Supplementary materials to

Thermostability improvement of a *Talaromyces leycettanus* xylanase by semi-rational protein engineering

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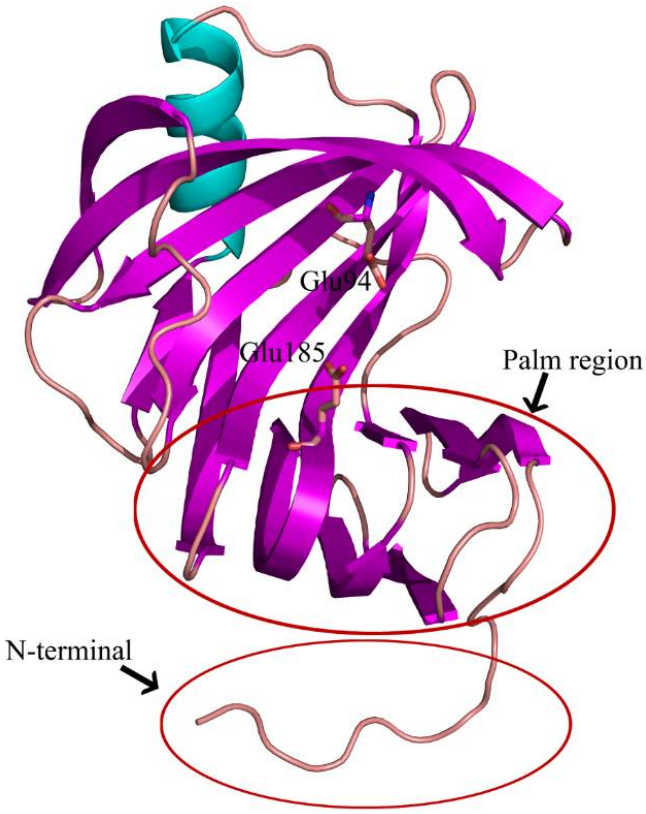
Supplementary Table 1 Summary of the recombinant *Tl*Xyn11B purification

Purification step	Protein concentration (μg/mL)	Total activity (U)	Specific activity (U/mg)	Recovery rate (%)
Crude enzyme	86	340,600	6,600	-
Vivaflow	532	180,900	6,800	53
Anion exchange	384	164,300	8,600	48

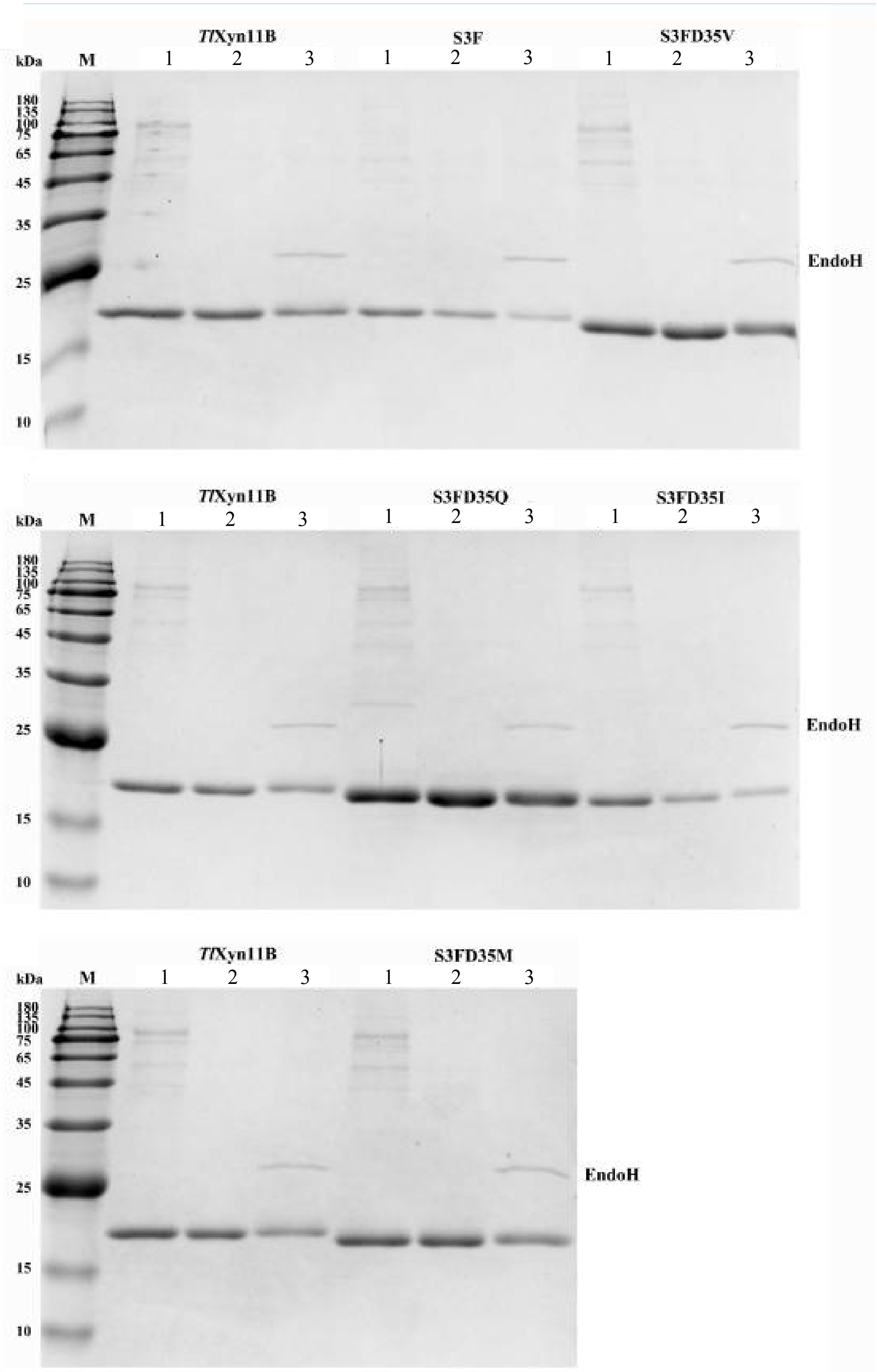
Supplementary Table 2 Primers used in this study

Primers	Sequences (5′→3′)[a]
*Tl*Xyn11BF	ATGGTGTCCTTCTCCTCCCTCGC
*Tl*Xyn11BR	CTAGGAAACAGTAATGGAAGAGGACCCG
*Tl*Xyn11B_EcoF	ACGAATTCGCTCCTAGCGAGCTCTCCAAACGC
*Tl*Xyn11B_NotR	ATTTGCGGCCGCCTAGGAAACAGTAATGGAAGAGGACCCG
*Tl*Xyn11B_T1-F	ACGAATTCCGCCAAACACTAACCTCAAGCTCC
*Tl*Xyn11B_T2-F	ACGAATTCACACTAACCTCAAGCTCCACTGGC
*Tl*Xyn11B_S3-F	ACGAATTCGCTCCTNNKGAGCTCTCCAAACGC
*Tl*Xyn11B_D35-F	GGAACGGTCNNKTACACTAATGGCAA
*Tl*Xyn11B_D35-R	ATTGCCATTAGTGTAMNNGACCGTTCC
5sAOX	TTGCGACTGGTTCCAATTGACAAGCTTTTG
3sAOX	TCCTCTTGATTAGAATCTAGCAAGACCGGTCTTC

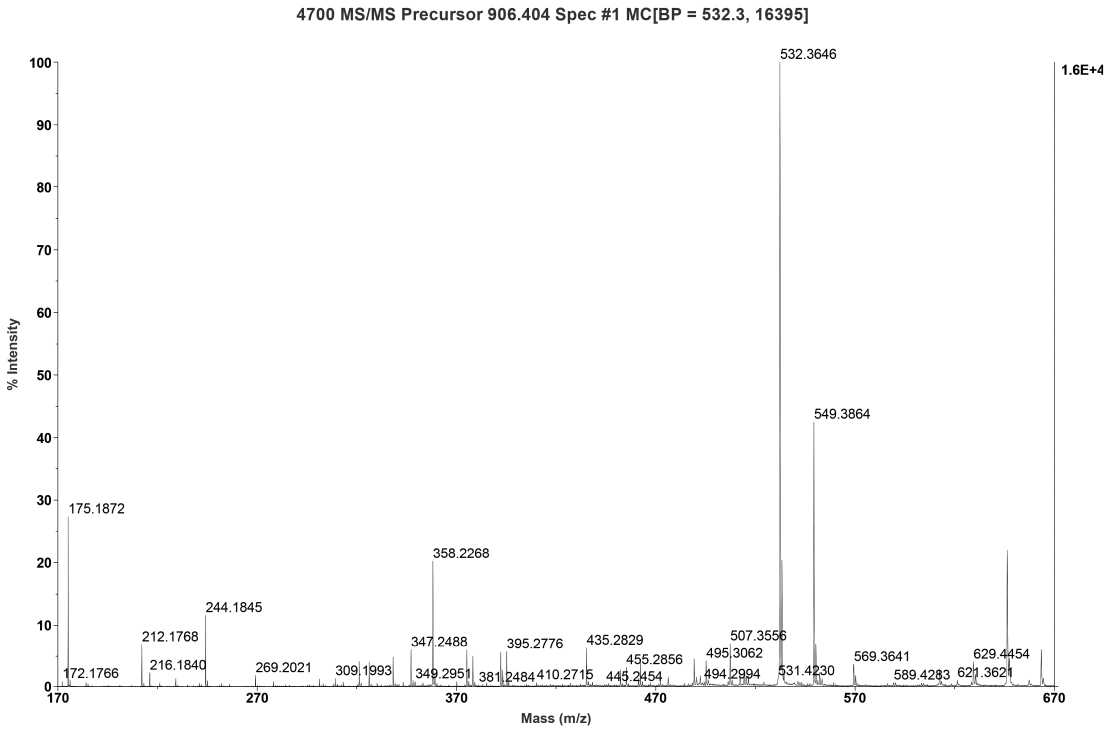
[a] The restriction sites are underlined



Supplementary Fig. 1 Homology modeling of *Tl*Xyn11B with the GH11 endo-1,4-β-xylanase from *T. cellulolyticus* (PDB: 3WP3) as template. The catalytic residues, palm region and N-terminus are indicated.



Supplementary Fig. 2 SDS-PAGE analysis of *Tl*Xyn11B and its mutants. Lanes: M, the molecular mass standards; 1, the crude enzymes; 2, the purified recombinant enzymes; 3, the deglycosylated enzymes with Endo H treatment.



Supplementary Fig. 3 MS identification of the purified recombinant *Tl*Xyn11B.