

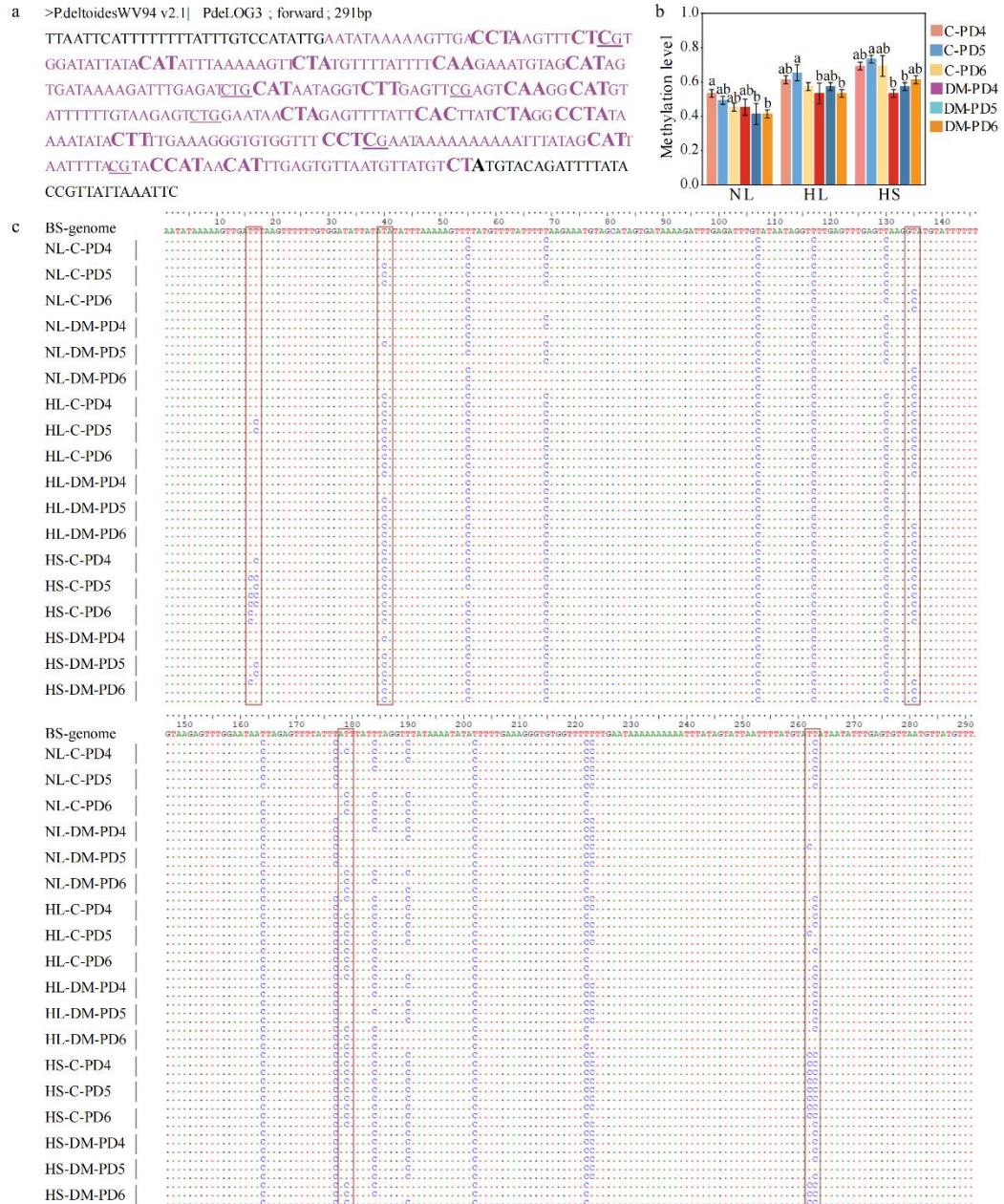


Fig. S8 Genomic distribution and methylation analysis of the *PdeLOG3* gene in *P. deltoides*. (a) Distribution of CG, CHG, and CHH C sites in the promoter region of the *PdeLOG3* gene in the *P. deltoides* reference genome. The target fragment (291bp, shown in purple font) along with its 30 bp upstream and downstream sequence is displayed. A total of 31 C sites were identified, including four CG sites, two CHG sites, and 25 CHH sites. (b) Average methylation level of C sites in the target fragment (291bp). Different lowercase letters indicate significant differences ($P < 0.05$) among genotypes/treatments within the same growth condition (Tukey test, $n = 3$). (c) Landscape of mCHH methylation sites in each sample detected by BS-PCR.