





Figure S1: RNAbound results of different parameter combinations, flank size ($f = 5, 10, 15, 20$) and base pairing probability threshold ($p_0 = 0.00005, 0.0005, 0.005, 0.05$), tested on window sizes 100 (a), 150 (b), and 200 (c) across Rfam families. In each panel, the left and right column represents the results of left and right boundary differences (between predicted and actual boundaries) for each Rfam family (row wise). The x -axis represents the different flank sizes, and the y -axis represents the median value of boundary differences.