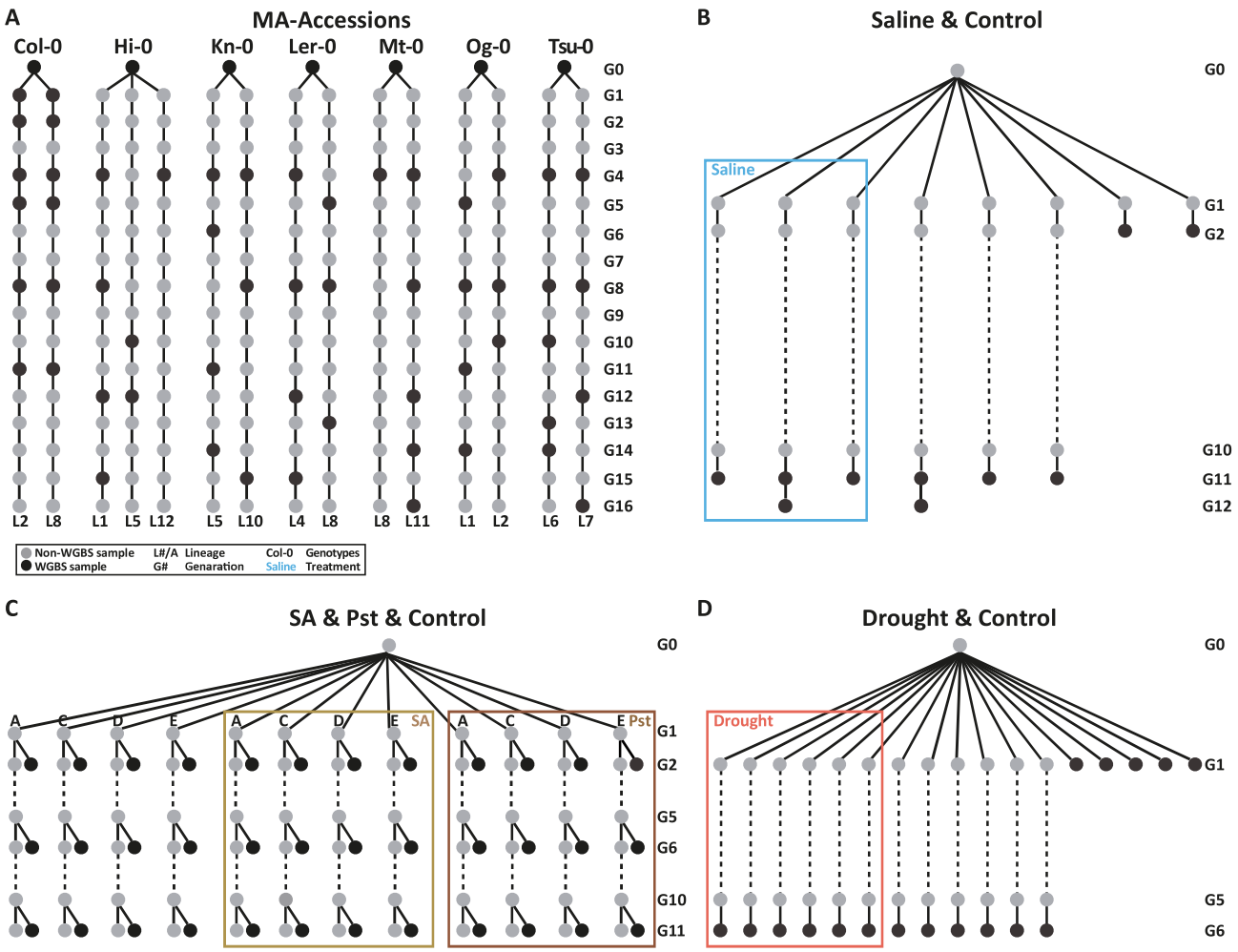


Fig. S1. Pedigrees of *A. thaliana* MA-lines. (A) The pedigrees of MA-Accessions from seven different natural accessions (i.e. genotypes) **(B-D)** MA-lines under multi-generational biotic (C) or abiotic (B and D) stress and their corresponding controls. The non-WGBS samples (grey circle) inside the rectangles are treated with stress, but the WGBS samples (black circle) are not, other samples outside the rectangles are treated as controls. A and C are newly produced data, whereas B and D are from previously published studies (B(23); D(24). B, C, and D were derived from a single Columbia (Col-0) genotype.

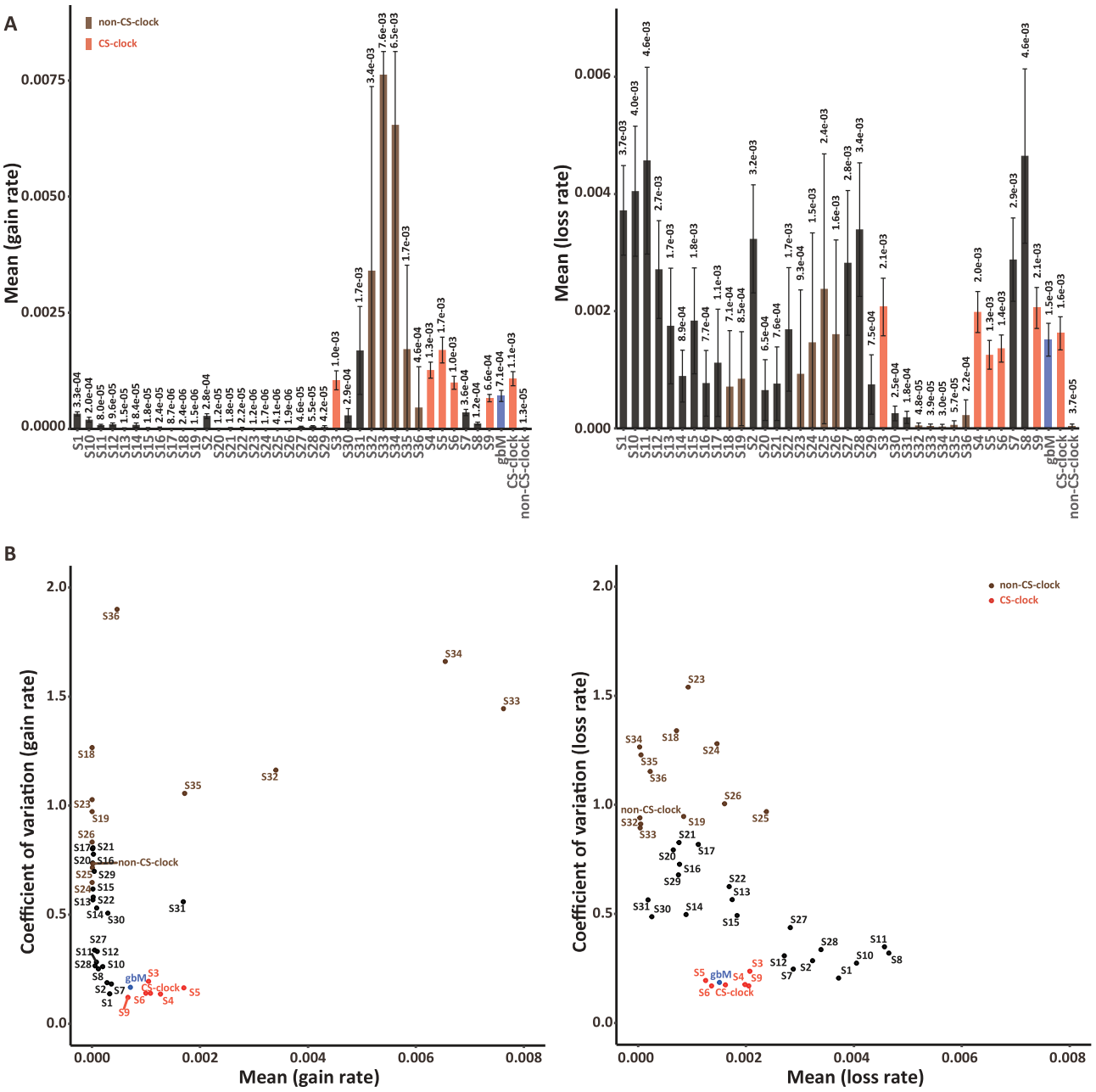
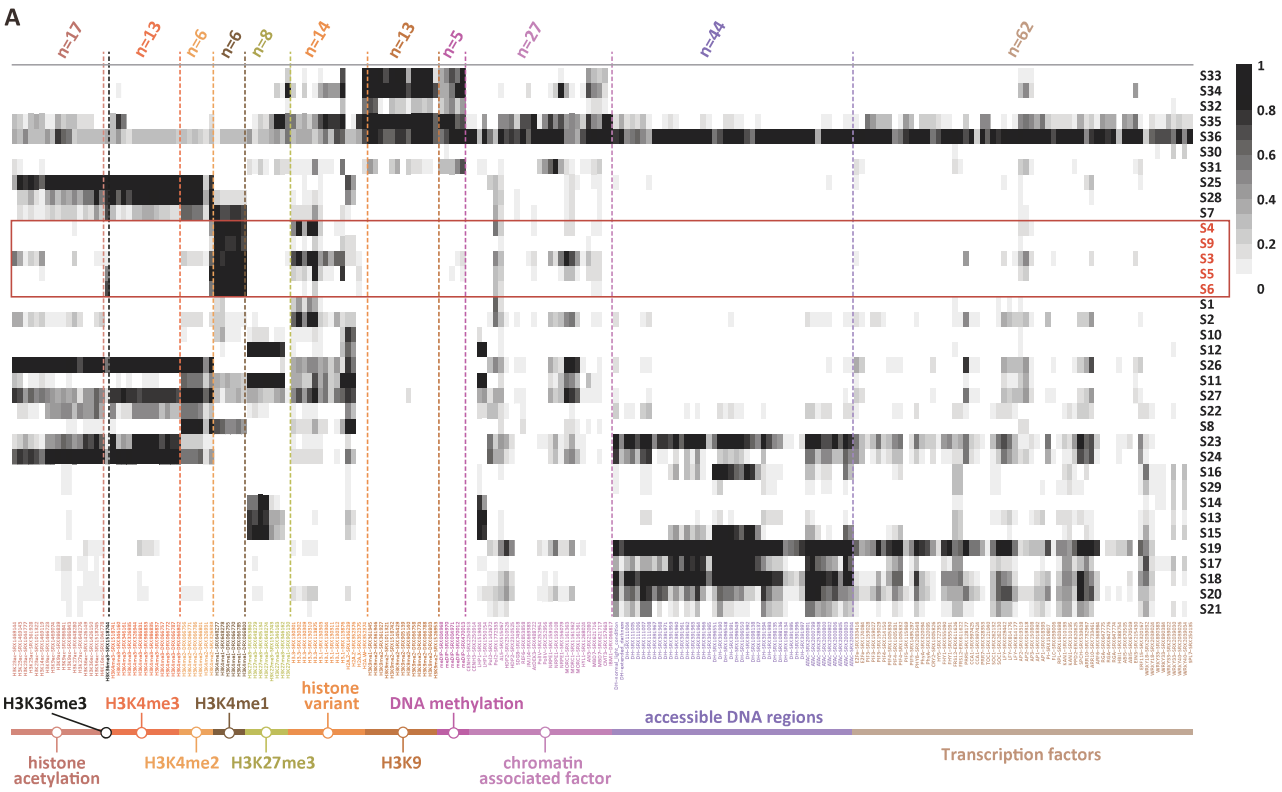


Fig. S2. Epimutation rate of each chromatin state across the 14 different genetic and environmental MA lines. (A) Mean of gain or loss rate. **(B)** Coefficient of variation versus the mean for gain or loss rate. This shows that the states with the lowest coefficient of variation (CS-clock states, red color) are not because they have the largest gain or loss rate.



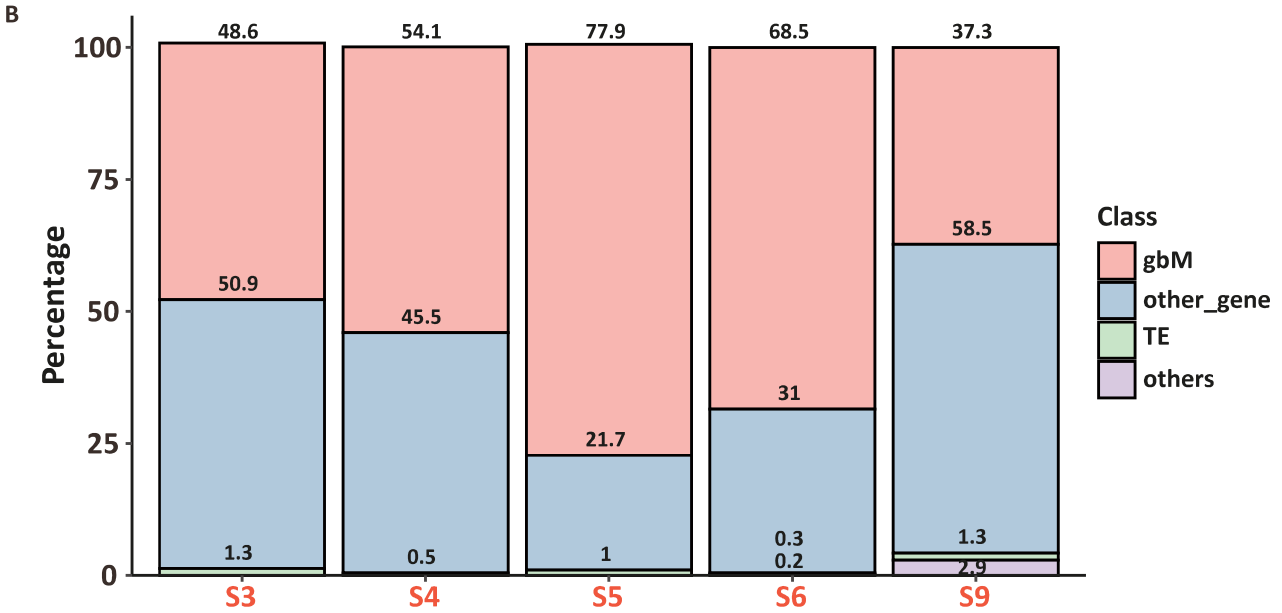


Fig. S3. Chromatin modifications and genomic annotations within defined chromatin states. (A) The enrichment of different chromatin modifications within each of the 36 chromatin states. **(B)** The percentage of genomic annotations of the five chromatin states that define the clock-like regions. "other_gene" was defined by removing gbM genes from the whole gene sets. "others" was defined by removing genes and TE from the whole genome.

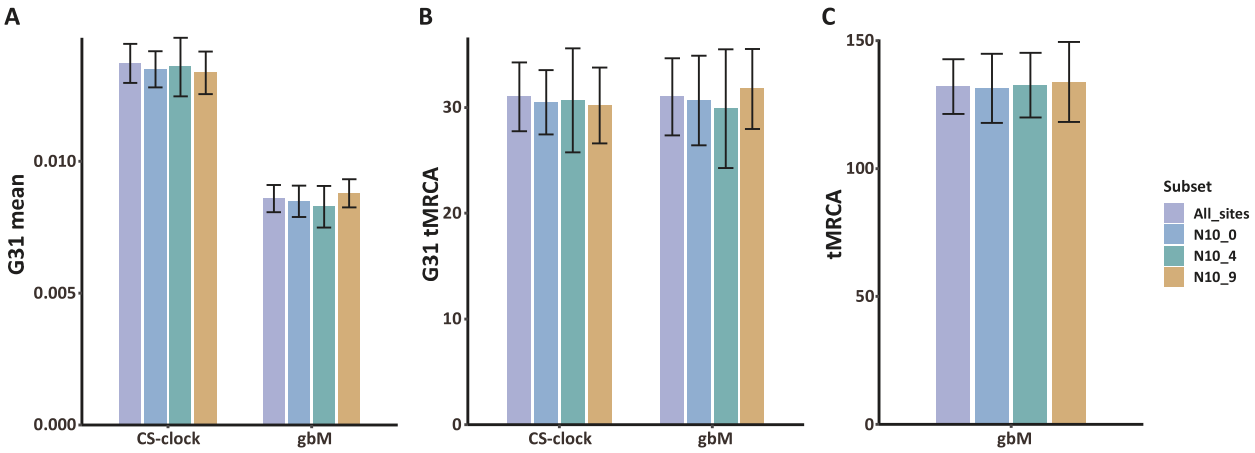


Fig. S4. Comparative analysis of depth and tMRCA in gbM and CS-clock subsets. This figure illustrates the measurement of depth and time to the most recent common ancestor (tMRCA) across subsets of CS-clock regions and gbM genes in *A. thaliana* MA1_1, MA1_2, and North American accessions. We created subsets by selecting one CG site per every ten (neighbourhood size = 10) from the original data, with the process replicated thrice, targeting the 1st, 5th, and 10th CG sites within each neighbourhood (N10_0, N10_4, N10_9). **(A)** Depth of the G31 samples from MA1_1 and MA1_2. **(B)** Estimated tMRCA for G31 samples, drawn from both gbM genes and CS-clock regions (including their respective subsets). The average epimutation rate across all gbM CpG sites in G31 was used for each gbM gene subset. Similarly, for each subset of CS-clock regions, the average epimutation rate from all corresponding CpG sites in G31 was used. **(C)** Estimated tMRCA for 12 non-recombining taxa from the North American accessions. These estimations used the average epimutation rate of all gbM sites, sourced from G31.

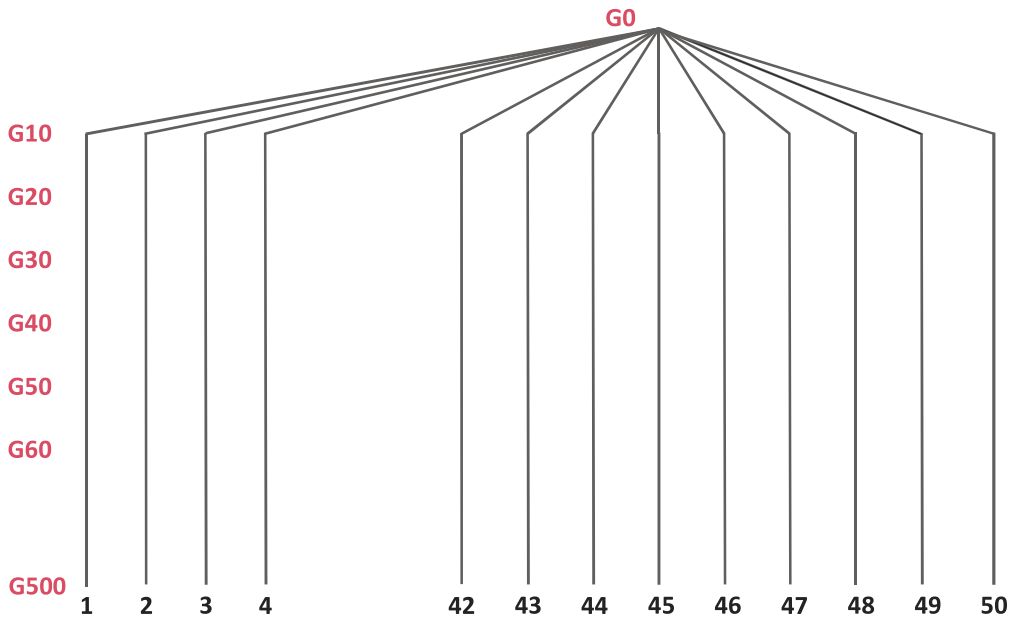


Fig. S5. Simulated MA lines. To study accumulation of SNPs and epimutations, we simulated 16 sets of MA lines. Each set of MA lines contained 50 MA lines that shared a single common ancestor (G0). The simulated MA lines were propagated with either selfing or clonal propagation for 500 generations. The substitution rates, generation time, and simulated sequence lengths were identical for all individuals in the same set of MA lines. Every 10 generations, the sequence divergence between the common ancestor and its descendants was measured and recorded.

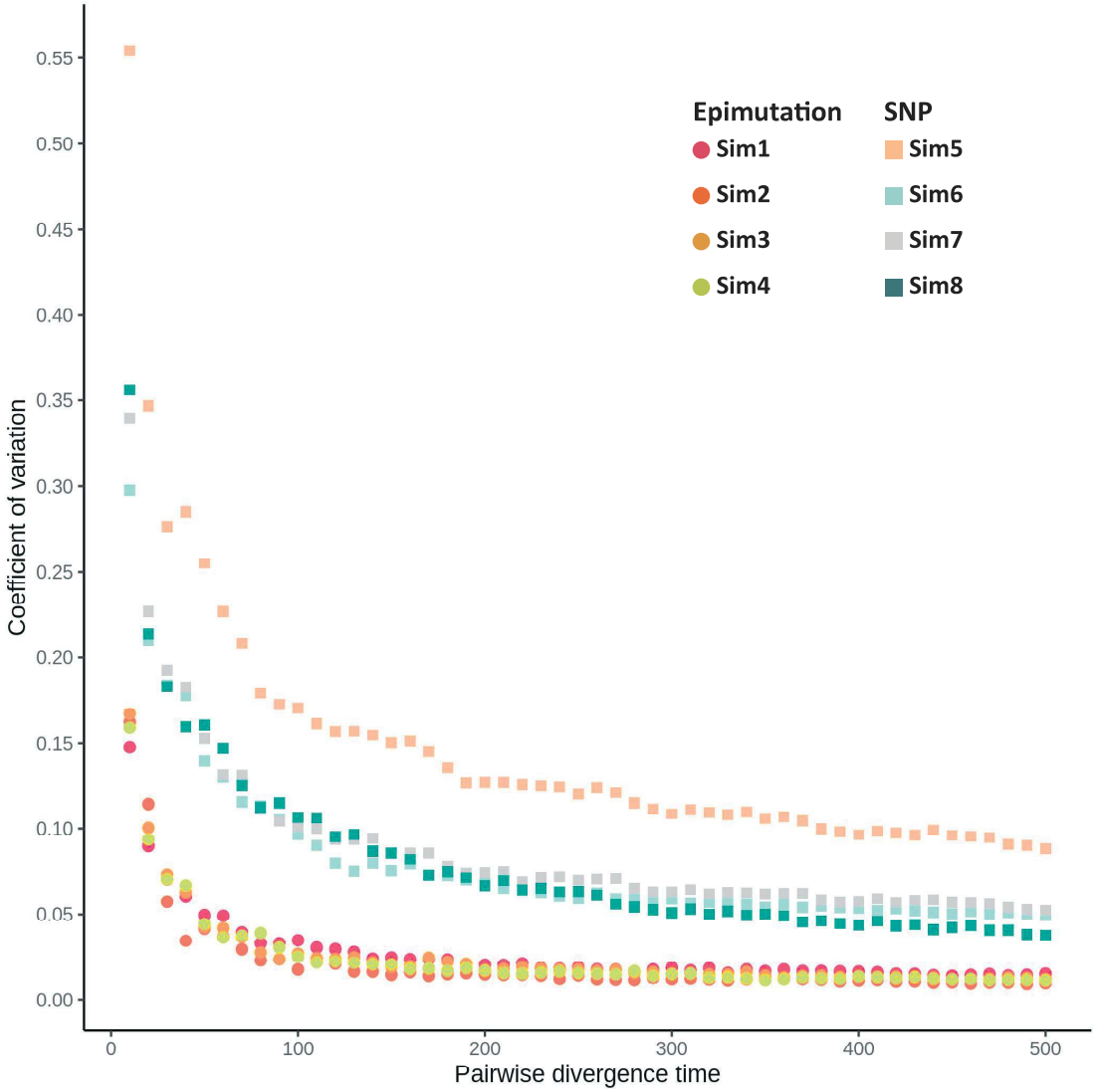


Fig. S6. Coefficient of variation of observed divergence in simulated selfing MA lines. We simulated accumulation of epimutations (Sim1-4, spots) and SNPs (Sim5-8, squares) on 8 sets of 50 simulated selfing MA lines. Within each set of MA lines, we measured the observed divergence every 10 generations and evaluated their dispersion via coefficient of variations (CVs). From G0 to G500, the CVs of observed epimutations are always ~50% lower than CVs of observed SNPs.

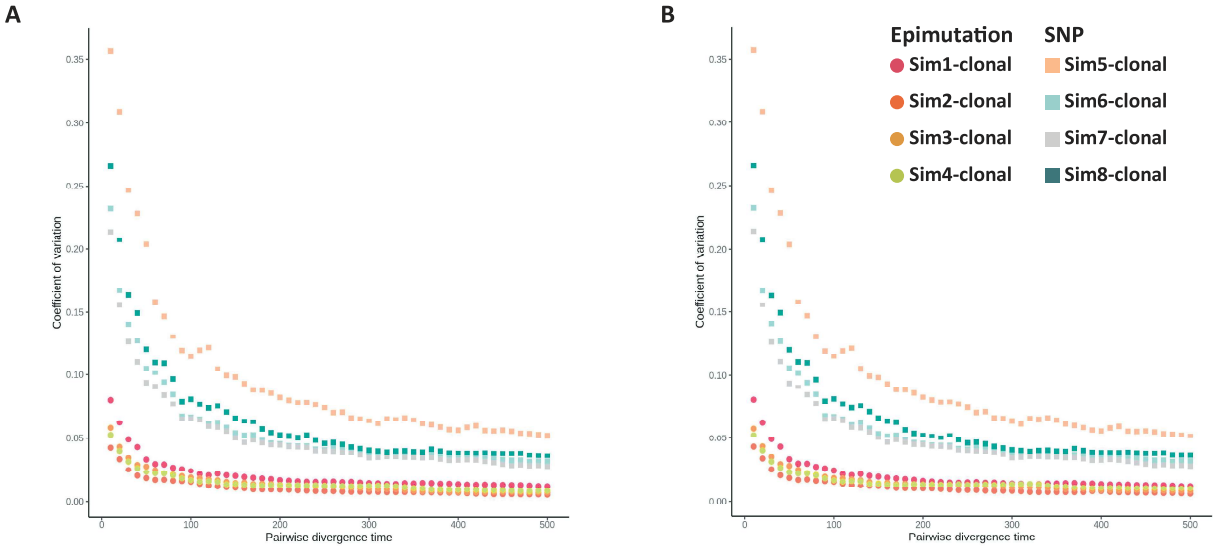


Fig. S7. Coefficient of variation of divergence in simulated clonal datasets. For clonal diploid plants, we also simulated the (epi)mutation accumulation on epigenetic clock regions (1×10^5 CpG sites, Sim1-clonal - Sim4-clonal) and genome (1×10^9 base pairs, Sim5-clonal - Sim8-clonal). There were eight sets of 50 simulated MA lines. Each set of the MA lines started from a single founder individual (G0) and reproduced through asexual reproduction for 500 generations. Every 10 generations, we measured the divergence between every single individual and G0. **(A)** Coefficient of variation of observed divergence (P-distance). **(B)** Coefficient of variation of estimated divergence. We used baseline distance to estimate the divergence on epigenetic clock regions. For simulated genomes, we used the K80 distance. Both observed and estimated divergence suggests the epigenetic clock has higher statistical robustness while inferring recent evolutionary histories.

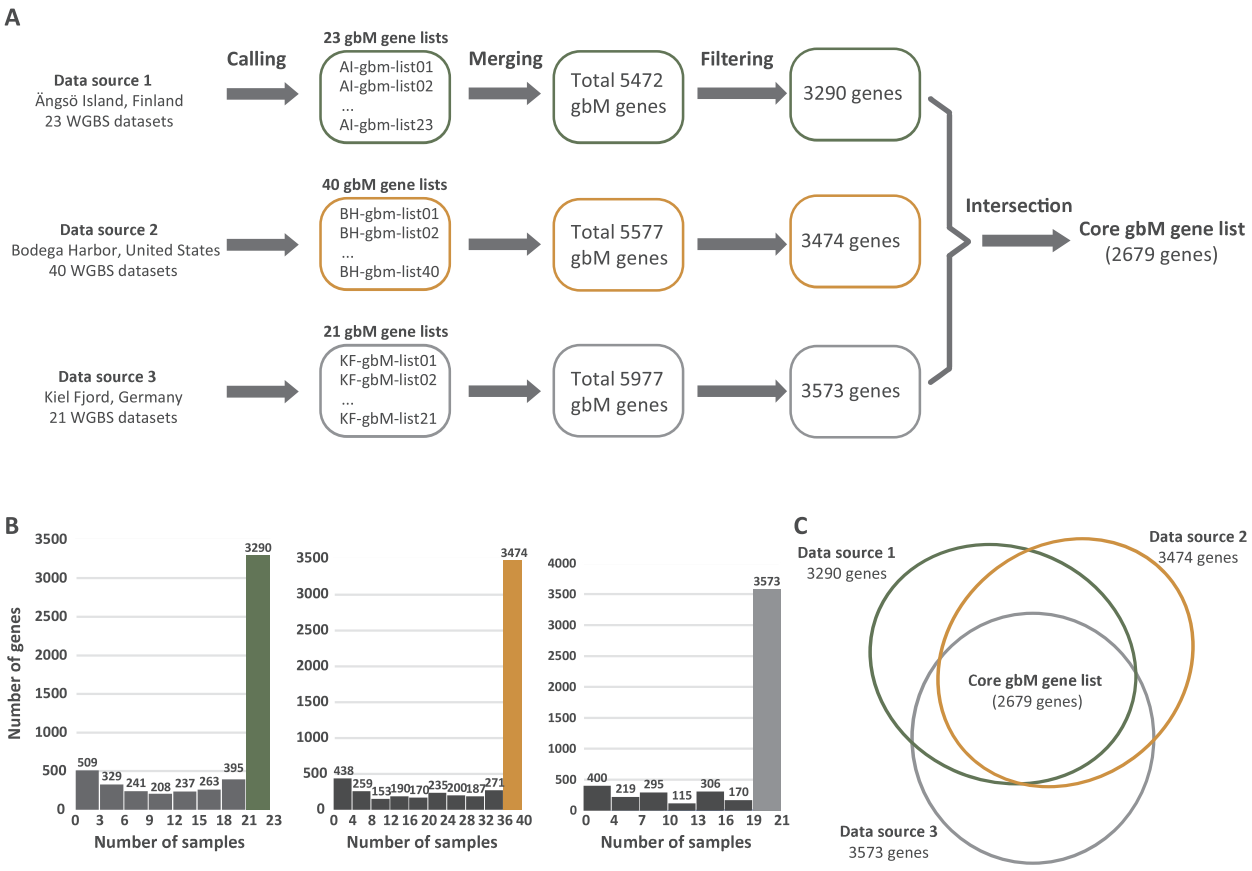


Fig. S8. Identifying gbM genes in *Z. marina* samples. (A) We identified gene-body methylation (gbM) genes from *Z. marina* samples from three data sources from various locations. From each sample, which corresponds to a WGBS dataset, a gbM gene list was generated with a published pipeline (30). **(B)** The gbM gene lists from the same data source showed high consistency. In samples from Ängsö Island, Finland (data source 1), 3,290 genes were identified as gbM genes in 90% samples (i.e., in at least 21 samples). With the same cut-off, 3,474 genes and 3,573 genes were identified in 90% of samples within each of the other two data sources. Thus, three lists of highly reliable gbM calls were obtained. **(C)** We defined the intersection of three lists in (B) as "core gbM gene list" and used them in for analyses.

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