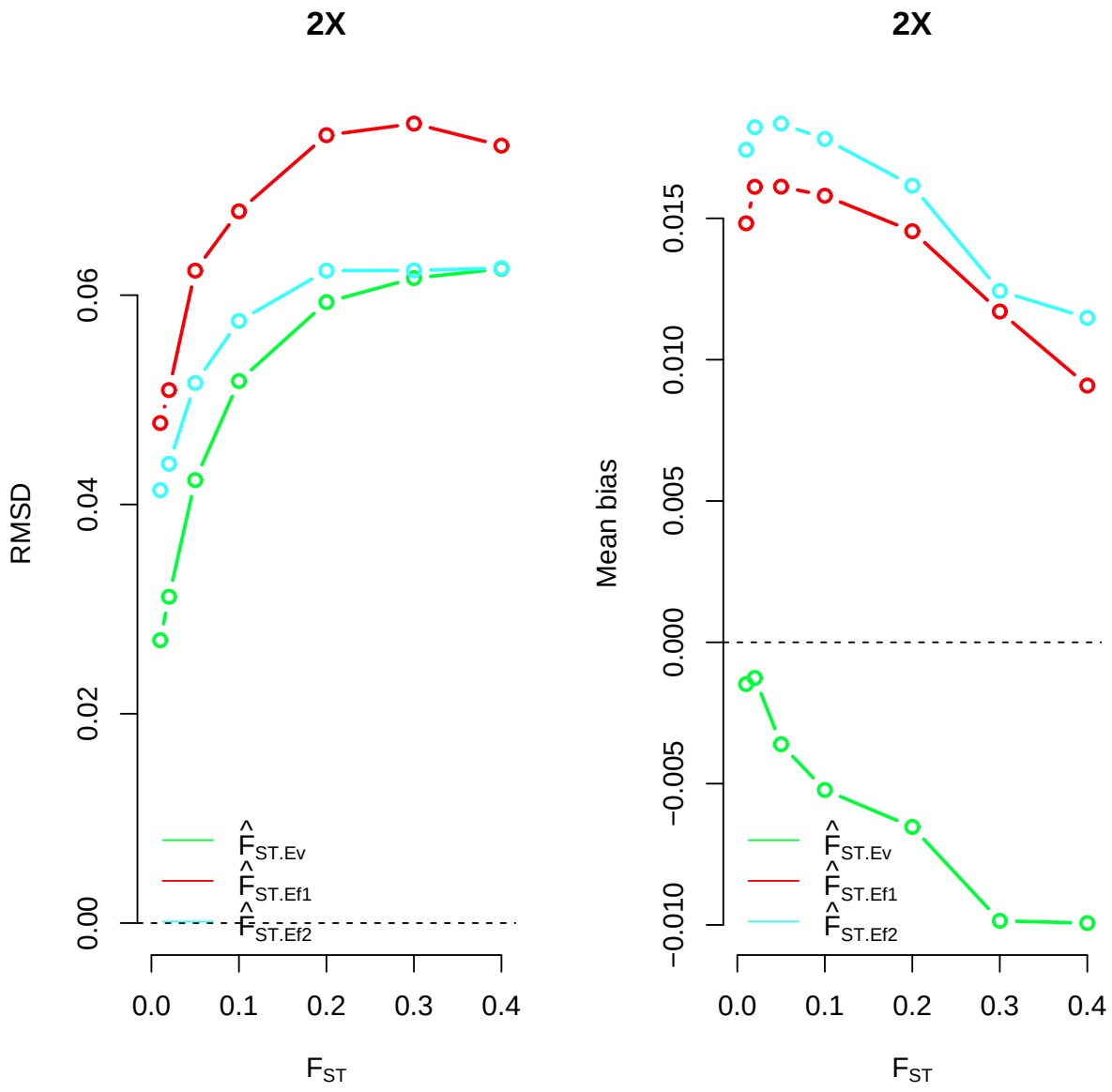

Figure S2: RMSD (left panel) and mean bias (right panel) for estimating F_{ST} at 2X sequencing coverage. We compared the accuracy of the new method which does not rely on genotype calling ($\hat{F}_{ST.Ev}$) and of two methods based on computing population allele frequency as the sample allele frequency with the highest posterior probability, $\hat{F}_{ST.Ef1}$, and as the expected allele frequency, $\hat{F}_{ST.Ef2}$ (see Material and Methods). We simulated 20 individuals for each population and $10,000$ sites for each scenario.