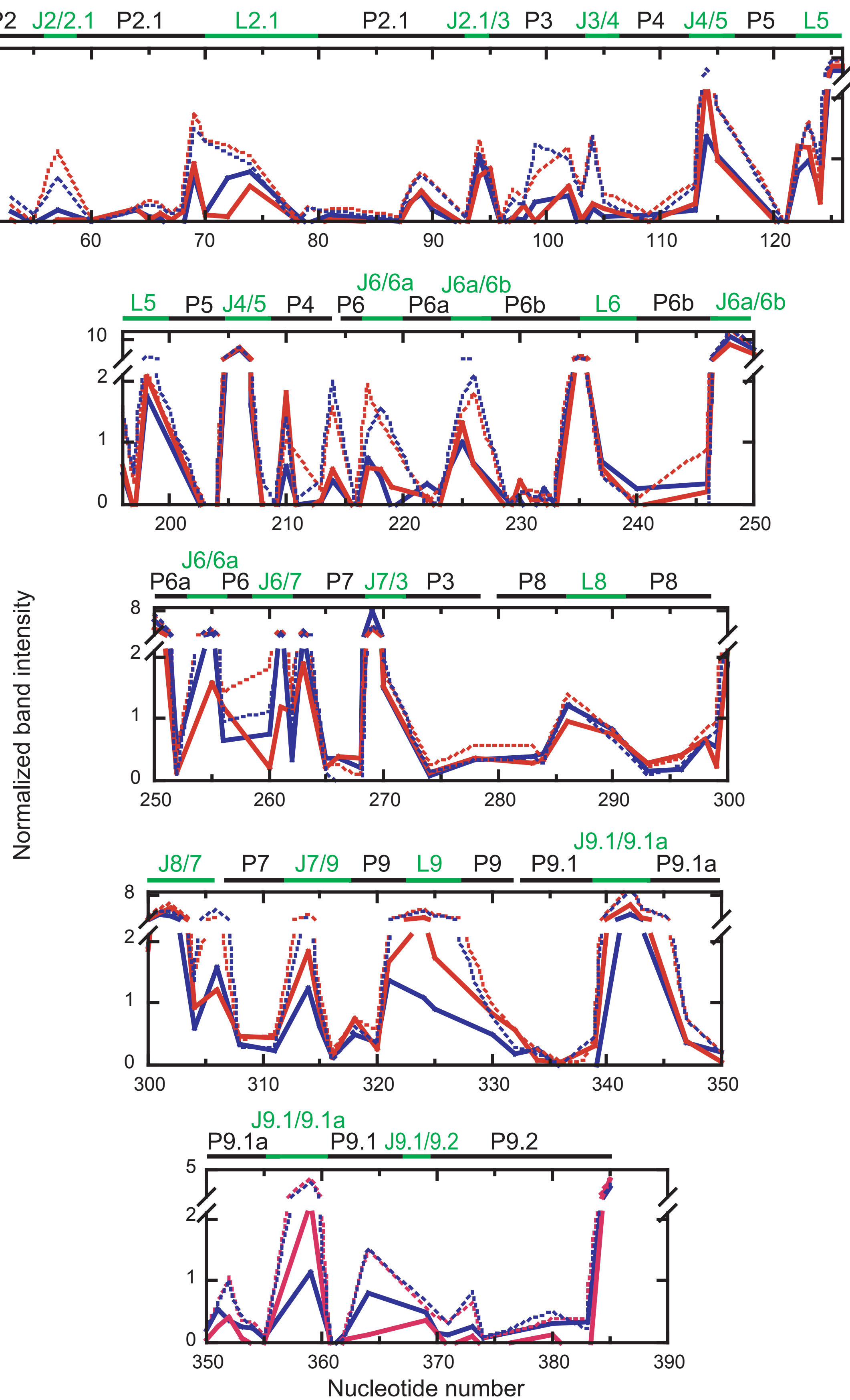

Fig. S1. DMS footprinting of the native and misfolded ribozyme and CYT-18 complexes. Data from the native ribozyme are shown in blue and data from the misfolded ribozyme are red. Solid lines show data with CYT-18 and dashed lines show data without CYT-18. Band intensity at each A and C nucleotide was normalized by dividing by the fully-extended product, and this value was multiplied by 1000 to obtain the y-axis values shown. Secondary structure elements are indicated in black and loops and joining sequences are indicated in green.