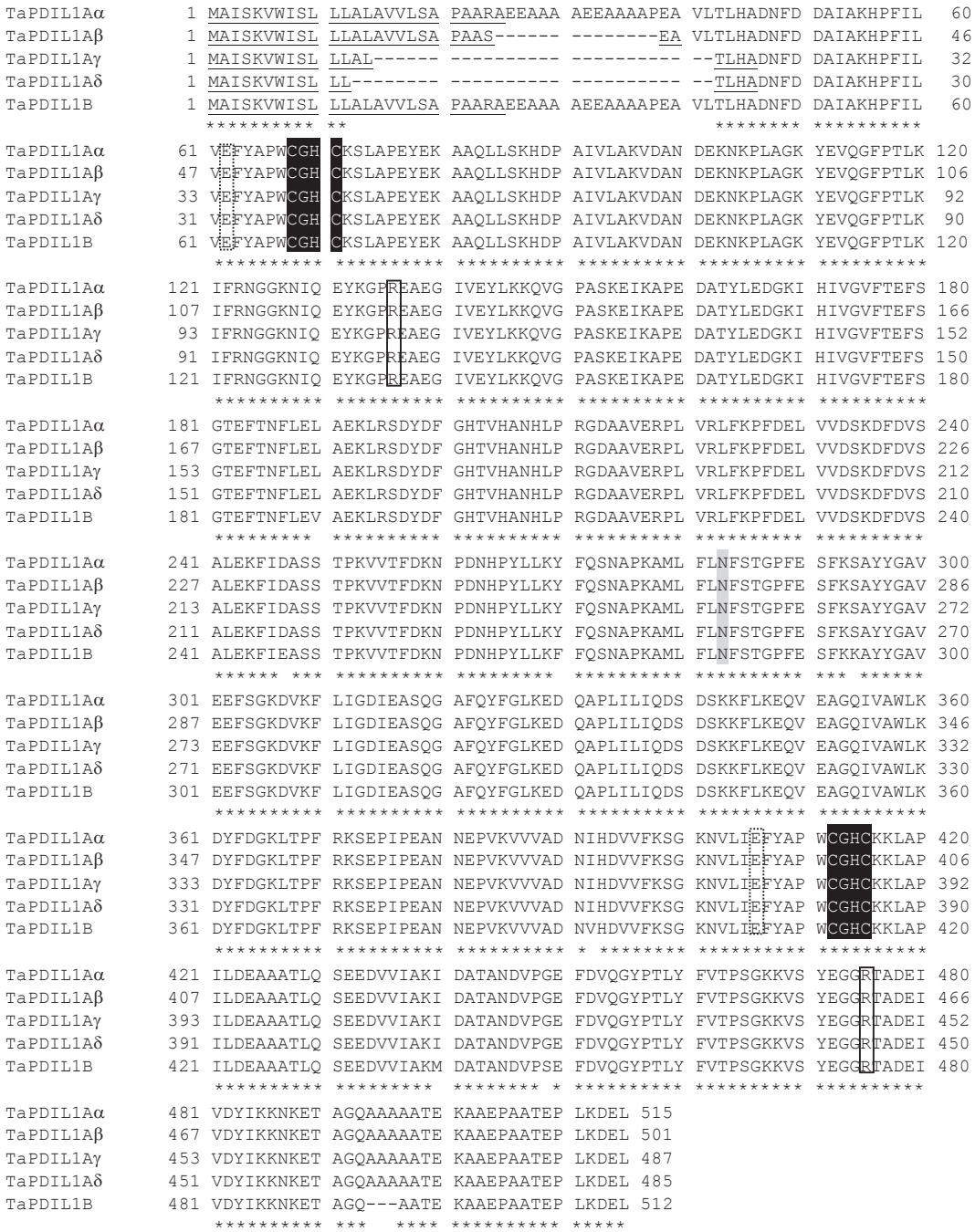

Figure S1. Alignment of amino acid sequences of TaPDIL1Aα, TaPDIL1Aβ, TaPDIL1Aγ, TaPDIL1Aδ, and TaPDIL1B. The putative signal peptide (underlined), active center CGHC motifs (shaded in black), N-glycosylation consensus asparagine (shaded in gray), conserved arginine (box with straight lines), and glutamic acid (box with dotted lines) are indicated. Asterisks indicate positions that have a single, fully conserved residue.