



Additional file 2: Figure S1. Taxonomic position of *Sus barbatus* and *S. scrofa vittatus* based on *cytb* nucleotide sequences. The maximum-likelihood phylogenetic tree was generated under the General Time Reversible model in MEGA7 with 500 bootstrap replicates. The scale-bar below the diagram indicates the number of inferred changes along each branch. Red triangles and square indicate sequences generated in this study.