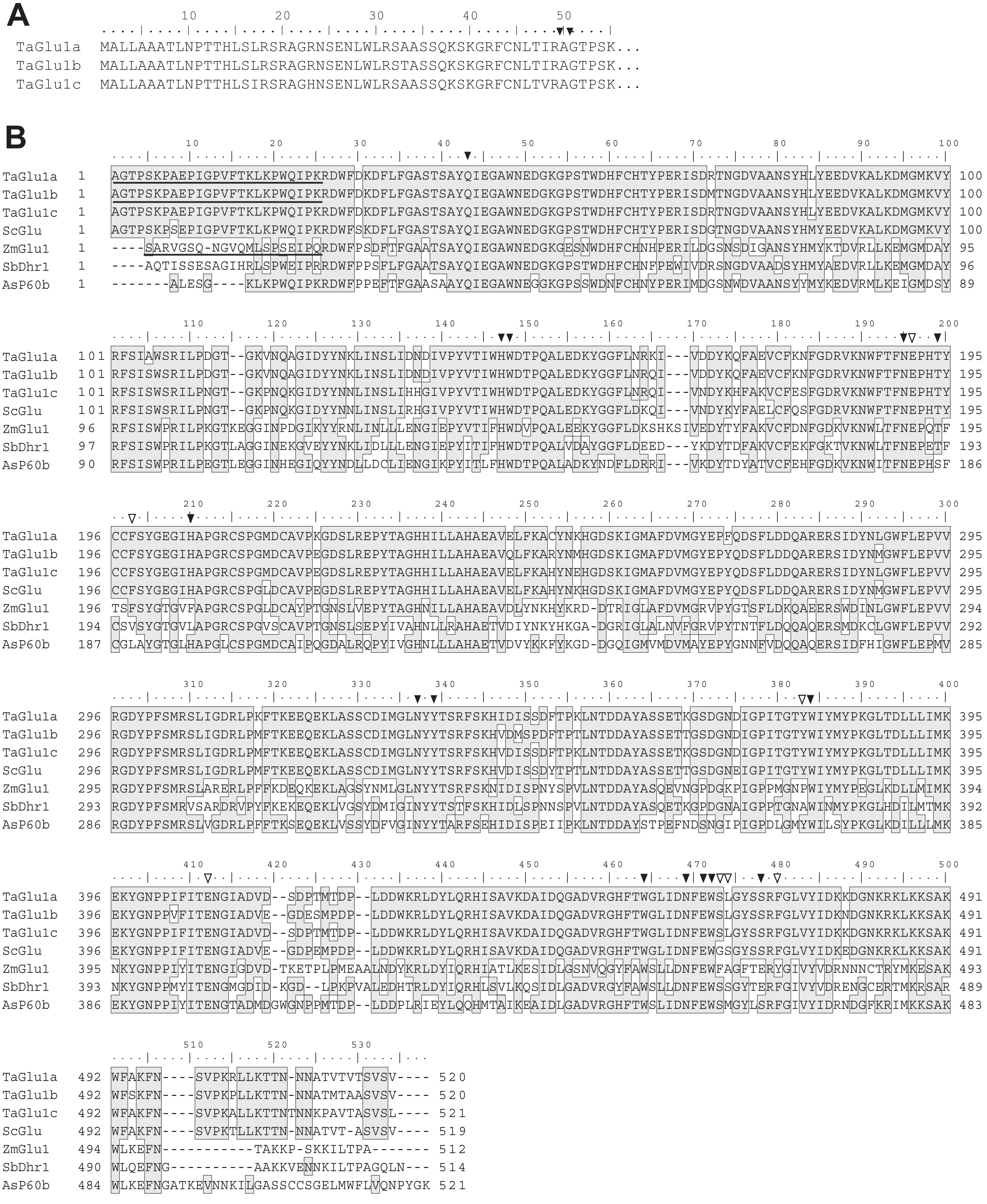
Supplemental Figure



Amino acid sequences of monocot β-D-glucosidases.
A, the amino acid sequences of the N-terminal region of TaGlu1a – TaGlu1c precursors. The possible cleavage sites of the signal peptides are indicated by downward arrowheads (see Supplemental Text). B, sequence alignment of mature glucosidases from monocotyledonous plants. The amino acid sequences were aligned by ClustalW. Identical residues are shaded. The residues that constitute the substrate binding pocket are indicated by downward open and closed triangles. The open triangles indicate the residues to which mutations were introduced in this study. The N-terminal sequences replaced with the corresponding part of ZmGlu1 were underlined. The DDBJ/EMBL/GenBank accession numbers of ZmGlu1, SbDhr1 and AsP60b are U25157, U33817 and AF082991, respectively. ScGlu is the sequence obtained in the present study. Residues A324 and S326 are substituted by G and L, respectively, in the sequence in data base (accession number AF293849).