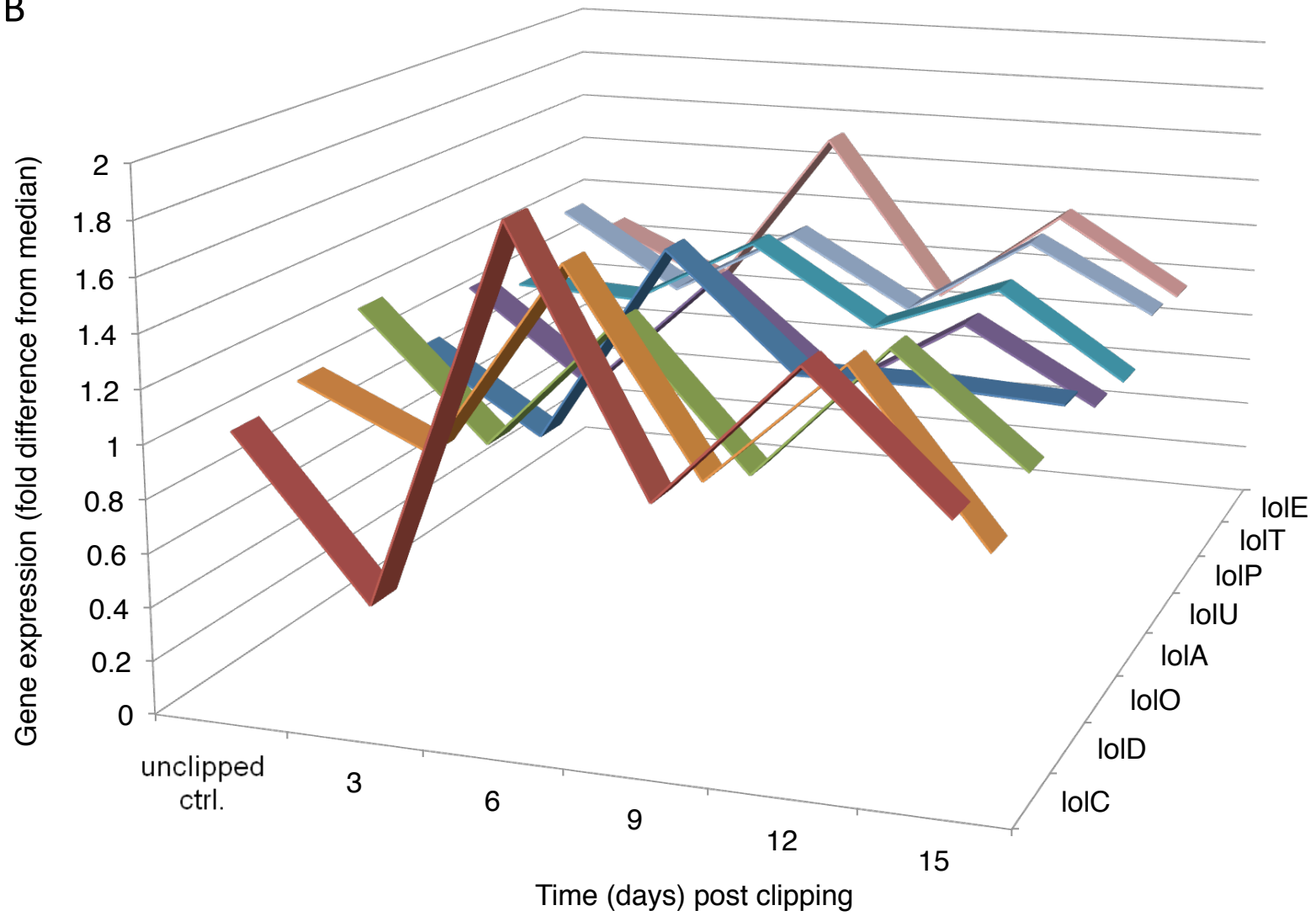
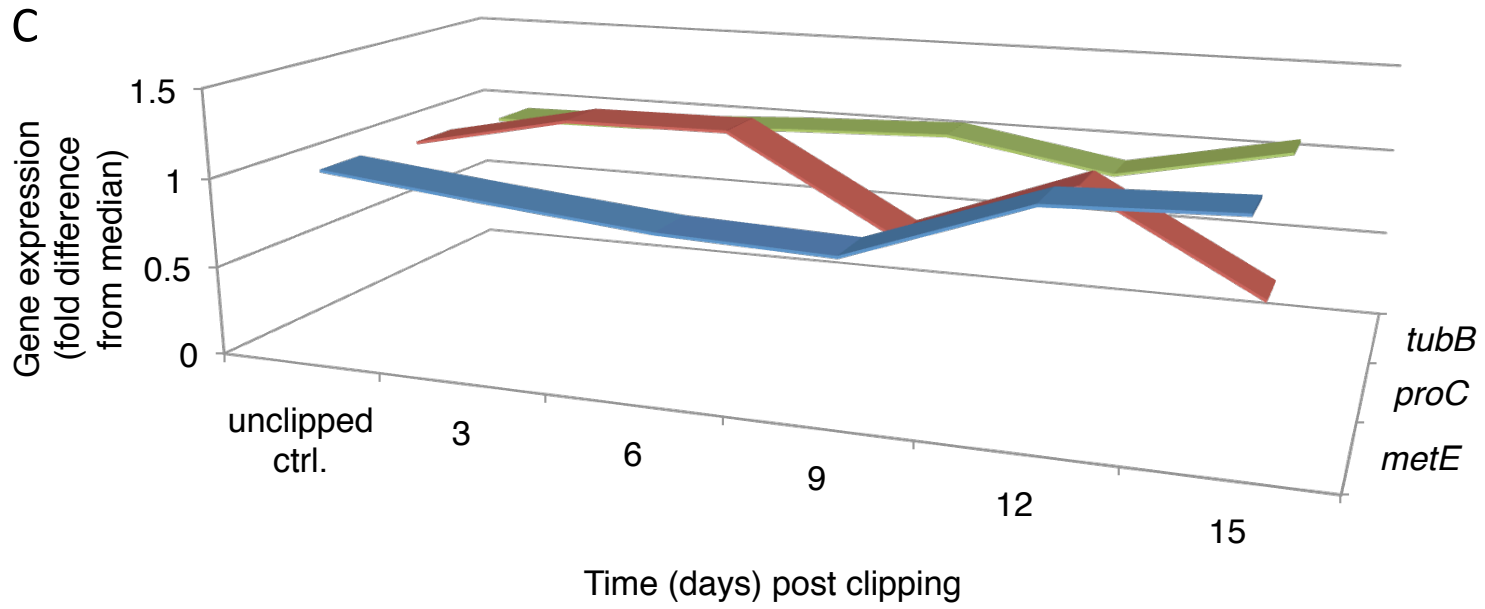


Supplemental Figure 1. Time course of *N. siegelii* gene expression in MF (**A**) basal and (**B** and **C**) regrowth tissues (n=2) after clipping, compared to unclipped controls (n=6). Gene expression is indicated as fold-difference from the median for each gene in the experiment, calculated from RT-qPCR as $2^{-\Delta\Delta Ct}$.

B

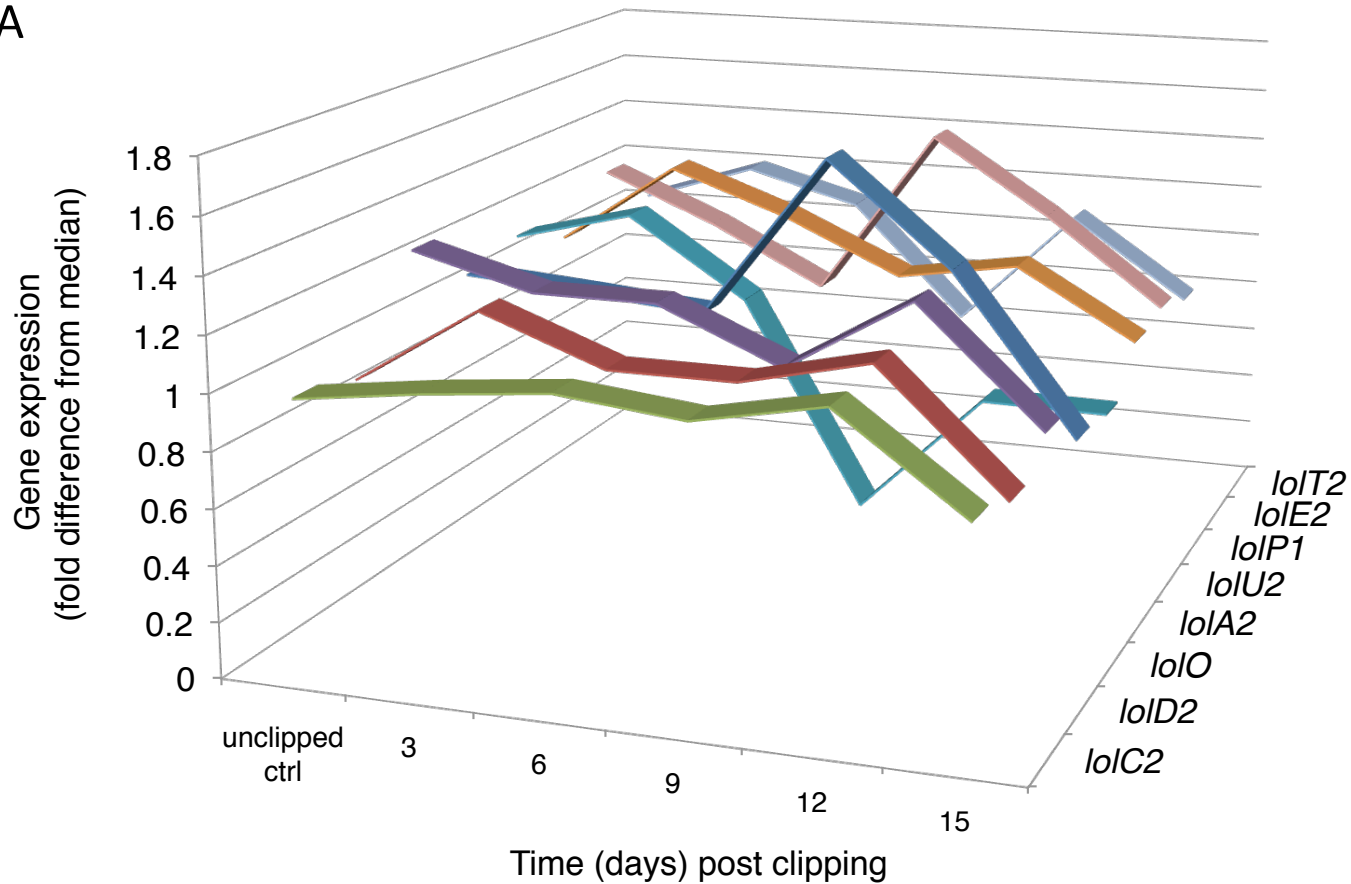


Supplemental Figure 1, panel **B**.



Supplemental Figure 1, panel **C**.

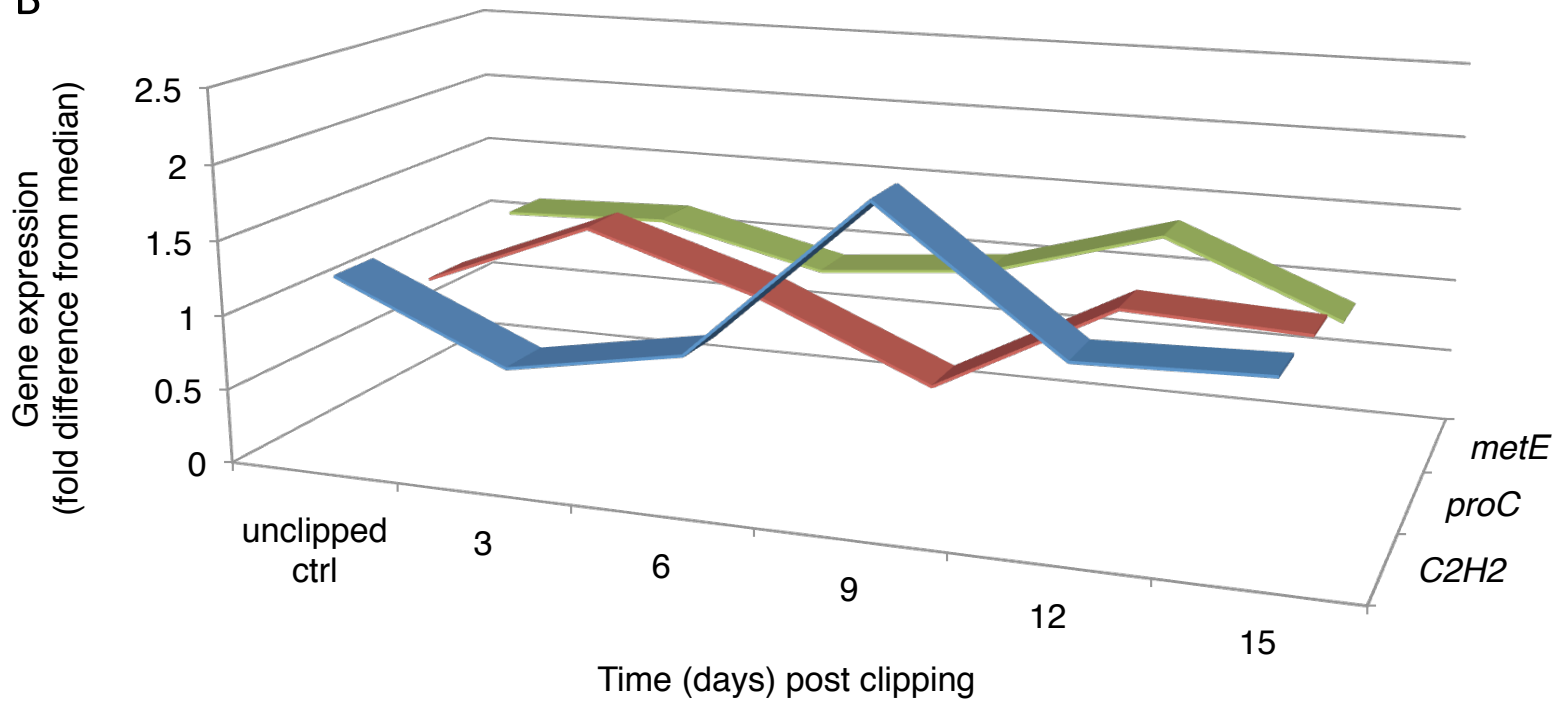
A



Supplemental Figure 2. Time course of *N. uncinatum* gene expression in MF regrowth tissues after clipping (n=2, except n = 1 at day 9 PC), compared to unclipped controls (n=4).

A. *LOL* gene expression;

B



Supplemental Figure 2 (continued).

B. Expression of *proC*, *metE* and *C2H2* genes.