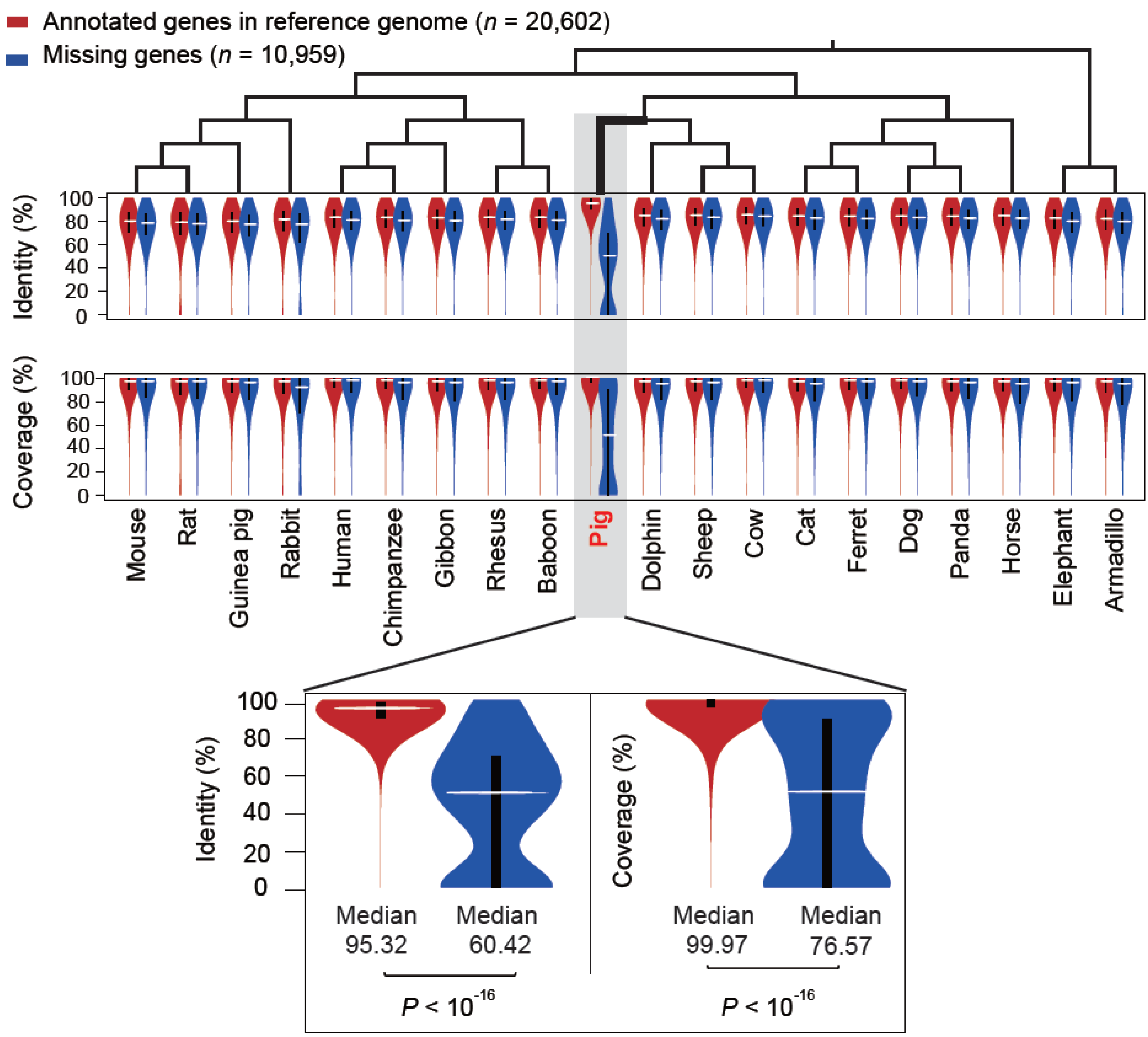

Supplemental Fig. S36. Comparisons of conservation level of missing genes and annotated genes in reference genome across 19 mammalian genomes and the reference pig genome (Ensemble release 83). The branching order was derived from the TimeTree database (Supplemental URLs). Aligning the protein sequences to genomes gave the similar identity (missing compared to annotated genes: 81.55% / 83.60%) and coverage (96.32% / 97.37%) between the missing genes and previously annotated genes across 18 mammalian genomes, with the exception of in pig reference genome with significantly lower identity (60.42% / 95.32%; $P < 10^{-16}$, Mann-Whitney *U* test) and coverage (76.57% / 99.97%; $P < 10^{-16}$)