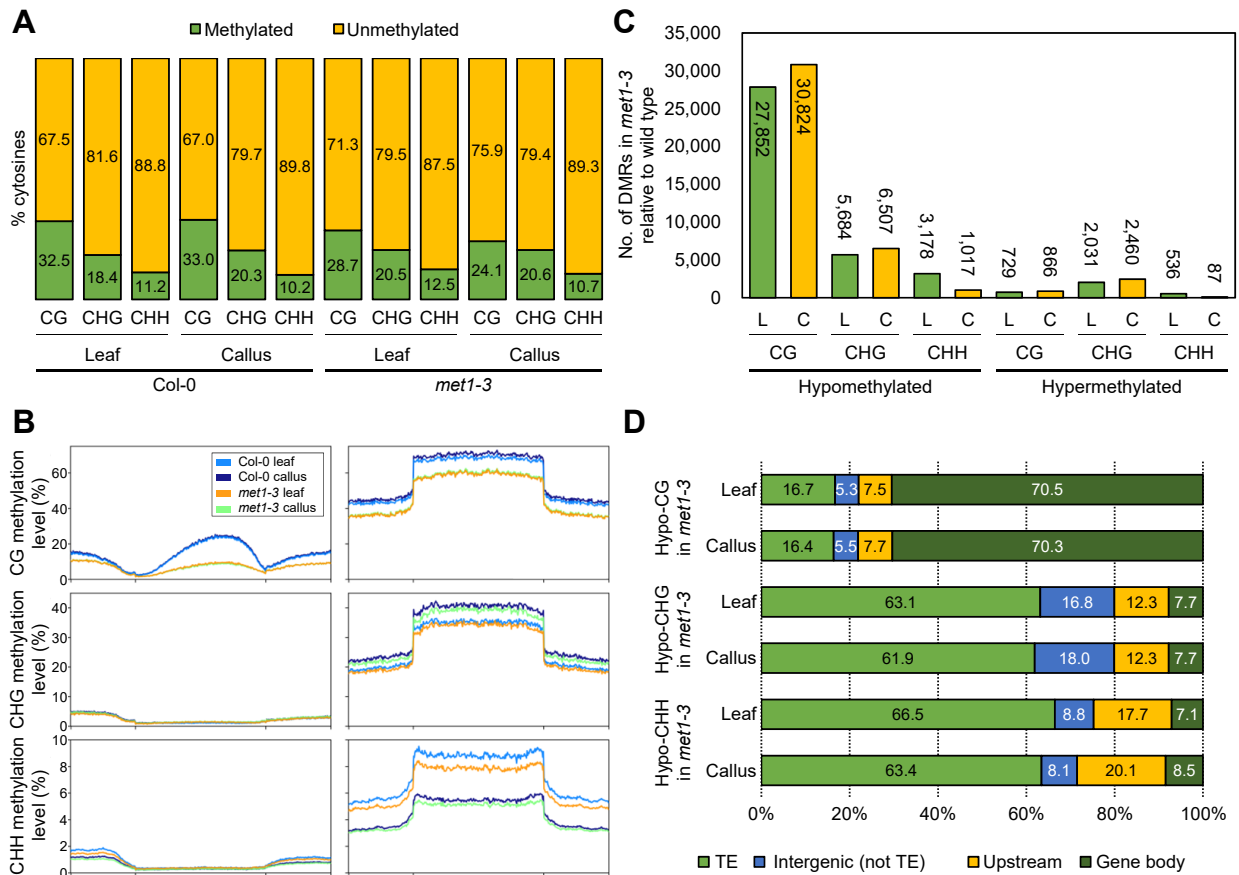
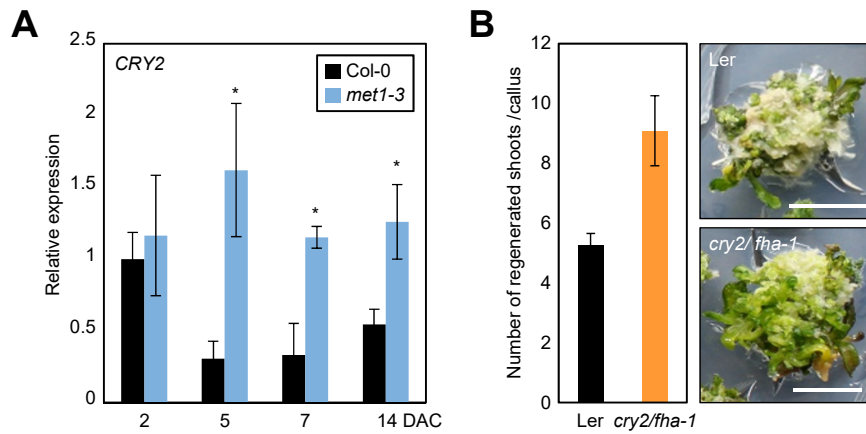


Supplementary Fig. S1. Cumulative cytosine coverage in leaf and callus tissues of *met1-3* and wild type. Red vertical dashed line indicates minimum depth threshold.



Supplementary Fig. S2. Genome-wide DNA methylation patterns in *met1-3* and wild type. (A) Fractions of methylated and unmethylated cytosines in *met1-3* and wild type. (B) Average level of DNA methylation over genic and TE regions. The flanking 1-kb regions were analyzed. TSS, transcription start site; TTS, transcription termination site. (C) Distribution of differentially methylated regions (DMRs). The number of DMRs in *met1-3* relative to wild type was analyzed in each sequence context. L, leaf; C, callus. (D) Distribution of DMRs in genic (upstream 1 kb and gene body), transposable element (TE) and intergenic regions.



Supplementary Fig. S3. Role of CRY2 in plant regeneration. (A) Transcript accumulation of *CRY2* in *met1-3* during callus formation. Transcript accumulation was analyzed by RT-qPCR. Three independent biological replicates were averaged, and statistical significance of the measurements was analyzed by a Student's *t*-test ($*P < 0.05$). (B) Shoot regeneration capacity of *cry2/fha-1* mutant. Callus preincubated for 7 days on CIM were transferred to SIM. The number of regenerated shoots from calli was measured ($n > 20$) at 3 weeks after incubation on SIM. Three independent biological replicates were averaged. Bars indicate the SEM. Scale bars = 10 mm.