



Figure 1: Mean (normalized) R10 ONT raw signal value conditioned on individual nucleotide base at a given (relative) position. Over a large set of sequences aligned to their respective raw signals, the value on the y-axis is calculated by computing the average signal value overall signal values where a base at a position relative to the aligned base attains the value indicated by the legend. The lighter area indicates the sequence of bases that forms the 10-mers used in this work. Our 10-mers extend the 9-mers used in ONTs Remora toolkit by the leftmost base at relative position -7 , which allows us to more effectively handle the step-back mechanism described later.