Figure S1: Comparison for different $\gamma$. The x-axis denotes genetic markers along a chromosome, the y-axis is inferred allele counts at each marker of an arbitrarily chosen ancestral population. The black lines are the simulated truth; the red lines are inferred values with different choice of mixing generations; the blue line are the results of the HapMix as a comparison. Each column denotes an individual, $\gamma = 50, 100, 200$ from top to bottom panels. The individual on the left is explained in the main text. For the individual on the right, the deviation error are 0.053, 0.054, 0.077, and correlations are 0.941, 0.946, 0.939 respectively. As an comparison, HAPMIX has deviation 0.086 and correlation 0.866.