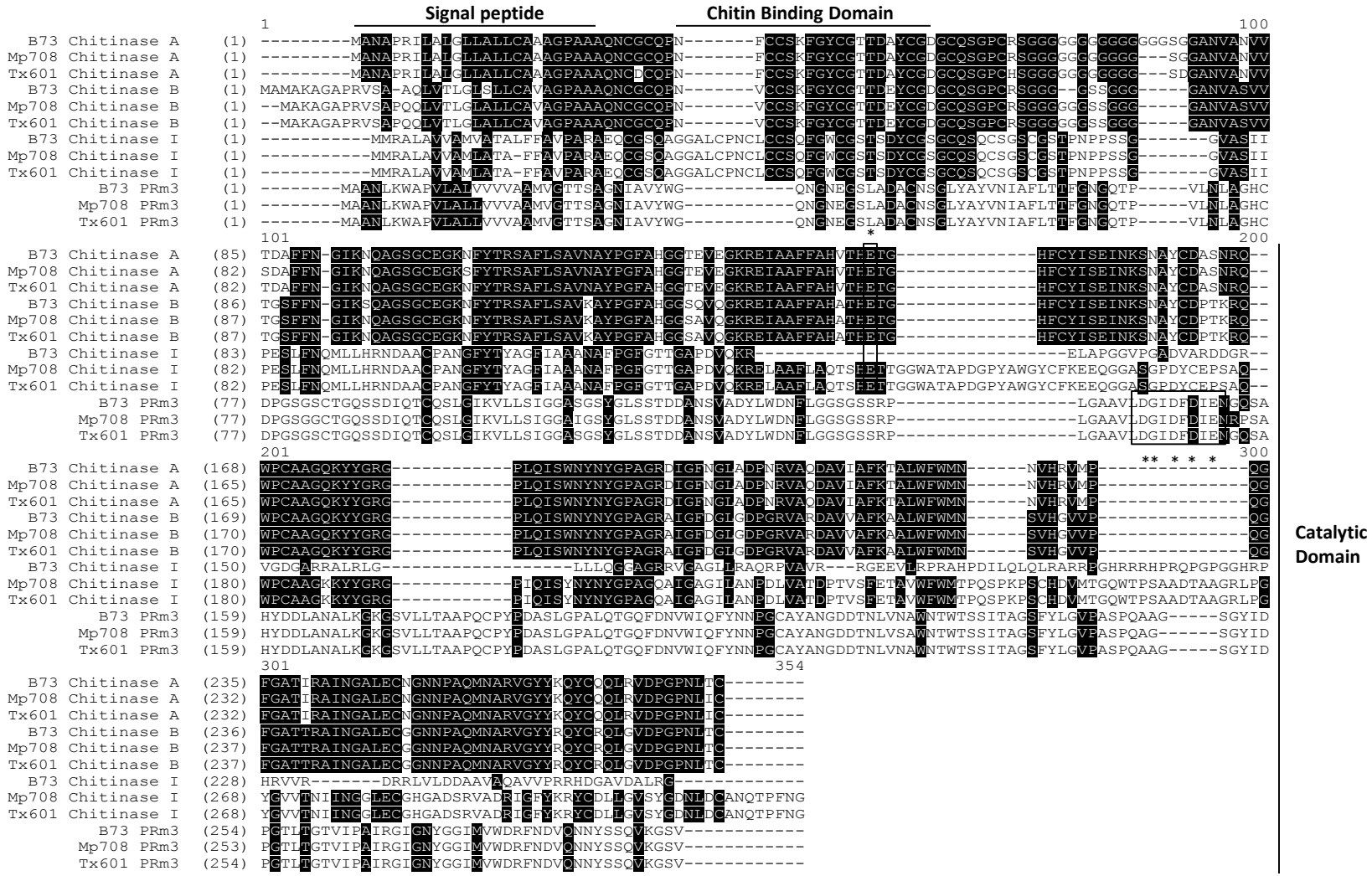

Supplemental Fig. 1 Alignment of endochitinase amino acid sequences from three different maize inbreds. The deduced amino acid sequences of chitinase A, chitinase B, chitinase I, and chitinase PRm3 were aligned from maize inbreds B73, Mp708, and Tx601. Numbers correspond to the amino acid position. Black backgrounds indicate identical or similar amino acids. The dashes denote spaces required for optimal alignment. The signal peptide, chitin-binding domain, and catalytic domain are labeled. The conserved catalytic residues were indicated by open black boxes and labeled with stars. The sources for plant chitinases were listed in Table 1. Sequences were aligned using Vector NTI 11 program from Invitrogen