



Figure S7: PCA plots from known genotypes and from called genotypes using genotype posterior probabilities. We simulated 3 populations of 20 individuals each at 20X sequencing coverage. Colors are coded according to each simulated population. Blue and green/red populations are differentiated by an F_{ST} of 0.4 while green and red populations are differentiated by an F_{ST} of 0.15. We simulated 10,000 sites, all variable in the population.