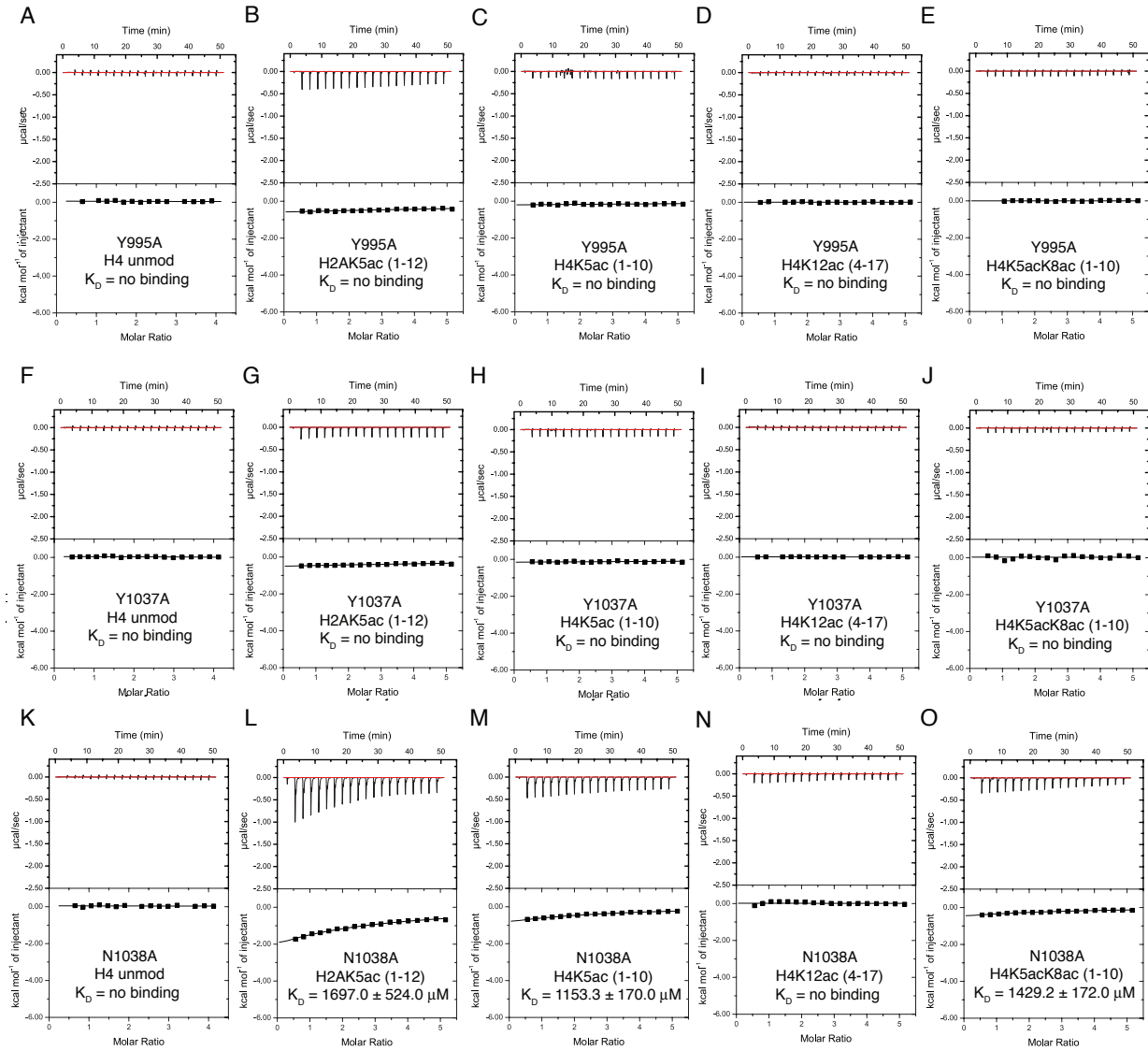


Supplemental Figure 1. ITC measurements of the interaction between acetylated histone ligands and mutant ATAD2B bromodomain proteins. (A-O) Exothermic ITC enthalpy plots for the binding of mutant ATAD2B bromodomain proteins to histone peptide ligands that are unmodified, mono- or di-acetylated. The calculated binding constants are indicated.



Supplemental Figure 2. Sequence alignment of the ATAD2 and ATAD2B bromodomains. Sequence alignment of the ATAD2 and ATAD2B bromodomain proteins corresponding to the amino acids in our ATAD2B bromodomain structure (residues 953-1085). Residues colored magenta are involved in hydrogen bonding to compound 38 for the ATAD2B bromodomain, and compound 42 for the ATAD2 bromodomain. Residues colored green are hydrophobic contacts. Residues that were mutated in this study are marked with a red vertical line. Sequence alignment was performed using the T-Coffee software [48].

