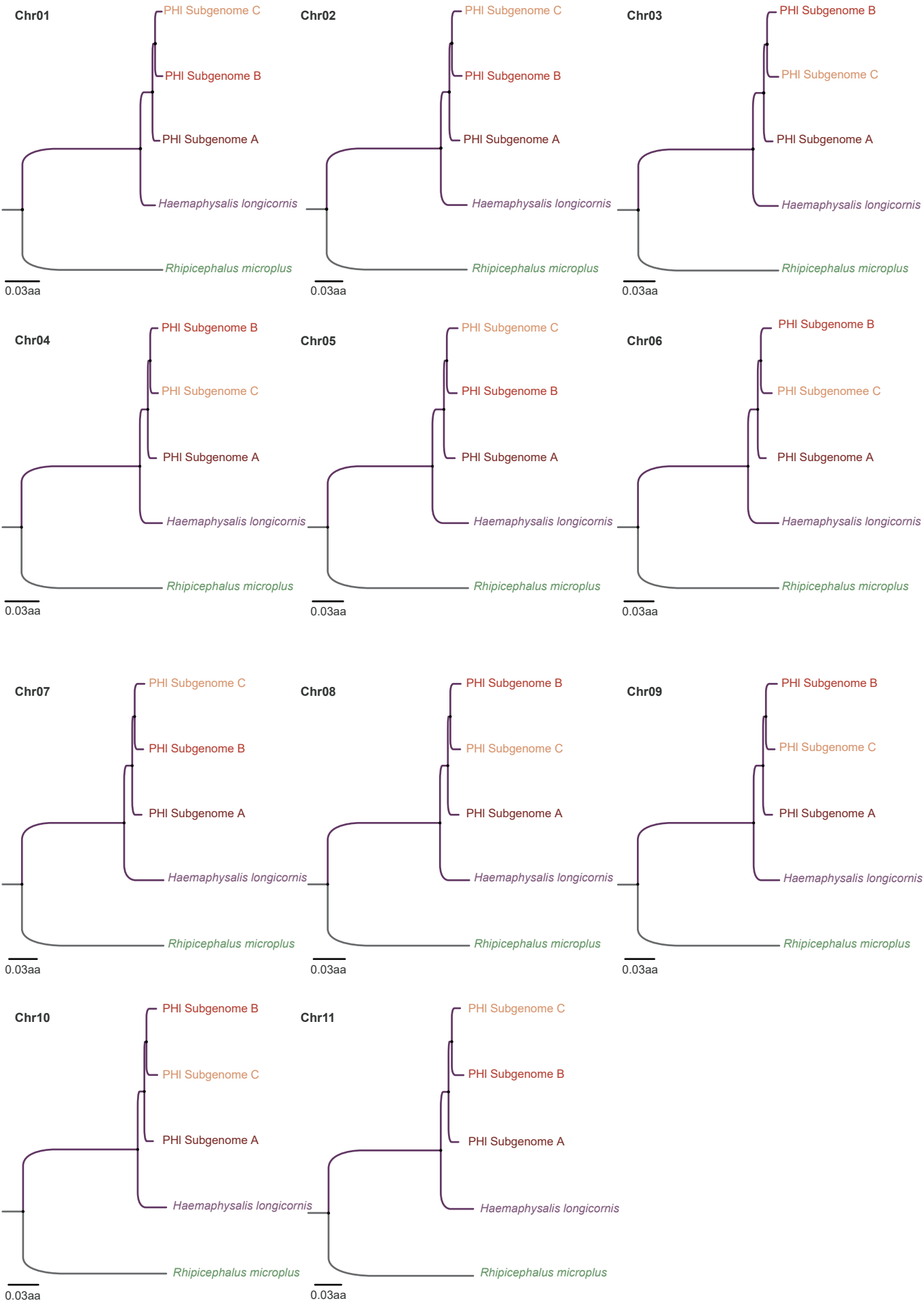
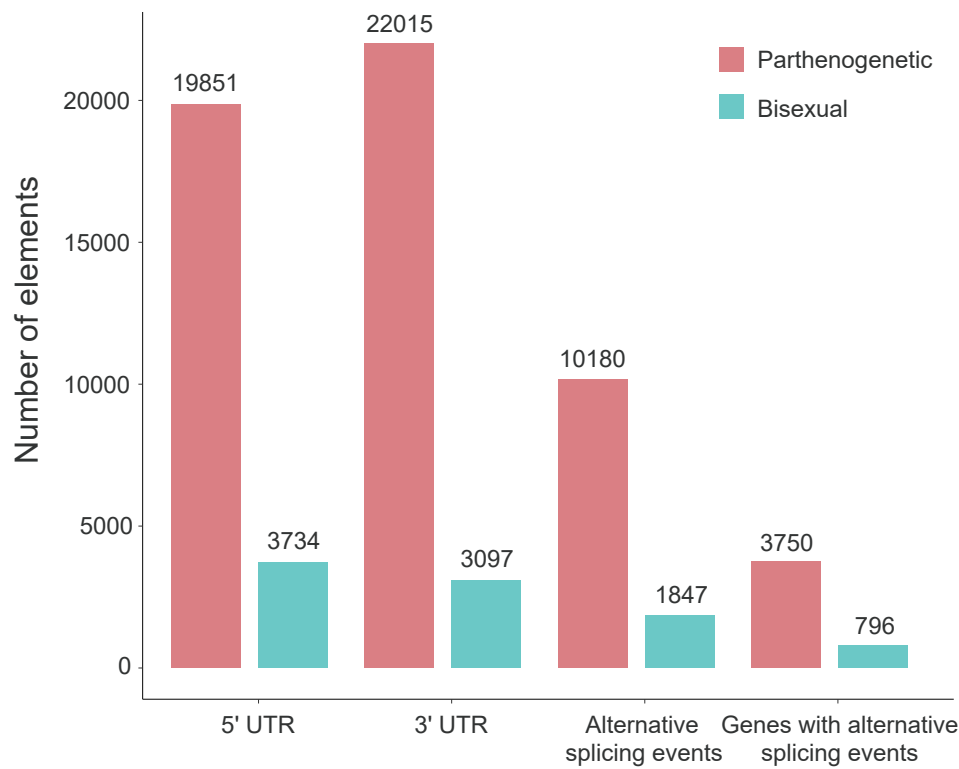


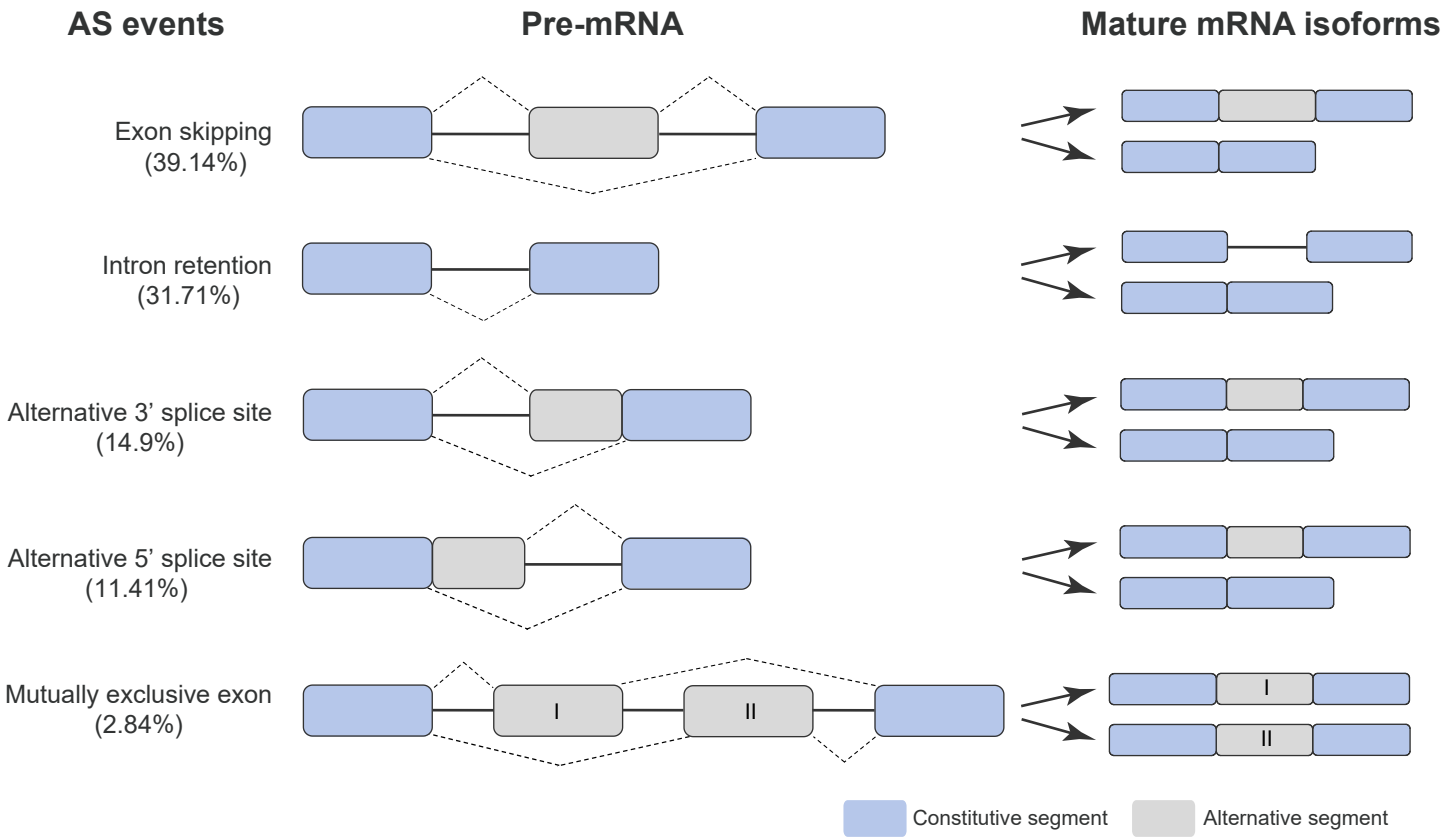
Supplementary Fig. 1



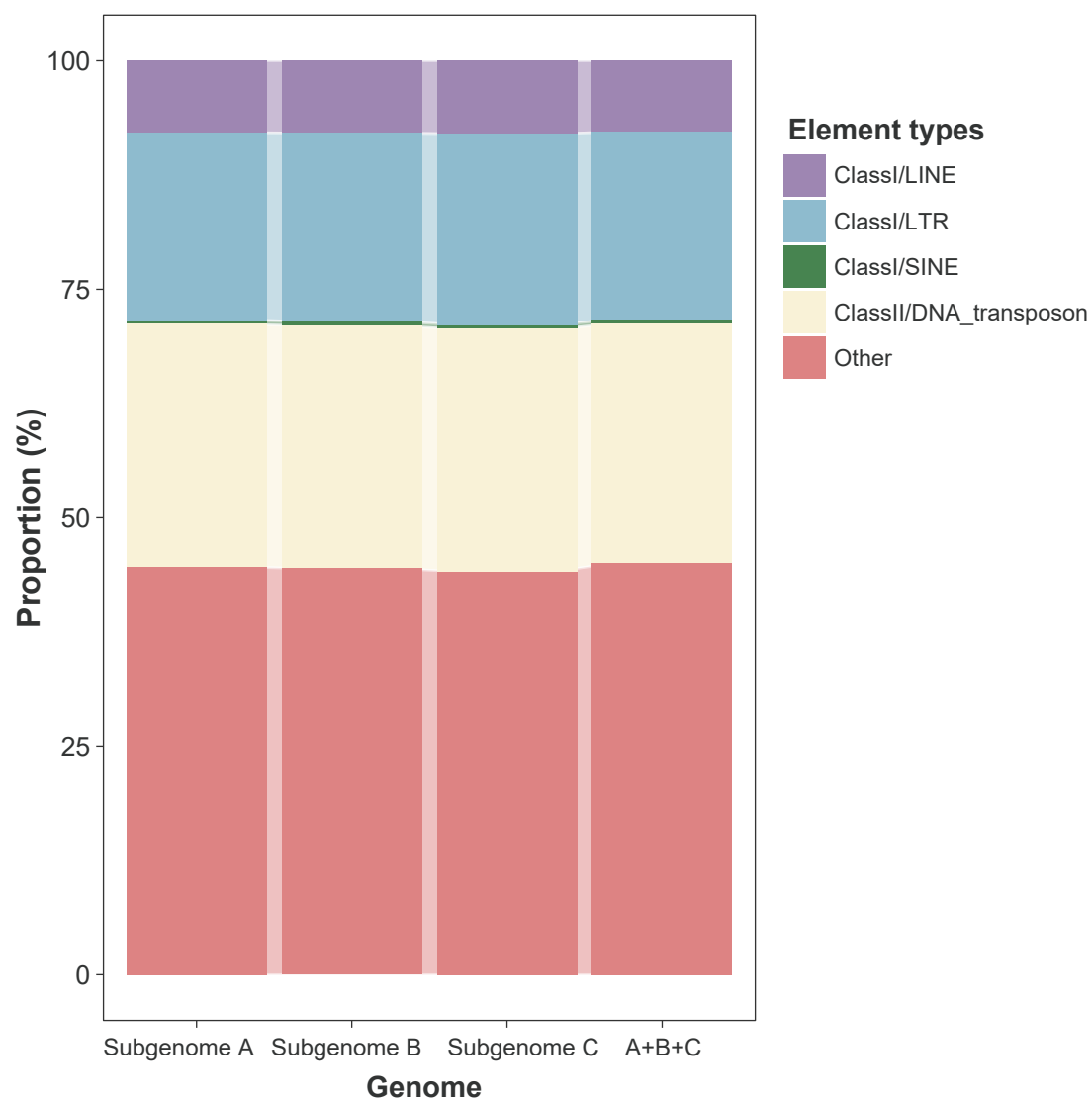
Supplementary Fig. 2



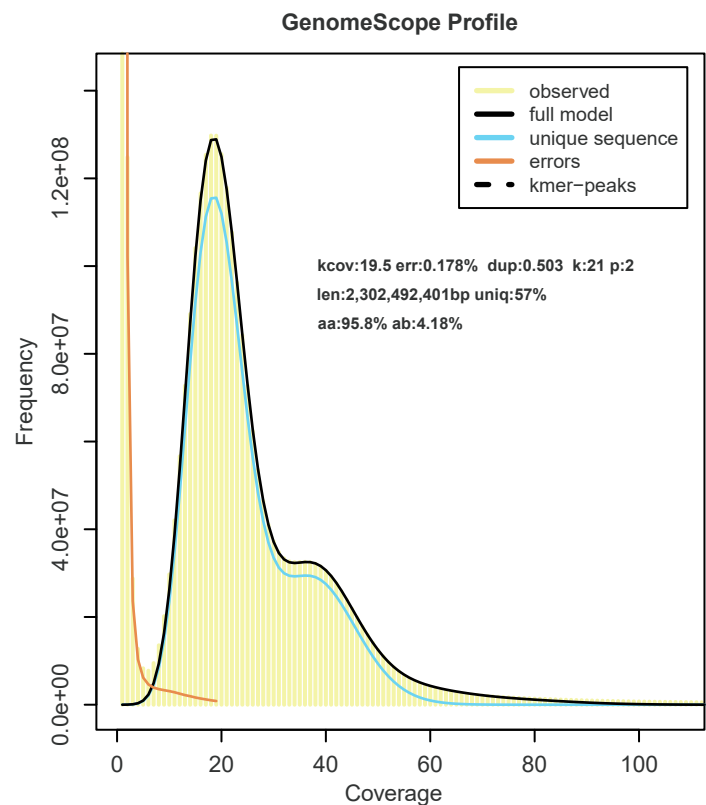
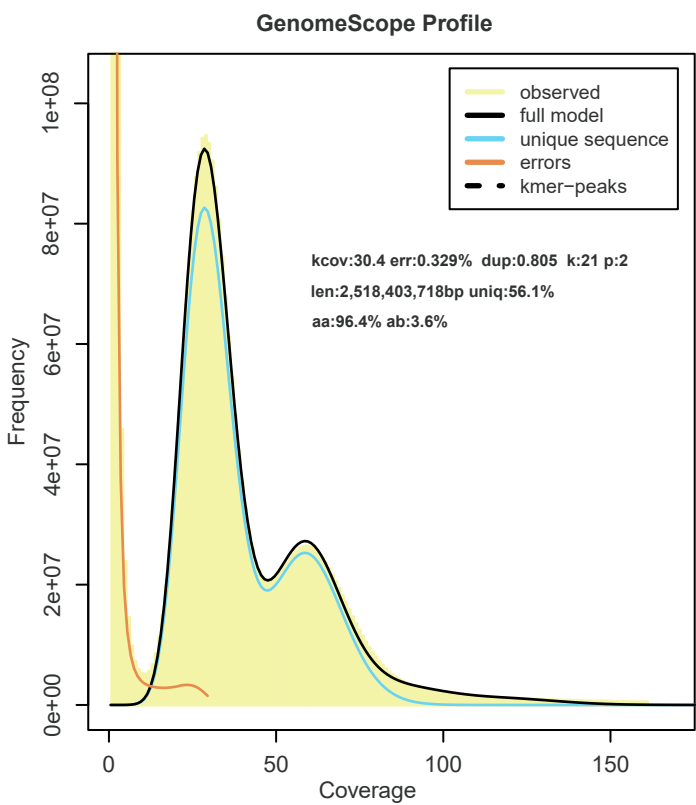
Supplementary Fig. 3



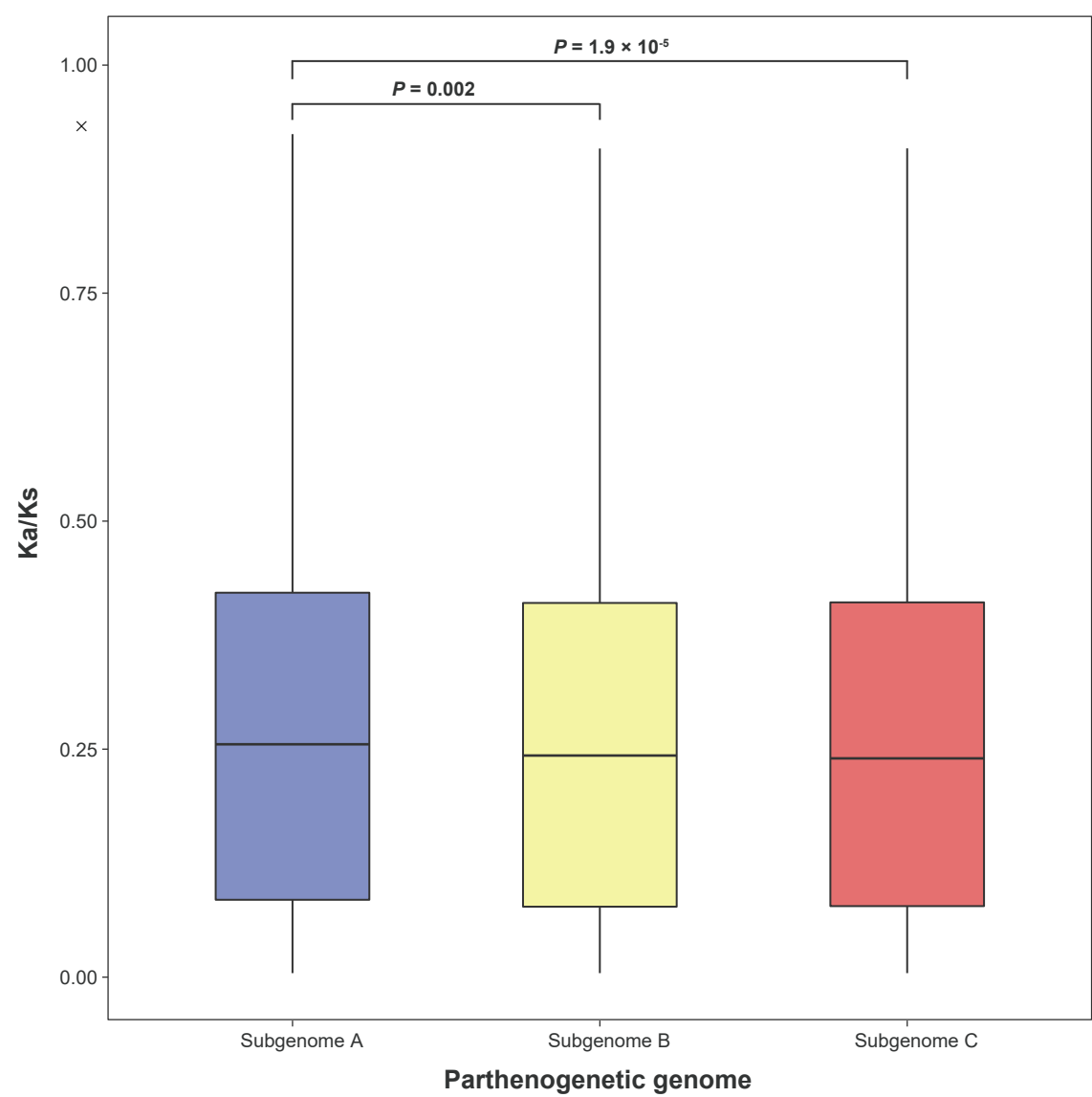
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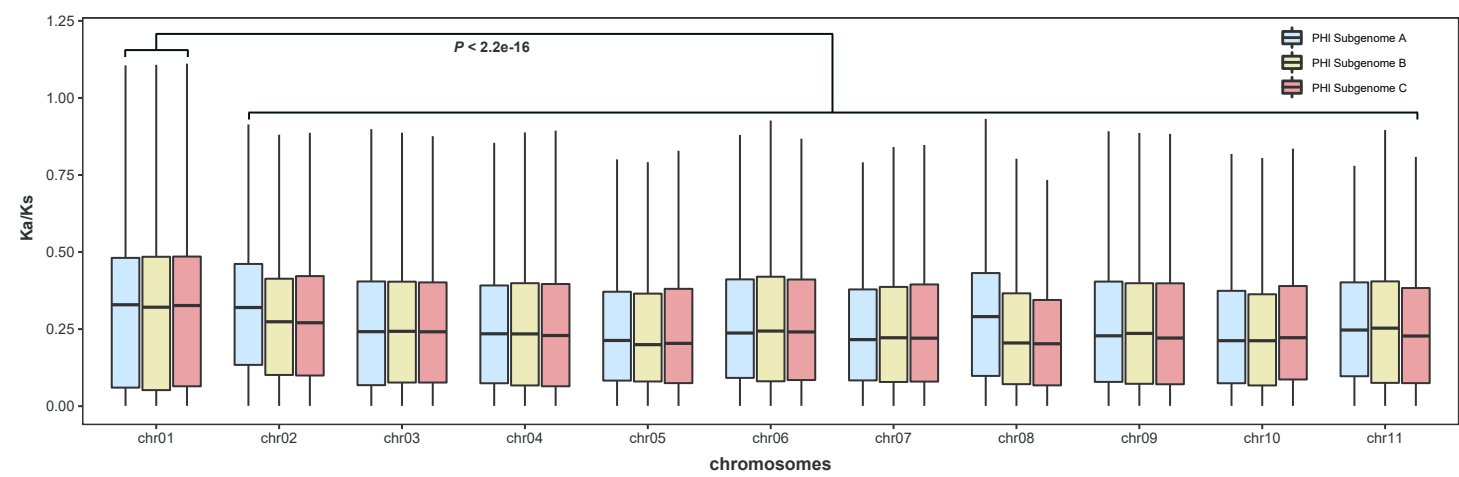
Supplementary Fig. 5



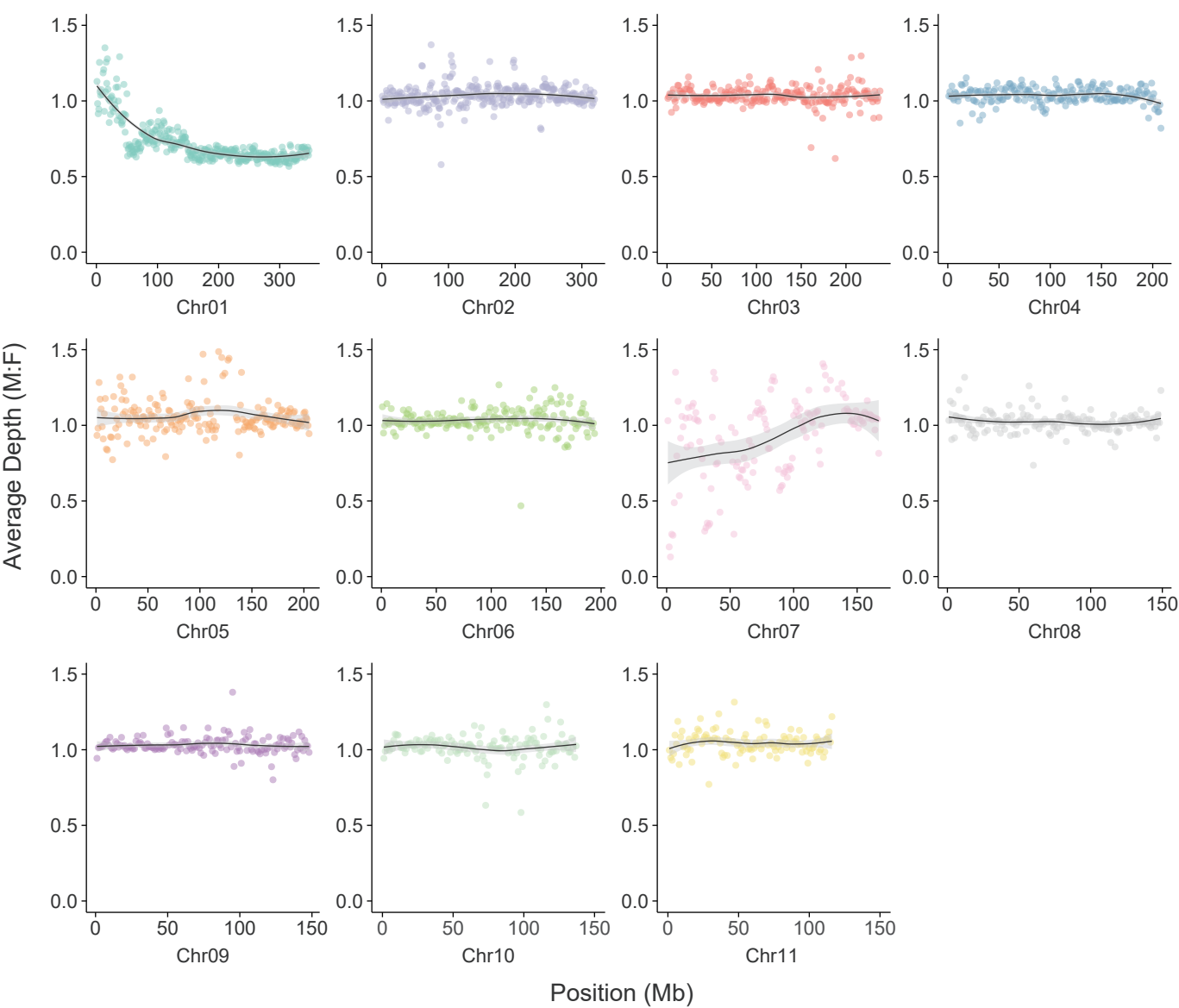
Supplementary Fig. 6



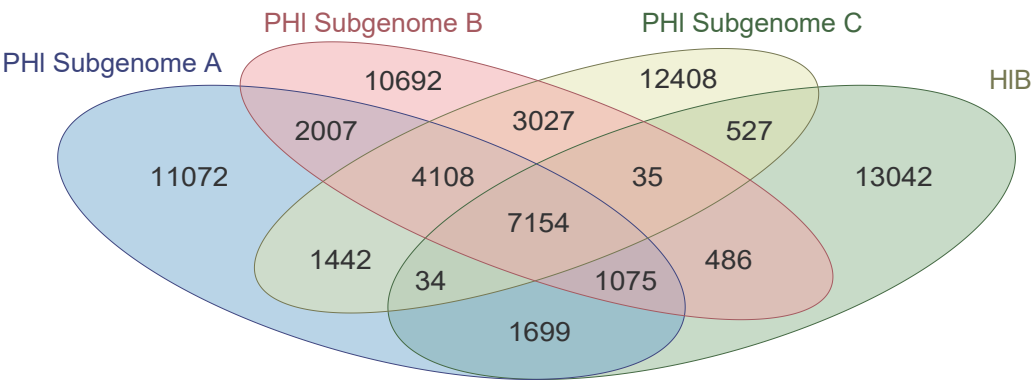
Supplementary Fig. 7



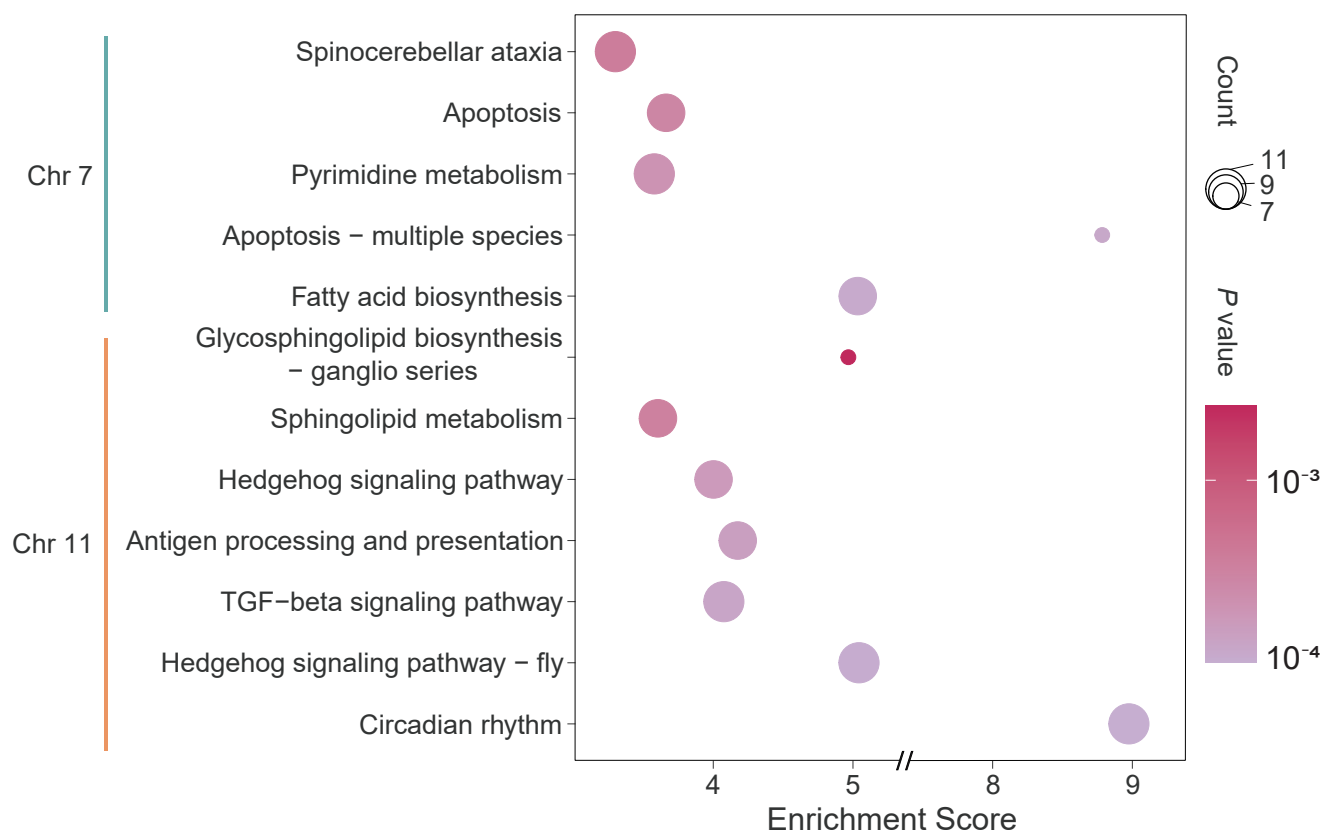
Supplementary Fig. 8



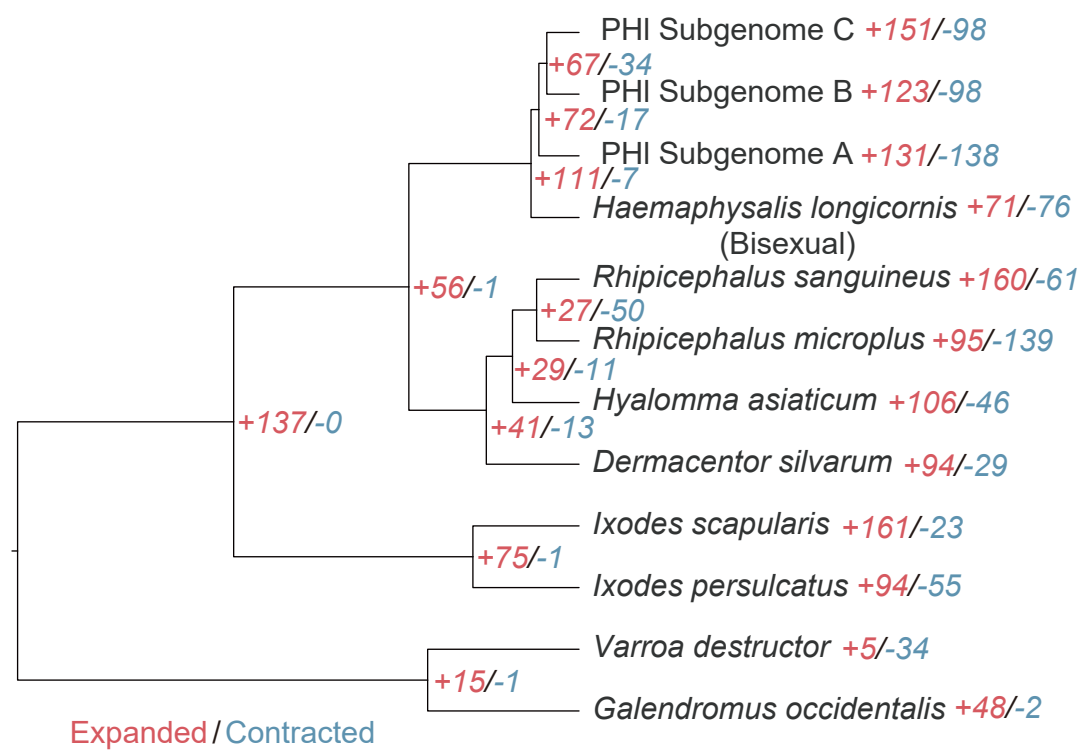
Supplementary Fig. 9



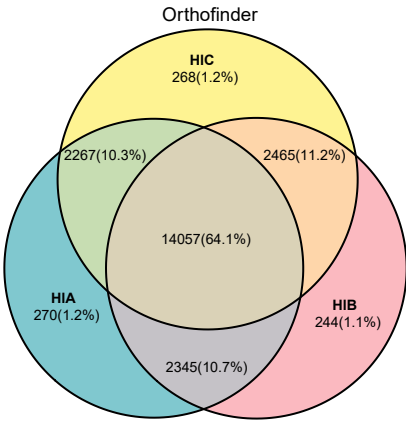
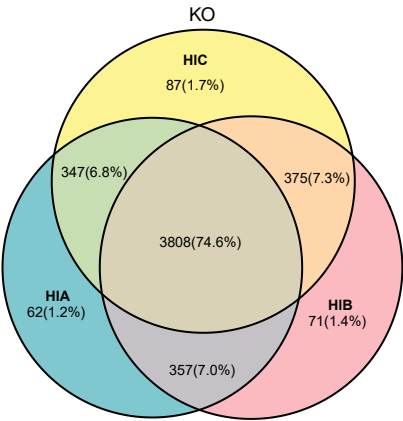
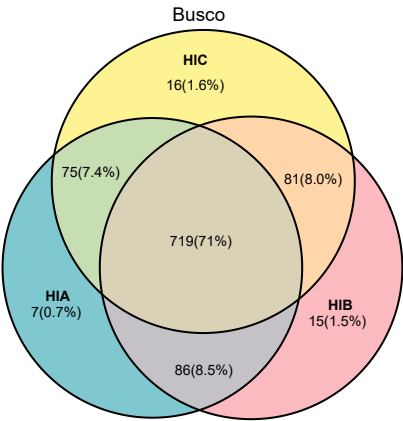
Supplementary Fig. 10



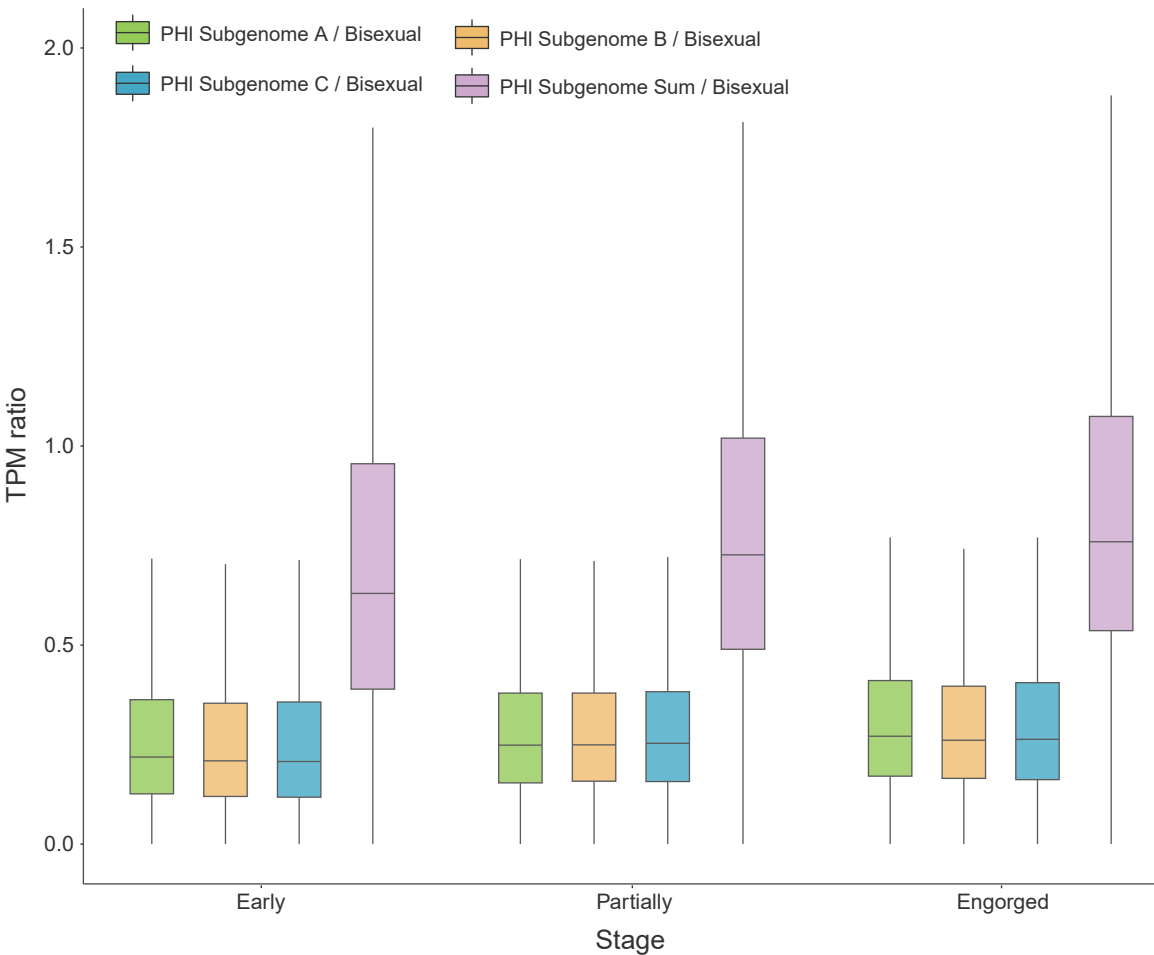
Supplementary Fig. 11



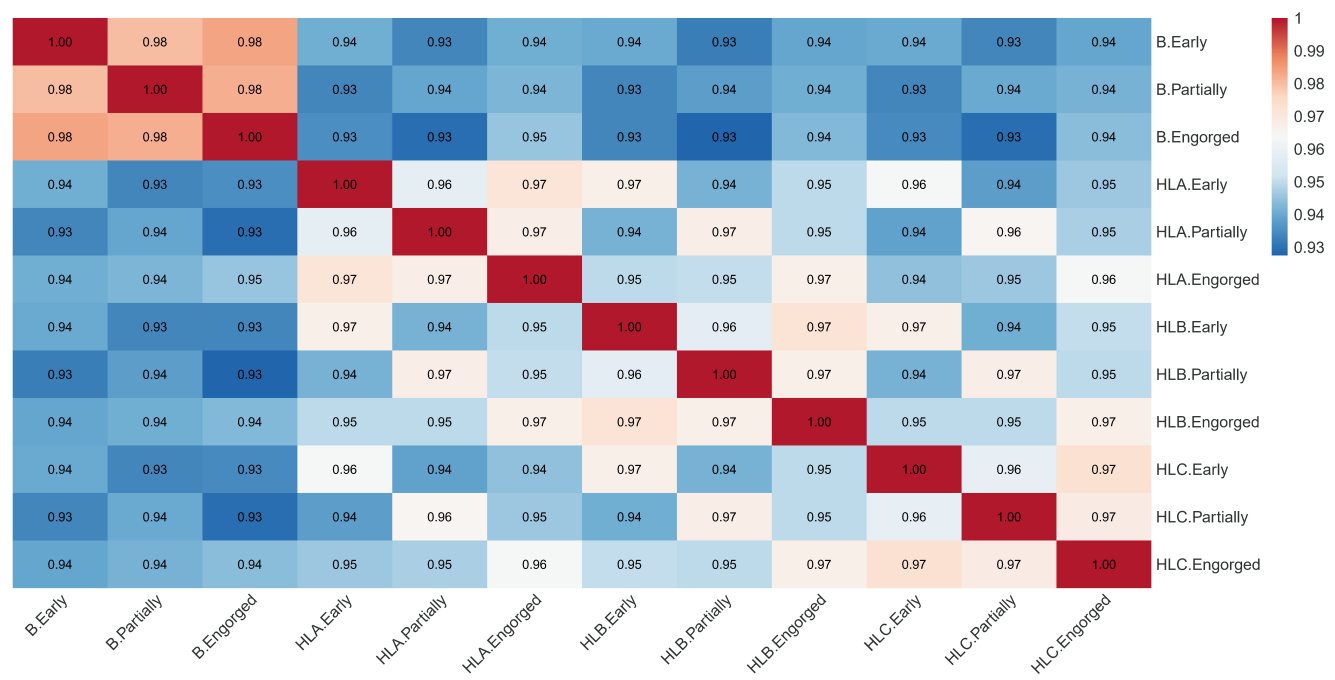
Supplementary Fig. 12



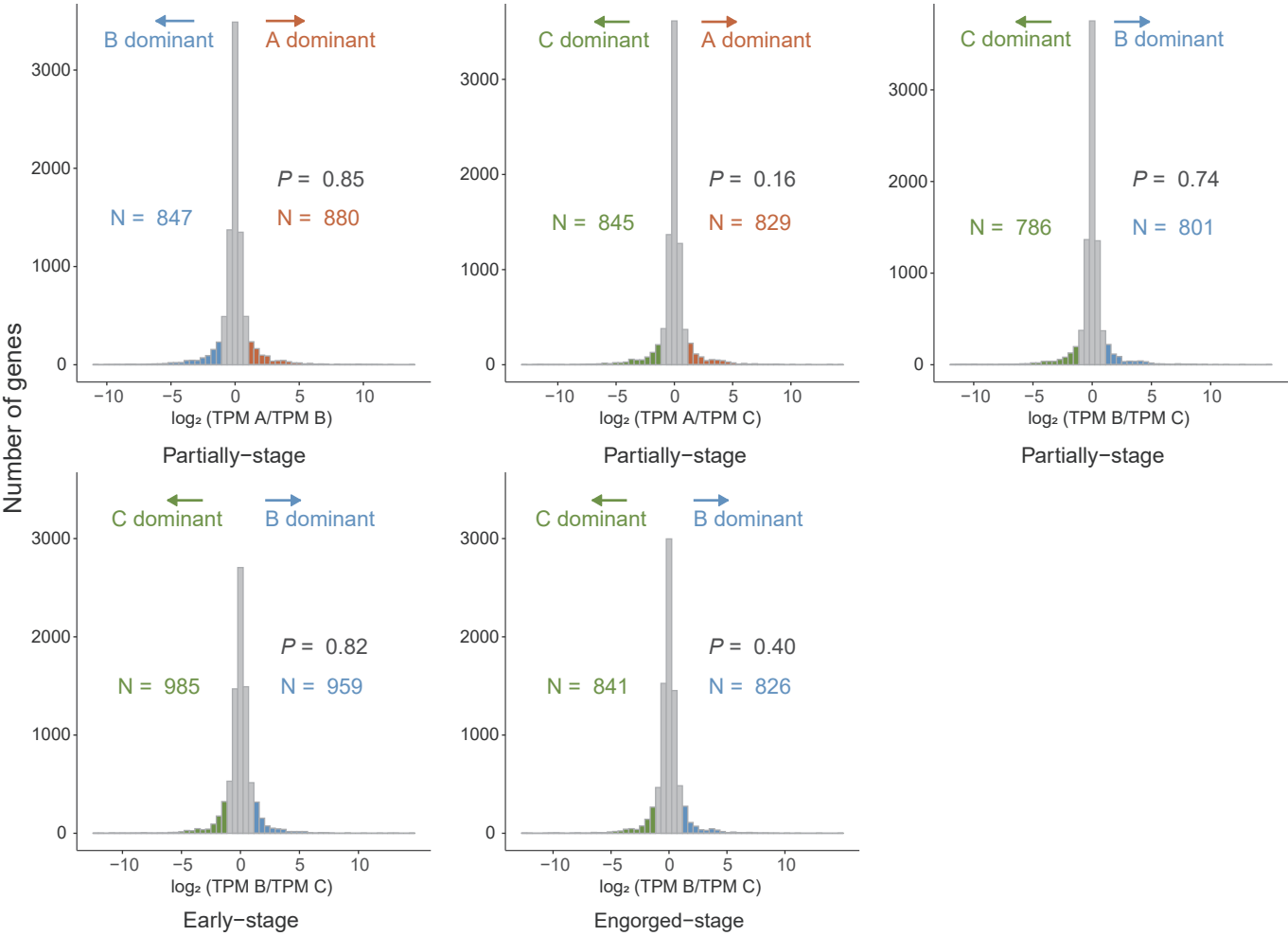
Supplementary Fig. 13



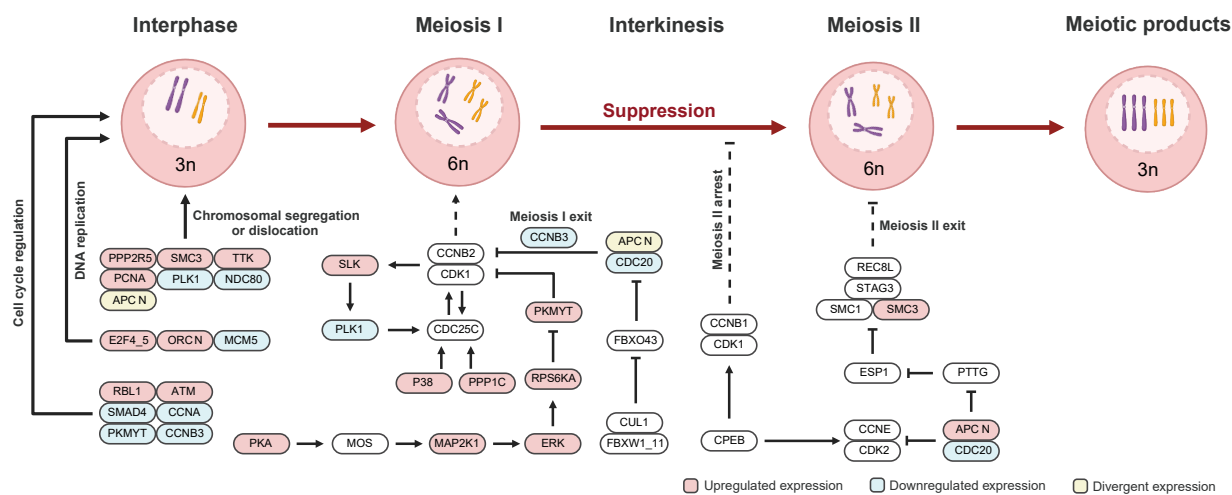
Supplementary Fig. 14

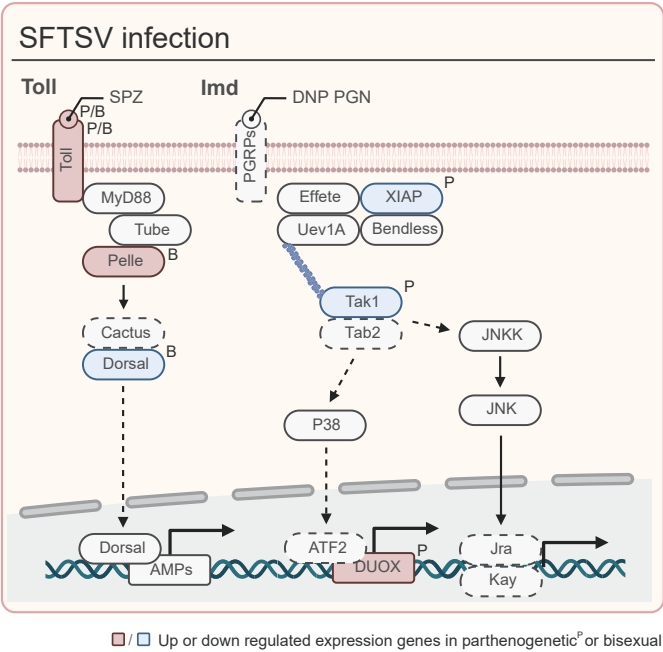


Supplementary Fig. 15

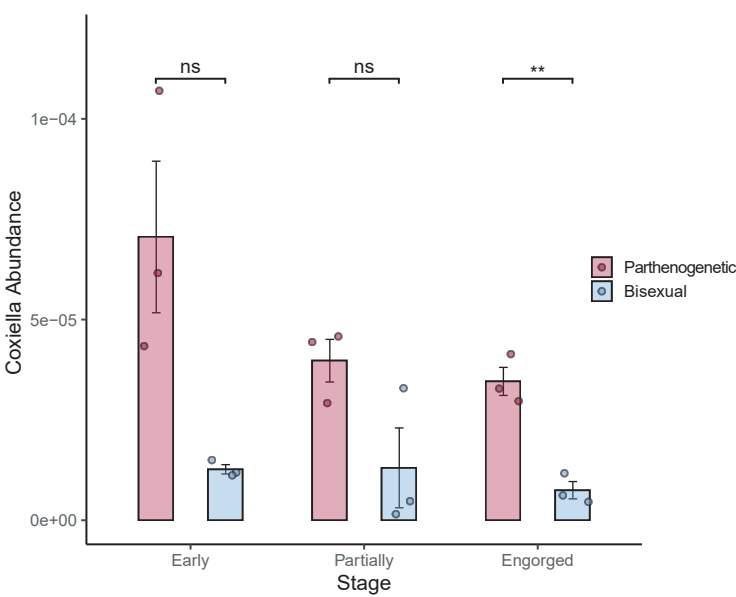


Supplementary Fig. 16

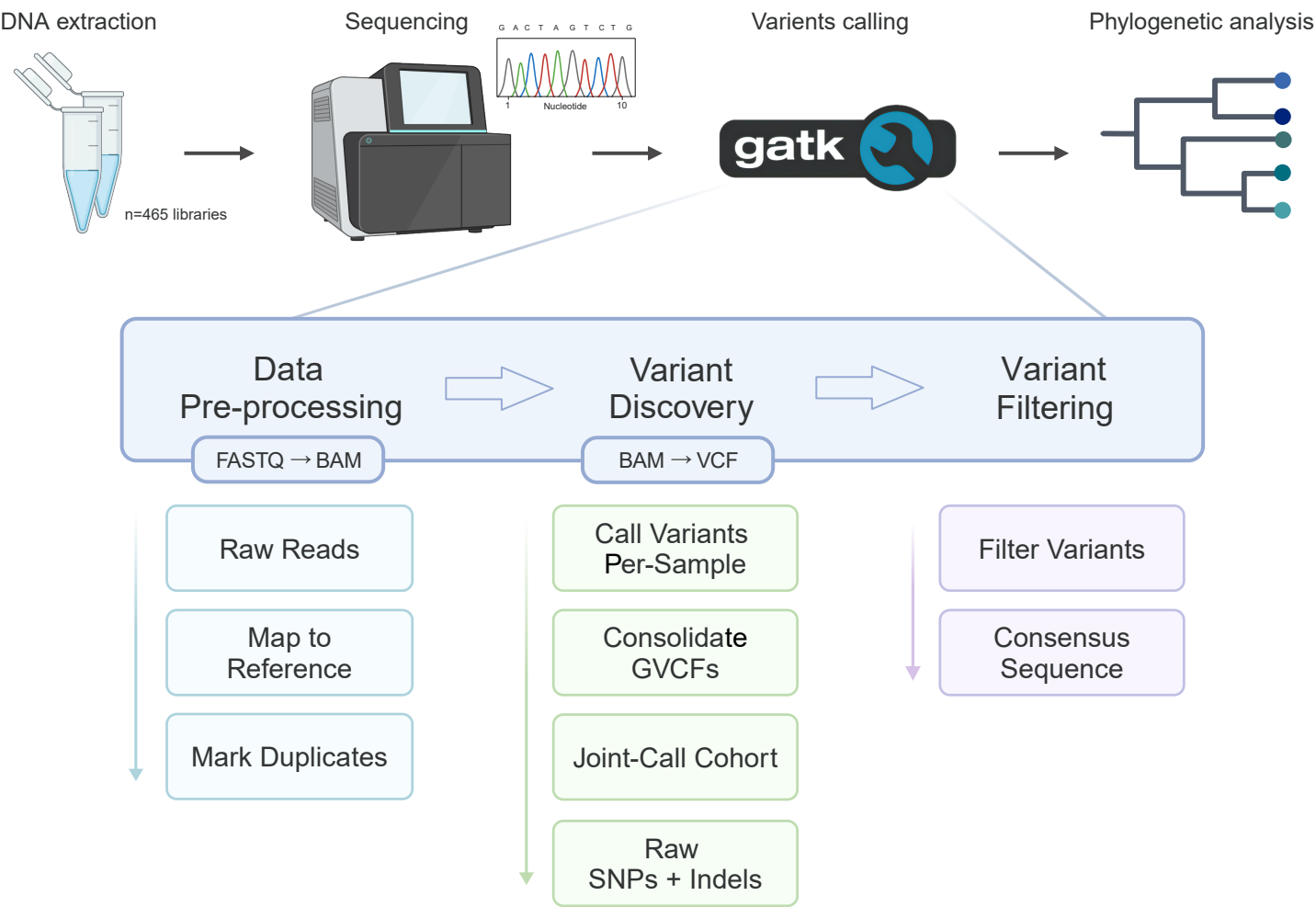




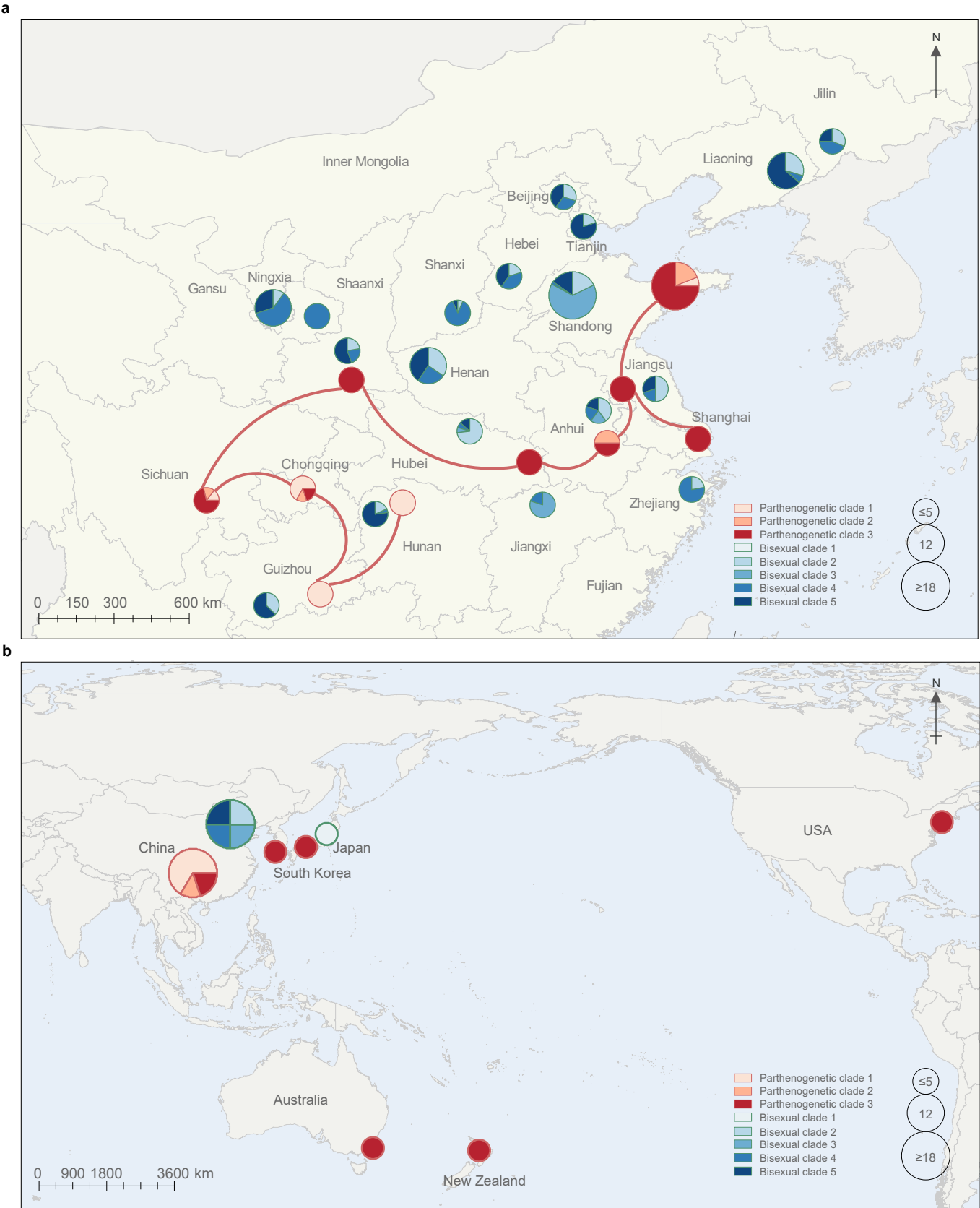
Supplementary Fig. 18



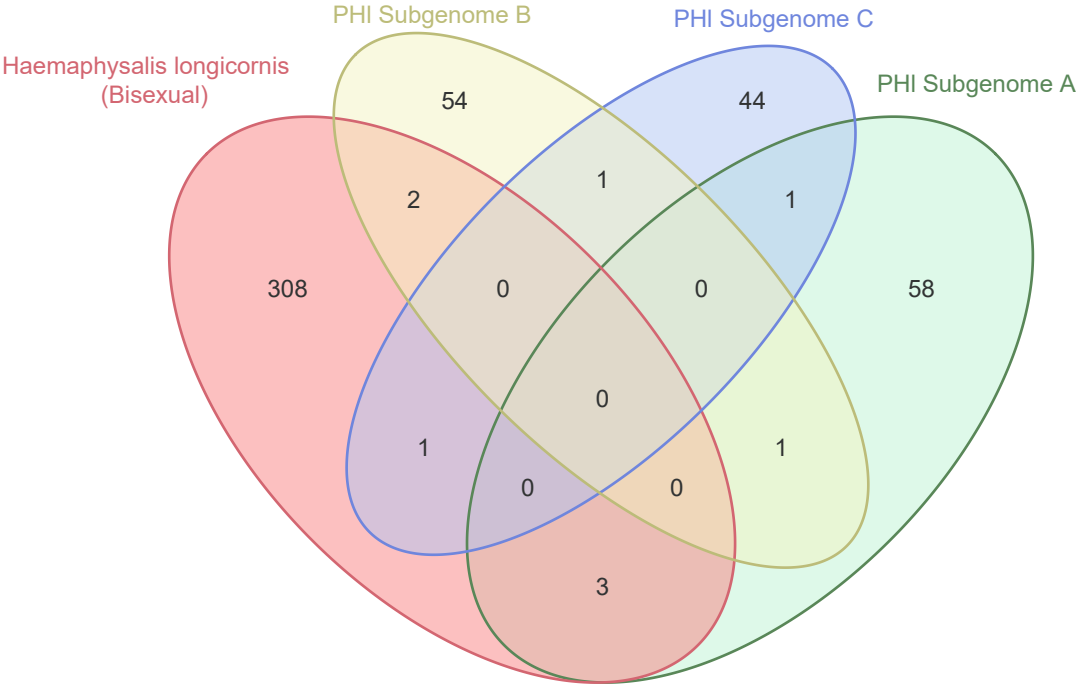
Supplementary Fig. 19



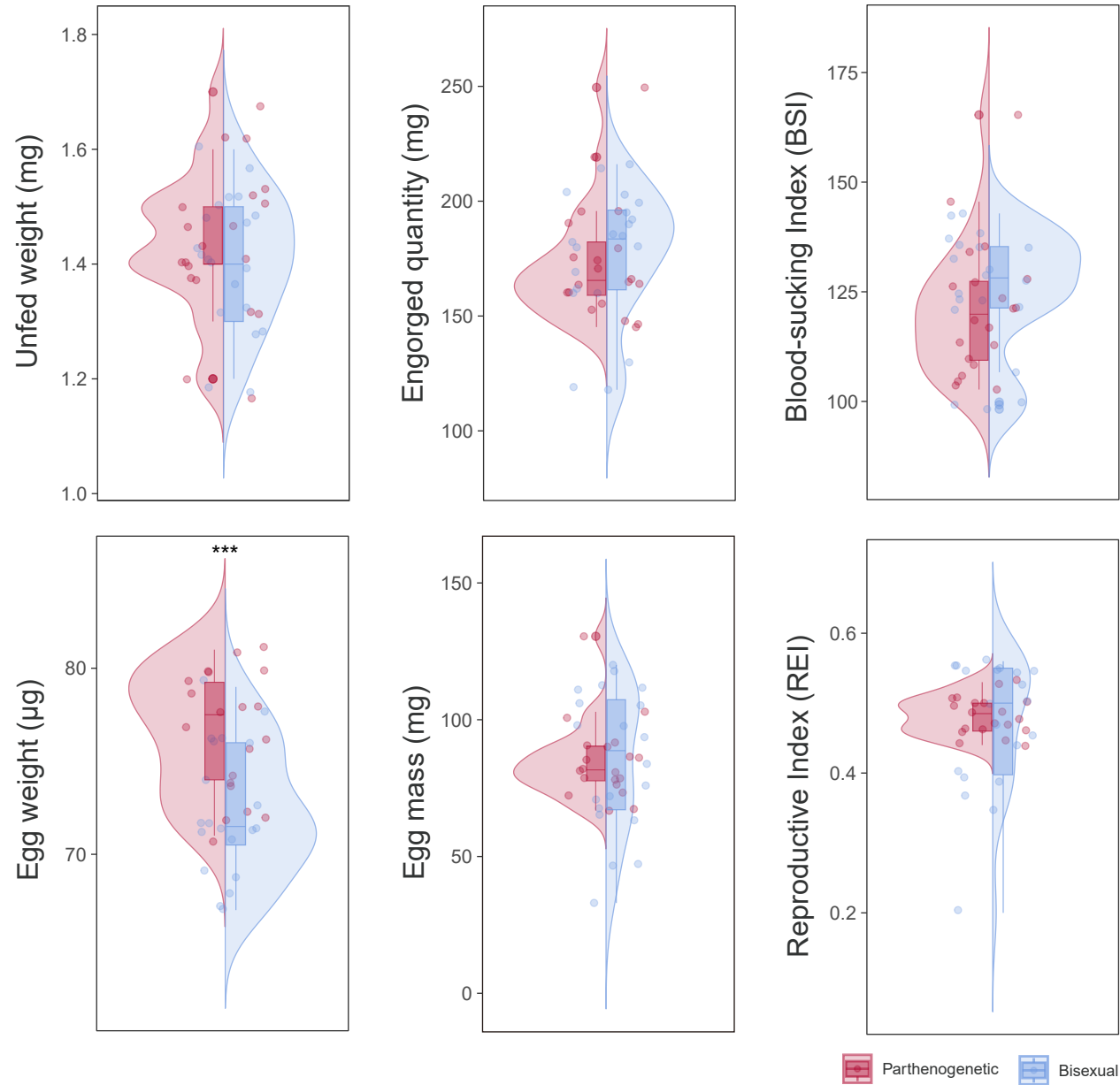
Supplementary Fig. 20

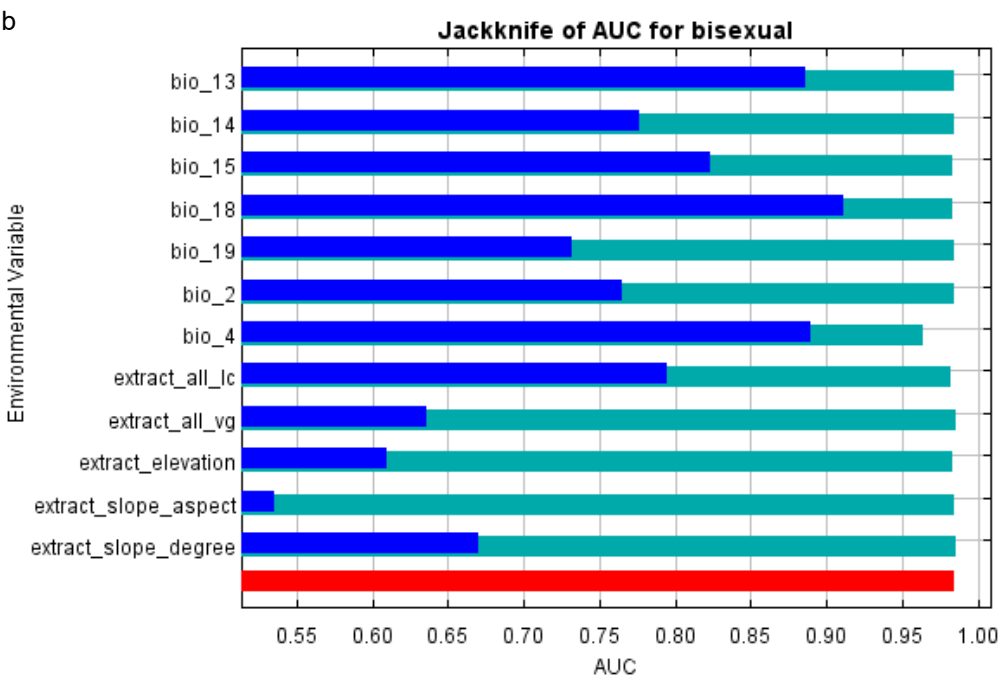
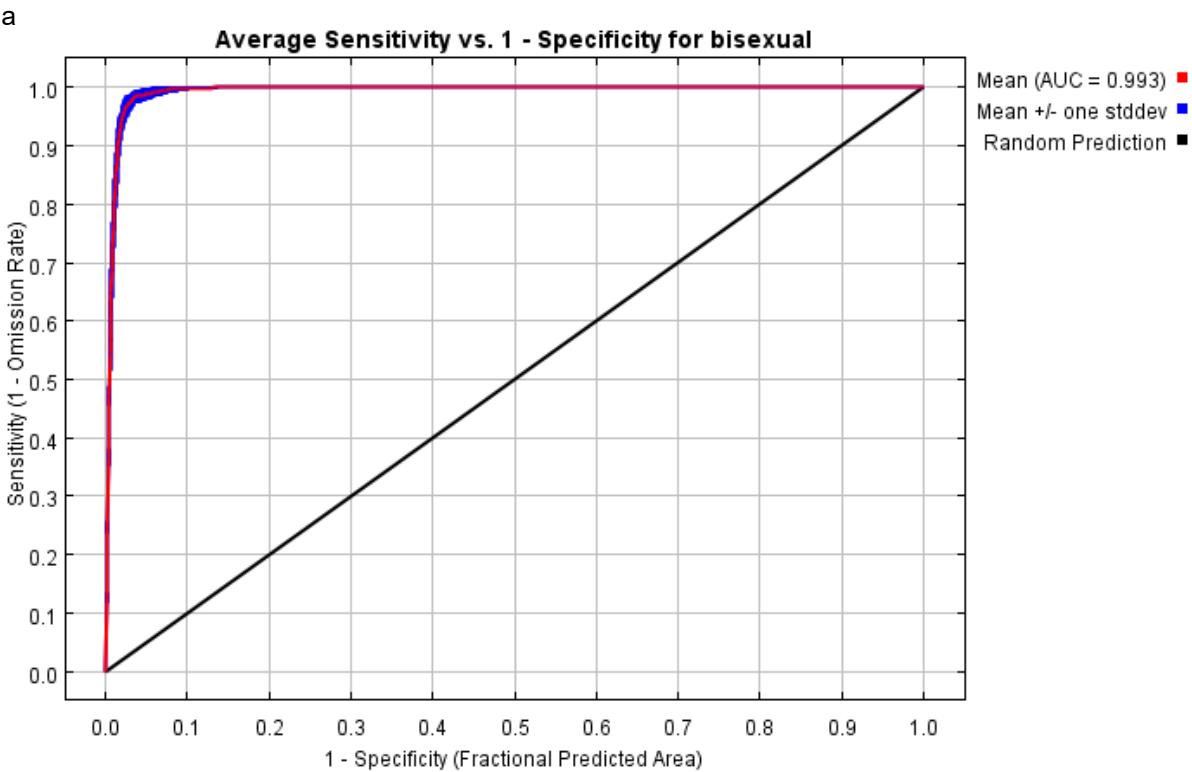


Supplementary Fig. 21

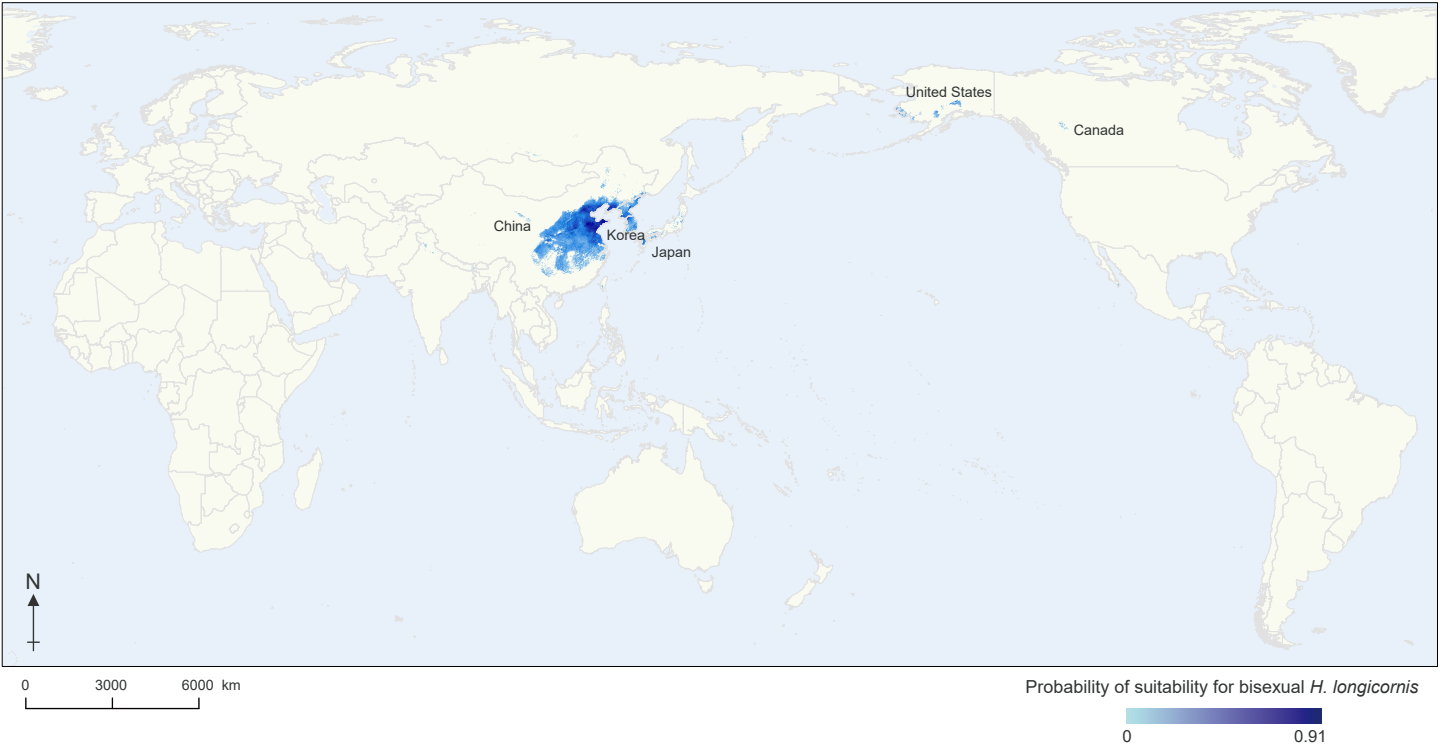


Supplementary Fig. 22

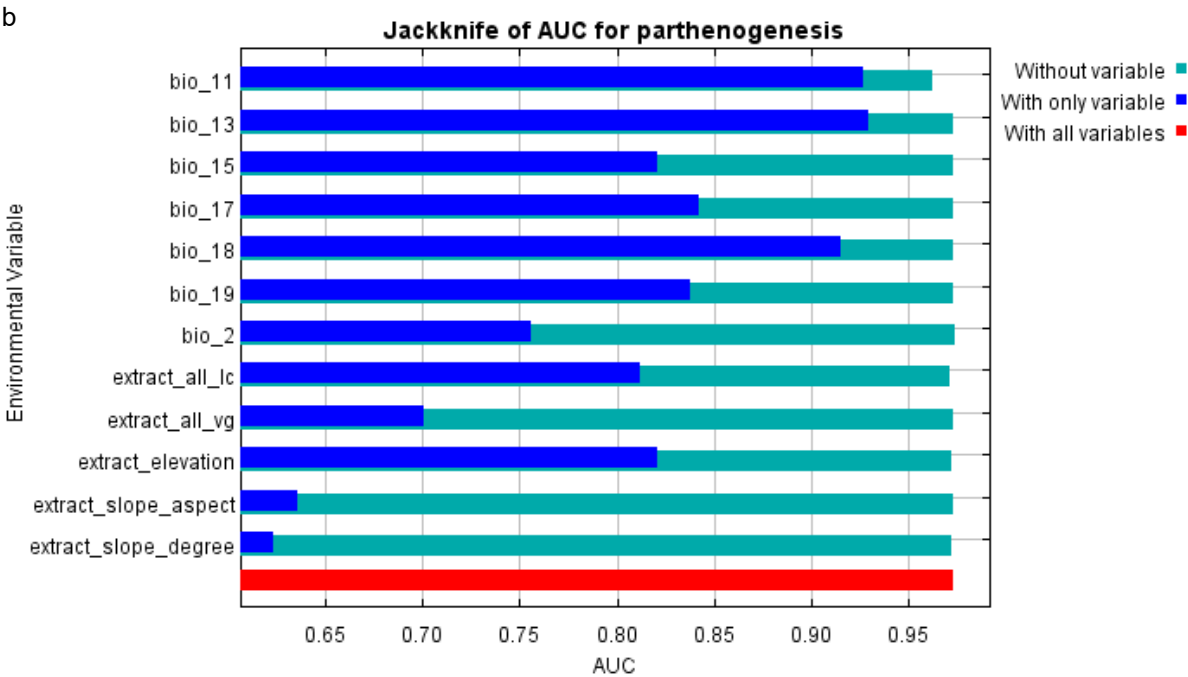
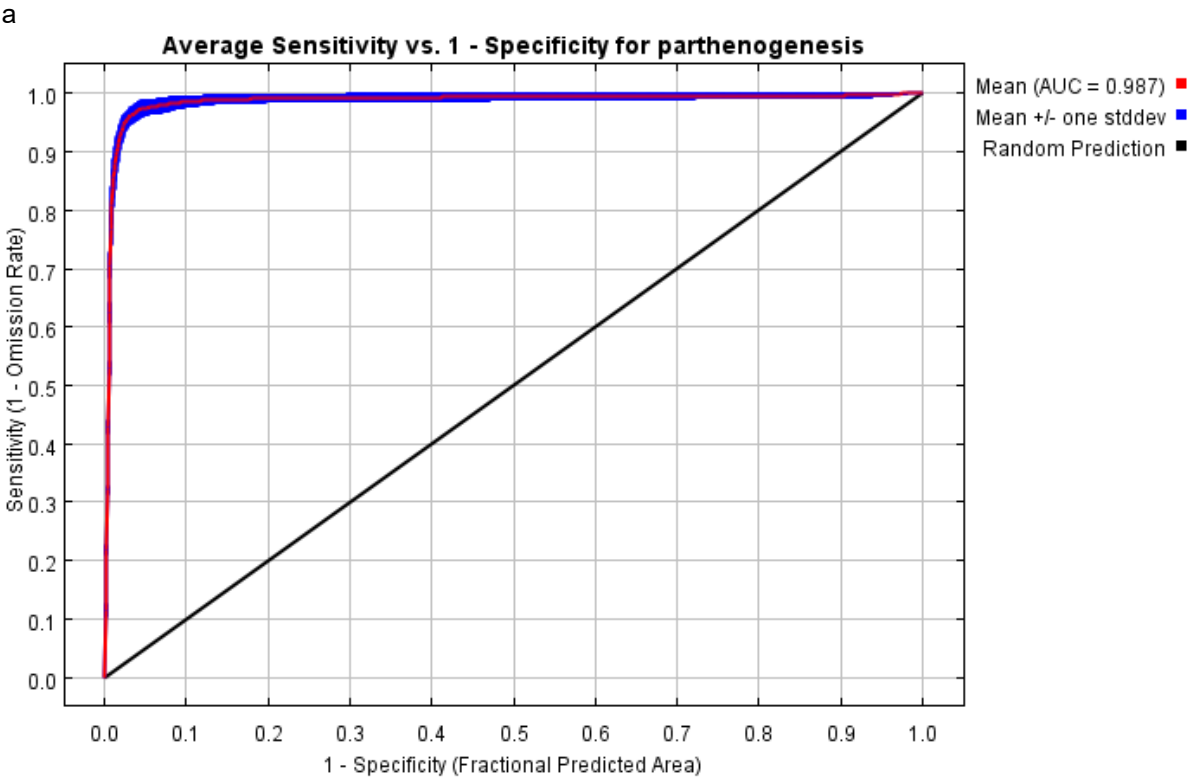




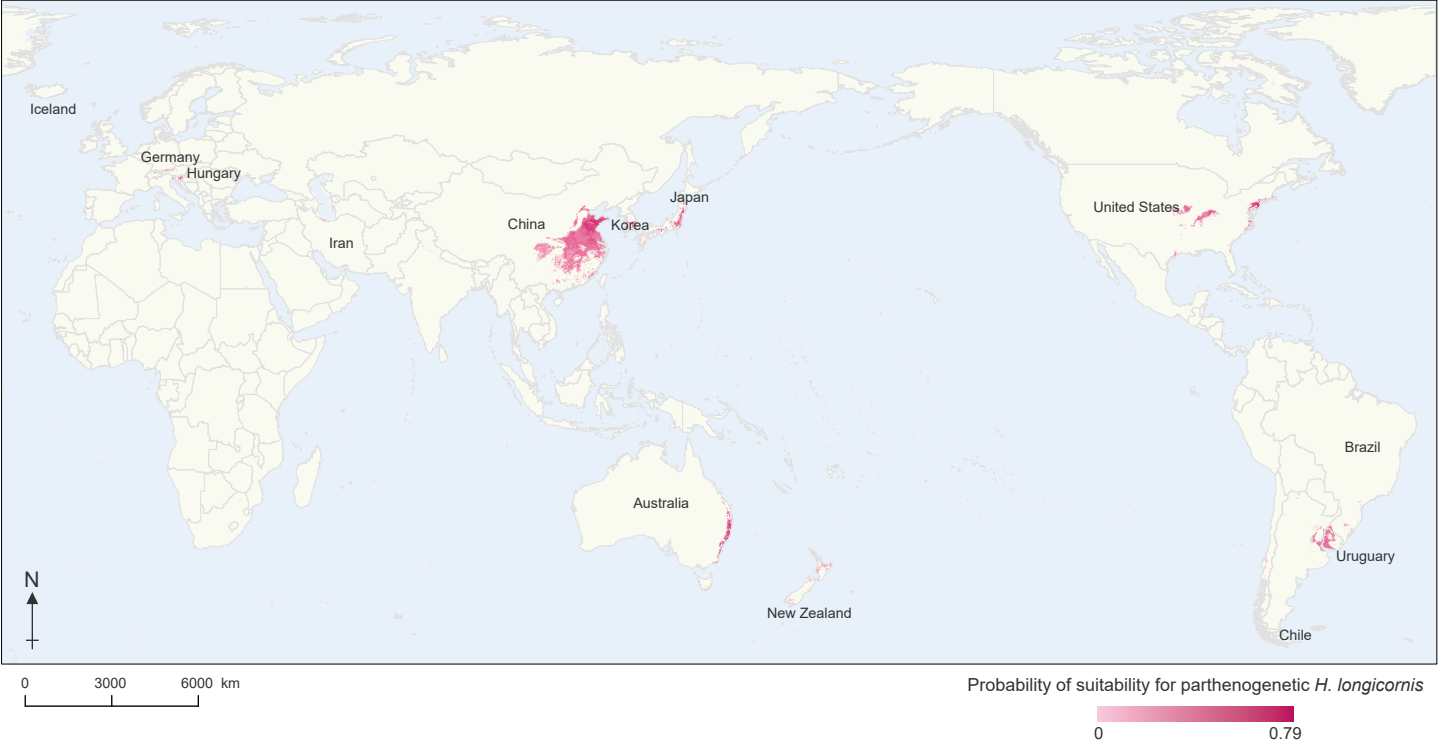
Supplementary Fig. 24



Supplementary Fig. 25



Supplementary Fig. 26



Supplementary Information

Supplementary Fig. 1 | Phylogenetic analysis of each chromosome in the three subgenomes of parthenogenetic *Haemaphysalis longicornis*. Maximum-likelihood tree was constructed using protein sequences from the single-copy gene families of each chromosome. PH1 denotes parthenogenetic *H. longicornis*.

Supplementary Fig. 2 | Statistics of alternative splicing annotations in the parthenogenetic *Haemaphysalis longicornis* genome. Red bars indicate alternative splicing annotations in the parthenogenetic genome integrated with Iso-Seq data; blue bars represent annotations in the previously published bisexual *H. longicornis* genome (without Iso-Seq data).

Supplementary Fig. 3 | A schematic structure of each alternative splicing category, along with the proportion of each category annotated in parthenogenetic *Haemaphysalis longicornis* genome.

Supplementary Fig. 4 | Proportion of annotated repeat elements in the three subgenomes and whole genome in parthenogenetic *Haemaphysalis longicornis*.

Supplementary Fig. 5 | K-mer spectra and fitted models of two bisexual *Haemaphysalis longicornis* samples. The plot was generated by GenomeScope software. The diploid genome has two major k-mer peaks. “ab” indicates the two nucleotides at given position of the genome are different.

Supplementary Fig. 6 | Boxplot of the Ka/Ks ratio distribution of protein-coding genes belonging to subgenome A, B and C, respectively. Wilcoxon rank-sum test was used to test the significance of the difference between subgenomes.

Supplementary Fig. 7 | Boxplot of the Ka/Ks ratio distribution of protein-coding genes in 33 chromosomes of parthenogenetic *Haemaphysalis longicornis*. Red, yellow and blue boxplots indicate the chromosomes belonging to subgenome A, B and C. Wilcoxon rank-sum test was used to test the difference between chr01 and other chromosomes.

Supplementary Fig. 8 | Short-read coverage ratio between male and female in a 100-kb fixed window of the bisexual *Haemaphysalis longicornis* genome. As bisexual females have two X chromosomes (XX) and males have only one (XO), the sequence read coverage of the X chromosome in males is expected to be half that of females. Only one chromosome, chr01, exhibited a male-to-female coverage ratio of approximately 0.5, while the ratios for the remaining autosomes were close to 1. Notably, the first 40–50 Mb region of chr01 showed a coverage ratio close to 1, suggesting a potential misassembly in the bisexual genome assembly. The lines represent smooth fitted curves generated using the LOESS method.

Supplementary Fig. 9 | Venn diagram of the homologue gene pairs in synteny blocks across three subgenomes of parthenogenetic *Haemaphysalis longicornis* and bisexual *Haemaphysalis longicornis*.

Supplementary Fig. 10 | KEGG pathway enrichment of the genes related to chromosome fission and fusion events. The size of each circle represents the number of genes in the pathways, and the color denotes the P-value of the enriched pathway using Fisher's exact test.

Supplementary Fig. 11 | Gene family contraction and expansion in tick species. Red indicates the number of significantly expanded gene families and green denotes the number of significantly contracted gene families.

Supplementary Fig. 12 | Gene family clustering analysis of three subgenomes. Complementary analyses were performed using BUSCO, KEGG Orthology (KO) annotation, and OrthoFinder-based gene family clustering.

Supplementary Fig. 13 | Dosage compensation effect of the homologous genes in three subgenomes. The y-axis represents the TPM ratio of homologous gene pairs between one parthenogenetic subgenome and the bisexual genome. Compared to diploid homologous genes, homologous genes in the three subgenomes exhibited reduced expression levels.

Supplementary Fig. 14 | Correlation between the gene expression of three subgenomes of parthenogenetic *Haemaphysalis longicornis* and bisexual *H. longicornis*. The number in each cell indicates the Spearman's correlation coefficient.

Supplementary Fig. 15 | Subgenome expression bias in the ovary during blood feeding. The x-axis represents the magnitude of expression differences between homoeologous gene pairs in the two subgenomes. N values indicate the number of dominant genes (fold change > 2) in one subgenome compared to the other. The P values indicate the significance of subgenome dominance by comparing the expression levels of homologous gene pairs of two subgenomes based on Wilcoxon rank-sum test.

Supplementary Fig. 16 | Functional genes related to reproduction and embryonic development in parthenogenetic *Haemaphysalis longicornis*.

Supplementary Fig. 17 | Differentially expressed genes in the Toll and Imd pathways in response to *SFTSV* infection in the parthenogenetic and bisexual ticks. The color represents the upregulation (red) or downregulation (blue) status of each gene, and dashed rectangles indicate genes that were not annotated by KEGG.

Supplementary Fig. 18 | Transcriptional abundance of *Coxiella* symbionts in parthenogenetic and bisexual *Haemaphysalis longicornis* in ovarian tissues across three feeding stages (early, partially engorged, and fully engorged).

Supplementary Fig. 19 | The workflow to call genetic variants and build phylogenetic tree.

Supplementary Fig. 20 | Geographical population structure of *Haemaphysalis longicornis* populations. **a**, Geographical population structure in Chian. Pie charts on the map summarized the number of samples for each clade in each province. Neighboring provinces with the most similar parthenogenetic population structure are connected. **b**, Geographical population structure in the world. Pie charts on the map summarized the number of samples for each clade in each country.

Supplementary Fig. 21 | Venn diagram for the positively selected genes in three subgenomes of parthenogenetic *Haemaphysalis longicornis* and bisexual *Haemaphysalis longicornis*.

Supplementary Fig. 22 | Reproductive characteristics of parthenogenetic and bisexual populations. Wilcoxon rank-sum test was used to test the significance of the difference between two colonies. P values less than 0.01 are summarized with three asterisks, and P values less than 0.0001 are summarized with four asterisks.

Supplementary Fig. 23 | Maxent model training for parthenogenetic *Haemaphysalis longicornis*. a. The average area under the curve (AUC) for parthenogenetic *H. longicornis* Maxent models. b. Relative importance of environmental variables for parthenogenetic *H. longicornis* under current environmental conditions based on Jack-knife test.

Supplementary Fig. 24 | Potential global distribution map of parthenogenetic *Haemaphysalis longicornis*. The probabilities of habitat suitability are shown as predicted by Maxent.

Supplementary Fig. 25 | Maxent model training for bisexual *Haemaphysalis longicornis*. a. The average area under the curve (AUC) for Maxent models. b. Relative importance of environmental variables for bisexual *H. longicornis* under current environmental conditions based on Jack-knife test.

Supplementary Fig. 26 | Potential global distribution map of bisexual *Haemaphysalis longicornis*. The probabilities of habitat suitability are shown as predicted by Maxent.

Supplementary Table 1 | Statistics of HiFi sequencing results.

Data type	Reads number	Reads base	Reads length N50	Average length	Reads length Max
CCS	10,643,777	210,418,098,556	20,607	19,769	50,685

Supplementary Table 2 | Statistics of Hi-C sequencing results.

Data type	Total read pairs	Reads base	Unique mapped read pairs	Valid interaction pairs
Hi-C	2,211,953,902	659,591,444,382	1,747,303,521	1,352,671,775

Supplementary Table 3 | Statistics of Iso-Seq sequencing results.

Samples	CCS* Number	Read bases	Average sequencing depth	Number of	Average
				consensus	consensus
				isoforms	isoforms
					read length
PF4	596,168	1,141,906,025	35	147,239	1,834

*CCS: circular consensus sequencing

Supplementary Table 4 | Mitochondrial sequences of *Haemaphysalis longicornis* obtained from GenBank.

ID	Country	B/P
MW642354.1	China	Bisexual
MW642377.1	China	Bisexual
MW642379.1	China	Bisexual
OM368291.1	China	Bisexual

MW642352.1	China	Bisexual
MW642395.1	China	Bisexual
MW642401.1	China	Bisexual
MW642387.1	China	Bisexual
MW642386.1	China	Bisexual
MW642388.1	China	Bisexual
MW642380.1	China	Bisexual
MW642399.1	China	Bisexual
MW642398.1	China	Bisexual
MW642400.1	China	Bisexual
NC_037493.	China	Bisexual
MG450553.1	China	Bisexual
MT780294.1	China	Bisexual
MW642349.1	China	Bisexual
MW642353.1	China	Bisexual
MW642351.1	China	Bisexual
MW642341.1	China	Bisexual
MW642346.1	China	Bisexual
OM368274.1	China	Bisexual
MW642378.1	China	Bisexual
OL741744.1	Japan	Bisexual
MW642370.1	China	Bisexual

MW642373.1	China	Bisexual
MW642381.1	China	Bisexual
MW642392.1	China	Bisexual
MW642396.1	China	Bisexual
MW642355.1	China	Bisexual
MW642345.1	China	Bisexual
MW642365.1	China	Bisexual
MW642344.1	China	Bisexual
OM368286.1	China	Bisexual
MW642393.1	China	Bisexual
MW642361.1	Japan	Bisexual
MW642356.1	China	Bisexual
MW642367.1	China	Bisexual
MW642371.1	China	Bisexual
MW642358.1	China	Bisexual
MW642337.1	China	Bisexual
MW642394.1	China	Bisexual
MK450606.1	China	Bisexual
MW642338.1	China	Parthenogenetic
MW642374.1	China	Parthenogenetic
MW642343.1	China	Parthenogenetic
OM368281.1	China	Parthenogenetic

PP376089.1	China	Parthenogenetic
PP376090.1	China	Parthenogenetic
MW642375.1	China	Parthenogenetic
PP376091.1	China	Parthenogenetic
PP376092.1	China	Parthenogenetic
MW642359.1	China	Parthenogenetic
MW642363.1	China	Parthenogenetic
MW642342.1	China	Parthenogenetic
MW642376.1	China	Parthenogenetic
MK439888.1	China	Parthenogenetic
MW642402.1	China	Parthenogenetic
MW642382.1	China	Parthenogenetic
MW642407.1	China	Parthenogenetic
MW642383.1	China	Parthenogenetic
MW642403.1	China	Parthenogenetic
MW642348.1	China	Parthenogenetic
MW642372.1	China	Parthenogenetic
PP386058.1	China	Parthenogenetic
MW642404.1	USA	Parthenogenetic
MW642405.1	Korea	Parthenogenetic
MW642369.1	China	Parthenogenetic
MW642384.1	China	Parthenogenetic

MW642385.1	China	Parthenogenetic
MW642390.1	China	Parthenogenetic
MW642364.1	Australia	Parthenogenetic
MW642366.1	Australia	Parthenogenetic
MW642360.1	Japan	Parthenogenetic
MW642406.1	New Zealand	Parthenogenetic
MW642347.1	China	Parthenogenetic
MW602986.1	USA	Parthenogenetic
ON800836.1	USA	Parthenogenetic
MW642368.1	China	Parthenogenetic
MW642357.1	China	Parthenogenetic
MW642339.1	China	Parthenogenetic
MW642350.1	China	Parthenogenetic
MW642397.1	China	Parthenogenetic
MW642389.1	China	Parthenogenetic
MW642340.1	China	Parthenogenetic
MW642362.1	China	Parthenogenetic
