



Figure S1. Position of the studied populations (Urals, Caucasus, Central Asia, Russian Far East) on the phylogenetic tree of main wild boar mtDNA lineages. The Bayesian (MCMC) haplotype tree based on the partial sequences of the mtDNA control region (547 bp) from the Eurasian wild boar. The tree reconstruction is based on the 17 haplotypes of wild boars sequenced in this work (haplotypes suspected to originate from hybrids between wild boar and domestic pig, DK4 and DK12, were excluded from the analysis) and 52 sequences representing haplotypes of animals classified as wild *S. scrofa* from Europe (n = 13) and Asia (n = 38) downloaded from GenBank. Haplotypes sequenced in this study begin with DK and are shown in red color. The haplotypes reported by Choi et al. (2020) are shown in green color. The haplotypes presented in Niedziałkowska et al. (2021) are shown in brown color. Haplotypes downloaded from GenBank and identical to those sequenced in this study were excluded from the analysis. The HKY+G model was implemented. Bayesian posterior probability is shown for branches having over 70% support. Major clades are indicated with different colors. The phylogeny was calculated in MrBayes 3.4 [44] with default values of priors.