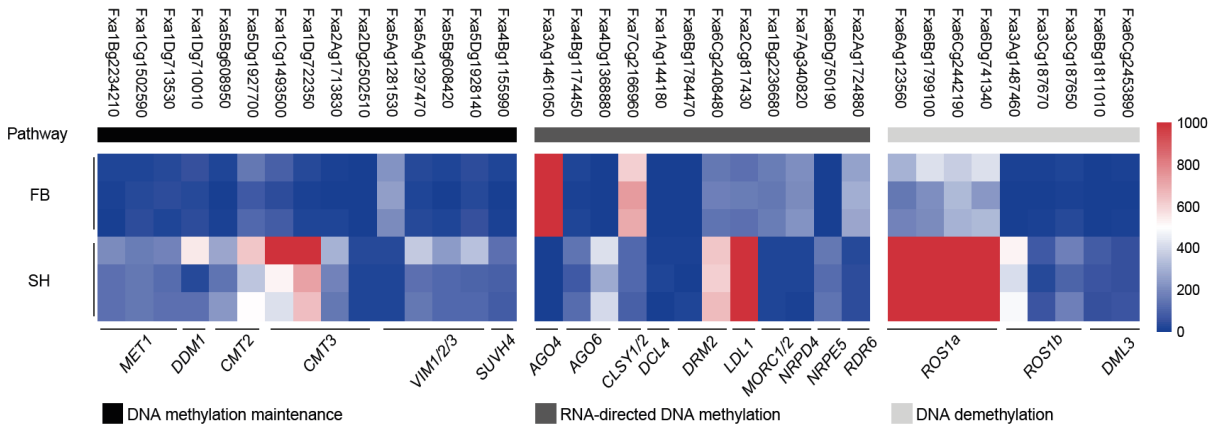

Supplementary Fig. S1. Expression of DNA methylation-related genes in FB and SH. Heatmap showing transcript abundance of genes involved in DNA methylation maintenance (black), RNA-directed DNA methylation (dark gray), and active DNA demethylation (light gray) pathways in Florida Brilliance (FB) and Seolhyang (SH) leaf tissues. Notably, SH exhibited higher expression of *CMT3*, while several RNA-directed DNA methylation components (e.g., *AGO4*, *CLSY1/2*) were expressed at lower levels compared to FB. In contrast, the demethylase gene *ROS1a* showed markedly elevated expression in SH. These differences may contribute to cultivar-specific variation in CHG methylation levels.