



Figure S1: Predicted sampling standard deviation of ML estimates of LD under a fixed total budget, as a function of the mean depth of coverage μ , when library preparation is three times more expensive than sequencing. Figure S1A shows the predicted sampling standard

deviation of the ML estimates of the LD coefficient D when all sequence reads cover both sites of interest (given by the square root of the theoretical sampling variance from Equations 9 and 13). Figure S1B shows that when all sequence reads cover just single polymorphic sites (given by the square root of the theoretical sampling variance from Equations 10 and 15). The major allele frequencies at two sites of interest are $p = q = 0.9$, and $D = 0.01$.