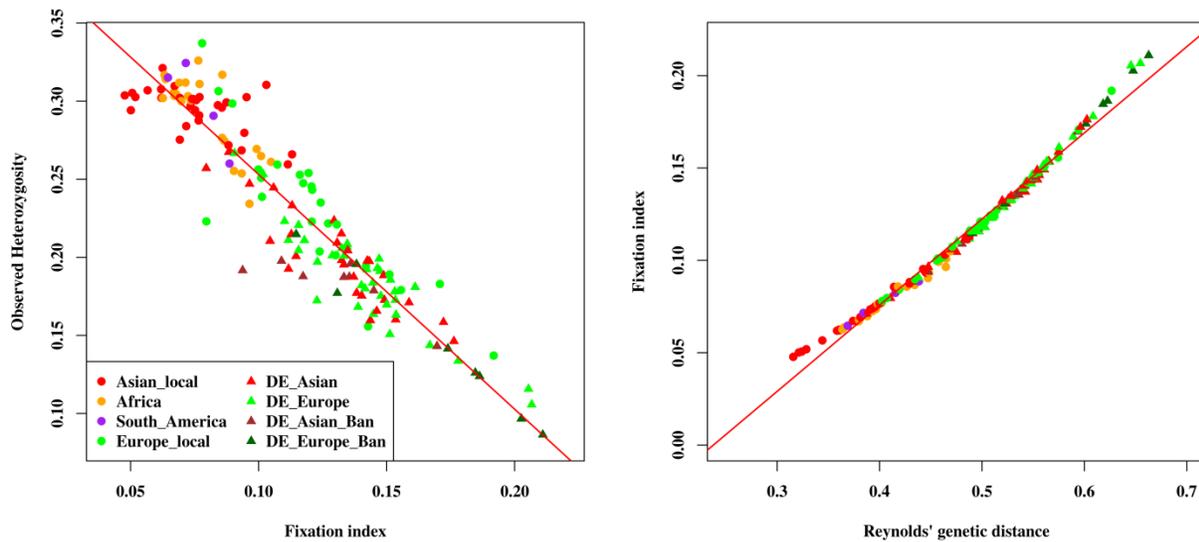
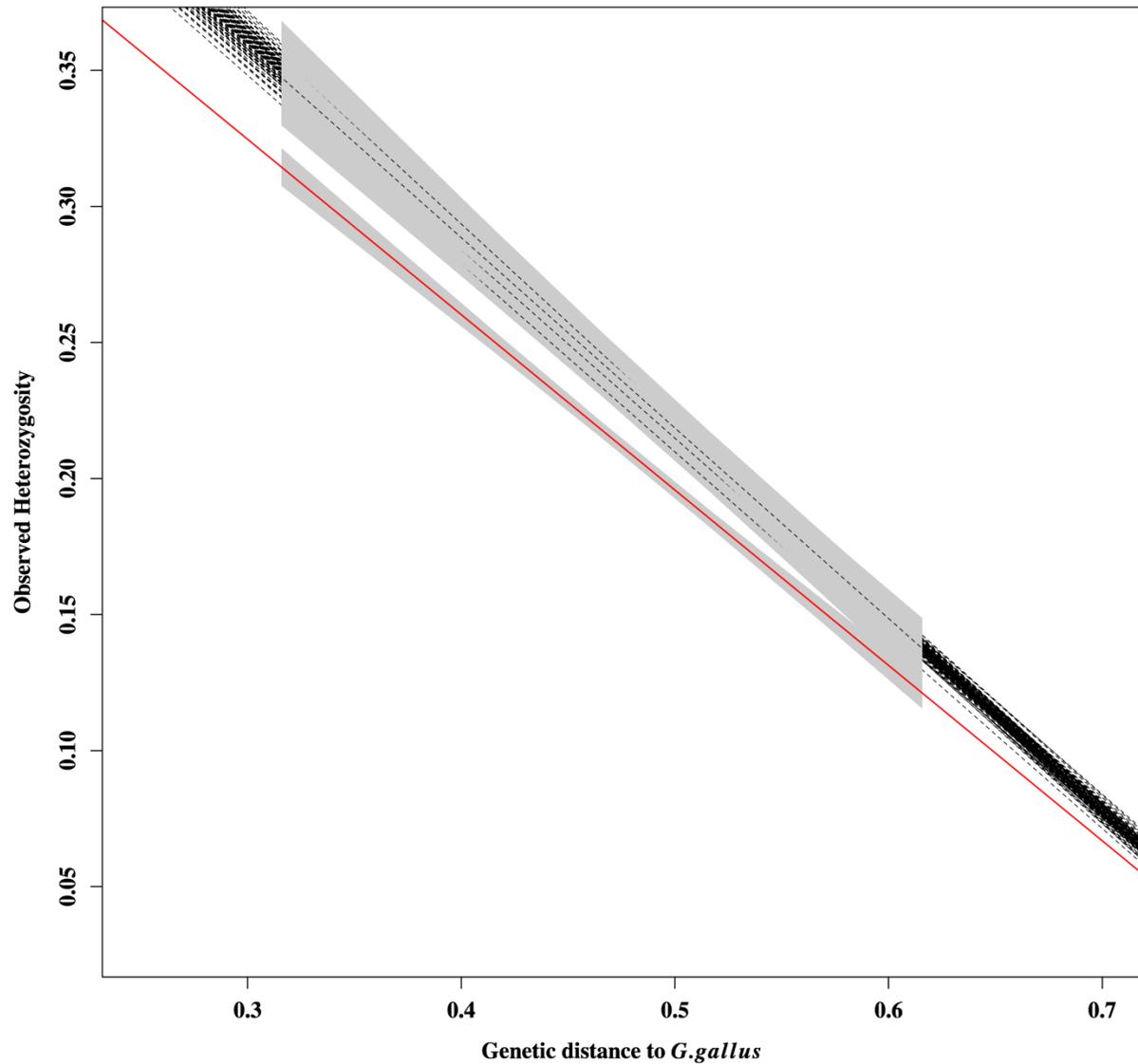


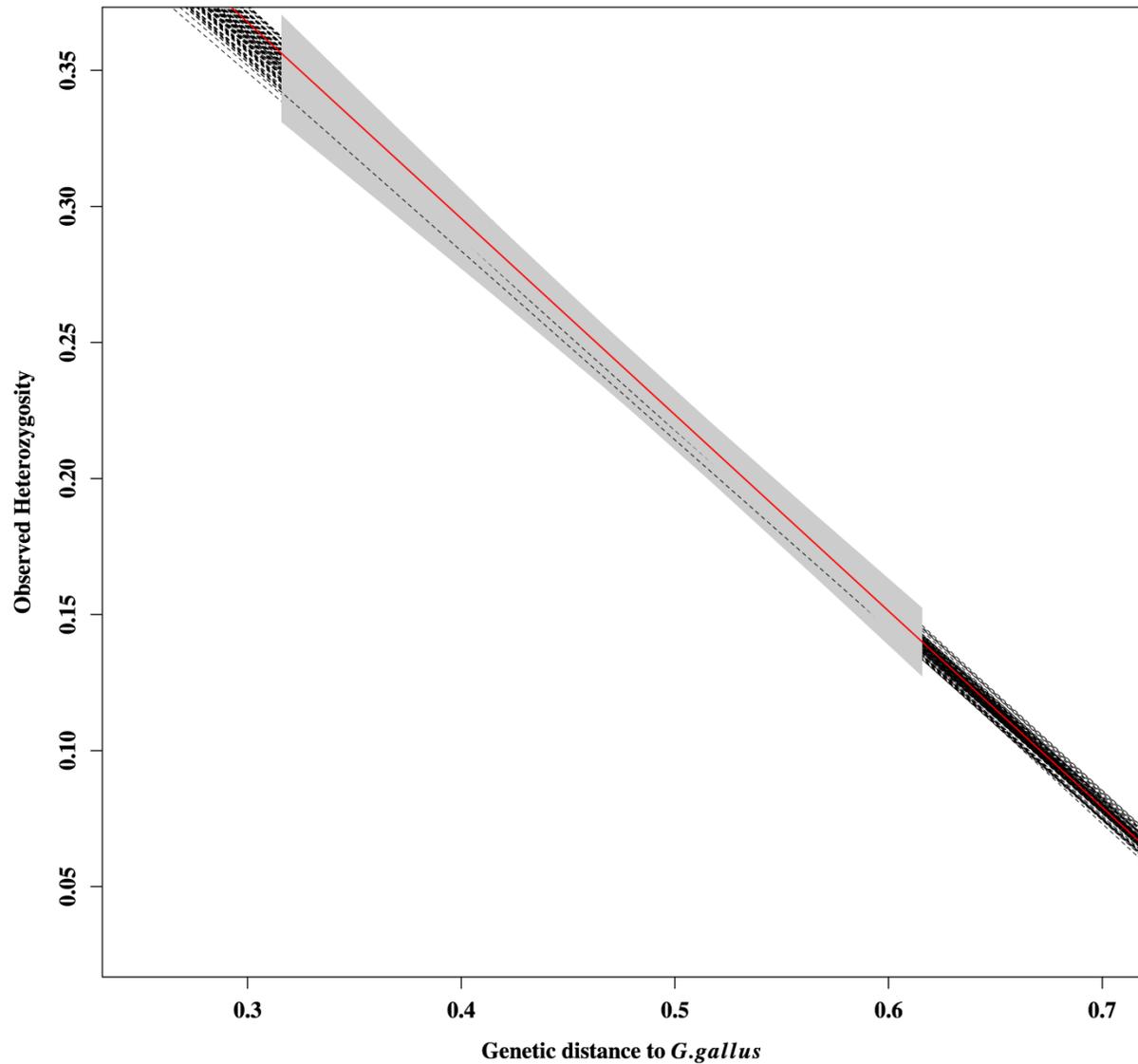
**Figure S1** Observed heterozygosity vs. Reynolds' genetic distance to the *Gallus gallus* estimated from 1000 SNP samples in 100 replicates. The dashed lines represent the 100 sample sets and the gray area shows a 95% confidence interval.



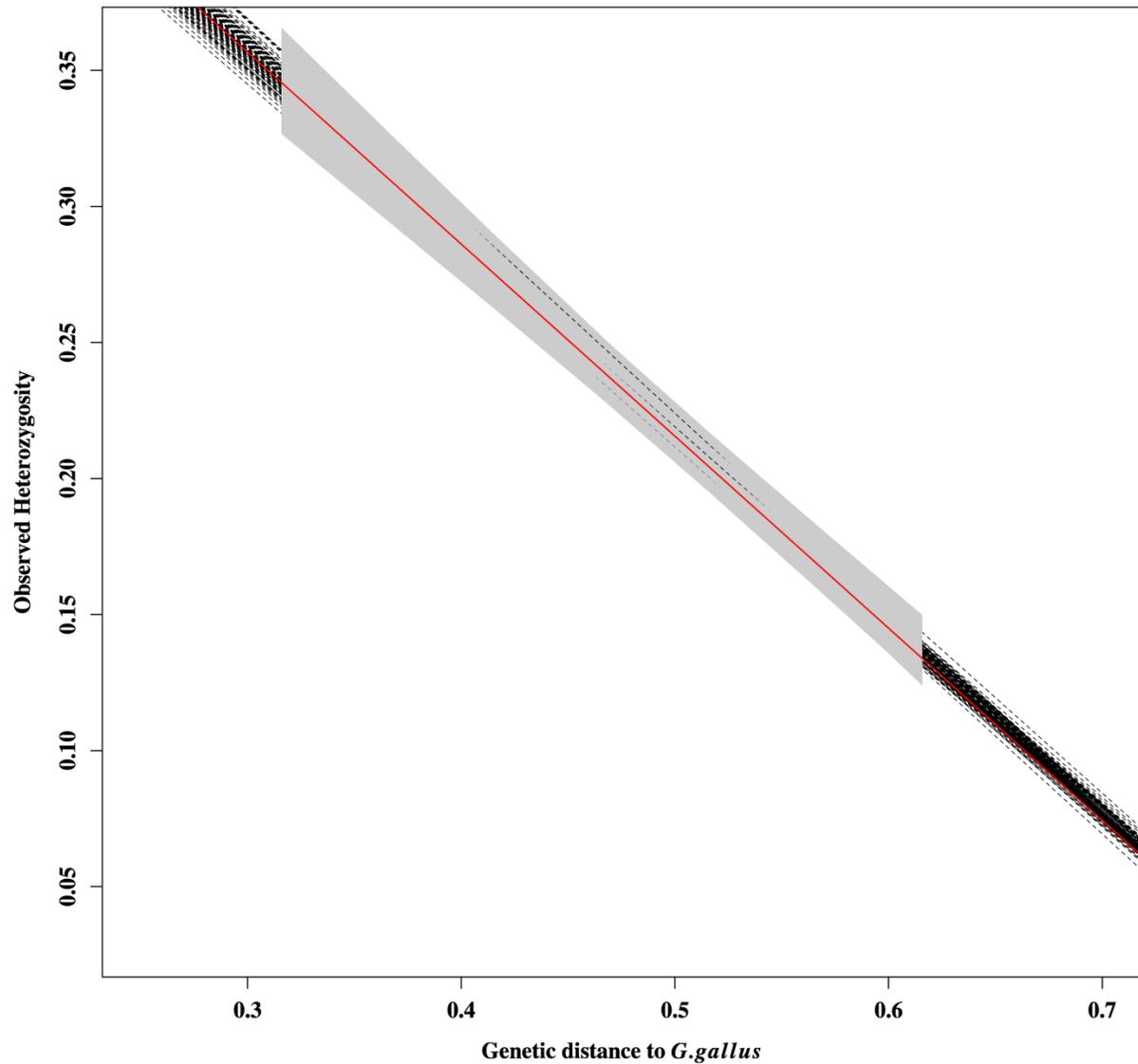
**Figure S2 Title: Relationship between the observed heterozygosity and genetic differentiation ( $F_{ST}$ ) from *G. gallus* (left), and the relationship between  $F_{ST}$  and Reynolds' genetic distance to *G. gallus* (right).** The regression lines of the relationships are drawn in red. The  $R^2$  is equal to 0.885 and 0.988, for the left and right figures, respectively. Different breed categories are denoted in different colors and/or shapes.



**Figure S3 Comparison of the relationship between the genetic distance to *G. gallus* and the observed heterozygosity estimated from the non-synonymous class vs. 100 random samples of the same number of SNPs as the non-synonymous class from the overall SNPs. The black dotted lines represent estimations with the overall SNPs, the red solid line represents the non-synonymous SNPs. The shaded areas represent the 95% confidence intervals of the regression lines. The mean  $R^2$  of the 100 samples is 0.880 and the mean slope is -0.708.**



**Figure S4 Comparison of the relationship between the genetic distances to *G. gallus* and the observed heterozygosity estimated from intronic SNPs vs. the overall set.** The black dashed lines represent estimations with the 100 replicates of 1000 randomly samples SNPs from the intronic SNPs and the red solid line represents overall SNPs. The 95% confidence intervals are shaded in gray. The mean  $R^2$  and slope of the 100 samples are 0.880 and -0.711, respectively.



**Figure S5 Comparison of the relationship between the genetic distance to *G. gallus* and the observed heterozygosity estimated from intergenic SNPs vs. the overall set.** The black dashed lines represent estimations with the 100 replicates of 1000 randomly sampled SNPs from the intergenic SNPs and the red solid line represents overall SNPs. The 95% confidence intervals are shaded in gray. The mean  $R^2$  and slope of the 100 samples are 0.878 and -0.701, respectively.