1 Supplemental Figures



3 Sup. Fig. 1 Geographic locations of the seven East Asian Populations





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А

7 B

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10 Sup. Fig. 2 Scaled maximum likelihood estimate of the divergence time plotted







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20 Fig. 3 Scaled maximum likelihood estimate of divergence time plotted against the true







26 Sup. Fig. 4 Maximum likelihood estimate of asymmetric dissimilarity measure plotted

against the expected value

28 Supplemental Figure Legends

- 29 Sup. Fig. 1 Geographic locations of the seven East Asian Populations
- 30

31 Sup. Fig. 2 Data were simulated from population structure shown in Fig. 1B with 32 population size A) N_1 =937.5 and N_2 =3750 and B) N_1 =937.5 and N_2 =312.5, and 33 different divergence times ranging from 3,000 years to 30,000 years. For each 34 combination of population sizes and divergence time, 1,000 data sets were simulated. 35 Average value of 1,000 maximum likelihood estimates was scaled by and plotted 36 against the true value of divergence time, with bars representing scaled standard 37 deviations. Red line represents the result from fully-parameterized method. Green line 38 represents the result from IS-based method. Blue line represents the result from 39 Beta-based method.

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Sup. Fig. 3 Data were simulated from population structure shown in Fig. 1B with 41 42 population size $N_1 = N_2 = 937.5$, and different divergence times ranging from 3,000 43 years to 30,000 years. For each combination of population sizes and divergence time, 44 1,000 data sets were simulated, each including A) 30,000, B) 10,000, C) 3,000 and D) 45 1,000 SNPs, respectively. Average value of 1,000 maximum likelihood estimates was scaled by and plotted against the true value of divergence time, with bars representing 46 47 scaled standard deviations. Red line represents the result from fully-parameterized 48 method. Green line represents the result from IS-based method. blue line represents the result from Beta-based method. 49

51	Sup. Fig. 4 Data were simulated using population tree shown in A) Fig. 4A. and B)
52	Fig. 4B. For each population tree, 1,000 data sets were simulated. Asymmetric
53	dissimilarity measures were estimated from each data set. The average of 1,000
54	maximum likelihood estimates was plotted against the expected value of the
55	corresponding asymmetric dissimilarity measure, with bars representing standard
56	deviations.