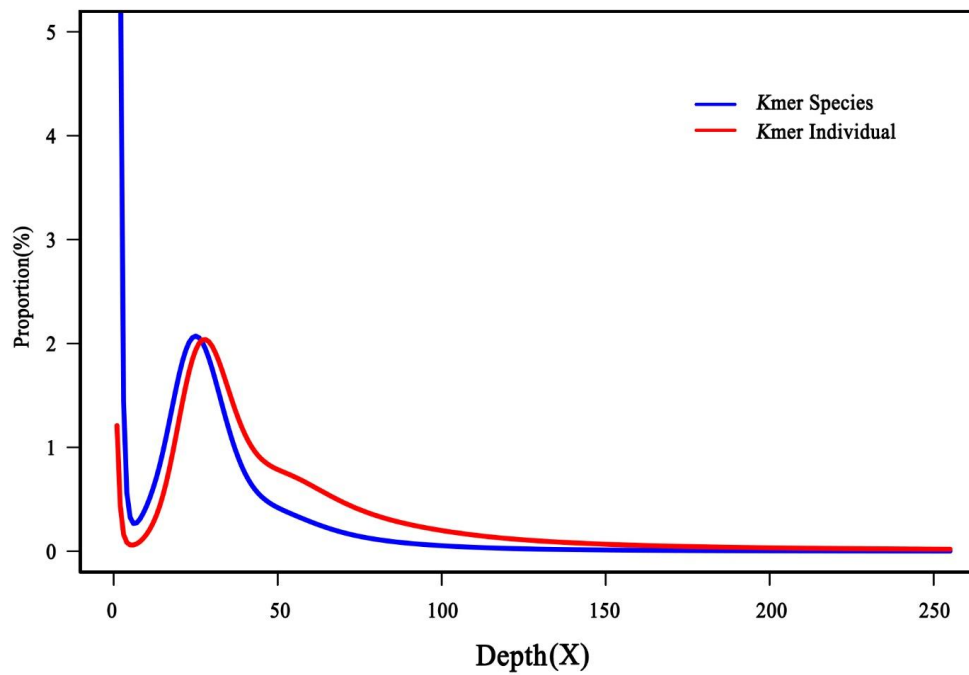


1 **Population genomic analysis provides strong evidence of the past**
2 **success and future strategies of South China tiger breeding**
3
4 **Chen Wang et al.**
5
6 **Supplementary Information.**

7 Supplementary Figures

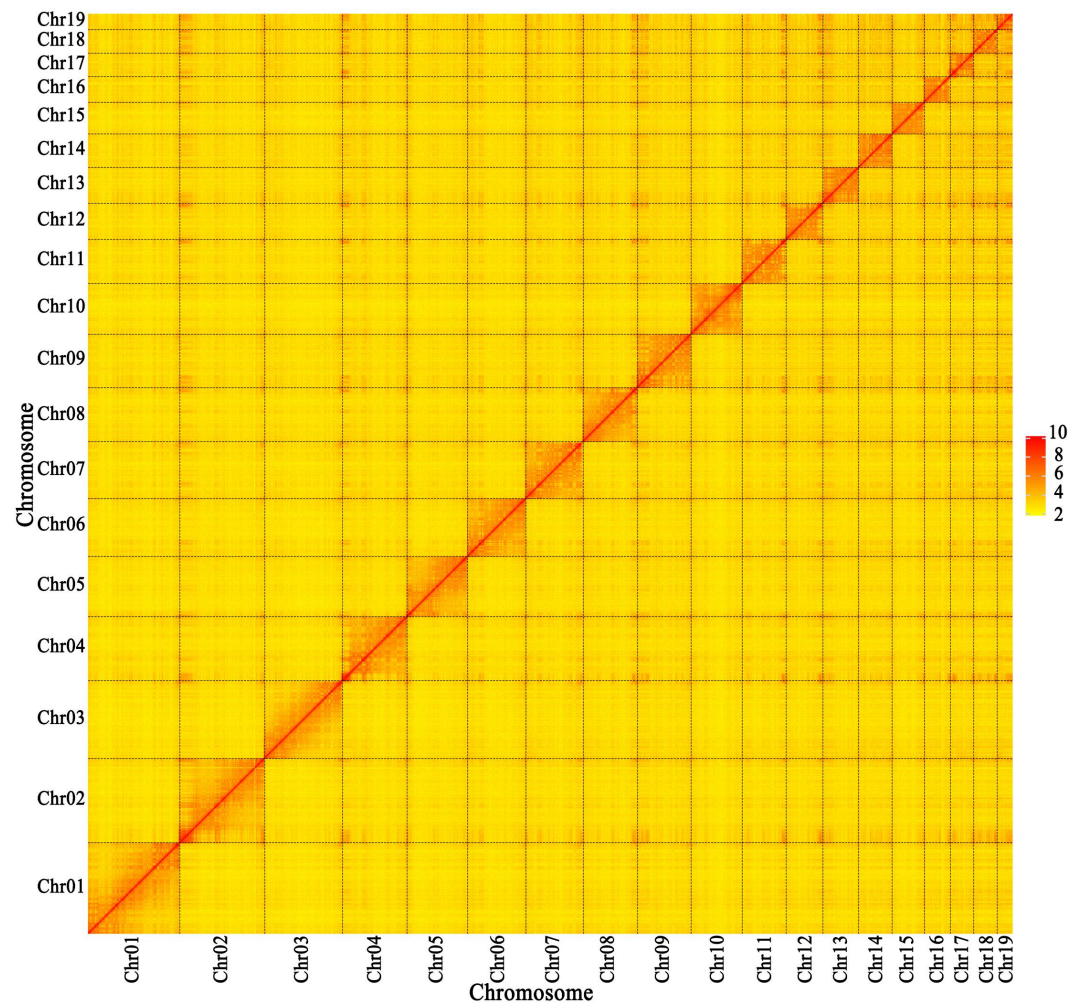


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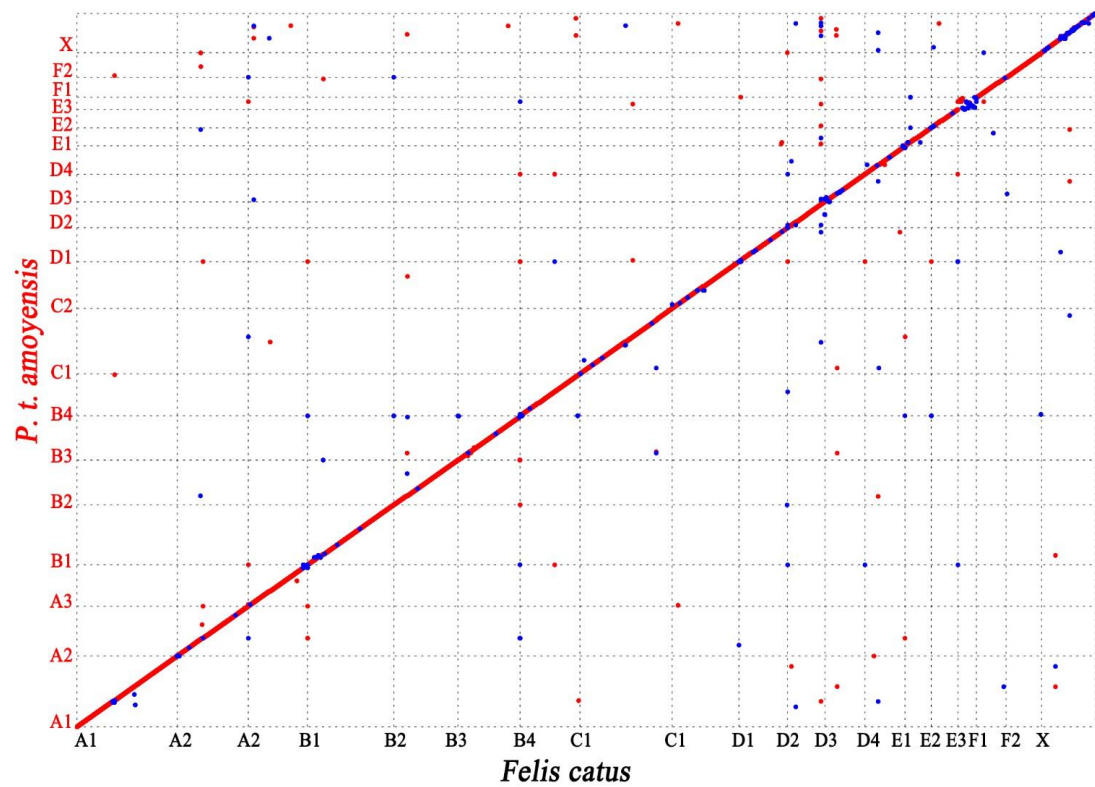
9

10 **Supplementary Figure S1.** Distribution of 17-mer depths for estimating the genome size.

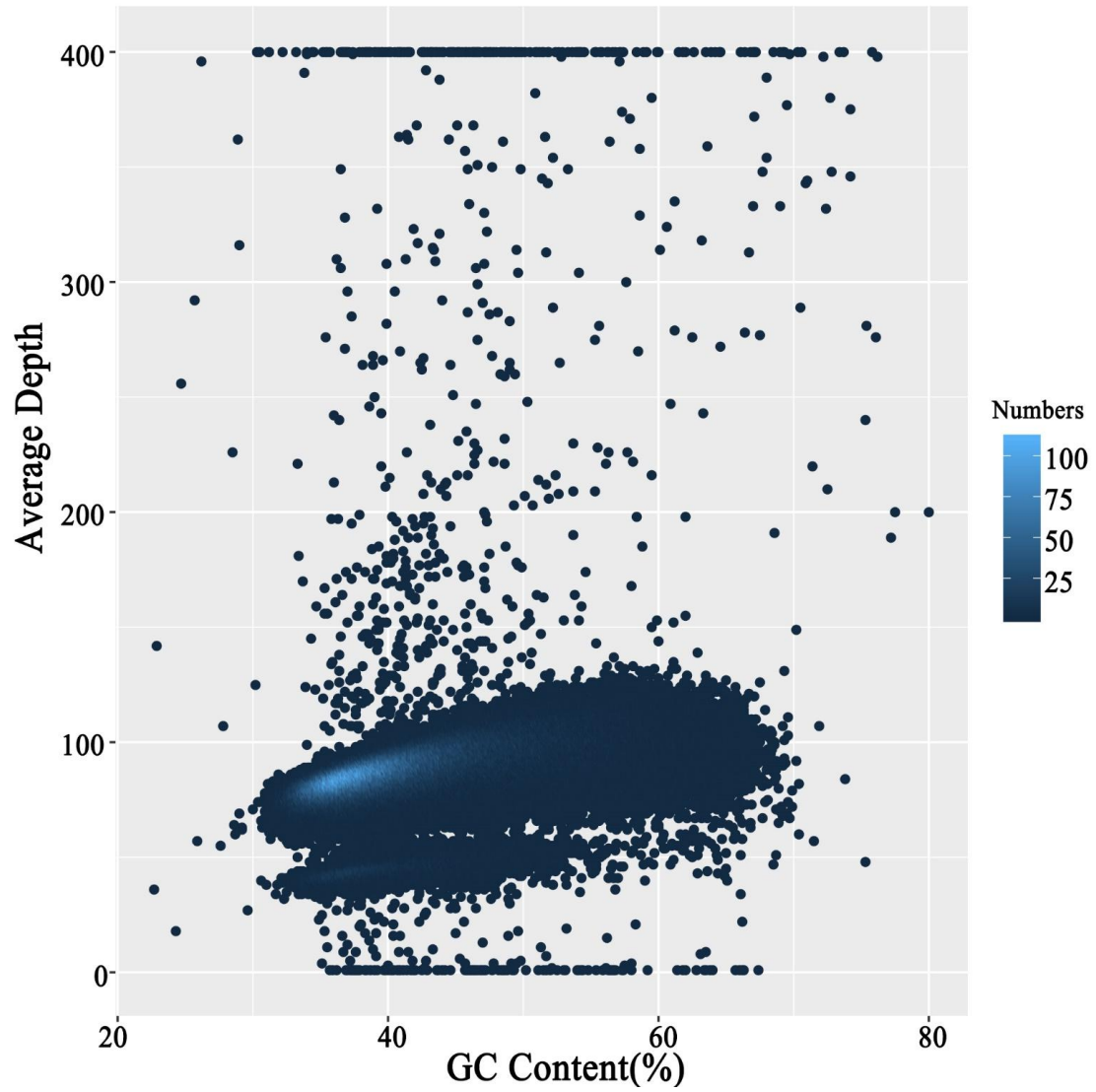
11 The x-axis represents k-mer depths while y-axis represents the proportion. The peak depth is
 12 at 25-fold and total number of k-mers is 61,791,522,108. The *P. t. amoyensis* genome size is
 13 estimated to be 2471.66 Mb from the formula $G = K_num / K_depth$.



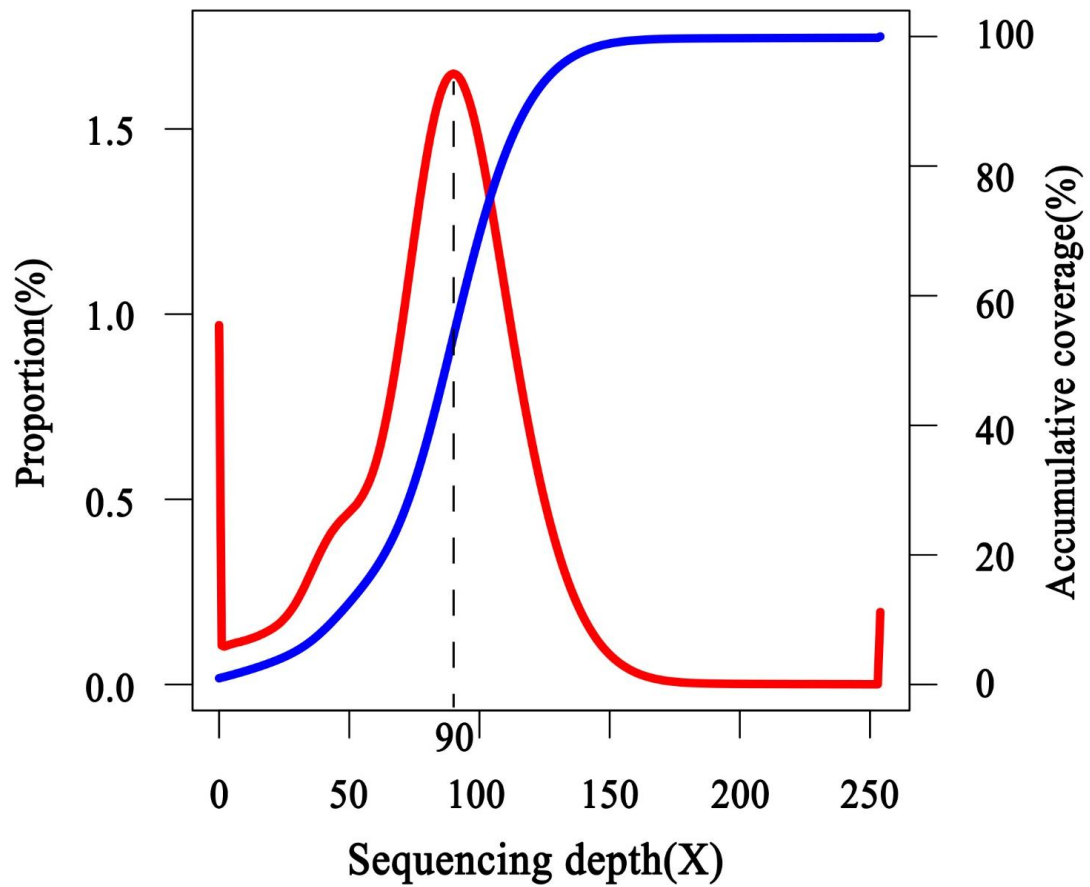
Supplementary Figure 2. Hi-C chromosomal contact heat map. A 500 kb resolution was used to calculate the number of Hi-C read pairs in any two bins.



Supplementary Figure 3. The collinearity between the South China tiger (*P. t. amoyensis*) and domestic cat (*Felis catus*) genomes. Each dot represents an aligned region while the minimum length is 10 kb.



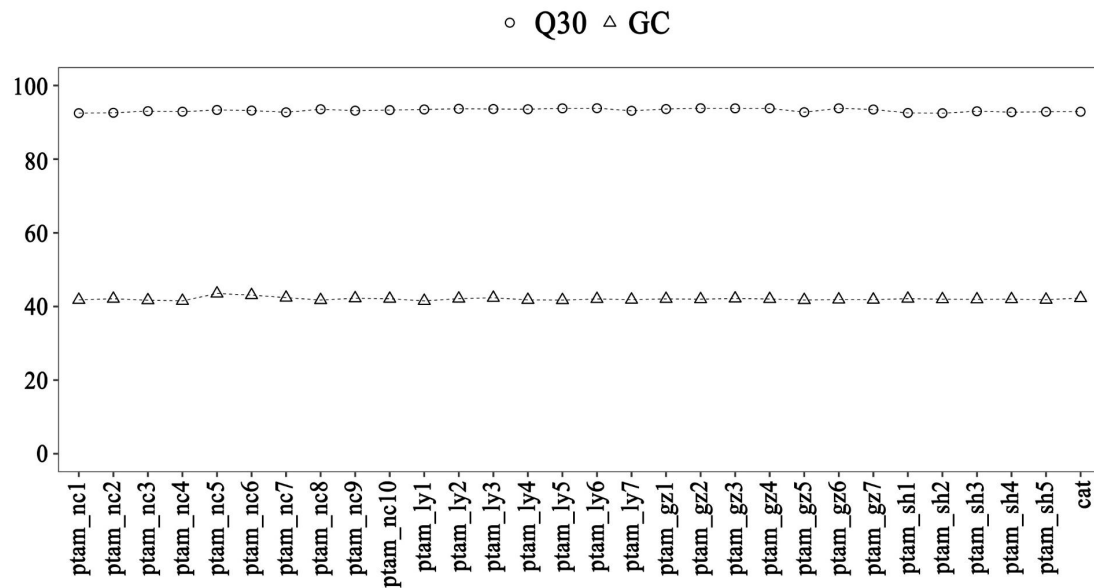
Supplementary Figure 4. Distribution of GC content versus sequencing depth. We used 20-kb sliding windows along the South China tiger genome, to calculate the GC content and average sequencing depth.



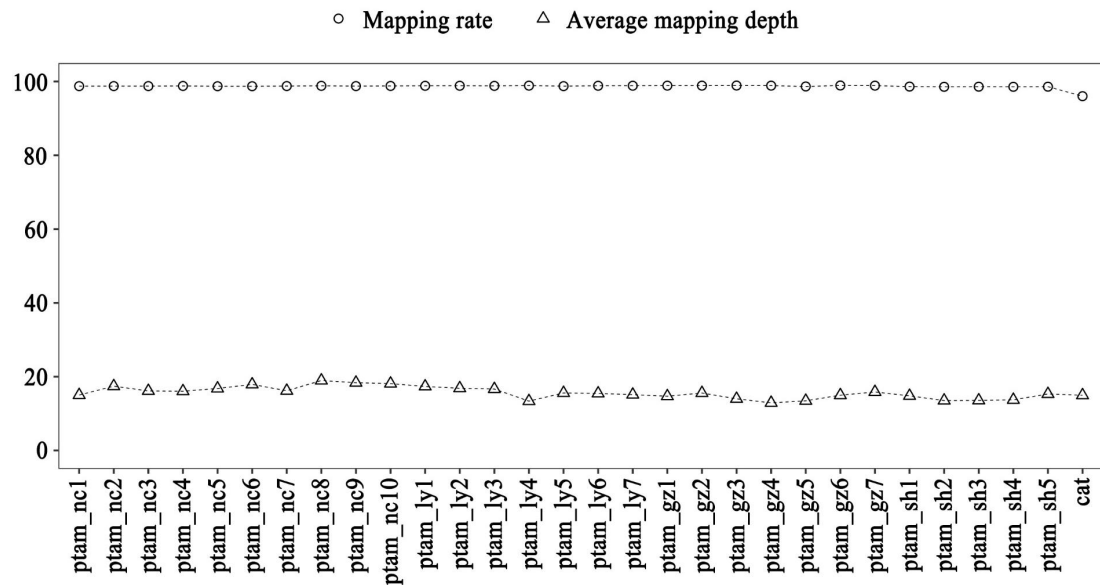
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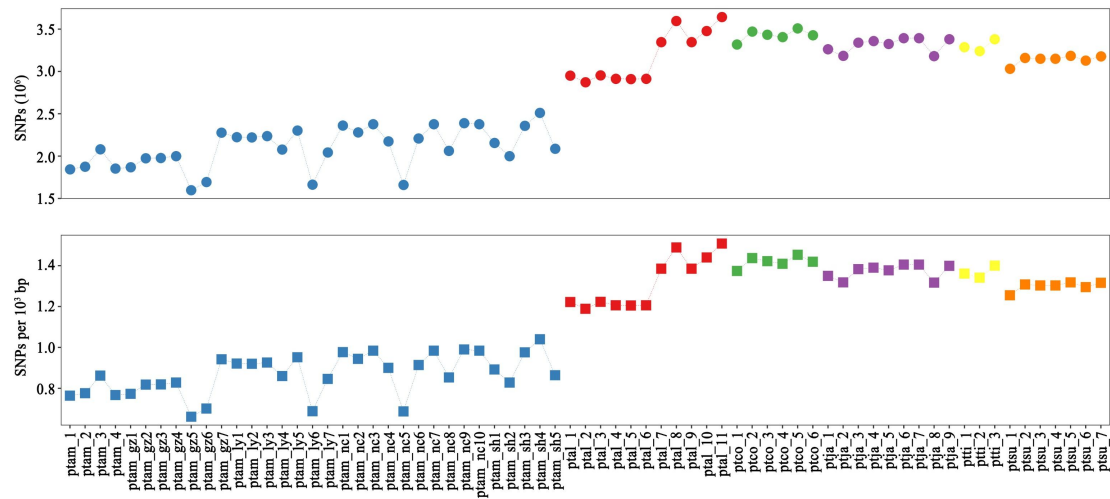
30 **Supplementary Figure 5.** Distribution of sequencing depth. We only used around 230 Gb
 31 data from Illumina short insert-size libraries (< 500 bp) for base depth analysis.



Supplementary Figure 6. Q30 and GC content for each samples. The average Q30 and GC content are 93.24 and 42.04, respectively. Their very low variation reflect our re-sequencing data to be high quality.

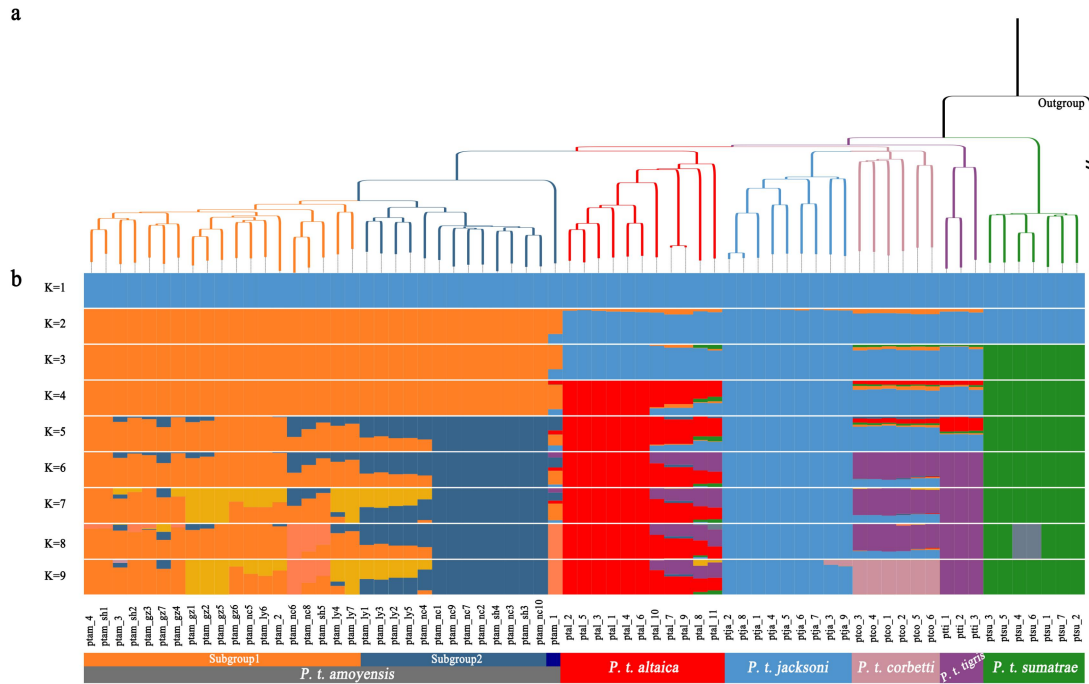


Supplementary Figure 7. The distribution of mapping rates and average mapping depths for each individual. The depths range from $12.91 \times$ to $18.96 \times$ while the rates vary from 96.03% to 98.92%.



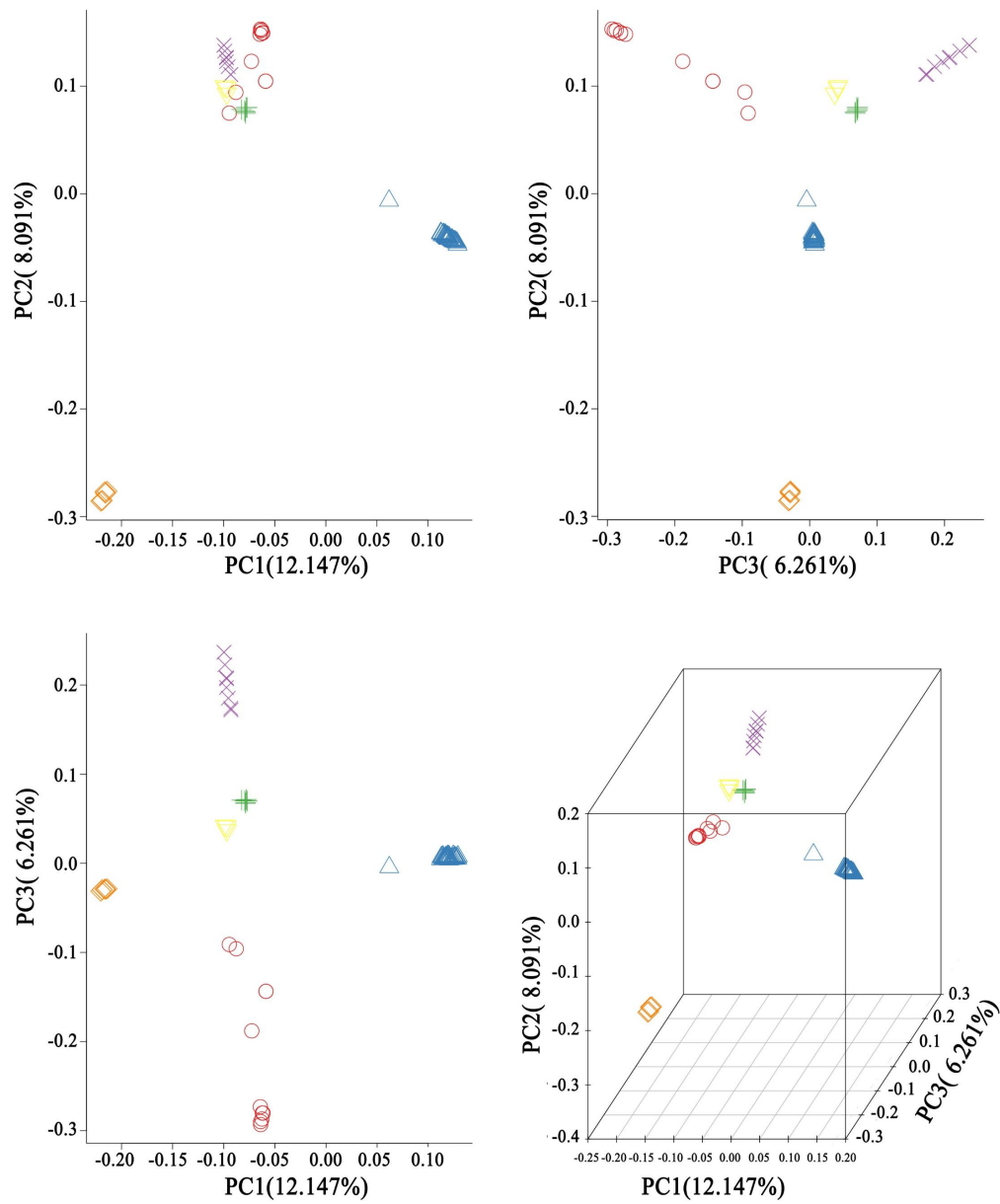
40

41 **Supplementary Figure 8.** The distribution of the SNP number and frequency. (up) Number
 42 of SNPs (up) and frequency of SNPs per 1 kb (down).



Supplementary Figure 9. Phylogeny and genetic structure analysis. (a) Neighbor-joining phylogenetic tree of all the 70 samples using 124,123 SNPs at the fourfold degenerate sites and with domestic cat as an outgroup. (b) ADMIXTURE plots for all tigers for *K* values from 1 to 9 based on 25,645 SNPs at fourfold degenerate sites. The result clearly separates six tiger subspecies from each other.

○ *P. t. altaica* △ *P. t. amoyensis* + *P. t. corbetti* ◇ *P. t. sumatrae* ▽ *P. t. tigris* × *P. t. jacksoni*



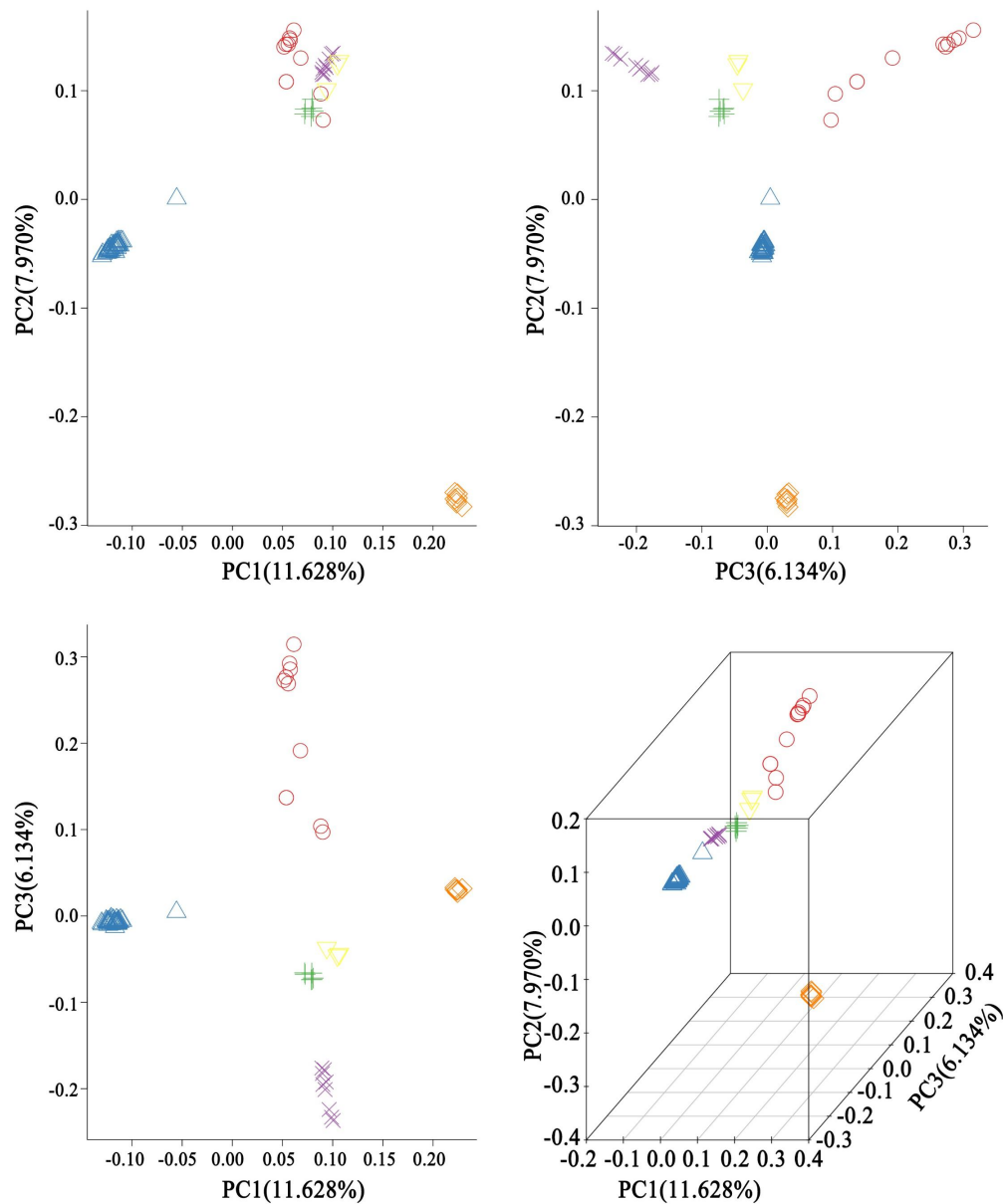
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52 **Supplementary Figure 10.** Principal component analysis using whole genome-wide SNPs.

53 The result clearly separates six tiger subspecies from each other.

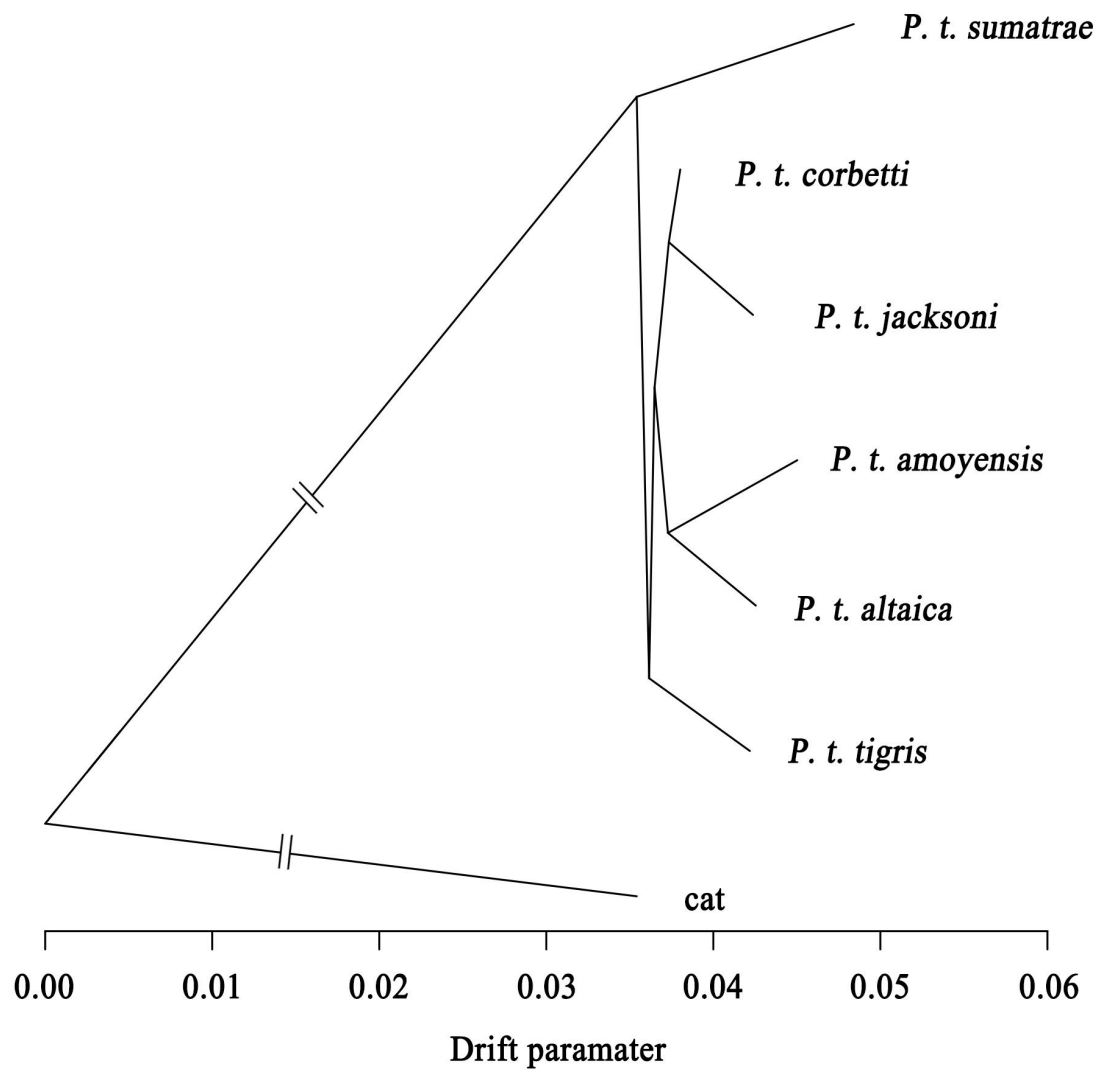
○ *P. t. altaica* △ *P. t. amoyensis* + *P. t. corbetti* ◇ *P. t. sumatrae* ▽ *P. t. tigris* × *P. t. jacksoni*



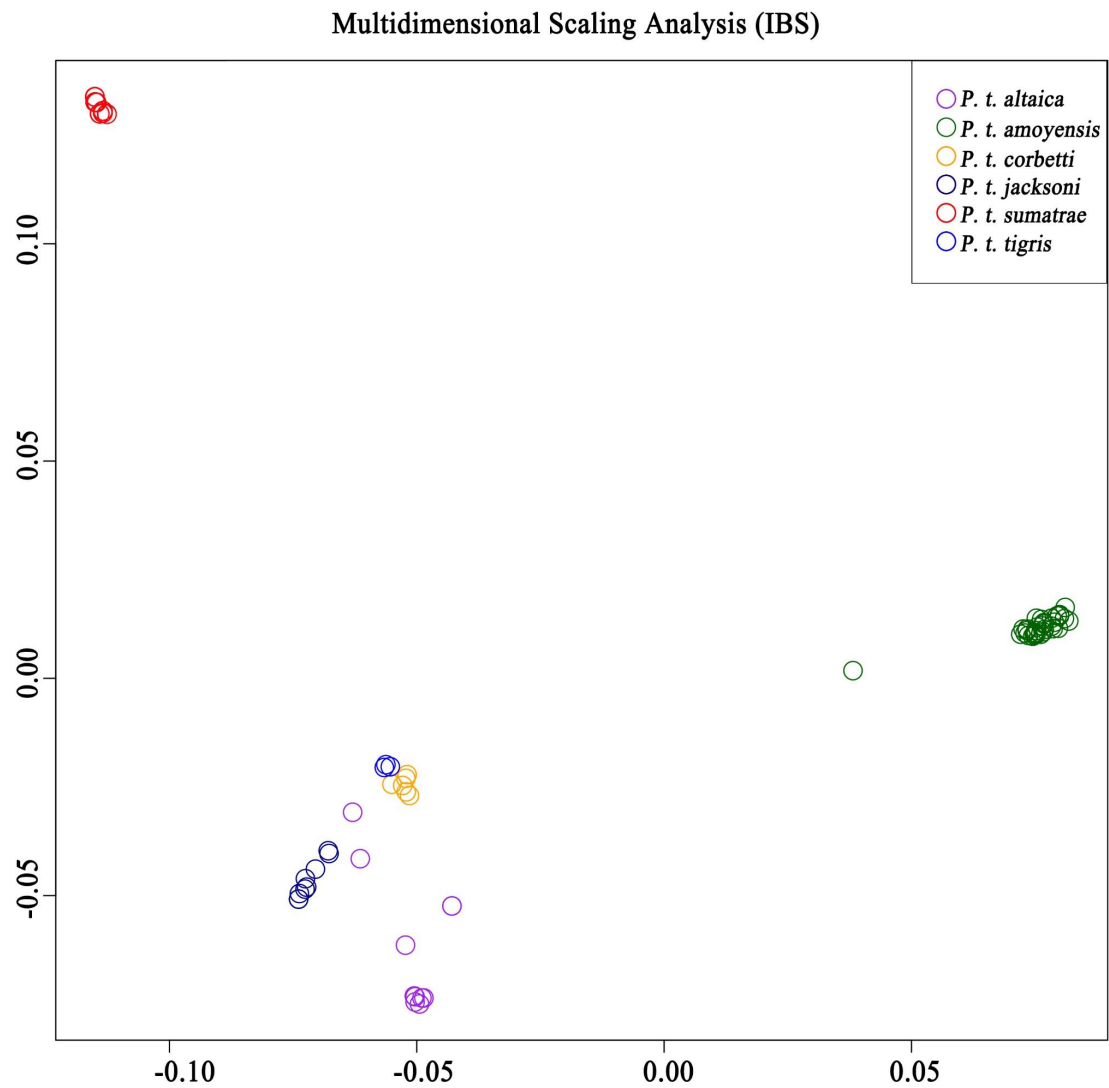
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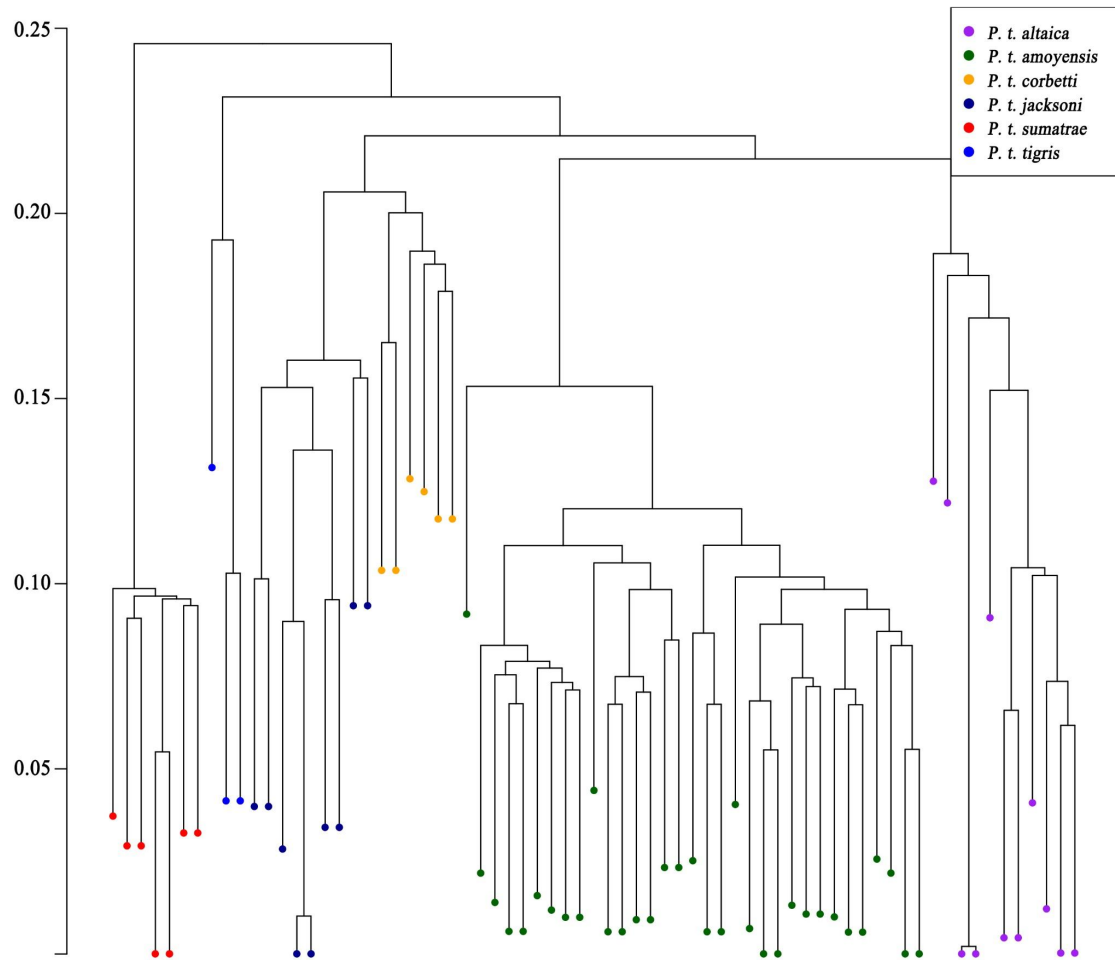
56 **Supplementary Figure 11.** Principal component analysis using SNPs at the fourfold
 57 degenerate sites. The result clearly separates six tiger subspecies from each other.



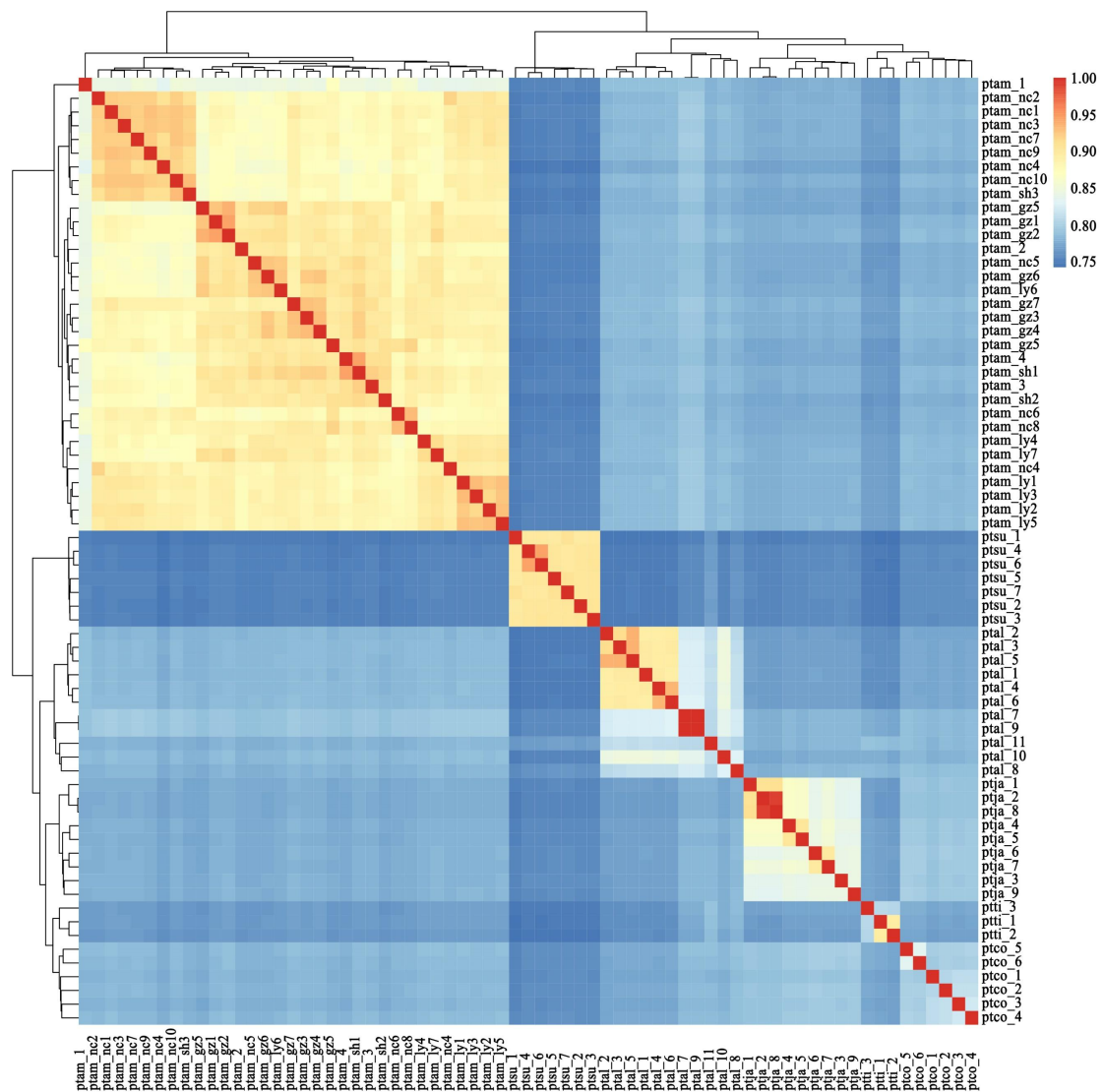
Supplementary Figure 12. A maximum likelihood tree was built using TreeMix software with whole-genome sequencing data of six tiger subspecies.



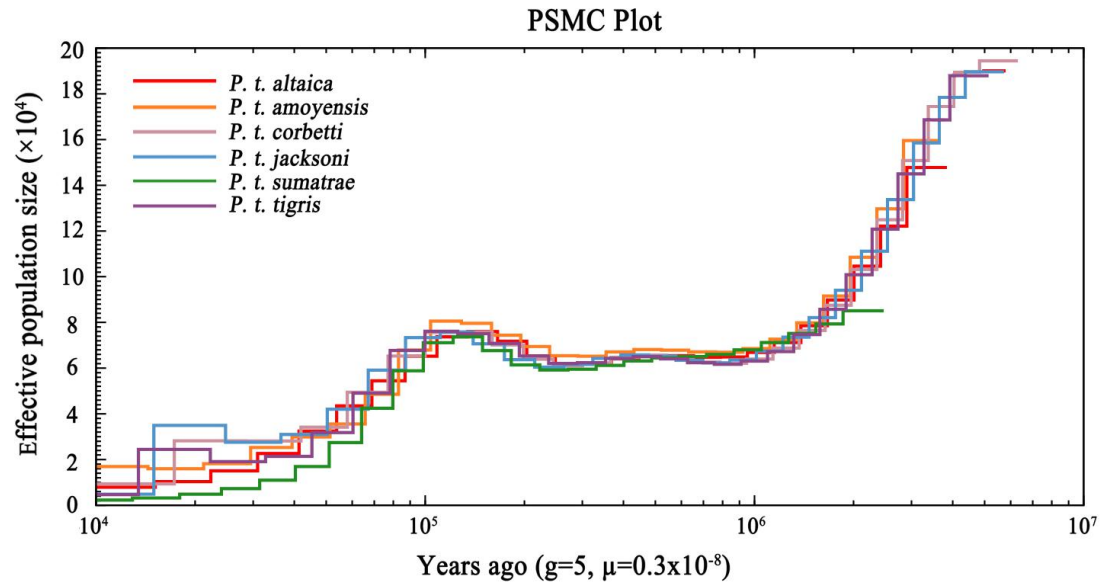
Supplementary Figure 13. Multidimensional scaling analysis based on the matrix of genome-wide identity-by-state (IBS) pairwise distances between six tiger subspecies.



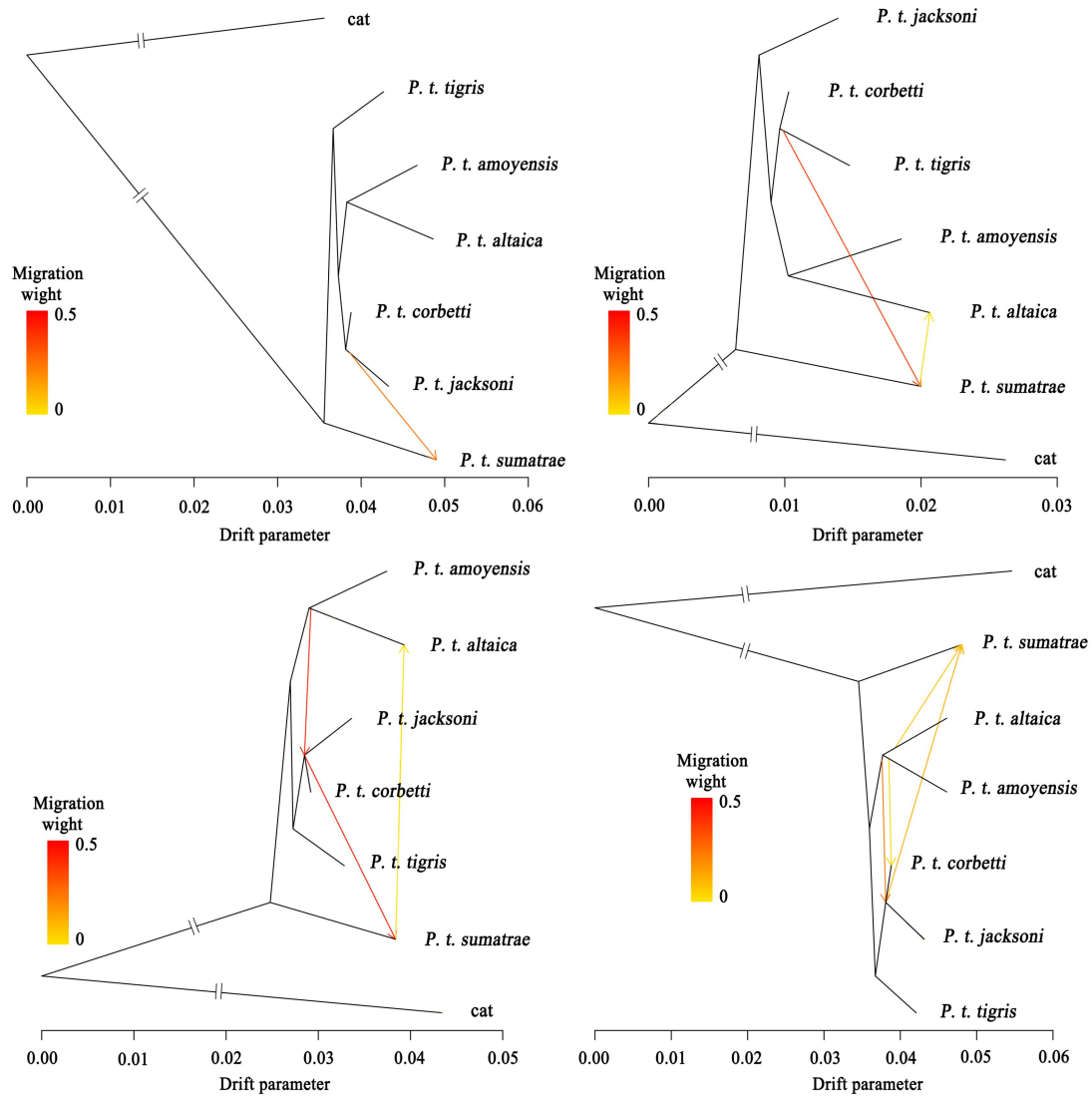
Supplementary Figure 14. Cluster analysis based on the matrix of genome-wide identity-by-state (IBS) pairwise distances between six tiger subspecies determined by a permutation score.



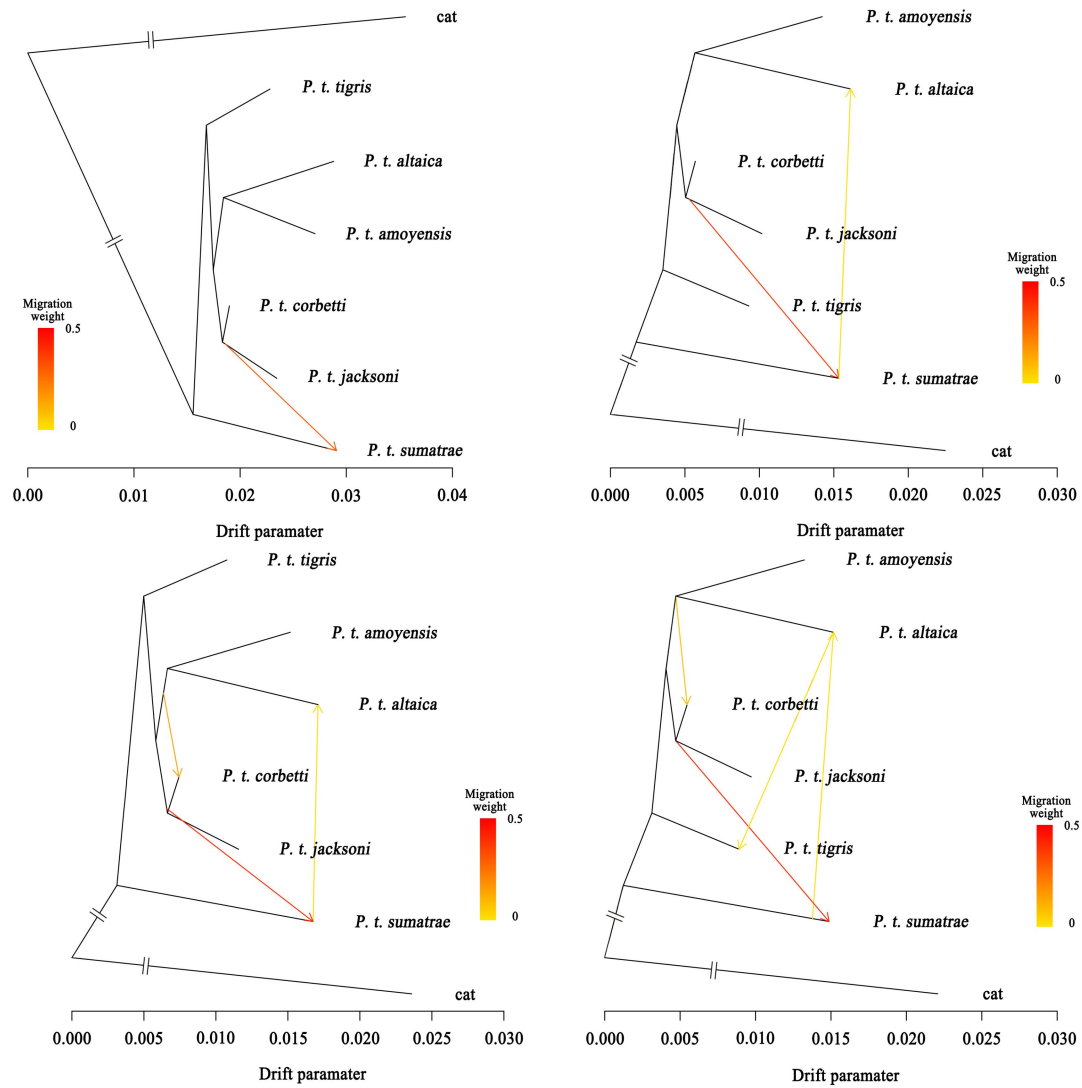
Supplementary Figure 15. Analysis of genome-wide average identity-by-state (IBS) pairwise identities between six tiger subspecies.



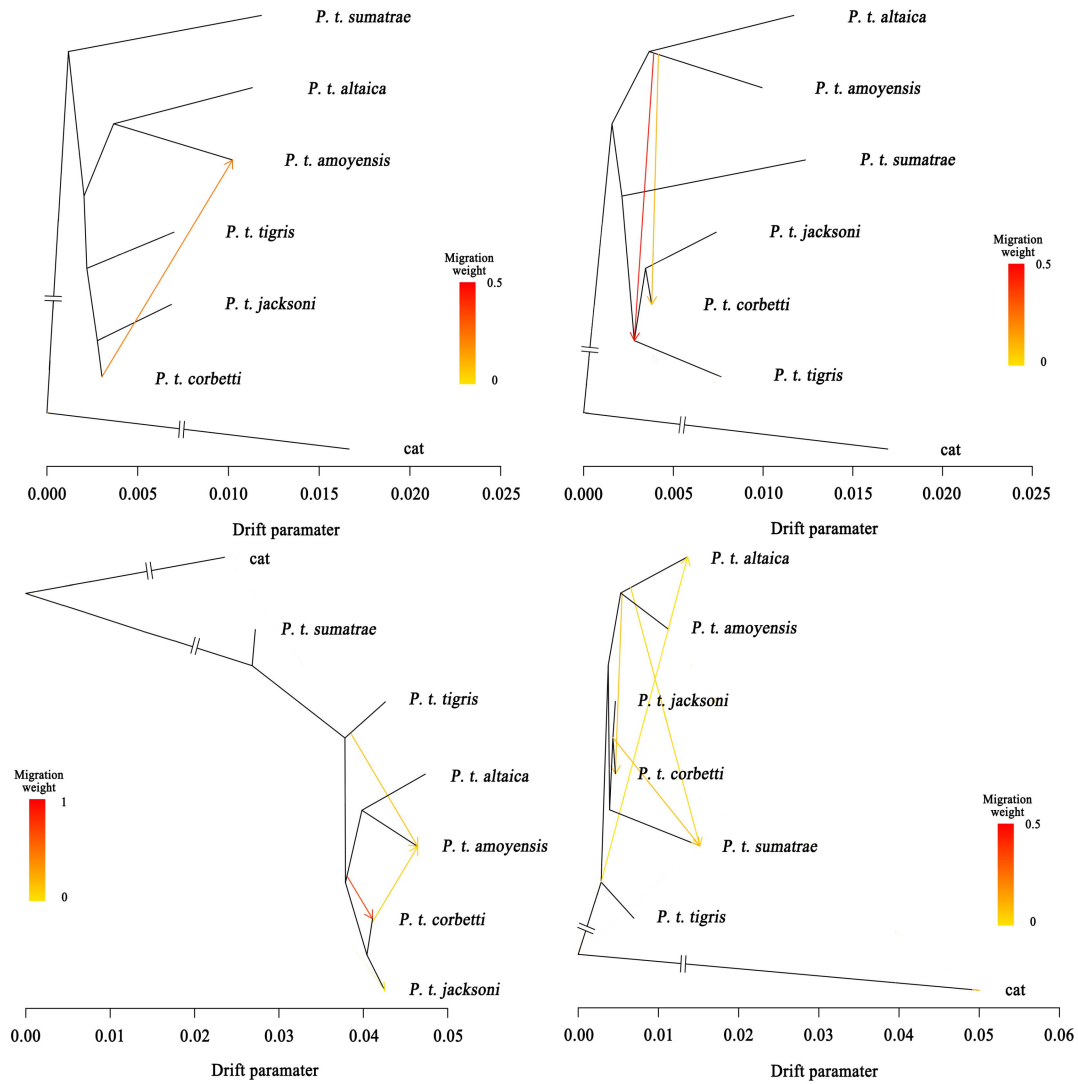
Supplementary Figure 16. PSMC plots of the inferred demographic histories of each tiger subspecies. The plot supports a previous observation by Liu et al. (2018).



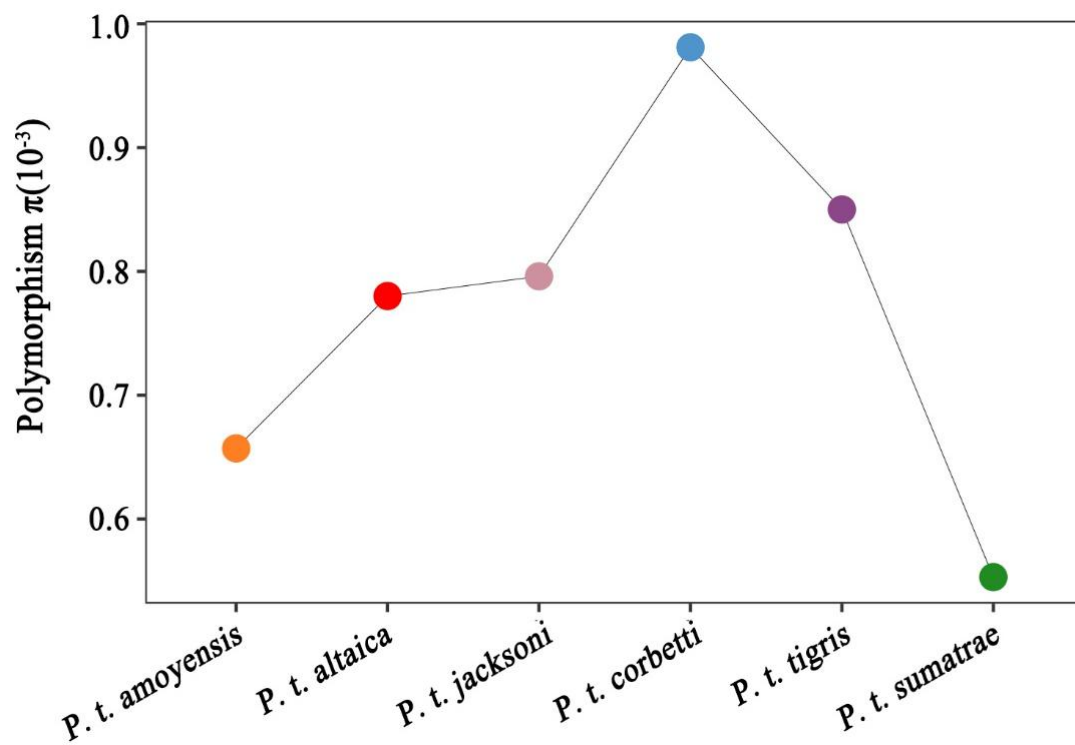
Supplementary Figure 17. Plot of migration events between the South China tiger subgroup1 population and other tiger subspecies inferred by the TreeMix method. The scale bar shows 10 times the average standard error of the entries in the sample covariance matrix.



Supplementary Figure 18. Plot of migration events between the South China tiger subgroup2 population and other tiger subspecies inferred by the TreeMix method. The scale bar shows 10 times the average standard error of the entries in the sample covariance matrix.



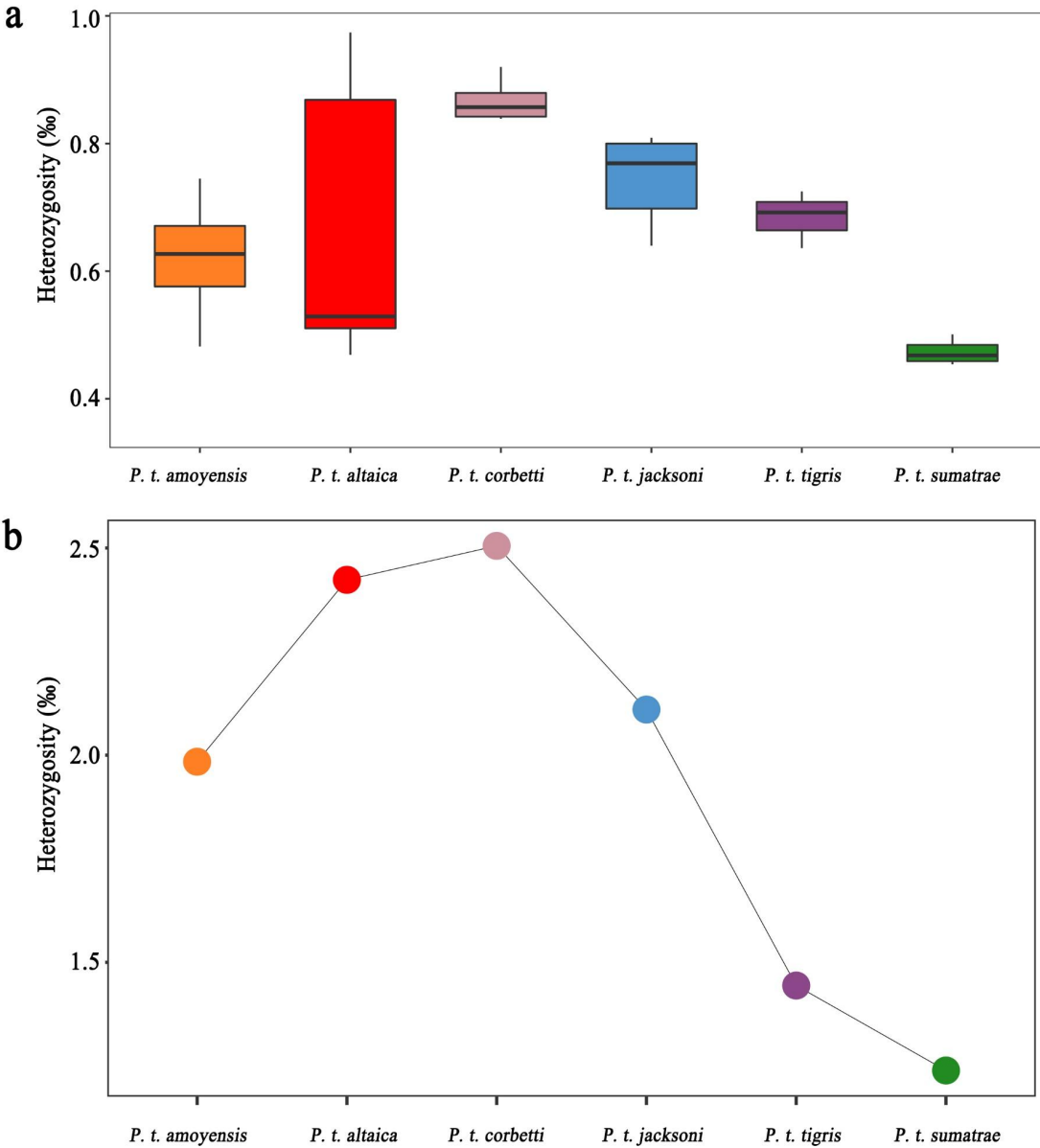
Supplementary Figure 19. Plot of migration events between the South China tiger ptam_1 individual and other tiger subspecies inferred by the TreeMix method. The scale bar shows 10 times the average standard error of the entries in the sample covariance matrix.



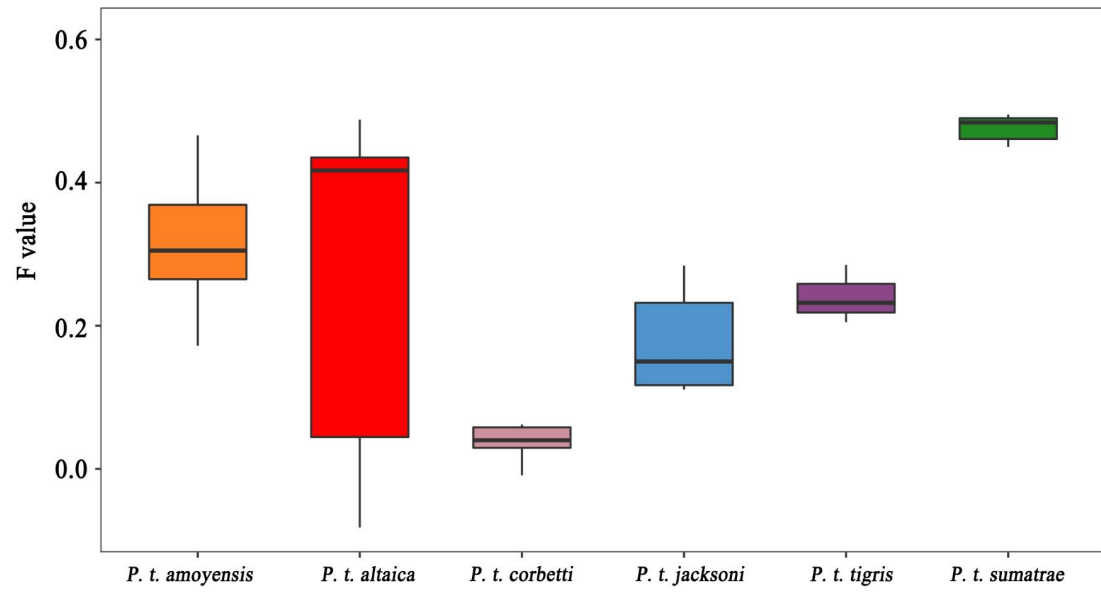
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97 **Supplementary Figure 20.** Nucleotide diversity π estimates of six tiger subspecies.



101 **Supplementary Figure 21.** Heterozygosity statistics of genome-wide SNPs. (a) Observed
102 heterozygosity across all individual genomes of each subspecies. (b) Averaged genomic
103 heterozygosity in each subspecies.



Supplementary Figure 22. Genomic inbreeding coefficients F_H in each tiger subspecies.