In Table S1, we simulated data for 3 cases:

1. **Sequence Independent Sample, Genotyping 100% Accurate.** We simulated GWAS and sequencing data as described in Scenario 1 of the main text except that genotyping accuracy was 100% and fine-mapping was not conditional on genome-wide significance.

2. **Sequence Independent Sample, Genotyping 97% Accurate.** We simulate data as in (1) except that genotyping accuracy is 97%.

3. **Sequence GWAS Discovery Sample, Genotyping 97% Accurate** We simulate data as in (2) except that fine-mapping is conditional on genome-wide significance at the tag SNP.

The results show that when fine-mapping is performed in an independent sample with 100% accurate genotyping, the power to detect the original effect at the causal SNP as well as the
localization success rate is high. When genotyping error is introduced, both power and localization success rate fall considerably. Re-using the original successful GWAS for the fine-mapping stage increases the probability that the causal SNP will be genome-wide significant because it is conditional on genome-wide significance at the GWAS tag SNP. However, re-using the GWAS data considerably decreases the probability that the causal SNP will be top-ranked.