

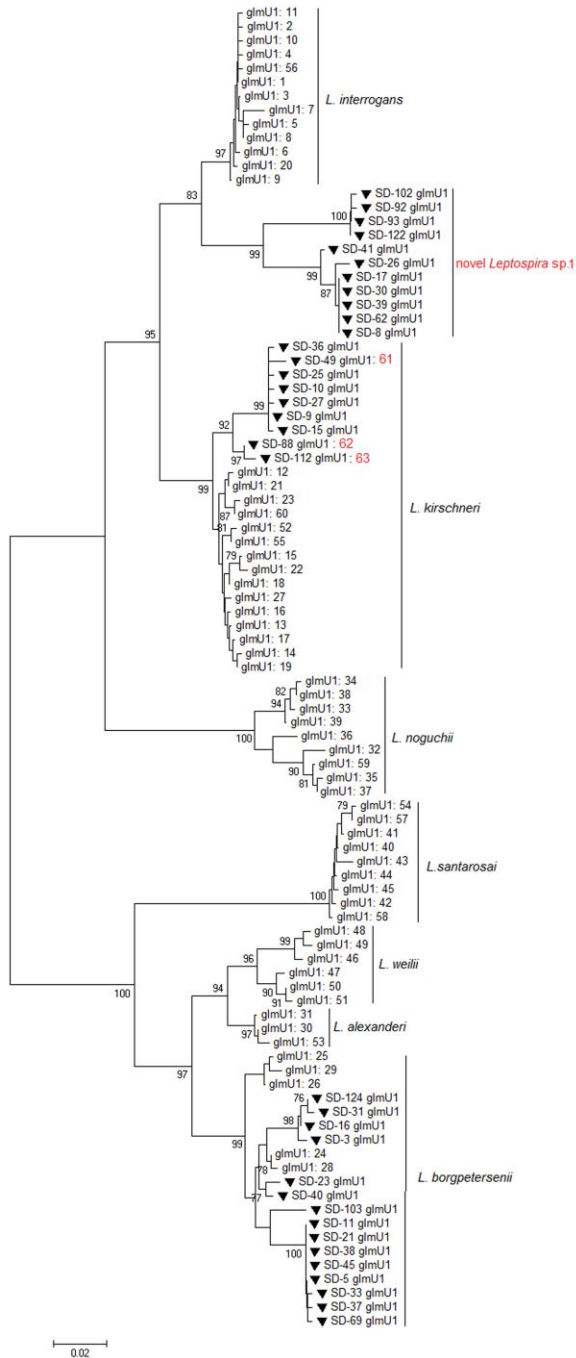
Pathogenic *Leptospira* Species in Insectivorous Bats, China, 2015

Technical Appendix

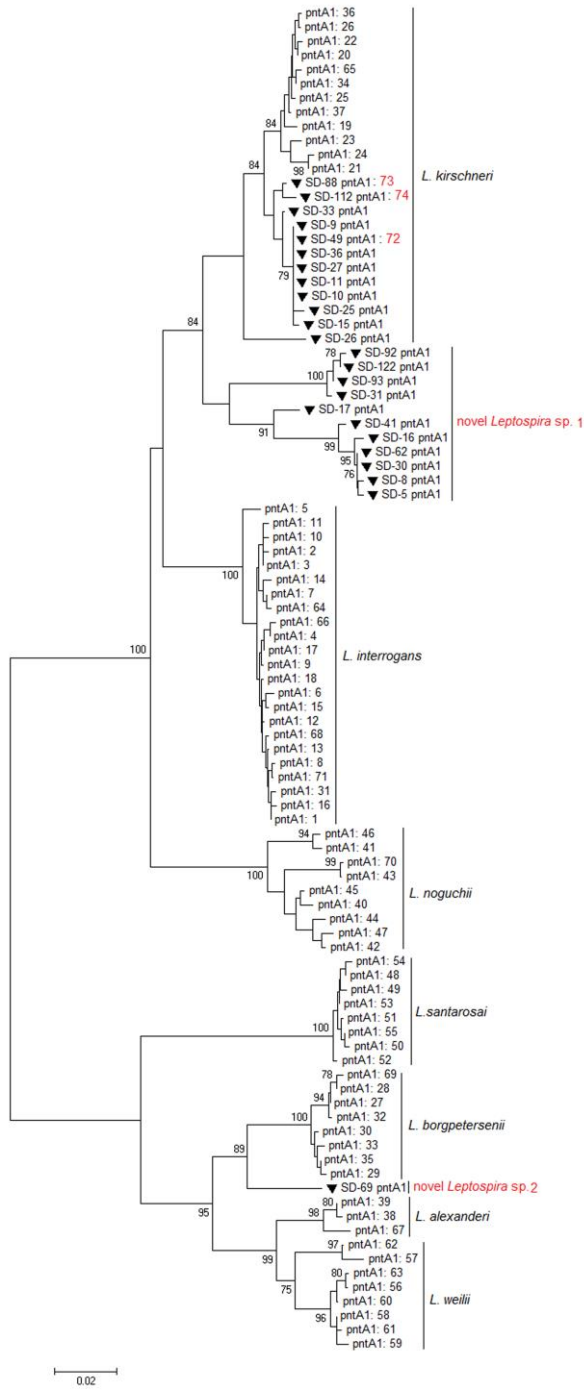
Technical Appendix Table. Multilocus sequence typing (MLST) of *Leptospira* in bats, Mengyin County, Shandong Province, China

Bat species	Bat no.	<i>glmU</i>	<i>pntA</i>	<i>sucA</i>	<i>tpiA</i>	<i>pfkB</i>	<i>mreA</i>	<i>caiB</i>	ST	Co-infection
<i>M. fimbriatus</i>	SD-88	Lk (62)	Lk (73)	Lk (68)	Lk (63)	Lk (88)	Lk (65)	Lk (60)	ST246	1
<i>M. fimbriatus</i>	SD-112	Lk (63)	Lk (74)	Lk (69)	Lk (64)	Lk (89)	Lk (66)	Lk (60)	ST245	1
<i>M. fimbriatus</i>	SD-124	Lb	—	Lb	—	—	—	—	—	1
<i>M. fimbriatus</i>	SD-122	N1	N1	N1	—	—	N1	—	—	1
<i>M. fimbriatus</i>	SD-93	N1	N1	N1	N1	N1	—	—	—	1
<i>M. fimbriatus</i>	SD-103	Lb	—	N2	Lb	Lb	Lb	—	—	2
<i>M. fimbriatus</i>	SD-102	N1	—	N1/N2	N1	N1/Lb	N1	—	—	3
<i>M. ricketti</i>	SD-92	N1	N1	N1/Lb	N1	N1	N1	—	—	2
<i>M. pequinius</i>	SD-49	Lk (61)	Lk (72)	Lk (67)	Lk (62)	Lk (87)	Lk (64)	Lk (59)	ST244	1
<i>M. pequinius</i>	SD-10	Lk	Lk	Lk	—	Lk	Lk	Lk	—	1
<i>M. pequinius</i>	SD-15	Lk	Lk	Lk	—	Lk	Lk	Lk	—	1
<i>M. pequinius</i>	SD-36	Lk	Lk	Lk	—	Lk	—	—	—	1
<i>M. pequinius</i>	SD-21	Lb	—	—	—	—	—	—	—	1
<i>M. pequinius</i>	SD-23	Lb	—	Lb	Lb	Lb	—	Lb	—	1
<i>M. pequinius</i>	SD-38	Lb	—	Lb	Lb	Lb	—	—	—	1
<i>M. pequinius</i>	SD-8	N1	N1	N1	—	—	N1	—	—	1
<i>M. pequinius</i>	SD-30	N1	N1	N1	—	N1	N1	—	—	1
<i>M. pequinius</i>	SD-62	N1	N1	N1	—	N1	N1	—	—	1
<i>M. pequinius</i>	SD-41	N1	N1	N1	N1	N1	—	—	—	1
<i>M. pequinius</i>	SD-39	N1	—	N1	—	N1	N1	—	—	1
<i>M. pequinius</i>	SD-25	Lk	Lk	Lk	—	Lb	—	Lk	—	2
<i>M. pequinius</i>	SD-9	Lk	Lk	Lk	Lb	Lk	Lk	Lk	—	2
<i>M. pequinius</i>	SD-27	Lk	Lk	Lk	Lb	Lk	Lk	Lk	—	2
<i>M. pequinius</i>	SD-3	Lb	—	Lb	—	N2	Lb	—	—	2
<i>M. pequinius</i>	SD-40	Lb	—	Lb	—	N2	Lb	—	—	2
<i>M. pequinius</i>	SD-5	Lb	N1	N1	—	Lb	—	—	—	2
<i>M. pequinius</i>	SD-69	Lb	N2	N2	—	Lb	Lb	—	—	2
<i>M. pequinius</i>	SD-33	Lb	Lk	N2	—	Lb	Lb	—	—	2
<i>M. pequinius</i>	SD-37	Lb	—	N2	—	Lb	Lb	—	—	2
<i>M. pequinius</i>	SD-45	Lb	—	N2	—	Lb	Lb	—	—	2
<i>M. pequinius</i>	SD-26	N1	Lk	N1	N1	N1	N1	Lk	—	2
<i>M. pequinius</i>	SD-31	Lb	N1	Lb	Lb	N2	N1	—	—	3
<i>M. pequinius</i>	SD-16	Lb	N1	Lb	—	N2	Lb	—	—	3
<i>M. pequinius</i>	SD-11	Lb	Lk	N4	—	—	—	Lk	—	3
<i>M. pequinius</i>	SD-17	N1	N1	N3	N1	N1	N1	Lk	—	3

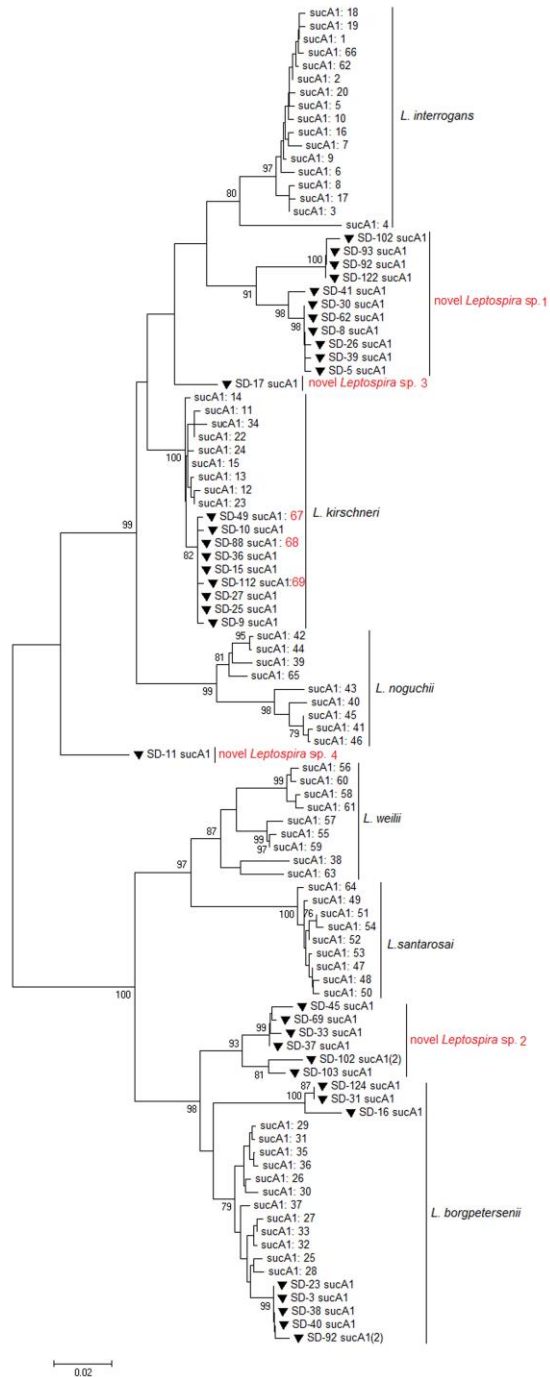
*For SD-49, SD-88, and SD-112, novel alleles assigned are shown in the parentheses. Lb, *L. borgpetersenii*; Lk, *L. kirschneri*; N1, potential new *Leptospira* sp. 1; N2, potential new *Leptospira* sp. 2; N3, potential new *Leptospira* sp. 3; N4, potential new *Leptospira* sp.



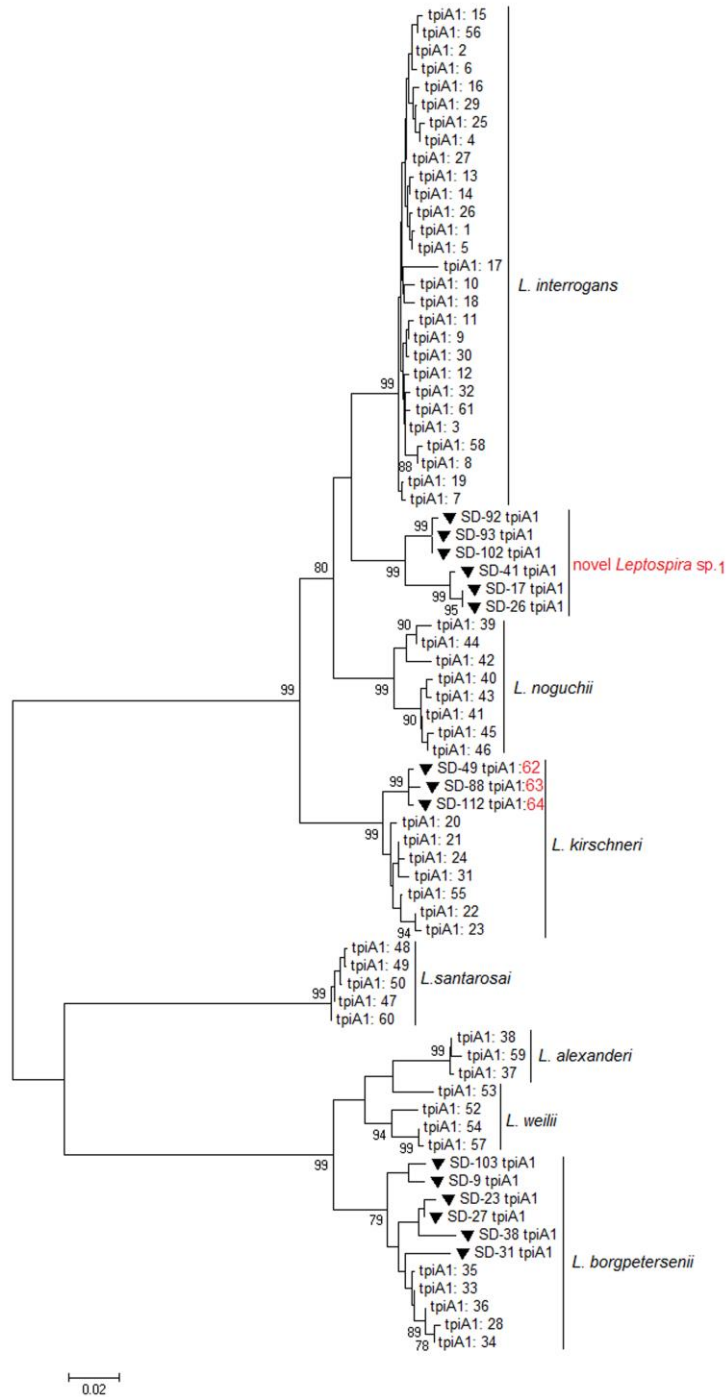
Technical Appendix Figure 1. Neighbor-joining phylogenetic tree for *glmU* gene of *Leptospira* in bats, Mengyin County, Shandong Province, China. The tree was constructed with Kimura's 2-parameter model using MEGA 7.0, and bootstrap values were calculated with 1,000 replicates. Alleles of each locus detected in this study are shown with the sample number highlighted with a triangle, and novel allele numbers assigned in this study are indicated in red. *Leptospira* species are shown on the right, and potential new *Leptospira* species detected in this study are shown in red.



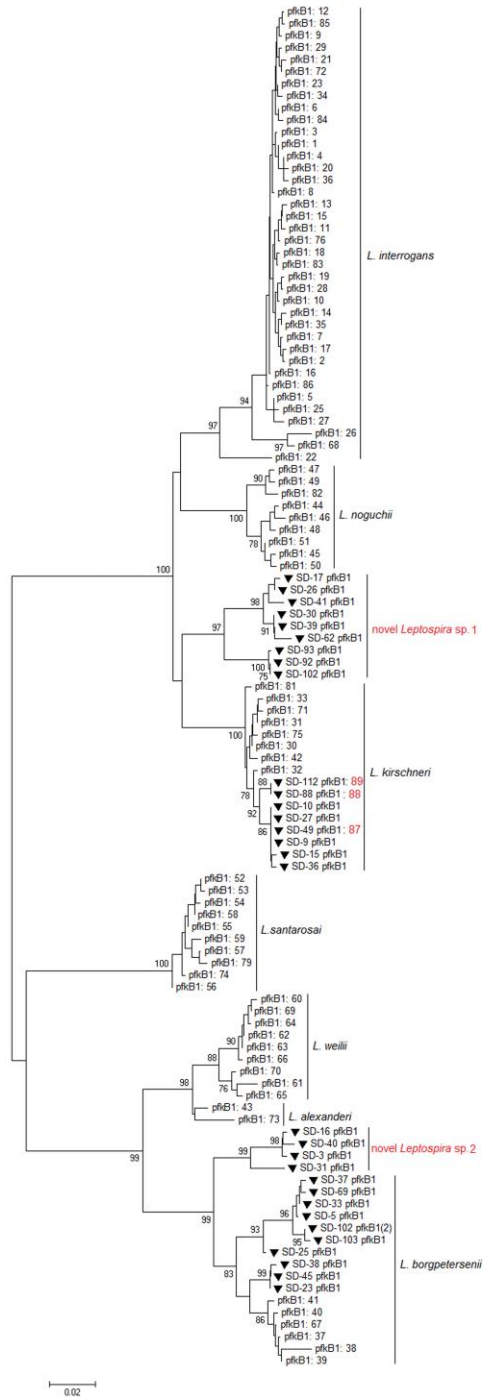
Technical Appendix Figure 2. Neighbor-joining phylogenetic tree for *pntA* gene of *Leptospira* in bats, Mengyin County, Shandong Province, China. The tree was constructed with Kimura's 2-parameter model using MEGA 7.0, and bootstrap values were calculated with 1,000 replicates. Alleles of each locus detected in this study are shown with the sample number highlighted with a triangle, and novel allele numbers assigned in this study are indicated in red. *Leptospira* species are shown on the right, and potential new *Leptospira* species detected in this study are shown in red.



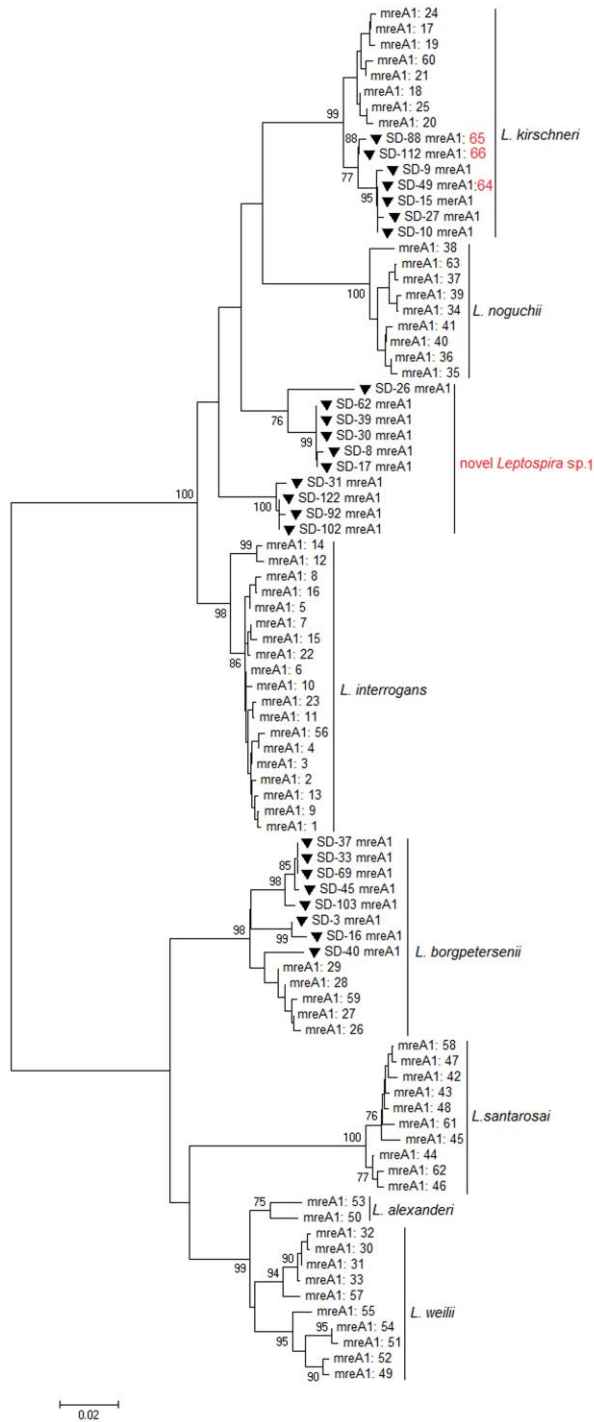
Technical Appendix Figure 3. Neighbor-joining phylogenetic tree for *sucA* gene of *Leptospira* in bats, Mengyin County, Shandong Province, China. The tree was constructed with Kimura's 2-parameter model using MEGA 7.0, and bootstrap values were calculated with 1,000 replicates. Alleles of each locus detected in this study are shown with the sample number highlighted with a triangle, and novel allele numbers assigned in this study are indicated in red. *Leptospira* species are shown on the right, and potential new *Leptospira* species detected in this study are shown in red.



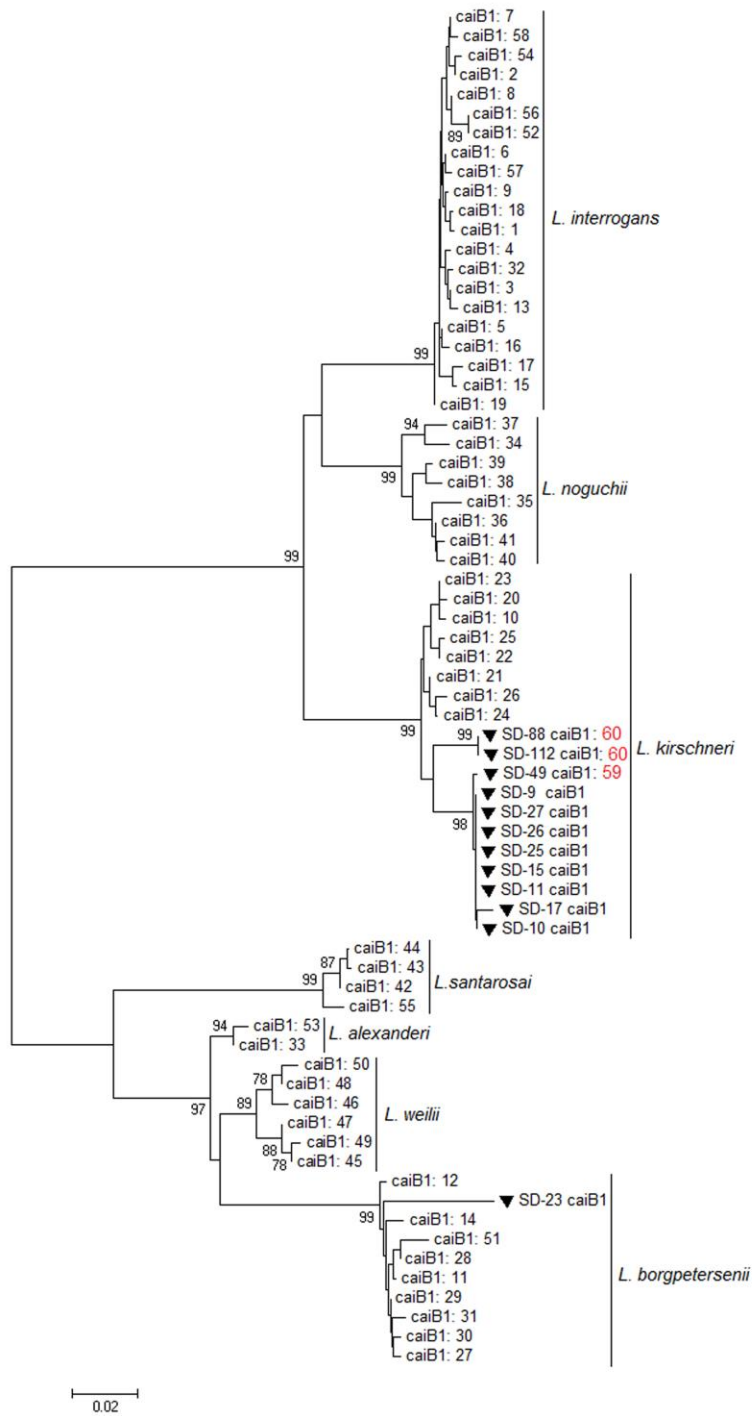
Technical Appendix Figure 4. Neighbor-joining phylogenetic tree for *tpiA* gene of *Leptospira* in bats, Mengyin County, Shandong Province, China. The tree was constructed with Kimura's 2-parameter model using MEGA 7.0, and bootstrap values were calculated with 1,000 replicates. Alleles of each locus detected in this study are shown with the sample number highlighted with a triangle, and novel allele numbers assigned in this study are indicated in red. *Leptospira* species are shown on the right, and potential new *Leptospira* species detected in this study are shown in red.



Technical Appendix Figure 5. Neighbor-joining phylogenetic tree for *pfkB* gene of *Leptospira* in bats, Mengyin County, Shandong Province, China. The tree was constructed with Kimura's 2-parameter model using MEGA 7.0, and bootstrap values were calculated with 1,000 replicates. Alleles of each locus detected in this study are shown with the sample number highlighted with a triangle, and novel allele numbers assigned in this study are indicated in red. *Leptospira* species are shown on the right, and potential new *Leptospira* species detected in this study are shown in red.



Technical Appendix Figure 6. Neighbor-joining phylogenetic tree for *mreA* gene of *Leptospira* in bats, Mengyin County, Shandong Province, China. The tree was constructed with Kimura's 2-parameter model using MEGA 7.0, and bootstrap values were calculated with 1,000 replicates. Alleles of each locus detected in this study are shown with the sample number highlighted with a triangle, and novel allele numbers assigned in this study are indicated in red. *Leptospira* species are shown on the right, and potential new *Leptospira* species detected in this study are shown in red.



Technical Appendix Figure 7. Neighbor-joining phylogenetic tree for *caiB* gene of *Leptospira* in bats, Mengyin County, Shandong Province, China. The tree was constructed with Kimura's 2-parameter model using MEGA 7.0, and bootstrap values were calculated with 1,000 replicates. Alleles of each locus detected in this study are shown with the sample number highlighted with a triangle, and novel allele numbers assigned in this study are indicated in red. *Leptospira* species are shown on the right, and potential new *Leptospira* species detected in this study are shown in red.