**SOURCE DATA:**

The dataset contains all the images, including protein and RNA blots. Raw image and source files can be found in the associated Zenodo dataset: ([www.zenodo.org](http://www.zenodo.org)) under the doi: [10.5281/zenodo.14037413](https://zenodo.org/records/14037413). DNA and protein sequences used for phylogenetic trees, do plots…, and any other type of source data, sorted by figure and figure panel can be found here as well as in the Zenodo dataset together with genome browser tracks ready to use. Plasmids generated for this study have been deposited in Addgene. They are listed below together with previously existing plasmids obtained from Addgene and used in this study. NGS data has been deposited on NCBI SRA, accession numbers of datasets used in each figure are listed accordingly in this document. The content of each file is:

**FIGURE 3:**

* **3A**: Picture of *Spirodela polyrhiza* (used as well in S19A, S26B, D).

**FIGURE 5:**

* **5A:** Western blot image files for the detection of H3K9me1, H3K9me2 and H3 in *Arabidopsis* and *Spirodela*.

**FIGURE 7:**

* **7A:** Western blot and Coomassie image files for the detection of FHA-AtAGO4\_gDNA and FHA-SpAGO4a\_cDNA in input and IP fractions from transient expression in *N. benthamiana*.
* **7D:** image files of *N. benthamiana* leaves infiltrated with RUBY or Scarlet hairpin (hpScarlet) and Northern blots image files for the detection of siRNAs produced by RUBY and hpScarlet transiently expressed in *N. benthamiana*.
* **7E:** image files of *Spirodela* cultures in dishes infiltrated with RUBY or Scarlet hairpin (hpScarlet) and Northern blots image files for the detection of siRNAs produced by RUBY and hpScarlet transiently expressed in *Spirodela*.

**SUPPLEMENTAL FIGURE S6:**

* Protein sequences, and their alignment, of several angiosperm DRB proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S7:**

* Protein sequences, and their alignment, of several angiosperm RDR proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S8:**

* Protein sequences, and their alignment, of several angiosperm DCL proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S9:**

* Protein sequences, and their alignment, of several angiosperm AGO proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S10:**

* DNA sequence of the Spirodela (Sp9509) Chromosome 7 fragment containing the AGO5 cluster.

**SUPPLEMENTAL FIGURE S11:**

* Protein sequences, and their alignment, of several angiosperm SHH proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S12:**

* Protein sequences, and their alignment, of several angiosperm Snf2 remodelers proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S13:**

* Protein sequences, and their alignment, of several angiosperm Class V SET-domain containing proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S14:**

* Protein sequences, and their alignment, of several angiosperm DNA methyltransferase proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S15:**

* Protein sequences, and their alignment, of several angiosperm RNA pol large subunit proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S16:**

* Protein sequences, and their alignment, of several angiosperm SPT5 and SPT5L proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S17:**

* Protein sequences, and their alignment, of several animal and plant Uhrf/VIM proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S18:**

* **S18A\_B:** Protein sequences, and their alignment, of several angiosperm SUVH4 and SUVH5/6 proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).
* **S18C\_D:** Protein sequences, and their alignment, of several angiosperm ASI1 proteins, including those identified in the *S. polyrhiza* 9509 genome, used to build phylogenetic tree in fasta (.fa) format. Machine readable tree file is also provided in Nexus format (.nxs).

**SUPPLEMENTAL FIGURE S19:**

* Picture of *Arabidopsis* (used as well in S26 A,C).

**SUPPLEMENTAL FIGURE S24:**

* **S24C:** image files of the coomassie staining of histone acid-extraction protein samples run on SDS-PAGE gel.
* **S24D:** Excel files with mass-spectrometry data used for quantification of histone modifications in Arabidopsis and Spirodela.

**SUPPLEMENTAL FIGURE S27:**

* **S27A:** image files of *Arabidopsis* interphase nuclei stained with DAPI.
* **S27B:** image files of *Spirodela* interphase nuclei stained with DAPI.

**SUPPLEMENTAL FIGURE S34:**

* DNA sequence files (fasta) of TEs used to generate dot plots.

**SUPPLEMENTAL FIGURE S35:**

* **S35A:** Western blot and Coomassie image files for the detection of *FHA-AtAGO4\_gDNA* and *FHA-SpAGO4a\_gDNA* in input and IP fractions from transient expression in *N. benthamiana*.
* **S35B:** Intron-annotated genomic DNA sequences of At*AGO4* and Sp*AGO4a* in GenBank (.gbk) format.
* **S35C:** image file of EtBr staining of agarose gel electrophoresis of splicing analysis of *SpAGO4a*.
* **S35D:** Western blot and Coomassie image files for the detection of *FHA-AtAGO4\_gDNA* and *FHA-SpAGO4a\_cDNA* in input and IP fractions from transient expression in *N. benthamiana*.

**SUPPLEMENTAL FIGURE S36:**

* DNA sequence files (fasta) of TEs used to generate dot plots.

**SUPPLEMENTAL FIGURE S38:**

* Pictures of *Spirodela* during pretreatment, manual and vacuum agroinfiltration and RUBY transient expression.

**NGS DATASETS:**

All the NGS data generated for this study can be found under the SRA BioProject ID PRJNA1164696. The data was used to generate the following figure panels:

* Figures: 1A-H, 2A-F, 3A-E, 4A-H, 5D-J, 6A-G, 7B, 7F-H
* Supplemental Figures: S1, S3, S4, S19, S20, S22, S23, S26, S28, S29, S30, S31, S32, S33, S35, S36, S37, S38.

Publicly available sequencing data (from indicated datasets) was used to generate the following figures:

* Figure 2A-F (Arabidopsis gene expression): GSM6892968

**MASS SPECTROMETRY DATA:**

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD050443. Data was used to generate:

* Supplemental Figure 24D

**PLASMIDS:**

The following plasmids generated in this study can be retrieved from Addgene under the following ID#:

* p35S:FHA-AtAGO4\_gDNA: #216838
* p35S:FHA-SpAGO4a\_gDNA: #216841
* p35S::FHA-SpAGO4a\_cDNA: #216842

The following plasmids used in this study were retrieved from Addgene under the following ID#:

* p35S:RUBY: #160908
* pZmUbq:RUBY: #160909
* p35S:GFP-GUS: #167122

The following plasmids were a gift from Dr. Marco Incarbone (Max Planck Institute of Molecular Plant Physiology, Potsdam Science Park, Potsdam 14476, Germany).

* pAtUBQ:hpScarlet