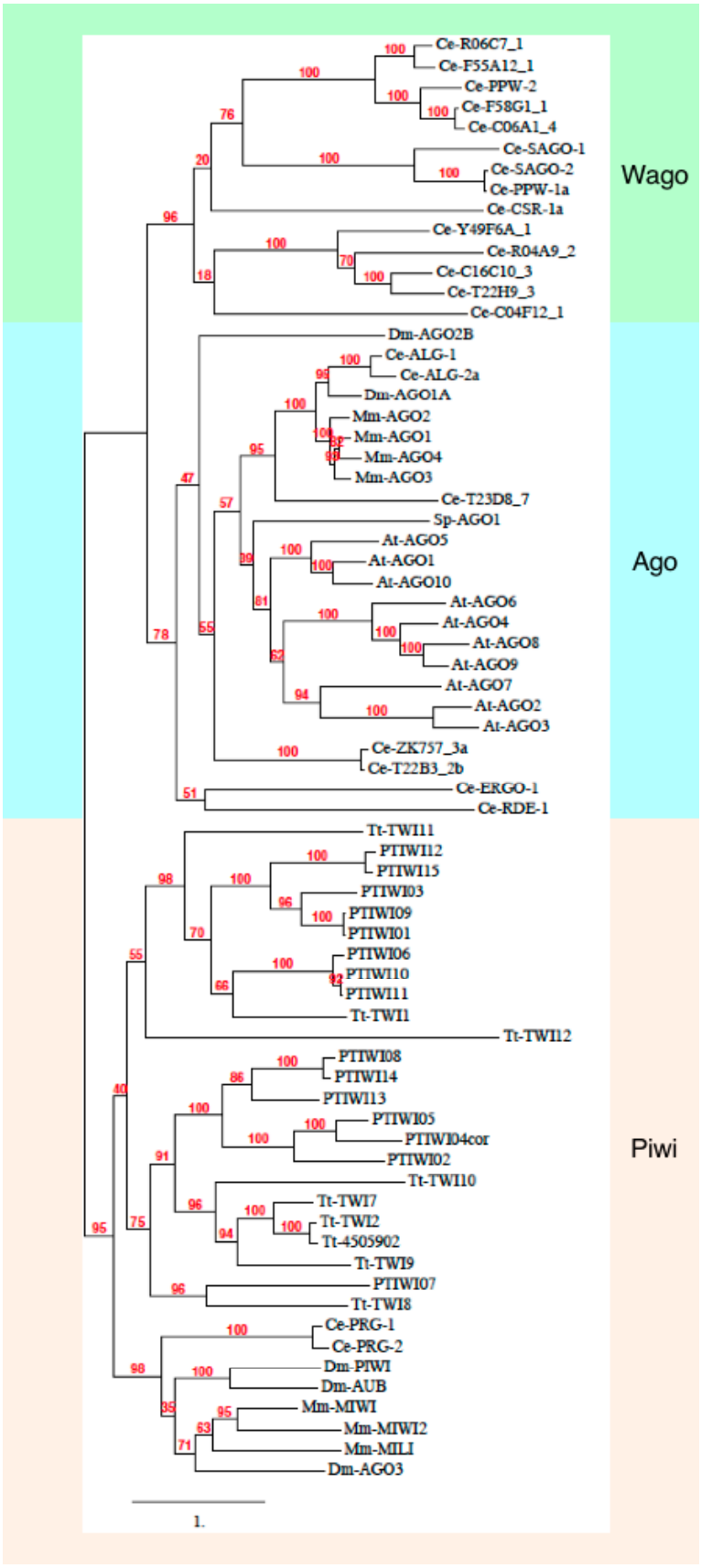
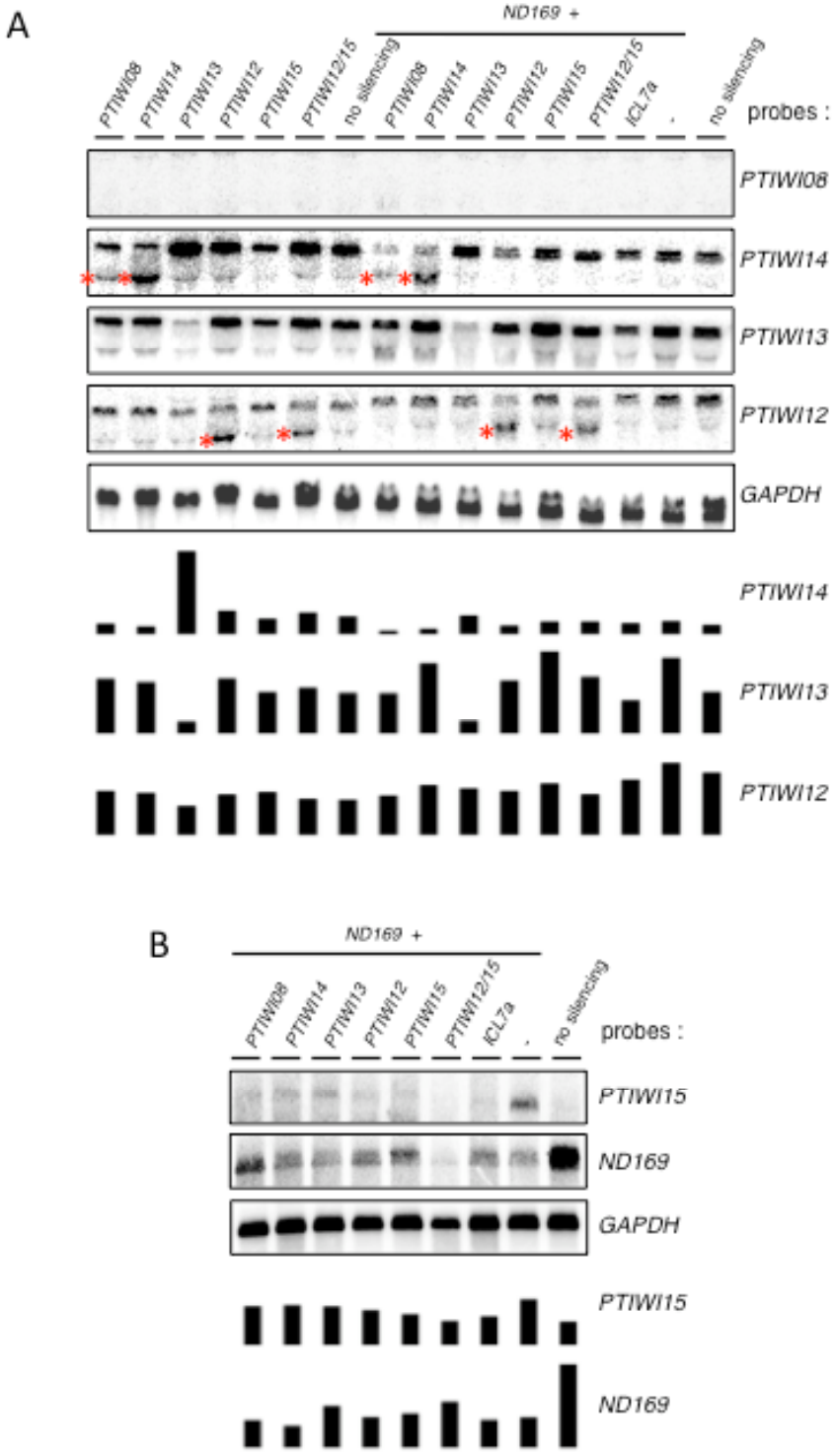
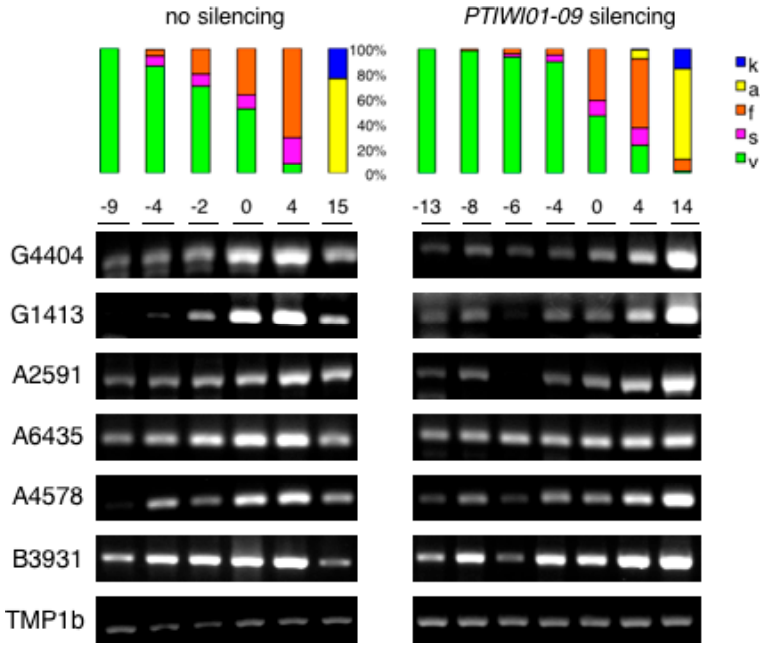
Sup. Figure S2. An Argonaute phylogenetic tree based on the alignment shown in Sup. Fig. S1. Bootstrap values are indicated. The scale bar indicates the branch length corresponding to 1 substitution per site (inferred using the WAG model).



Sup. Figure S3. Northern blot analyses of steady-state mRNA levels after dsRNA-induced silencing of *PTIWI* genes. **(A)** A northern blot of total RNA samples from cultures silenced for different *PTIWI* genes or for the *ICL7a* centrin gene as a control (as indicated above each lane), with or without co-silencing of the *ND169* reporter gene, was hybridized with different probes, as indicated on the right of each panel. Lower molecular weight material indicated by red stars (a smear compressed by the small ribosomal RNA) provides qualitative evidence for the degradation of the *PTIWI14* mRNA upon feeding of *PTIWI14* or *PTIWI08* dsRNAs, and of the *PTIWI12* mRNA upon feeding of *PTIWI12* dsRNA. The histograms below represent quantification of full-length mRNAs, after normalization with the *GAPDH* mRNA signal. **(B)** A northern blot of purified polyA+ RNAs from the *ND169* co-silencing samples was hybridized with *PTIWI15*, *ND169*, or *GAPDH* probes.



Sup. Figure S4. Gel images of PCR analyses of IES excision (see Fig. 4B).



Sup. Figure S5. Dot-blot quantification of the Sardine transposon and of the *A* surface antigen gene. Total DNA samples from the post-autogamous progeny of wild-type cells, and of cells silenced for *PTIWI01*, *PTIWI03*, and/or *PTIWI09*, were spotted on the membrane and hybridized with probes specific for *A* surface antigen gene, for the Sardine transposon, or for mitochondrial DNA as a loading control.