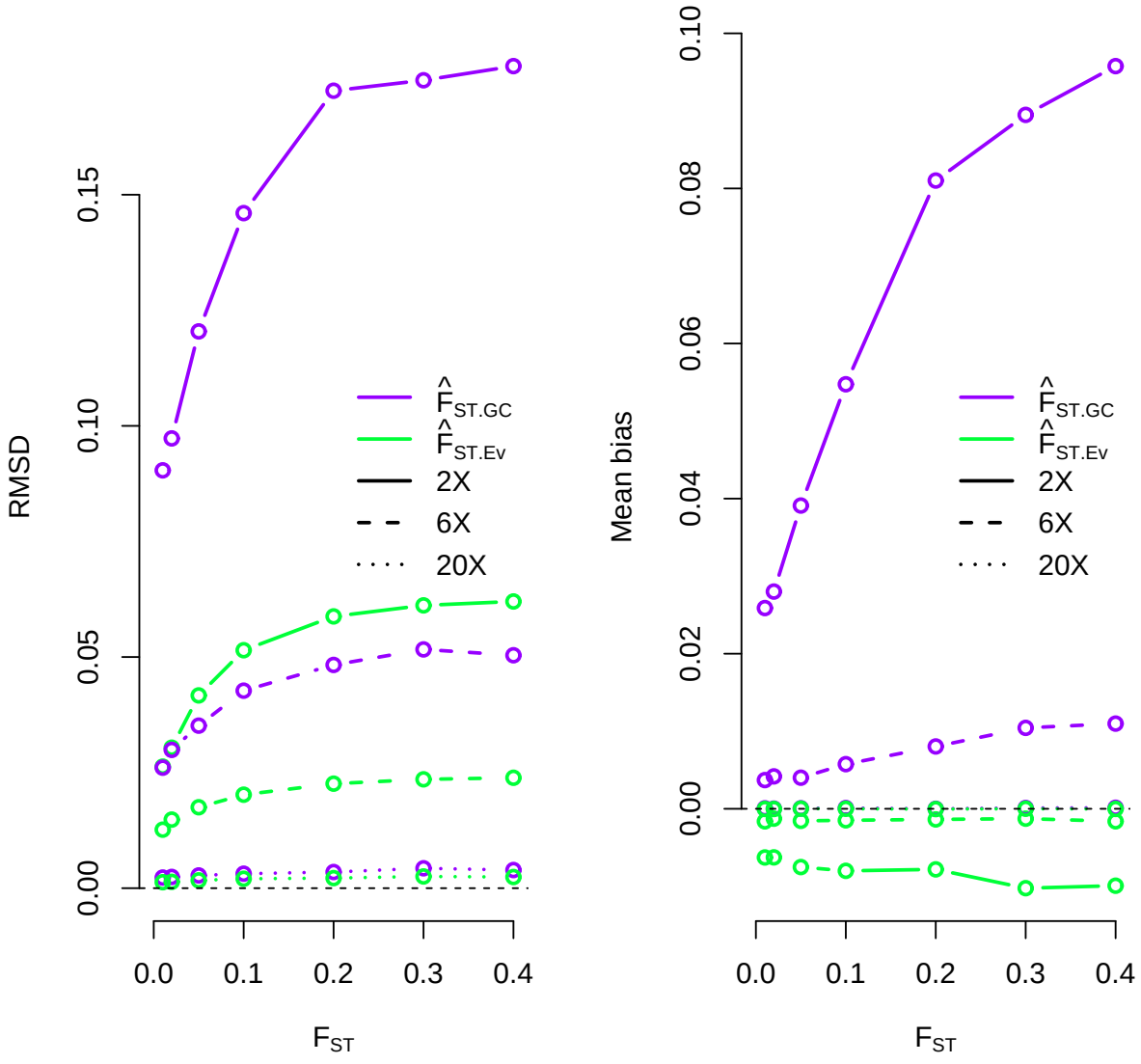

Figure S1: RMSD (left panel) and mean bias (right panel) for estimating F_{ST} under different sequencing coverage (2X, 6X and 20X). We compared the accuracy of the new method which does not rely on genotype calling ($\hat{F}_{ST.Ev}$), while also using the true 2D-SFS as a prior, and a method based on allele frequencies after calling genotypes ($\hat{F}_{ST.GC}$) (see Material and Methods). We simulated 20 individuals for each population and $10,000$ sites for each scenario.