

Table S1. Statistics of nanopore sequenced reads and BLASTn identification.

Species	Code	Consensus	No. reads	Length (bp)	BLASTn Identification	% identity
<i>C. orientalis</i>	PR2	Consensus_01	14,131	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	2,558	272	<i>L. orientalis</i> 378 (KY982674)	99.63
<i>C. (Trithecoides) sp.</i>	PR3	Consensus_01	14,037	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	4,662	270	<i>L. orientalis</i> 378 (KY982674)	98.89
<i>C. (Trithecoides) sp.</i>	PR5	Consensus_01	2,239	273	<i>L. orientalis</i> 340 (KY982673)	99.63
		Consensus_02	479	320	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. (Trithecoides) sp.</i>	PR6	Consensus_01	15,242	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. (Trithecoides) sp.</i>	PR8	Consensus_01	17,204	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	3,561	306	<i>L. martiniquensis</i> 770605 (KY982650)	99.64
<i>C. (Trithecoides) sp.</i>	PR10	Consensus_01	23,000	279	<i>L. martiniquensis</i> SK4-1 (MK603826)	99.64
<i>C. (Trithecoides) sp.</i>	PR11	Consensus_01	13,364	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	3,747	273	<i>L. orientalis</i> PCM2 (JX195640)	99.26
		Consensus_03	1,836	313	<i>L. martiniquensis</i> 770605 (KY982650)	99.64
<i>C. (Trithecoides) sp.</i>	PR15	Consensus_01	17,343	279	<i>L. martiniquensis</i> SK4-1 (MK603826)	98.92
<i>C. jacobsoni</i>	PR21	Consensus_01	15,408	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. maharakhamense</i>	PR22	Consensus_01	15,462	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	5,228	273	<i>L. orientalis</i> 340 (KY982673)	100
<i>C. jacobsoni</i>	PR23	Consensus_01	14,569	280	<i>L. martiniquensis</i> 770605 (KY982650)	99.64
		Consensus_02	2,235	273	<i>L. orientalis</i> 340 (KY982673)	99.63
		Consensus_03	1,645	313	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. (Trithecoides) sp.</i>	PR24	Consensus_01	14,232	282	<i>L. martiniquensis</i> 770605 (KY982650)	99.29
		Consensus_02	2,428	275	<i>L. orientalis</i> 609106 (KY982677)	99.27
<i>C. maharakhamense</i>	GS1	Consensus_01	18,970	280	<i>L. martiniquensis</i> 770605 (KY982650)	97.15
<i>C. oxystoma</i>	GS10	Consensus_01	8,516	281	<i>L. martiniquensis</i> 770605 (KY982650)	99.64
		Consensus_02	6,043	273	<i>L. orientalis</i> 609106 (KY982677)	98.54
		Consensus_03	1,512	312	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. oxystoma</i>	GS12	Consensus_01	13,130	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	1,484	273	<i>L. orientalis</i> 409537 (KY982675)	100
<i>C. maharakhamense</i>	TP33	Consensus_01	12,061	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	3,734	271	<i>L. orientalis</i> 409537 (KY982675)	99.26
<i>C. guttifer</i>	TP34	Consensus_01	14,131	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	862	273	<i>L. orientalis</i> 409537 (KY982675)	100
<i>C. guttifer</i>	TP38	Consensus_01	13,894	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	790	272	<i>L. orientalis</i> 378 (KY982674)	100

Table S1. Statistics of nanopore sequenced reads and BLASTn identification. (Continued)

Species	Code	Consensus	No. reads	Length (bp)	BLASTn Identification	% identity
<i>C. guttifer</i>	TP39	Consensus_01	14,850	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. mahasarakhamense</i>	TP43	Consensus_01	13,242	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. mahasarakhamense</i>	TP45	Consensus_01	16,963	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	2,381	273	<i>L. orientalis</i> 409537 (KY982675)	100
<i>C. mahasarakhamense</i>	TP47	Consensus_01	10,410	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. guttifer</i>	TP48	Consensus_01	1,298	272	<i>L. orientalis</i> 378 (KY982674)	100
		Consensus_02	12,317	279	<i>L. martiniquensis</i> SK4-1 (MK603826)	98.56
		Consensus_03	3,673	309	<i>L. martiniquensis</i> SK4-1 (MK603826)	98.92
		Consensus_04	2,575	309	<i>L. martiniquensis</i> SK4-1 (MK603826)	99.28
<i>C. mahasarakhamense</i>	TP49	Consensus_01	16,714	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. mahasarakhamense</i>	TP50	Consensus_01	17,396	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. mahasarakhamense</i>	TP51	Consensus_01	13,551	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	3,257	275	<i>L. orientalis</i> 272078 (KY982669)	99.64
<i>C. guttifer</i>	TP53	Consensus_01	13,509	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	3,265	273	<i>L. orientalis</i> 409537 (KY982675)	100
<i>C. mahasarakhamense</i>	TP54	Consensus_01	1,319	273	<i>L. orientalis</i> 378 (KY982674)	100
		Consensus_02	16,190	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. mahasarakhamense</i>	TP55	Consensus_01	14,892	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. guttifer</i>	TP56	Consensus_01	16,861	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. mahasarakhamense</i>	TP57	Consensus_01	14,464	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	1,189	272	<i>L. orientalis</i> 378 (KY982674)	99
<i>C. guttifer</i>	TP58	Consensus_01	13,718	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. mahasarakhamense</i>	TP59	Consensus_01	12,848	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	1,802	273	<i>L. orientalis</i> 409537 (KY982675)	100
<i>C. mahasarakhamense</i>	TP60	Consensus_01	11,610	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. guttifer</i>	TP61	Consensus_01	14,104	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. guttifer</i>	TP62	Consensus_01	15,557	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
<i>C. guttifer</i>	TP63	Consensus_01	20,660	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	3,804	272	<i>L. orientalis</i> 378 (KY982674)	100
<i>C. mahasarakhamense</i>	TP64	Consensus_01	19,052	279	<i>L. martiniquensis</i> SK4-1 (MK603826)	98.56
		Consensus_02	1,197	273	<i>L. orientalis</i> 409537 (KY982675)	99.26
<i>C. guttifer</i>	TP65	Consensus_01	12,702	281	<i>L. martiniquensis</i> 770605 (KY982650)	100
		Consensus_02	2,541	272	<i>L. orientalis</i> 409537 (KY982675)	99.63

Table S2. Haplotypes of 49 *L. martiniquensis* and 23 *L. orientalis* ITS1 sequences amplified from *Culicoides* biting midges collected in this study and patients previously reported from Northern Thailand.

Species	Haplotypes (frequency)	Length (bp)	Accession numbers of associated <i>Leishmania</i> ITS1 sequences and hosts
<i>L. martiniquensis</i>	Hap_1 (36)	259	PP586221 (<i>C. orientalis</i> _PR2; <i>C. (Trithecoides)</i> sp._PR3, PR5, PR6, PR8, PR11; <i>C. jacobsoni</i> _PR21, PR23; <i>C. oxystoma</i> _GS10, GS12; <i>C. mahasarakhamense</i> _PR22, TP33, TP43, TP45, TP47, TP49, TP50, TP54, TP55, TP57, TP59, TP60; <i>C. guttifer</i> _TP34, TP38, TP39, TP53, TP56, TP58, TP61, TP62, TP63, TP65), OM688240 (patient from Chiang Rai), JX898938 (a patient from Lamphun), KJ210834, and KJ210836 (two patients from Chiang Mai)
	Hap_2 (1)	259	PP586222 (<i>C. oxystoma</i> _GS10)
	Hap_3 (1)	259	PP586223 (<i>C. (Trithecoides)</i> sp._PR08)
	Hap_4 (1)	257	PP586224 (<i>C. (Trithecoides)</i> sp._PR10)
	Hap_5 (1)	258	PP586225 (<i>C. jacobsoni</i> _PR23)
	Hap_6 (1)	259	PP586226 (<i>C. (Trithecoides)</i> sp._PR11)
	Hap_7 (1)	259	PP586227 (<i>C. mahasarakhamense</i> _TP51)
	Hap_8 (1)	257	PP586228 (<i>C. mahasarakhamense</i> _GS1)
	Hap_9 (1)	259	PP586229 (<i>C. (Trithecoides)</i> sp._PR24)
	Hap_10 (1)	257	PP586230 (<i>C. (Trithecoides)</i> sp._PR15)
	Hap_11 (2)	257	PP586231 (<i>C. guttifer</i> _TP48; <i>C. mahasarakhamense</i> _TP64)
	Hap_12 (1)	257	PP586232 (<i>C. guttifer</i> _TP48)
	Hap_13 (1)	257	PP586233 (<i>C. guttifer</i> _TP48)
<i>L. orientalis</i>	Hap_14 (5)	251	PP586234 (<i>C. mahasarakhamense</i> _PR22, TP45; <i>C. oxystoma</i> _GS12; <i>C. guttifer</i> _TP53) and MG731230 (a patient from Nan)
	Hap_15 (1)	251	PP586235 (<i>C. (Trithecoides)</i> sp._PR11)
	Hap_16 (1)	253	PP586236 (<i>C. (Trithecoides)</i> sp._PR24)

Table S2. Haplotypes of 49 *L. martiniquensis* and 23 *L. orientalis* ITS1 sequences amplified from *Culicoides* biting midges collected in this study and patients previously reported from Northern Thailand. (Continued)

Species	Haplotypes (frequency)	Length (bp)	Accession numbers of associated <i>Leishmania</i> ITS1 sequences and hosts
	Hap_17 (1)	251	PP586237 (<i>C. (Trithecoides)</i> sp._PR5)
	Hap_18 (1)	248	PP586238 (<i>C. (Trithecoides)</i> sp._PR3)
	Hap_19 (1)	250	PP586239 (<i>C. mahasarakhamense</i> _TP54)
	Hap_20 (1)	250	PP586240 (<i>C. orientalis</i> _PR2)
	Hap_21 (3)	250	PP586241 (<i>C. guttifer</i> _TP38, TP48, TP63)
	Hap_22 (1)	249	PP586242 (<i>C. mahasarakhamense</i> _TP33)
	Hap_23 (1)	251	PP586243 (<i>C. mahasarakhamense</i> _TP59)
	Hap_24 (1)	251	PP586244 (<i>C. oxystoma</i> _GS10)
	Hap_25 (1)	250	PP586245 (<i>C. guttifer</i> _TP65)
	Hap_26 (1)	253	PP586246 (<i>C. mahasarakhamense</i> _TP51)
	Hap_27 (1)	250	PP586247 (<i>C. mahasarakhamense</i> _TP57)
	Hap_28 (1)	251	PP586248 (<i>C. guttifer</i> _TP34)
	Hap_29 (1)	251	PP586249 (<i>C. jacobsoni</i> _PR23)
	Hap_30 (1)	251	PP586250 (<i>C. mahasarakhamense</i> _TP64)