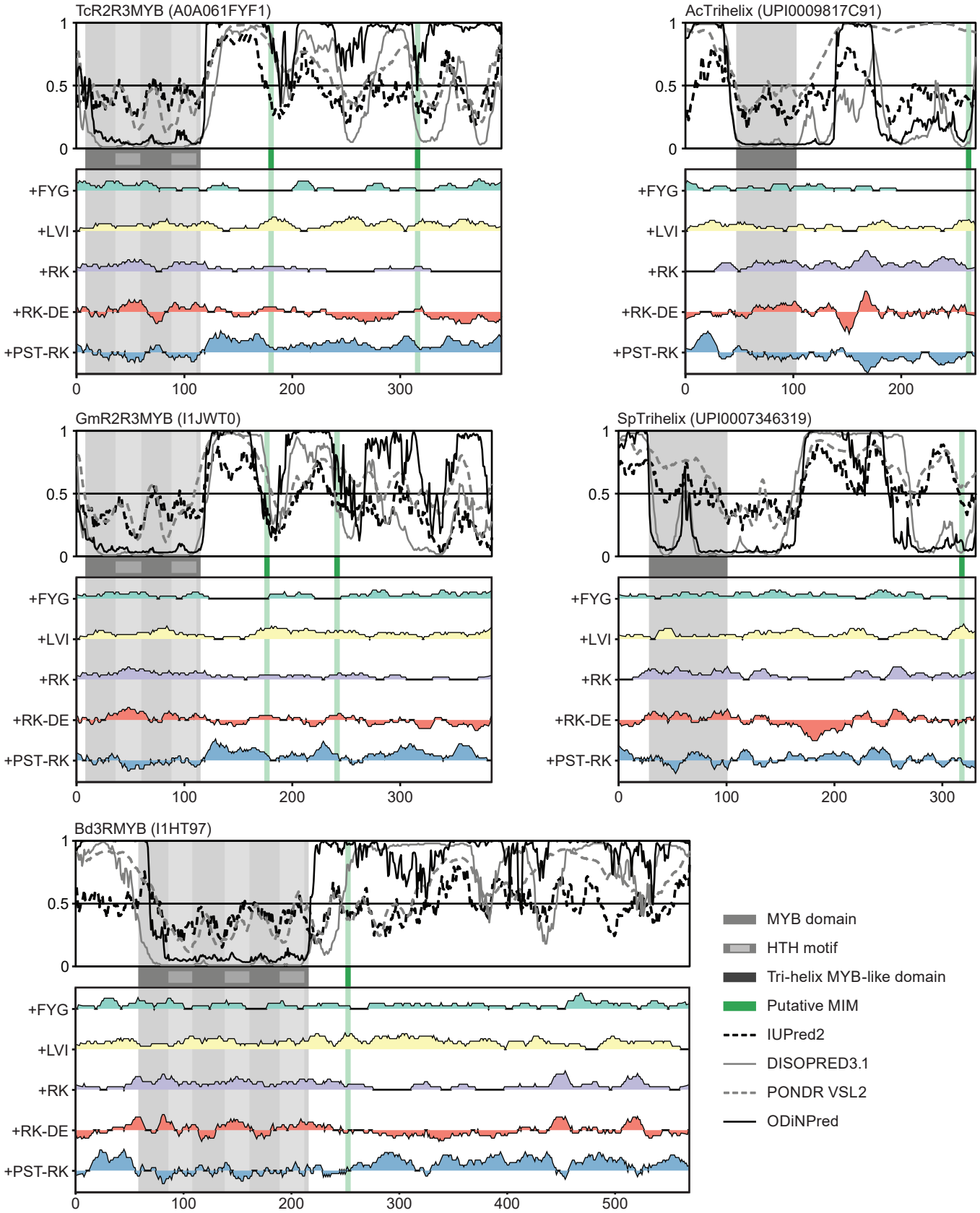

Supplemental Figure 1. Disorder prediction and IDDomainSpotter profiles for putative MIM containing proteins. Top panels show sequence specific disorder predictions using IUPred2 [49], DISOPRED3.1 [50], PONDR VSL2 [51,52], and ODiNPred [53]. Bottom panels show IDDomainSpotter profiles: Each curve shows the fraction of a different set of residues within sliding windows of 15 residues [48]. Domain information was obtained from PROSITE [41]. The putative motif is shown by a green bar.