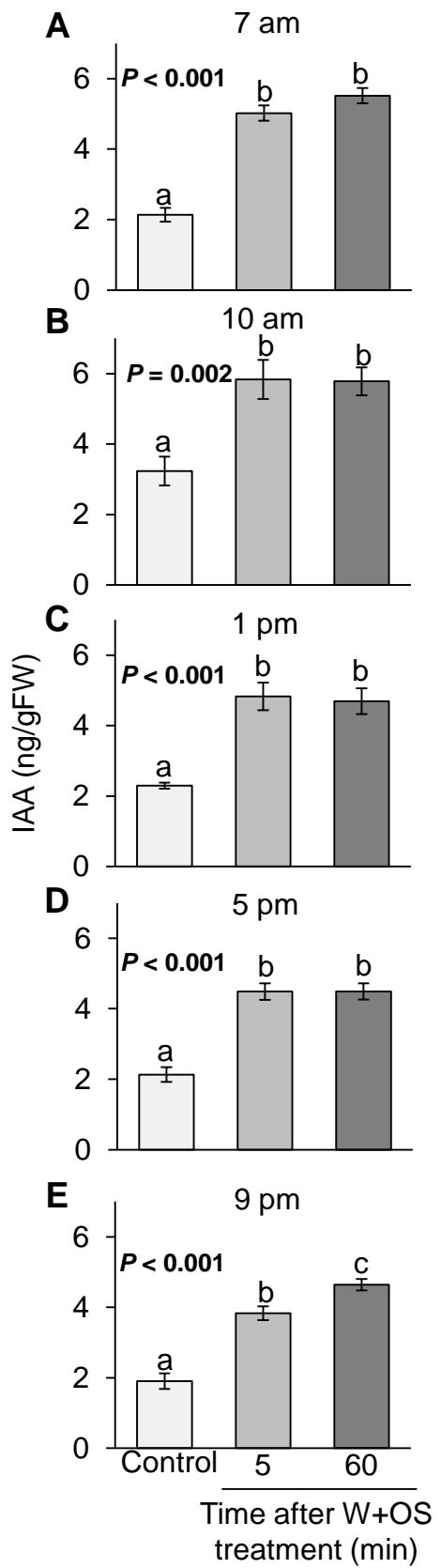


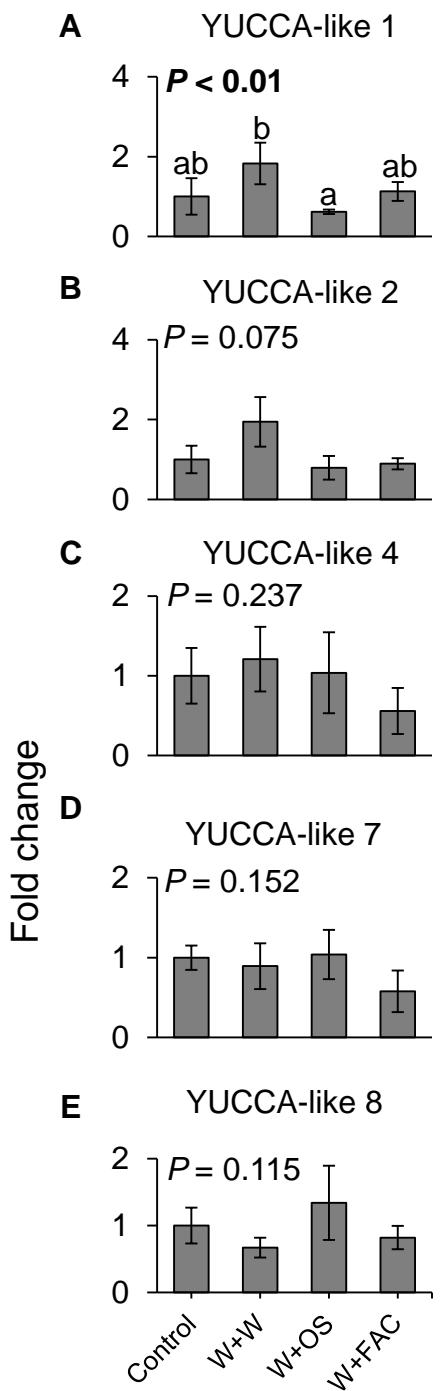
# Supplementary material



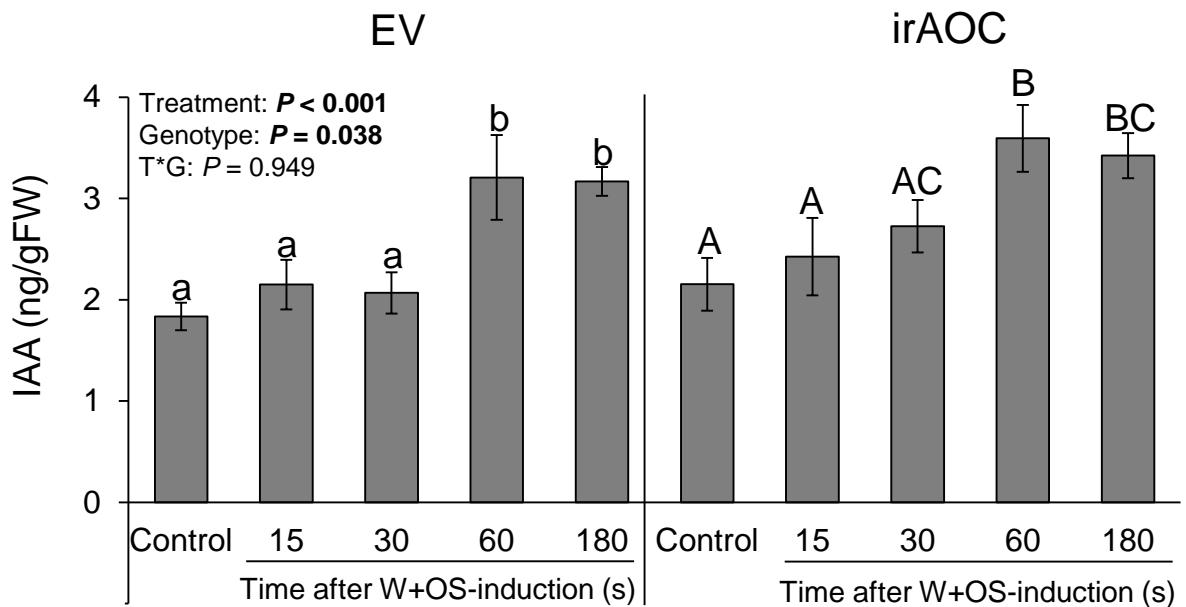
**Figure S1.** IAA is induced locally in response to simulated *M. sexta* herbivory independently of time of day. Average ( $\pm$ SE) IAA content in the leaves of plants that were subjected to simulated *M. sexta* attack at 7 am (a), 10 am (b), 1pm (c), 5pm (d) or 9pm (e) 5 and 60 minutes after treatments. Different letters indicate significant differences between treatments ( $P < 0.05$ ).

	<b>FAD-binding</b>	<b>Hallmark 1</b>	<b>NADH-binding</b>	<b>Hallmark 2</b>
<b>NaYUCCA-like 1</b>	GAGPSGLA	WLVVATGENAE	GCGNSGME	DSVVLATGYCSNVP
<b>NaYUCCA-like 2</b>	GAGPSGLA	WLVVATGENAE	GCGNSGME	DSVILATGYCSNVP
<b>NaYUCCA-like 3</b>	GAGPSGLA	WLVVATGENAE	GCGNSGME	DSVVLATGYCSNVP
<b>NaYUCCA-like 4</b>	GGGPSGLA	WLVVATGENAE	GCGNSGME	DSVVLATGYCSNVP
<b>NaYUCCA-like 5</b>	GAGPAGLA	FLVLASGENSE	GCGNSGME	DVIVFATGFKRTTH
<b>NaYUCCA-like 6</b>	GAGPSGLA	WLVVATGENAE	GCGNSGME	DSIILATGYKSNVP
<b>NaYUCCA-like 7</b>	GGGPSGLA	WLVVATGENAE	GCGNSGME	DAIILATGYKSNVP
<b>NaYUCCA-like 8</b>	GAGPSGLA	WLVVATGENAE	GCGNSGME	DAIILATGYKSNVP
<b>NaYUCCA-like 9</b>	GAGPAGIA	FLVLASGENSE	GCGNSGME	DAMVFATGYKSTVT

**Figure S2.** *N. attenuata* genome contains nine *YUCCA-like* genes. Multiple alignment of four conserved amino acid motifs found in the ten-membered NaYUCCA-like gene family.



**Figure S3.** Gene expression patterns of YUCCA-like genes upon simulated *M. sexta* attack. Average ( $\pm$ SE) transcript abundance relative to control of YUCCA-like 1 (A), YUCCA-like 2 (B), YUCCA-like 4 (C), YUCCA-like 7 (D) and YUCCA-like 8 (E) genes followed simulated *M. sexta* attack (n=3). Different letters indicate significant differences between treatments ( $P < 0.05$ ).



**Figure S4.** Jasmonate signaling is not required for the *M. sexta*-induced accumulation of IAA. Average ( $\pm$ SE) IAA levels in local, treated leaves of wild type plants (empty vector; EV) and jasmonate-deficient inverted repeat allene-oxide cyclase (irAOC) plants ( $n=5$ ). Different letters indicate significant differences between treatments within each genotype ( $P < 0.05$ ). W+OS: wounded and *M. sexta* oral secretions-treated plants.