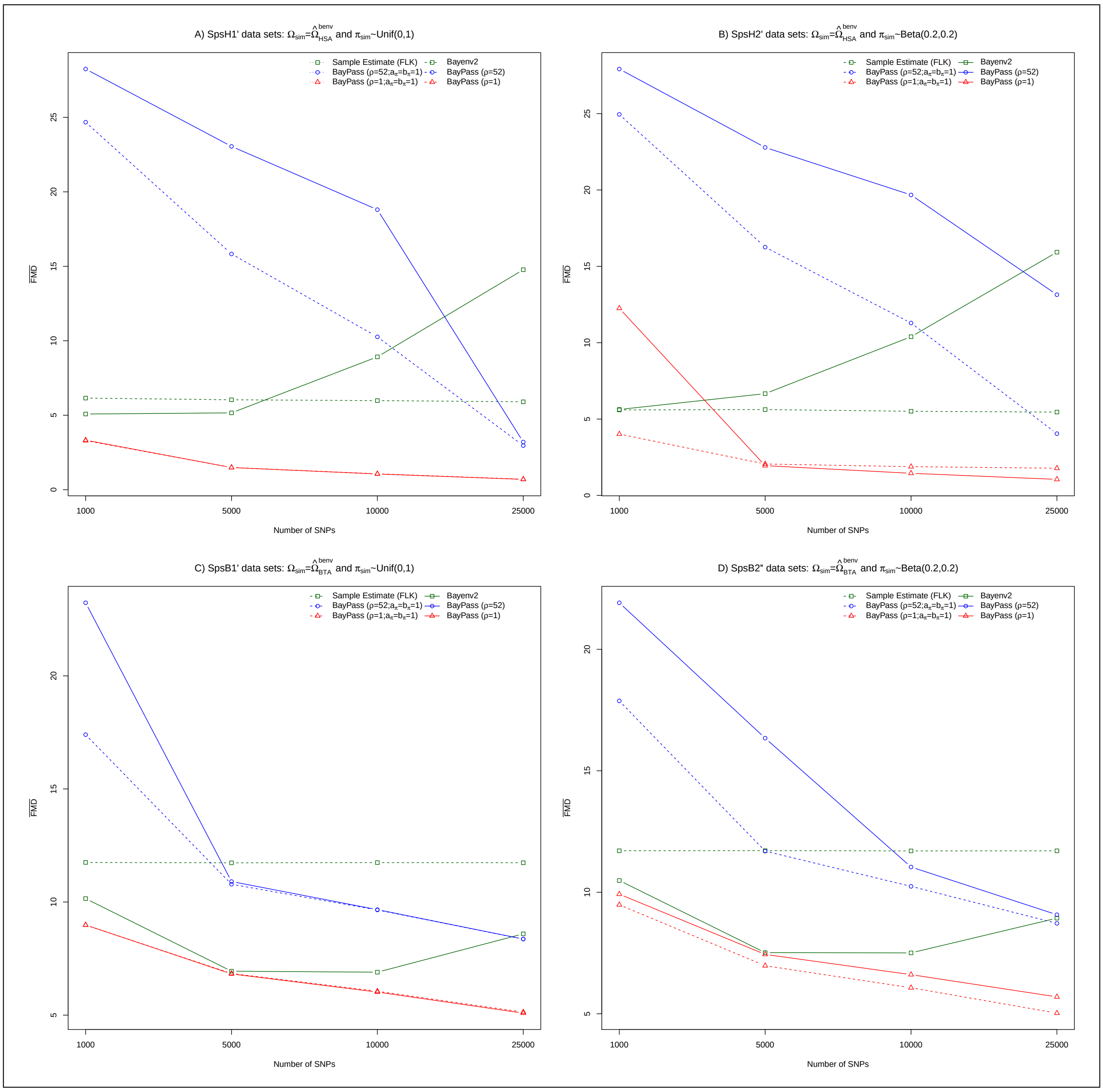

Figure S4: FMD distances (Förstner and Moonen, 2003) between the matrices used to simulate the data sets and their estimates. Simulation scenarios are defined according to the matrix $\mathbf{\Omega}_{\text{sim}}$ used to simulated the data ($\widehat{\mathbf{\Omega}}^{\text{benv}}_{\text{HSA}}$ in A and B; and $\widehat{\mathbf{\Omega}}^{\text{benv}}_{\text{BTA}}$ in C and D) and the parameters of the Beta distribution used to sample the simulated ancestral allele frequencies π_i (Unif(0,1) in A and C; and Beta(0.2,0.2) in B and D). For each scenario, ten independent data sets of 1,000, 5,000, 10,000 and 25,000 markers were simulated (160 data sets in total) and analyzed with BayEnv2 (Coop *et al.*, 2010) and four alternative BayPass model parameterizations (i) $\rho = 1$; ii) $\rho = 1$ and $a_\pi = b_\pi = 1$; iii) $\rho = J$ and ; iv) $\rho = J$ and $a_\pi = b_\pi = 1$). As a matter of comparisons, the FLK frequentist estimate(Bonhomme *et al.*, 2010) of the covariance matrices was also computed. Each point in the curves is the average of the ten pairwise FMD distances between the underlying $\mathbf{\Omega}_{\text{sim}}$ and each of the $\widehat{\mathbf{\Omega}}$ estimated in the ten corresponding simulation replicates.