



**S6 Fig. Averaged ZDOCK scores for the PfR6–HMG-box *Pf* complex.** Binding of the selected aptamers 3D ssDNA structures to the HMG-box *Pf* were predicted using ZDOCK server. A) The ZDOCK score of 2,000 iterations were averaged using Graphpad Prism 7.02. B) Highest ZDOCK score of each aptamer.