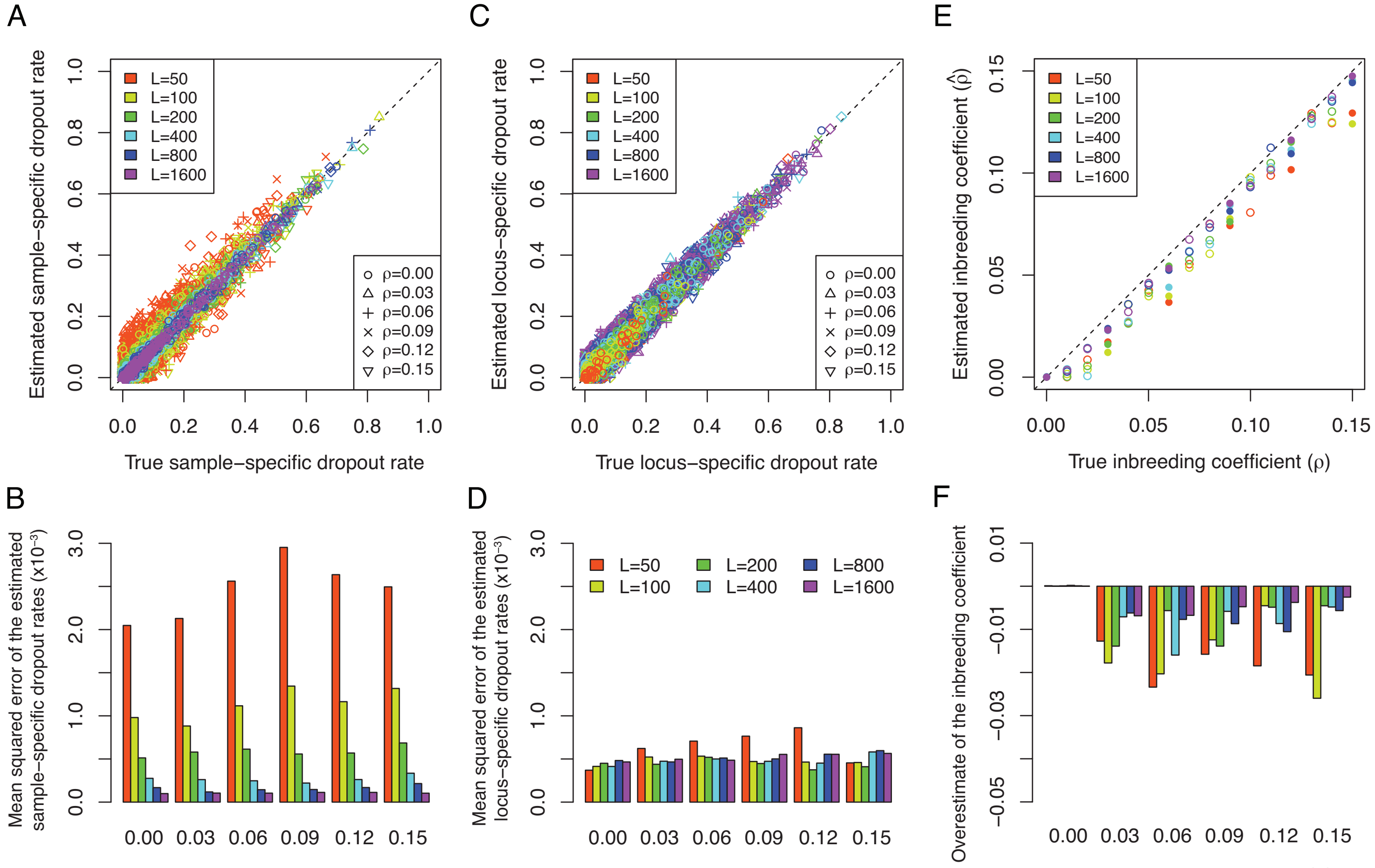

Figure S5: Estimated dropout rates and inbreeding coefficients for simulated data with different numbers of loci and the same number of individuals ($N = 250$). The allele frequencies for the loci were sampled with replacement from the MLEs of the Native American data. Each data set was simulated with no population structure and no genotyping errors other than allelic dropout. (A) Comparison of the estimated sample-specific dropout rates and the assumed true sample-specific dropout rates. (B) Mean squared errors across all the estimated sample-specific dropout rates for each of the 36 data sets shown in panel A. (C) Comparison of the estimated locus-specific dropout rates and the assumed true locus-specific dropout rates. (D) Mean squared errors across all the estimated locus-specific dropout rates for each of the 36 data sets shown in panel C. (E) Comparison of the estimated inbreeding coefficient and the assumed true inbreeding coefficient, in which each point corresponds to one of 96 simulated data sets. The 36 solid points correspond to the simulated data sets shown in the other panels (A, B, C, D, and F). (F) Overestimation of the inbreeding coefficient, calculated by subtracting the assumed true inbreeding coefficient from the estimated inbreeding coefficient, or $\hat{\rho} - \rho$.