

**File S1**  
**Supplementary Document**

**Application of kernel-ABC for three populations**

We applied the kernel-ABC method to infer the demography of macaques using the IGS data of Indonesian-Malaysian *M. fascicularis* ( $2N = 30$ ), Philippine *M. fascicularis* ( $2N = 18$ ), and Burmese *M. mulatta* ( $2N = 10$ ), which was previously analyzed using a different method (NAKAGOME *et al.* 2012; OSADA *et al.* 2010). The sequence data were summarized into SFS in each population ( $SFS_{IM}$ ,  $SFS_P$ , and  $SFS_R$ ) and three dimensional tensors of HFS (3D-HFS) (Figure S1). The demographic model is shown in Figure S2. In order to investigate the trend of population size change in two *M. fascicularis* populations, we set no assumption for the population size changes and used the same prior density of  $LN(100000, 100000^2)$  for  $N_R$ ,  $N_{C-anc}$ ,  $N_{IM}$ , and  $N_P$ , respectively. The conditions of kernel-ABC and coalescent simulations were the same as those described in Materials and Methods. The estimated parameters are shown in Table S1, supporting the population expansion in the Indonesian-Malaysian *M. fascicularis* and population contraction in the Philippine *M. fascicularis*.

**Validation of kernel-ABC in two population models**

We generated samples that have the same number of loci (26 loci) and similar parameter values to our estimated parameter values in a constant population size model, Model 1, and Model 2 with 25% size. For each model, we generated 10,000 simulated datasets using the parameter values shown in Table S2, and calculated the average of summary statistics (2D-SFS and 2D-HFS) across all datasets. Next, we chose a typical dataset as an observation, which has the smallest sum of squared deviations from the average. Posterior means of demographic parameters were estimated using the kernel-ABC method with 20,000 samples, and the process was repeated for 100 times.

**References**

- Nakagome, S., K. Fukumizu and S. Mano, 2012 Kernel approximate bayesian computation for population genetic inferences. ArXiv e-prints: arXiv:1205.3246.
- Oada, N., Y. Uno, K. Mineta, Y. Kameoka, I. Takahashi *et al.*, 2010 Ancient genome-wide admixture extends beyond the current hybrid zone between *Macaca fascicularis* and *M. mulatta*. *Mol. Ecol.* **19**: 2884-2895.