-pre-exposed wild-type (WT) and irAOC tobacco plants were treated with simulated herbivory (SH +) or left untreated (SH -), and levels (mean $\pm$ SE) of *NtAOC1* and *NtJAR4* (A) and the contents of secondary metabolites nicotine (B), chlorogenic acid (C), rutin (D), and dicaffeoyl spermindine (E) were determined in samples collected at 2 h (for a) or 48 h (for b-e). n = 6-8. Different letters ($P < 0.05$, Duncan's multiple range test) indicate significant differences between treatment groups within the same gene (for A) or genotype (for B-E).



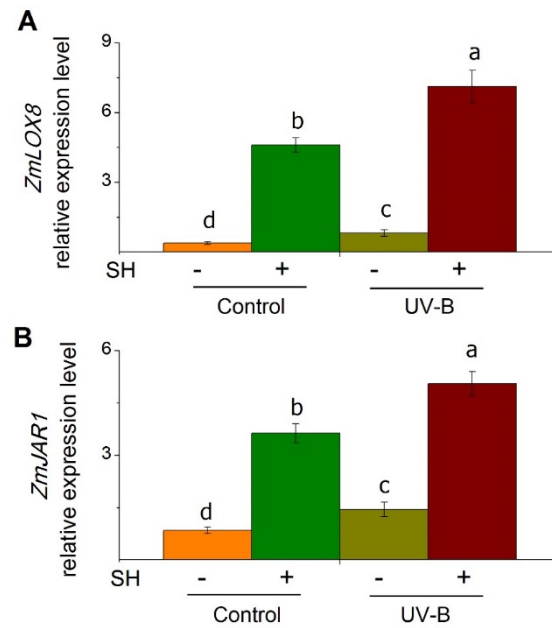
Supplementary Figure 3. Gene expression and secondary metabolites of rice in response to UV-B treatments and simulated herbivory. Control and UV-B-pre-exposed wild-type (WT) and *irCOI1* rice plants were treated with simulated herbivory (SH +) or left untreated (SH -), and the levels (mean ± SE) of *OsLOX*, and *OsJAR1* (A) and the contents of secondary metabolites feruloylputrescine (B), caffeoylputrescine (C), and *p*-coumaroylputrescine (D) were

51 determined in samples collected at 2 h (for A) or 48 h (for B-D). n = 6-8. Different
52 letters ($P < 0.05$, Duncan's multiple range test) indicate significant differences
53 between treatment groups within the same gene (for A) or genotype (for B-D).
54



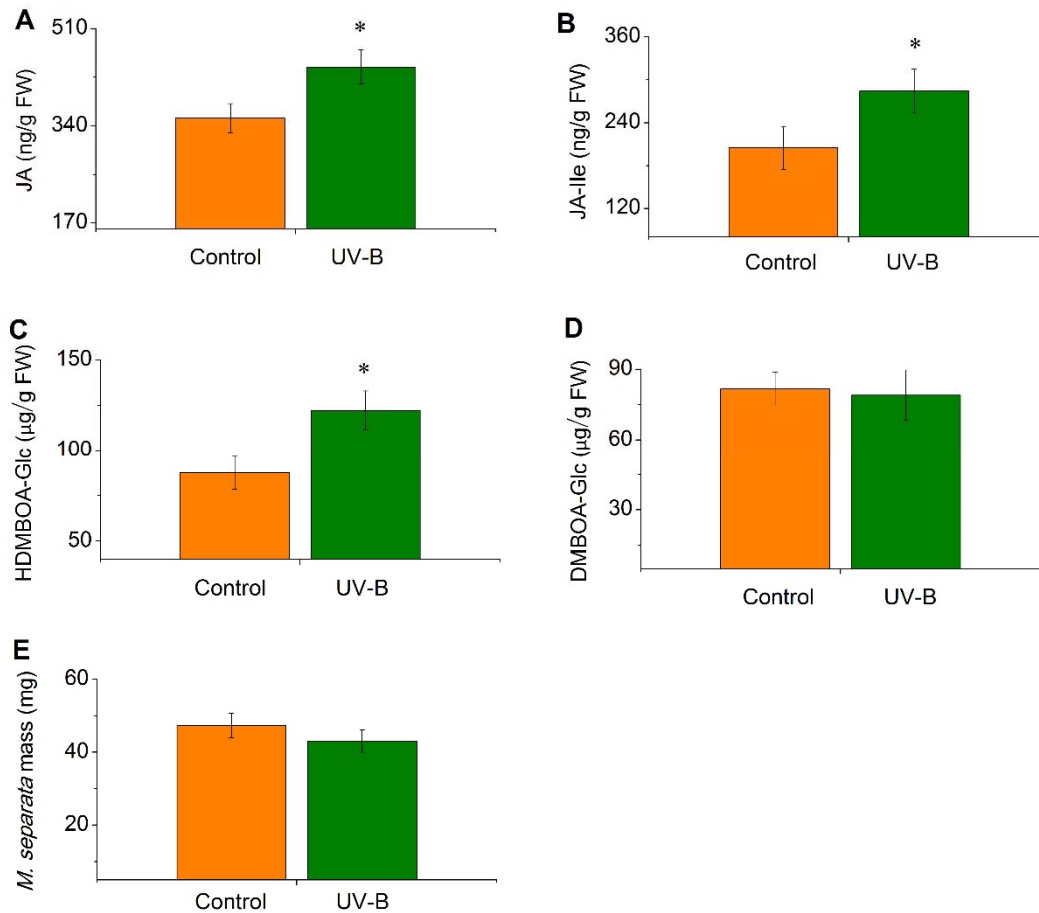
Supplementary Figure 4. UV-B-enhanced rice defense traits against the striped stem borer (SSB) *C. suppressalis*.

Control and UV-B-pre-exposed rice plants were infested by SSB (A-C) and levels (mean $\pm$ SE) of JA (A), JA-Ile (B), and TPI activity (C) were determined in samples collected at 2 h (for A and B) or 48 h (C); mean masses ($\pm$ SE) of SSB after 12 days feeding on control and UV-B-pretreated WT rice plants (D). For A-C, $n = 6-8$, for D, $n = 30-50$. Asterisks (* $P < 0.05$, Student's t test) indicate significant differences between treatments.



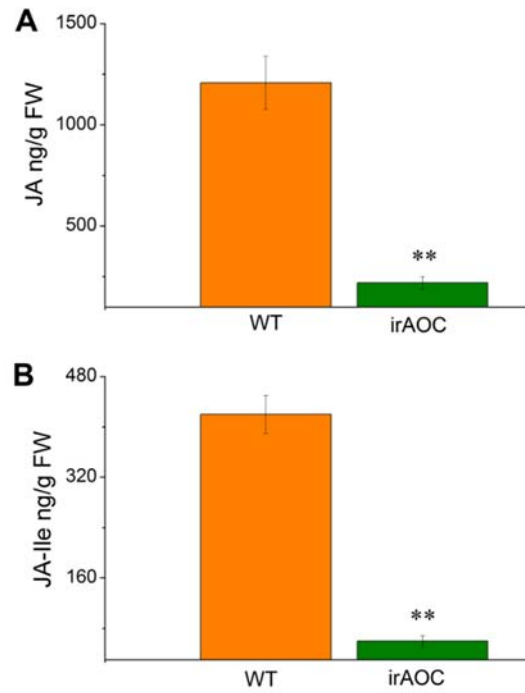
Supplementary Figure 5. Responses of maize to UV-B pre-treatment and simulated *M. separata* feeding.

Control and UV-B-pre-exposed maize plants were treated with simulated herbivory (SH +) or left untreated (SH -), and the levels (mean $\pm$ SE) of *ZmLOX8* (A) and *ZmJAR1* (B) were determined in samples collected at 2 h. $n = 6-8$, letters ($P < 0.05$, Duncan's multiple range test) indicate significant differences between treatments.



Supplementary Figure 6. Growth of *M. separata* on control and UV-B--pre-treated maize plants.

Both control and UV-B-pre-exposed (UV-B) maize plants were treated with simulated herbivory, and contents (mean $\pm$ SE) of JA (A), JA-Ile (B), HDMBOA-Glc (C) and DMBOA-Glc (D) were determined in samples collected at 2 h (for A and B) or 48 h (C); mean masses ($\pm$ SE) of *M. separata* 8 days after feeding on control and UV-B-pretreated maize (E). For a-c, $n = 6-8$, for D, $n = 30-50$. Asterisks (* $P < 0.05$, Student's t test) indicate significant differences between treatments.



76

77 **Supplementary Figure 7.** Silencing efficiently of irAOC tobacco plants.

78 Wild-type (WT) and irAOC plants were treated with wounding, and the levels (mean
 79 $\pm$ SE) of JA (A), JA-Ile (B) were determined in samples collected at 1 h. Asterisks (**
 80 $P < 0.01$, Student's t -test, $n = 5$) indicate significant differences between genotypes.

Supplementary Table 1. Primers used in this study

Gene name	Gene ID	Forward Primer (5' to 3')	Reverse Primer (5' to 3')
<i>AtPP2AA3</i>	AT1G13320	ACCTGCGGTAATAACTGCATCTAA	ACCAAGCATGGCCGTATCAT
<i>AtOPR3</i>	AT2G06050	GAAGATTTCGATCTCTCTCATCG	GGTCCGTTGAGCATAATACTC
<i>AtJAR1</i>	AT2G46370	AGACGATCCGCACCAAATGT	TTTGGCACATACGGCTCCAT
<i>NtACT</i>	XM_009633597	TGATAACGGAACAGGAATGG	TCGAGGTCGACCAACAATAC
<i>NtJAR</i>	DQ359729.1	GCCTCCCGAGCTTGTTACAT	GACCGTCTAAATTTTCCATGAGA
<i>NtAOC</i>	NM_001324978.1	GAGCCAGCACCTGAAGCTAA	TTCTCCGGAAATGACCCAC
<i>NtAOC</i> for RNAi	NM_001324978.1	CACCTCCACCAACTCCAAGT	TGCTGCAATTTCACTTGACC
<i>OsACT</i>	Os03g50885	TGGACAGGTTATCACCATTGGT	CCGCAGCTTCCATTCTCTATG
<i>OsLOX</i>	Os08g39840	TCAAGGAGATCGAGGGCGT	TCGGAGAAGGGCTTCATCAG
<i>OsJAR1</i>	Os05g50890	AAGGTTTGTGAACCCATCAAACAGC	AATAATACTTTGCAGCACTTGTTACG
<i>ZmACT</i>	GRMZM2G006765	GGAGCTCGAGAATGCCAAGAGCAG	GACCTCAGGGCATCTGAACCTCTC
<i>ZmJAR1</i>	GRMZM2G091276	GGTCCATGGAGCCATACCTG	TAGAGCCGACCCATCCTTCA
<i>ZmLOX8</i>	GRMZM2G104843	CATCAAGAGTAAGCCAGCGC	GTTTCGATGTTGACGGGGTTG