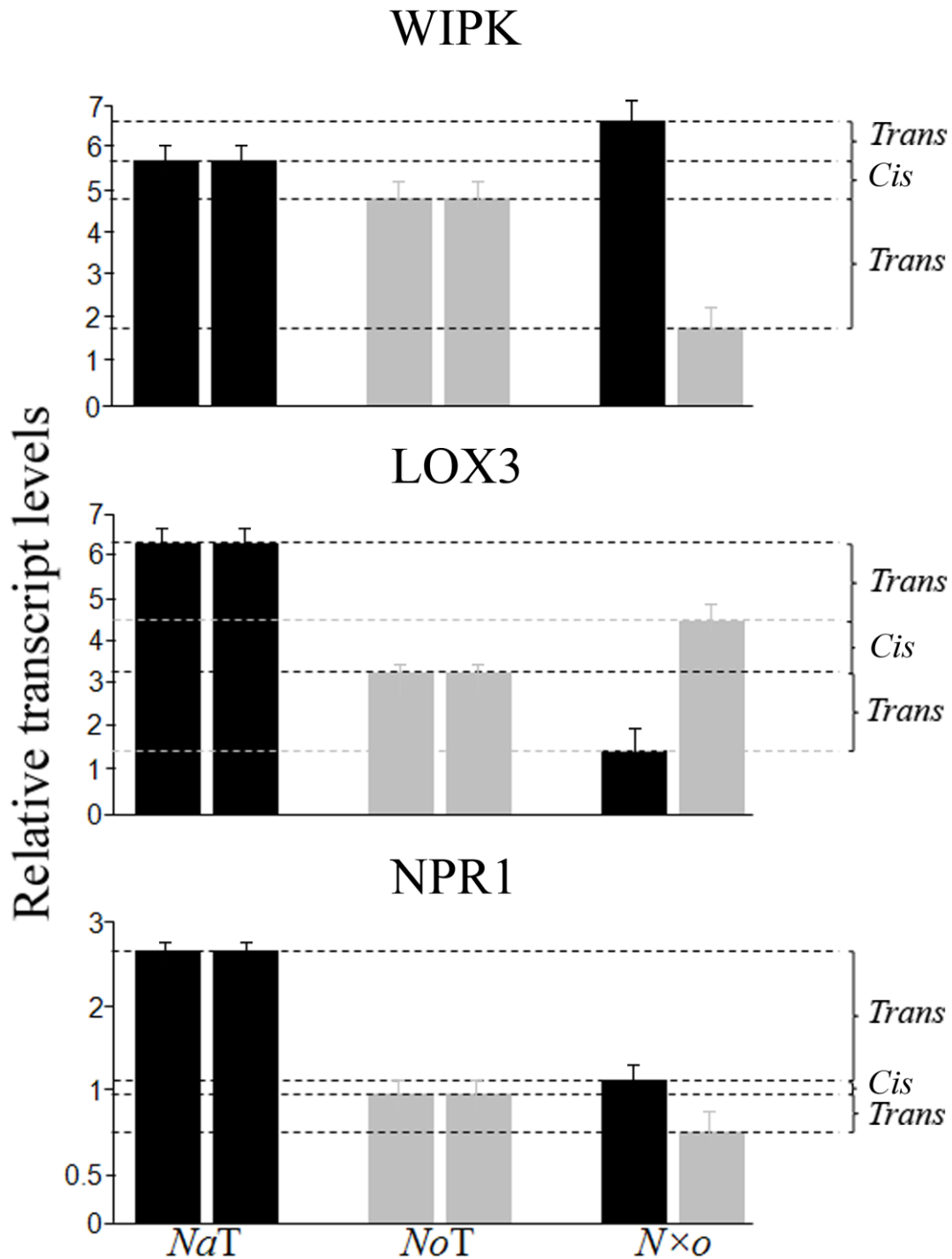


1 **Supplemental Figure S1.** OS elicitation enhances the accumulation of uni-parental transcript  
 2 patterns of WIPK and LOX3, but not NPR1 in  $N \times o$  lines (2-5).

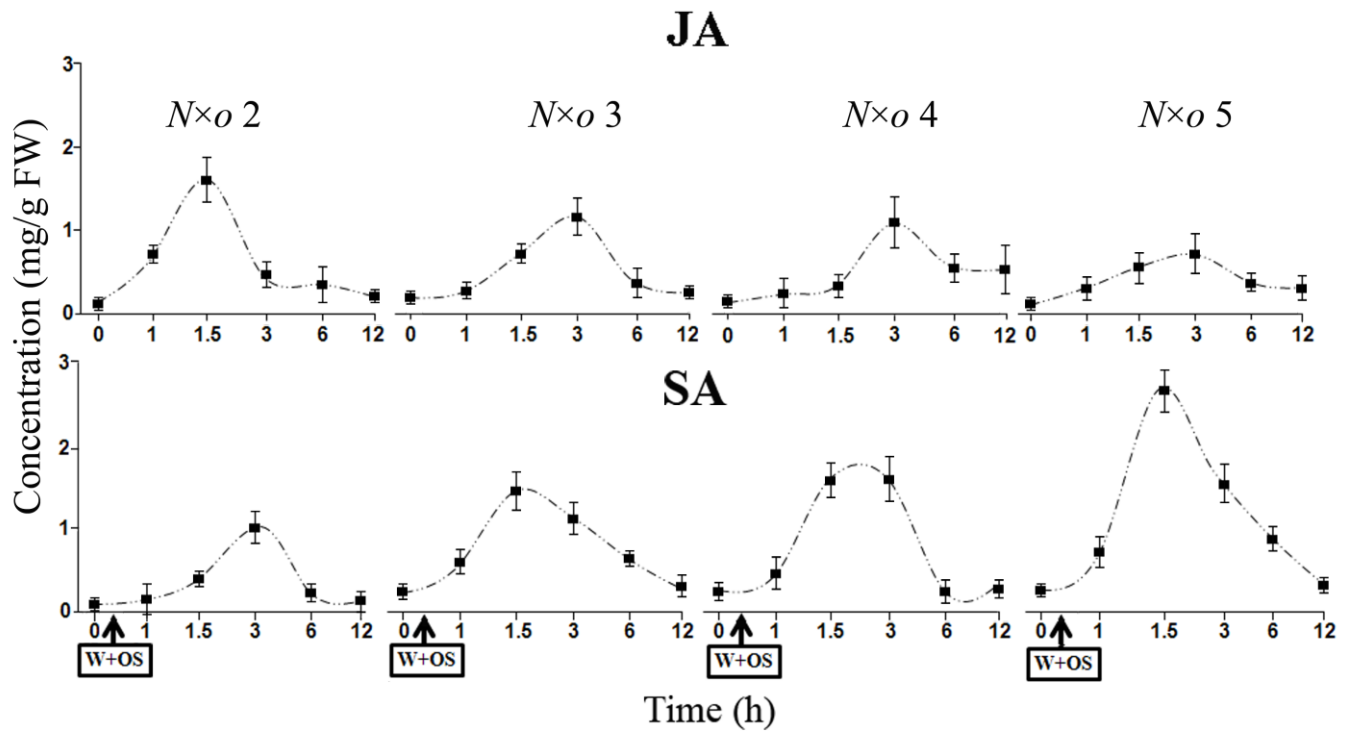
3 After elicitation with *M. sexta* oral secretions (OS), *N. × obtusiata* ( $N \times o$ ) lines 2-5  
 4 induced an increase in the accumulation of *N. attenuata*-wound induced protein kinase (*Na*-  
 5 WIPK), and *N. obtusifolia*- lipoxygenase 3 (*No*-LOX3), and attenuated levels of *Na*-LOX3,  
 6 *Na* and *No*- non-expressor of pathogenesis-related (NPR1) transcripts. Asterisks indicate  
 7 levels of significant difference between the maximum values of the pairs plotted together on  
 8 the same graph (\* $P < 0.05$ ; \*\* $P < 0.01$ ).



1 **Supplemental Figure S2.** Both *cis* and *trans* regulatory elements act on the expression of  
 2 WIPK, LOX3 and NPR1 genes elicited by *M. sexta* OS.

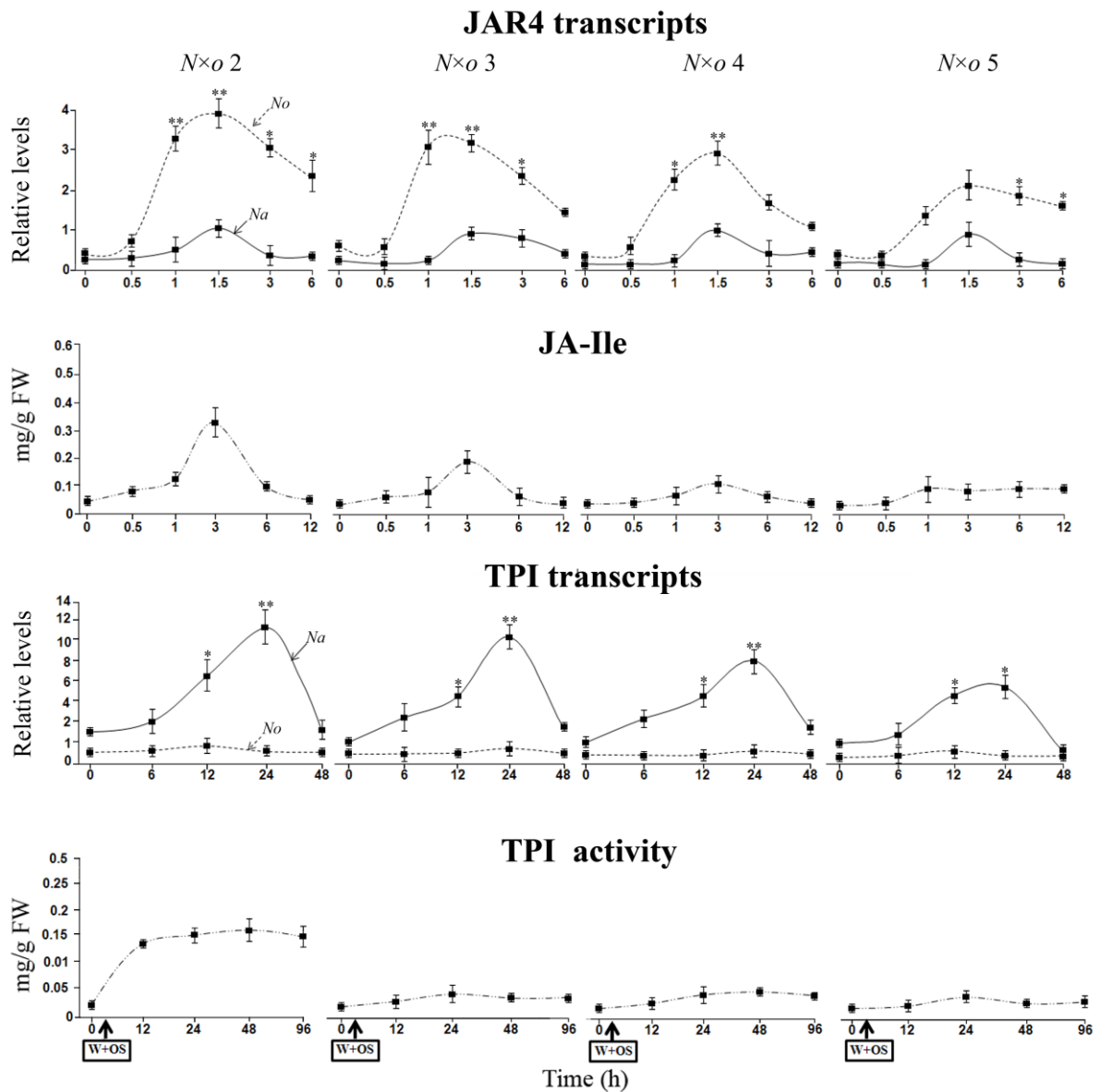
3 Wound induced protein kinase (WIPK), lipoxygenase 3 (LOX3) and pathogenesis-  
 4 related (NPR1) transcripts accumulation was compared among *N. attenuata* tetraploid (*NaT*),  
 5 *N. obtusifolia* tetraploid (*NoT*) and *N. ×obtusata* (*Nxo*) using the approach described by  
 6 Zhang and Borevitz (2009). Briefly, the authors consider that a given gene is under the control

1 of only *cis* genetic elements if the specific parental expression difference is equal to the allele  
2 expression difference in the hybrid; otherwise, both *cis* and *trans* elements are involved. Our  
3 analysis revealed that the parental WIPK, LOX3 and NPR1 transcript accumulation difference  
4 between *NaT* and *NoT* is not equal to the difference of *Na* and *No* transcripts in *N×o*,  
5 suggesting that the regulation of the expression of these genes involves not only *cis*, but also  
6 *trans* elements. In this analysis, we considered only the maximal relative values of transcript  
7 accumulation elicited by *M. sexta* oral secretions (OS).



1 **Supplemental Figure S3.** Patterns of OS-elicited SA and JA accumulation in *N×o* 2-5 after  
 2 OS elicitation.

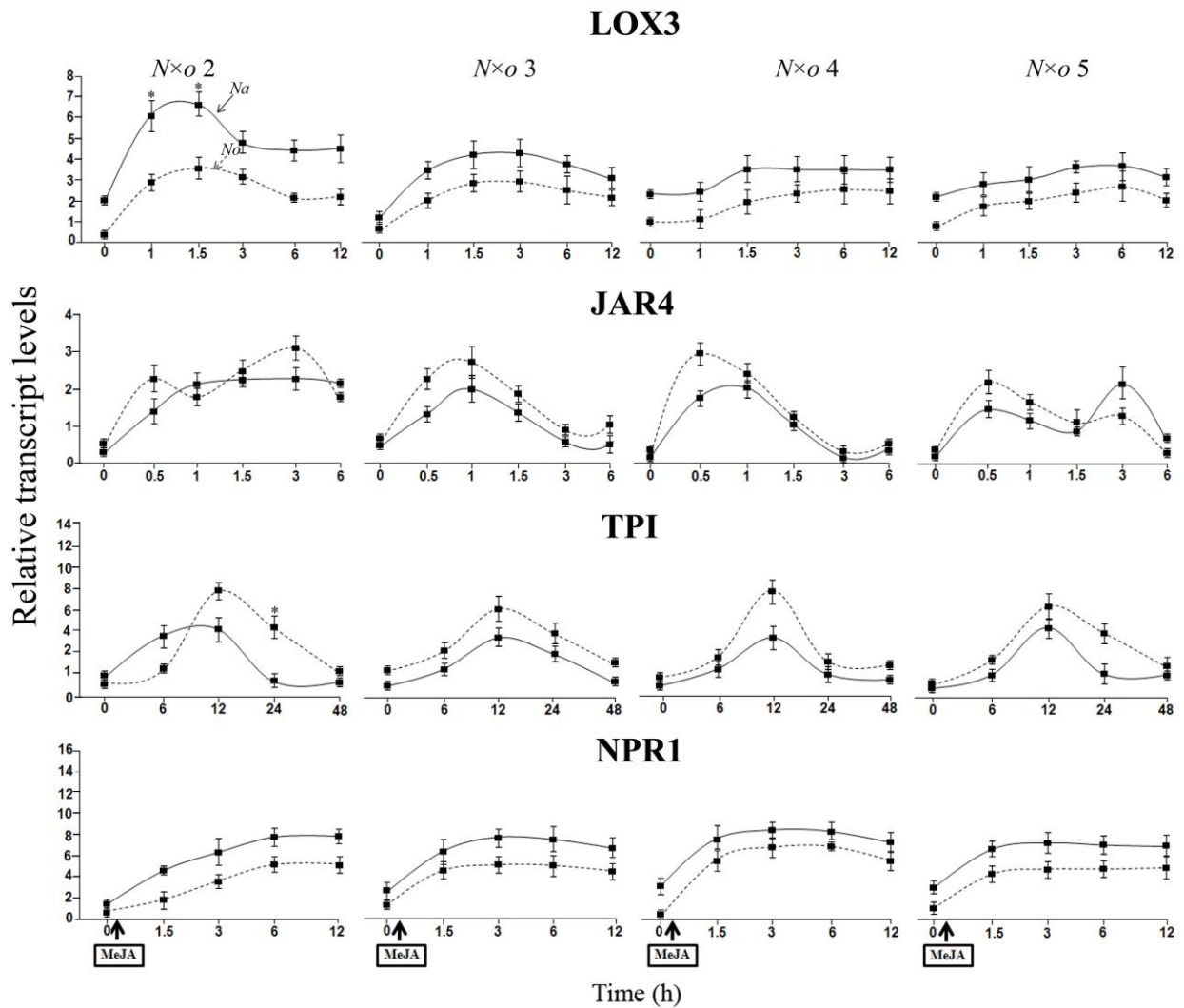
3            After elicitation with *M. sexta* oral secretions (OS), *N. ×obtusata* (*N×o*) lines 2-5  
 4 accumulated high levels of *salicylic acid* (SA) and low levels of jasmonic acid (JA). Only the  
 5 accumulation of JA was associated with a delay in the synthetic polyploids compared to their  
 6 parental lines.



1 **Supplemental Figure S4.** *N* × *o* lines (2-5) enhance the accumulation of only one parental  
 2 transcript of JAR4 and TPI, and accumulated different levels of JA-Ile and TPI activity after  
 3 *M. sexta* OS elicitation.

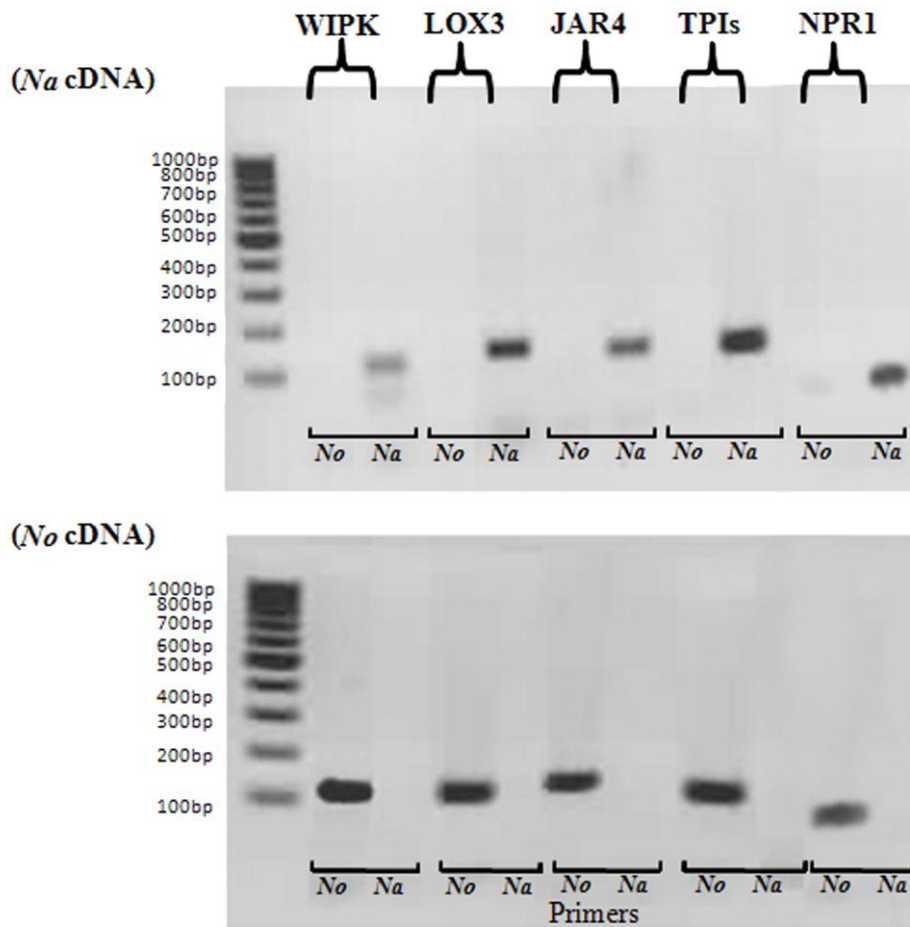
4 After elicitation with *M. sexta* oral secretions (OS), *N. × obtusiata* (*N* × *o*) lines 2-5  
 5 accumulated only *N. obtusifolia*-jasmonate-resistant4 (*No*-JAR4) transcripts and *N. attenuata*-  
 6 trypsin protease inhibitor (*Na*-TPI) transcripts, but not that of *Na*-JAR4 and *No*-TPIs. The  
 7 maximum levels of accumulated jasmonic acid–isoleucine (JA-Ile) and active TPIs were  
 8 different among *N* × *o* lines. All polyploid lines showed a delay in the accumulation of JAR4,  
 9 JA-Ile as well as transcript and active TPI levels compared to their parental lines. Asterisks

- 1 indicate levels of significant difference between the maximum values of the pairs plotted
- 2 together on the same graph (\*\*P<0.01).



1 **Supplemental Figure S5.** Methyl jasmonate treatment of *N*×o1-5 elicits transcripts of both  
 2 parental LOX3, JAR4 and TPis, demonstrating that the uniparental pattern of transcript  
 3 accumulation observed after OS elicitation is not due to gene inactivation.

4 After methyl jasmonate (MeJA) application, *N. × obtusiata* line 2-5 (*N*×o 2-5)  
 5 accumulated both parental lipoxygenase 3 (LOX3), jasmonate-resistant 4 (JAR4) and trypsin  
 6 protease inhibitor (TPI). Application of MeJA restored the delay in the accumulation of JAR4  
 7 and TPI transcripts observed after OS elicitation. Asterisks indicate levels of significant  
 8 difference between the maximum values of the pairs plotted together on the same graph  
 9 (\* $P < 0.05$ ; \*\* $P < 0.01$ )



1

2

3 **Supplemental Figure S6.** PCR products amplified in *N. attenuata* (*Na*) and *N. obtusifolia*  
 4 (*No*) cDNA using RT primer pairs specific for *Na* and *No*- wound induced protein kinase  
 5 (WIPK), lipoxygenase 3 (LOX3), jasmonate-resistant 4 (JAR4), trypsin protease inhibitor  
 6 (TPI) and non-expressor of pathogenesis-related (NPR1)

7

8 PCR products (10  $\mu$ L/well) were run in a 1.5% agarose gel and visualized with  
 9 ethidium bromide staining.

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