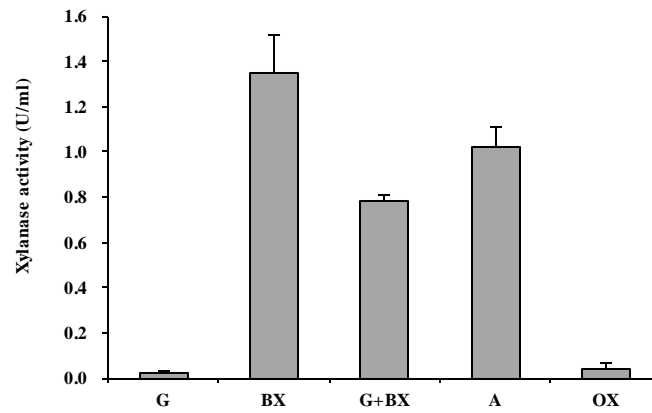
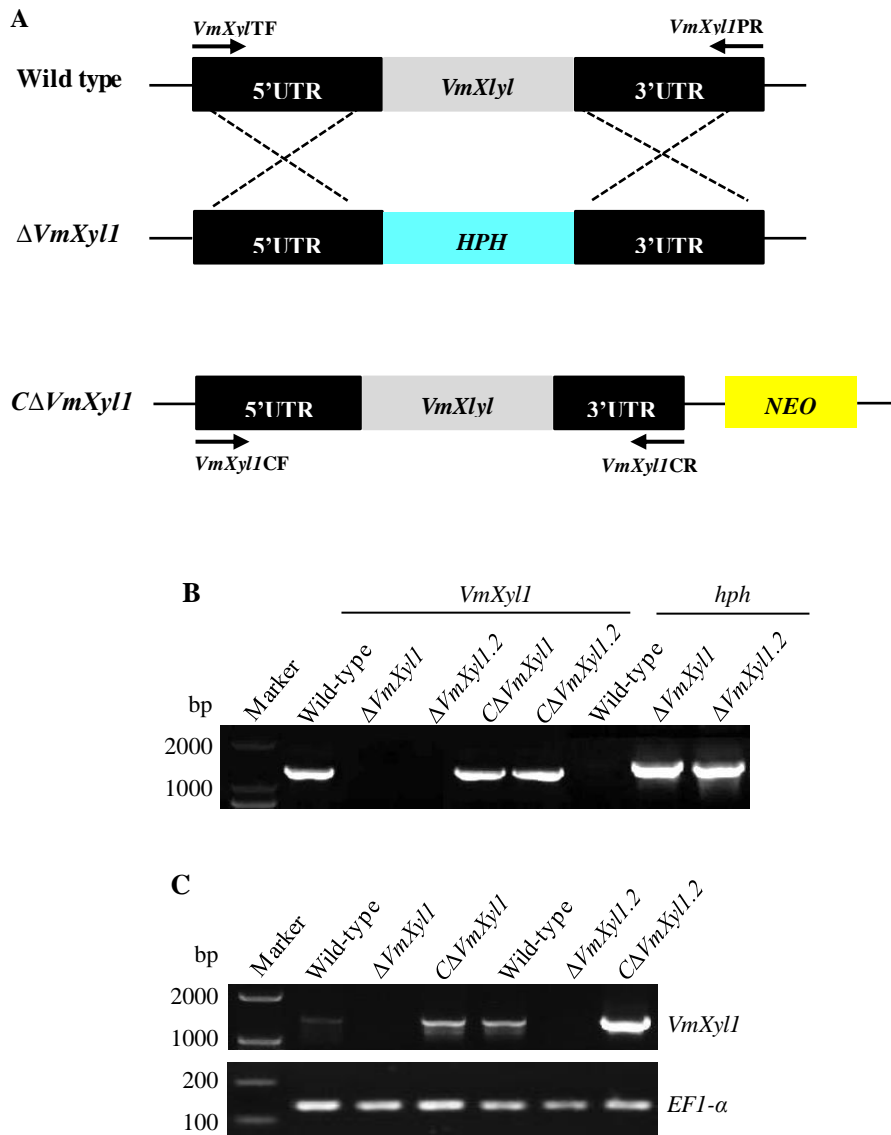


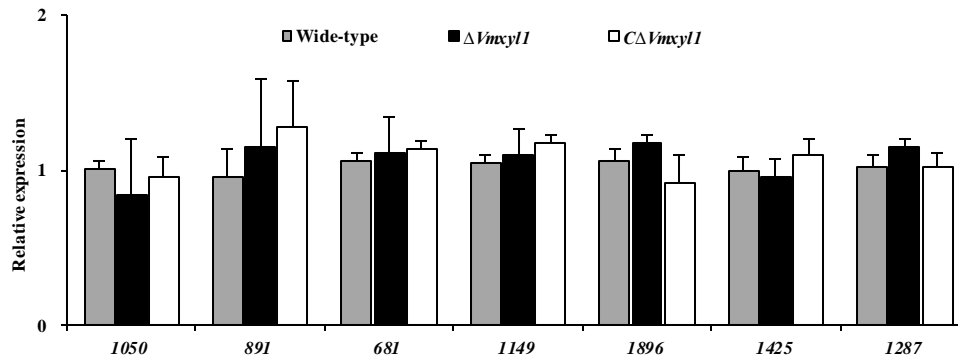
## Supplementary material



**FIGURE S1 | The xylanase activity produced by wild-type LXS080601 in medium containing different carbon sources after 3 days of growth.** The bars (G, BX, G+X, A, and OX) represent glucose, beechwood xylan, glucose+beechwood xylan, apple branch extract, and oat spelt xylan, respectively. The xylanase activity was expressed as units per min per ml (U/ml).



**FIGURE S2 | Generation of *VmXylI* deletion and complementation mutants.** (A) Schematic diagram of gene disruption and complemented constructs. (B) Mutants were confirmed by genomic PCR with the primer pair *VmXylIF/VmXylIR*. (C) The RT-PCR analysis of *VmXylI* expression with the primer pair *VmXylIF/VmXylIR* in wild-type, gene deletion ( $\Delta VmXylI$  and  $\Delta VmXylI.2$ ), and complemented ( $C\Delta VmXylI$  and  $C\Delta VmXylI.2$ ) strains. The expression of *EF1- $\alpha$*  was the internal control with the primer pair *EF1- $\alpha$ F/EF1- $\alpha$ R*.



**FIGURE S3 | The expression of endoxylanase genes in wild-type, *VmXyII* deletion and complemented strains.** Relative expression of seven endoxylanase genes from family GH10 and GH11 in the lesion border of apple tree bark were compared between wild-type and *VmXyII* mutant strains at 5 dpi. The expression of *EFL- $\alpha$*  was used to normalize in each sample. Transcript levels of wild-type strain were normalized to one. The means and standard deviation of the transcription levels were calculated of three independent biological replicates. Bars represent the standard error.