Figure S1: Mean pairwise diversity, π, after a selective sweep from standing genetic variation in evolutionary rescue (blue; $d = 0.05$) or in a population of roughly constant size (red; $d = 0$). The thick solid curves are our approximations (Equation 9). The dashed blue curves replace $\mathbb{E}[\pi|\text{unlinked}]$ with the observed genome-wide average π (excluding sites within 5cM of the selected site as we simulate only a portion of a genome). The thinnest curves are 100 replicate simulations (rescue only for clarity) and the slightly thicker curves are simulation means (often obscured by prediction). Parameters: $N(0) = 10^4$.