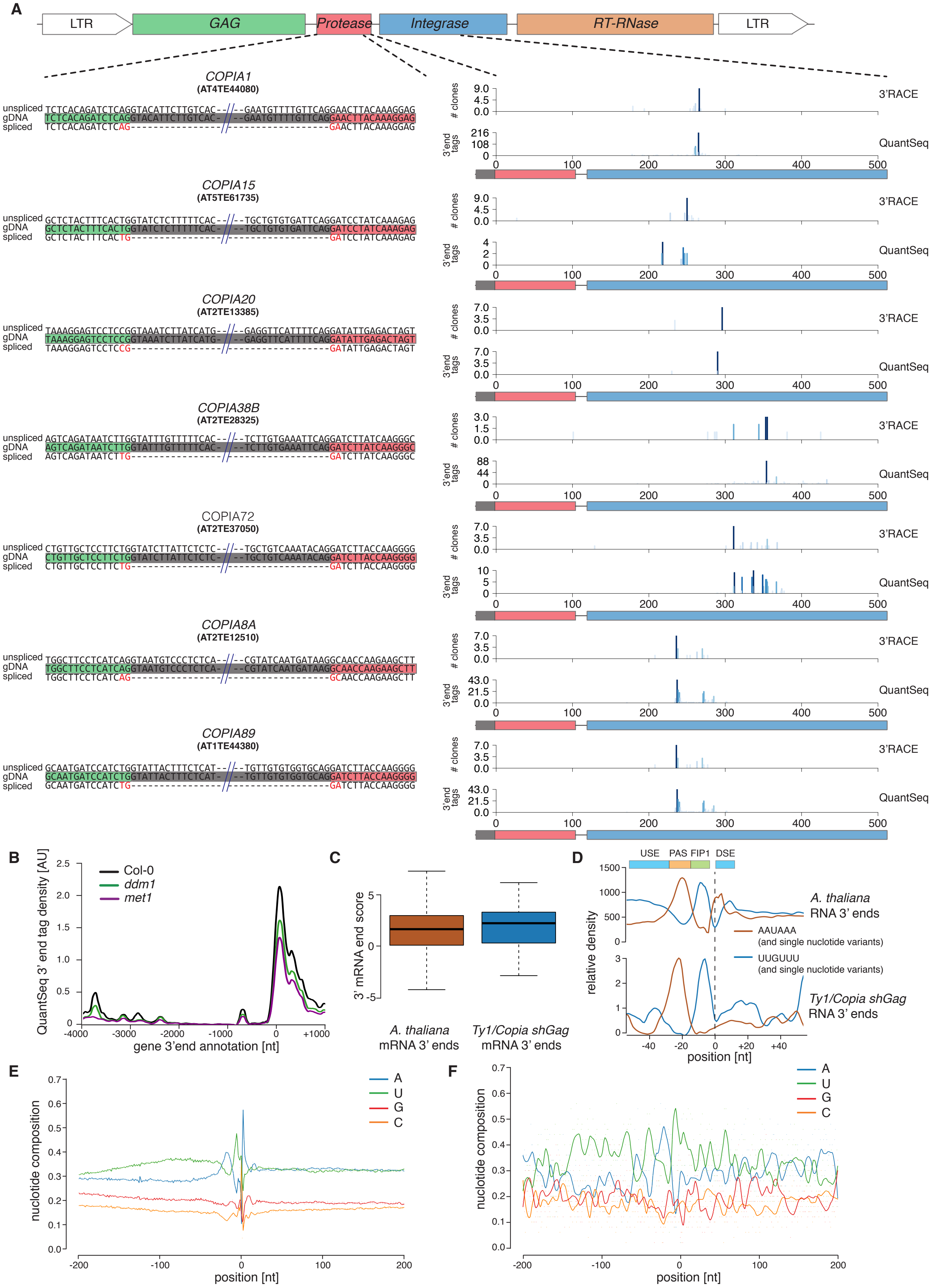

Supplemental Figure S4. 3' RACE validation of the QuantSeq data and features of *shGAG* RNA 3'ends.
(A) Left panel: nucleotide sequences of splice junctions of seven distinct Ty1/Copia elements. Right panel: 3' RACE analysis of those *Ty1/Copia* elements (top diagrams) versus RNA 3' ends identified in the integrase domain (blue) using the QuantSeq approach (bottom diagrams). Sequenced 3' RACE clones terminating in the integrase domain were exclusively spliced. (B) Kernel density plot of mRNA 3' end tags of annotated genes identified by the QuantSeq method. (C) Position-specific scoring matrix scores for A. thaliana mRNA 3' ends versus *Ty1/Copia shGAG* mRNA 3' ends. (D) Cleavage and polyadenylation site features of total A. thaliana and *Ty1/Copia shGAG* mRNAs. (USE) Upstream sequence element, (PAS) poyl(A)-site; (FIP1) FIP1 bidning site; (DSE) downstream sequence element. (E) Nucleotide composition around the major RNA 3' end within each cluster of total Arabidopsis RNA termination sites. (F) As in (E) but only using termination sites of *Ty1/Copia* shGAG RNAs.