

Supplemental Information for:

Assessing population structure and migration patterns of wild boar (*Sus scrofa*) in Japan

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Supplementary Figures:

Supplementary Figure 1 - Results of parameter using in discriminant analysis of principal components (DAPC).

Supplementary Figure 2 - Results of discriminant analysis of principal components (DAPC) analysis.

Supplementary Figure 3 - EEMS output.

Supplementary Figure 4 - Prefectures and regions of Japan used in this study.

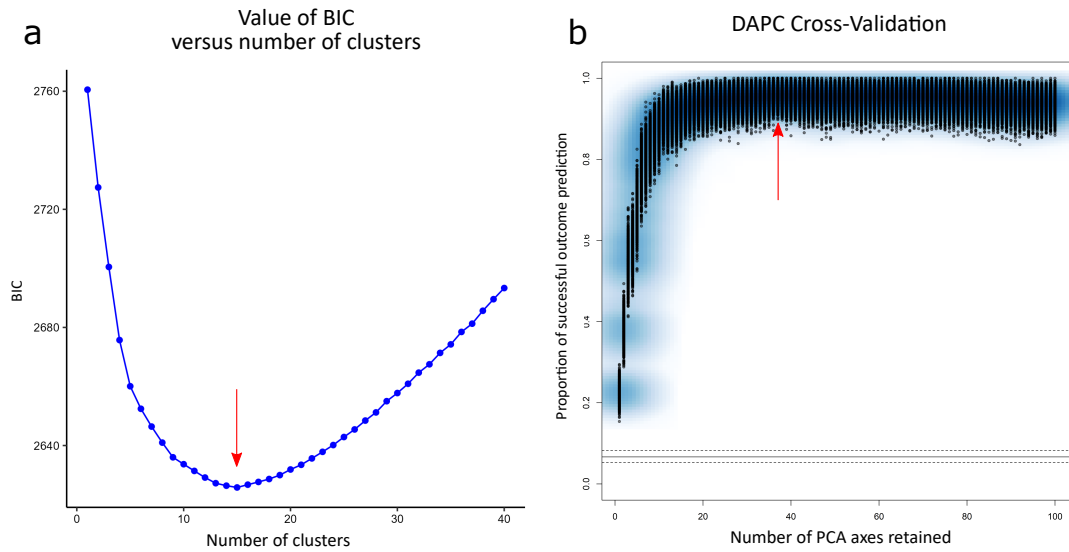
Supplementary Data:

Supplementary Data 1 - Results of linkage disequilibrium expressed as standardised index of association, measured with 999 resampling using the poppr package in R.

Supplementary Data 2 - Summary of locus characteristics of 29 microsatellites of wild boar in Japan.

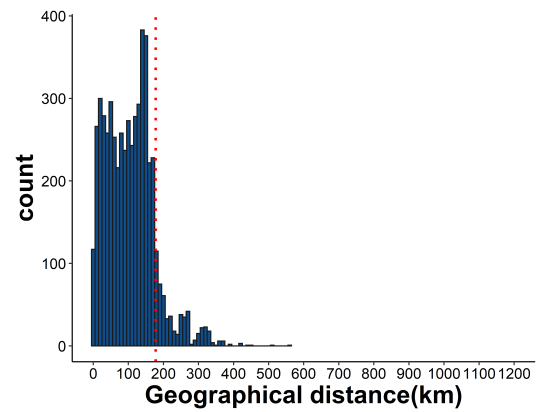
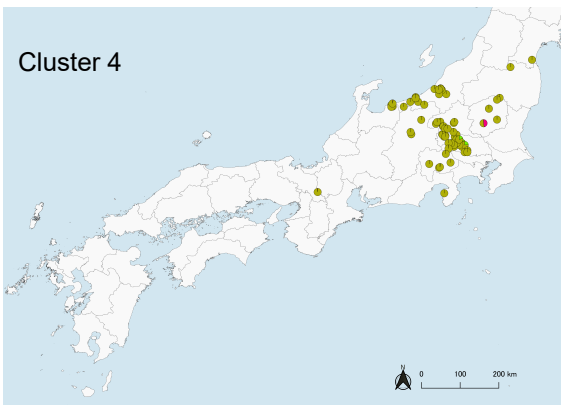
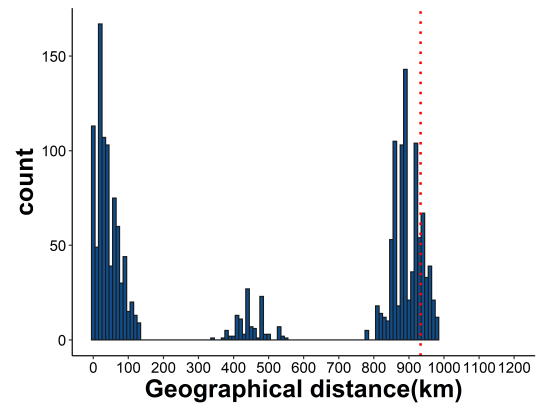
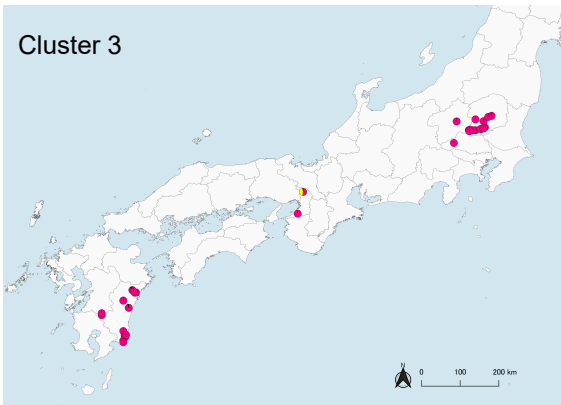
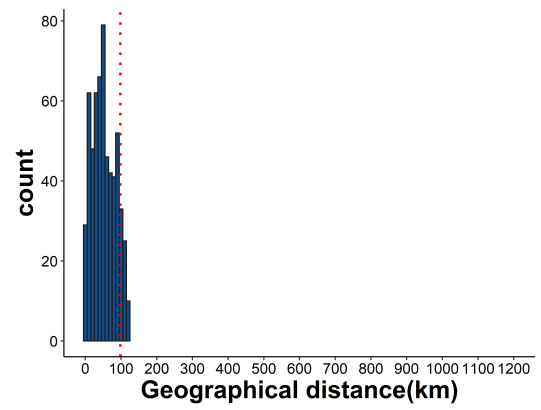
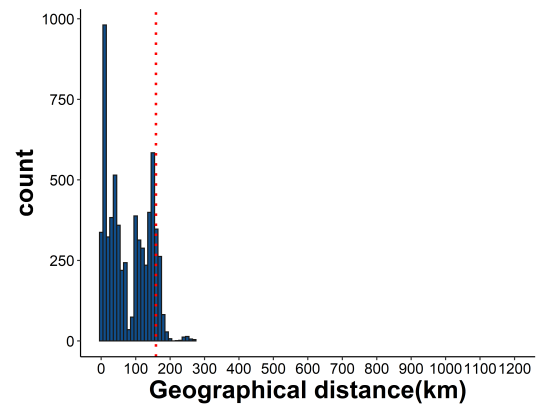
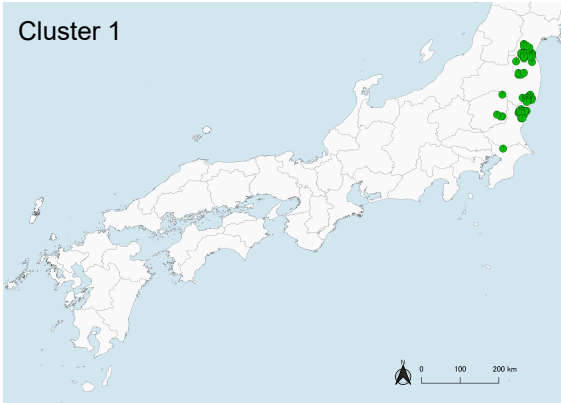
Supplementary Data 3 - Allele values of wild boar collected between 2014 and 2020 in Japan.

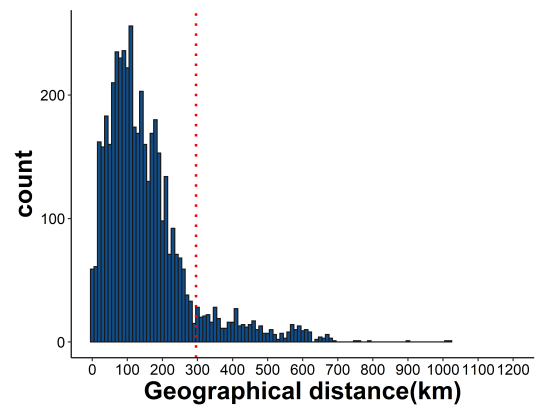
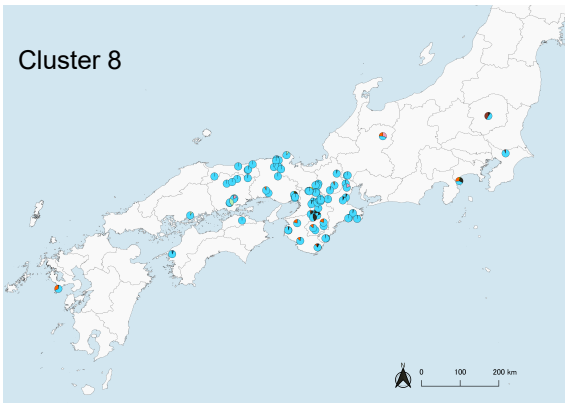
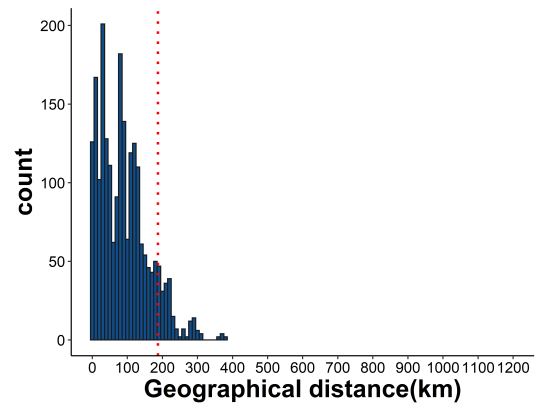
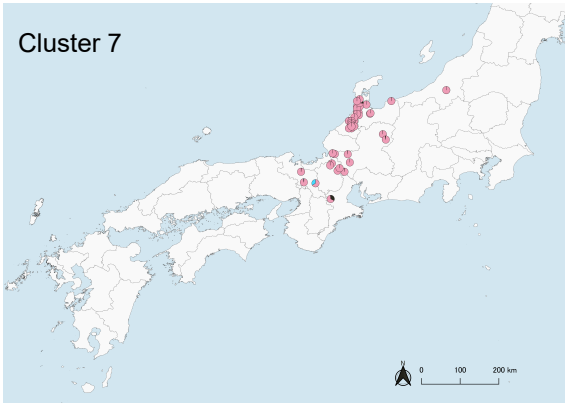
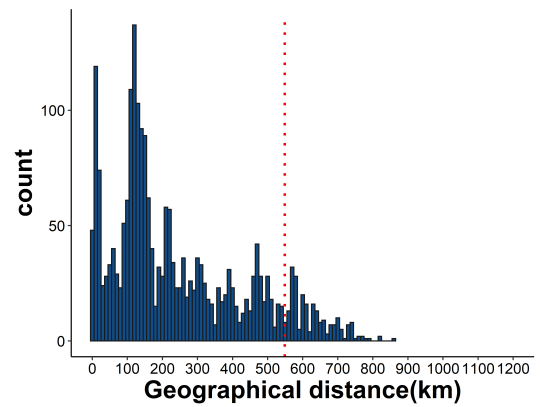
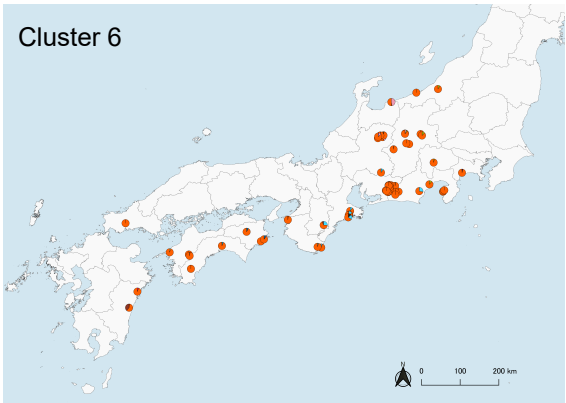
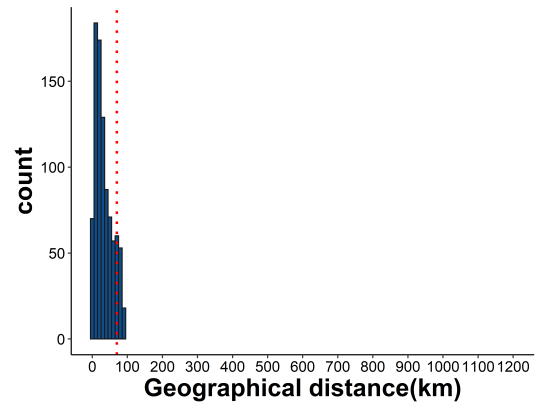
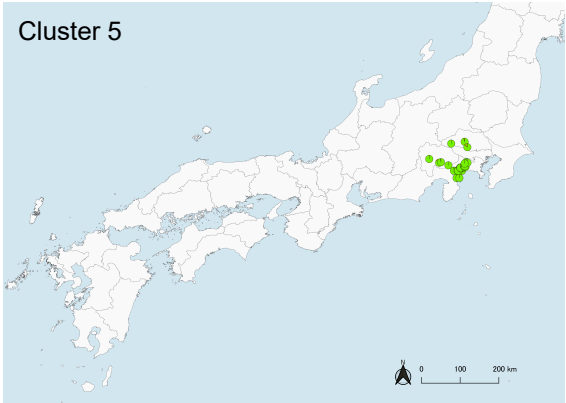
Supplementary Data 4 - List of 30 microsatellite markers.

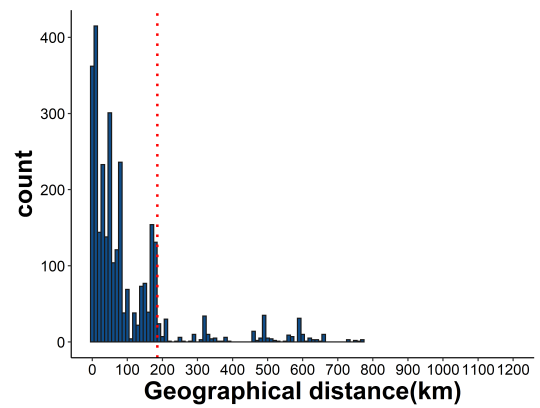
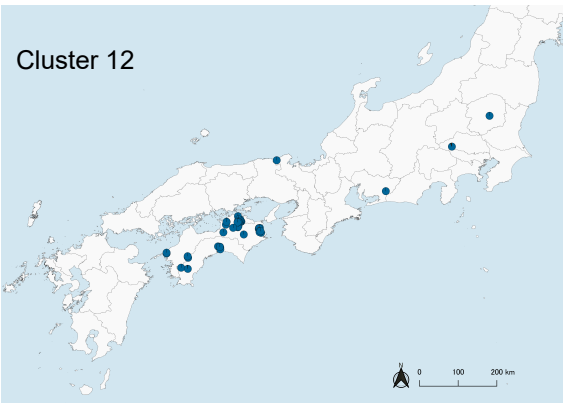
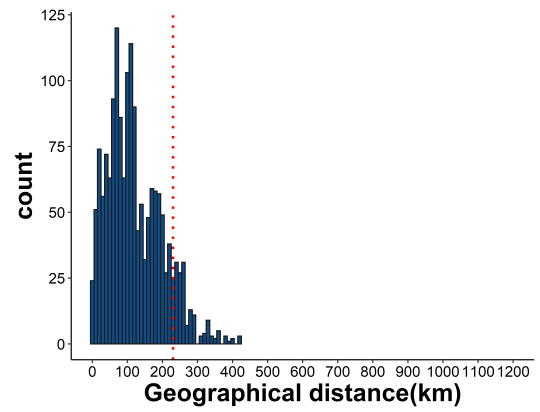
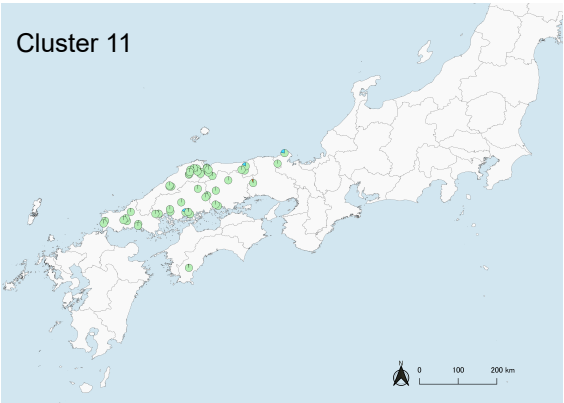
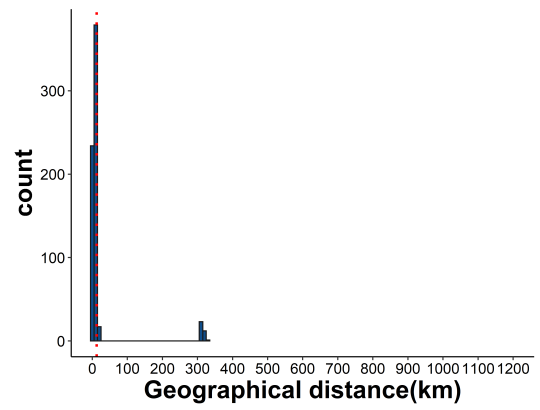
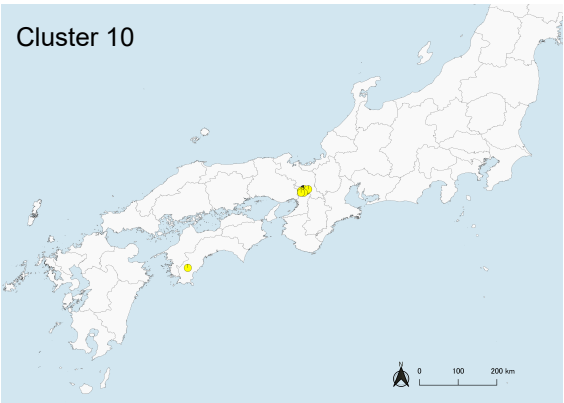
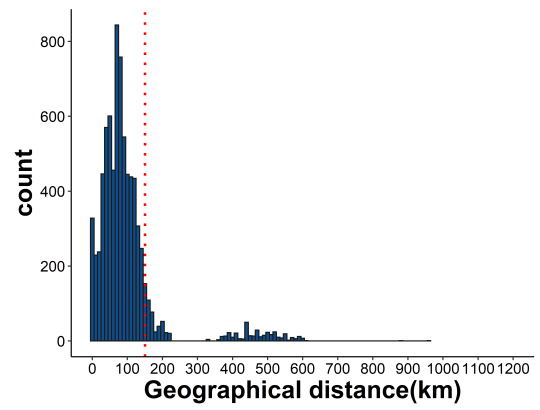
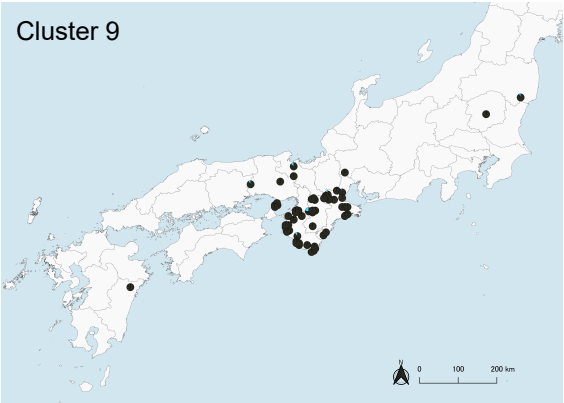


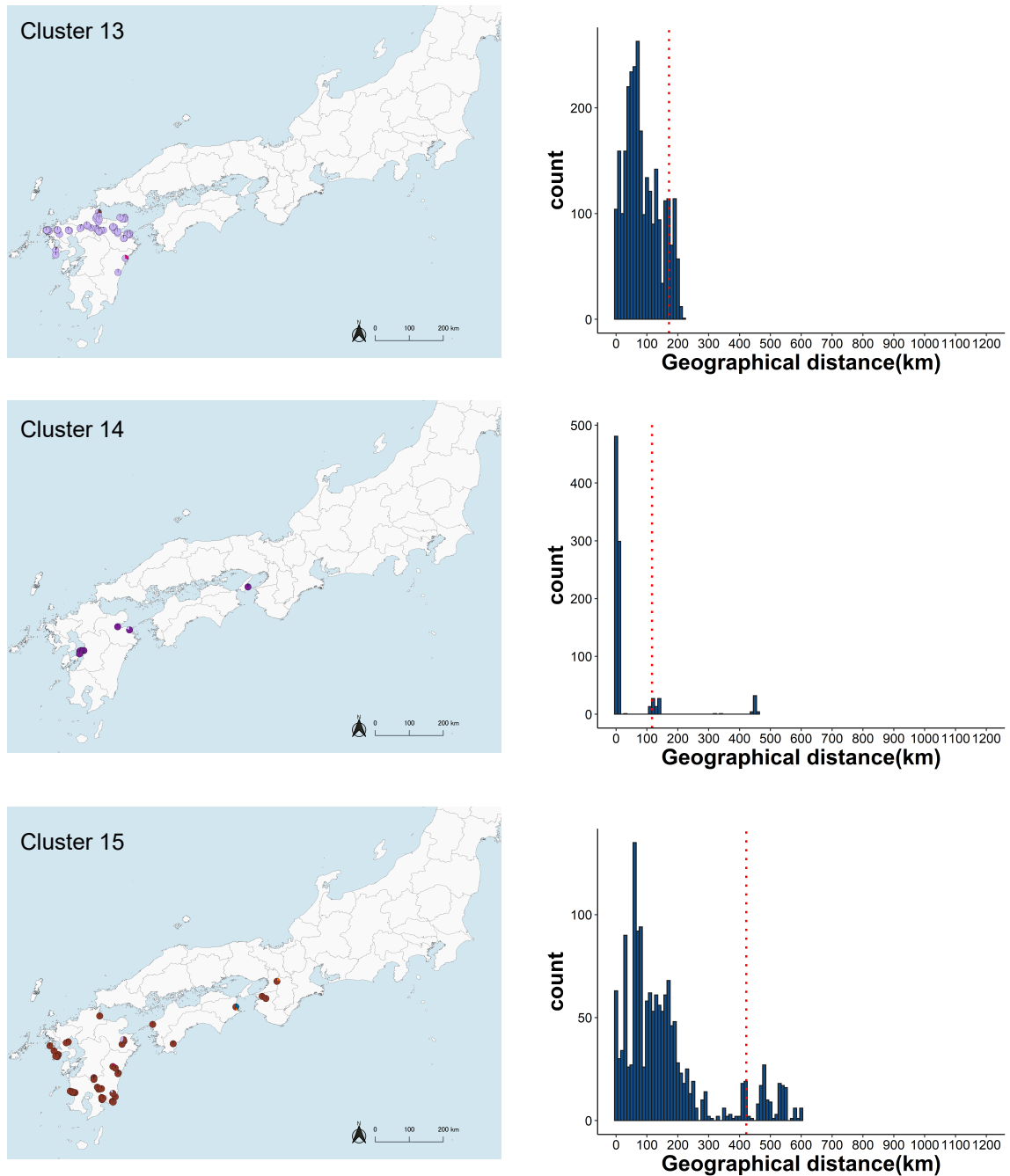
Supplementary Figure 1. Results of parameter using in discriminant analysis of principal components (DAPC).

(a) Bayesian information criterion (BIC) values for each number of clusters. The lowest values were indicated by an arrow ($K=15$). (b) The plot of DAPC cross validation. The x-axis is the number of PCA axes retained for DAPC, and the y-axis is the proportion of successful outcome predictions. Individual replicates appear as point, and the density of these points in different regions of the plot is shown in blue.



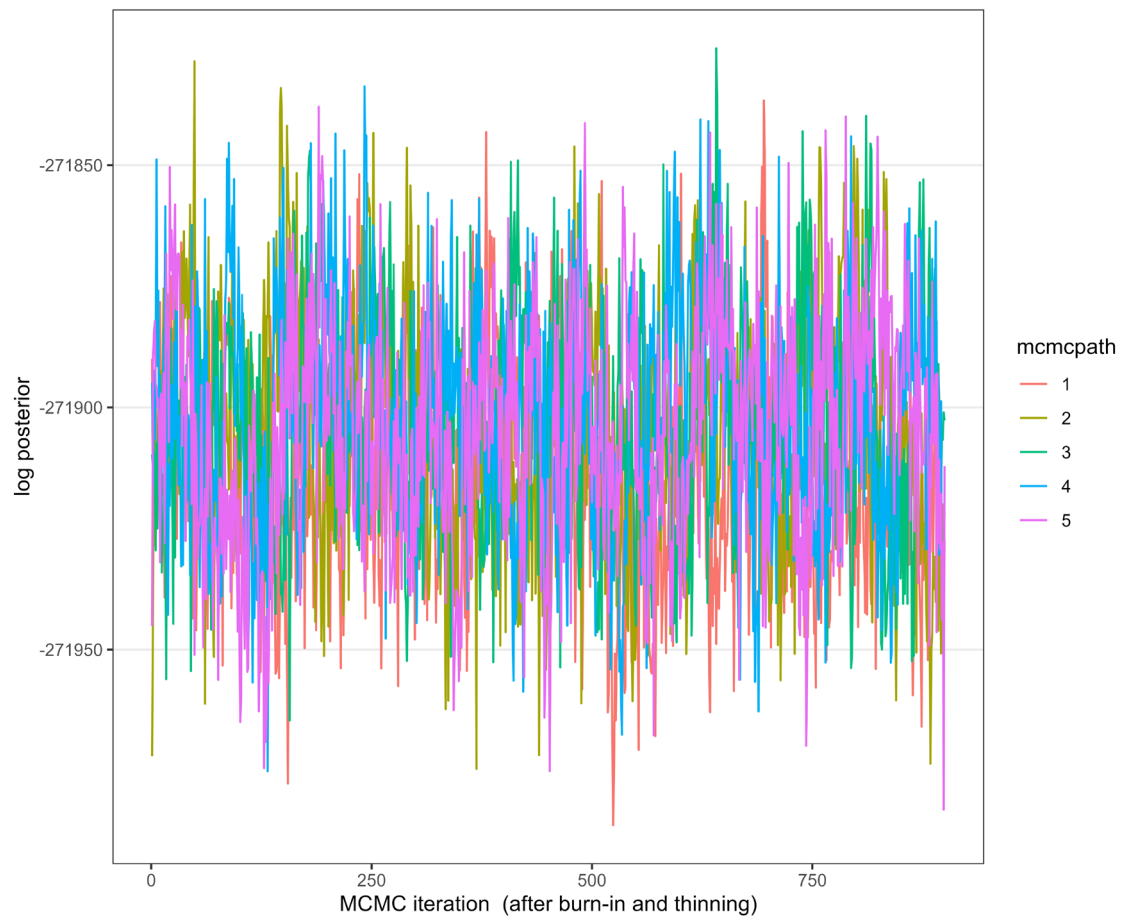






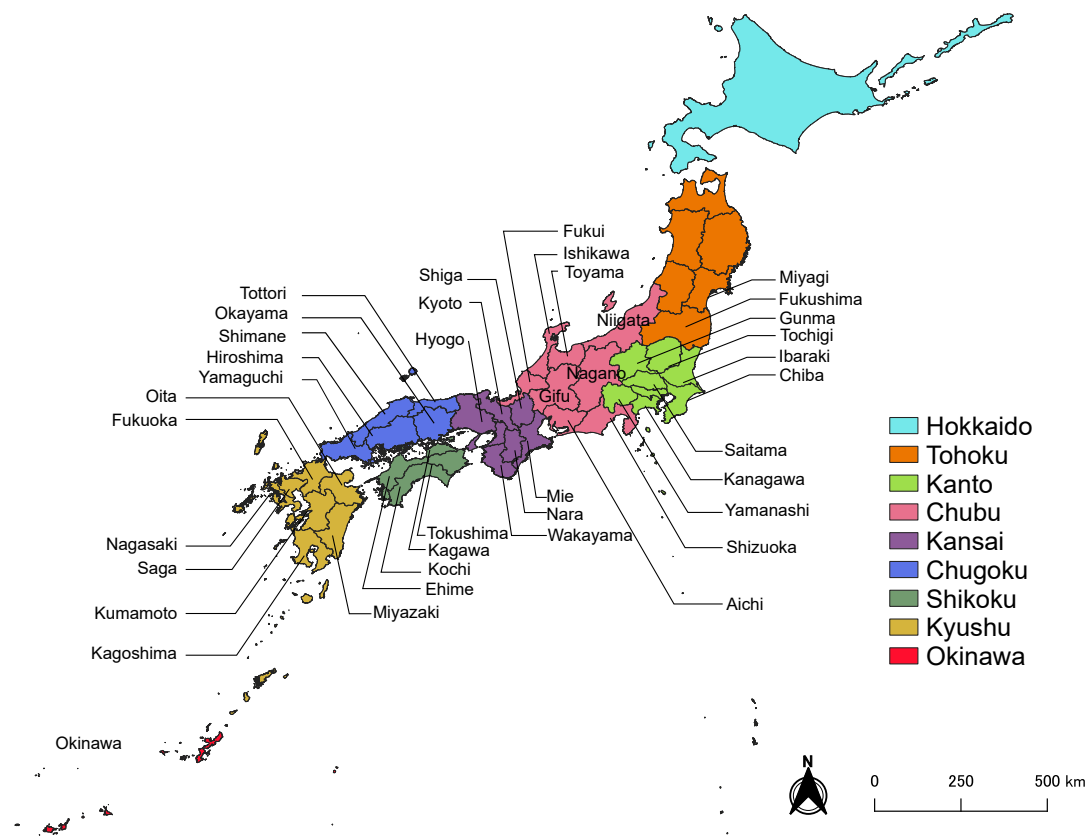
Supplementary Figure 2. Results of discriminant analysis of principal components (DAPC) analysis.

These figures show the distribution of individuals belonging to each cluster (left) and the pairwise geographic distance histogram (right). The red dotted line indicates the 90th percentile of distance within each cluster.



Supplementary Figure 3. EEMS output.

Posterior traces of five MCMC runs. We confirmed that all MCMC runs converged.



Supplementary Figure 4. Prefectures and regions of Japan used in this study.