



Supplementary Figure 1. To determine TP, FP and FN values, we evaluated the overlap between a predicted and a true binding region, which starts from the first intermolecular base-pair and ends with the last intermolecular base-pair. In the image above, the green region of a target RNA represents a verified binding region while the orange line shows a computational prediction by an algorithm. Therefore, TP values are the number of nucleotides inside an overlap. FP scores show the false predictions, so those values are the number of non-overlapping nucleotides in a predicted binding region, which leads to a lower PPV. Lastly, FN scores are the nucleotide counts of a verified region ignored by a prediction algorithm. We manually confirmed that all binding regions are consecutive with only few mismatches in order to use this assessment model.