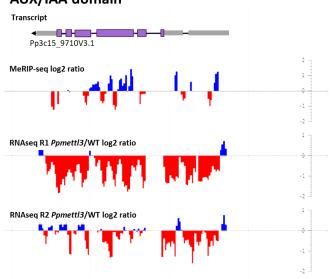
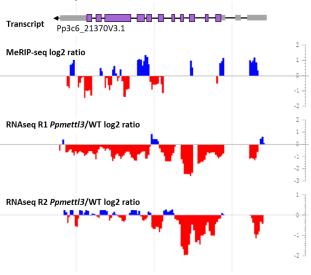
(a)
AUX/IAA domain

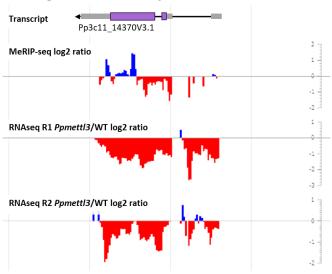




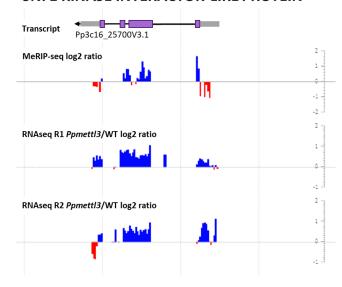


UDP-glucuronate 4-epimerase

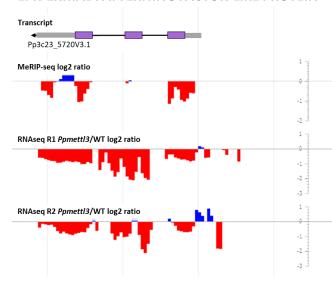
(b)



SNF1 KINASE INTERACTOR-LIKE PROTEIN



EPIDERMAL PATTERNING FACTOR-LIKE PROTEIN



INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE

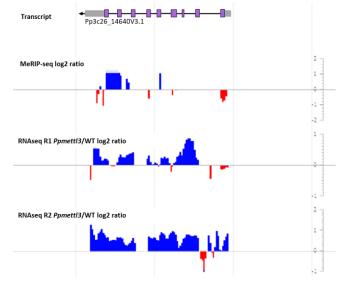


Figure S7. Selected transcripts showing m⁶A presence and their corresponding differential accumulation in *Ppmta* and wild type plants.

Diagrams show the structure of genes encoding factors related to (a) auxin signaling and (b) others found in development-related GO categories shown in Figure 5B. The plots below each gene indicate the position of enriched peaks found by MeRIP-seq shown as the log² ratio of IP/input (in blue and red bars). The accumulation levels obtained in the RNA-seq replicate 1 and 2 are indicated below as log² ratio of *Ppmta*/WT, shown as blue bars (up-regulated) or red bars (down-regulated).