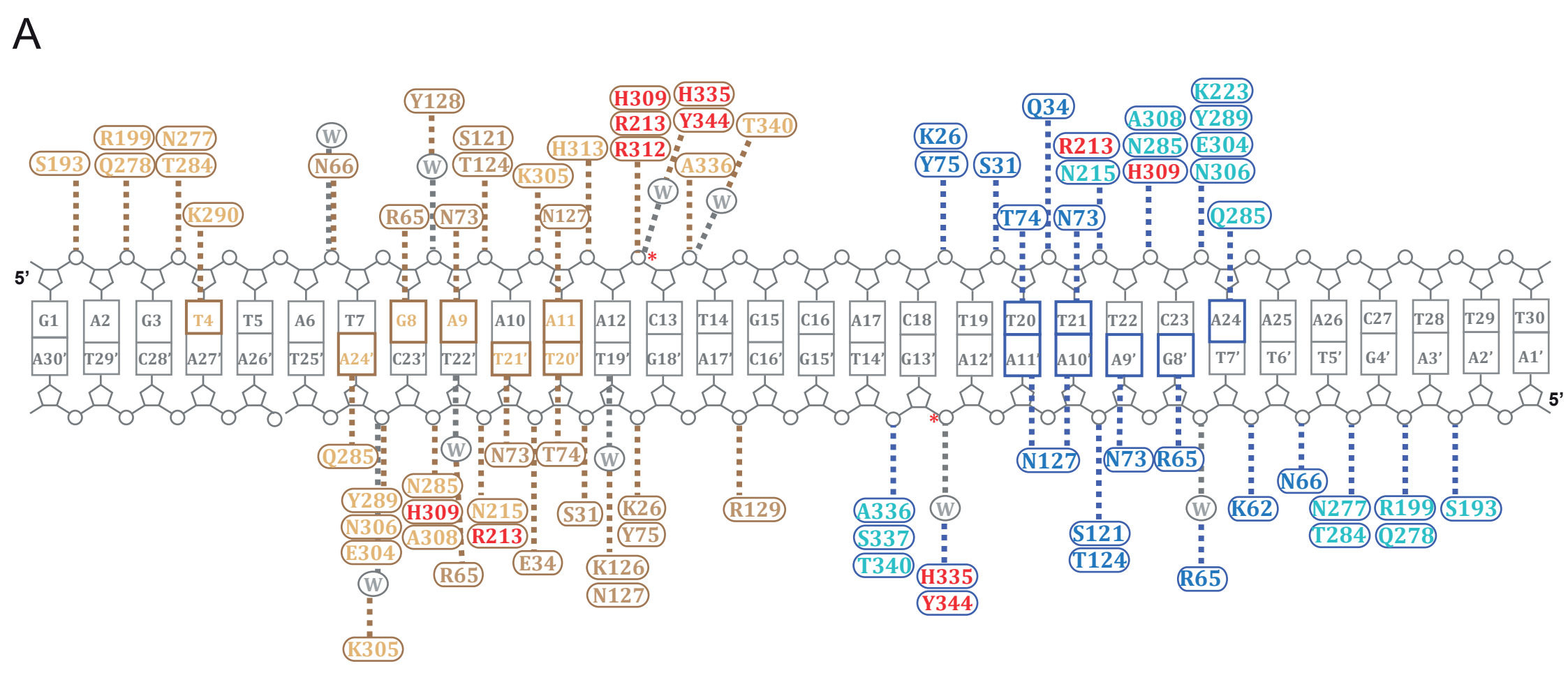

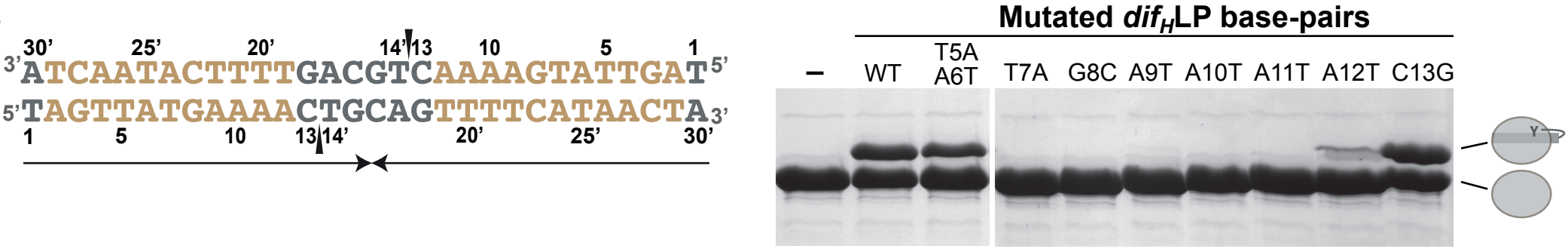

Figure 2-figure supplement 4: Interactions between XerH and the *dif*$_H$ site.

A) Schematic view of the interactions observed in the XerH-*dif*$_H$ synaptic complex crystal structure. Amino acids of the XerH subunits bound to the left and right *dif*$_H$ arms are shown in gold and blue, respectively. The residues of the N-terminal domain are shown with a darker color, and the catalytic residues are shown in red. Dashed lines indicate hydrogen bonds. Bases directly contacted by XerH are colored gold or blue. Interacting water molecules are shown in grey. The diagram is based on protein-DNA interaction analysis performed with NUCPLOT (Luscombe et al., 1997).

B) Mutational analysis of XerH-*dif*$_H$ interactions. The left-arm palindrome *dif*$_H$ (*dif*$_H$LP) substrate is shown on the left with the left arm sequences in gold. Note that the sequence is written in the 3' to 5' direction as in the main figure. Arrows beneath the sequence indicate the palindromic region, and triangles mark the introduced nicks. On the right, *in vitro* XerH cleavage assays with various substrate variants. The DNA mutations numbered as in (A) are indicated above the gel. In this assay, upon cleavage XerH becomes covalently attached to the cleaved DNA strand via a phosphotyrosyl bond, which is trapped by the use of double-nicked 'suicide' substrates (see schematic representation in Figure 3C). The XerH-DNA covalent intermediate and unmodified XerH can be separated on SDS-PAGE.