

Figure S1. ML tree of domestic dog (D) and wolf (W) mt genomes, constructed on the basis of the GTR+I model (logL = -45701.2). Numbers on branches are percentages of 1000 bootstrap samples supporting the branch; only values $\geq 50\%$ are shown.

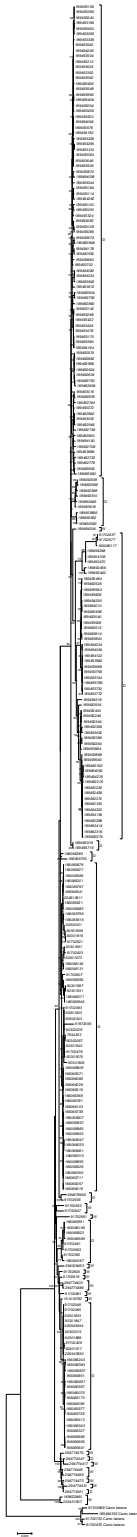


Figure S2. ML tree of domestic pig (D) and wild boar (W) mt genomes, constructed on the basis of the TN93+G+I model (logL = -41231.1). Numbers on branches are percentages of 1000 bootstrap samples supporting the branch; only values $\geq 50\%$ are shown.

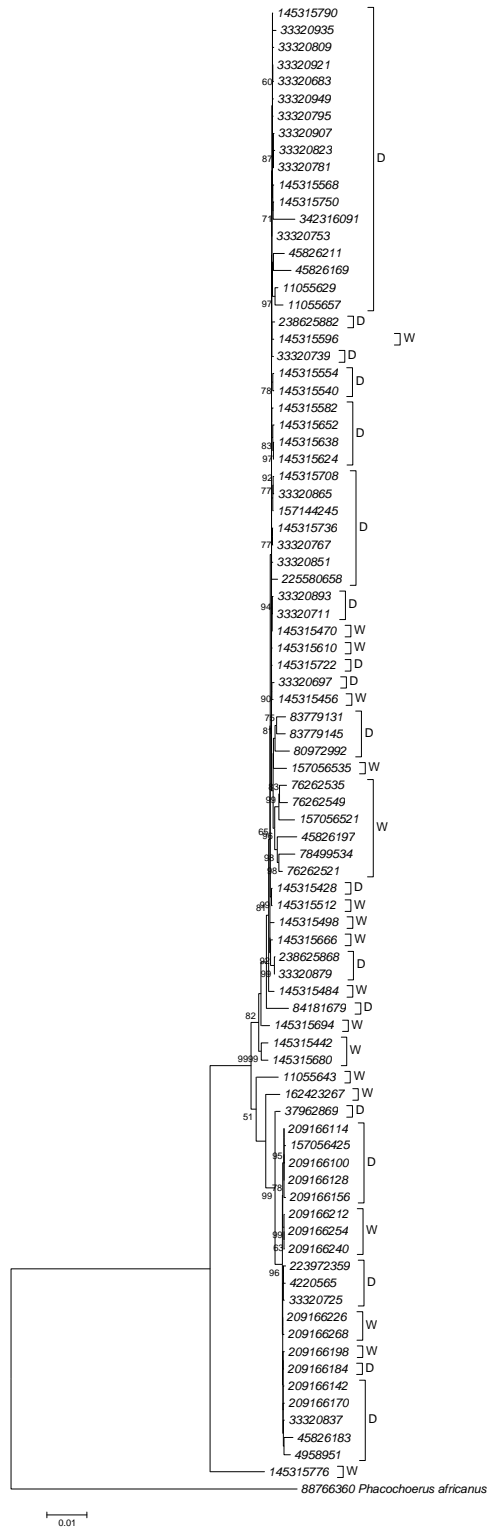


Figure S3. ML tree of domestic chicken (D) and red junglefowl (W) mt genomes, constructed on the basis of the HKY+G+I model (logL = -29453.3). Numbers on branches are percentages of 1000 bootstrap samples supporting the branch; only values $\geq 50\%$ are shown.

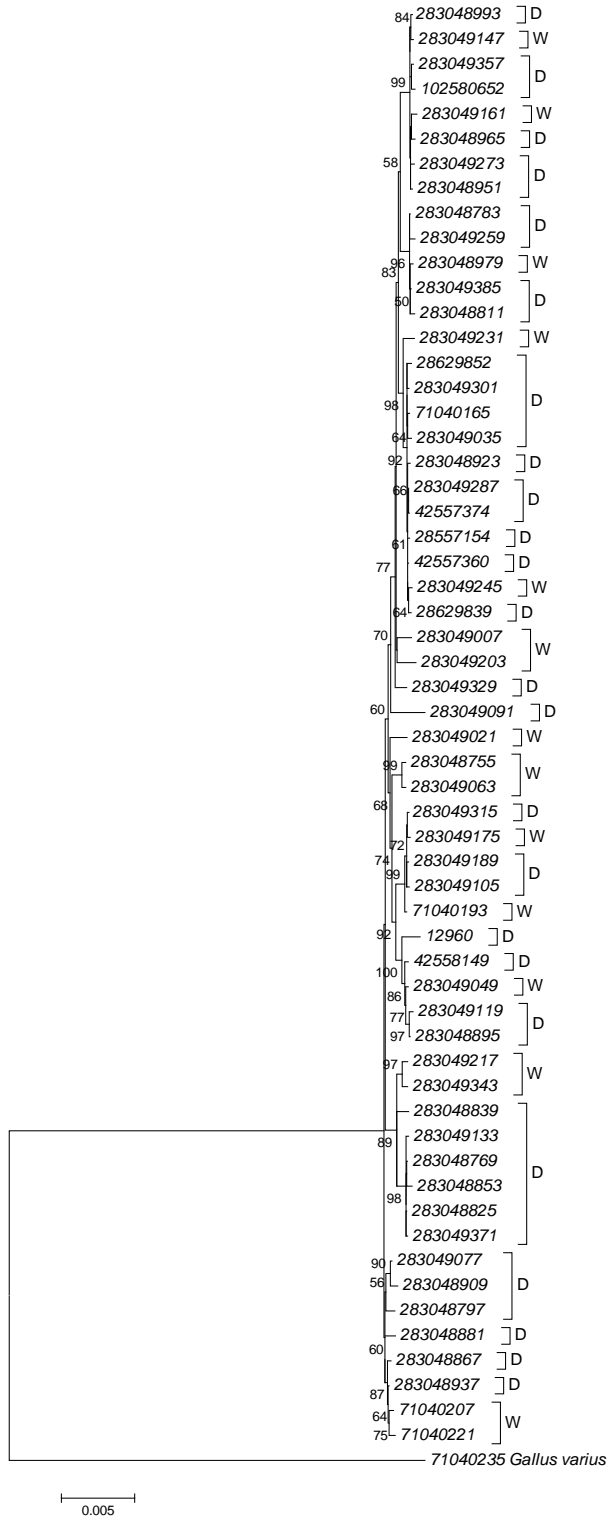


Figure S4. ML tree of domestic silkworm (*B. mori*) and wild silkworm (*B. mandarina*) mt genomes, constructed on the basis of the GTR+G+I model (logL = -45798.0). Numbers on branches are percentages of 1000 bootstrap samples supporting the branch; only values $\geq 50\%$ are shown.

