Supplementary Material for "Discriminating protein tags on a dsDNA construct using a Dual Nanopore Device"

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VI. INDIVIDUAL DWELL TIME DISTRIBUTION OF THE TAGS FROM THE SIMULATION

In the Brownian dynamics simulation the dwell time distributions of the partially charged sidechain tags are calculated from the residence time in the left/right nanopore regions for $L \rightarrow R/R \rightarrow L$ scans shown in the Fig. S1 (a) and (b) respectively. During the $L \rightarrow R$ scans for an individual tag, the left pore dwell time distribution is wider than the right pore and the opposite is observed for the $R \rightarrow L$ scans. It is also worth mentioning that for the closely separated tag pairs (T_2, T_3 and T_4, T_5, T_6) the dwell time increases the most for the left pore during the $L \rightarrow R$ scans and in the right pore during the $R \rightarrow L$ scans.

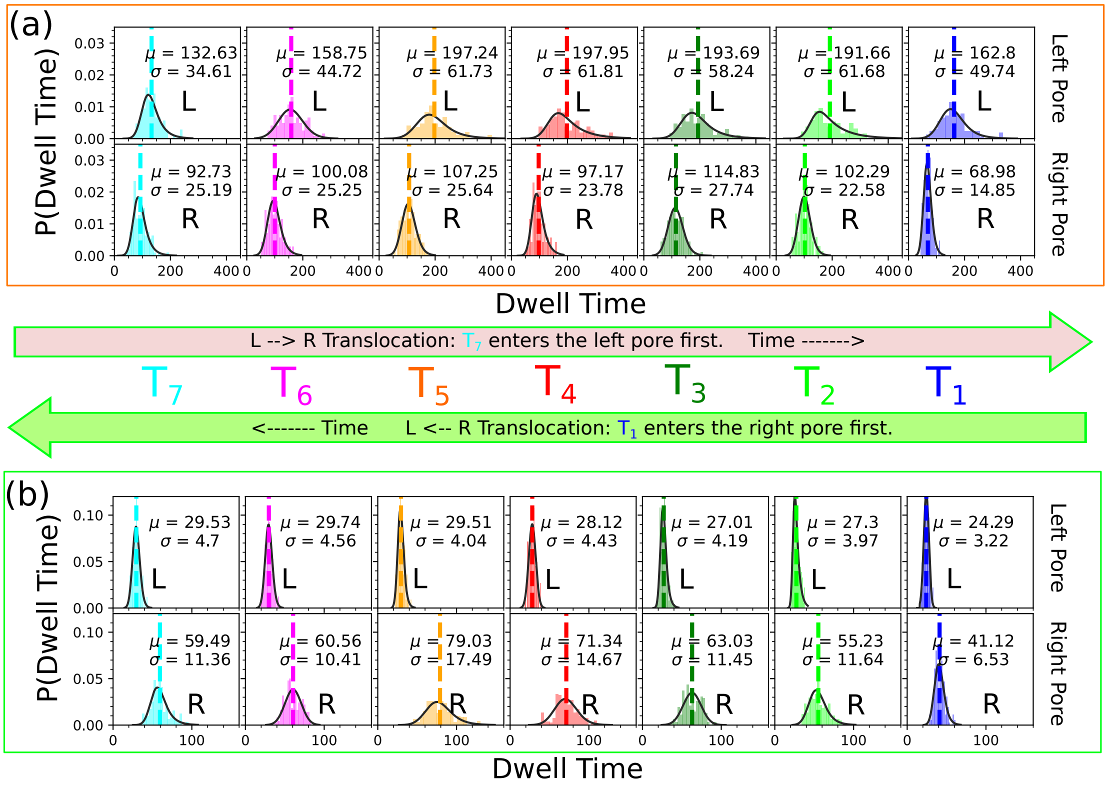

FIG. S1. The panel figures show the individual dwell time distribution of the seven sidechain tags obtained from the BD simulation for the voltages $V_L = 3$ and $V_R = 6$ for the $L \rightarrow R$ scans, and for $R \rightarrow L$ scans the left/right pore voltages are $V_L = 13$ and $V_R = 6$ respectively. (a) The first/second row represents the dwell time of the tags in the left/right pore respectively during the $L \rightarrow R$ scans. (b) The dwell time distributions for the individual sidechain tags for the $R \rightarrow L$ scans. The black dotted lines represent dwell time averages with the average values mentioned in the μ. The standard deviations are denoted by the σ. The black envelops represent the exponentially modified Gaussian distribution fit of the dwell time histograms.