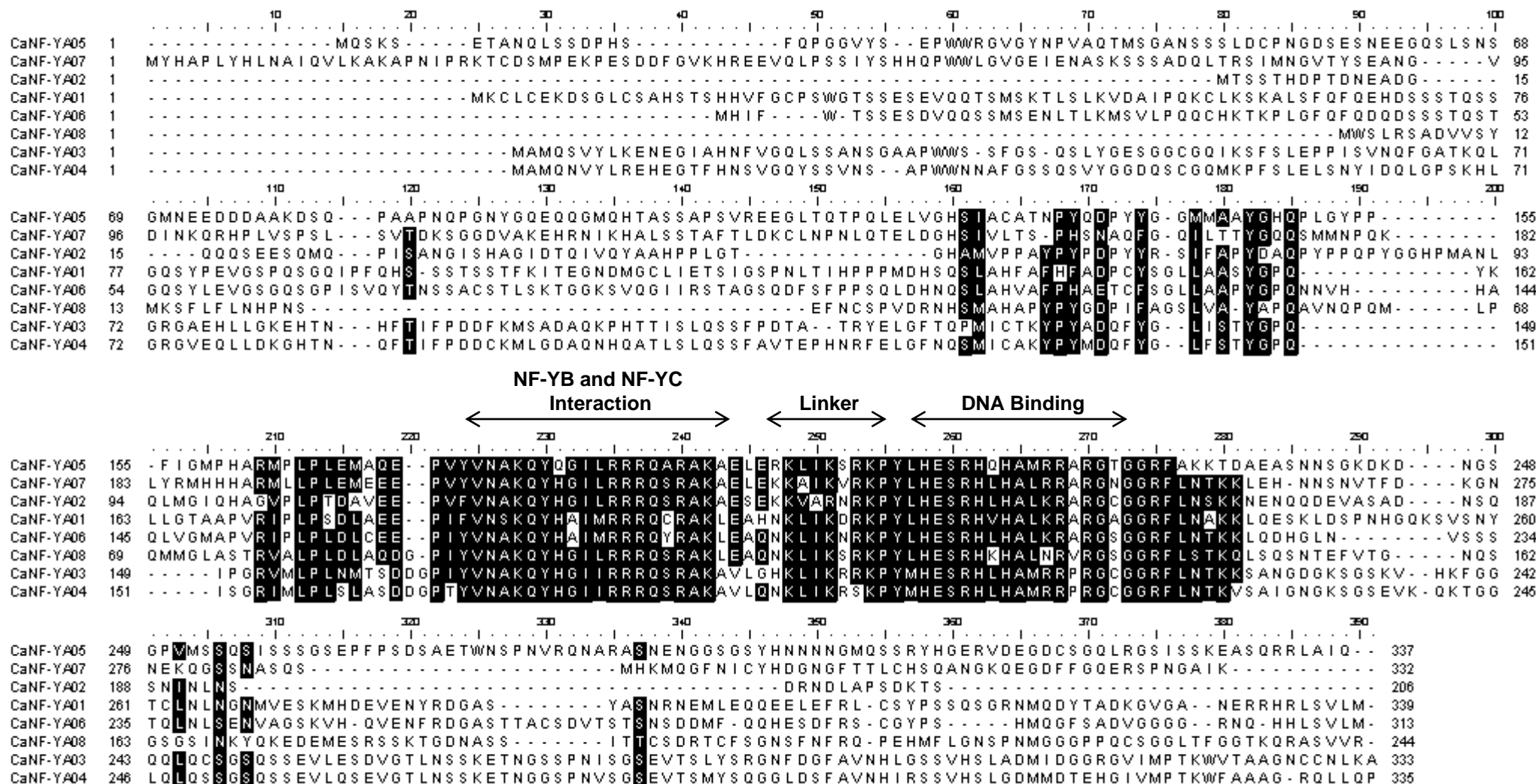


Figure S1A. The multiple alignments of full-length CaNF-YA TFs as determined using Clustal X (v. 2.1) software.

Conserved domains were indicated by thick black lines above the sequences. The conserved residues were marked in white color in the black background.



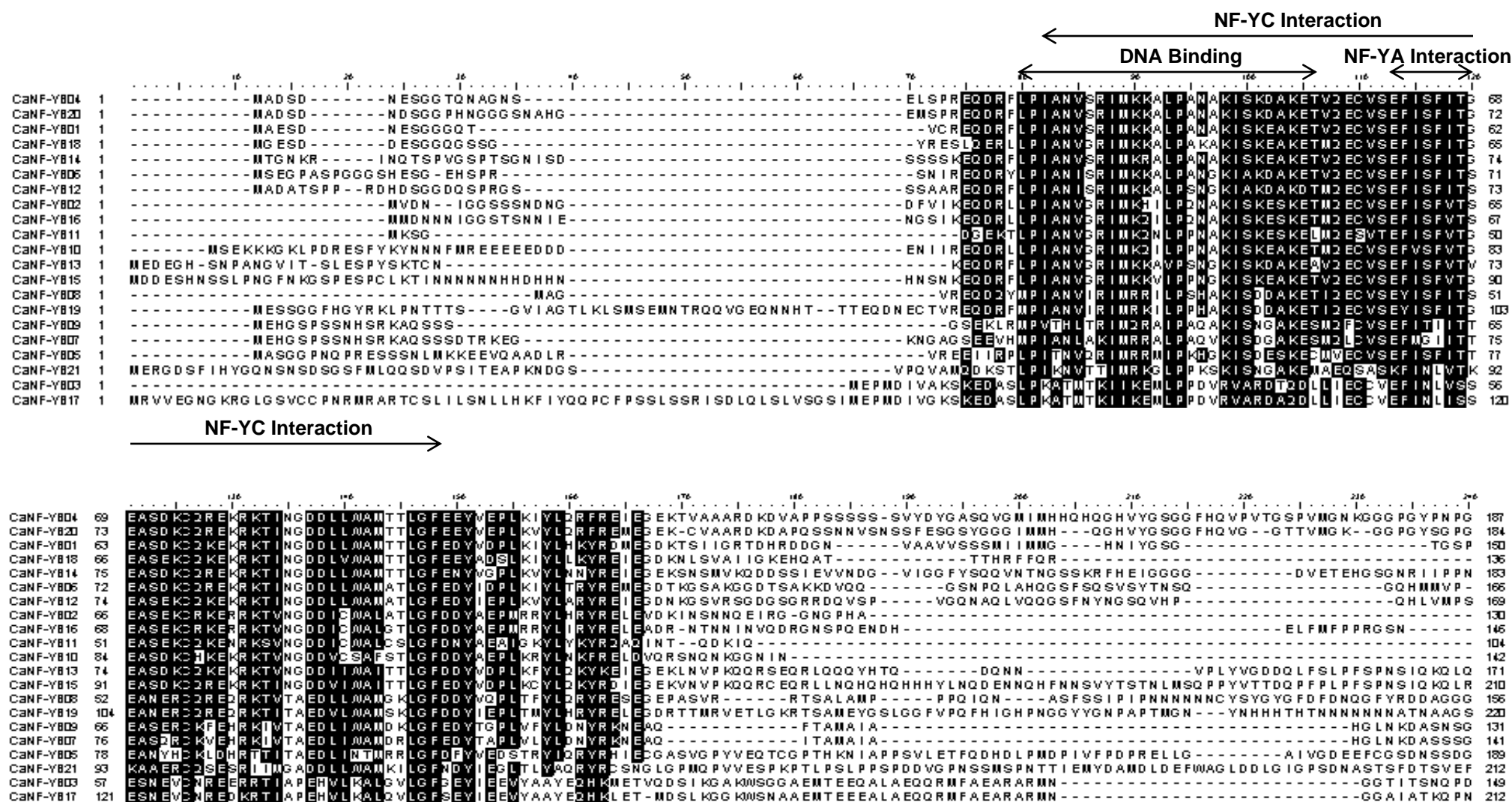


Figure S1B. The multiple alignments of full-length CaNF-YB TFs as determined using Clustal X (v. 2.1) software. Conserved domains were indicated by thick black lines above the sequences. The conserved residues were marked in white color in the black background.

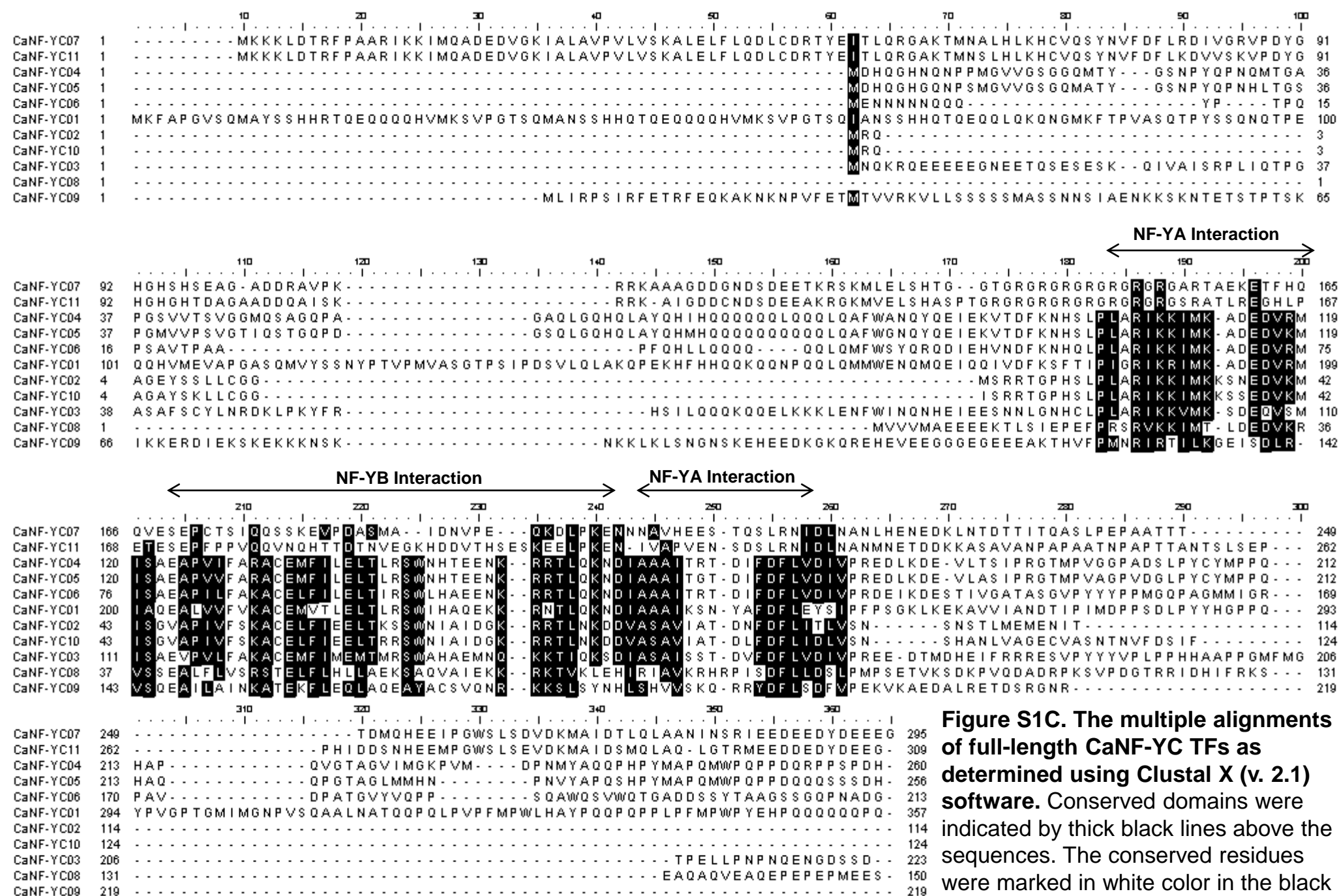


Figure S1C. The multiple alignments of full-length CaNF-YC TFs as determined using Clustal X (v. 2.1) software. Conserved domains were indicated by thick black lines above the sequences. The conserved residues were marked in white color in the black background.