## Supplemental Datasets

Supplementary Dataset 1 MethylC sequencing statistics

Supplementary Dataset 2 *strs2* DMRs

Supplementary Dataset 3 mRNA sequencing statistics

Supplementary Dataset 4 Differentially expressed genes following triggering stress in naive plants

Supplementary Dataset 5 Differentially expressed genes following triggering stress in primed plants

Supplementary Dataset 6 Dampened transcripts

Supplementary Dataset 7 Enriched GO terms among dampened transcripts

Supplementary Dataset 8 Genotyping primers

Figure S1 Exploratory transcriptome analysis of naive and primed plants

A Multi-dimensional scaling plot of all samples where distance reflects the typical log2 fold change between samples.

B-D Mean-difference plots for B primed versus naive libraries, C naive-triggered versus naive libraries, and D primed-triggered versus primed libraries with smearing of low abundance transcripts. Each dot represents a transcript plotted by its average abundance (log2 CPM) against the log2 fold change from the specified comparison. Red and blue dots indicate differentially expressed transcripts as determined by quasi-likelihood F-tests (FDR < 0.05). Blue lines denote 2-fold change.