Table S1: Average distance between inferred and true ancestry locations in simulated admixed individuals from POPRES data. Simulations assume 4 generations in the mixture process. Independent SNP model denotes the extension of SPA that ignores admixture-LD. It can also be understood as SPAMIX with completely random transition probability between nearby SNPs. SPAMIX (logistic) represents simulation results starting from haplotypes generated at a location on a map using a Bernoulli sampling from the logistic gradients (see Methods). Parenthesis denotes the standard deviations. We found that Linkage Disequilibrium (LD) significantly affects the ancestry inference as well as the local ancestry inference. We observe more recombination events than expected if using the correct recombination probability (used in simulations). We circumvent this bias multiplying the transition probability by a factor $10^{-1}$, $10^{-2}$, $10^{-4}$ and $10^{-5}$ for the pruned SNP list with 0.1, 0.2, 0.5 and 0.8 pruning thresholds. 44,699, 72,418, 136,284, 194,432 SNPs were retained at the 4 pruning thresholds.

| No. of ancestry | | 1 | 2 | 3 | 4 |
|---|---|---|---|---|---|
| Independent SNP model | Pruned SNP (0.1) | 425(252) | 961(540) | 977(599) | 982(655) |
| | Pruned SNP (0.2) | 443(265) | 880(491) | 898(530) | 880(578) |
| | Pruned SNP (0.5) | 420(245) | 823(448) | 855(502) | 810(494) |
| | Pruned SNP (0.8) | 421(259) | 810(429) | 845(491) | 813(505) |
| SPAMIX | Pruned SNP (0.1) | 425(252) | 558(314) | 596(353) | 621(405) |
| | Pruned SNP (0.2) | 443(265) | 550(326) | 591(367) | 639(423) |
| | Pruned SNP (0.5) | 420(245) | 557(359) | 630(522) | 657(617) |
| | Pruned SNP (0.8) | 421(259) | 589(557) | 809(895) | 878(848) |