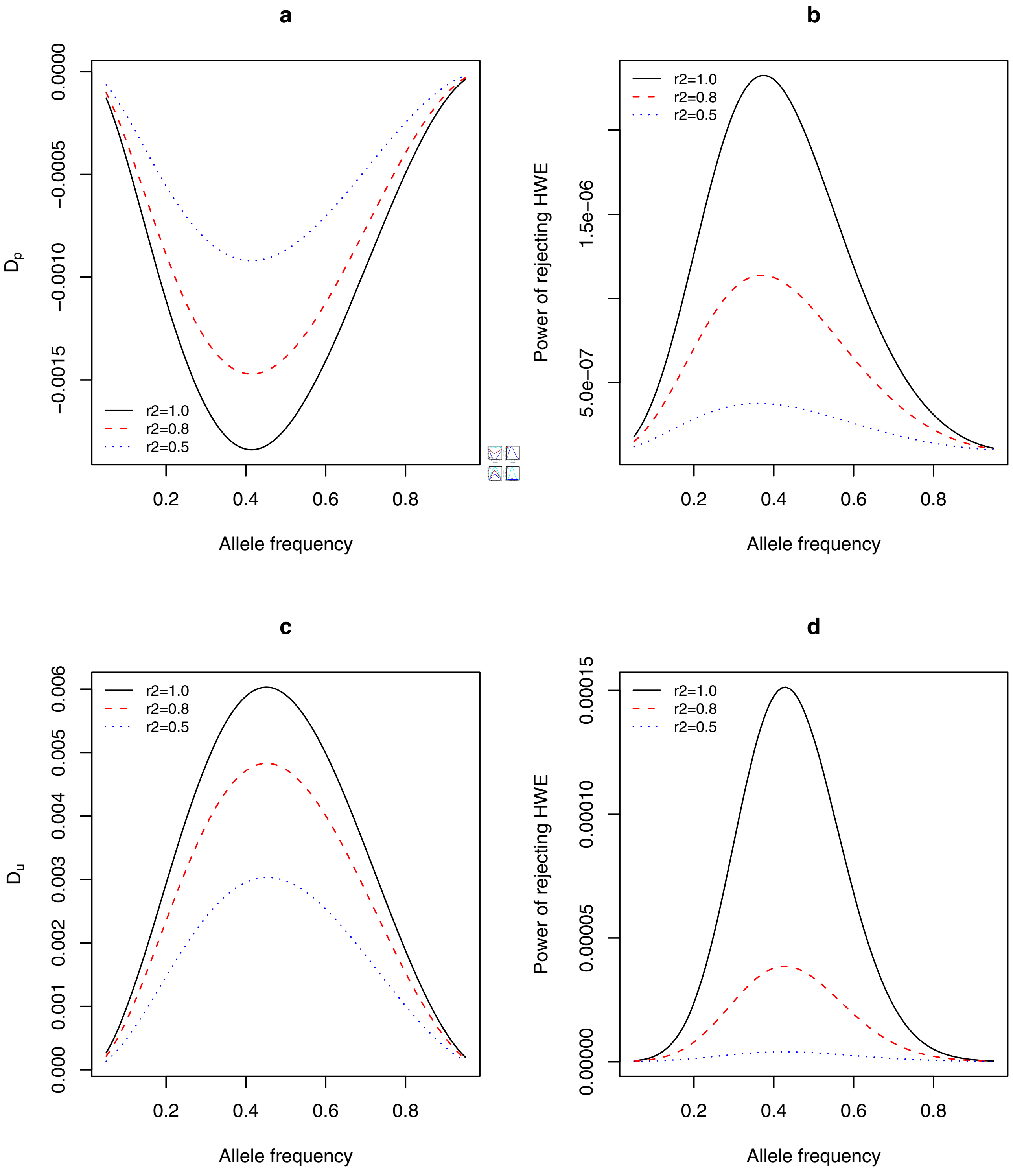
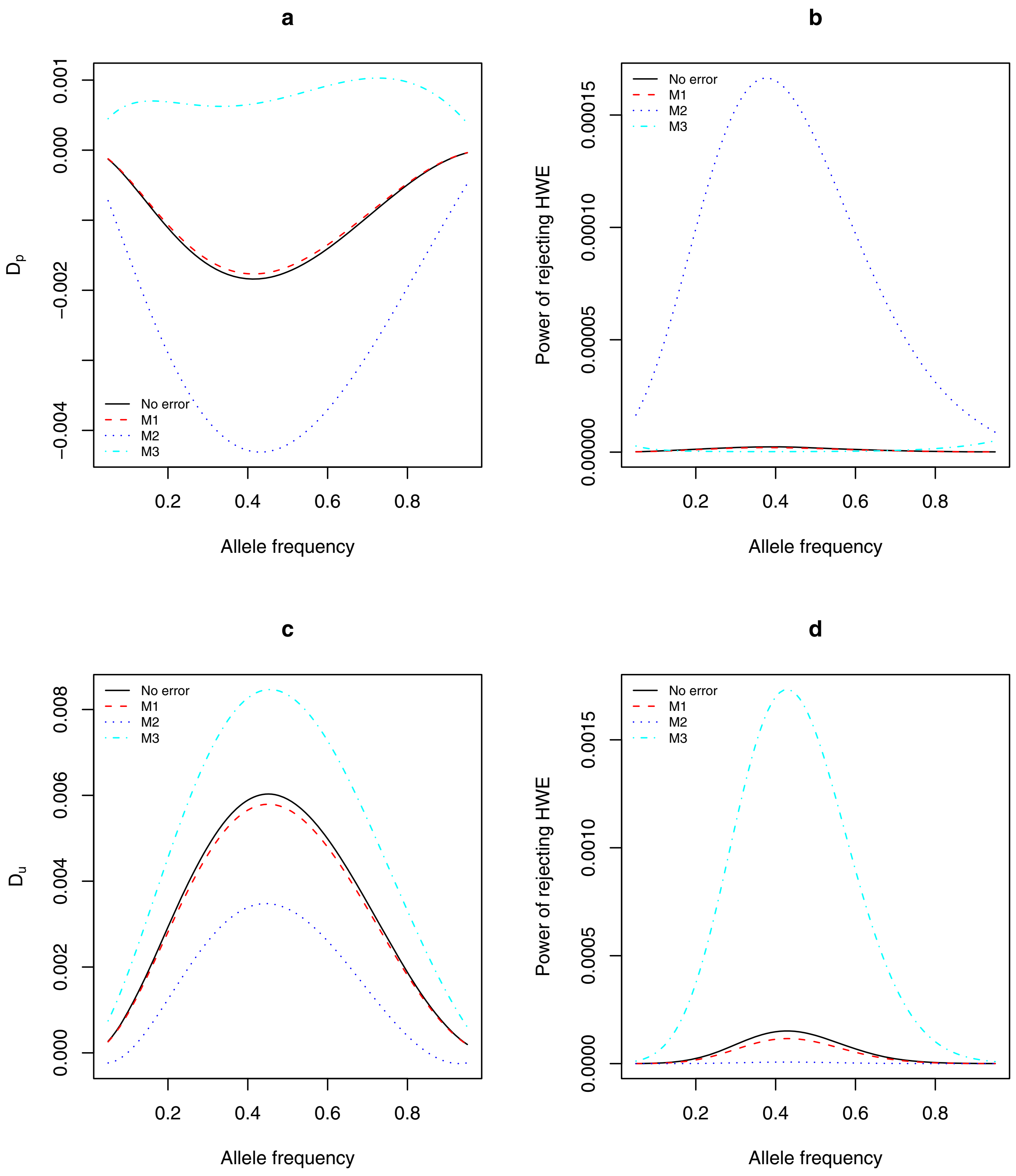
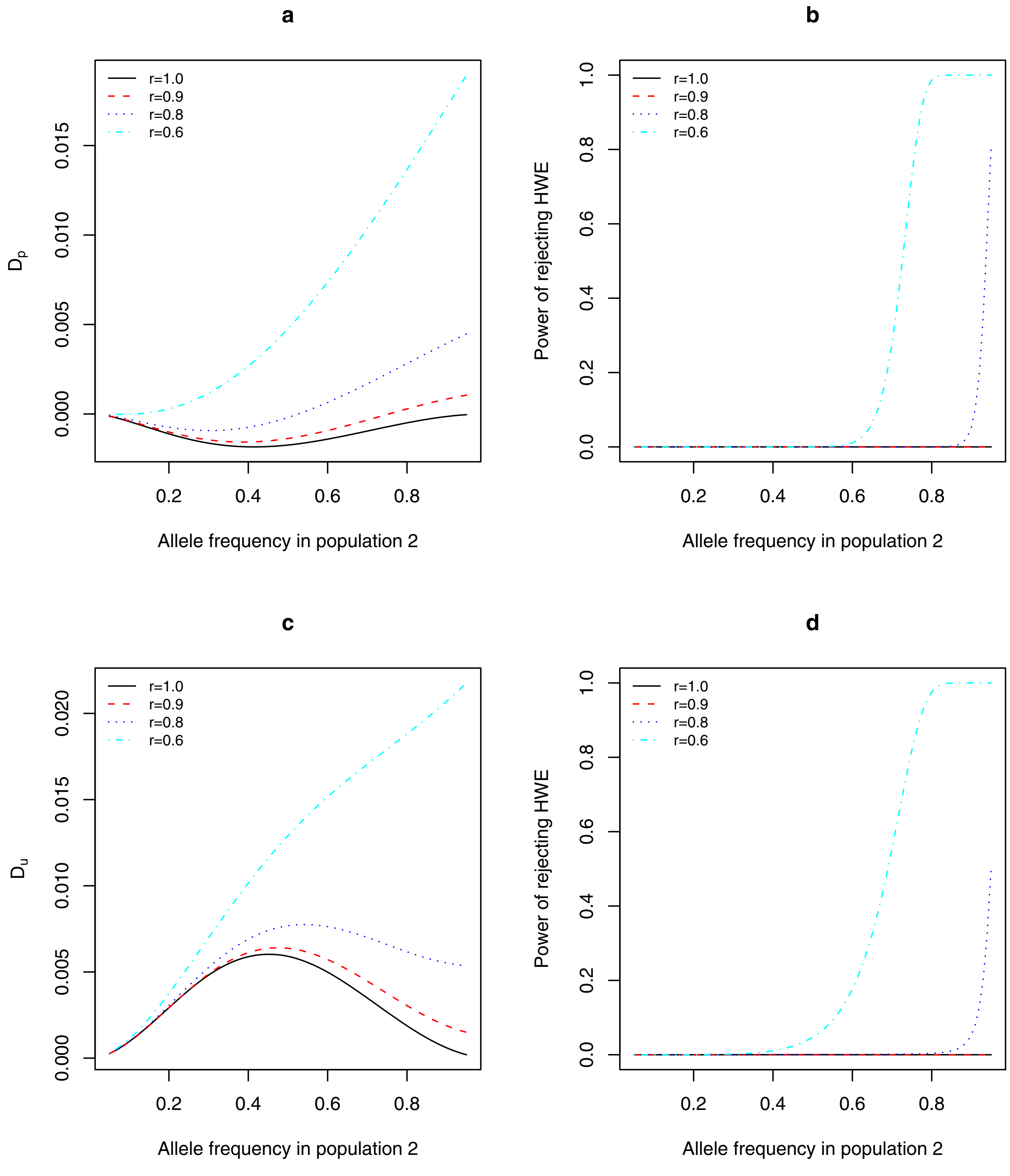


Supplemental Fig. 1: Displays the effect of LD (r^2) on the HWD coefficient (a) and the power of rejecting HWE (b) in parental genotype data for the additive model and the effect of LD on the HWD coefficient (c) and power of rejecting HWD (d) in unaffected sibling genotype data for the recessive model for $\gamma_1 = 1.5$ at $\alpha = 1\text{x}10^{-7}$.



Supplemental Fig. 2: Displays the effect of genotyping error on the HWD coefficient (a) and power of rejecting HWE (b) in parental genotype data for the additive model and the effect of genotyping error on the HWD coefficient (c) and power of rejecting HWD (d) in unaffected sibling genotype data for the recessive model for $\gamma_1 = 1.5$ at $\alpha = 1\text{x}10^{-7}$. Three genotyping error models are shown: random error model (M1), homozygote to heterozygote error model (M2) and heterozygote to homozygote error model (M3).



Supplemental Fig. 3: Displays the effect of population substructure on the HWD coefficient (a) and power of rejecting HWE (b) in parental genotype data for the additive model and the effect of population substructure on the HWD coefficient (c) and power of rejecting HWD (d) in unaffected sibling genotype data for the recessive model for γ_1 = 1.5 at $\alpha = 1\text{x}10^{-7}$. The ratio of the allele frequency between population 1 and 2 is denoted by r.