

Supplementary information, Data S13 Dating admixture times using HAPMIX

The HAPMIX package has a set of parameters (e.g., recombination, mutation and miscopying parameter, etc) that are fine-tuned for human populations. Following the guidelines provided in the original publication, we first did a local search for the optimal parameter settings for dog populations. Next, using these fine-tuned parameters for dogs, we plotted the maximum likelihood curve for the time of admixture for the northern Chinese dogs using the European breeds and the southern Chinese indigenous dogs as two source populations. Supplementary information, Figure S13 shows the likelihood curve peaking around 3,500 generation, which was around 10,500 years ago. The admixture for the northern Chinese indigenous groups was quite ancient and was only a few thousand years after leaving Asia.