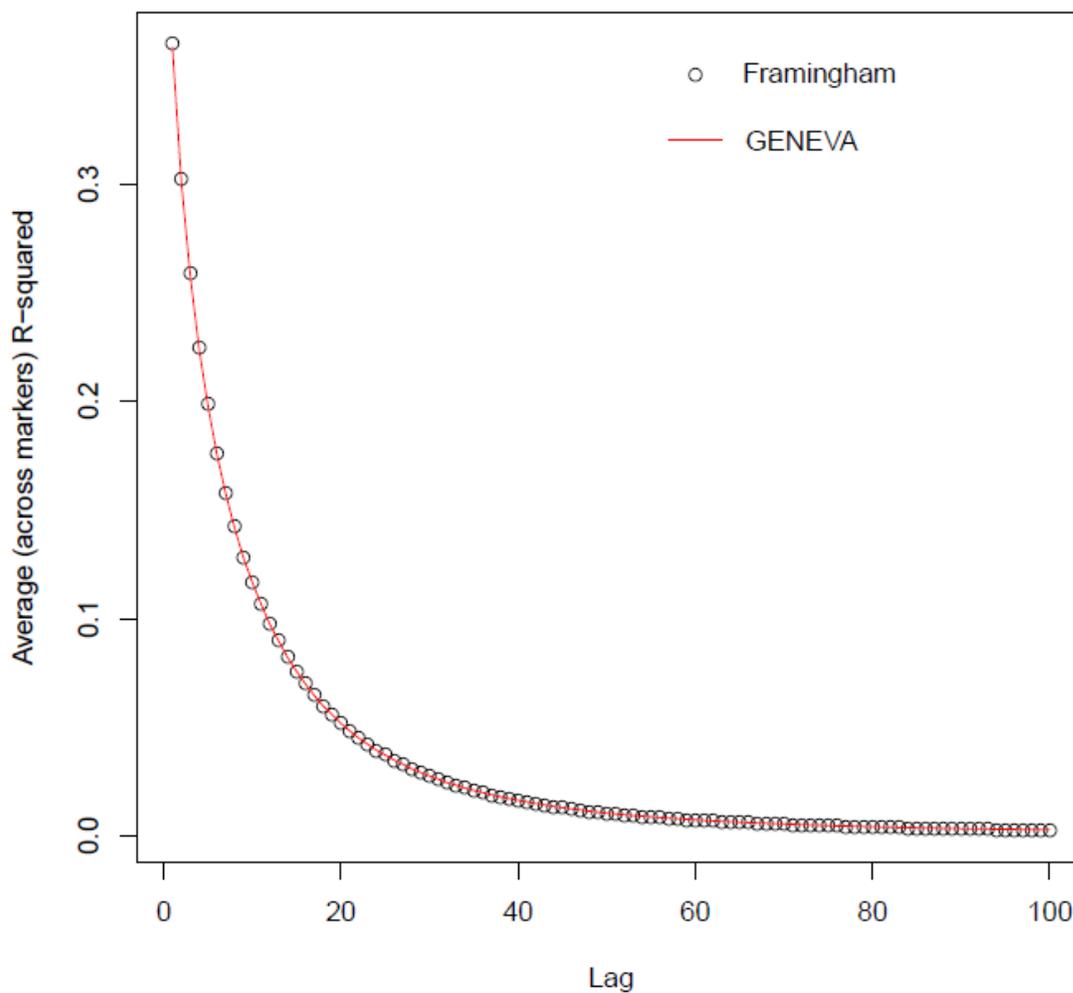**Figure S2.** Average squared correlation between genotypes at various lags (number of markers in between the two used to compute the squared correlation) observed in FHS (dots) and GEN (line). The average inter-marker distance in the platform was 7.2 kb.