De novo DNA methylation of the 35S enhancer revealed by high-resolution methylation analysis of an entire T-DNA segment in transgenic gentian [Plant Biotechnol. 28(2): 223-230 (2011)]

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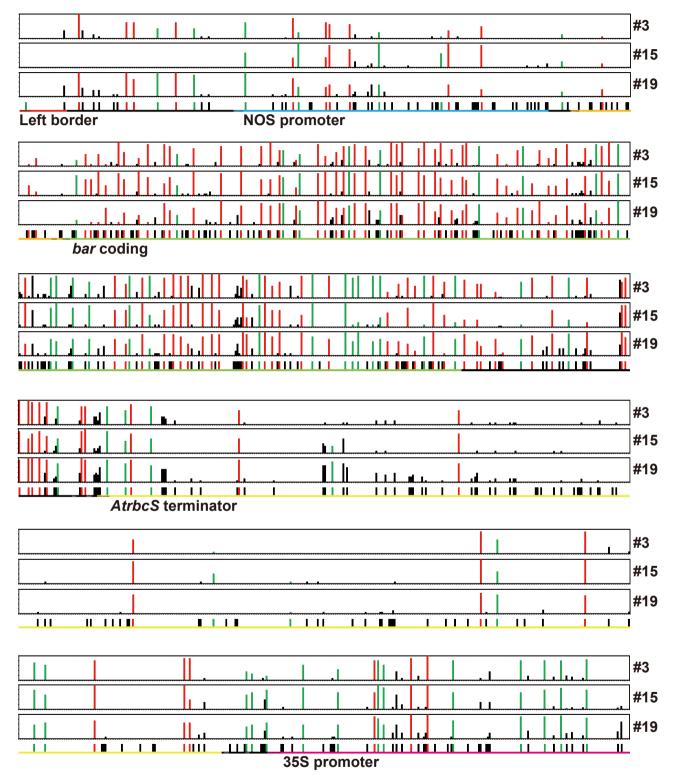


Figure S1. Comparison of the DNA methylation map of the full-length T-DNA sequence among the transgenic gentian plant lines #3, #15, and #19.

The percentage of methylated cytosine is represented by bar charts (red, CpG; green, CpWpG; black, CpHpH and CpCpG), and the position of each cytosine is represented below. Each promoter, coding, terminator, and T-DNA border region is indicated by a different color. Crossbars at the bottom within the 35S promoter region indicate the region of the probes for EMSA.

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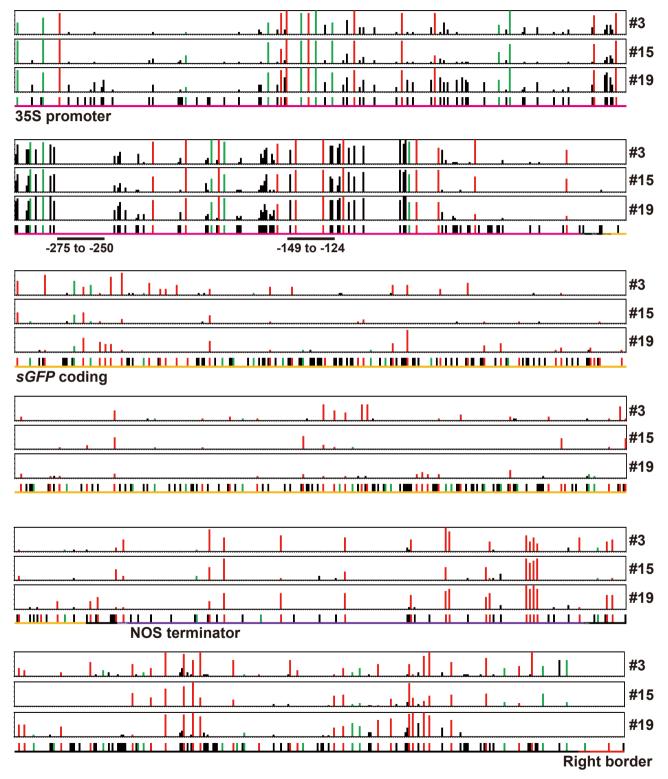


Figure S1. (Continued.)