

Figure S1. Size and strand polarity distribution of PSTVd-sRNA (18 to 26 nt) derived from the tomato (T3 and T4) and *N. benthamiana* PSTVd-infected samples. RPM, reads per million.

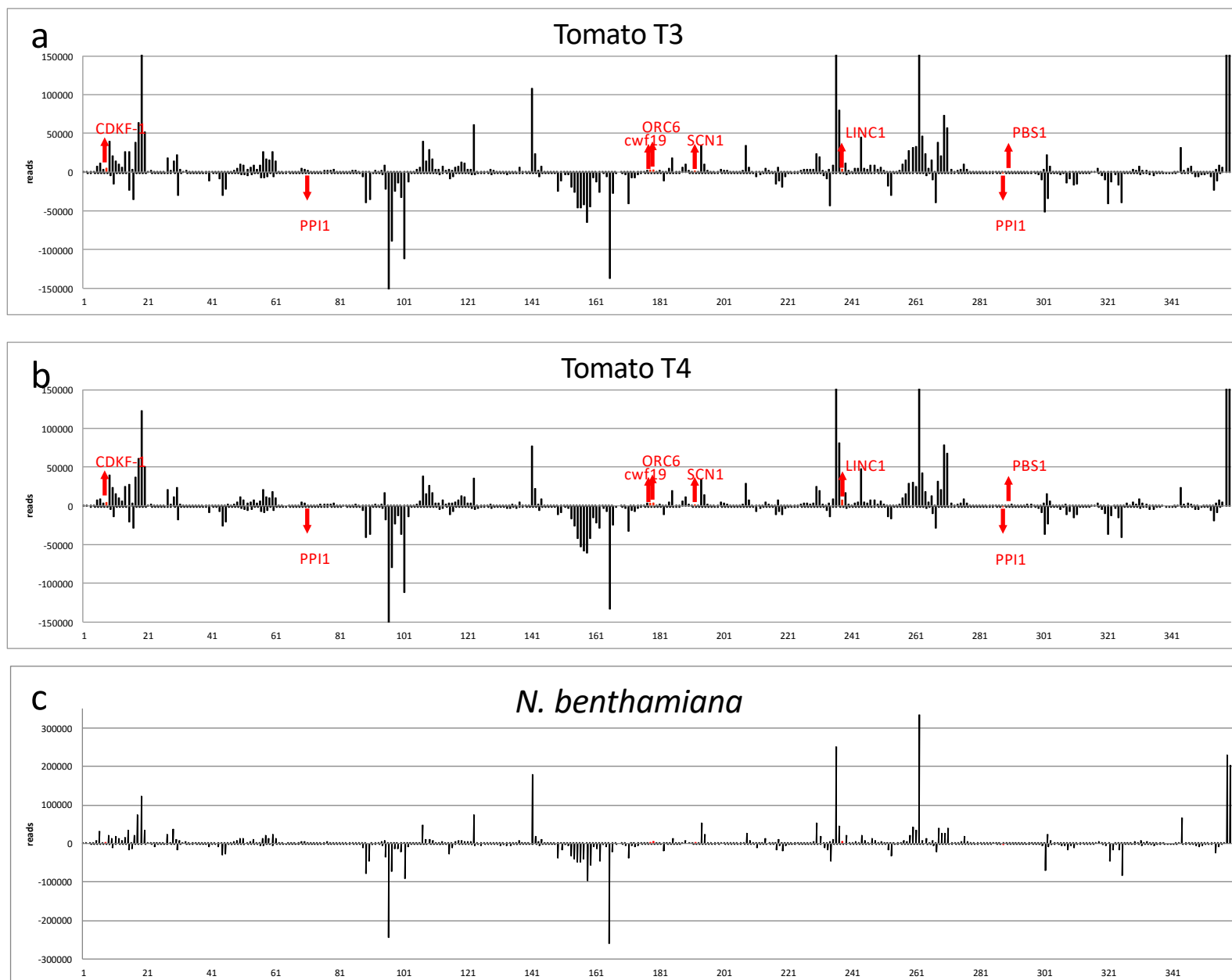


Figure S2. Distribution of PSTVd-sRNAs along PSTVd genome. Location and frequencies in the genomic PSTVd RNA (variant Nb) of the 5'-terminal nucleotide of the plus-strand (positive values) and minus-strand (negative values) PSTVd-sRNAs from the viroid-infected tomato T3 and T4 (**a** and **b**, respectively) and *N. benthamiana* (**c**) plants. Red arrows indicate the PSTVd-sRNAs identified in the degradome analysis that mediate the cleavage of a *bona-fide* mRNA target (the name of which is in red).

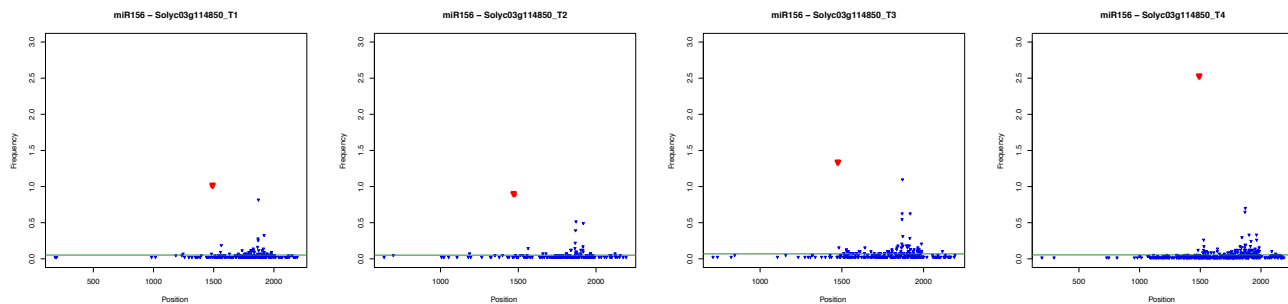
Mock
(T1)

Mock
(T2)

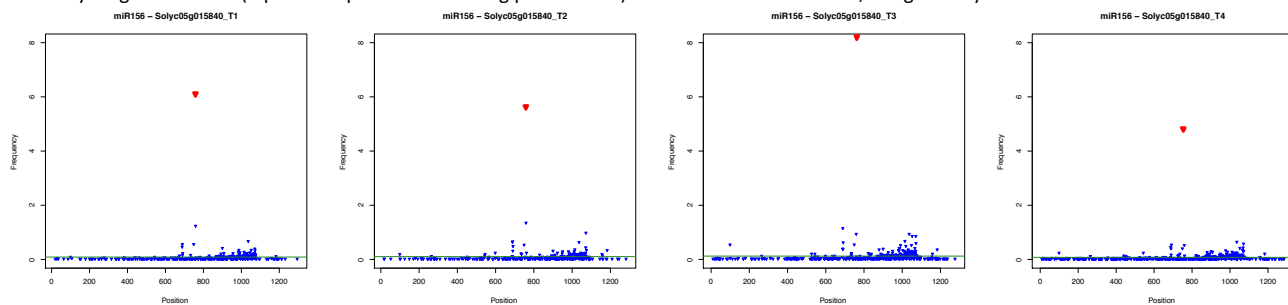
PSTVd-infected
(T3)

PSTVd-infected
(T4)

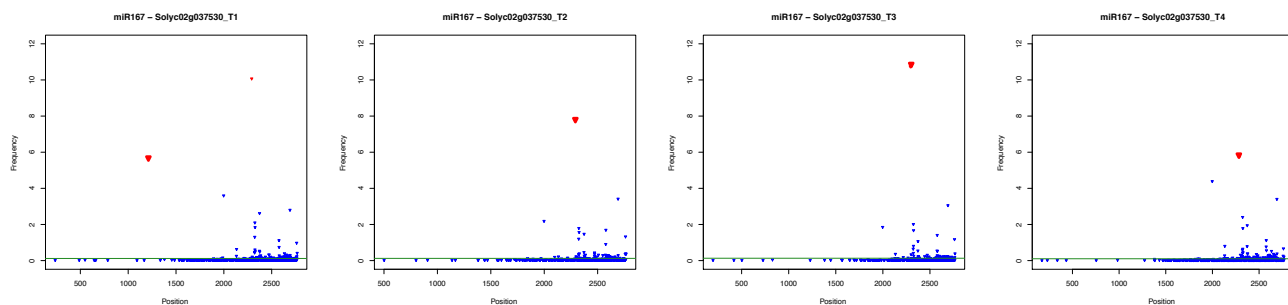
Solyc03g114850.2.1 (Squamosa promoter-binding protein-like) CLEAVAGE POSITION 1481 Targeted by mir156



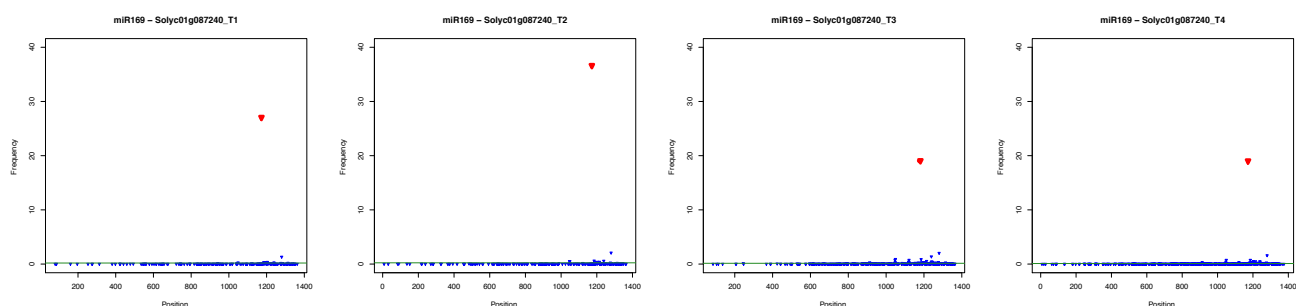
Solyc05g015840.2.1 (Squamosa promoter-binding protein-like) CLEAVAGE POSITION 760; Targeted by mir156



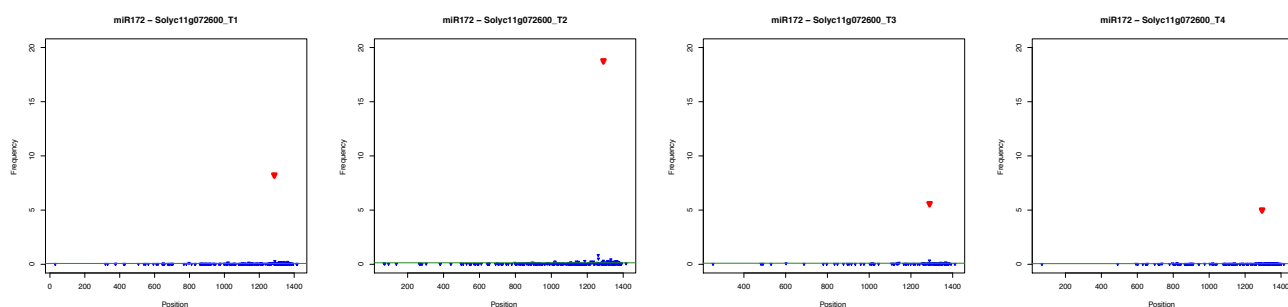
Solyc02g037530.2.1 (auxin response factor 8) CLEAVAGE POSITION 2291; targeted by miR167



Solyc01g087240.2.1 (nuclear factor Y, subunit A9) CLEAVAGE POSITION 1171 ; targeted by miR169



Solyc11g072600.1.1 (related to AP2.7) CLEAVAGE POSITION 1288 ; targeted by miR172



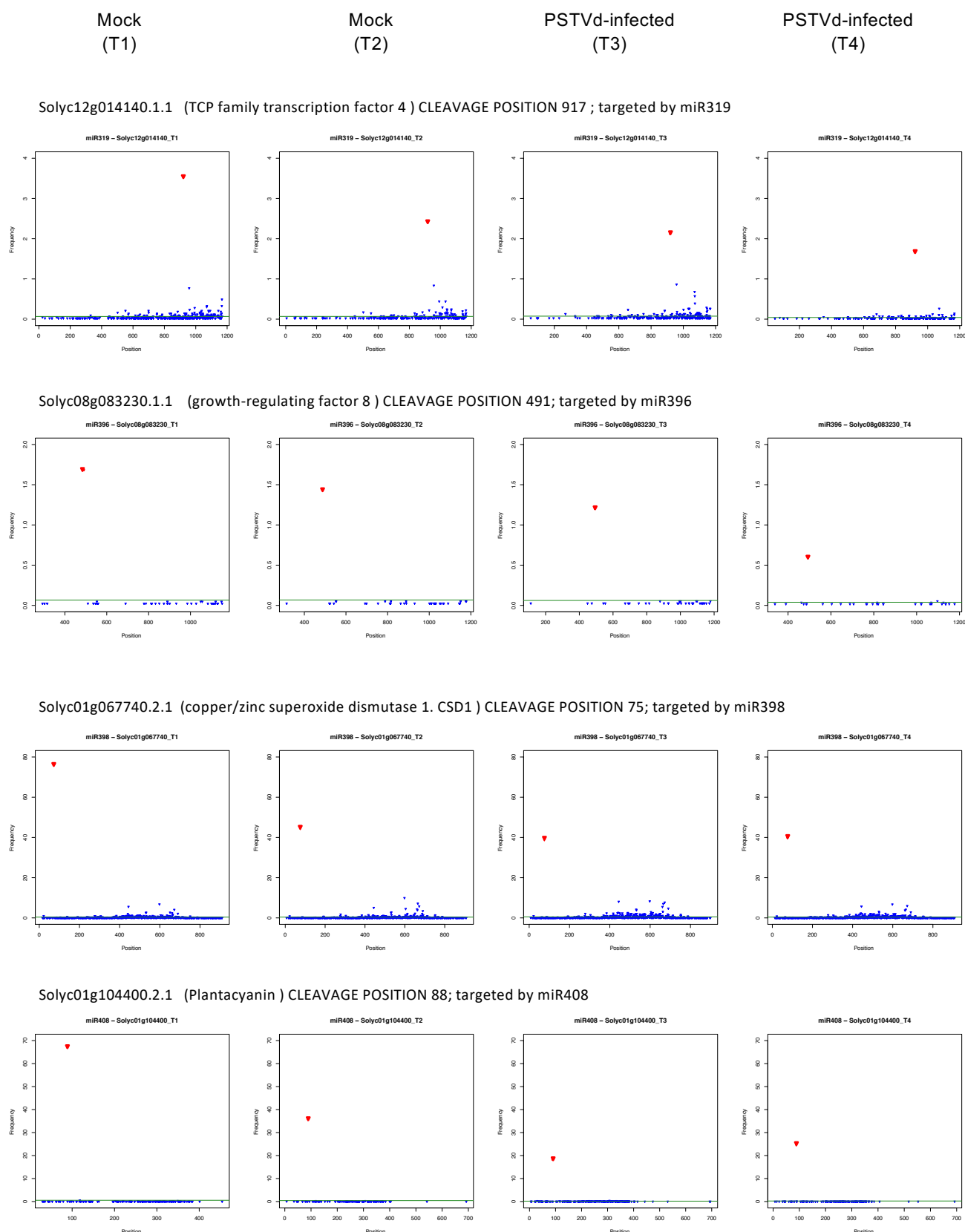


Figure S3. T-plots of mRNA targets of representative conserved miRNAs in mock (T1 and T2) and PSTVd-infected (T3 and T4) replicates. The abundance of each degradome tag is plotted as a function of the position of its 5' end in the transcript. In each t-plot, the tag abundance at the cleavage site predicted according with the cognate miRNA is reported in red.

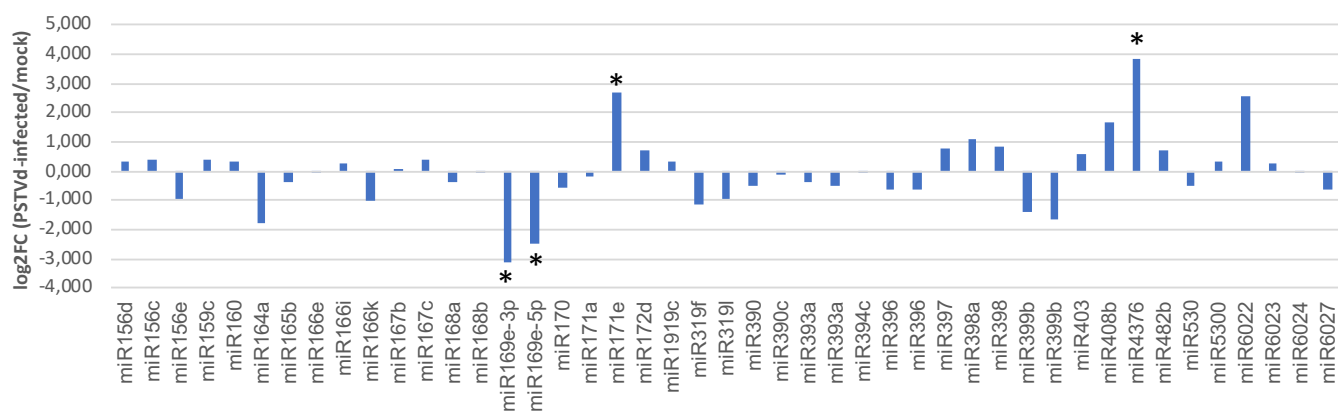


Figure S4. Changes in accumulation levels of miRNAs upon PSTVd-infection. log₂ of the fold change (FC) of miRNAs accumulation in PSTVd-infected with respect to mock-inoculated tomato plant are shown. The read per million average in the two replicates was used to calculate the FC. Statistical significance for t-test ($P < 0.01$) is indicated by asterisks.

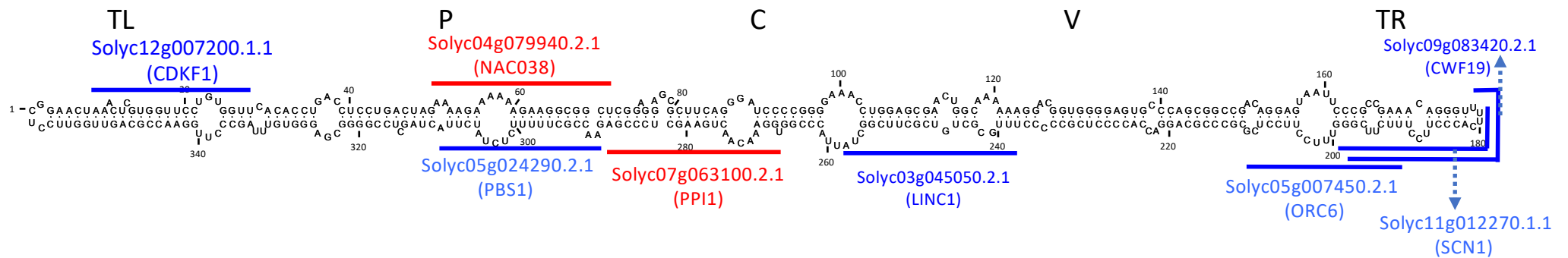


Figure S5. Localization in the PSTVd proposed secondary structure of the PSTVd-sRNAs targeting for cleavage eight *bona fide* tomato mRNAs. Blue and red lines denote the plus and minus polarity strand of the PSTVd-sRNAs, respectively. The ID and the name of the mRNAs targeted by each PSTVd-sRNA are indicated.

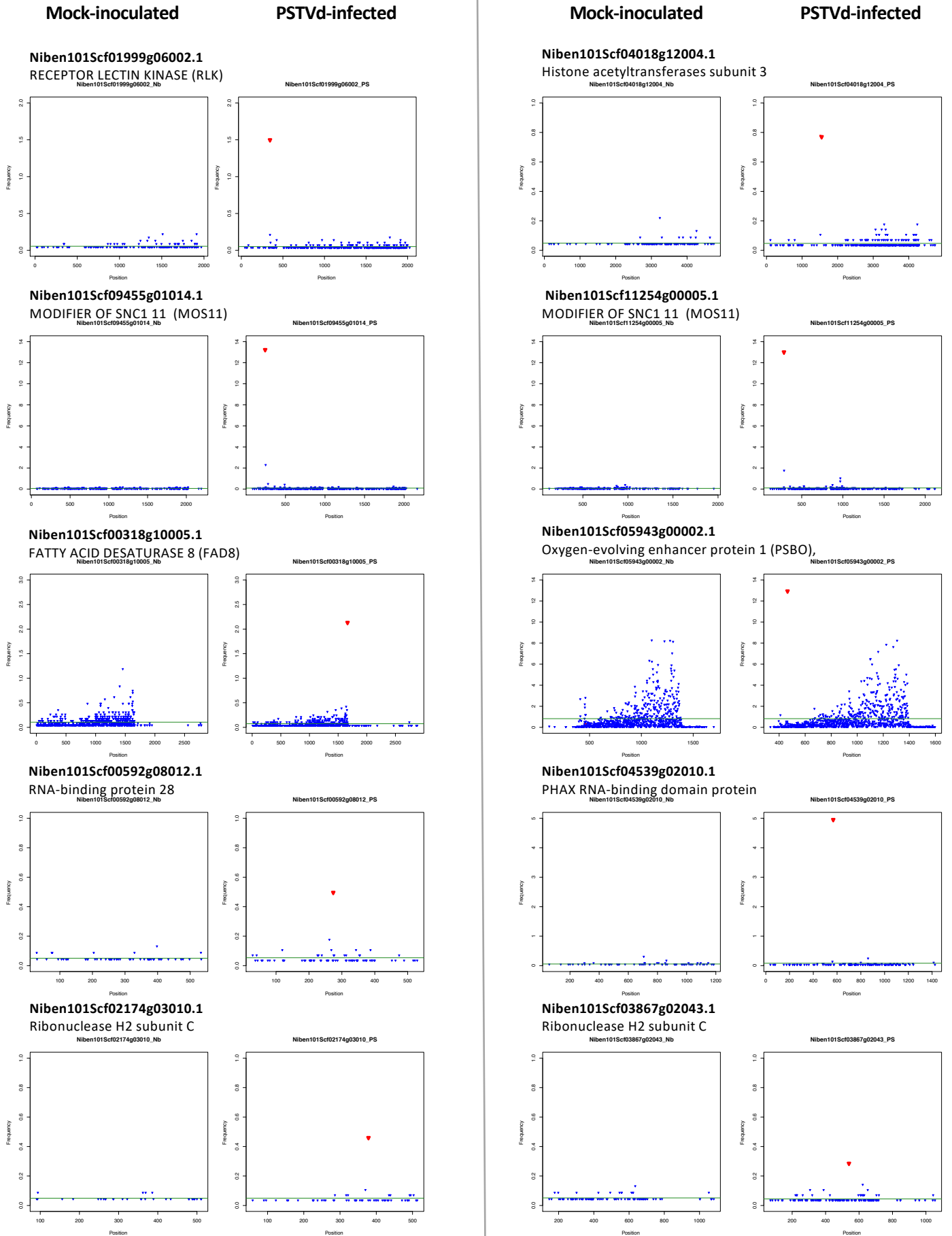


Figure S6. T-plots of ten representative specific mRNA targets of PSTVd-sRNA identified in mock-inoculated and PSTVd-infected inoculated *N. benthamiana*. The abundance of each degradome tag is plotted as a function of the position of its 5' end in the transcript. In each t-plot from PSTVd-infected sample, the tag abundance at the cleavage site predicted according with the cognate PSTVd-sRNA is reported in red. The ID and the name of the mRNAs targeted by each PSTVd-sRNA are indicated.