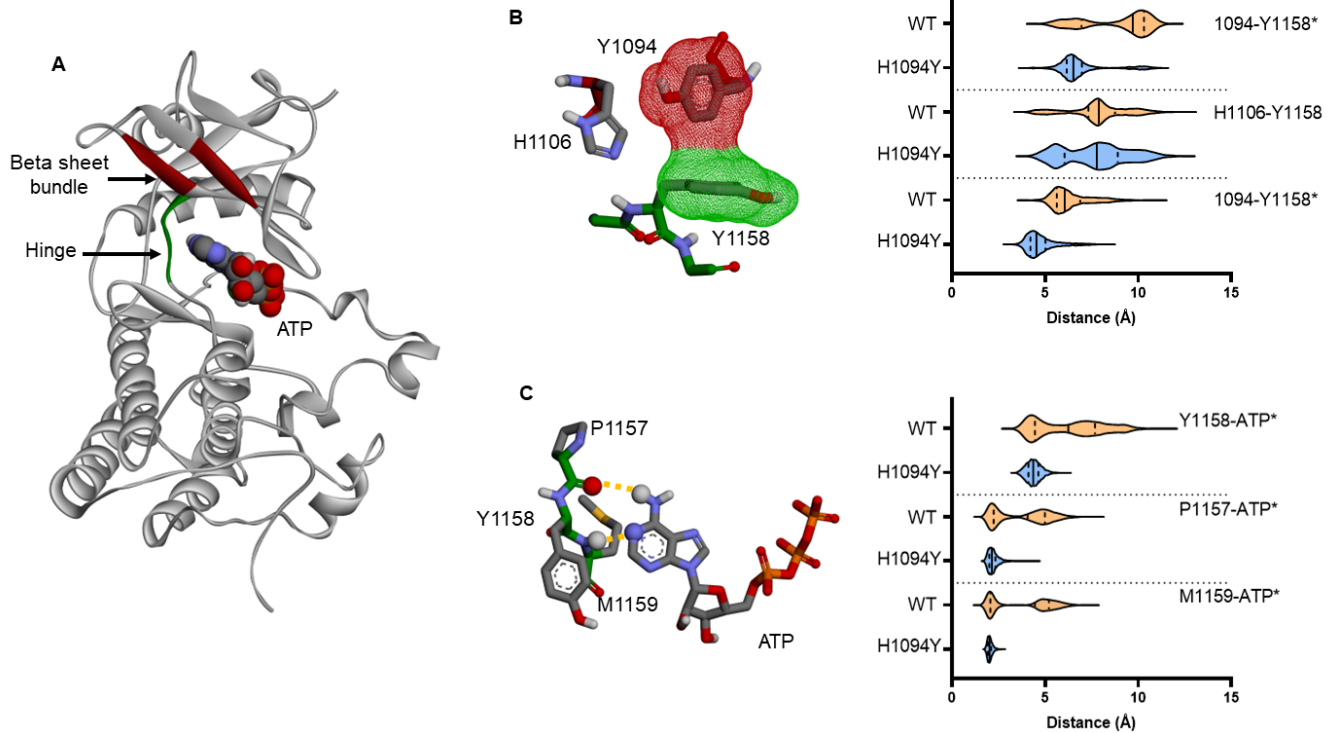


# Supplementary Figure 17



**Supplementary Figure 17. Equilibration of interactions that drives ATP affinity in the presence *MET* H1094Y mutant.** (A) Representative structure of the ATP bound cMET H1094Y with the regions of interest highlighted [subsection of the 5 pleated beta sheet bundle containing H1094Y and direct interactions (red), hinge binding region (green)]. (B) H1094Y forms novel  $\pi$ - $\pi$  stacking interactions (T stacking with an upper cut-off of 5.0 angstroms) with Y1158. (C)  $\pi$ - $\pi$  stacking from Y1158 stabilizes the ATP hydrogen bonding network. \*Indicates that statistical testing with the Mann–Whitney–Wilcoxon test resulted in a P value < 0.01. Values above 12 angstroms were excluded due to ATP unbinding.