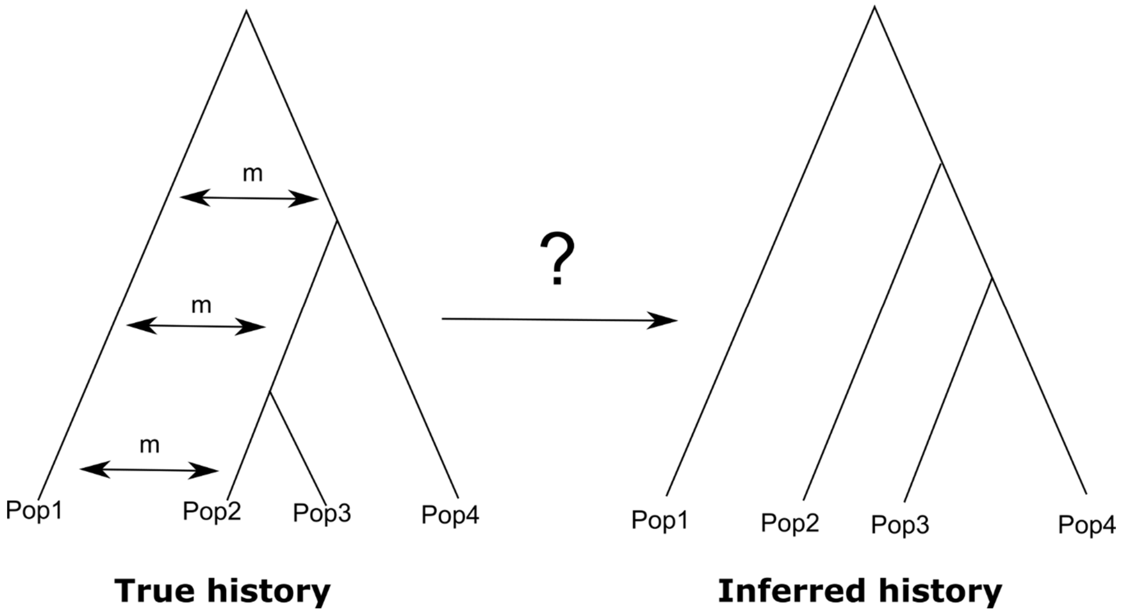
Supplementary Figure S9



Supplementary Information, Figure S9. Robustness of the basal positioning of Southern Chinese Indigenous dogs to mild gene flow between dogs and wolves

We simulated a scenario similar to the case of dog domestication. After domestication (assumed to be 33,000 years ago), two groups separated (corresponding to the East Asian and non-East Asian groups) and diverged from each other 15,000 years ago. The East Asian group consists of two populations (Pop2 and 3) and non-East Asian group consists of Pop4. There is continuous migrations between Pop2 (similar to Southern Chinese indigenous dogs) and the outgroup (wolves). Here, based on inferred levels of migration, we are testing whether the inferred tree topologies will deviate from the true population relationship and make population 2 become more basal.

We simulated the genome wide data similar to our dataset.

The ms code is

```
ms 8 48000 -t 50 -r 50 10000 -I 4 2 2 2 2 \
    -n 1 1 -n 2 0.25 -n 3 0.10 -n 4 0.20 \
    -m 2 1 $migration \
    -m 1 2 $migration \
    -ej 0.00521 3 2 \
    -ej 0.015625 4 2 \
    -en 0.015625 2 0.1 \
    -eM 0.034375 0 \
    -ej 0.034375 2 1
```