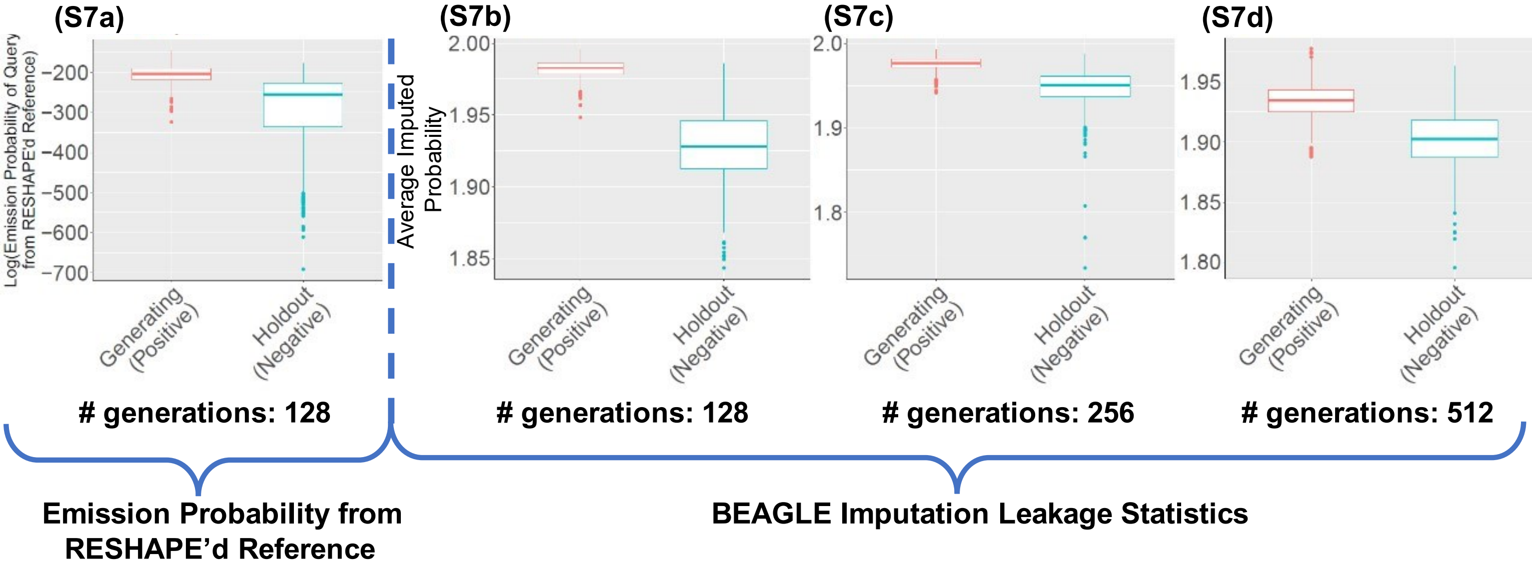

Supplemental Figure S7. **Leakage from sampled panels generated by RESHAPE. (a)** Bar plots show the distribution of log10 emission probability of genomes in positive (red) and negative (green) samples. Note that the genomes in positive sample are assigned higher emission probability when the RESHAPE'd panel is used. **(b)** Bar plots show the average imputed probability of haplotypes per genome (between 0 and 2) for the positive (red) and negative (green) samples after RESHAPE'd panel with 128-generations is used as reference and the positive (and negative) panels are used as query panels in a BEAGLE run. **(c)** Average total imputed probability distributions for positive and negative samples calculated by BEAGLE when 256 generation RESHAPE'd panel is used as reference. Note the separation between the positive and negative samples. **(d)** Average imputed probability distributions for the samples with 512 generation RESHAPE'd reference panel.