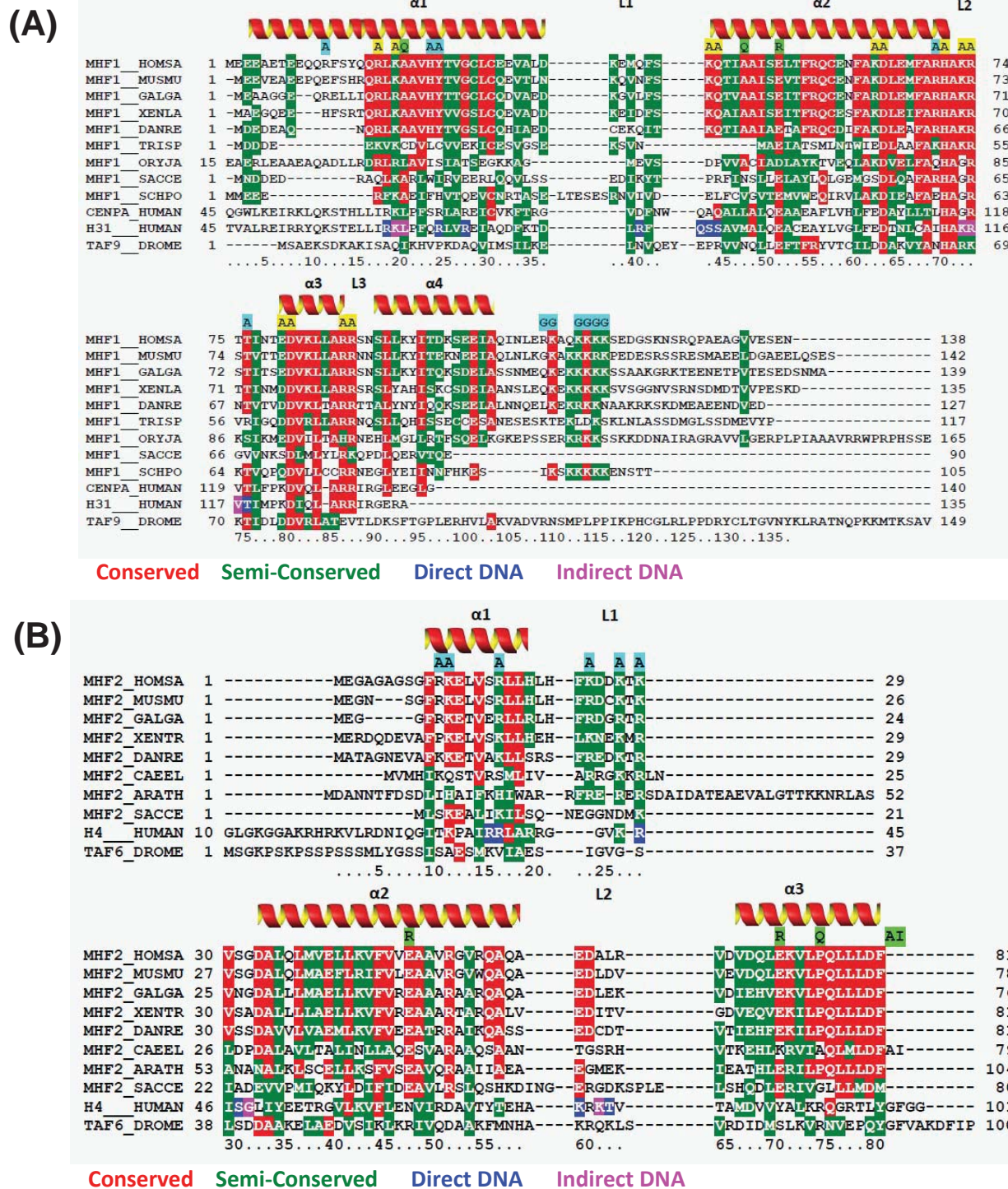


## Both MHF1 and MHF2 are conserved structurally and functionally



**Figure S2. (A)** Primary sequence alignment of MHF1 including sequences from human (HOMSA), mouse (MUSMU), chicken (GALGA), fish (DANRE and TRISP), plant (ORYJA) and yeast (SACCE and SCHPO). **(B)** Alignment of MHF2 including sequences from human (HOMSA), mouse (MUSMU), chicken (GALGA), frog (XENTR), fish (DANRE), worm (CAEEL), plant (ARATH), and yeast (SACCE). Alignment is also shown for related histone-fold proteins including histone H4 and TAF6. For both alignments, the secondary structure as seen in the MHF crystal structure is shown above the alignment. Identical residues are marked red, while semi-conserved residues are marked green, relative to the human sequence. Known direct (blue) and indirect (magenta) DNA interaction residues for histone H3.1 are indicated. Mutations in Figures 2 and 6 are shown above the alignment with the mutation indicated by the single letter amino acid code and colored according to function: blue (DNA-interaction mutation), green (MID-MHF1 or MID-MHF2 interaction mutation), or yellow (other interface mutations of interest).