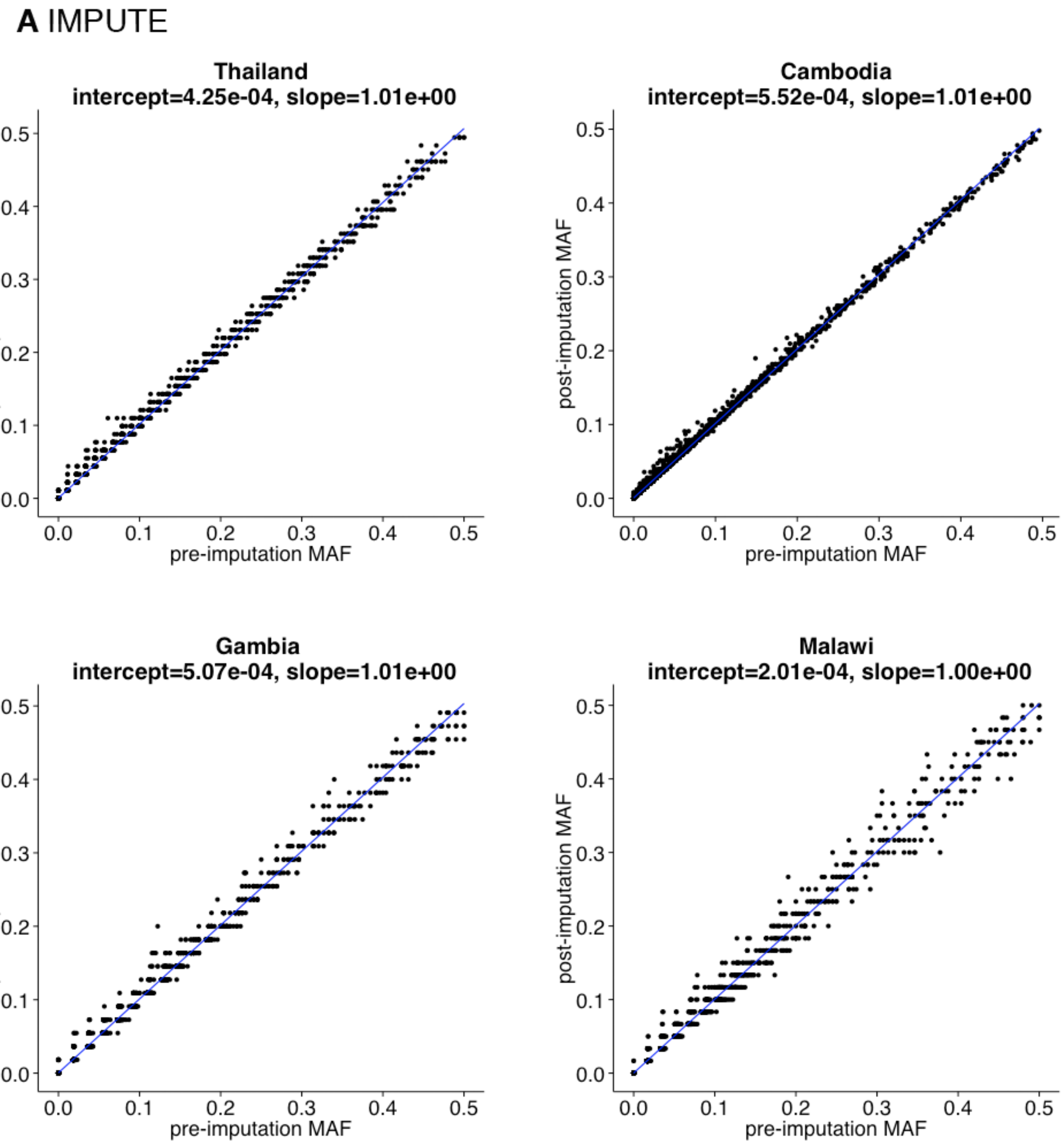
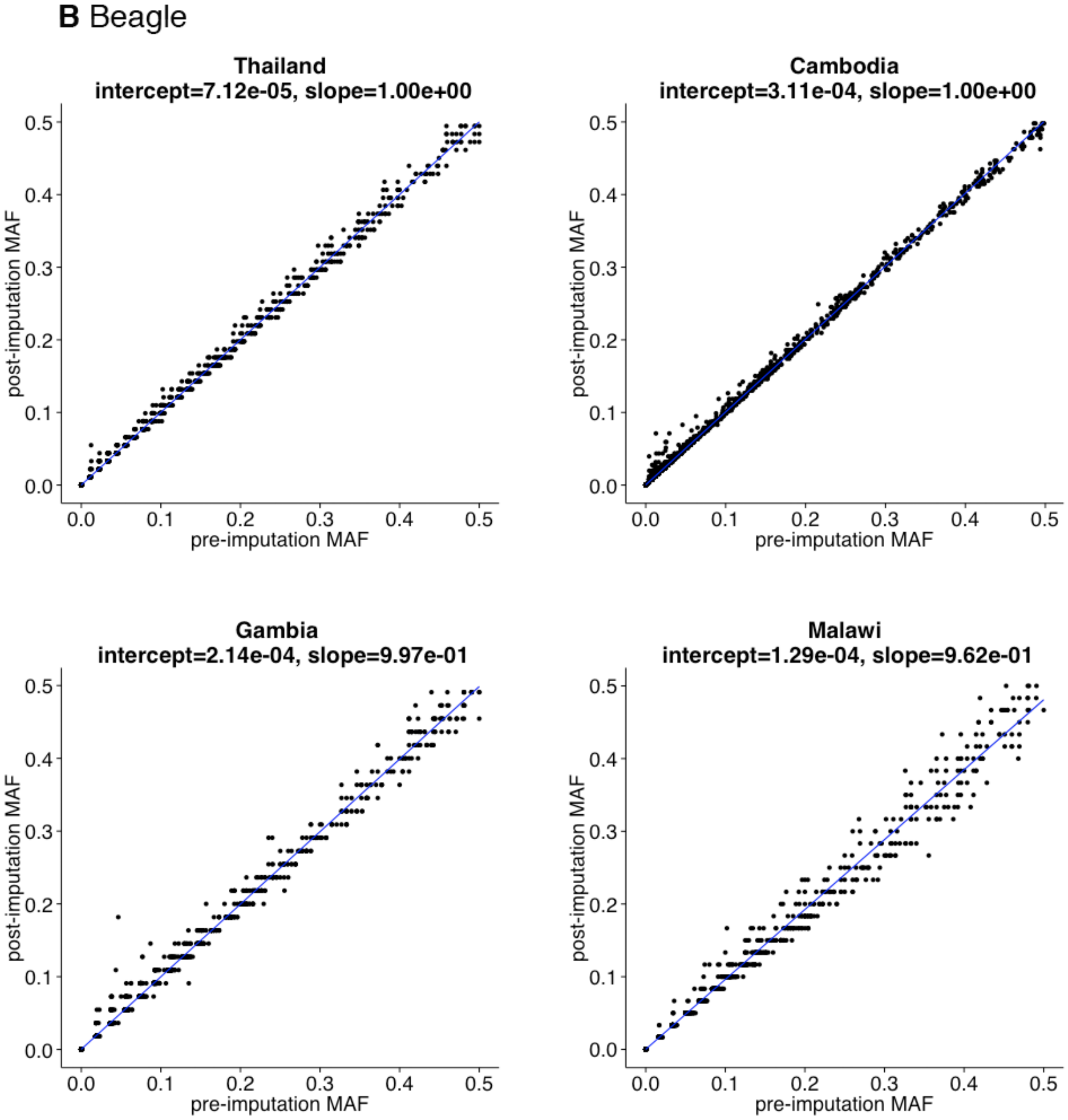


S. Figure 2A. MAF of a sample of 5,000 SNPs in each population pre-and post-imputation, using IMPUTE (recombination map: LDhat, reference panel: population-specific). No systematic increase or decrease was detected.



S. Figure 2B. MAF of a sample of 5,000 SNPs in each population pre-and post-imputation, using Beagle. No systematic increase or decrease was detected.