

Supplementary information: Table S1-S7 and Figure S1-S6

**Fragmented mitochondrial genomes in two suborders of parasitic lice of
eutherian mammals (Anoplura and Rhynchophthirina, Insecta)**

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Table S1. PCR primers used to verify the mitochondrial minichromosomes of the elephant louse, *Haematomyzus elephantis*

Primer	Target gene or region	Sequence (5'-3')	Use
YSC3F	<i>cox3</i>	TACTTGCACTTGCGCA GCTTTGTGGTGACG	Verifying <i>atp8-atp6-trnP-cox3</i> minichromosome with YSC3R
YSC3R	<i>cox3</i>	GCGATCCACCTAGTTA CAGCCCCTATGAAG	Verifying <i>atp8-atp6-trnP-cox3</i> minichromosome with YSC3F
YSCBF	<i>cob</i>	GTAGAAGAAATCCAT TAGGGTTGTCGAGGG	Verifying <i>cob-trnA-trnW-trnF-nad6</i> minichromosome with YSCBR
YSCBR	<i>cob</i>	GGGCCGCAATGTGCG TAATAGCCAAGCTTA	Verifying <i>cob-trnA-trnW-trnF-nad6</i> minichromosome with YSCBF
YSC1F(2)	<i>cox1</i>	GTTATTGCTATTCCTA CTGGAGTAAAAGTG	Verifying <i>trnI-cox1-trnE</i> minichromosome with YSC1R(2)
YSC1R(2)	<i>cox1</i>	GTAGCACTTGTAAGT AAGCACGACTGTCA	Verifying <i>trnI-cox1-trnE</i> minichromosome with YSC1F(2)
YSC2F(2)	<i>cox2</i>	TGAGATGTTTCGCCTTT TAAGAGTTGATCAG	Verifying <i>trnY-cox2-trnE</i> minichromosome with YSC2R(2)
YSC2R(2)	<i>cox2</i>	CCCTTATTATGTAAGA ATCGAAGGAAACTC	Verifying <i>trnY-cox2-trnE</i> minichromosome with YSC2F(2)
YSN1F	<i>nad1</i>	GGGAAAGTGAAGTAG TAGCAGGTTACACAG	Verifying <i>trnT-nad1-trnQ</i> minichromosome with YSN1R
YSN1R	<i>nad1</i>	CTTCTGAAAGGTCAA AAGGTCTCCGACCCC	Verifying <i>trnT-nad1-trnQ</i> minichromosome with YSN1F
YSN3F	<i>nad3</i>	GGTCAAATGAGCCTTT TGAATGTGGAATGG	Verifying <i>trnS₂(tga)-trnR-nad4L-trnM-trnG-nad3</i> minichromosome with YSN3R
YSN3R	<i>nad3</i>	GCTTTAATTCGGACCC TGAGAATAAACCTC	Verifying <i>trnS₂(tga)-trnR-nad4L-trnM-trnG-nad3</i> minichromosome with YSN3F
YSN4F	<i>nad4</i>	CCCATTAGAGGGGAG TATCCTCTTAGCCGC	Verifying <i>trnK-nad4-trnC</i> minichromosome with YSN4R
YSN4R	<i>nad4</i>	GCTTCAACATGTGCTT TAGGGAGCCACGAA	Verifying <i>trnK-nad4-trnC</i> minichromosome with YSN4F
YSN5F(2)	<i>nad5</i>	ATTTGACCTTGCCCTTG TTTCATATAATGGC	Verifying <i>trnH-nad5</i> minichromosome with YSN5R(2)
YSN5R(2)	<i>nad5</i>	TTGAAGGGCAACAGA GTTAATCATTACTCC	Verifying <i>trnH-nad5</i> minichromosome with YSN5F(2)
YSHF	<i>trnH</i>	TGGAGTCATAAATGG GCTCTCCCCCCTTCC	Verifying <i>trnH-nad5</i> minichromosome with YSHR
YSHR	<i>trnH</i>	GTCACAGTTTTACAAT TAAACTACCCTTC	Verifying <i>trnH-nad5</i> minichromosome with YSHF
YSrSF	<i>rrnS</i>	CAGGTCAAGGTGCAG	Verifying <i>trnL₂(taa)-rrnS</i>

		GTTATATTTATGGGG	minichromosome with YSrSR
YSrSR	<i>rrnS</i>	CAGCCACGTATTCCAC ATATGAGTGCTGAT	Verifying <i>trnL₂(taa)-rrnS</i> minichromosome with YSrSF
YSrLF	<i>rrnL</i>	GTTGAACTATTAGACC CTCCACAGCGAGGG	Verifying <i>trnL₁(tag)-rrnL-trnV</i> minichromosome with YSrLR
YSrLR	<i>rrnL</i>	CCGCCCCAGACAAA TACTTTTCATCTCT	Verifying <i>trnL₁(tag)-rrnL-trnV</i> minichromosome with YSrLF

Table S2. Polymorphic sites in the non-coding region of *I-cox1-E* minichromosome

Name	Type	Minimum	Maximum	Length	Coverage	Polymorphism Type	Variant Frequency
A	Polymorphism	103	103	1	2,563	SNP	43.10%
T	Polymorphism	103	103	1	2,563	SNP	56.90%
A	Polymorphism	148	148	1	1,452	SNP	63.00%
C	Polymorphism	148	148	1	1,452	SNP	36.80%
C	Polymorphism	152	152	1	1,387	SNP	62.90%
T	Polymorphism	152	152	1	1,387	SNP	37.10%
C	Polymorphism	186	186	1	1,012	SNP	40.60%
T	Polymorphism	186	186	1	1,012	SNP	59.40%
A	Polymorphism	304	304	1	1,515	SNP	42.40%
T	Polymorphism	304	304	1	1,515	SNP	52.70%
A	Polymorphism	305	305	1	1,531	SNP	57.90%
G	Polymorphism	305	305	1	1,531	SNP	40.80%
A	Polymorphism	307	307	1	1,540	SNP	40.50%
G	Polymorphism	307	307	1	1,540	SNP	59.50%
A	Polymorphism	308	308	1	1,555	SNP	58.80%
G	Polymorphism	308	308	1	1,555	SNP	41.20%
A	Polymorphism	311	311	1	1,586	SNP	61.90%
G	Polymorphism	311	311	1	1,586	SNP	34.20%
A	Polymorphism	431	431	1	1,968	SNP	39.30%
T	Polymorphism	431	431	1	1,968	SNP	60.50%
A	Polymorphism	447	447	1	1,931	SNP	80.30%
G	Polymorphism	447	447	1	1,931	SNP	18.50%
A	Polymorphism	448	448	1	1,926	SNP	18.20%
G	Polymorphism	448	448	1	1,926	SNP	81.80%
A	Polymorphism	452	452	1	1,914	SNP	18.20%
G	Polymorphism	452	452	1	1,914	SNP	81.80%
C	Polymorphism	457	457	1	1,882	Indel	78.60%
	Polymorphism	457	457	1	1,882	Indel	19.60%
C	Polymorphism	460	460	1	1,876	SNP	78.10%
T	Polymorphism	460	460	1	1,876	SNP	21.90%
A	Polymorphism	469	469	1	1,822	Indel	85.90%
	Polymorphism	469	469	1	1,822	Indel	12.00%
T	Polymorphism	470	470	1	1,816	Indel	86.30%
	Polymorphism	470	470	1	1,816	Indel	12.00%
T	Polymorphism	471	471	1	1,791	Indel	87.50%
	Polymorphism	471	471	1	1,791	Indel	12.20%
A	Polymorphism	473	473	1	1,803	SNP	12.30%
C	Polymorphism	473	473	1	1,803	SNP	87.00%
C	Polymorphism	503	503	1	1,704	SNP	45.60%
T	Polymorphism	503	503	1	1,704	SNP	54.40%
A	Polymorphism	505	505	1	1,703	SNP	39.00%
T	Polymorphism	505	505	1	1,703	SNP	61.00%
C	Polymorphism	507	507	1	1,711	SNP	60.60%
T	Polymorphism	507	507	1	1,711	SNP	39.30%

A	Polymorphism	572	572	1	1,402 SNP	46.40%
T	Polymorphism	572	572	1	1,402 SNP	53.40%
C	Polymorphism	632	632	1	2,054 SNP	43.30%
T	Polymorphism	632	632	1	2,054 SNP	56.70%
C	Polymorphism	838	838	1	3,379 SNP	19.70%
T	Polymorphism	838	838	1	3,379 SNP	80.30%
C	Polymorphism	842	842	1	3,347 SNP	20.10%
T	Polymorphism	842	842	1	3,347 SNP	79.80%
C	Polymorphism	849	849	1	3,348 SNP	15.30%
T	Polymorphism	849	849	1	3,348 SNP	84.60%
G	Polymorphism	853	853	1	3,341 SNP	16.10%
T	Polymorphism	853	853	1	3,341 SNP	83.70%
C	Polymorphism	1,650	1,650	1	3,058 SNP	71.50%
T	Polymorphism	1,650	1,650	1	3,058 SNP	27.80%
C	Polymorphism	1,652	1,652	1	3,074 SNP	29.00%
T	Polymorphism	1,652	1,652	1	3,074 SNP	70.10%
A	Polymorphism	1,653	1,653	1	3,073 SNP	28.90%
C	Polymorphism	1,653	1,653	1	3,073 SNP	27.50%
T	Polymorphism	1,653	1,653	1	3,073 SNP	43.50%
C	Polymorphism	1,654	1,654	1	3,083 SNP	88.00%
T	Polymorphism	1,654	1,654	1	3,083 SNP	12.00%
C	Polymorphism	1,655	1,655	1	3,108 SNP	72.40%
T	Polymorphism	1,655	1,655	1	3,108 SNP	27.60%
A	Polymorphism	1,656	1,656	1	3,109 SNP	83.70%
T	Polymorphism	1,656	1,656	1	3,109 SNP	15.90%
C	Polymorphism	1,660	1,660	1	3,128 SNP	36.10%
T	Polymorphism	1,660	1,660	1	3,128 SNP	63.90%
C	Polymorphism	1,661	1,661	1	3,132 SNP	83.60%
T	Polymorphism	1,661	1,661	1	3,132 SNP	16.30%
G	Polymorphism	1,665	1,665	1	3,151 SNP	83.70%
T	Polymorphism	1,665	1,665	1	3,151 SNP	16.10%
C	Polymorphism	1,721	1,721	1	3,149 SNP	55.70%
T	Polymorphism	1,721	1,721	1	3,149 SNP	44.30%
A	Polymorphism	1,736	1,736	1	3,048 SNP	80.90%
G	Polymorphism	1,736	1,736	1	3,048 SNP	19.10%
A	Polymorphism	1,856	1,856	1	3,278 SNP	45.60%
C	Polymorphism	1,856	1,856	1	3,278 SNP	54.30%
C	Polymorphism	1,877	1,877	1	3,154 SNP	14.50%
T	Polymorphism	1,877	1,877	1	3,154 SNP	85.50%
C	Polymorphism	2,100	2,100	1	2,919 SNP	71.20%
T	Polymorphism	2,100	2,100	1	2,919 SNP	28.70%
C	Polymorphism	2,105	2,105	1	2,960 SNP	28.80%
T	Polymorphism	2,105	2,105	1	2,960 SNP	71.10%
C	Polymorphism	2,110	2,110	1	2,973 SNP	37.80%
T	Polymorphism	2,110	2,110	1	2,973 SNP	62.00%
A	Polymorphism	2,187	2,187	1	2,901 SNP	70.10%

G	Polymorphism	2,187	2,187	1	2,901 SNP	29.80%
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Table S3. Heteroplasmic sites in the non-coding region of *T-nad1-Q* minichromosome

Name	Type	Minimum	Maximum	Length	Coverage	Polymorphism Type	Variant Frequency
A	Polymorphism	264	264	1	1,300	Indel	88.10%
	Polymorphism	264	264	1	1,300	Indel	10.20%
C	Polymorphism	265	265	1	1,257	Indel	89.20%
	Polymorphism	265	265	1	1,257	Indel	10.60%
G	Polymorphism	269	269	1	1,121	SNP	19.60%
T	Polymorphism	269	269	1	1,121	SNP	80.20%
C	Polymorphism	275	275	1	946	Indel	72.30%
	Polymorphism	275	275	1	946	Indel	25.80%
C	Polymorphism	279	279	1	893	SNP	60.20%
T	Polymorphism	279	279	1	893	SNP	39.80%
C	Polymorphism	280	280	1	880	SNP	57.70%
G	Polymorphism	280	280	1	880	SNP	41.70%
A	Polymorphism	281	281	1	862	SNP	12.30%
C	Polymorphism	281	281	1	862	SNP	43.40%
T	Polymorphism	281	281	1	862	SNP	43.70%
A	Polymorphism	282	282	1	855	SNP	46.40%
C	Polymorphism	282	282	1	855	SNP	14.20%
G	Polymorphism	282	282	1	855	SNP	38.70%
C	Polymorphism	283	283	1	850	SNP	64.60%
G	Polymorphism	283	283	1	850	SNP	34.80%
C	Polymorphism	284	284	1	859	Indel	49.70%
G	Polymorphism	284	284	1	859	Indel	39.10%
	Polymorphism	284	284	1	859	Indel	11.20%
A	Polymorphism	285	285	1	877	Indel	16.10%
C	Polymorphism	285	285	1	877	Indel	72.90%
	Polymorphism	285	285	1	877	Indel	10.90%
C	Polymorphism	286	286	1	867	Indel	76.10%
G	Polymorphism	286	286	1	867	Indel	12.80%
	Polymorphism	286	286	1	867	Indel	11.10%
A	Polymorphism	287	287	1	895	Indel	76.20%
	Polymorphism	287	287	1	895	Indel	10.70%
G	Polymorphism	287	287	1	895	Indel	10.50%
A	Polymorphism	289	289	1	916	SNP	64.30%
G	Polymorphism	289	289	1	916	SNP	11.40%
T	Polymorphism	289	289	1	916	SNP	24.30%
G	Polymorphism	293	293	1	1,046	Indel	78.70%
	Polymorphism	293	293	1	1,046	Indel	21.30%
A	Polymorphism	345	345	1	2,481	SNP	33.50%
G	Polymorphism	345	345	1	2,481	SNP	66.40%
A	Polymorphism	349	349	1	2,537	SNP	67.30%
G	Polymorphism	349	349	1	2,537	SNP	32.60%
G	Polymorphism	364	364	1	2,701	Indel	83.20%

	Polymorphism	364	364	1	2,701 Indel	16.20%
G	Polymorphism	376	376	1	2,491 SNP	13.70%
T	Polymorphism	376	376	1	2,491 SNP	85.90%
C	Polymorphism	379	379	1	2,375 SNP	22.90%
T	Polymorphism	379	379	1	2,375 SNP	77.00%
A	Polymorphism	380	380	1	2,342 SNP	77.80%
T	Polymorphism	380	380	1	2,342 SNP	22.00%
G	Polymorphism	386	386	1	2,093 SNP	87.80%
T	Polymorphism	386	386	1	2,093 SNP	12.10%
A	Polymorphism	389	389	1	1,948 SNP	10.50%
C	Polymorphism	389	389	1	1,948 SNP	89.50%
A	Polymorphism	419	419	1	1,747 SNP	84.30%
G	Polymorphism	419	419	1	1,747 SNP	15.70%
G	Polymorphism	424	424	1	1,872 Indel	84.30%
	Polymorphism	424	424	1	1,872 Indel	15.70%
T	Polymorphism	425	425	1	1,894 Indel	78.70%
	Polymorphism	425	425	1	1,894 Indel	15.10%
A	Polymorphism	468	468	1	2,372 SNP	39.10%
T	Polymorphism	468	468	1	2,372 SNP	60.60%
A	Polymorphism	484	484	1	2,583 SNP	74.50%
G	Polymorphism	484	484	1	2,583 SNP	25.10%
A	Polymorphism	485	485	1	2,600 SNP	24.50%
G	Polymorphism	485	485	1	2,600 SNP	75.50%
A	Polymorphism	489	489	1	2,640 SNP	24.10%
G	Polymorphism	489	489	1	2,640 SNP	75.90%
C	Polymorphism	494	494	1	2,734 Indel	69.20%
	Polymorphism	494	494	1	2,734 Indel	29.00%
C	Polymorphism	497	497	1	2,752 SNP	68.10%
T	Polymorphism	497	497	1	2,752 SNP	31.90%
A	Polymorphism	506	506	1	2,891 Indel	83.80%
	Polymorphism	506	506	1	2,891 Indel	14.40%
T	Polymorphism	507	507	1	2,905 Indel	84.40%
	Polymorphism	507	507	1	2,905 Indel	14.30%
T	Polymorphism	508	508	1	2,934 Indel	85.50%
	Polymorphism	508	508	1	2,934 Indel	14.10%
A	Polymorphism	510	510	1	2,961 SNP	12.30%
C	Polymorphism	510	510	1	2,961 SNP	87.00%
C	Polymorphism	540	540	1	3,160 SNP	69.60%
T	Polymorphism	540	540	1	3,160 SNP	30.30%
A	Polymorphism	542	542	1	3,165 SNP	60.40%
T	Polymorphism	542	542	1	3,165 SNP	39.50%
C	Polymorphism	544	544	1	3,182 SNP	39.60%
T	Polymorphism	544	544	1	3,182 SNP	60.30%
A	Polymorphism	609	609	1	2,408 SNP	60.80%
T	Polymorphism	609	609	1	2,408 SNP	39.00%
C	Polymorphism	669	669	1	2,795 SNP	59.80%

T	Polymorphism	669	669	1	2,795 SNP	40.20%
C	Polymorphism	875	875	1	3,655 SNP	21.00%
T	Polymorphism	875	875	1	3,655 SNP	79.00%
C	Polymorphism	877	877	1	3,689 SNP	24.50%
T	Polymorphism	877	877	1	3,689 SNP	75.40%
A	Polymorphism	878	878	1	3,705 SNP	24.10%
C	Polymorphism	878	878	1	3,705 SNP	73.50%
C	Polymorphism	879	879	1	3,707 SNP	42.50%
T	Polymorphism	879	879	1	3,707 SNP	57.40%
C	Polymorphism	880	880	1	3,748 SNP	27.50%
T	Polymorphism	880	880	1	3,748 SNP	72.30%
A	Polymorphism	881	881	1	3,772 SNP	74.90%
T	Polymorphism	881	881	1	3,772 SNP	24.50%
C	Polymorphism	885	885	1	3,911 SNP	73.40%
T	Polymorphism	885	885	1	3,911 SNP	26.60%
C	Polymorphism	886	886	1	3,956 SNP	29.40%
T	Polymorphism	886	886	1	3,956 SNP	70.50%
G	Polymorphism	890	890	1	4,039 SNP	34.60%
T	Polymorphism	890	890	1	4,039 SNP	65.30%
A	Polymorphism	919	919	1	4,883 SNP	10.40%
C	Polymorphism	919	919	1	4,883 SNP	88.60%
C	Polymorphism	1,337	1,337	1	2,509 SNP	31.70%
T	Polymorphism	1,337	1,337	1	2,509 SNP	67.30%
A	Polymorphism	1,338	1,338	1	2,550 Indel	25.30%
C	Polymorphism	1,338	1,338	1	2,550 Indel	57.70%
	Polymorphism	1,338	1,338	1	2,550 Indel	10.20%
C	Polymorphism	1,341	1,341	1	2,616 SNP	21.00%
T	Polymorphism	1,341	1,341	1	2,616 SNP	69.00%
	Polymorphism	1,341	1,340	0	2,565 Indel	89.40%
A	Polymorphism	1,341	1,340	0	2,565 Indel	10.60%
A	Polymorphism	1,342	1,342	1	2,642 SNP	78.40%
T	Polymorphism	1,342	1,342	1	2,642 SNP	18.10%
A	Polymorphism	1,344	1,344	1	2,727 Indel	70.30%
	Polymorphism	1,344	1,344	1	2,727 Indel	20.00%
G	Polymorphism	1,352	1,352	1	2,765 SNP	55.40%
T	Polymorphism	1,352	1,352	1	2,765 SNP	44.40%
C	Polymorphism	1,404	1,404	1	4,374 SNP	22.50%
T	Polymorphism	1,404	1,404	1	4,374 SNP	77.40%
C	Polymorphism	1,687	1,687	1	5,402 SNP	79.70%
T	Polymorphism	1,687	1,687	1	5,402 SNP	19.00%
C	Polymorphism	1,689	1,689	1	5,381 SNP	19.60%
T	Polymorphism	1,689	1,689	1	5,381 SNP	79.10%
A	Polymorphism	1,690	1,690	1	5,367 SNP	19.40%
C	Polymorphism	1,690	1,690	1	5,367 SNP	15.10%
T	Polymorphism	1,690	1,690	1	5,367 SNP	65.40%
C	Polymorphism	1,692	1,692	1	5,350 SNP	84.90%

T	Polymorphism	1,692	1,692	1	5,350 SNP	15.00%
A	Polymorphism	1,693	1,693	1	5,345 SNP	80.80%
T	Polymorphism	1,693	1,693	1	5,345 SNP	18.70%
C	Polymorphism	1,697	1,697	1	5,233 SNP	39.40%
T	Polymorphism	1,697	1,697	1	5,233 SNP	60.50%
C	Polymorphism	1,698	1,698	1	5,222 SNP	83.60%
T	Polymorphism	1,698	1,698	1	5,222 SNP	16.20%
G	Polymorphism	1,702	1,702	1	5,150 SNP	84.60%
T	Polymorphism	1,702	1,702	1	5,150 SNP	15.30%
T	Polymorphism	1,725	1,725	1	4,783 Indel	80.70%
	Polymorphism	1,725	1,725	1	4,783 Indel	16.30%
C	Polymorphism	1,727	1,727	1	4,791 SNP	82.20%
T	Polymorphism	1,727	1,727	1	4,791 SNP	17.80%
A	Polymorphism	1,732	1,732	1	4,787 SNP	77.70%
C	Polymorphism	1,732	1,732	1	4,787 SNP	18.90%
C	Polymorphism	1,758	1,758	1	4,613 SNP	40.70%
T	Polymorphism	1,758	1,758	1	4,613 SNP	59.20%
A	Polymorphism	1,773	1,773	1	4,541 SNP	68.80%
G	Polymorphism	1,773	1,773	1	4,541 SNP	31.20%
C	Polymorphism	1,914	1,914	1	4,274 SNP	42.00%
T	Polymorphism	1,914	1,914	1	4,274 SNP	58.00%
C	Polymorphism	2,137	2,137	1	4,048 SNP	44.00%
T	Polymorphism	2,137	2,137	1	4,048 SNP	55.90%
C	Polymorphism	2,142	2,142	1	4,045 SNP	56.30%
T	Polymorphism	2,142	2,142	1	4,045 SNP	43.70%
C	Polymorphism	2,147	2,147	1	4,077 SNP	63.80%
T	Polymorphism	2,147	2,147	1	4,077 SNP	36.20%
A	Polymorphism	2,224	2,224	1	4,411 SNP	78.20%
G	Polymorphism	2,224	2,224	1	4,411 SNP	21.70%
	Polymorphism	2,362	2,361	0	3,305 Indel	89.60%
G	Polymorphism	2,362	2,361	0	3,305 Indel	10.40%
	Polymorphism	2,362	2,361	0	3,305 Indel	89.60%
A	Polymorphism	2,362	2,361	0	3,305 Indel	10.40%

Table S4. Heteroplasmic sites in the non-coding region of *K-nad4-C* minichromosome

Name	Type	Minimum	Maximum	Length	Coverage	Polymorphism Type	Variant Frequency
A	Polymorphism	158	158	1	4,637	SNP	13.80%
C	Polymorphism	158	158	1	4,637	SNP	86.20%
C	Polymorphism	162	162	1	4,467	SNP	13.60%
T	Polymorphism	162	162	1	4,467	SNP	86.40%
C	Polymorphism	196	196	1	3,571	SNP	18.30%
T	Polymorphism	196	196	1	3,571	SNP	81.70%
A	Polymorphism	200	200	1	3,476	SNP	84.10%
G	Polymorphism	200	200	1	3,476	SNP	15.90%
A	Polymorphism	202	202	1	3,458	SNP	27.40%
T	Polymorphism	202	202	1	3,458	SNP	72.40%

A	Polymorphism	203	203	1	3,447 SNP	27.30%
T	Polymorphism	203	203	1	3,447 SNP	72.60%
C	Polymorphism	246	246	1	3,221 SNP	84.80%
T	Polymorphism	246	246	1	3,221 SNP	15.20%
A	Polymorphism	331	331	1	3,479 SNP	82.70%
G	Polymorphism	331	331	1	3,479 SNP	17.10%
A	Polymorphism	335	335	1	3,597 SNP	25.50%
G	Polymorphism	335	335	1	3,597 SNP	74.50%
G	Polymorphism	350	350	1	3,676 Indel	85.90%
	Polymorphism	350	350	1	3,676 Indel	13.20%
C	Polymorphism	365	365	1	3,344 SNP	31.30%
T	Polymorphism	365	365	1	3,344 SNP	68.60%
A	Polymorphism	366	366	1	3,325 SNP	68.80%
T	Polymorphism	366	366	1	3,325 SNP	31.00%
A	Polymorphism	454	454	1	4,281 SNP	75.40%
T	Polymorphism	454	454	1	4,281 SNP	24.40%
A	Polymorphism	470	470	1	4,429 SNP	74.10%
G	Polymorphism	470	470	1	4,429 SNP	25.40%
A	Polymorphism	471	471	1	4,433 SNP	25.30%
G	Polymorphism	471	471	1	4,433 SNP	74.70%
A	Polymorphism	475	475	1	4,456 SNP	24.80%
G	Polymorphism	475	475	1	4,456 SNP	75.20%
C	Polymorphism	480	480	1	4,473 Indel	63.60%
	Polymorphism	480	480	1	4,473 Indel	33.50%
C	Polymorphism	483	483	1	4,415 SNP	61.70%
T	Polymorphism	483	483	1	4,415 SNP	38.20%
A	Polymorphism	492	492	1	4,442 Indel	80.30%
	Polymorphism	492	492	1	4,442 Indel	17.90%
T	Polymorphism	493	493	1	4,453 Indel	80.70%
	Polymorphism	493	493	1	4,453 Indel	17.90%
T	Polymorphism	494	494	1	4,482 Indel	81.90%
	Polymorphism	494	494	1	4,482 Indel	17.70%
C	Polymorphism	526	526	1	4,318 SNP	64.30%
T	Polymorphism	526	526	1	4,318 SNP	35.70%
A	Polymorphism	528	528	1	4,330 SNP	55.90%
T	Polymorphism	528	528	1	4,330 SNP	44.00%
C	Polymorphism	530	530	1	4,332 SNP	44.00%
T	Polymorphism	530	530	1	4,332 SNP	55.90%
A	Polymorphism	595	595	1	3,509 SNP	39.30%
T	Polymorphism	595	595	1	3,509 SNP	60.60%
C	Polymorphism	655	655	1	5,113 SNP	80.20%
T	Polymorphism	655	655	1	5,113 SNP	19.80%
C	Polymorphism	861	861	1	7,796 SNP	18.20%
T	Polymorphism	861	861	1	7,796 SNP	81.70%
C	Polymorphism	863	863	1	7,800 SNP	13.30%
T	Polymorphism	863	863	1	7,800 SNP	86.70%

A	Polymorphism	864	864	1	7,771 SNP	12.60%
C	Polymorphism	864	864	1	7,771 SNP	81.10%
C	Polymorphism	865	865	1	7,764 SNP	27.10%
T	Polymorphism	865	865	1	7,764 SNP	72.90%
C	Polymorphism	866	866	1	7,785 SNP	19.30%
T	Polymorphism	866	866	1	7,785 SNP	80.60%
A	Polymorphism	867	867	1	7,809 SNP	86.80%
T	Polymorphism	867	867	1	7,809 SNP	12.80%
C	Polymorphism	871	871	1	8,086 SNP	84.30%
T	Polymorphism	871	871	1	8,086 SNP	15.70%
C	Polymorphism	872	872	1	8,172 SNP	23.50%
T	Polymorphism	872	872	1	8,172 SNP	76.40%
G	Polymorphism	876	876	1	8,382 SNP	26.50%
T	Polymorphism	876	876	1	8,382 SNP	73.20%
C	Polymorphism	900	900	1	9,311 SNP	10.70%
T	Polymorphism	900	900	1	9,311 SNP	88.90%
A	Polymorphism	946	946	1	10,071 SNP	88.30%
G	Polymorphism	946	946	1	10,071 SNP	11.60%
G	Polymorphism	1,338	1,338	1	7,364 SNP	67.60%
T	Polymorphism	1,338	1,338	1	7,364 SNP	32.20%
C	Polymorphism	1,390	1,390	1	8,283 SNP	34.40%
T	Polymorphism	1,390	1,390	1	8,283 SNP	65.50%
C	Polymorphism	1,673	1,673	1	9,348 SNP	77.90%
T	Polymorphism	1,673	1,673	1	9,348 SNP	21.00%
C	Polymorphism	1,675	1,675	1	9,365 SNP	21.60%
T	Polymorphism	1,675	1,675	1	9,365 SNP	77.10%
A	Polymorphism	1,676	1,676	1	9,428 SNP	21.50%
T	Polymorphism	1,676	1,676	1	9,428 SNP	68.50%
A	Polymorphism	1,679	1,679	1	9,567 SNP	80.70%
T	Polymorphism	1,679	1,679	1	9,567 SNP	18.20%
C	Polymorphism	1,683	1,683	1	9,522 SNP	33.00%
T	Polymorphism	1,683	1,683	1	9,522 SNP	66.90%
C	Polymorphism	1,684	1,684	1	9,536 SNP	89.30%
T	Polymorphism	1,684	1,684	1	9,536 SNP	10.20%
G	Polymorphism	1,688	1,688	1	9,425 SNP	85.70%
T	Polymorphism	1,688	1,688	1	9,425 SNP	14.20%
T	Polymorphism	1,711	1,711	1	8,915 Indel	64.80%
	Polymorphism	1,711	1,711	1	8,915 Indel	31.10%
C	Polymorphism	1,713	1,713	1	8,890 SNP	66.40%
T	Polymorphism	1,713	1,713	1	8,890 SNP	33.50%
A	Polymorphism	1,718	1,718	1	8,714 SNP	53.90%
C	Polymorphism	1,718	1,718	1	8,714 SNP	38.10%
C	Polymorphism	1,726	1,726	1	8,733 SNP	10.30%
G	Polymorphism	1,726	1,726	1	8,733 SNP	89.70%
C	Polymorphism	1,744	1,744	1	9,260 SNP	59.20%
T	Polymorphism	1,744	1,744	1	9,260 SNP	40.80%

A	Polymorphism	1,759	1,759	1	9,504 SNP	66.10%
G	Polymorphism	1,759	1,759	1	9,504 SNP	33.90%
A	Polymorphism	1,879	1,879	1	9,025 SNP	18.40%
C	Polymorphism	1,879	1,879	1	9,025 SNP	81.60%
C	Polymorphism	1,900	1,900	1	8,321 SNP	10.80%
T	Polymorphism	1,900	1,900	1	8,321 SNP	89.20%
C	Polymorphism	2,123	2,123	1	8,082 SNP	29.30%
T	Polymorphism	2,123	2,123	1	8,082 SNP	70.70%
C	Polymorphism	2,128	2,128	1	8,095 SNP	70.70%
T	Polymorphism	2,128	2,128	1	8,095 SNP	29.20%
C	Polymorphism	2,133	2,133	1	8,143 SNP	77.80%
T	Polymorphism	2,133	2,133	1	8,143 SNP	22.10%
A	Polymorphism	2,210	2,210	1	7,940 SNP	36.00%
G	Polymorphism	2,210	2,210	1	7,940 SNP	64.00%

Table S5. Heteroplasmic sites in the non-coding region of *H-nad5* minichromosome

Name	Type	Minimum	Maximum	Length	Coverage	Polymorphism Type	Variant Frequency
A	Polymorphism	23	23	1	3,279	SNP	42.30%
G	Polymorphism	23	23	1	3,279	SNP	57.60%
G	Polymorphism	315	315	1	2,555	SNP	31.80%
T	Polymorphism	315	315	1	2,555	SNP	67.80%
G	Polymorphism	363	363	1	2,738	SNP	61.70%
T	Polymorphism	363	363	1	2,738	SNP	36.40%
	Polymorphism	364	363	0	2,703	Indel	65.80%
A	Polymorphism	364	363	0	2,703	Indel	34.10%
G	Polymorphism	370	370	1	2,633	SNP	14.60%
T	Polymorphism	370	370	1	2,633	SNP	85.20%
G	Polymorphism	410	410	1	2,668	Indel	86.50%
	Polymorphism	410	410	1	2,668	Indel	12.60%
A	Polymorphism	411	411	1	2,692	SNP	19.50%
T	Polymorphism	411	411	1	2,692	SNP	78.00%
A	Polymorphism	413	413	1	2,728	SNP	48.60%
G	Polymorphism	413	413	1	2,728	SNP	47.60%
A	Polymorphism	418	418	1	2,774	Indel	70.30%
	Polymorphism	418	418	1	2,774	Indel	28.60%
A	Polymorphism	425	425	1	2,760	SNP	20.80%
T	Polymorphism	425	425	1	2,760	SNP	78.40%
A	Polymorphism	468	468	1	2,737	SNP	51.00%
T	Polymorphism	468	468	1	2,737	SNP	48.80%
A	Polymorphism	484	484	1	2,721	SNP	69.90%
G	Polymorphism	484	484	1	2,721	SNP	29.10%
A	Polymorphism	485	485	1	2,717	SNP	28.80%
G	Polymorphism	485	485	1	2,717	SNP	71.20%
A	Polymorphism	489	489	1	2,703	SNP	28.80%
G	Polymorphism	489	489	1	2,703	SNP	70.80%
	Polymorphism	494	494	1	2,749	Indel	58.10%

C	Polymorphism	494	494	1	2,749 Indel	41.80%
C	Polymorphism	497	497	1	2,782 SNP	41.70%
T	Polymorphism	497	497	1	2,782 SNP	57.40%
	Polymorphism	506	506	1	2,749 Indel	64.90%
A	Polymorphism	506	506	1	2,749 Indel	35.00%
	Polymorphism	507	507	1	2,749 Indel	64.90%
T	Polymorphism	507	507	1	2,749 Indel	35.00%
	Polymorphism	508	508	1	2,748 Indel	64.90%
T	Polymorphism	508	508	1	2,748 Indel	35.00%
A	Polymorphism	510	510	1	2,775 SNP	33.10%
C	Polymorphism	510	510	1	2,775 SNP	63.20%
C	Polymorphism	538	538	1	2,412 SNP	89.10%
T	Polymorphism	538	538	1	2,412 SNP	10.90%
C	Polymorphism	540	540	1	2,428 SNP	73.10%
T	Polymorphism	540	540	1	2,428 SNP	26.90%
A	Polymorphism	542	542	1	2,425 SNP	61.70%
T	Polymorphism	542	542	1	2,425 SNP	38.10%
C	Polymorphism	544	544	1	2,436 SNP	38.60%
T	Polymorphism	544	544	1	2,436 SNP	61.30%
A	Polymorphism	609	609	1	1,896 SNP	52.80%
T	Polymorphism	609	609	1	1,896 SNP	47.00%
C	Polymorphism	669	669	1	2,496 SNP	79.90%
T	Polymorphism	669	669	1	2,496 SNP	20.10%
C	Polymorphism	875	875	1	3,688 SNP	18.50%
T	Polymorphism	875	875	1	3,688 SNP	81.50%
C	Polymorphism	877	877	1	3,663 SNP	19.20%
T	Polymorphism	877	877	1	3,663 SNP	80.80%
A	Polymorphism	878	878	1	3,627 SNP	18.80%
C	Polymorphism	878	878	1	3,627 SNP	80.50%
C	Polymorphism	879	879	1	3,615 SNP	35.60%
T	Polymorphism	879	879	1	3,615 SNP	64.30%
C	Polymorphism	880	880	1	3,638 SNP	20.10%
T	Polymorphism	880	880	1	3,638 SNP	79.80%
A	Polymorphism	881	881	1	3,729 SNP	79.50%
T	Polymorphism	881	881	1	3,729 SNP	19.90%
C	Polymorphism	885	885	1	3,794 SNP	77.40%
T	Polymorphism	885	885	1	3,794 SNP	22.60%
C	Polymorphism	886	886	1	3,830 SNP	24.70%
T	Polymorphism	886	886	1	3,830 SNP	75.10%
G	Polymorphism	890	890	1	3,881 SNP	30.50%
T	Polymorphism	890	890	1	3,881 SNP	69.30%
A	Polymorphism	919	919	1	4,412 SNP	10.90%
C	Polymorphism	919	919	1	4,412 SNP	88.80%
C	Polymorphism	1,404	1,404	1	3,895 SNP	17.20%
T	Polymorphism	1,404	1,404	1	3,895 SNP	82.80%
A	Polymorphism	1,419	1,419	1	3,908 SNP	14.30%

G	Polymorphism	1,419	1,419	1	3,908 SNP	85.60%
C	Polymorphism	1,464	1,464	1	4,065 SNP	69.80%
T	Polymorphism	1,464	1,464	1	4,065 SNP	30.10%
C	Polymorphism	1,687	1,687	1	4,725 SNP	73.20%
T	Polymorphism	1,687	1,687	1	4,725 SNP	25.80%
C	Polymorphism	1,689	1,689	1	4,753 SNP	26.60%
T	Polymorphism	1,689	1,689	1	4,753 SNP	72.20%
A	Polymorphism	1,690	1,690	1	4,758 SNP	26.70%
C	Polymorphism	1,690	1,690	1	4,758 SNP	18.80%
T	Polymorphism	1,690	1,690	1	4,758 SNP	54.30%
C	Polymorphism	1,692	1,692	1	4,805 SNP	81.30%
T	Polymorphism	1,692	1,692	1	4,805 SNP	18.60%
A	Polymorphism	1,693	1,693	1	4,811 SNP	74.40%
T	Polymorphism	1,693	1,693	1	4,811 SNP	25.00%
C	Polymorphism	1,697	1,697	1	4,748 SNP	34.10%
T	Polymorphism	1,697	1,697	1	4,748 SNP	65.90%
C	Polymorphism	1,698	1,698	1	4,738 SNP	82.10%
T	Polymorphism	1,698	1,698	1	4,738 SNP	17.60%
G	Polymorphism	1,702	1,702	1	4,688 SNP	88.80%
T	Polymorphism	1,702	1,702	1	4,688 SNP	11.10%
T	Polymorphism	1,725	1,725	1	4,489 Indel	83.50%
	Polymorphism	1,725	1,725	1	4,489 Indel	13.90%
C	Polymorphism	1,727	1,727	1	4,469 SNP	85.20%
T	Polymorphism	1,727	1,727	1	4,469 SNP	14.80%
A	Polymorphism	1,732	1,732	1	4,404 SNP	73.00%
C	Polymorphism	1,732	1,732	1	4,404 SNP	17.00%
C	Polymorphism	1,758	1,758	1	4,698 SNP	56.20%
T	Polymorphism	1,758	1,758	1	4,698 SNP	43.80%
A	Polymorphism	1,773	1,773	1	4,649 SNP	43.30%
G	Polymorphism	1,773	1,773	1	4,649 SNP	56.70%
A	Polymorphism	1,893	1,893	1	4,660 SNP	14.50%
C	Polymorphism	1,893	1,893	1	4,660 SNP	85.40%
C	Polymorphism	1,914	1,914	1	4,253 SNP	33.30%
T	Polymorphism	1,914	1,914	1	4,253 SNP	66.60%
C	Polymorphism	2,137	2,137	1	4,178 SNP	59.20%
T	Polymorphism	2,137	2,137	1	4,178 SNP	40.80%
C	Polymorphism	2,142	2,142	1	4,204 SNP	41.50%
T	Polymorphism	2,142	2,142	1	4,204 SNP	58.40%
C	Polymorphism	2,147	2,147	1	4,183 SNP	47.90%
T	Polymorphism	2,147	2,147	1	4,183 SNP	52.00%
A	Polymorphism	2,224	2,224	1	3,690 SNP	60.70%
G	Polymorphism	2,224	2,224	1	3,690 SNP	39.30%

Table S6. PCR primers used to amplify and sequence the mitochondrial genes and genomes of the elephant louse, *Haematomyzus elephantis*

Primer	Target gene or region	Sequence (5'-3')	Use
mtd6	<i>cox1</i>	GGAGGATTTGGAAAT TGATTAGTTCC	Amplifying <i>cox1</i> fragment with mtd11
mtd11	<i>cox1</i>	ACTGTAAATATATGAT GAGCTCA	Amplifying <i>cox1</i> fragment with mtd6
mtd16	<i>cox2</i>	ATTGGACATCAATGAT ATTGA	Amplifying <i>cox2</i> fragment with mtd18
mtd18	<i>cox2</i>	CCACAAATTTCTGAAC ATTGACCA	Amplifying <i>cox2</i> fragment with mtd16
12SA	<i>rrnS</i>	TACTATGTTACGACTT AT	Amplifying <i>rrnS</i> fragment with 12SB
12SB	<i>rrnS</i>	AAACTAGGATTAGAT ACCC	Amplifying <i>rrnS</i> fragment with 12SA
mtd32m	<i>rrnL</i>	ACGCCGGTCTGAACTC AAATCATGTAA	Amplifying <i>rrnL</i> fragment with mtd34
mtd34	<i>rrnL</i>	CGCCTGTTTAACAAAA ACAT	Amplifying <i>rrnL</i> fragment with mtd34
ELC1F	<i>cox1</i>	TTTATTCTGGTTTTTTG GTCATCCAGAAGT	Amplifying <i>trnI-cox1-trnE</i> minichromosome with ELC1R
ELC1R	<i>cox1</i>	AGCATAGTAATCGCC CCTGCAAGGACCGG	Amplifying <i>trnI-cox1-trnE</i> minichromosome with ELC1F
ELC2F	<i>cox2</i>	GAGTTGATCAGAGTG TGATTCTCCCGTTTC	Amplifying <i>trnY-cox2-trnE</i> minichromosome with ELC2R1
ELC2R1	<i>cox2</i>	GCGAACATCTCAGAC ATTTAAATCCCTTAT	Amplifying <i>trnY-cox2-trnE</i> minichromosome with ELC2F
EL12SF1	<i>rrnS</i>	AATTTGTGGTAAGATG TTCGTGTAATTCG	Amplifying <i>trnL₂(taa)-rrnS</i> minichromosome with EL12SR
EL12SR	<i>rrnS</i>	ATTGTCCTTGCACACC GCCGTCGGAAGGG	Amplifying <i>trnL₂(taa)-rrnS</i> minichromosome with EL12SF1
EL16SF	<i>rrnL</i>	GCGGCCCTTCACATCA AGGGTGCAGCGGG	Amplifying <i>trnL₁(tag)-rrnL-trnV</i> minichromosome with LX16SR
LX16SR	<i>rrnL</i>	GACTGTGCTAAGGTAGCA TAAT	Amplifying <i>trnL₁(tag)-rrnL-trnV</i> minichromosome with EL16SF
ELC1seqF	<i>cox1</i>	TTATTGGTGTAATGT TACTTCTTCCCTC	Sequencing by primer walking
ELC1seqR	<i>cox1</i>	TCAATTGGCGAAACCT CCAATTATAATTGG	Sequencing by primer walking
EL16SF1	<i>rrnL</i>	CAAAGGTACAGGAA CAACCCTTACTTGTC	Sequencing by primer walking
ELNCRf	NCR*	CATGAGTCACGTCATG GAGGCTGTGTGGAG	Sequencing by primer walking

ELNCRr	NCR	AATTAGGGTCAAATTT CGACCTCCCAAGGG	Sequencing by primer walking
ELNCRf1	NCR	CTTCTTATCCATCTCT ATGGATAATTACCC	Sequencing by primer walking
ELNCRf2	NCR	TTAGCCAGGTAAAAG GGTGATTTTGCCTTC	Sequencing by primer walking
ELNCRf3	NCR	GATTTCAATCTCTGAT GAGATGGCCTCTAC	Sequencing by primer walking
ELNCRf4	NCR	GGGAGAGTACCCCA GAGAGGATACCCACT	Sequencing by primer walking
ELNCRf5	NCR	AATCCTCAGGTGATA GAGAGATGGAACCTC	Sequencing by primer walking
ELNCRf6	NCR	AAGTGAGATAGGACC ATCTTCATCGATCGA	Sequencing by primer walking
USFB1567	NCR	TGAGAATTGATTTCAA TCCTCAGGTGATAG	Amplifying coding regions of all minichromosomes with ELR
ELR	NCR	AATAACATATTTTCTG TTGCAAAGTCACTC	Amplifying coding regions of all minichromosomes with USFB1567

*Note: NCR for non-coding region.

Table S7. Species of insects for phylogenetic analyses

Species	Common name	GenBank accession number	Reference
<i>Haematomyzus elephantis</i>	Elephant louse	KF933032-41	This manuscript
<i>Pediculus humanus</i>	Human body louse	FJ499473-90	Shao et al. ⁸
<i>Pediculus capitis</i>	Human head louse	JX080388-407	Shao et al. ⁹
<i>Pthirus pubis</i>	Human pubic louse	EU219988-95, HM241895-8	Shao et al. ⁹
<i>Haematopinus suis</i>	Domestic pig louse	KC814602–10	Jiang et al. ¹¹
<i>Haematopinus apri</i>	Wild pig louse	KC814611–19	Jiang et al. ¹¹
<i>Polyplax asiatica</i>	Rat louse	KF647751-61	Dong et al. ¹⁰
<i>Polyplax spinulosa</i>	Rat louse	KF647762-72	Dong et al. ¹⁰
<i>Bothriometopus macrocnemis</i>	Screamer louse	NC_009983	Cameron et al. ⁵
<i>Campanulotes bidentatus compar</i>	Small pigeon louse	NC_007884	Covacin et al. ⁴
<i>Ibidoecus bisignatus</i>	Glossy ibis head louse	NC_015999	Cameron et al. ⁶
<i>Heterodoxus macropus</i>	Wallaby louse	NC_002651	Shao et al. ³
<i>Liposcelis bostrychophila</i>	Booklouse	JN645275-6	Wei et al. ³⁸
<i>Psococerastis albimaculata</i>	Barklouse	NC_021400	Li et al. ³⁹
<i>Longivalvus hyalospilus</i>	Barklouse	JQ910986	Li et al. ³⁹
Lepidopsocid sp.	Barklouse	NC_004816	Shao et al. ⁴⁰
<i>Alloeorhynchus bakeri</i>	True bug	NC_016432	Li et al. ⁴¹

NCR (*I-cox1-E*) -----ATTTCTTAGCATTGTTGGTTTATGTTGCCATGAGTCACGTCATGGAGGCTGTGTGGAGGTTTTAGGCCTTAAAAGGGTTAAATTTGGCCTTAATCTTCACTTTAGCCTAATTTTTGAGTGACTTTG 127
NCR (*T-nad1-Q*) TCTCAGTTTATCCGTTTGTGATGCTCAAGAGCATTGTTATTTTATGTTGCCATGAGTCACGTCATGGAGGCTGTGTGGAGGTTTTAGGCCTTAAAAGGGTTAAATTTGGCCTTAATCTTCACTTTAGCCTAATTTTTGAGTGACTTTG 150
NCR (*K-nad4-C*) -----ATTGTTGATGCTTCAAGAGCATTGTTATTTTATGTTGCCATGAGTCACGTCATGGAGGCTGTGTGGAGGTTTTAGGCCTTAAAAGGGTTAAATTTGGCCTTAATCTTCACTTTAGCCTAATTTTTGAGTGACTTTG 137
NCR (*H-nad5*) -----GTGATGCTTCAAGAGCATTGTTGTTTATGTTGCCATGAGTCACGTCATGGAGGCTGTGTGGAGGTTTTAGGCCTTAAAAGGGTTAAATTTGGCCTTAATCTTCACTTTAGCCTAATTTTTGAGTGACTTTG 133

NCR (*I-cox1-E*) CAACAGAAAATATGTTATTTATGACATATCGATTGTAATAATCCTTCAGGATATTTTATATGAAAATTTAAGAGGGAGAGTACCCCCAGAGAGGATACCCACTATACCTAGATACCCAGATACC-----ACC 254
NCR (*T-nad1-Q*) CAACAGAAAATATGTTATTTCTGATATATCGATTGTAATAATCCTTCAGGATATTTTACATGGAATTTTACCCAGGGGGGATACCCAGGGGGGACTACCCACTACCCAGATACCCCATATACCCGTACGT-----ACC 284
NCR (*K-nad4-C*) CAACAGAAAATATGTTATTTCTGATATATCGATTGTAATAATCCTTCAGGATATTTTATATGAAATTTTACCAGGTTGGAAACCATACGGGGGGGATACCCACTATACCCAGATACCCAGATACC--GTATGT-----ACC 270
NCR (*H-nad5*) CAACAGAAAATATGTTATTTCTGATATATCGATTGTAATAATCCTTCAGGATATTTTACATGGAATTTTACCAGGGGGGATACCCAGGGGGGACTACCCACTACCCAGATACCCCATATACCCGTACCCGGGAGGGGATACCCACC 283

NCR (*I-cox1-E*) ACC-ATAGTGGATACCCCAT-----AGGGATACATATA-TAGATAGAGTACTAGAATAAGAAAAGCAGTGATTACCA-TATACCCAGAGGGACTACCCGGGACTGATTAATTTGGTTAATAG-GGGGGTAGGAAAAGAGAAGAAACAT 393
NCR (*T-nad1-Q*) CCAGAGGGGAGAGACTACTACTAGATAGAGAGATAGTATA-TAGATAGAGTACTAGAATAAGAAAAGCAGTGATTACCA-TATACCCAGAGGGACTACCCGGGACTGATTAATTTGGTTAATAG-GGGGGTAGGAAAAGAGAAGAAACAT 430
NCR (*K-nad4-C*) CCAGAGGGGAGAGACTACTACTAGATAGAGAGATAGTATA-TAGATAGAGTACTAGAATAAGAAAAGCAGTGATTACCA-TATACCCAGAGGGACTACCCGGGACTGATTAATTTGGTTAATAG-GGGGGTAGGAAAAGAGAAGAAACAT 416
NCR (*H-nad5*) CCGAGTGGGAGAGACTACTACTAGATAGAGATA-GATATACATATATAGGATACAGAATAAGAAAAGCAGTGATTACCA-TATACCCAGAGGGACTACCCGGGACTGATTAATTTGGTTAATAGGGGGGGTARGAAAAGAGAAGTAAACAT 430

NCR (*I-cox1-E*) ACAGGGGTGGAGACCCCTGTATACCTGCTAGTCGGCTGCCGACTAGCATGTAAGAAGGCCTCCCTGCCCTTCTATTATCCCTTCCTATCCATCTCTATGGATAATTAACCCCTTACAGGGGGTACATAGGGGGATCCGTCCCCATATCCTACG 543
NCR (*T-nad1-Q*) ACAGGGGTGGAGACCCCTGTATACCTGCTAGTCGGCTGCCGACTAGCATGTAAGAAGGCCTCCCTGCCCTTCTATTATCCCTTCCTATCCATCTCTATGGATAATTAACCCCTTACAGGGGGTACATAGGGGGATCCGTCCCCATATCCTACG 580
NCR (*K-nad4-C*) ACAGGGGTGGAGACCCCTGTATACCTGCTAGTCGGCAGCCGACTAGCATGTAAGAAGGCCTCCCTGCCCTTCTATTATCCCTTCCTATCCATCTCTATGGATAATTAACCCCTTACAGGGGGTACATAGGGGGATCCGTCCCCATATCCTACG 566
NCR (*H-nad5*) ACAGGGGTGGAGACCCCTGTATACCTGCTAGTCGGCAGCCGACTAGCATGTAAGAAGGCCTCCCTGCCCTTCTATTATCCCTTCCTATCCATCTCTATGGATAATTAACCCCTTACAGGGGGTACATAGGGGGATCCGTCCCCATATCCTACG 580

NCR (*I-cox1-E*) ATCCCTCCCTTAGCAATAGAGATCCAATTCATTATATAAAATATCATAAATAATAATTTAAAATAAAGCAGAATCTCCTACTTCTTATTCGGTAACGTAAGTCCCTCAGGGGAACTAACGACACGCCCTCCTCCTTTGGCTGATTCCTAGAG 693
NCR (*T-nad1-Q*) ATCCCTCCCTTAGCAATAGAGATCCAATTCATTATATAAAATATCATAAATAATAATTTAAAATAAAGCAGAATCTCCTACTTCTTATTCGGTAACGTAAGTCCCTCAGGGGAACTAACGACACGCCCTCCTCCTTTGGCTGATTCCTAGAG 730
NCR (*K-nad4-C*) ATCCCTCCCTTAGCAATAGAGATCCAATTCATTATATAAAATATCATAAATAATAATTTAAAATAAAGCAGAATCTCCTACTTCTTATTCGGTAACGTAAGTCCCTCAGGGGAACTAACGACACGCCCTCCTCCTTTGGCTGATTCCTAGAG 716
NCR (*H-nad5*) ATCCCTCCCTTAGCAATAGAGATCCAATTCATTATATAAAATATCATAAATAATAATTTAAAATAAAGCAGAATCTCCTACTTCTTATTCGGTAACGTAAGTCCCTCAGGGGAACTAACGACACGCCCTCCTCCTTTGGCTGATTCCTAGAG 730

NCR (*I-cox1-E*) GCGGTGGGTAGCTGATCCATCCCATCTCCAACTTTGATTGAGCATCAATCAAAGTGAGATAGGACCCTTTCATCGATCGATTAGAAATCATCCCTAGTATAGGATGAATTTGATTTCAATCTCTGATGAGATGGCCTTACCATCTCTT 843
NCR (*T-nad1-Q*) GCGGTGGGTAGCTGATCCATCCCATCTCCAACTTTGATTGAGCATCAATCAAAGTGAGATAGGACCCTTTCATCGATCGATTAGAAATCATCCCTAGTATAGGATGAATTTGATTTCAATCTCTGATGAGATGGCCTTACCATCTCTT 880
NCR (*K-nad4-C*) GCGGTGGGTAGCTGATCCATCCCATCTCCAACTTTGATTGAGCATCAATCAAAGTGAGATAGGACCCTTTCATCGATCGATTAGAAATCATCCCTAGTATAGGATGAATTTGATTTCAATCTCTGATGAGATGGCCTTACCATCTCTT 866
NCR (*H-nad5*) GCGGTGGGTAGCTGATCCATCCCATCTCCAACTTTGATTGAGCATCAATCAAAGTGAGATAGGACCCTTTCATCGATCGATTAGAAATCATCCCTAGTATAGGATGAATTTGATTTCAATCTCTGATGAGATGGCCTTACCATCTCTT 880

NCR (*I-cox1-E*) ACCACTTTATCTGAGTGAGGCGTCACCTCTCCCTCCATCCACACAGAGATGGAGAGGTAATTCCTGAATTAACGCCCAAACCTCAGTGAGTCTTGGTTCATCAACTTTAATTTAGCATCAACTTAAAGTGAGATGAAACCATCTCCA 993
NCR (*T-nad1-Q*) ACCACTTTATCTGAGTGAGGCGTCACCTCTCCCTCCATCCACACAGAGATGGAGAGGTAATTCCTGAATTAACGCCCAAACCTCAGTGAGTCTTGGTTCATCAACTTTAATTTAGCATCAACTTAAAGTGAGATGAAACCATCTCCA 1030
NCR (*K-nad4-C*) ACCACTTTATCTGAGTGAGGCGTCACCTCTCCCTCCATCCACACAGAGATGGAGAGGTAATTCCTGAATTAACGCCCAAACCTCAGTGAGTCTTGGTTCATCAACTTTAATTTAGCATCAACTTAAAGTGAGATGAAACCATCTCCA 1016
NCR (*H-nad5*) ACCACTTTATCTGAGTGAGGCGTCACCTCTCCCTCCATCCACACAGAGATGGAGAGGTAATTCCTGAATTAACGCCCAAACCTCAGTGAGTCTTGGTTCATCAACTTTAATTTAGCATCAACTTAAAGTGAGATGAAACCATCTCCA 1030

NCR (*I-cox1-E*) TCAATCGATTAGAAATCATCCCTAGTATAGGTTGATTTGATTTCAATCTCTGATAAGATGGAGAGGTTGAAATTTAGTAAATTAACGCCCTTACCCCTTGGGAGGTCGAAATTTGACCCATAATTTCTGAGGAAATCCCATAGAAATTT 1143
NCR (*T-nad1-Q*) TCAATCGATTAGAAATCATCCCTAGTATAGGTTGATTTGATTTCAATCTCTGATAAGATGGAGAGGTTGAAATTTAGTAAATTAACGCCCTTACCCCTTGGGAGGTCGAAATTTGACCCATAATTTCTGAGGAAATCCCATAGAAATTT 1180
NCR (*K-nad4-C*) TCAATCGATTAGAAATCATCCCTAGTATAGGTTGATTTGATTTCAATCTCTGATAAGATGGAGAGGTTGAAATTTAGTAAATTAACGCCCTTACCCCTTGGGAGGTCGAAATTTGACCCATAATTTCTGAGGAAATCCCATAGAAATTT 1166
NCR (*H-nad5*) TCAATCGATTAGAAATCATCCCTAGTATAGGTTGATTTGATTTCAATCTCTGATAAGATGGAGAGGTTGAAATTTAGTAAATTAACGCCCTTACCCCTTGGGAGGTCGAAATTTGACCCATAATTTCTGAGGAAATCCCATAGAAATTT 1180

NCR (*I-cox1-E*) CCTTCCAAGAGGGGAAAATAGGTCGTAATCCATCTCCAACTTTAAATGAGCATCAATTTAAAGTGAGATGAAACCATCTCCATCAACTGATTAGAAATCATCTCTAGTATATGAGAAATGATTTCAATCCTCAGGTGATAGAGAGAT 1293
NCR (*T-nad1-Q*) CCTTCCAAGAGGGGAAAATAGGTCGTAATCCATCTCCAACTTTAAATGAGCATCAATTTAAAGTGAGATGAAACCATCTCCATCAACTGATTAGAAATCATCTCTAGTATATGAGAAATGATTTCAATCCTCAGGTGATAGAGAGAT 1330
NCR (*K-nad4-C*) CCTTCCAAGAGGGGAAAATAGGTCGTAATCCATCTCCAACTTTAAATGAGCATCAATTTAAAGTGAGATGAAACCATCTCCATCAACTGATTAGAAATCATCTCTAGTATATGAGAAATGATTTCAATCCTCAGGTGATAGAGAGAT 1316
NCR (*H-nad5*) CCTTCCAAGAGGGGAAAATAGGTCGTAATCCATCTCCAACTTTAAATGAGCATCAATTTAAAGTGAGATGAAACCATCTCCATCAACTGATTAGAAATCATCTCTAGTATATGAGAAATGATTTCAATCCTCAGGTGATAGAGAGAT 1330

NCR (*I-cox1-E*) GGAACTCTCTACACTCCTTAGCTGAGTGAGGCGTCACCTCTCCCTCCCAACACACAGATGGAGAGGTAATTTCTGAATTAACGCCCTCAGACTCAGTGAGTCTTGGTTCATCAACTTTAATTTAGCATCAATTTAAAGTGAGATGAAA 1443
NCR (*T-nad1-Q*) GGAACTCTCTACACTCCTTAGCTGAGTGAGGCGTCACCTCTCCCTCCCAACACACAGATGGAGAGGTAATTTCTGAATTAACGCCCTCAGACTCAGTGAGTCTTGGTTCATCAACTTTAATTTAGCATCAATTTAAAGTGAGATGAAA 1480
NCR (*K-nad4-C*) GGAACTCTCTACACTCCTTAGCTGAGTGAGGCGTCACCTCTCCCTCCCAACACACAGATGGAGAGGTAATTTCTGAATTAACGCCCTCAGACTCAGTGAGTCTTGGTTCATCAACTTTAATTTAGCATCAATTTAAAGTGAGATGAAA 1466
NCR (*H-nad5*) GGAACTCTCTACACTCCTTAGCTGAGTGAGGCGTCACCTCTCCCTCCCAACACACAGATGGAGAGGTAATTTCTGAATTAACGCCCTCAGACTCAGTGAGTCTTGGTTCATCAACTTTAATTTAGCATCAACTTTAAAGTGAGATGAAA 1480

(Fig. S1)

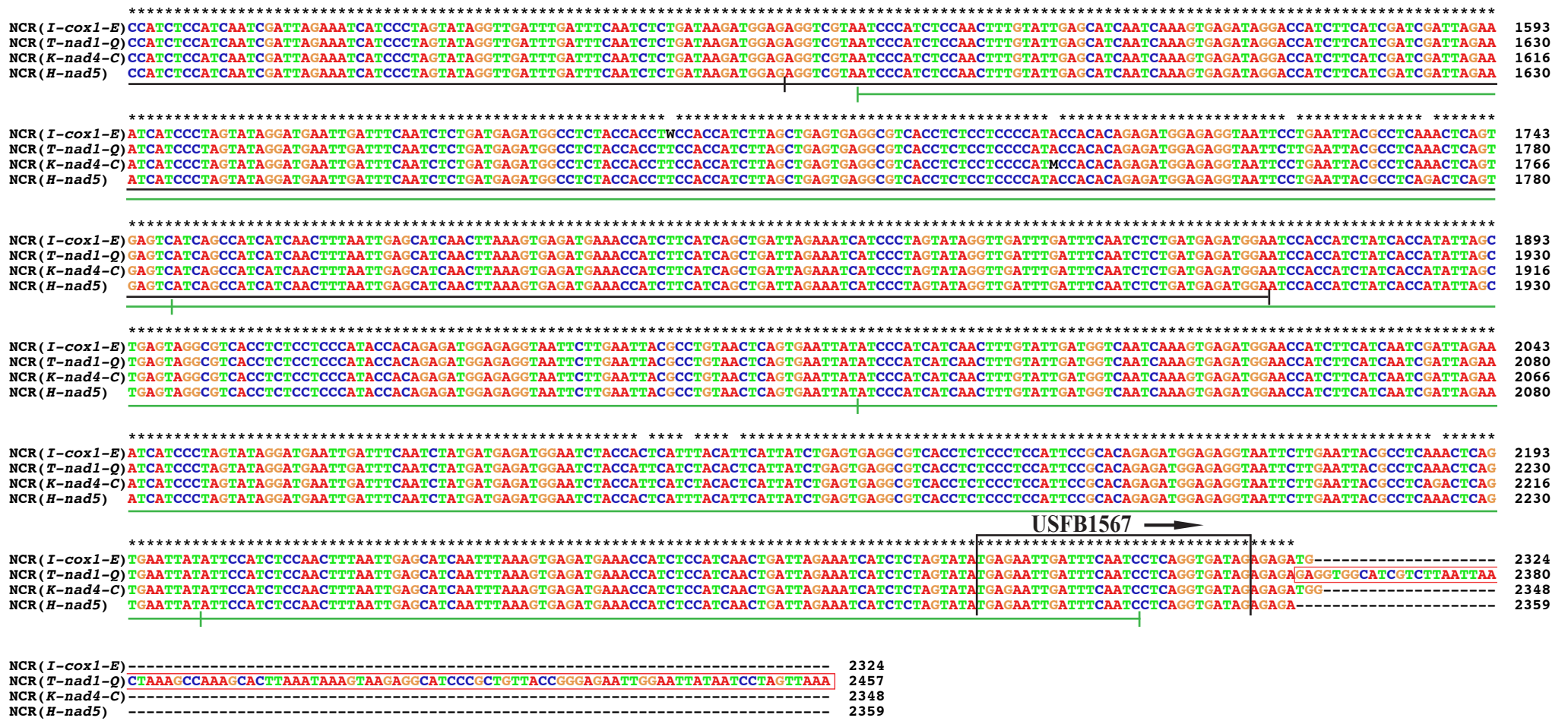


Fig. S1. Alignment of the full-length sequences of the non-coding regions of four mitochondrial minichromosomes of the elephant louse, *Haematomyzus elephantis*. USFB1567 and ELR are the primers used to amplify the coding regions of the 10 minichromosomes identified in the current study. The two 346-bp repeat units are underlined in black and the four 225-bp repeat units are underlined in green. Short vertical lines in black and green separate repeat units. The 99-bp sequence at the 3' end unique to *T-nad1-Q* minichromosome is in red-line box. Asterisks "*" indicate identical nucleotides whereas hyphens "-" indicate absent nucleotides.

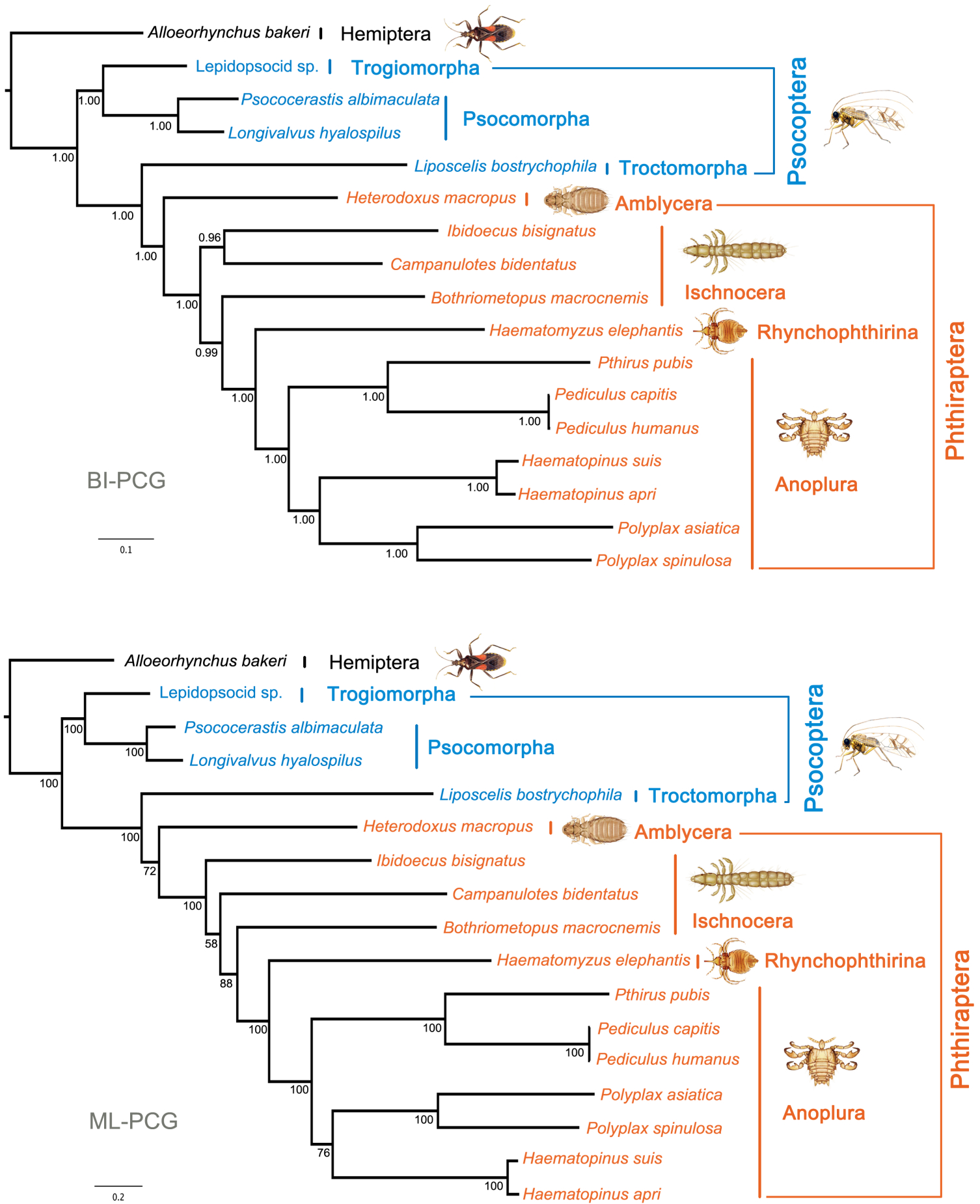


Fig. S3(A). Phylogenetic relationship of the elephant louse, *Haematomyzus elephantis*, with other parasitic lice (Phthiraptera), booklice and barklice (Psocoptera). The trees were constructed using Bayesian (upper) and maximum likelihood (lower) methods with concatenated sequences of 11 mitochondrial protein-coding genes (8,040 nucleotides). Posterior probability (BI-PCG tree) and bootstrap support value (%; ML-PCG tree) for each grouping were indicated near the branch nodes. Trees were rooted with the true bug, *Alloeorhynchus bakeri*.

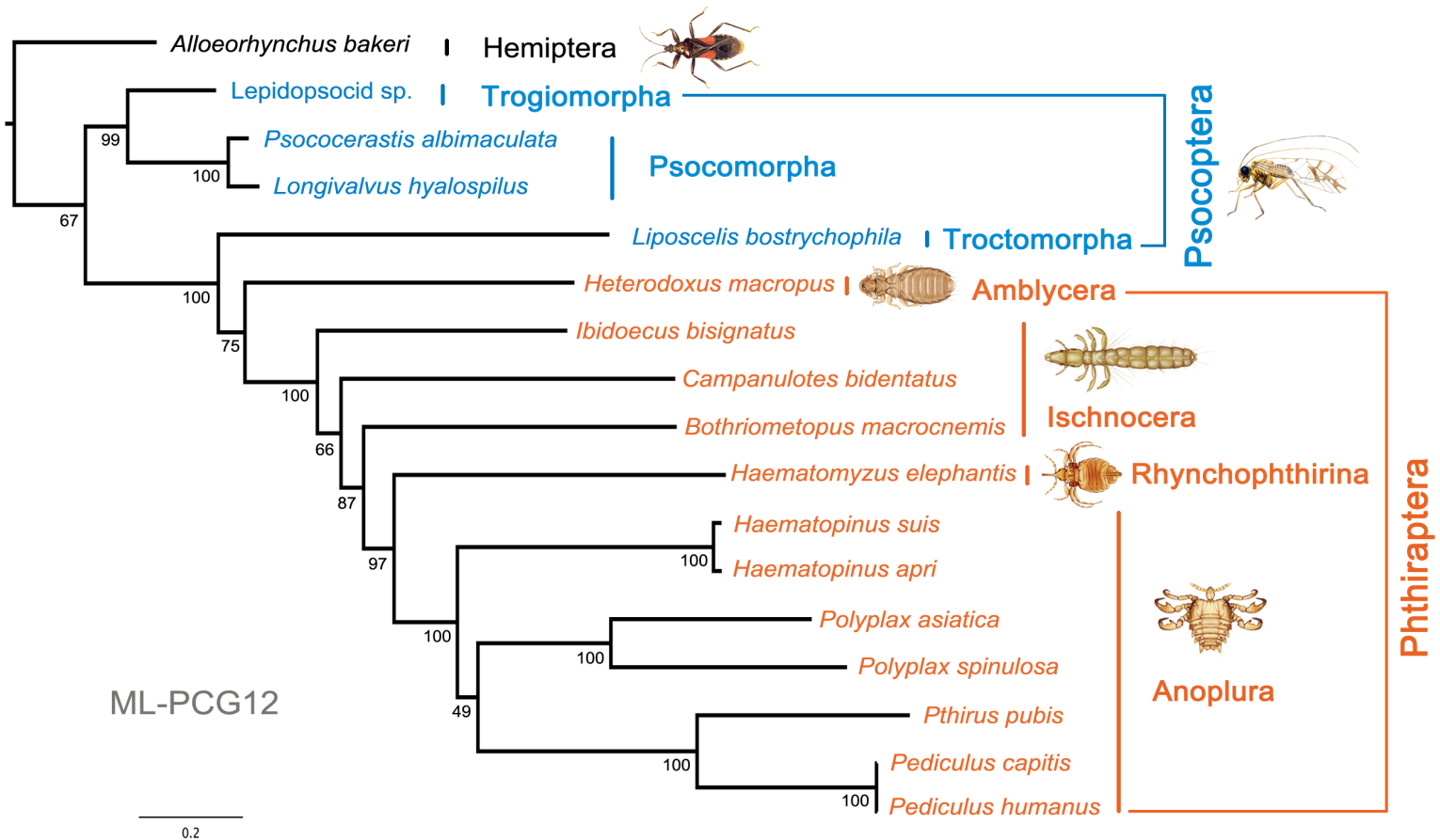
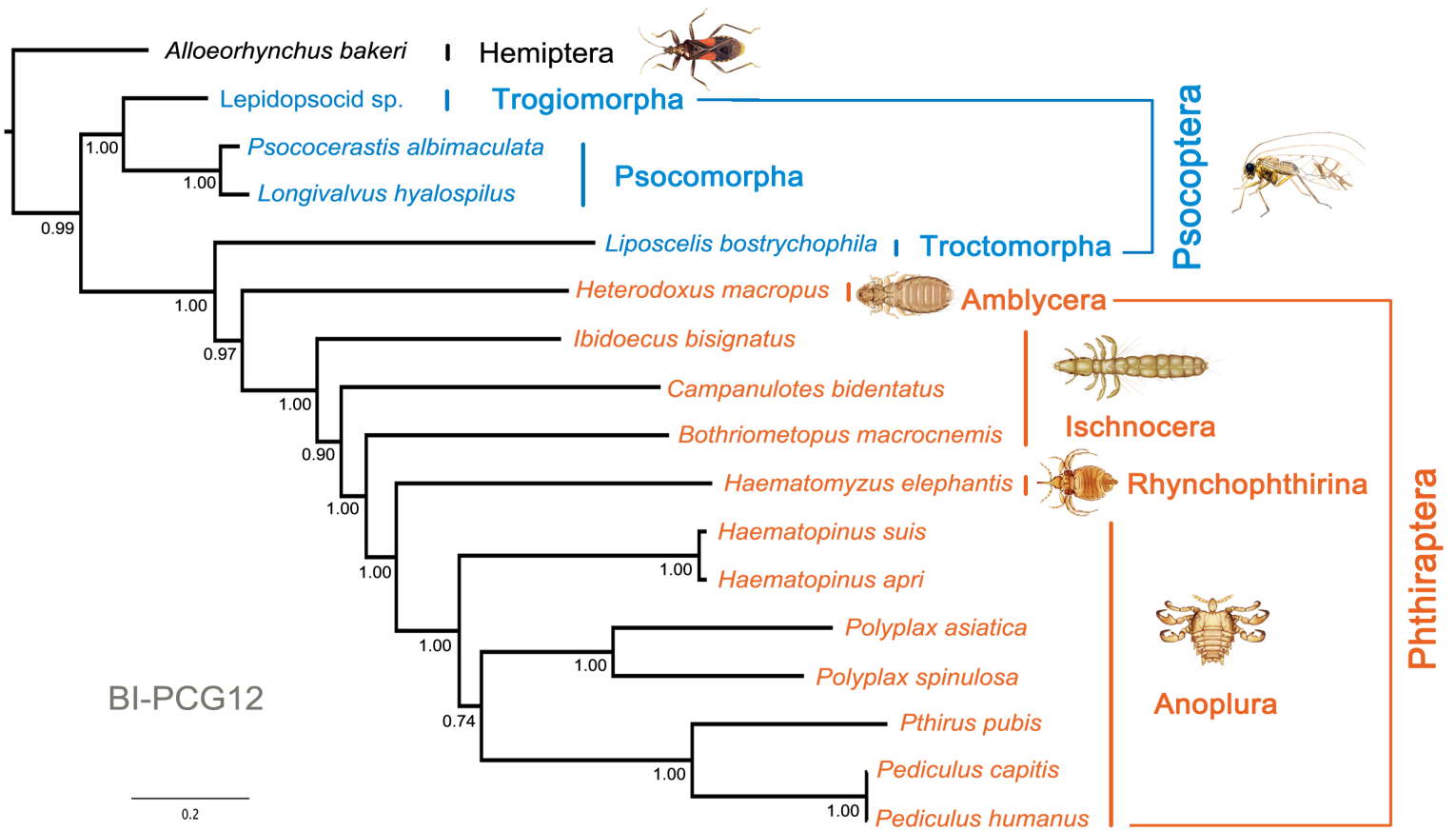


Fig. S3(B). Phylogenetic relationship of the elephant louse, *Haematomyzus elephantis*, with other parasitic lice (Phthiraptera), booklice and barklice (Psocoptera). The trees were constructed using Bayesian (upper) and maximum likelihood (lower) methods with concatenated sequences of 11 mitochondrial protein-coding genes at the first and second coding positions (5,360 nucleotides). Posterior probability (BI-PCG12 tree) and bootstrap support value (%; ML-PCG12 tree) for each grouping were indicated near the branch nodes. Trees were rooted with the true bug, *Alloeorhynchus bakeri*.

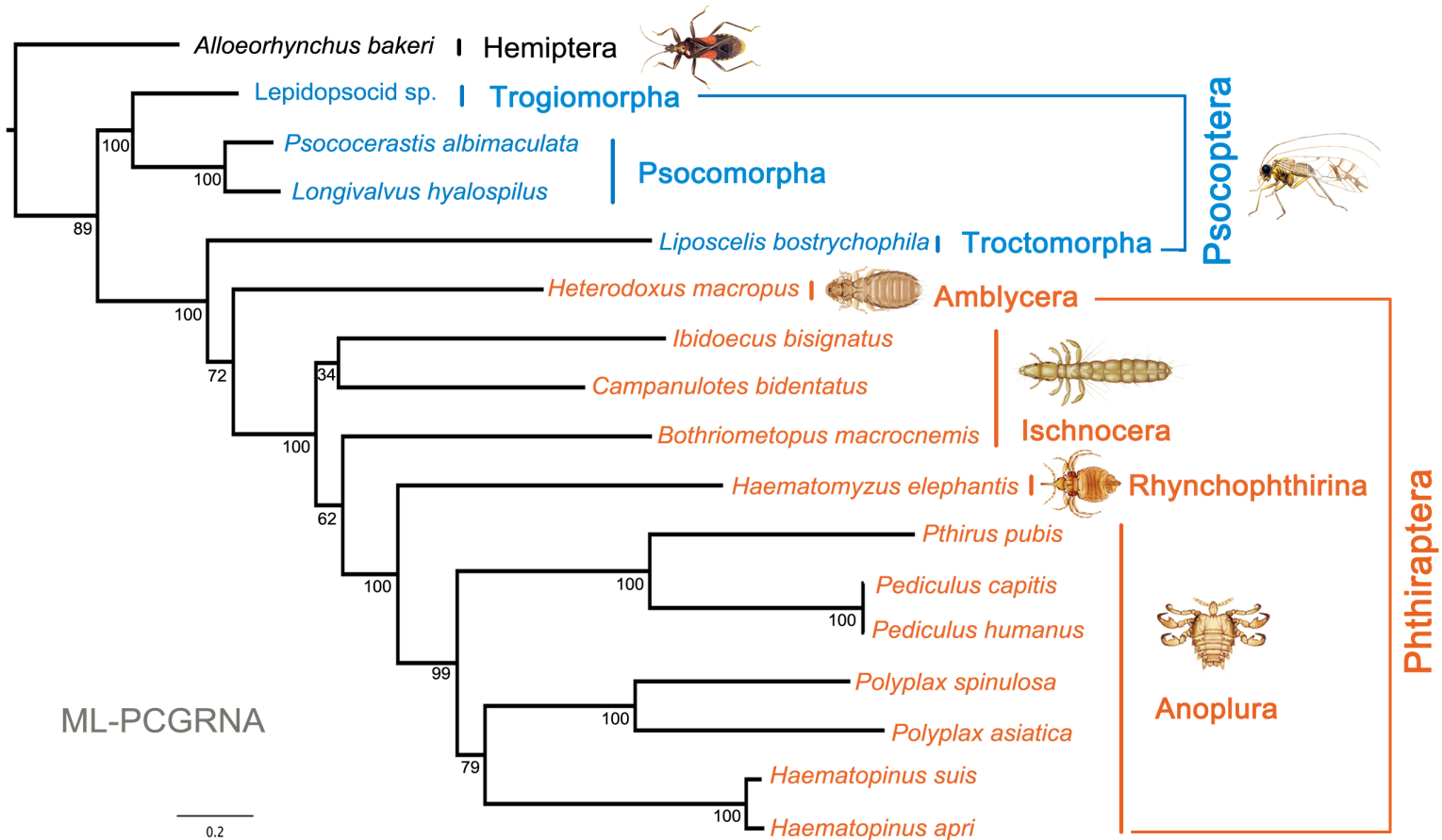
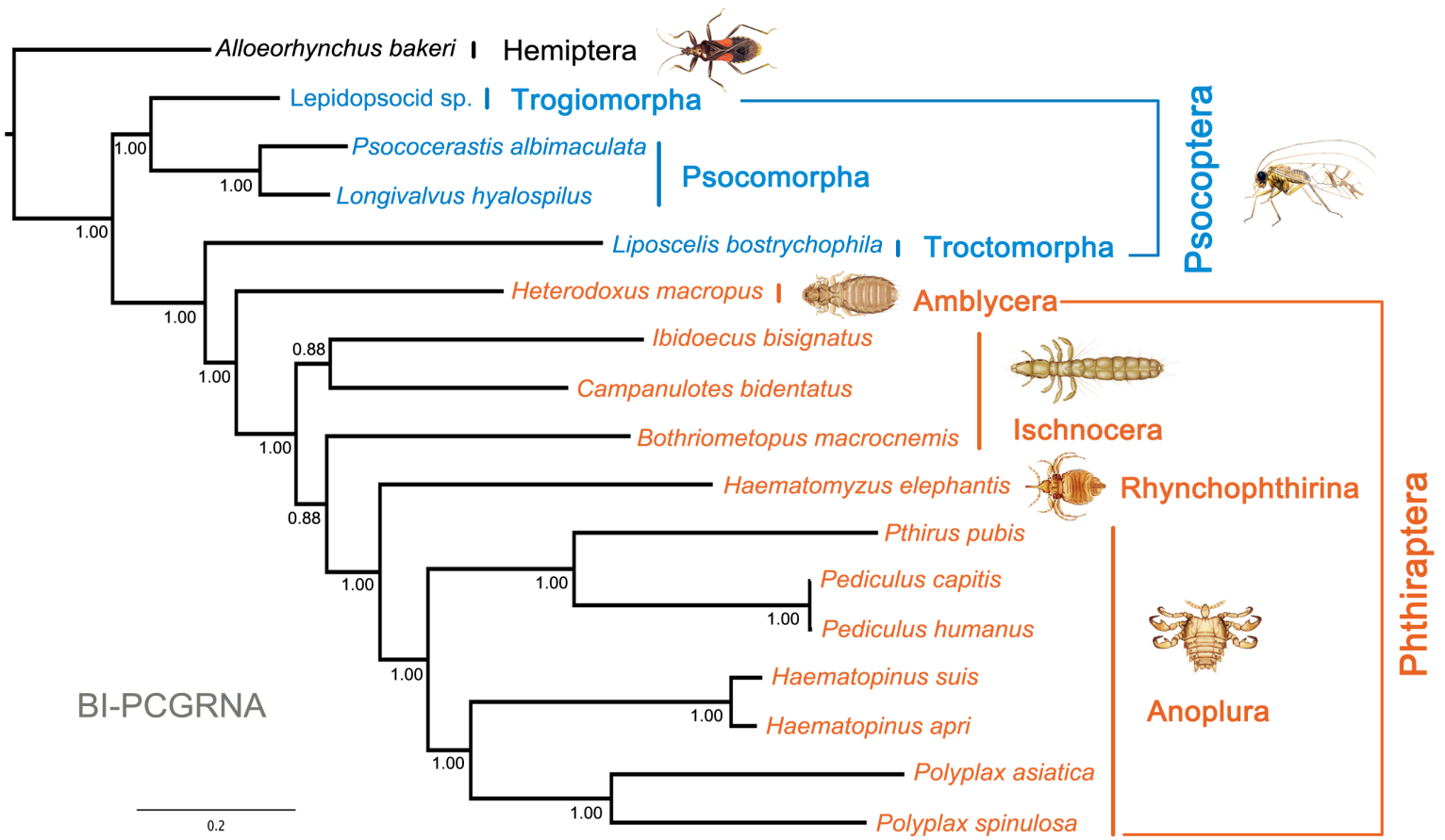


Fig. S3(C). Phylogenetic relationship of the elephant louse, *Haematomyzus elephantis*, with other parasitic lice (Phthiraptera), booklice and barklice (Psocoptera). The trees were constructed using Bayesian (upper) and maximum likelihood (lower) methods with concatenated sequences of 11 mitochondrial (mt) protein-coding genes and the mt rRNA genes (9,530 nucleotides). Posterior probability (BI-PCGRNA tree) and bootstrap support value (% ML-PCGRNA tree) for each grouping were indicated near the branch nodes. Trees were rooted with the true bug, *Alloeorhynchus bakeri*. Drawing of insects here and in Fig. S3(A) and (B) was by Hu Li.

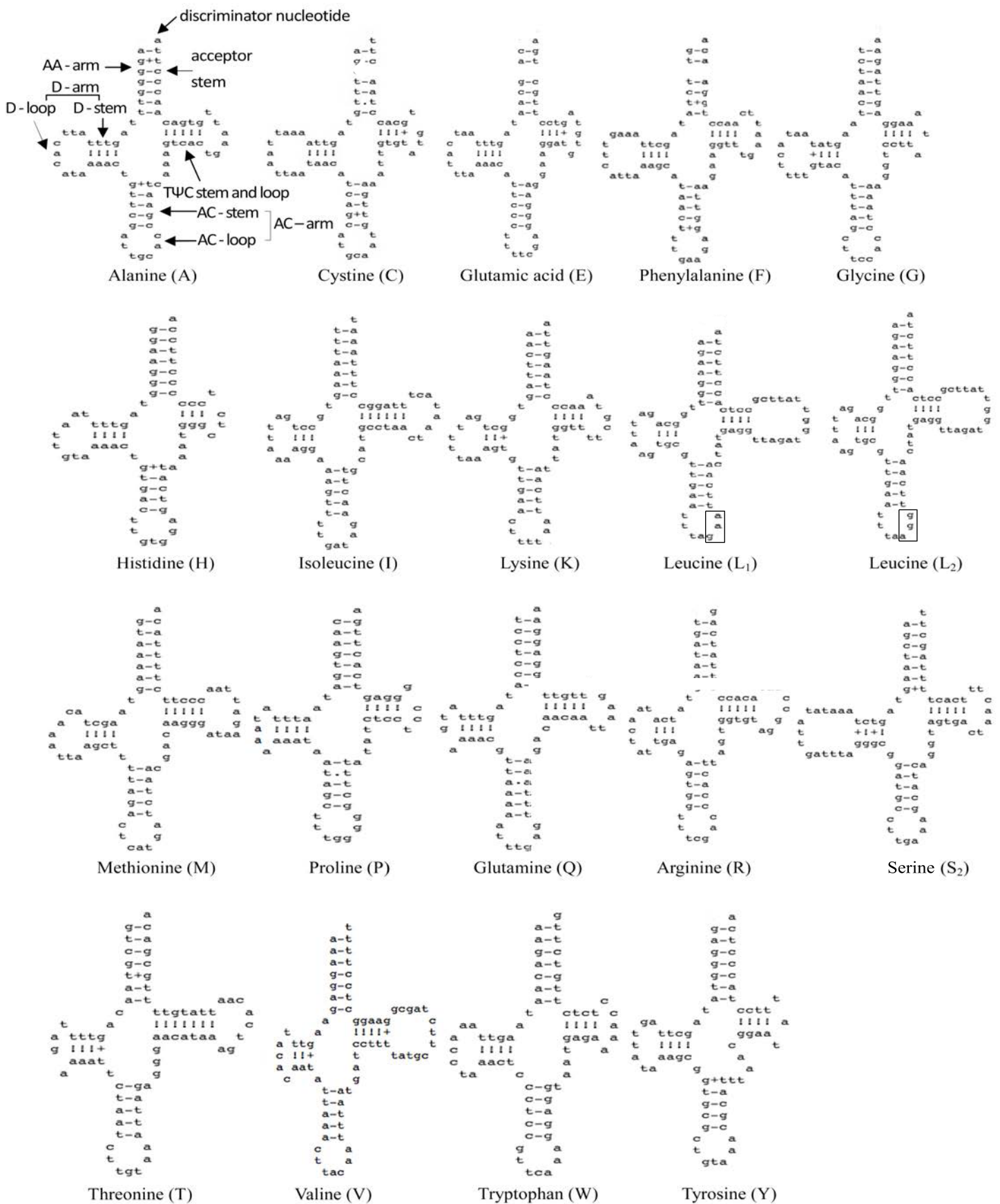


Fig. S4. Inferred secondary structures of the mitochondrial tRNAs of the elephant louse, *Haematomyus elephantis*. The three nucleotides that differ between L1 and L2 are boxed.

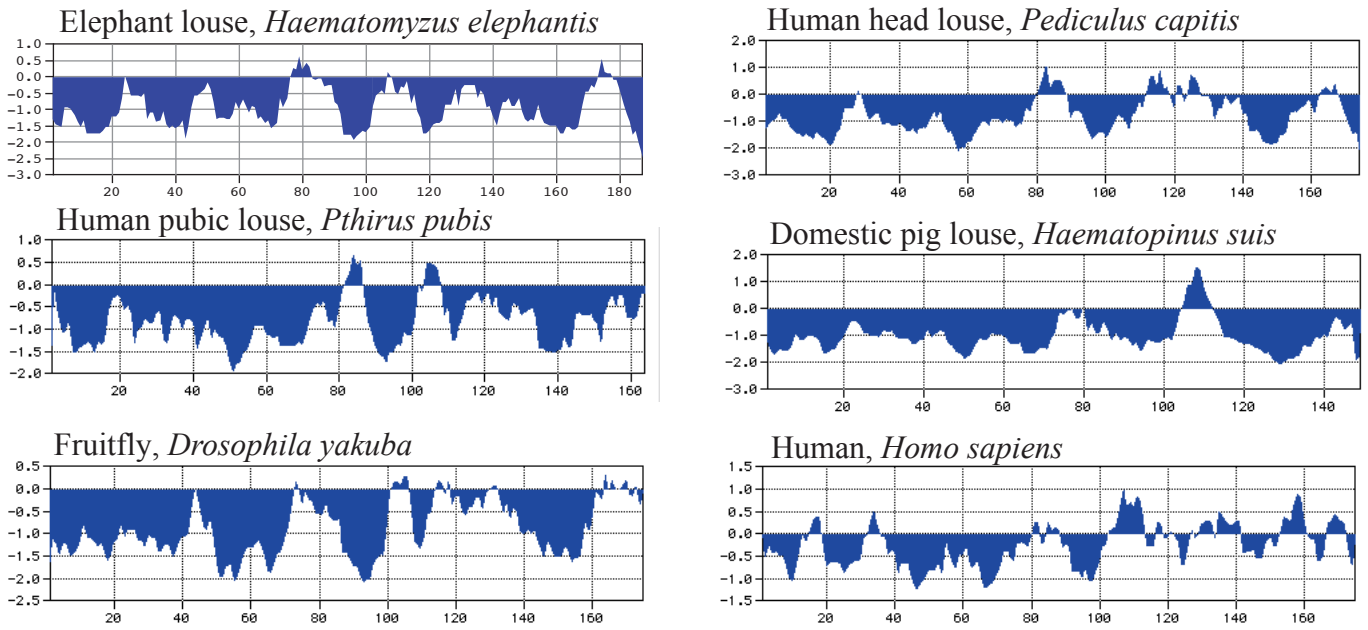


Fig. S5. Comparison of the Hopp/Woods hydrophilicity profiles of NAD6 proteins of the elephant louse, *Haematomyzus elephantis*, with the human lice, pig louse, fly and human. Amino acids are along the horizontal lines. Hydrophilicity values of amino acids are along the vertical lines.

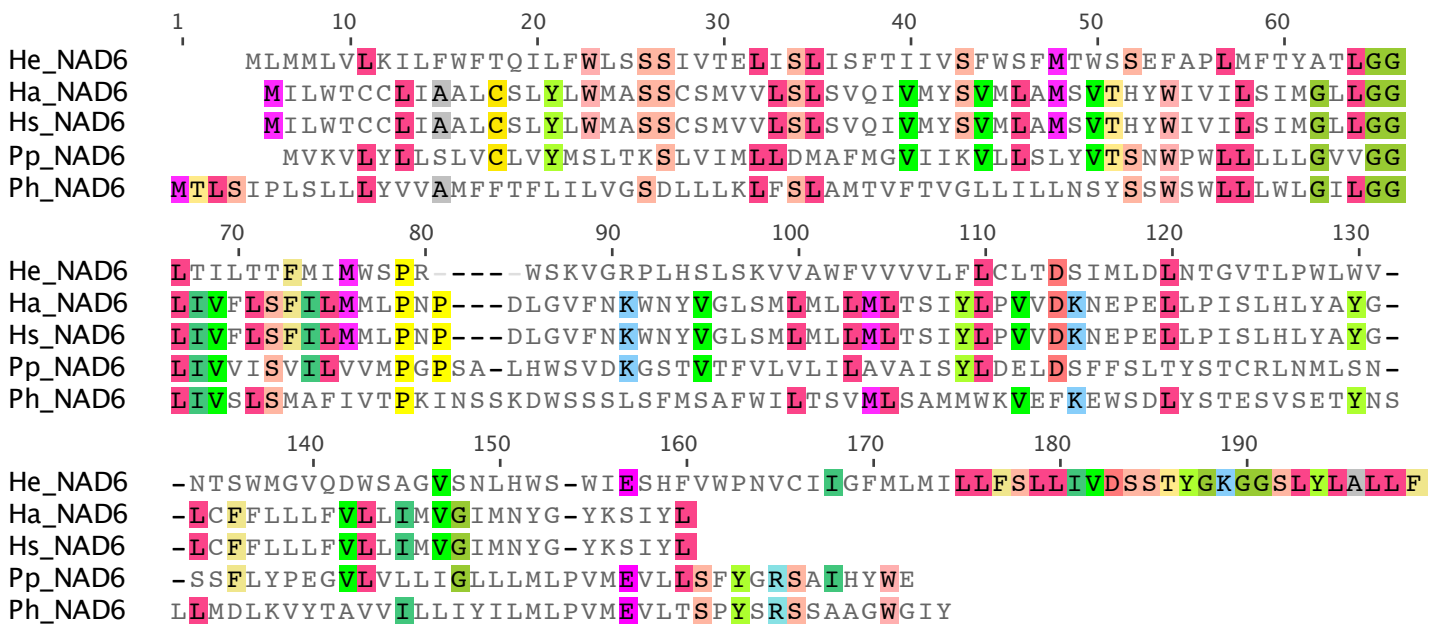


Fig. S6. Alignment of the putative amino acid sequences of mitochondrial NAD6 proteins of the elephant louse and four sucking lice (Anoplura). Conserved amino acid sequences were highlighted in colors. Abbreviations of species names are: He – *Haematomyzus elephantis* (elephant louse), Ha – *Haematopinus apri* (wild pig louse), Hs – *Haematopinus suis* (domestic pig louse), Pp – *Pthirus pubis* (human pubic louse), and Ph – *Pediculus humanus* (human body louse). Alignment was with Geneious 7.0.4. BLOSUM cost matrix was used; gap open cost was 10 and gap extend cost was 5.