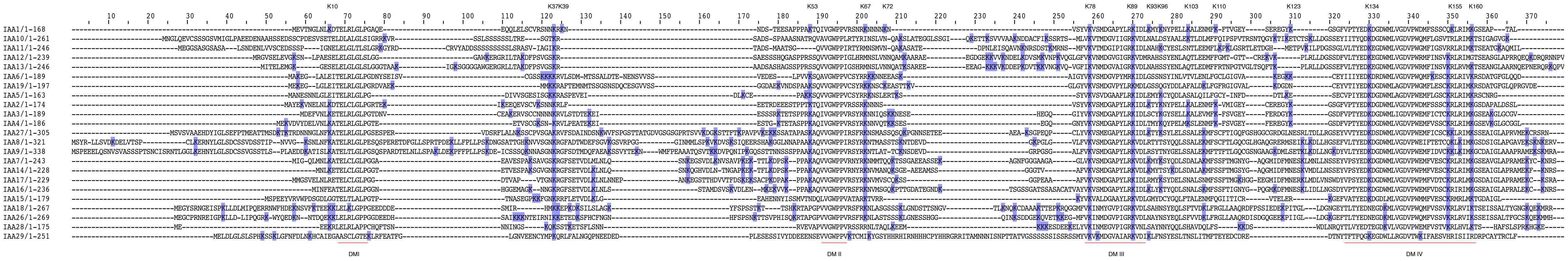

Supplemental Figure 1. Alignment of the 23 Arabidopsis IAA proteins that contain a conserved domain II (DMII) and interact with TIR1 in yeast 2-hybrid interaction assays.

Amino acid sequences of 23 Arabidopsis IAA proteins (listed on left with length of sequence shown) from TAIR10 were aligned using Jalview (jalview.org) and manually adjusted to maximize alignment in the 4 conserved domains (I-IV) indicated with bars below the alignment. All lysine residues are highlighted in blue. IAA1 is in the top row for convenience. The16 lysine residues in IAA1 are indicated above the alignment with their position indicated.