

Supplementary Tables and Figures

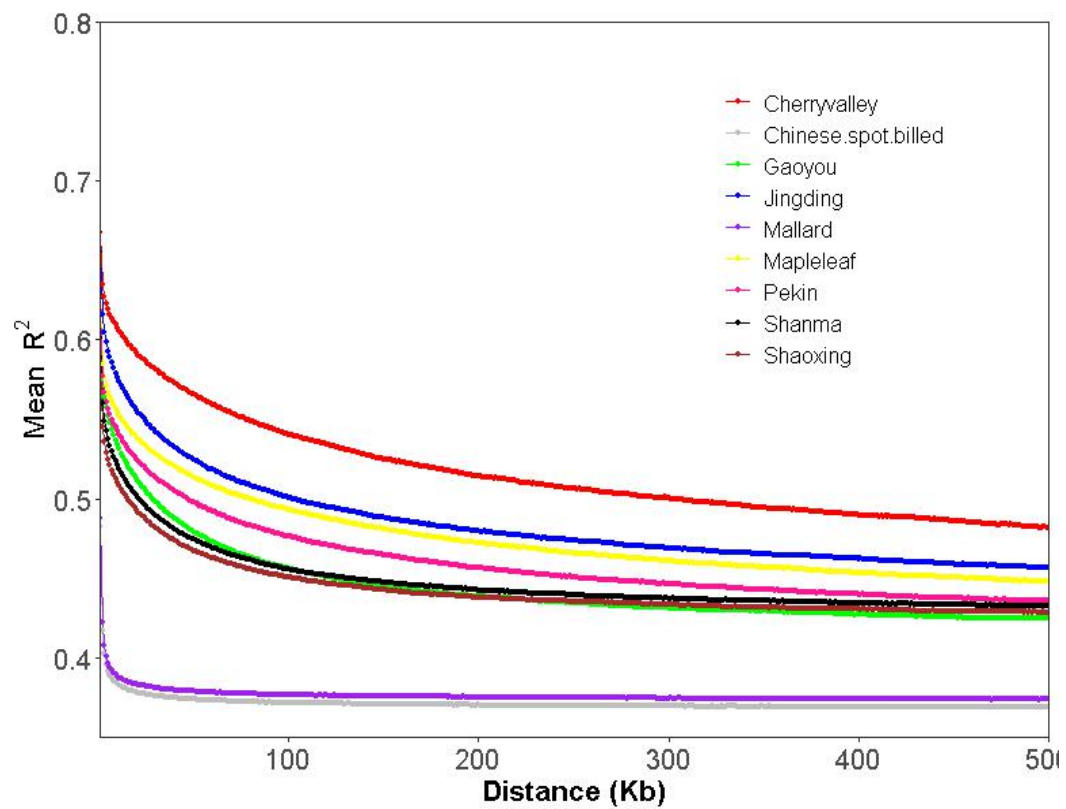
Supplementary Table S1. Summary of genomic data for 118 ducks.

Supplementary Table S2. D-statistics for D (Muscovy duck, mallard; P1, P2) or D (Muscovy duck, Chinese spot-billed duck; P1, P2). P1 and P2 represent different domestic duck groups. $Z < -3$ indicates admixture between mallards or Chinese spot-billed ducks and P1.

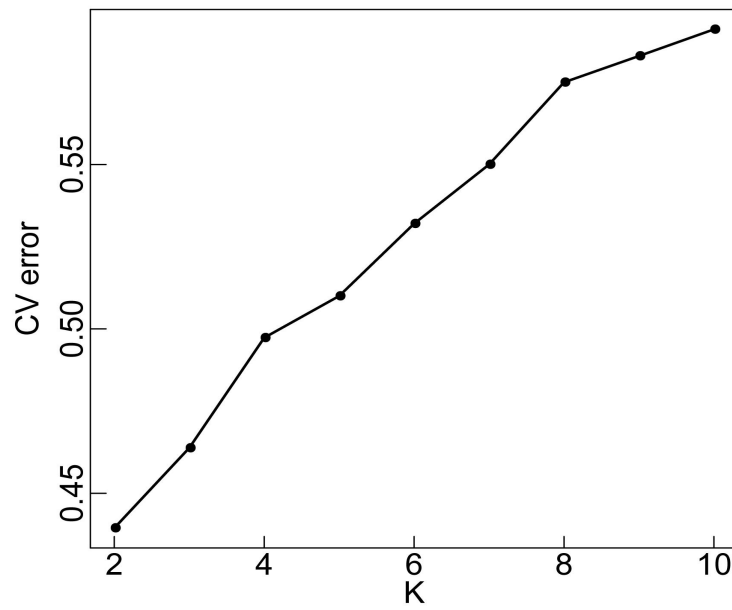
Supplementary Table S1, S2 are listed as a separate file due to their large size.



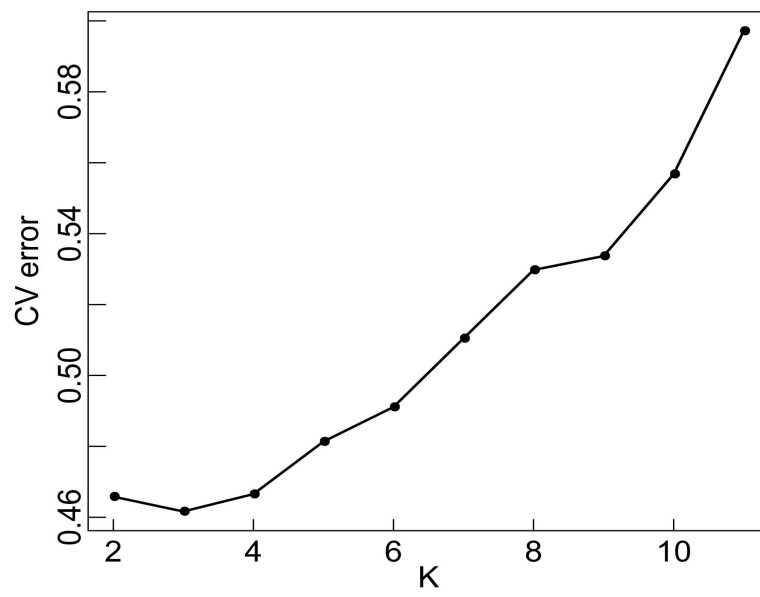
Supplementary Figure S1. Geographic distribution of samples used in this study.



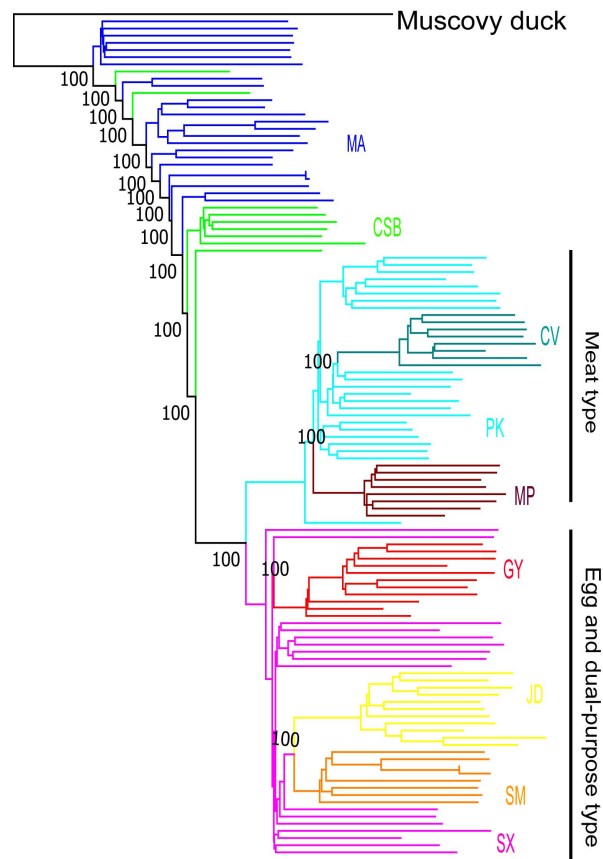
Supplementary Figure S2. LD decay determined by squared correlations of allele frequencies (R^2) against distance between polymorphic sites.



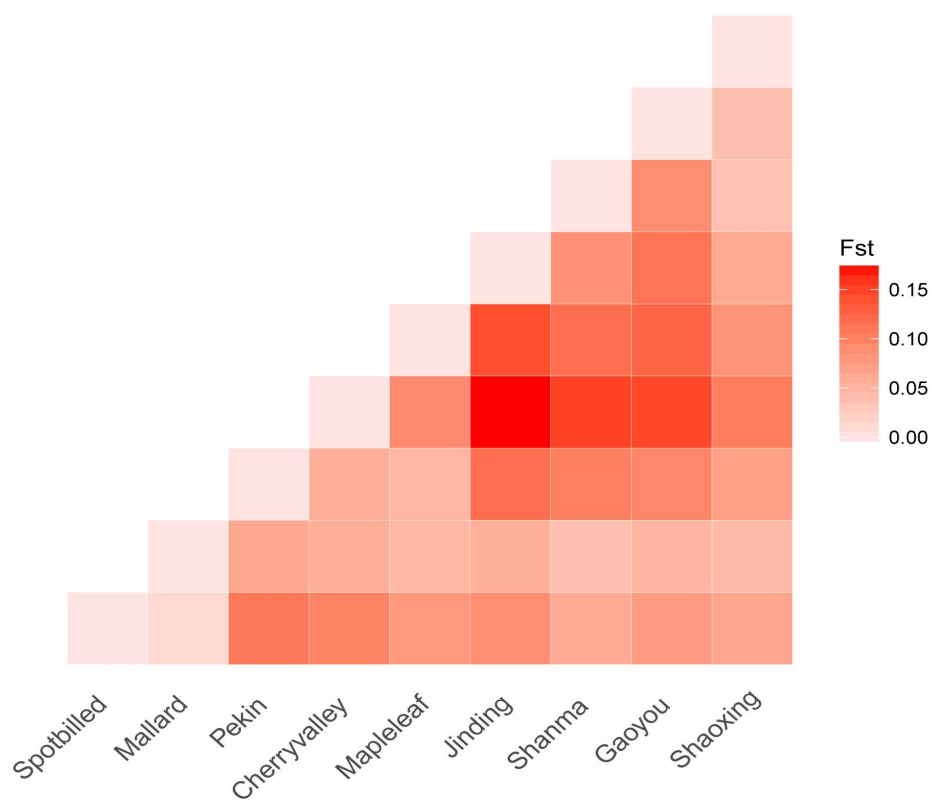
Supplementary Figure S3. CV error for ADMIXTURE analysis of two wild duck species. K values ranged from 2 to 10. K=2 is best.



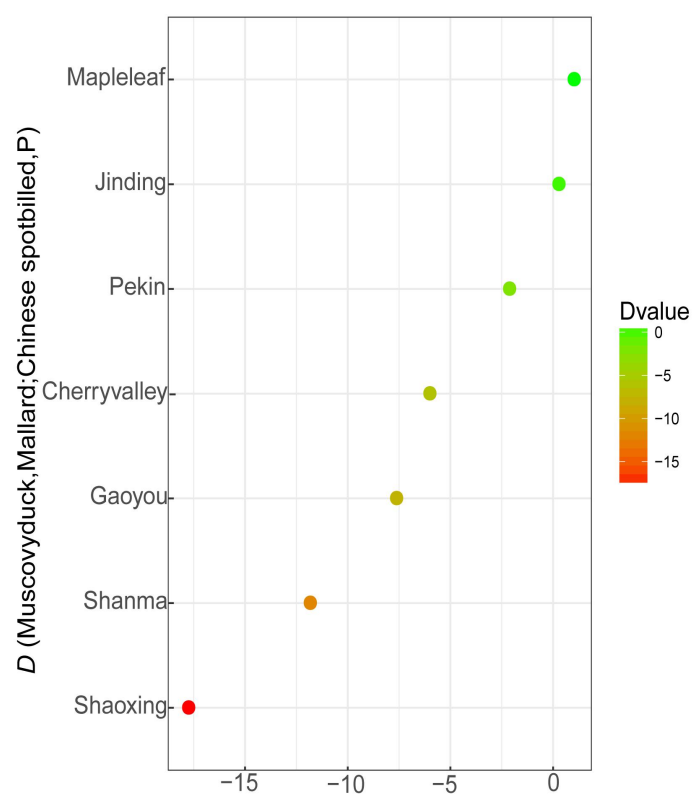
Supplementary Figure S4. CV error for ADMIXTURE analysis of 117 ducks. K values ranged from 2 to 11. K=3 is best.



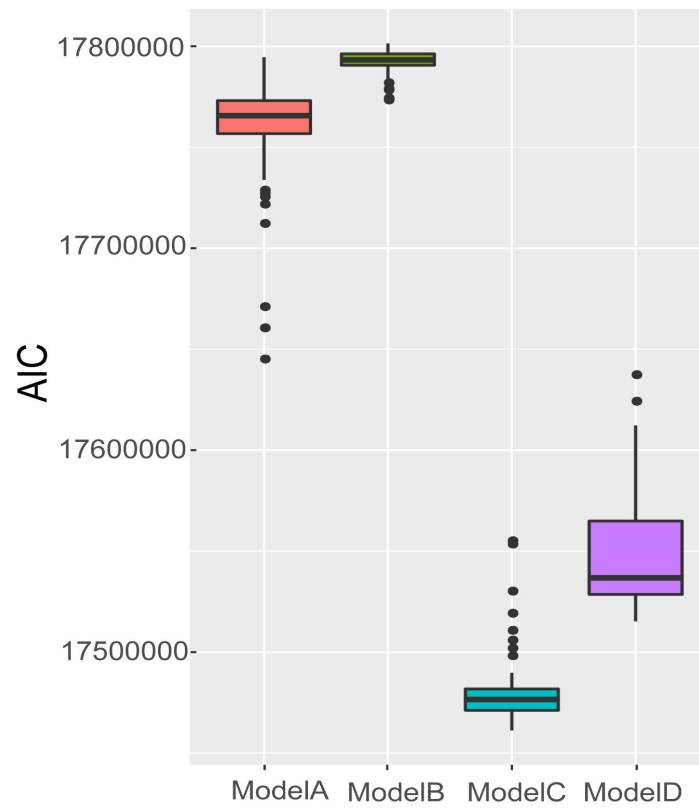
Supplementary Figure S5. Phylogenetic trees constructed using neighbor-joining method based on variants along autosomes. MA, mallard; CSB, Chinese spot-billed; PK, pekin; CV, cherry valley; MP, maple leaf; GY gaoyou; JD, jinding; SM; shanma; SX, shaoxing.



Supplementary Figure S6. F_{ST} for all possible pairwise combinations of nine duck populations.



Supplementary Figure S7. D-statistics for D (Muscovy duck, Mallard; Chinese spot-billed duck, P). $Z < -3$ indicates admixture between mallards and Chinese spot-billed ducks.



Supplementary Figure S8. Boxplot of AIC values for four demographic scenarios (Model C is best).