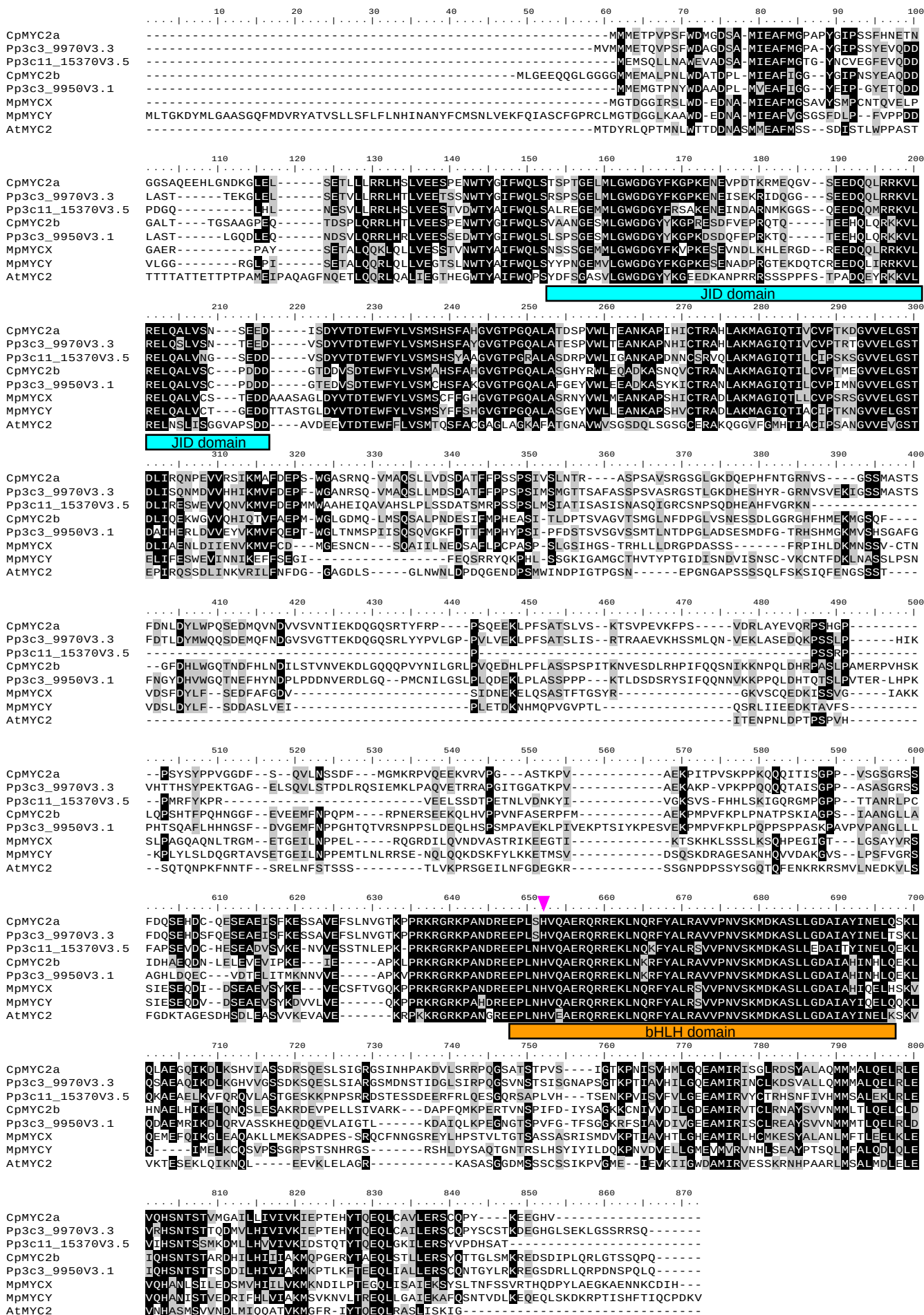




Supplementary Figure 5. Sequence alignment of MYC2

Sequences of MYC2 homologs were aligned by MEGA version X using Muscle. Sequence alignments were drawn using BioEdit software version 7.2.5. The Shading thresholds of identical or similar residues were 40%. Identical and similar residues were highlighted by black and gray, respectively. JID and bHLH domains were indicated by blue and orange squares, respectively. A magenta triangle indicates the histidine residue involving the binding to the G-box (CACGTG)