Supplemetary Figures

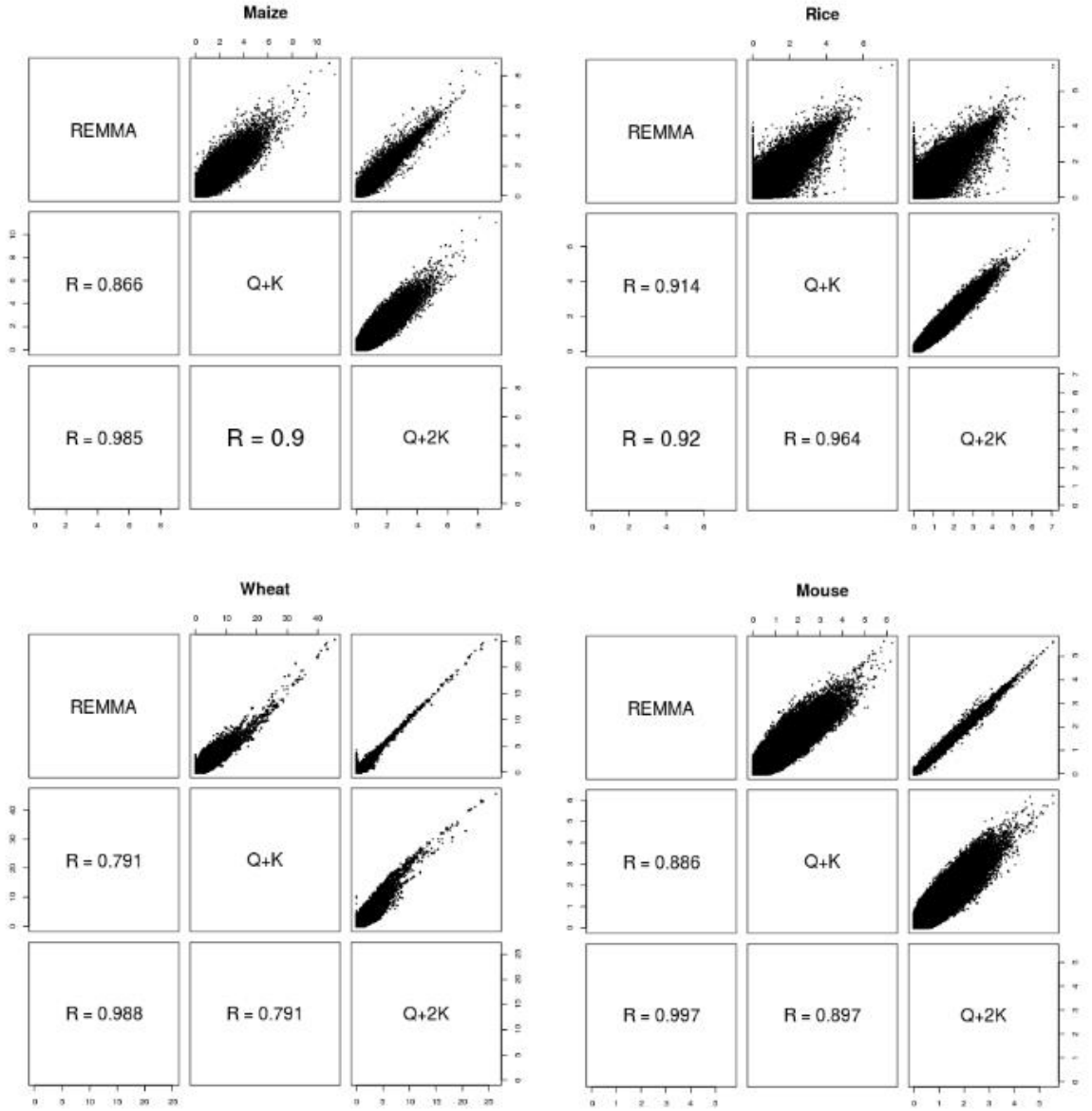

Figure S1. Comparison of the $-\log_{10}(p)$ values for epistatic effects obtained using the REMMA, Q+K and Q+2K model in the four empirical data sets. In each panel, the $-\log_{10}(p)$ values in each model were plotted against each of the other models in the upper-triangular part. The correlation between the $-\log_{10}(p)$ values for each pair of models was shown in the lower-triangular part.

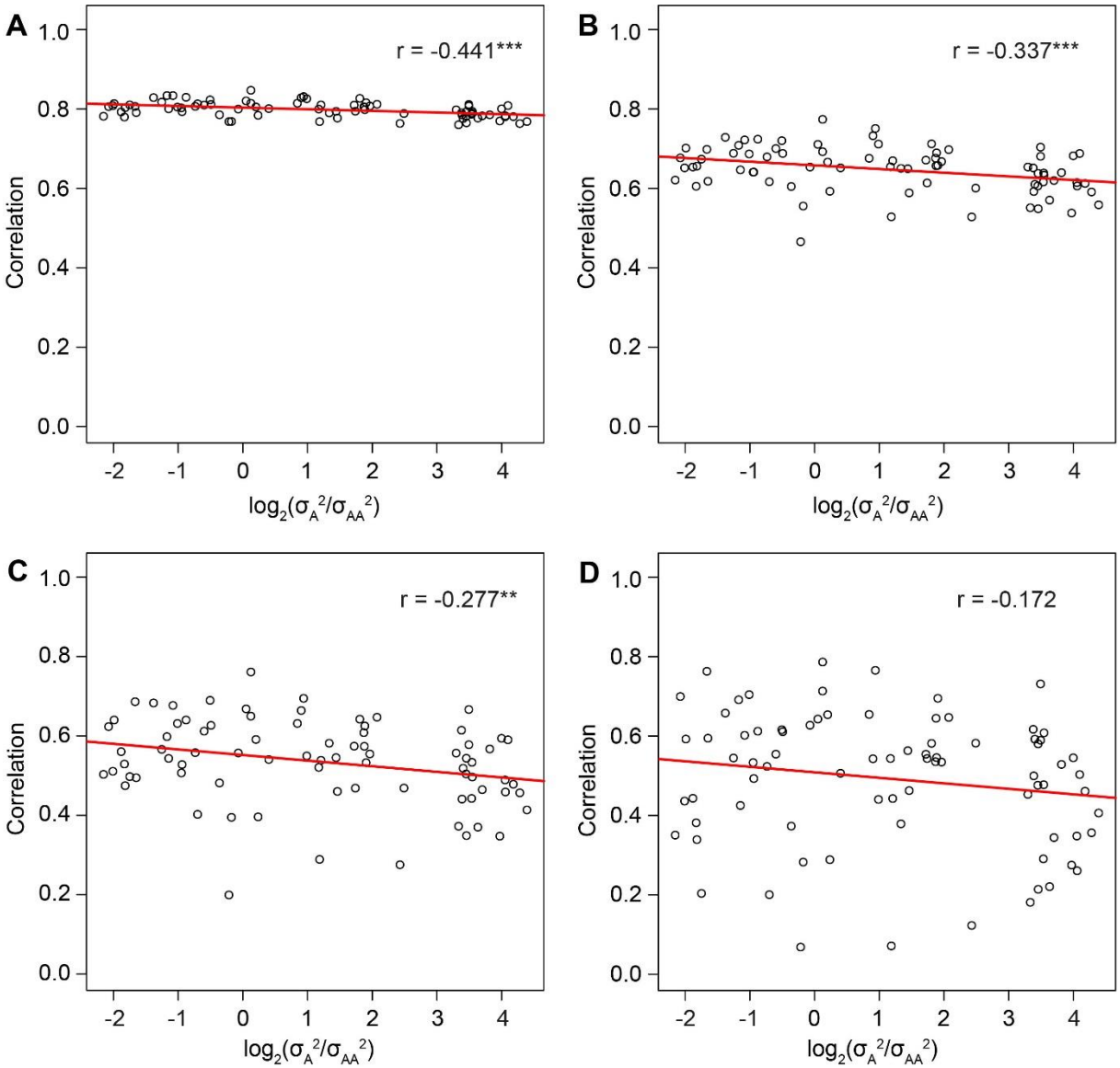

Figure S2. The correlations between the $-\log_{10}(p)$ values for the epistatic effects obtained using the REMMA and the Q+2K model in simulated data sets with $0.4 \leq h^2 < 0.7$ and different σ_A^2/σ_{AA}^2 ratios. Each point in the figure represented the correlation between the $-\log_{10}(p)$ values from the two models calculated in a specific simulated data set. The overall correlation between the correlations and the $\log_2(\sigma_A^2/\sigma_{AA}^2)$ values across all data sets was displayed as the r value together with an indication of significance (*$p < 0.1$, ** $p < 0.05$, *** $p < 0.01$). A threshold of $-\log_{10}(p)$ values was applied to filter the marker pairs. Namely, only the marker pairs whose $-\log_{10}(p)$ values were above the threshold in at least one of the two models were considered. In different panels, distinct threshold values were applied: A) 1, B) 2, C) 3 and D) 4.

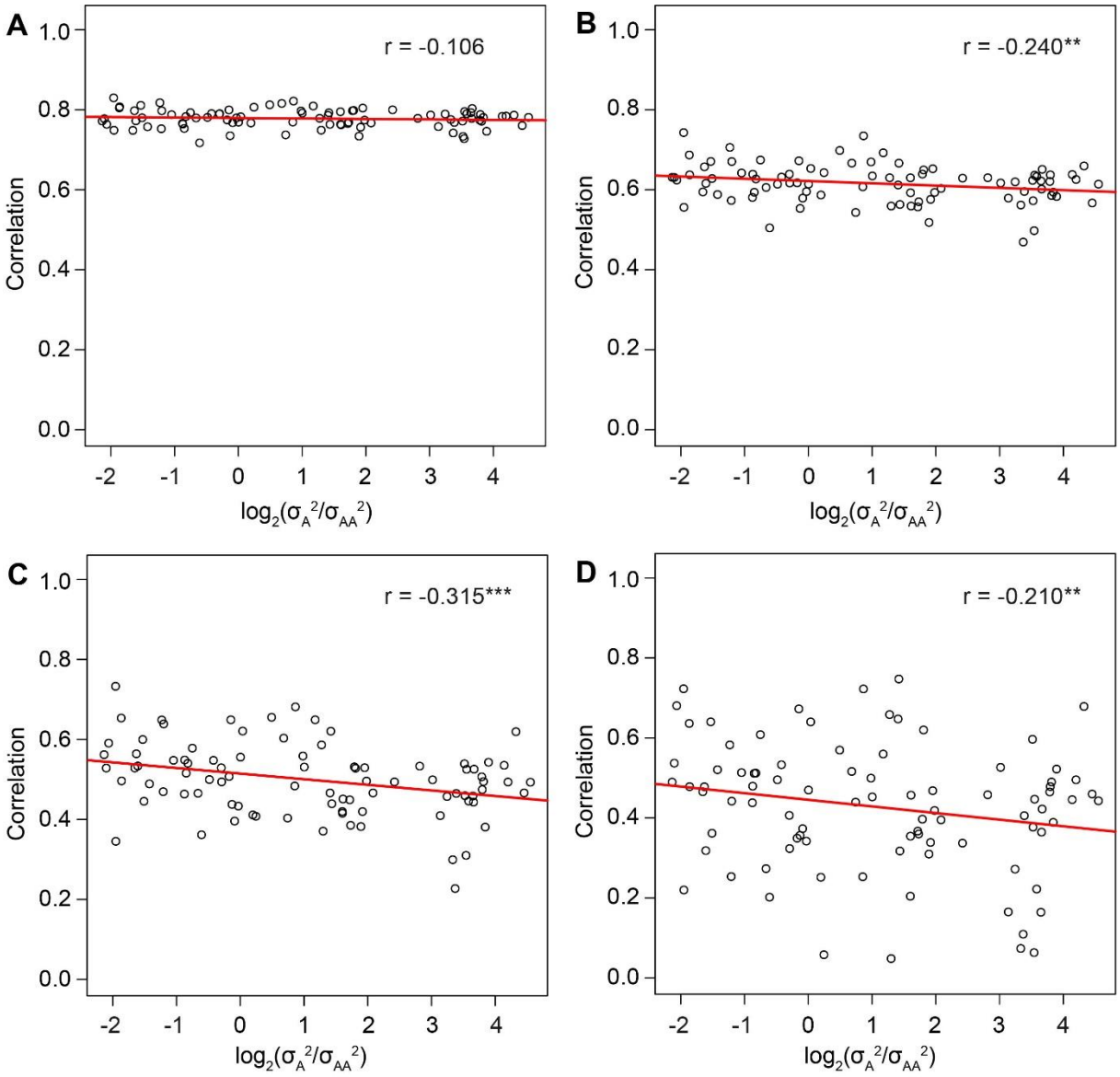

Figure S3. The correlations between the $-\log_{10}(p)$ values for the epistatic effects obtained using the REMMA and the Q+2K model in simulated data sets with $h^2 < 0.4$ and different σ_A^2/σ_{AA}^2 ratios. Each point in the figure represented the correlation between the $-\log_{10}(p)$ values from the two models calculated in a specific simulated data set. The overall correlation between the correlations and the $\log_2(\sigma_A^2/\sigma_{AA}^2)$ values across all data sets was displayed as the r value together with an indication of significance (*$p < 0.1$, ** $p < 0.05$, *** $p < 0.01$). A threshold of $-\log_{10}(p)$ values was applied to filter the marker pairs. Namely, only the marker pairs whose $-\log_{10}(p)$ values were above the threshold in at least one of the two models were considered. In different panels, distinct threshold values were applied: A) 1, B) 2, C) 3 and D) 4.

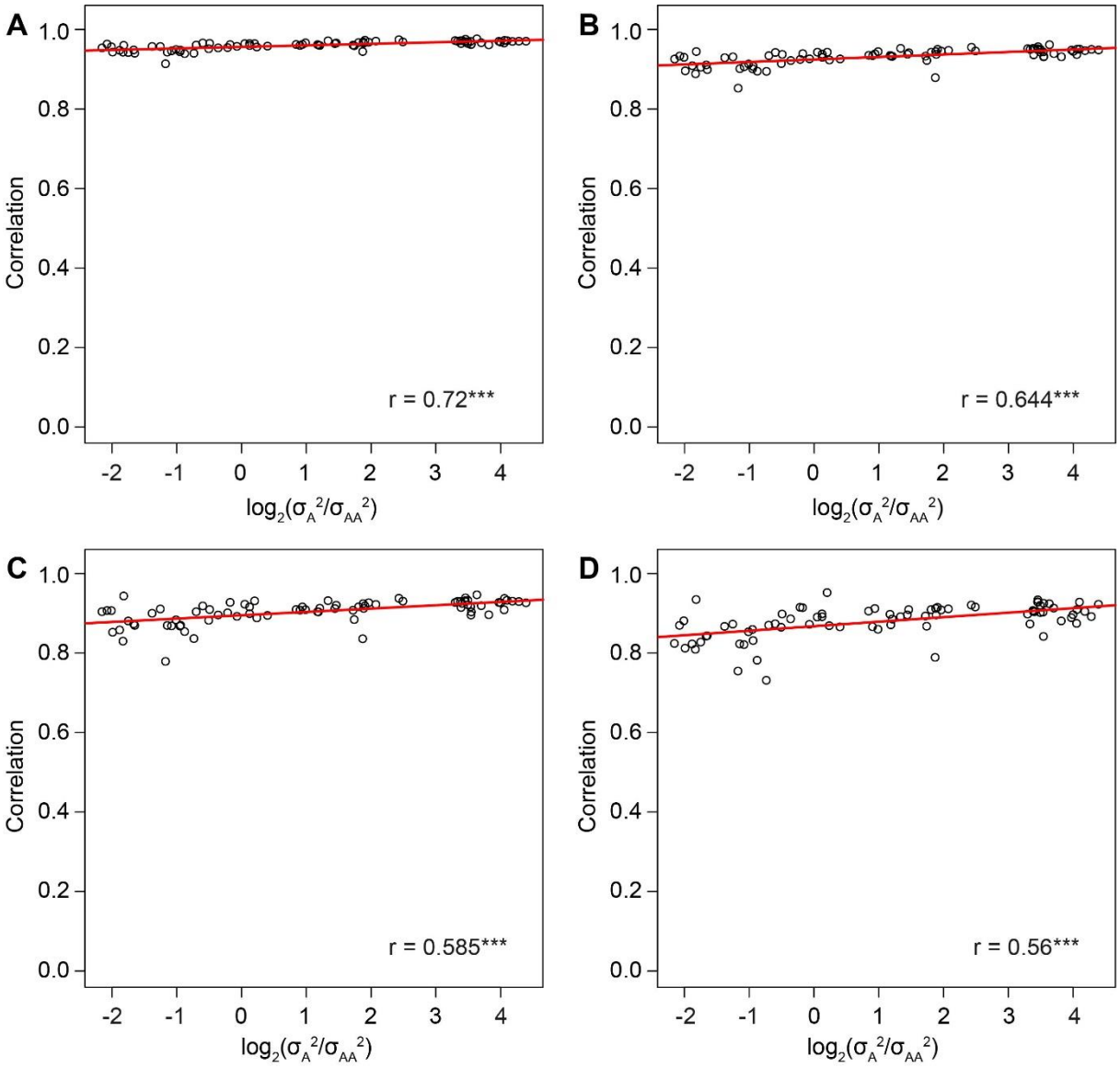

Figure S4. The correlations between the $-\log_{10}(p)$ values for the epistatic effects obtained using the Q+K and the Q+2K model in simulated data sets with $0.4 \leq h^2 < 0.7$ and different σ_A^2/σ_{AA}^2 ratios. Each point in the figure represented the correlation between the $-\log_{10}(p)$ values from the two models calculated in a specific simulated data set. The overall correlation between the correlations and the $\log_2(\sigma_A^2/\sigma_{AA}^2)$ values across all data sets was displayed as the r value together with an indication of significance (*$p < 0.1$, ** $p < 0.05$, *** $p < 0.01$). A threshold of $-\log_{10}(p)$ values was applied to filter the marker pairs. Namely, only the marker pairs whose $-\log_{10}(p)$ values were above the threshold in at least one of the two models were considered. In different panels, distinct threshold values were applied: A) 1, B) 2, C) 3 and D) 4.

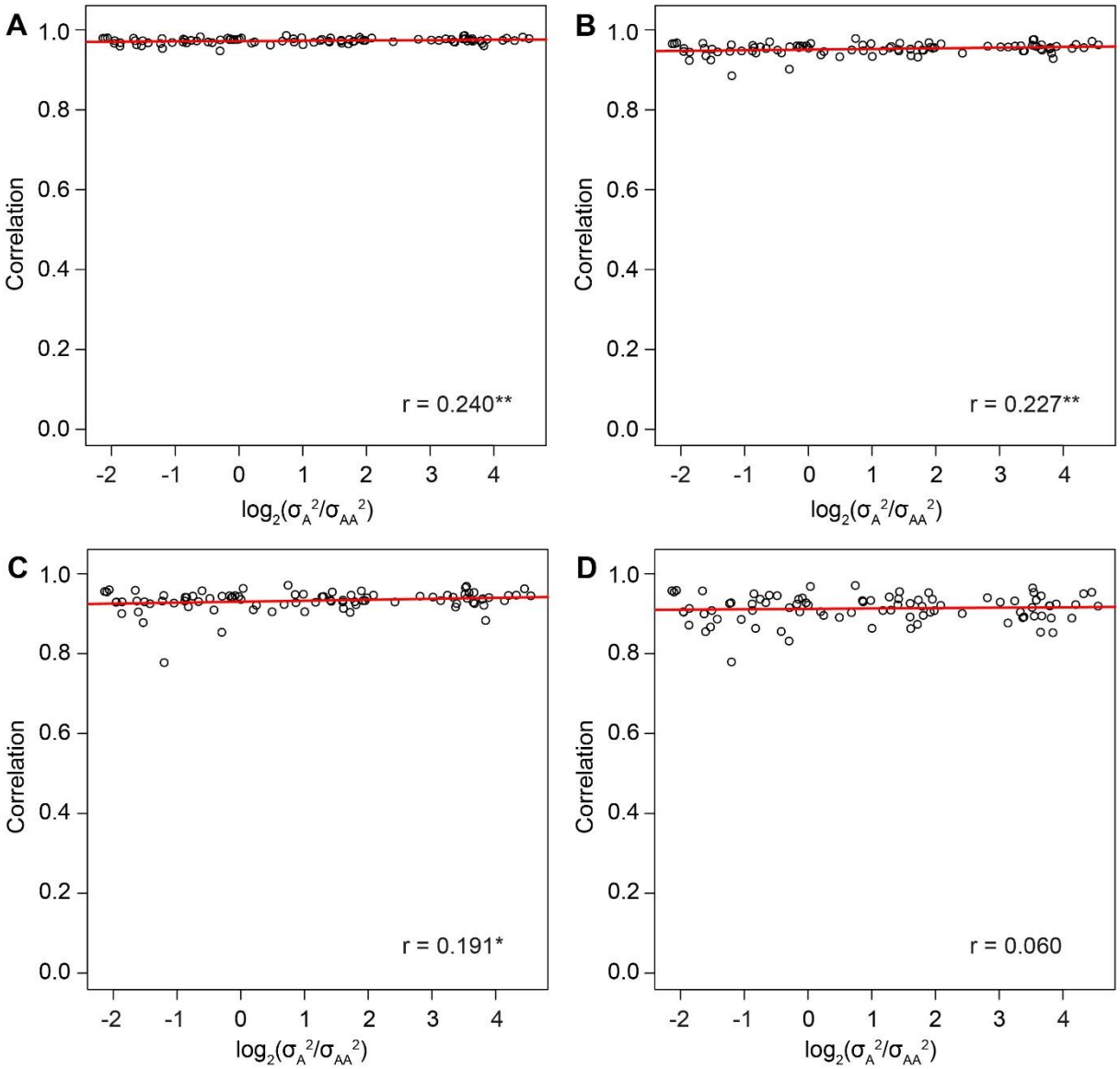

Figure S5. The correlations between the $-\log_{10}(p)$ values for the epistatic effects obtained using the Q+K and the Q+2K model in simulated data sets with $h^2 < 0.4$ and different σ_A^2/σ_{AA}^2 ratios. Each point in the figure represented the correlation between the $-\log_{10}(p)$ values from the two models calculated in a specific simulated data set. The overall correlation between the correlations and the $\log_2(\sigma_A^2/\sigma_{AA}^2)$ values across all data sets was displayed as the r value together with an indication of significance (*$p < 0.1$, ** $p < 0.05$, *** $p < 0.01$). A threshold of $-\log_{10}(p)$ values was applied to filter the marker pairs. Namely, only the marker pairs whose $-\log_{10}(p)$ values were above the threshold in at least one of the two models were considered. In different panels, distinct threshold values were applied: A) 1, B) 2, C) 3 and D) 4.

Supplemetary Tables

Table S1. The intervals defined for each simulated heritability (h^2) as a criterion to filter the simulated data sets. When the estimated value ($\hat{h}^2$) was contained in the corresponding interval, the simulated data set was kept.

Simulated value (h^2)	Interval for the estimation ($\hat{h}^2$)
0.1	(0.05, 0.15)
0.2	(0.15, 0.25)
0.3	(0.25, 0.35)
0.4	(0.35, 0.45)
0.5	(0.45, 0.55)
0.6	(0.55, 0.65)
0.7	(0.65, 0.75)
0.8	(0.75, 0.85)
0.9	(0.85, 0.95)

Table S2. The intervals defined for each simulated ratio of additive to additive-by-additive genetic variance (σ_A^2/σ_{AA}^2) as a criterion to filter the simulated data sets. When the estimated value ($\hat{\sigma}_A^2/\hat{\sigma}_{AA}^2$) was contained in the corresponding interval, the simulated data set was kept.

Simulated value (σ_A^2/σ_{AA}^2)	Interval for the estimation ($\hat{\sigma}_A^2/\hat{\sigma}_{AA}^2$)
0.25	(0.125, 0.375)
0.5	(0.375, 0.75)
1	(0.75, 1.5)
2	(1.5, 3)
4	(3, 6)
8	(6, 12)
16	(12, 24)