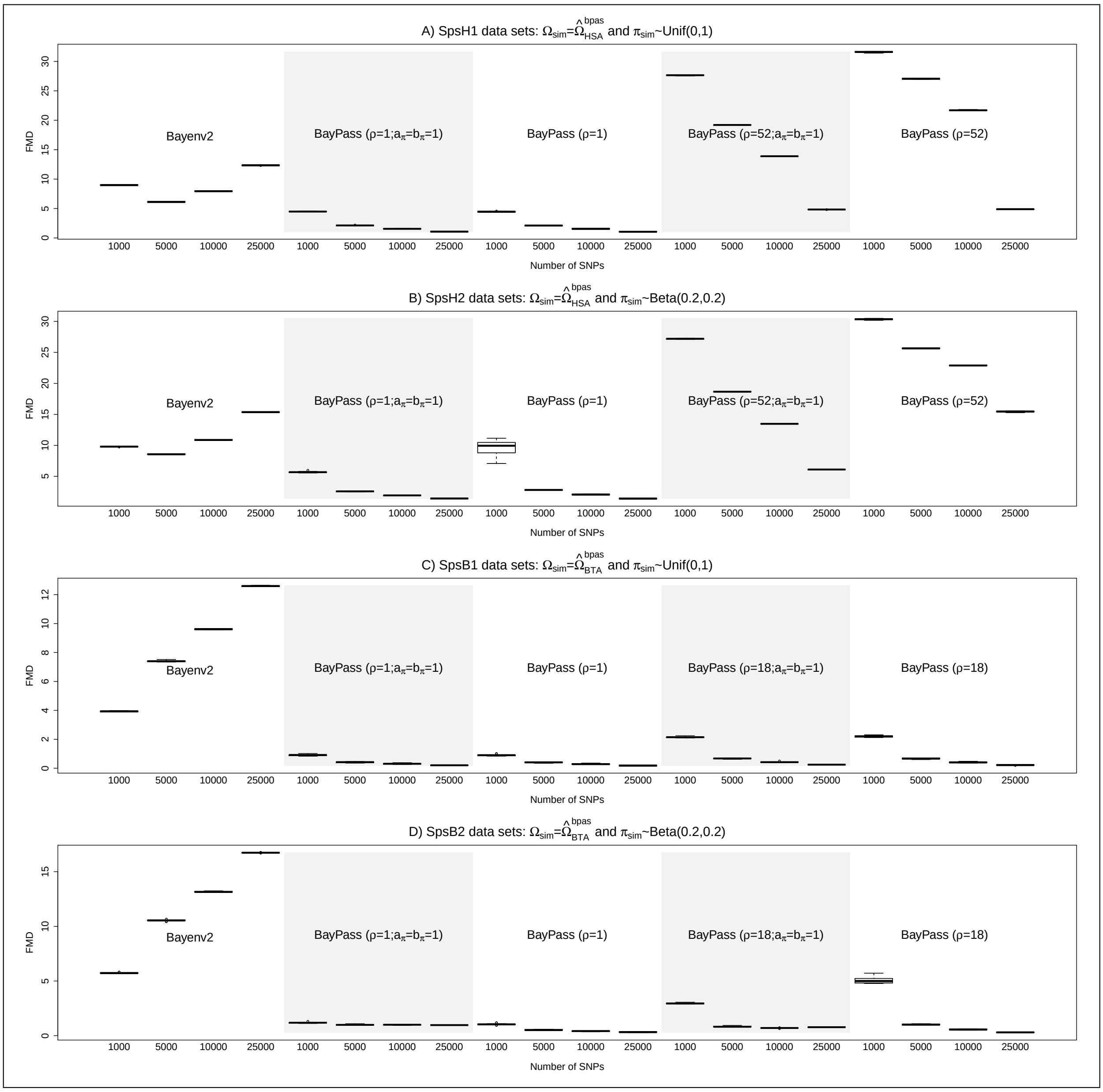

Figure S3: FMD distances (Förstner and Moonen, 2003) between the matrices used to simulate the data sets ($\widehat{\Omega}^{\text{bpas}}_{\text{HSA}}$ or $\widehat{\Omega}^{\text{bpas}}_{\text{BTA}}$) and their estimates obtained with BayEnv2 (Coop *et al.*, 2010) and four alternative BayPass model parameterizations (i) $\rho = 1$; ii) $\rho = 1$ and $a_\pi = b_\pi = 1$; iii) $\rho = J$ and ; iv) $\rho = J$ and $a_\pi = b_\pi = 1$). Each boxplot contains 10 FMD distances computed with estimates from 10 independent data sets simulated with the same parameters (scenarios SspH1, SspH2, SspB1 or SspB2; and 1,000, 5,000, 10,000 or 25,000 markers). In total, 160 different data sets were thus considered (10 replicates × 4 scenarios × 4 SNP numbers).