

Figure S1: NbAGO2 (Unigene No. Nbv3K585706870, retrieved from www.benthamgenome.com) was aligned with *Arabidopsis thaliana* NbAGO2 (Accession No. NM_102866.3), *Nicotiana tabacum* NtAGO2 (Accession No. XM_016619080.1), *Solanum lycopersicum* SlyAGO2 (Accession No. NM_001279306.2), and *Glycine max* GmAGO2 (Accession No. XM_006605460.3) by DNAMAN software (Version

6.0.3.99, Lynnon Biosoft, San Ramon, CA, USA). The sequences for amiR target sites were shown on top by lines with different colors.

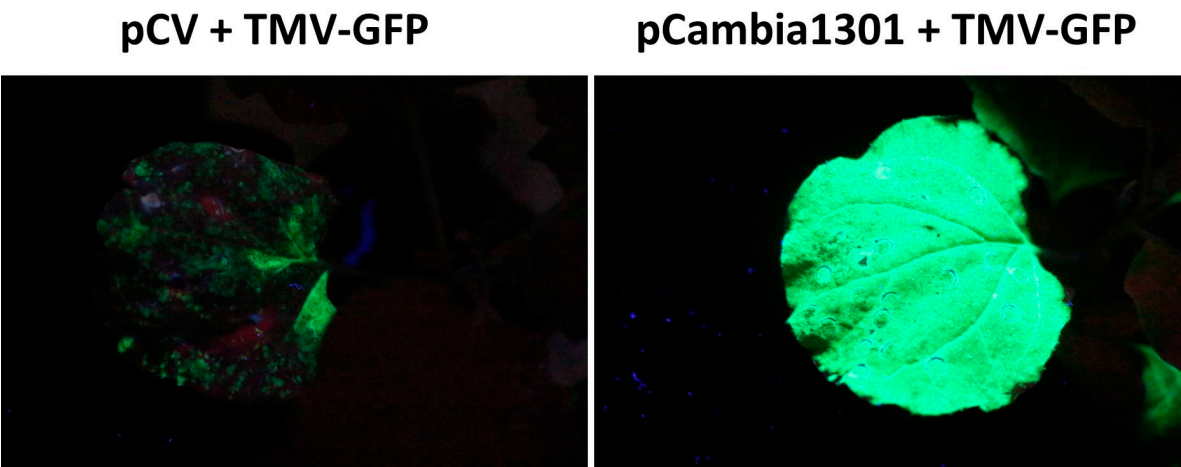


Figure 2. *N. benthamiana* leaves were first inoculated with pCV (both pCVA and pCVB), and then were infected with TMV-GFP (pJL24) one day later. As a control, pCambia1301, the backbone of pCV infectious clone used here, was inoculated. The result showed that first inoculation of pCV impeded TMV-GFP infections.

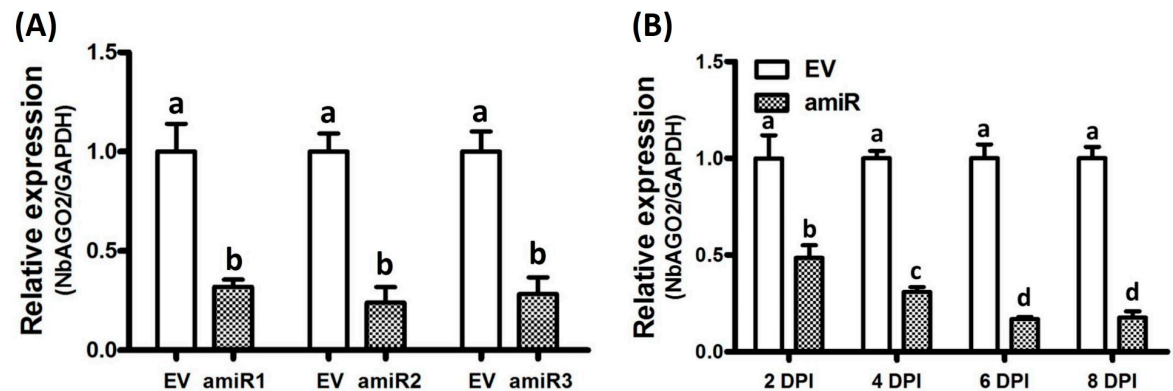


Figure S3: The experiments in (A) and (B) were performed the same as Figure 1 and 2, respectively. The only difference is *Actin* gene was used as internal control here instead of *GAPDH* in Figure 1 and 2.



Figure S4: Sequence alignment between miR403a and target *NbAGO2* gene from 17Wt *Nicotiana Benthamiana*. “|” indicates perfect match, while gap shows mismatches.