



Figure S10: Sum-of-squares (SS) between PC1 and PC2 computed from called genotypes (on x-axis) or with the new proposed method which does not rely on genotype calling (on y-axis). We simulated 1 populations of 40 individuals: half of them were sequenced at 2X coverage and the other half were sequenced at 20X coverage. We simulated 10,000 sites with 10% of sites being variable in the population.