SUPPLEMENTARY FIGURE

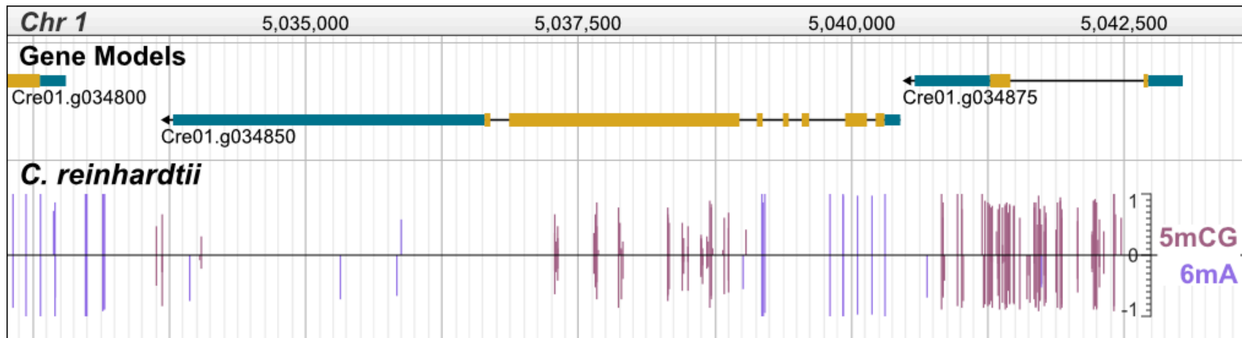

Fig. S1. Base modifications of *C. reinhardtii*. Viewing 5mC in the CG sequence context and 6mA in *C. reinhardtii* with the plugin. Height and direction of bar indicates methylation level and strand, respectively. Bars are colored by 5mCG and 6mA.

SUPPLEMENTARY METHODS

Genomes.

Arabidopsis thaliana: Reference sequence, gene models, and transposable element models were from the TAIR10 genome (https://www.arabidopsis.org).

Chlamydomonas reinhardtii: Reference sequence (v5.0) and gene models (v5.5) were from Phytozome 12 (https://phytozome.jgi.doe.gov/pz/portal.html).

Fig. 1: *A. thaliana* 5-methylcytosine.

Samples were previously published [1] and raw reads were downloaded SRR342383, SRR342378, and SRR342381 for sample 1, sample 2, and sample 3, respectively. Briefly reads were processed and aligned as described in Schultz *et al.* [2]. Reads were trimmed using Cutadapt v1.3 [3] with parameters "-a AGATCGGAAGAGCTCGTATGCC -m 30 -q 10". Reads were mapped to the TAIR10 genome using Bowtie v1.1.0 [4] with parameters "-k 1 -m 1 --chunkmbs 3072 --best --strata -o 4 -e 80 -l 20 -n 0". PCR duplicated were removed using Samtools v1.2 [5]. Only uniquely mapped, non-clonal reads were retained.

Resulting output files were converted to BigWig format using custom scripts available with the plugin. Methylated cytosines were determined as described in [2]. At each methylated cytosine, weighted methylation level [6] was computed as mC / (mC + uC) where mC is the number of methylated reads and uC is the number of unmethylated reads at the position. Positions were split into separate bedGraph files based on sequence context and files were converted using bedGraphToBigWig [7].

Fig. 2: *A. thaliana* small RNAs.

This sample was previously published [8] and raw reads were downloaded from SRR1266859. Reads were trimmed using Cutadapt v1.9.dev1 [3] with parameters "-a TGGAATTCTCGGGTGCCAAGGAACTCCAGT -g TGTGTTCTCAGGTCGCCCCTG -m 18 -M 30". Reads were then mapped to the TAIR10 genome using Bowtie v1.1.1 [4]

with parameters "--phred33-quals -n 0 -l 18 -M 1 --best". Samtools v1.2 [5] was used for subsequent file conversion.

Fig. 3: *A. thaliana* stranded coverage and sequence motif density.

Sample 1 methylation coverage was computed using only the uniquely mapped, non-clonal reads processed as described above in Fig. 1. Resulting BAM file was converted to BigWig format using custom scripts available with the plugin. Briefly, using the genomecov module from bedtools v2.24.0 [9], strand-specific coverage was found using the parameters "-bga -strand +" for the positive strand coverage and "-bga -strand -" for the negative strand coverage. The resulting bedGraph files were converted to BigWig format with bedGraphToBigWig [7].

CN dinucleotide (CA, CC, CG, and CT) motif density was computed using sliding windows with window size 100 base-pair (bp) and step size 10 bp. Using only the forward strand, density of the window was computed as nCN / nNN where nCN is the number of CN dinucleotides in the window and nNN is the number of dinucleotides in the window.

Figure S1: Base modifications in *C. reinhardtii*.

For 5-methylcytosine, raw reads were downloaded from SRR2022686. Paired-end reads were mapped as described in Schultz *et al.* [2]. Reads were trimmed using Cutadapt v1.14 [3] and mapped using Bowtie2 v2.2.9 [10]. PCR duplicates were removed using Picard tools v2.4.1 [11]. Only uniquely mapped, non-clonal reads were retained. Samtools v1.3.1 [5] was used for additional file conversions. Methylated reads and methylation level were determined as described above in Fig. 1.

For 6-methyladenine, processed WT data was downloaded from GSE68860. The "frac" attribute of each reported 6mA position was used to indicate methylation level.

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