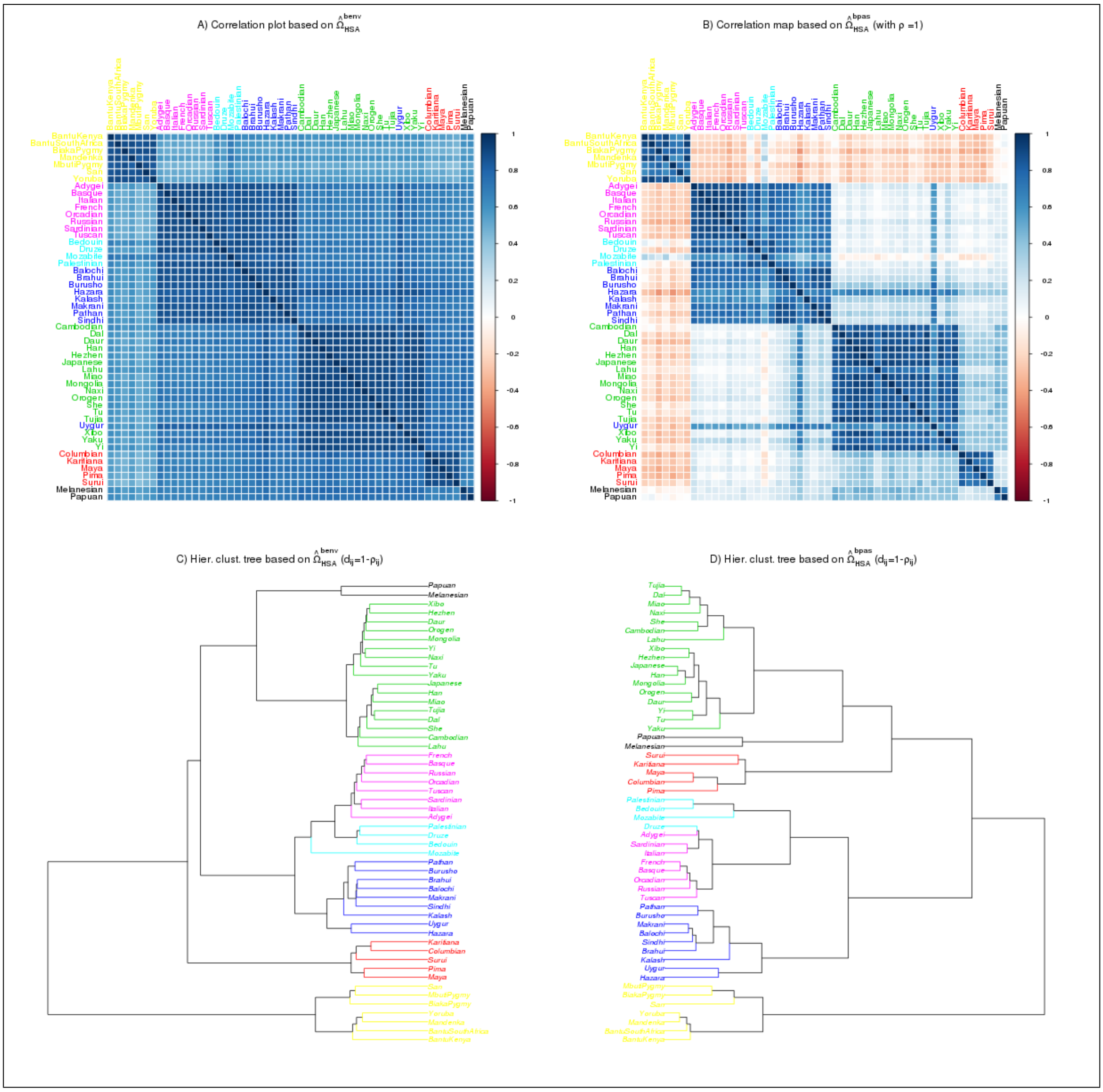

A) Correlation plot based on $\hat{\Omega}^{benv}_{HSA}$

B) Correlation map based on $\hat{\Omega}^{bpas}_{HSA}$ (with ρ =1)

C) Hier. clust. tree based on $\hat{\Omega}^{benv}_{HSA}$ ($d_{ij}=1-\rho_{ij}$)

D) Hier. clust. tree based on $\hat{\Omega}^{bpas}_{HSA}$ ($d_{ij}=1-\rho_{ij}$)

Figure S1: Representation of the scaled covariance matrices Ω among 52 human populations $\widehat{\Omega}^{\text{benv}}_{\text{HSA}}$ (A and C) as estimated from BayEnv2 (Coop *et al.*, 2010) and $\widehat{\Omega}^{\text{bpas}}_{\text{HSA}}$ (B and D) as estimated from BayPass under the core model with $\rho = 1$. Both estimates are based on the analysis of the HSA_{snp} data set consisting of 2,333 autosomal SNPs (see the main text). Population codes (and branches) are colored according to the broad group origins as defined in Conrad *et al.* (2006) (see Günther and Coop (2013))