



Supplementary Figure S1. A phylogenetic tree of *Leptospira* isolates originating from Thailand

A maximum likelihood tree was reconstructed from the 443 bp of 16S rDNA sequences using MEGA X version 10.0.5. Only the sequences from isolates originating from Thailand were used in this analysis demonstrating the genetic relatedness among pathogenic *Leptospira* isolated from different hosts and the environment. All 19 sequences from rodent samples in this study (red dots) and 35 reference sequences of pathogenic *Leptospira* spp. (yellow highlighted letters) and *Leptospira* spp. in intermediate group (green highlighted letters) were included. Hosts of isolates are shown in different shapes; dots for rodents, squares for human, tri-angle for other animals, and stars for environmental samples. Abbreviations are exemplified by the following: BRR, samples from Burirum; SUR, samples from Surin; SSK, samples from Sisaket; BRR0914K, the partial 16S rDNA sequences of the kidney sample from rodent no. 0914 trapped in Burirum; BRR0914U, the partial 16S rDNA sequences from the *Leptospira* isolated from a urine sample from rodent no. 0914 trapped in Burirum.