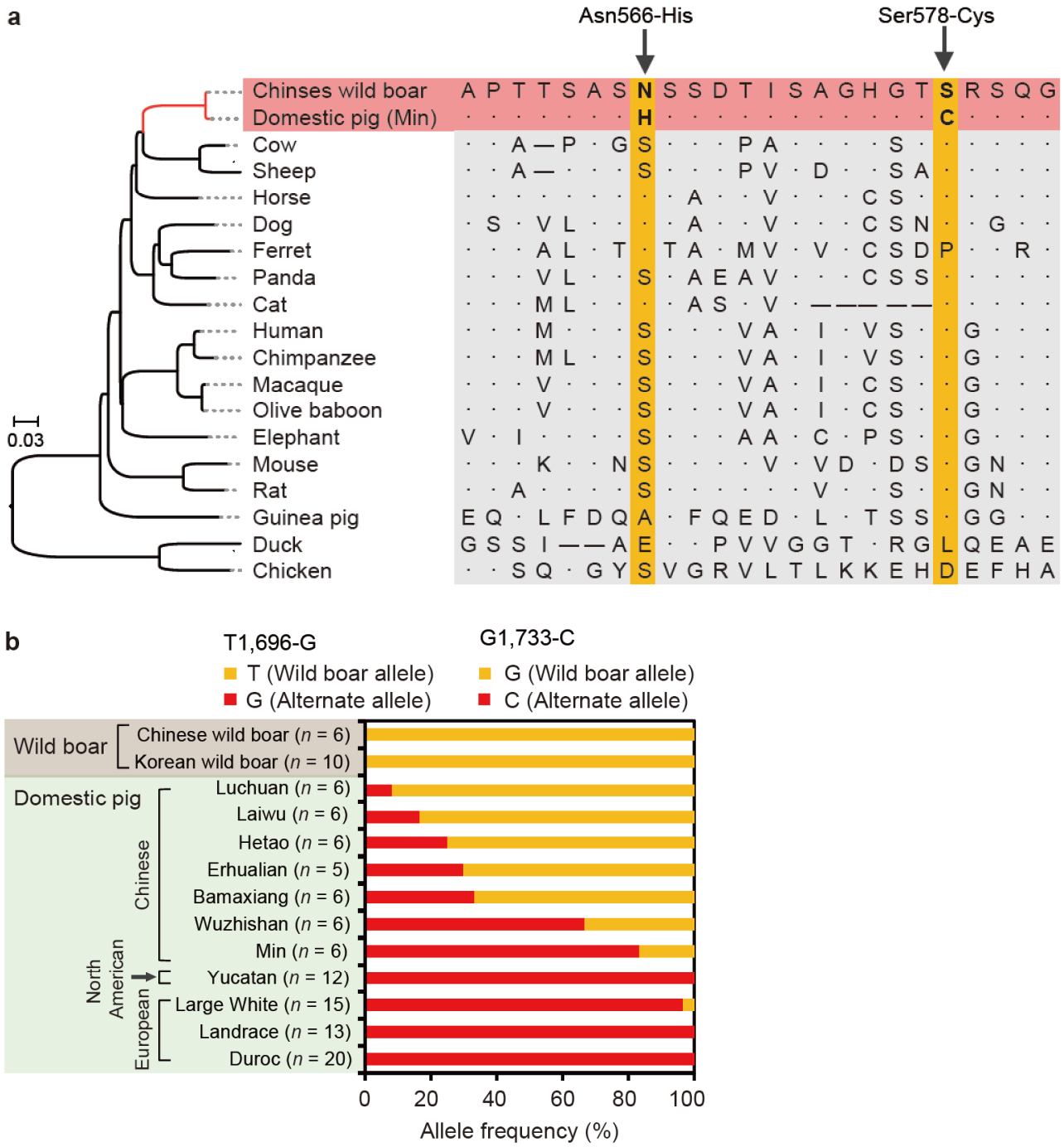

Supplemental Fig. S48. Two selected missense mutations in *ALPK3*. (**a**) Two amino acid variants (Asn566-His and Ser578-Cys) in *ALPK3*. Left panels: the phylogenetic tree of the orthologous protein sequences of pig and 19 vertebrates (Ensemble release 83) were derived from multiple alignment as implemented in the Clustal Omega tool[35], which were in accordance with the evolutionary distance with pig lineage. Right panels: multispecies alignment of proteins for two selected missense mutations. Protein coordinates were based on the longest gene model of inter-assembly collinear genes (RCGENE17759). Dots indicate identities to the Chinese wild boar sequence and dashes indicate missing data. (**b**) Two relevant missense mutations (T1,696-G and G1,733-C) had identical frequency in domestic pigs.