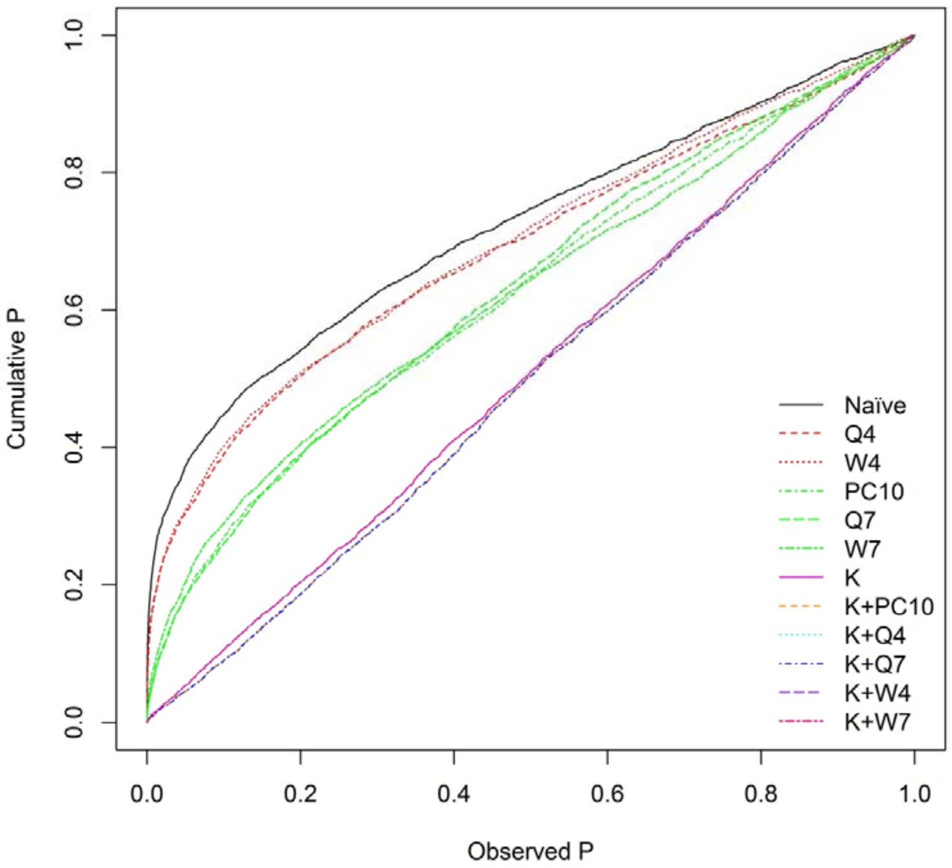

Figure S1 Plot of observed *vs.* expected cumulative *P* values using different GWAS models. The compared models are based on the IT data from UC Davis, 2011. **Naïve**: no population structure correction; **Q4 and Q7**: general linear model (GLM) with STRUCTURE membership coefficients from the four main groups or the 7 subgroups as covariates; **Ward 4 and Ward 7**: GLM with Ward cluster coefficients from the four main groups or the 7 subgroups as covariates; **PC10**: GLM with first 10 principal components as covariates; **K**: mixed linear model (MLM) with the 875 × 875 kinship matrix of identity-by-state (IBS). **K** was then combined with the previous 5 models (**K+Q4, K+Q7, K+W4, K+W7, K+PC10**). Genetic similarities were calculated using all 4,585 SNPs.