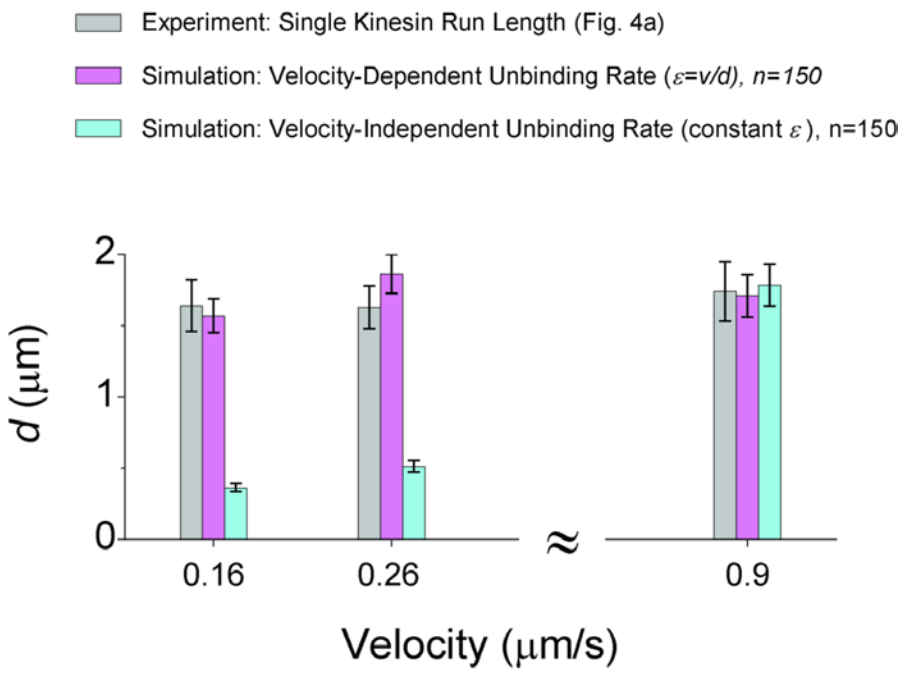

Figure S1. Simulated *vs*. measured single-motor travel distance for kinesin. Shown are mean±SEM, and simulation sample size. To evaluate single motor travel distances, we employed a previously developed Monte Carlo algorithm detailed in (10). We utilized the same parameters as described for kinesin in (10) with the following exceptions. We constrained the unbinding rate ε at $v_{max} = 0.9\mu$m/s, using single-kinesin travel measured at 1mM ATP. We then allowed the unbinding rate to either vary linearly with velocity (magenta bars), or to remain constant regardless the motor's speed (cyan bars). Our simulation demonstrates explicitly that a velocity-independent unbinding rate does not agree with the measured single-kinesin travel distance (grey bars). Intuitively, the time required to cover a particular distance is linearly proportional to velocity. Thus, with a velocity-independent unbinding rate, the single-motor travel distance should reduce linearly with reducing velocity. This does not agree with measurements (cyan *vs*. blue bars). A velocity dependent unbinding rate ($\varepsilon = {}^{v}/_{d}$), on the other hand, recaptures the experimental measurements quite well (magenta *vs*. grey bars).