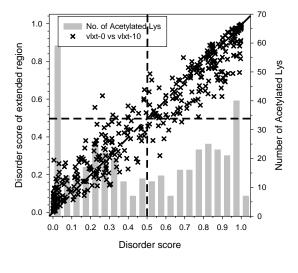
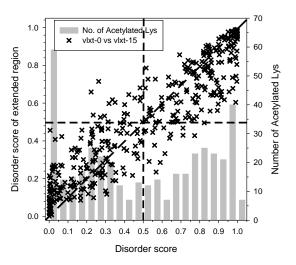
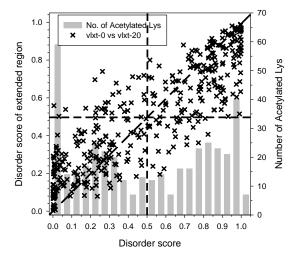
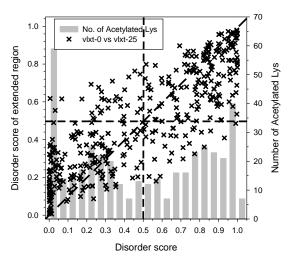


**Supplementary Figure S1**. Comparison between PONDR<sup>®</sup> VLXT and IUPred predictions for acetylated lysines in (a) extracellular and (b) intracellular tachyzoites. The correlation coefficients for two datasets between PONDR<sup>®</sup> VLXT and IUPred predictions are (a) 0.70 and (b) 0.72, respectively.









Supplementary Figure S2. Disorder scores of acetylated lysines and analysis of their local environment within the amino acid sequences of 274 tachyzoite proteins. Disorder score of each acetylated lysine is predicted by PONDR® VLXT. Influence of neighboring residues was measured by the averaging disorder score over peptides centered at the Lys but extended on both sides by a specific number of residues. The lengths of the extension in one direction are 10 (A), 15 (B), 20 (C), and 25 residues (B), respectively, and the corresponding scores are labeled as vlxt-10, vlxt-15, vlxt-20, and vlxt-25, whereas vlxt-0 is the original prediction score without extension. Each "x" in the figure is an acetylated lysine with x-axis being the original disorder scores for the acetylated lysines predicted by PONDR® VLXT (x-axis) and y-axis being averaged disorder score over the extended regions also predicted by PONDR® VLXT. The grey bars represent the distribution of the original PONDR® VLXT scores for the acetylated lysines.