



Figure S8: Sum-of-squares (SS) between PC1 and PC2 computed with the new proposed method, which does not rely on genotype calling, (on y-axis) or with the new method but without weighting each site for its probability to be variable (on x-axis). We simulated 3 populations of 20 individuals at 2X, 6X and 20X sequencing coverage. Populations are differentiated by F_{ST} of 0.4 - 0.15, 0.2 - 0.05 and 0.1 - 0.02. We simulated 10,000 sites with 2% and 10% of sites being variable in the population.