

Supplementary Table S1: Summary table for characteristics of the complete mitogenome of *Nilaparvata lugens*_1 (NCBI Accession Number: OK585089)

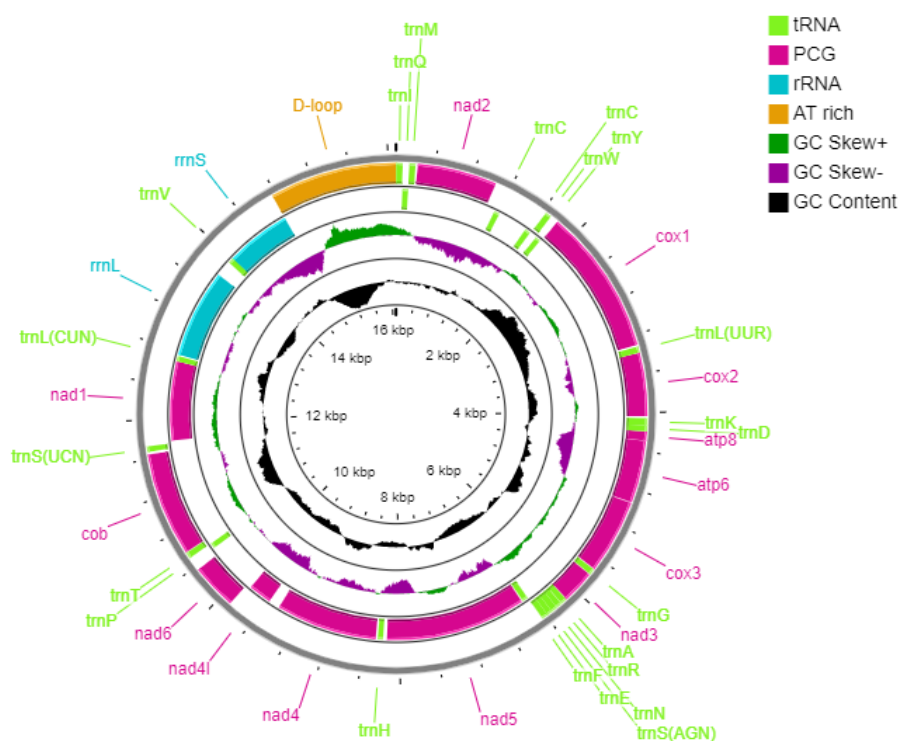
<i>Gene</i>	<i>Location</i>	<i>Direction</i>	<i>Size</i>	<i>Intergenic Spacers</i>	<i>Anticodon</i>	<i>Start codon</i>	<i>Stop codon</i>
<i>tRNA-Ile</i>	1-69	+	69		<i>atc</i>		
<i>tRNA-Gln</i>	73-139	-	67	3	<i>caa</i>		
<i>tRNA-Met</i>	139-202	+	64	-1	<i>atg</i>		
<i>NADH dehydrogenase subunit 2</i>	224-1045	+	822	21		<i>ata</i>	<i>tta</i>
<i>tRNA-Cys</i>	1157-1219	-	63	111	<i>tgc</i>		
<i>tRNA-Cys</i>	1565-1627	-	63	345	<i>tgc</i>		
<i>tRNA-Trp</i>	1638-1702	+	65	10	<i>tga</i>		
<i>tRNA-Tyr</i>	1712-1774	-	63	9	<i>tac</i>		
<i>cytochrome c-oxidase subunit 1</i>	1788-3302	+	1515	13		<i>atg</i>	<i>taa</i>
<i>tRNA-Leu</i>	3322-3387	+	66	19	<i>tta</i>		
<i>cytochrome c-oxidase subunit 2</i>	3388-4041	+	654	0		<i>att</i>	<i>tga</i>
<i>tRNA-Lys</i>	4062-4132	+	71	20	<i>aaa</i>		
<i>tRNA-Asp</i>	4133-4196	+	64	0	<i>gac</i>		
<i>ATPase subunit 8</i>	4197-4289	+	93	0		<i>att</i>	<i>t</i>
<i>ATPase subunit 6</i>	4292-4939	+	648	2		<i>ata</i>	<i>taa</i>
<i>cytochrome c-oxidase subunit 3</i>	4947-5717	+	771	7		<i>atg</i>	<i>tga</i>
<i>tRNA-Gly</i>	5725-5786	+	62	7	<i>gga</i>		
<i>NADH dehydrogenase subunit 3</i>	5793-6134	+	342	6		<i>ata</i>	<i>t</i>
<i>tRNA-Ala</i>	6139-6199	+	61	4	<i>gca</i>		
<i>tRNA-Arg</i>	6204-6263	+	60	4	<i>cga</i>		
<i>tRNA-Asn</i>	6263-6326	+	64	-1	<i>aac</i>		
<i>tRNA-Ser</i>	6326-6384	+	59	-1	<i>aga</i>		
<i>tRNA-Glu</i>	6384-6448	+	65	-1	<i>gaa</i>		
<i>tRNA-Phe</i>	6449-6514	-	66	0	<i>ttc</i>		
<i>NADH dehydrogenase subunit 5</i>	6528-8144	-	1617	13		<i>atg</i>	<i>tt</i>
<i>tRNA-His</i>	8190-8250	-	61	45	<i>cac</i>		
<i>NADH dehydrogenase subunit 4</i>	8274-9437	-	1164	23		<i>att</i>	<i>taa</i>
<i>NADH dehydrogenase subunit 4L</i>	9566-9829	-	264	128		<i>atg</i>	<i>taa</i>
<i>NADH dehydrogenase subunit 6</i>	9884-10357	+	474	54		<i>att</i>	<i>t</i>
<i>tRNA-Pro</i>	10448-10509	-	62	90	<i>cca</i>		
<i>tRNA-Thr</i>	10510-10572	+	63	0	<i>aca</i>		
<i>apocytochrome b</i>	10580-11653	+	1074	7		<i>atg</i>	<i>t</i>
<i>tRNA-Ser</i>	11682-11738	+	57	28	<i>tca</i>		
<i>NADH dehydrogenase subunit 1</i>	11768-12673	-	906	29		<i>atg</i>	<i>t</i>

<i>tRNA-Leu</i>	12675-12736	-	62	1	<i>Cta</i>		
<i>16S ribosomal RNA</i>	12753-13772	-	1020	16			
<i>tRNA-Val</i>	13956-14024	-	69	183	<i>Gta</i>		
<i>12S ribosomal RNA</i>	14019-14768	-	750	-6			
<i>Probable D-loop</i>	14769-16072		1304	0			

Supplementary Table S2: Summary table for characteristics of the complete mitogenome of *Nilaparvata lugens*_2 (NCBI Accession Number: OM372598)

<i>Gene</i>	<i>Location</i>	<i>Direct ion</i>	<i>Size</i>	<i>Intergenic Spacers</i>	<i>Anticodon</i>	<i>Start codon</i>	<i>Stop codon</i>
<i>tRNA-Ile</i>	1-69	+	69		<i>atc</i>		
<i>tRNA-Gln</i>	73-139	-	67	3	<i>caa</i>		
<i>tRNA-Met</i>	139-202	+	64	-1	<i>atg</i>		
<i>NADH dehydrogenase subunit 2</i>	224-1045	+	822	21		<i>ata</i>	<i>tta</i>
<i>tRNA-Cys</i>	1157-1219	-	63	111	<i>tgc</i>		
<i>tRNA-Cys</i>	1565-1626	-	63	345	<i>tgc</i>		
<i>tRNA-Trp</i>	1637-1701	+	65	10	<i>tga</i>		
<i>tRNA-Tyr</i>	1711-1773	-	63	9	<i>tac</i>		
<i>cytochrome c-oxidase subunit 1</i>	1787-3301	+	1515	13		<i>atg</i>	<i>taa</i>
<i>tRNA-Leu</i>	3321-3386	+	66	19	<i>tta</i>		
<i>cytochrome c-oxidase subunit 2</i>	3387-4040	+	654	0		<i>att</i>	<i>tga</i>
<i>tRNA-Lys</i>	4061-4131	+	71	20	<i>aaa</i>		
<i>tRNA-Asp</i>	4132-4195	+	64	0	<i>gac</i>		
<i>ATPase subunit 8</i>	4196-4288	+	93	0		<i>att</i>	<i>t</i>
<i>ATPase subunit 6</i>	4291-4938	+	648	2		<i>ata</i>	<i>taa</i>
<i>cytochrome c-oxidase subunit 3</i>	4946-5716	+	771	7		<i>atg</i>	<i>tga</i>
<i>tRNA-Gly</i>	5724-5785	+	62	7	<i>gga</i>		
<i>NADH dehydrogenase subunit 3</i>	5792-6133	+	342	6		<i>ata</i>	<i>t</i>
<i>tRNA-Ala</i>	6138-6198	+	61	4	<i>gca</i>		
<i>tRNA-Arg</i>	6203-6262	+	60	4	<i>cga</i>		
<i>tRNA-Asn</i>	6262-6325	+	64	-1	<i>aac</i>		
<i>tRNA-Ser</i>	6325-6383	+	59	-1	<i>aga</i>		
<i>tRNA-Glu</i>	6383-6447	+	65	-1	<i>gaa</i>		
<i>tRNA-Phe</i>	6448-6513	-	66	0	<i>ttc</i>		
<i>NADH dehydrogenase subunit 5</i>	6527-8143	-	1617	13		<i>atg</i>	<i>tt</i>
<i>tRNA-His</i>	8189-8249	-	61	45	<i>cac</i>		
<i>NADH dehydrogenase subunit 4</i>	8273-9436	-	1164	23		<i>att</i>	<i>taa</i>
<i>NADH dehydrogenase</i>	9565-9828	-	264	128		<i>atg</i>	<i>taa</i>

<i>subunit 4L</i>							
<i>NADH dehydrogenase subunit 6</i>	9883-10356	+	474	54		<i>att</i>	<i>t</i>
<i>tRNA-Pro</i>	10442-10503	-	62	85	<i>cca</i>		
<i>tRNA-Thr</i>	10504-10566	+	63	0	<i>aca</i>		
<i>apocytochrome b</i>	10574-11647	+	1074	7		<i>atg</i>	<i>t</i>
<i>tRNA-Ser</i>	11676-11732	+	57	28	<i>aga</i>		
<i>NADH dehydrogenase subunit 1</i>	11762-12667	-	906	29		<i>atg</i>	<i>t</i>
<i>tRNA-Leu</i>	12669-12730	-	62	1	<i>tta</i>		
<i>16S ribosomal RNA</i>	12747-13766	-	1020	16			
<i>tRNA-Val</i>	13950-14018	-	69	183	<i>gta</i>		
<i>12S ribosomal RNA</i>	14013-14762	-	750	-6			
<i>Probable D-loop</i>	14763-16081		1319	0			



Supplementary Figure S1. Mitochondrial genome map of *Nilaparvata lugens* sample-2. From outer to inner, the 1st circle shows the gene map (PCGs, rRNA, tRNAs & CR) and tRNA genes are abbreviated by one letter symbols according to the IUPAC-IUB single-letter amino acid codes. The 2nd circle shows the GC content and the 3rd shows GC skew calculated as $(G-C)/(G+C)$. GC content and GC skew are plotted as the deviation from the average value of the entire sequence.