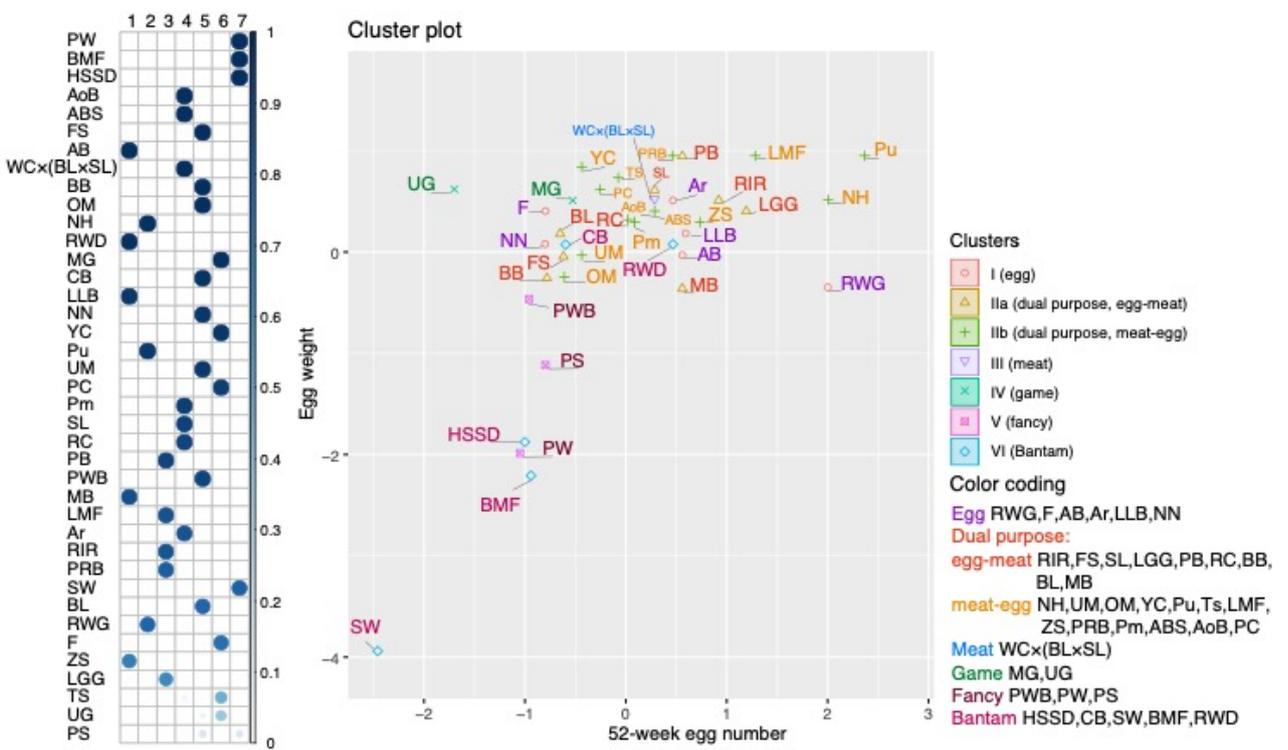
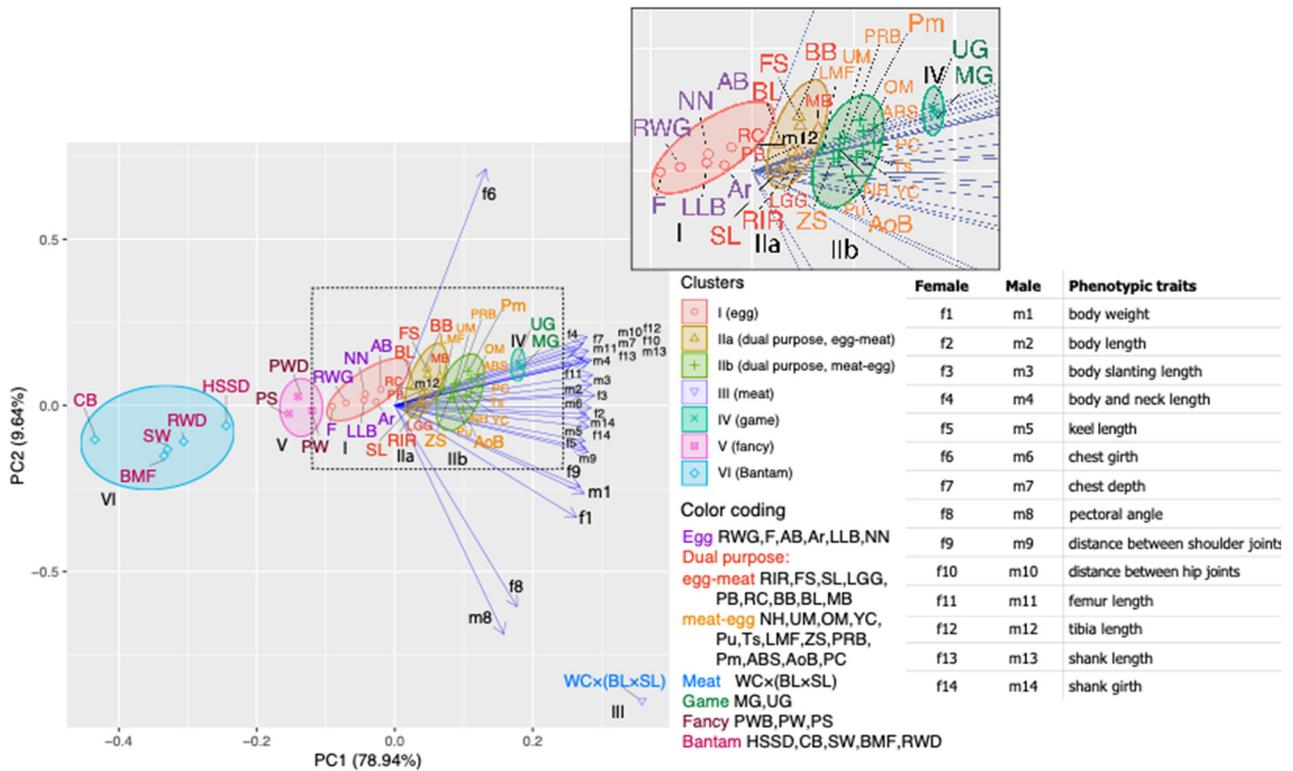


(a)

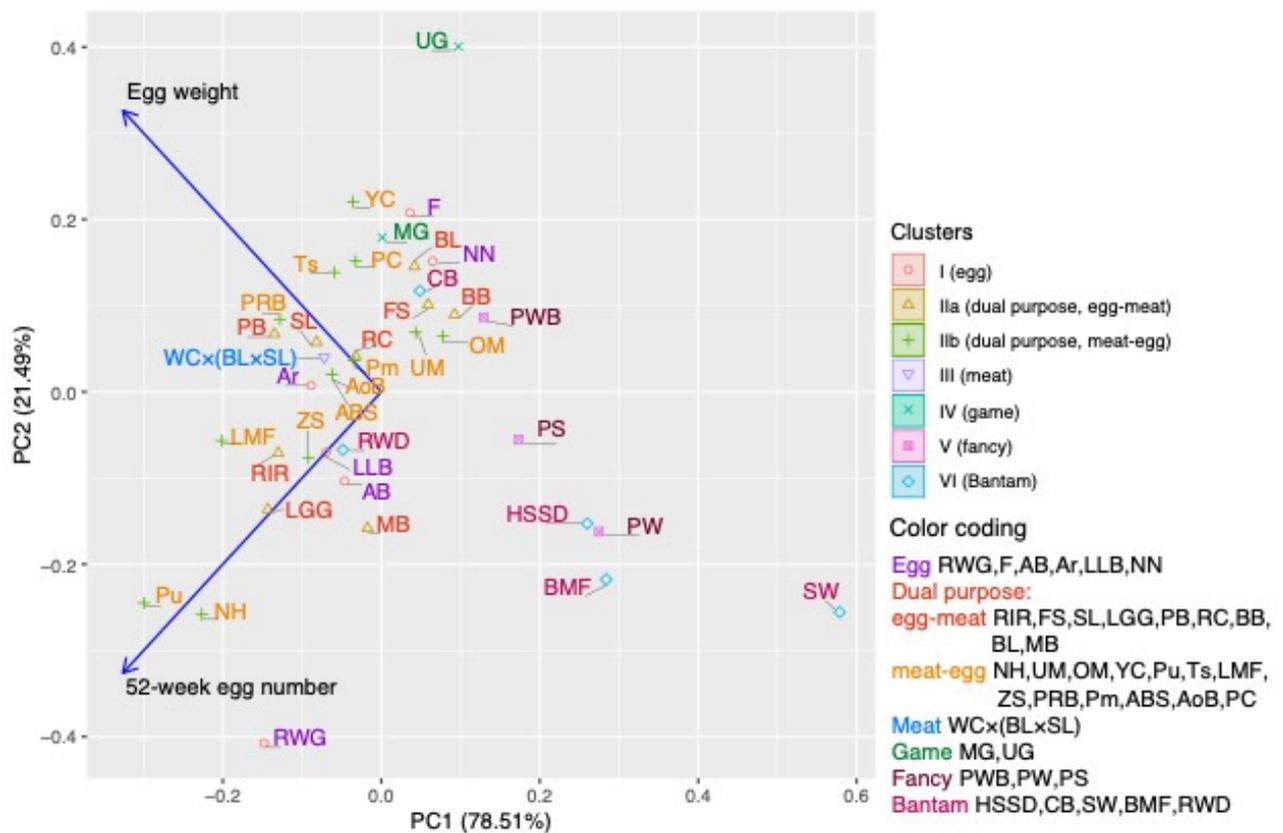


(b)

Figure S1. Fuzzy Analysis Clustering-based plots showing the distribution of the 39 phenotyped breeds/populations and built using (a) morphometric traits and (b) egg production traits. Clustering pattern in the graph (a) basically repeats PCM (Figure 1a), and that in the graph (b) has a number of differences as compared to PCM. Population abbreviations are given according to Table S1.

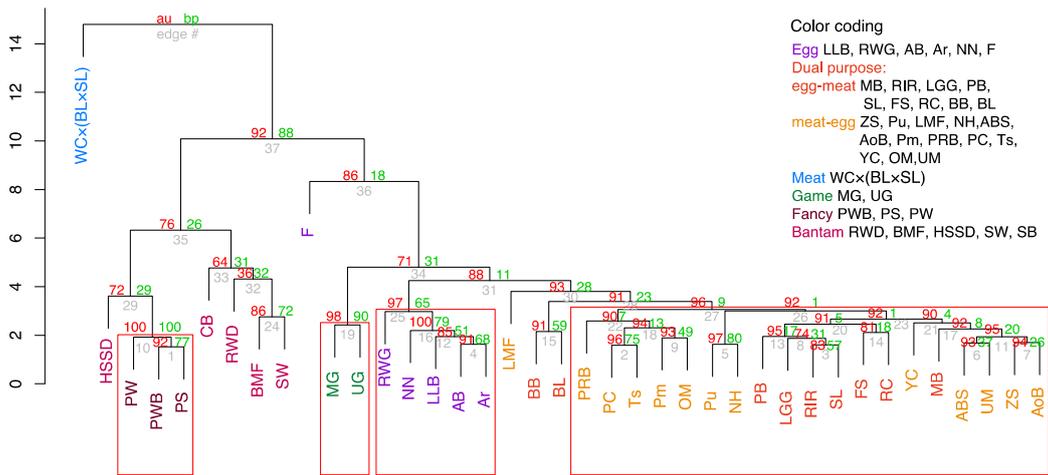


(a)

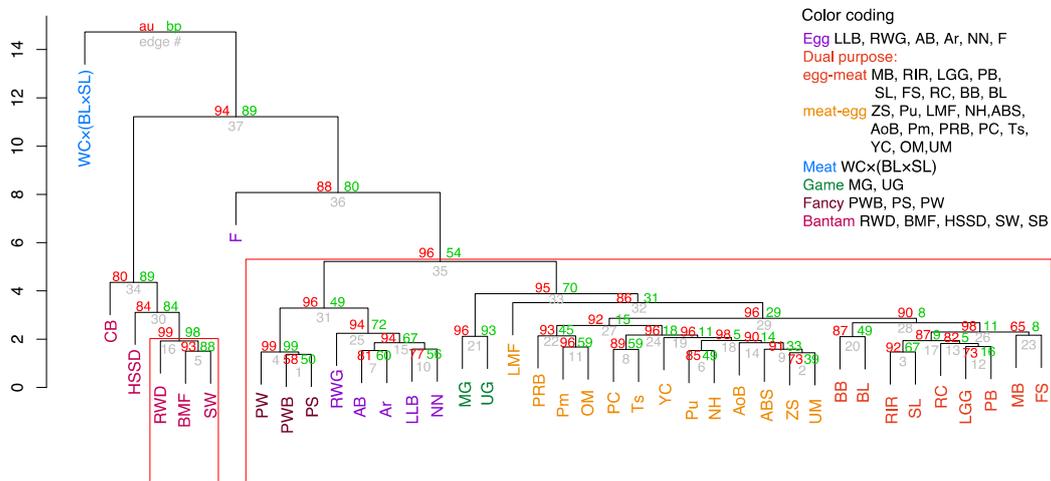


(b)

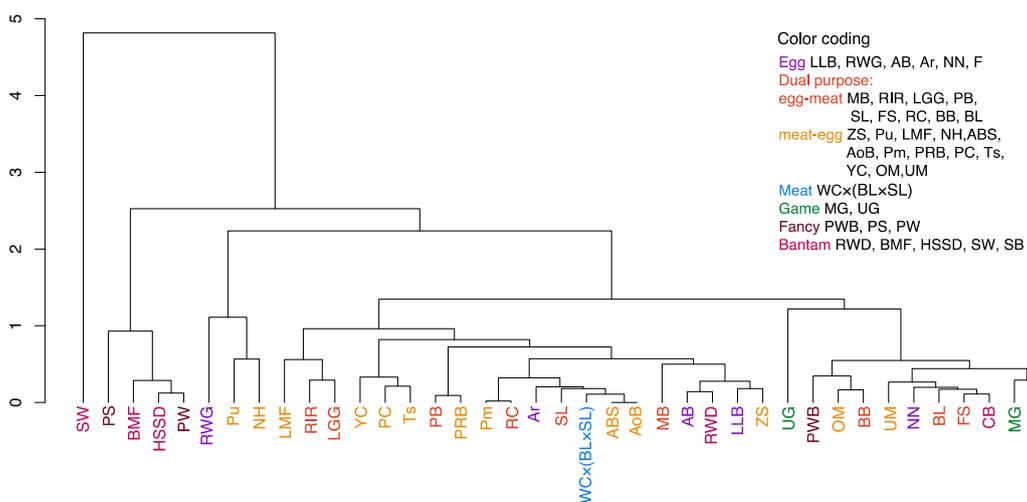
Figure S2. PCA plots showing the distribution of the 39 phenotyped breeds/populations and built using (a) morphometric traits and (b) egg production traits. Clustering pattern in the graph (a) basically repeats PCM (Figure 1b), and that in the graph (b) has a number of differences as compared to PCM. Population abbreviations are given according to Table S1.



(a)

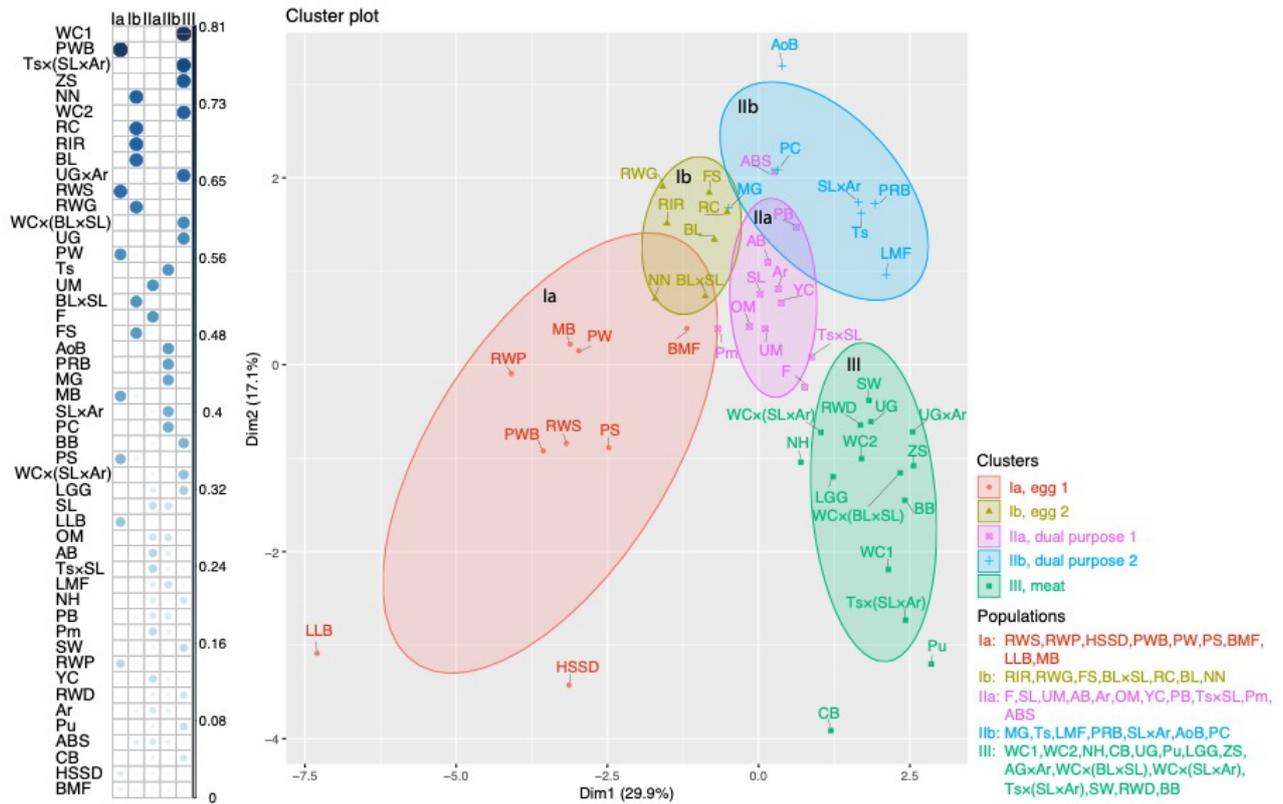


(b)

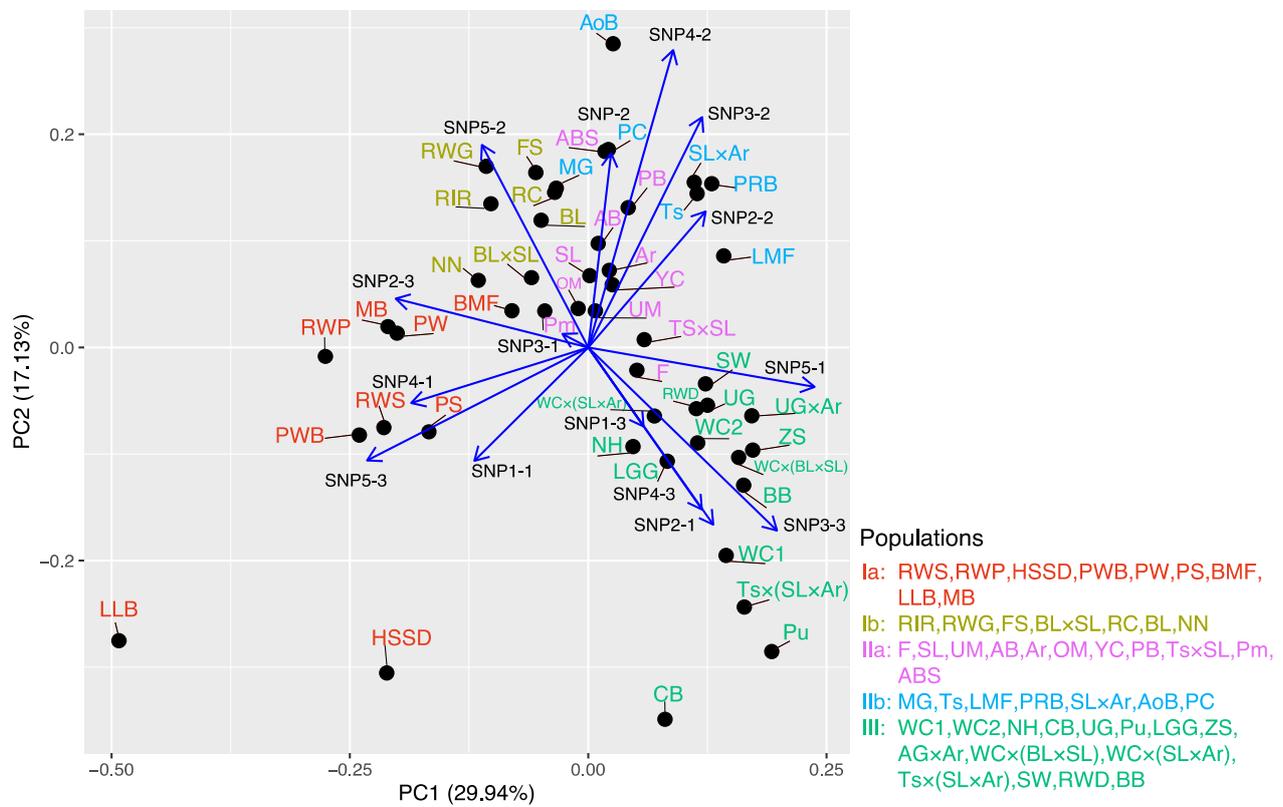


(c)

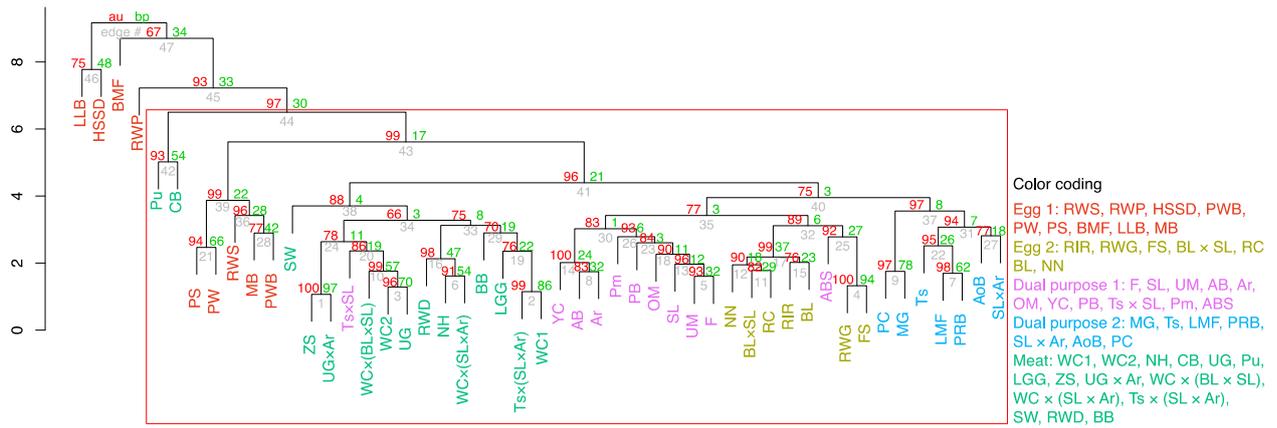
Figure S3. Plots of phylogenetic UPGMA-based trees constructed in comparison with PCM (shown via color coding) and using Euclidean distances for different sets of phenotypic traits: (a) all, (b) morphometric, and (c) egg production traits. A number of discrepancies in clustering patterns for the 39 phenotypic chicken breeds/populations were noted as compared to PCM (Figures 1, S2a and S3a). Population abbreviations are given according to Table S1.



(a)



(b)



(c)

Figure S4. Clustering plots for the 49 chicken breeds/populations based on their genotypes in the five SNPs at the *NCAPG-LCORL* locus and produced using (a) Fuzzy Analysis Clustering, (b) PCA, and (c) an UPGMA-assisted tree using Euclidean metrics. The clustering pattern seen in the graphs (a) and (b) forms the basis of GCM1 (genotypic clustering model 1), while that in the graph (c) has a number of differences as compared to GCM1 (shown via color coding) and was designated GCM2. Population abbreviations (a,b) and abbreviations (c) are given according to Table S1.

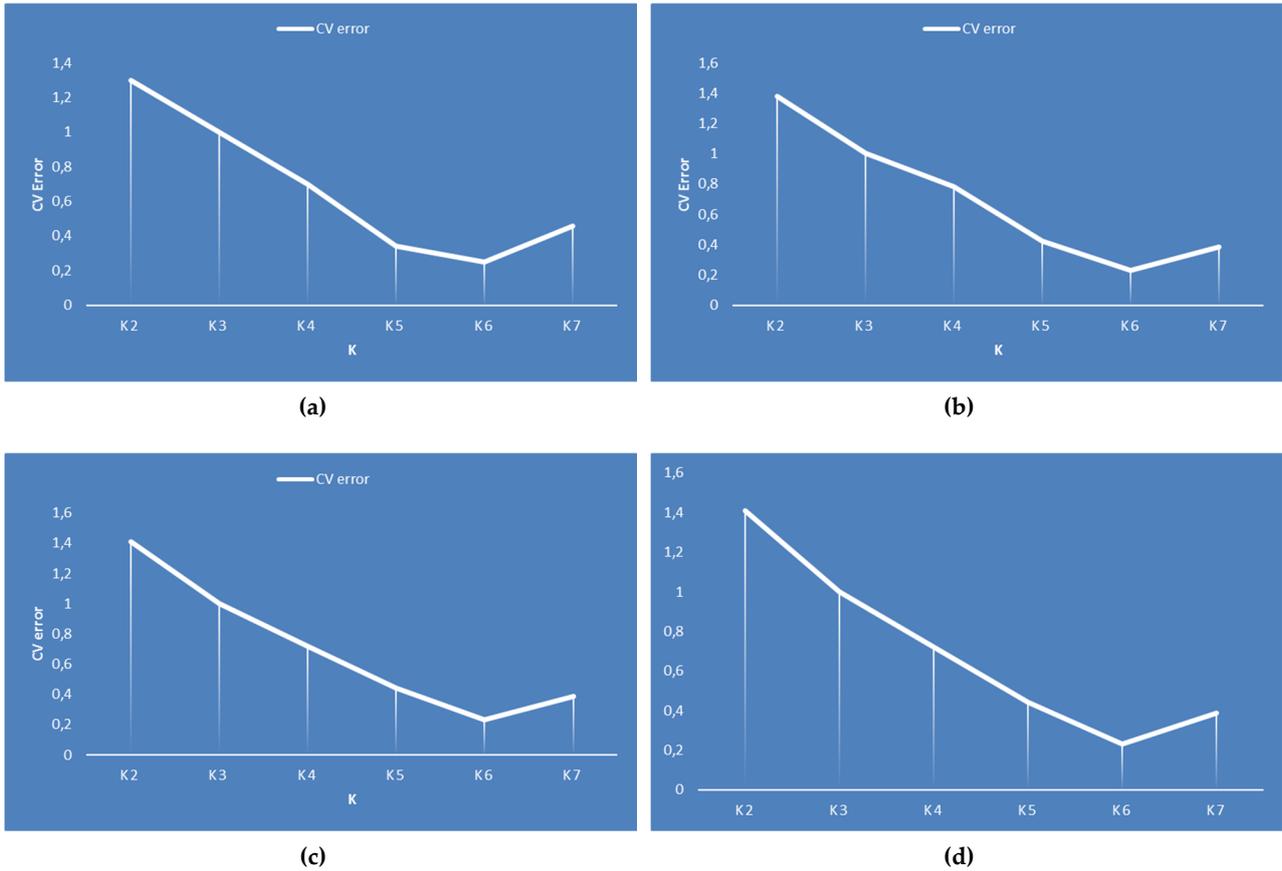
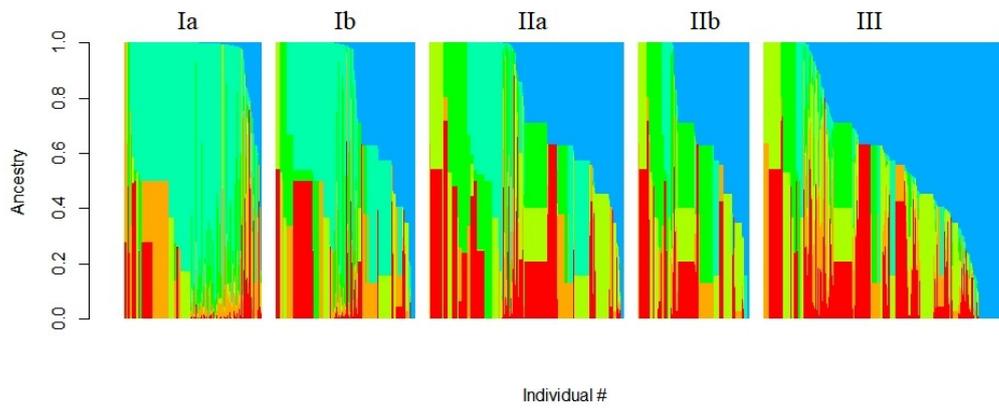
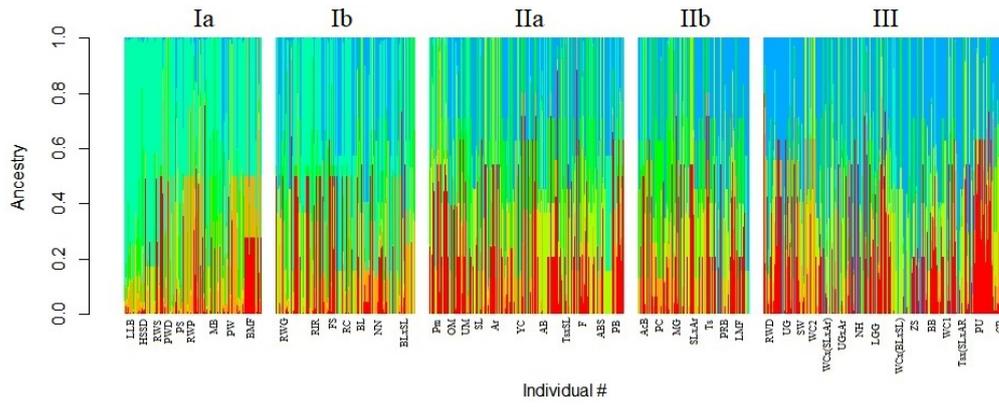
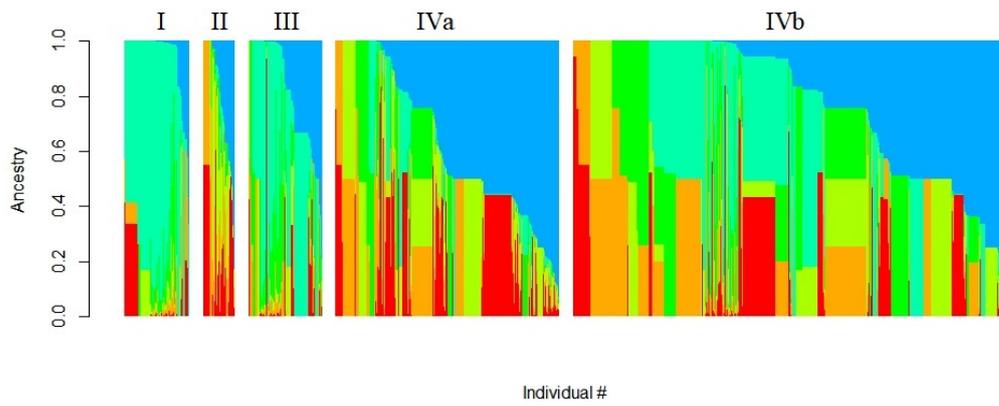
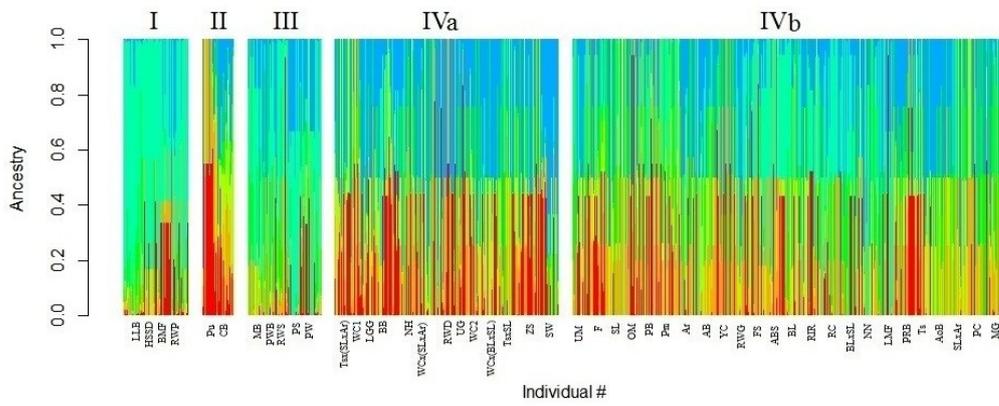


Figure S5. Number of ancestral populations using genotypes in the five SNPs at the *NCAPG-LCORL* locus for the 49 genotyped chicken breeds/populations and applying different clustering models: **(a)** TCM, $K = 6$, at minimal cross-validation (CV) error (0.2481); **(b)** PCM, $K = 6$, at minimum CV error (0.2294); **(c)** GCM1, $K = 6$, at minimum CV error (0.2319); and **(d)** GCM2, $K = 6$, at minimum CV error (0.2223). Each plot shows CV errors (Y-axis) for different K-values (X-axis) and was generated using the ADMIXTURE program.



(c)



(d)

Figure S6. Population structure based on the genetic variability in the 49 genotyped chicken breeds/populations for five SNP markers at the *NCAPG-LCORL* locus and produced by Bayesian clustering using the ADMIXTURE program (as visualized in color in R v.4.1.0). Each admixture plot represents a cluster structure of the studied population groups relative to the respective clustering (classification) models and the appropriate number of clusters within a model: (a) TCM, (b) PCM, (c) GCM1, and (d) GCM2. Each clustering (classification) model is shown in two versions, with populations within a cluster being unsorted (upper plot) and sorted by color (lower plot). Population abbreviations are given according to Table S1. Population RWD, a dwarf broiler breeder strain, was arbitrarily moved in TCM (a) to the DPB/MEB class since it does not actually look like a typical MTB.

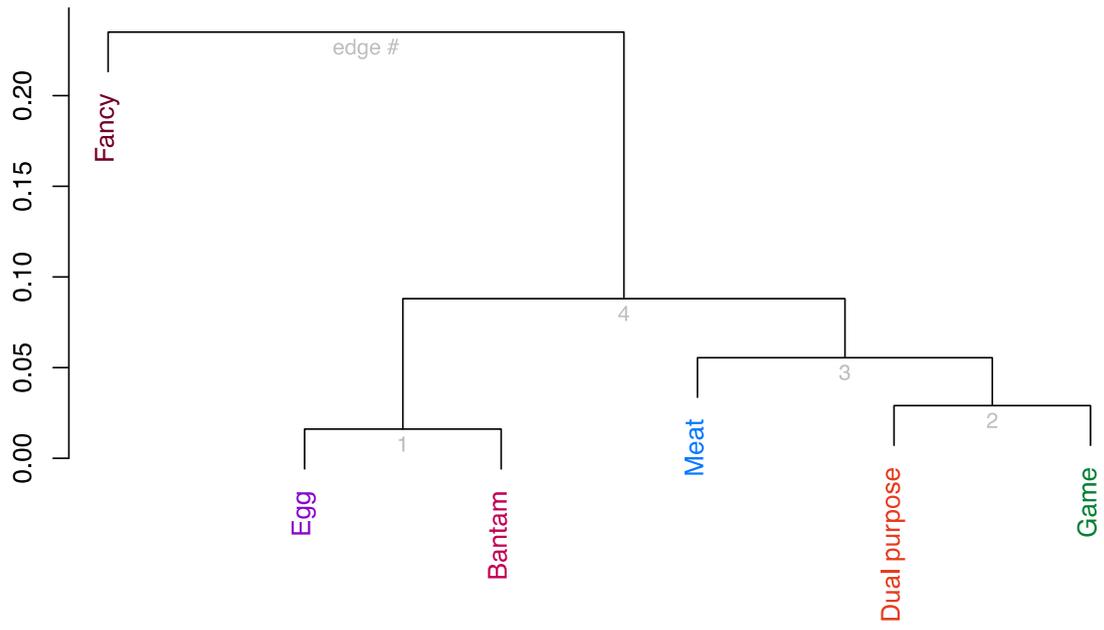


Figure S7. An UPGMA-based tree using Euclidean distances for six chicken breed clusters according to PCM and based on genotype frequencies in the five SNPs at the *NCAPG-LCORL* locus among the 49 genotyped chicken breeds/populations.