Supplementary information, Data S11 Genetic evidence for a single origin

Even though multiple geographic locations have been proposed for the origin of domestic dogs, all dogs show tight clustering in the PCA analysis, suggesting a single origin for domestic dogs (Figure 1G inset).

In order to explore potential alternative histories, we asked whether multiple origins could be compatible with the observed data. We simulated a simple demographic history where an ancestral population gives rise to two descendant populations around the same time (Supplementary information, Figure S11A, left panel). From each population, 20 haplotypes were sampled. When we conducted PCA analysis on these 60 haplotypes, we found that there are three distinct clusters in the PCA plot (Supplementary information, Figure S11B, top panels). In other words, if there are multiple origins for dogs, the descendant populations tend to reside in separate clusters, which is in contrast to what we observe in dogs.

The simulation on the independent history seems to suggest that multiple origins are not compatible with our data. Then the question is whether a single origin can produce data that is similar to the observed PCA results in Figure 1G. We then simulated two new scenarios where there is a single origin of dogs followed by some levels of divergence. The time of divergence is an important factor determining the amount of differentiation between the two dog populations (Supplementary information, Figure 11A, right panel). When we simulate a deep divergence between these two populations (e.g. 20,000 years), the PCA analysis still displays two distinct clusters in the PCA analysis (Supplementary information, Figure S11B, middle panel). It is only when the divergence time is fairly close (in this case 10,000 years ago), the two dog populations start to cluster into one group. (Supplementary information, Figure S11B, bottom panels) matching our observations in Figure 1G.

In summary, the simulation data strongly support a single origin for domestic dogs and the results suggest that the times of divergence between the major dog groups are fairly close to each other. It is important to emphasize that, many species (e.g., rice and pigs) with known multiple origins also show distinct clustering in the PCA analysis. Independent subsampling of the same ancestral population often leads to high differentiation between subgroups, which will be distinctly separated from each other in the PCA plots[21, 22]. The genetic pattern presented for dogs strongly suggests a single origin for domestic dogs.