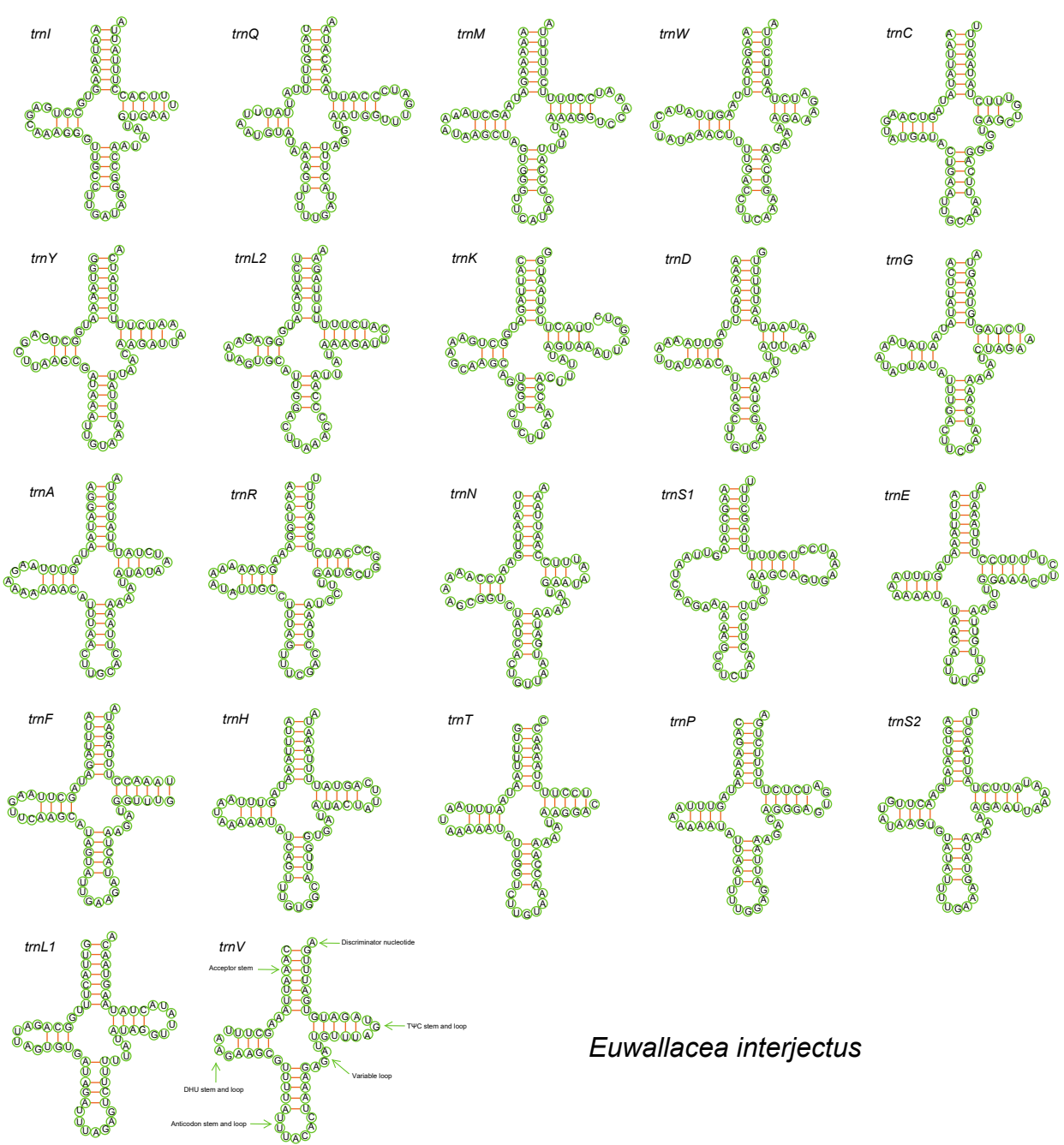
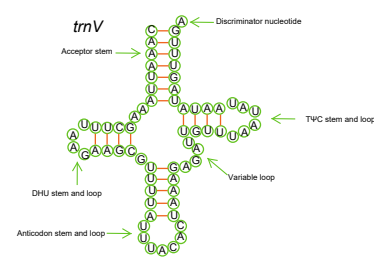
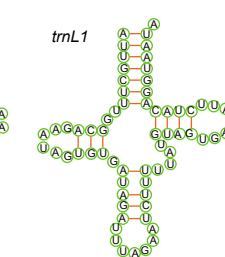
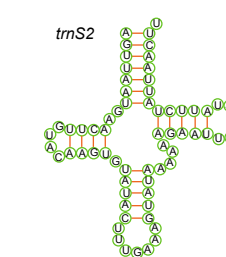
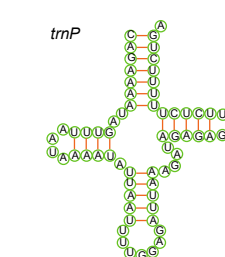
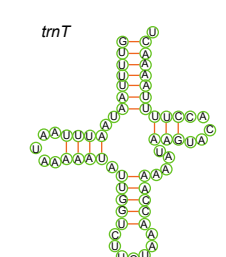
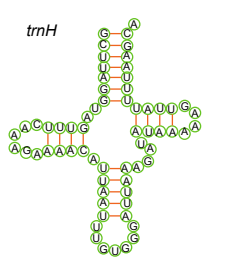
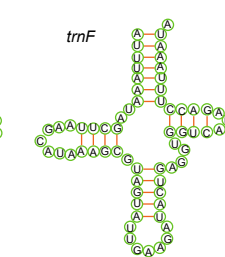
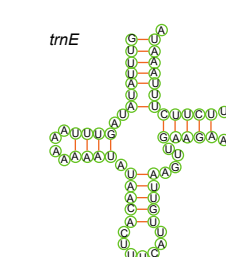
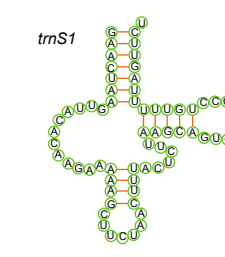
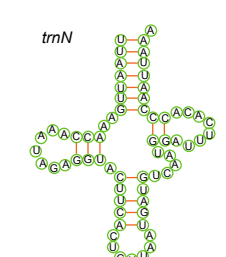
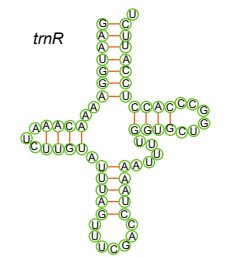
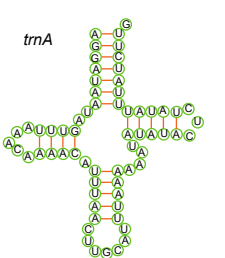
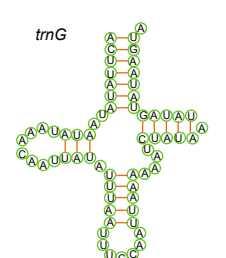
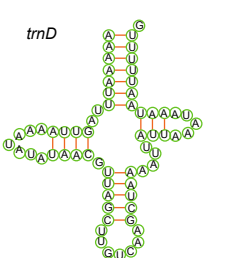
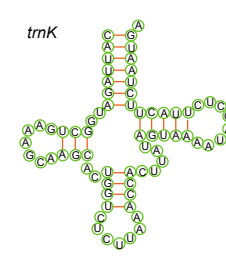
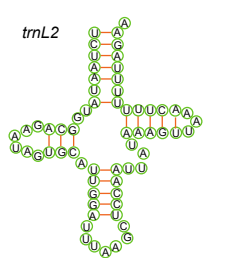
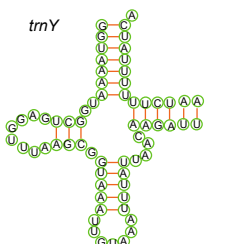
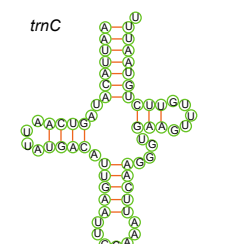
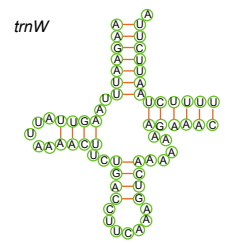
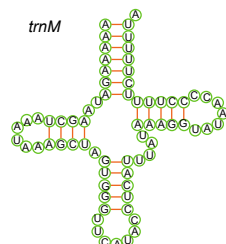
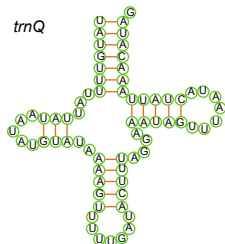
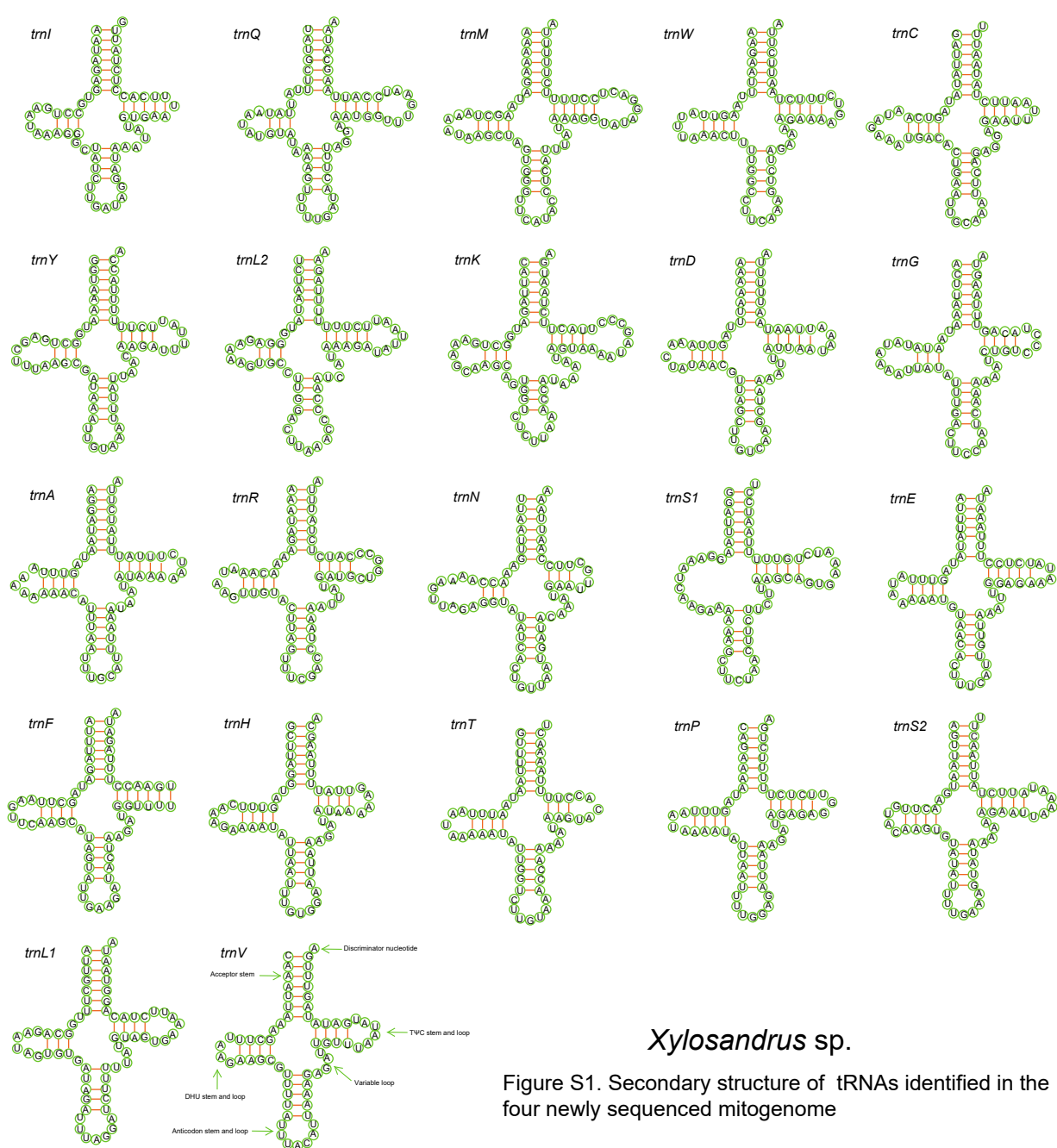


Euwallacea fornicatus





Euwallacea similis



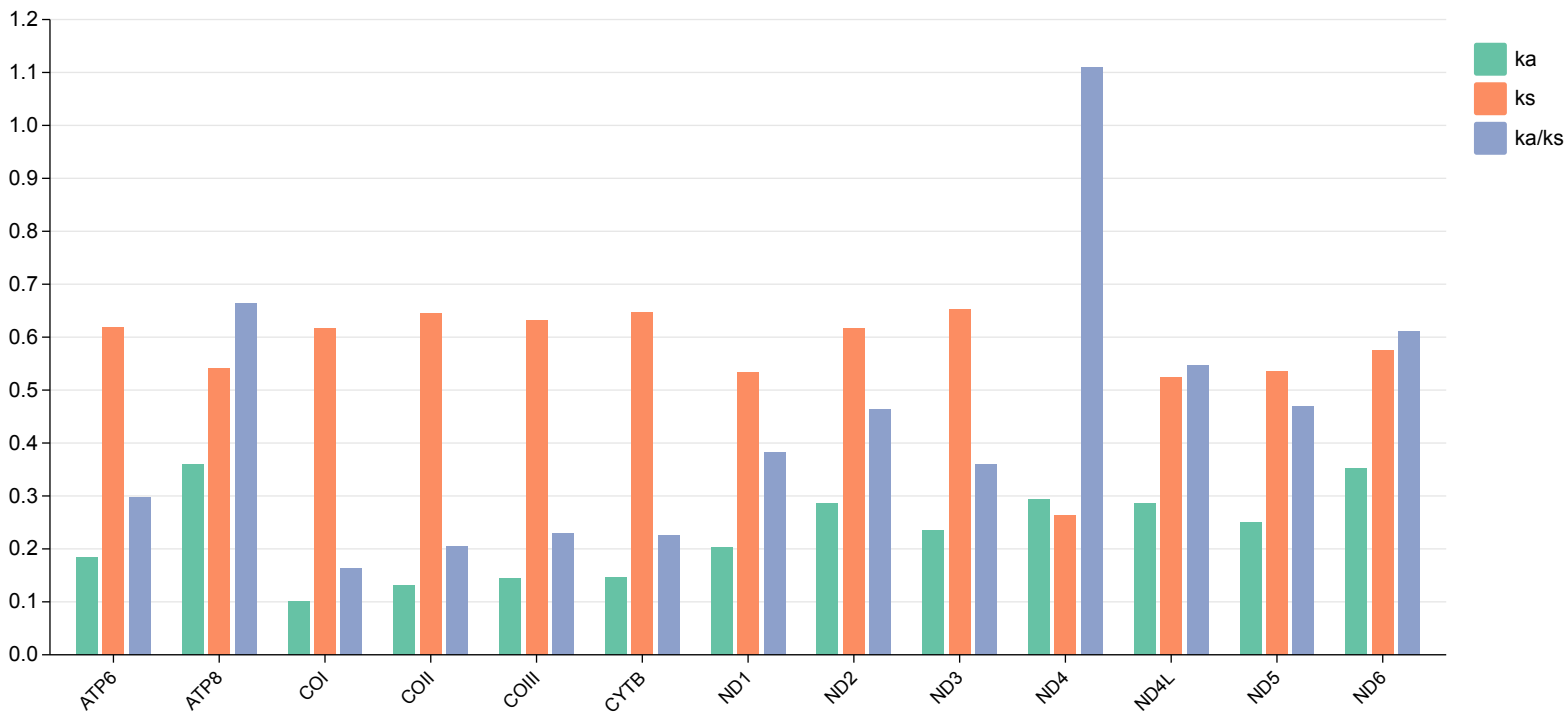


Figure S2. The Ka/Ks ratios of 13 PCGs of Scolytinae mitogenomes. Ka is the nonsynonymous substitution rate, and Ks is the synonymous substitution rate.

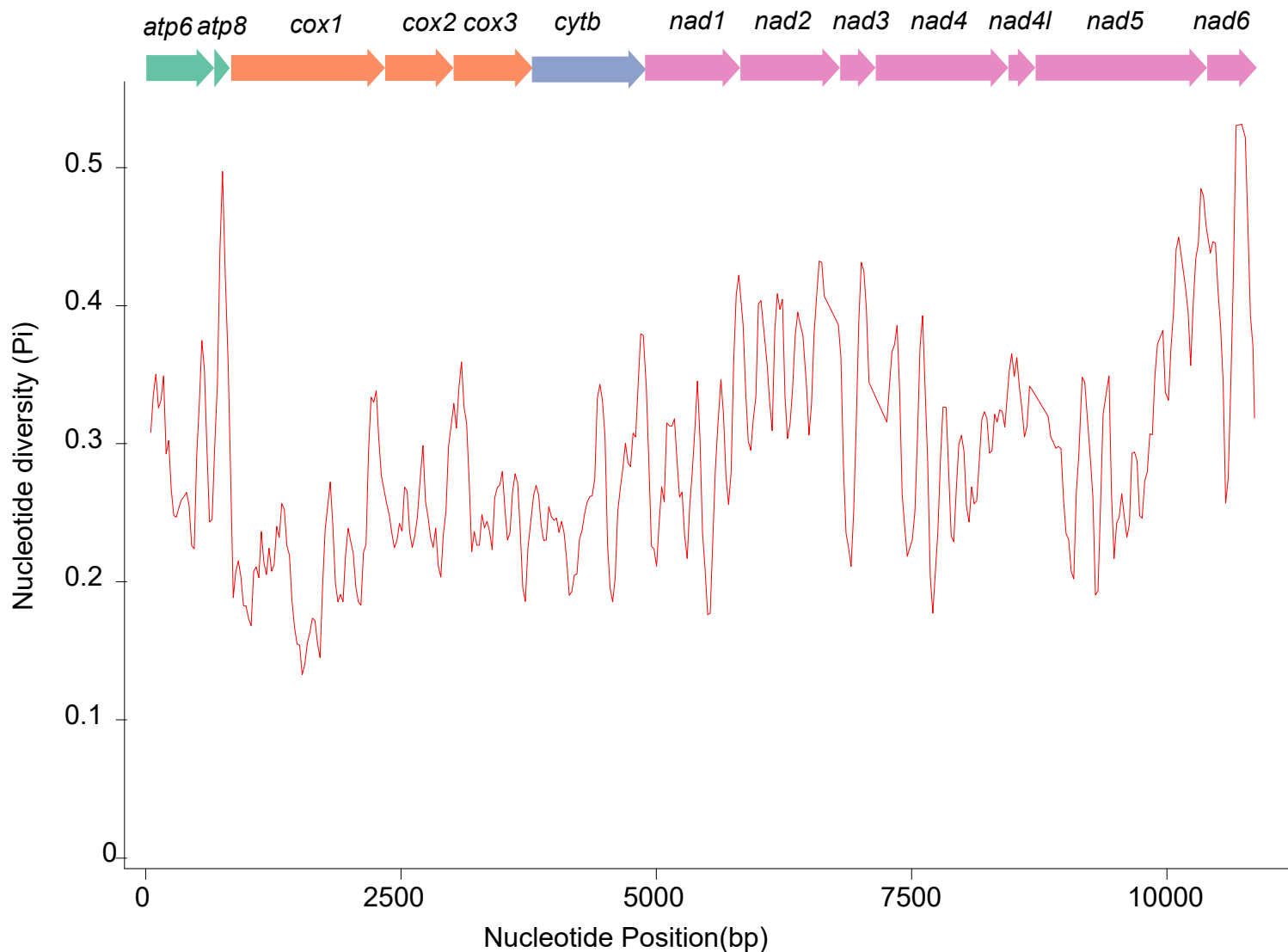


Figure S3. Sliding window analysis of 13 PCGs based on 52 Scolytinae mitogenomes. The red line shows the value of nucleotide diversity P_i (window size = 100 bp, step size = 20 bp). The P_i value for each gene is shown in the graph

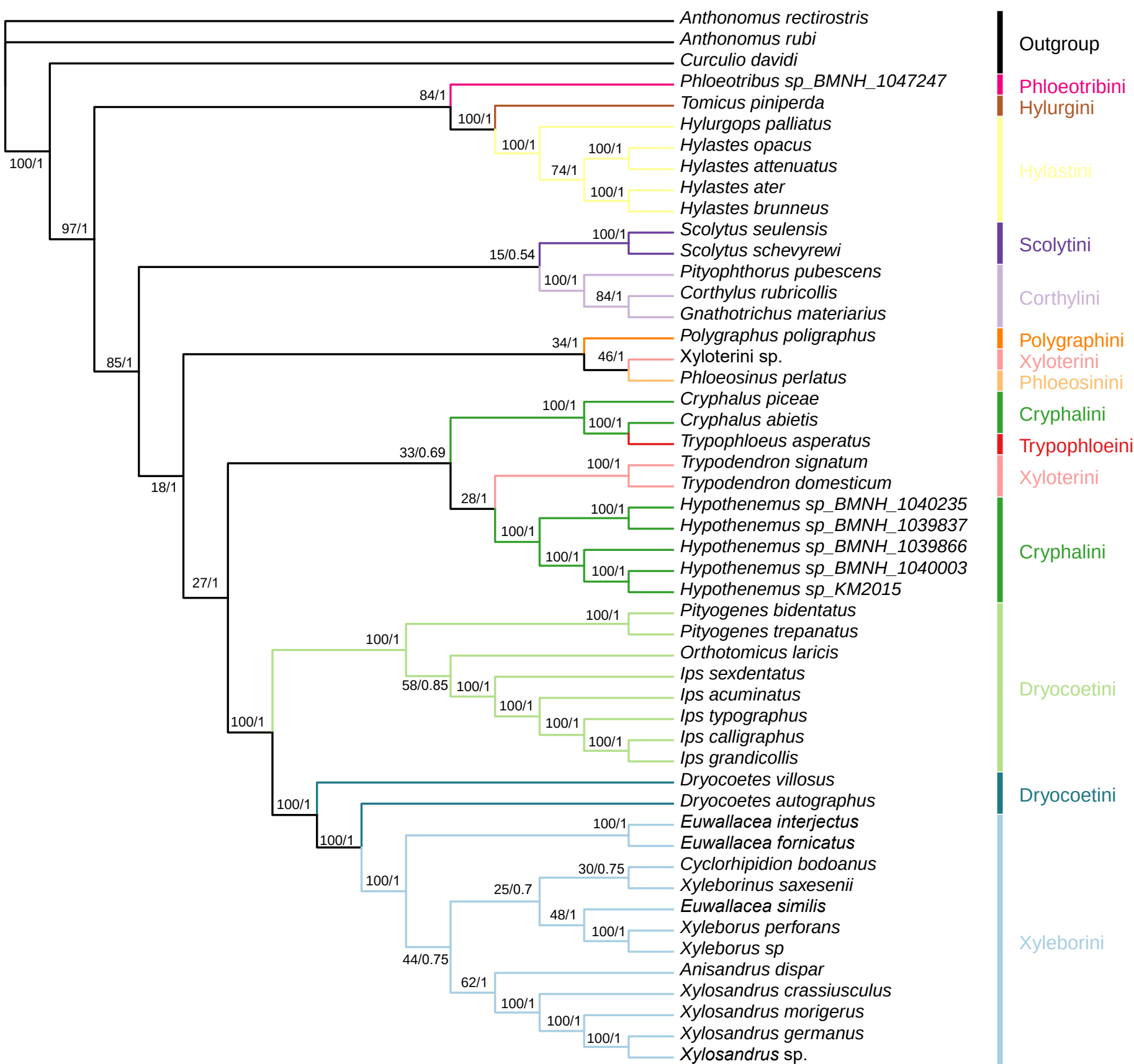


Figure S4. Phylogenetic tree inferred from RAxML and MrBayes analysis based on PCG12R matrix. Bootstrap values (BS) and Bayesian posterior probabilities (PP) are indicated on branches. Clades with different colors indicate different tribes.

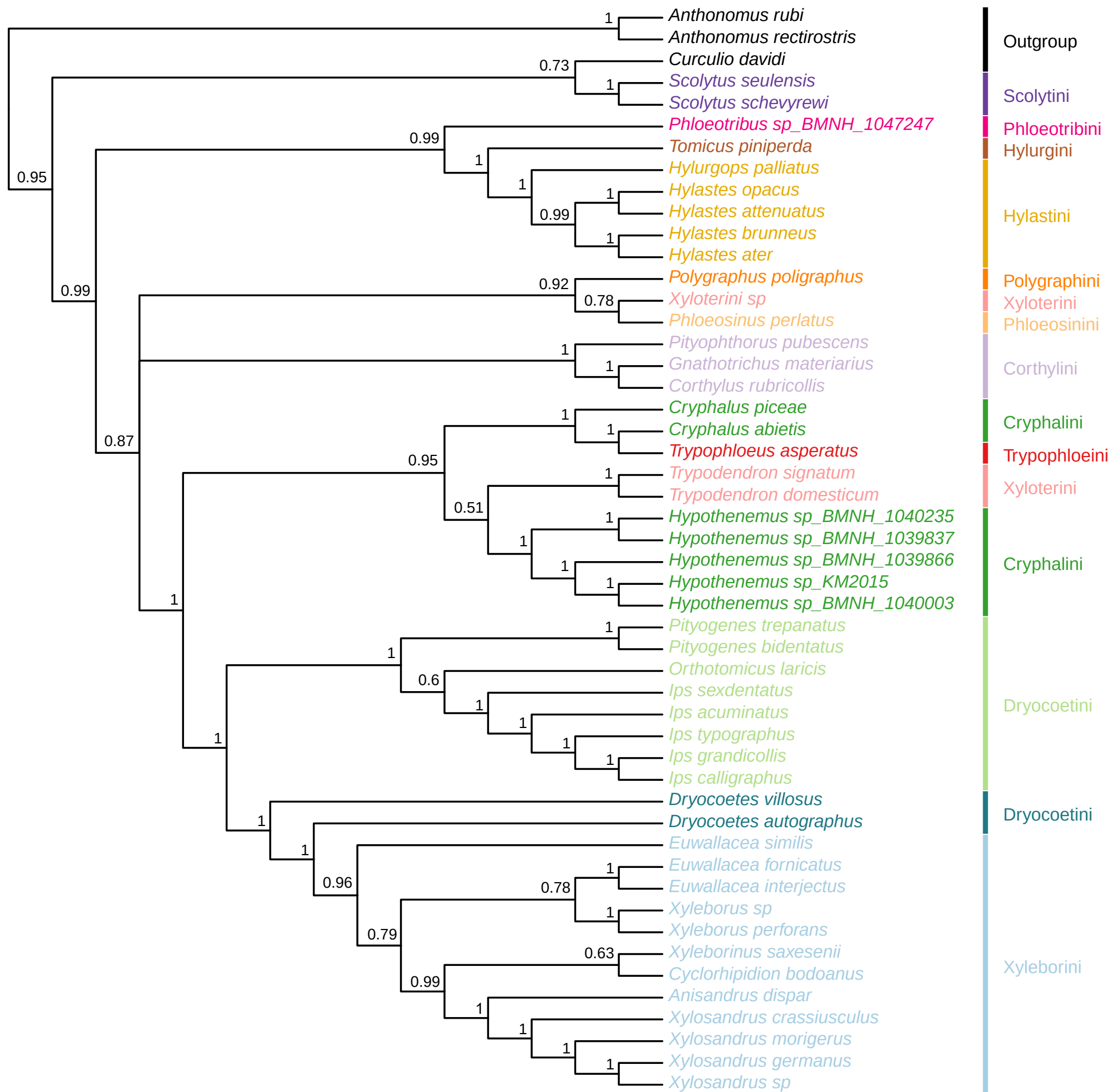


Figure S5. Phylogenetic tree inferred from PhyloBayes analysis based on PCG12R matrix. Bayesian posterior probabilities (PP) are indicated on branches. Clades with different colors indicate different tribes.

Table S1. The mitogenome sequences used in this study.

Tribe	Genus	Species	Size(bp)	GenBank
Corthylini	<i>Corthylus</i>	<i>Corthylus rubricollis</i>	10,450	MH473537
	<i>Gnathotrichus</i>	<i>Gnathotrichus materiarius</i>	16,871	NC_036294
	<i>Pityophthorus</i>	<i>Pityophthorus pubescens</i>	17,316	NC_036288
Cryphalini	<i>Cryphalus</i>	<i>Cryphalus abietis</i>	15,088	MT410860
		<i>Cryphalus piceae</i>	14,890	MT862373
	<i>Hypothenemus</i>	<i>Hypothenemus</i> sp BMNH 1039837	17,469	KX035163
		<i>Hypothenemus</i> sp BMNH 1039866	16,388	KX035165
		<i>Hypothenemus</i> sp BMNH 1040003	16,098	KX035175
		<i>Hypothenemus</i> sp BMNH 1040235	17,530	KX035186
		<i>Hypothenemus</i> sp KM2015	16,391	KX035224
Dryocoetini	<i>Dryocoetes</i>	<i>Dryocoetes autographus</i>	17,055	NC_036287
		<i>Dryocoetes villosus</i>	15,859	NC_036282
Hylastini	<i>Hylastes</i>	<i>Hylastes ater</i>	15,307	KX035206
		<i>Hylastes attenuatus</i>	17,409	NC_036290
		<i>Hylastes brunneus</i>	15,774	NC_036262
		<i>Hylastes opacus</i>	16,093	KX035200
	<i>Hylurgops</i>	<i>Hylurgops palliatus</i>	16,233	KX035201
Hylurgini	<i>Tomicus</i>	<i>Tomicus piniperda</i>	17,021	KX035226
Ipini	<i>Ips</i>	<i>Ips acuminatus</i>	19,580	MK988441
		<i>Ips calligraphus</i>	19,144	MW589547
		<i>Ips grandicollis</i>	11,553	KY952780
		<i>Ips sexdentatus</i>	18,579	NC_036281
		<i>Ips typographus</i>	17,054	KY952782
		<i>Orthotomicus</i>	18,887	NC_036291
		<i>Pityogenes</i>	18,781	NC_036289
		<i>Pityogenes trepanatus</i>	17,930	KX035225
Phloeosinini	<i>Phloeosinus</i>	<i>Phloeosinus perlatus</i>	17,054	NC_057470
Phloeotribini	<i>Phloeotribus</i>	<i>Phloeotribus</i> sp BMNH 1047247	15,449	KX035210
Polygraphini	<i>Polygraphus</i>	<i>Polygraphus poligraphus</i>	15,302	MN528600
Scolytini	<i>Scolytus</i>	<i>Scolytus schevyrewi</i>	15,891	NC_046589
		<i>Scolytus seulensis</i>	16,396	NC_046588
Trypophloeini	<i>Trypophloeus</i>	<i>Trypophloeus asperatus</i>	17,039	NC_036285
Xyleborini	<i>Anisandrus</i>	<i>Anisandrus dispar</i>	16,665	NC_036293
	<i>Cyclorhipidion</i>	<i>Cyclorhipidion bodoanus</i>	15,899	NC_036295
	<i>Euwallacea</i>	<i>Euwallacea fornicatus</i> *	16,265	ON169988
		<i>Euwallacea interjectus</i> *	16,179	ON169989
		<i>Euwallacea similis</i> *	15,419	ON169990
	<i>Xyleborinus</i>	<i>Xyleborinus saxesenii</i>	15,299	KX035203
	<i>Xyleborus</i>	<i>Xyleborus perforans</i>	10,788	JX412850
		<i>Xyleborus</i> sp.	16,450	KX035179
	<i>Xylosandrus</i>	<i>Xylosandrus crassiusculus</i>	16,875	NC_036284
		<i>Xylosandrus germanus</i>	16,099	NC_036280

		<i>Xylosandrus morigerus</i>	16,246	NC_036283
		<i>Xylosandrus</i> sp*.	16,056	ON169991
Xyloterini	<i>Trypodendron</i>	<i>Trypodendron domesticum</i>	16,986	NC_036286
		<i>Trypodendron signatum</i>	16,909	NC_036292
		<i>Xyloterini</i> sp.	16,971	ON169992
Outgroups				
	<i>Curculio</i>	<i>Curculio davidi</i>	16,852	NC_034293
	<i>Anthonomus</i>	<i>Anthonomus rectirostris</i>	17,676	NC_044713
		<i>Anthonomus rubi</i>	17,476	NC_044714

* Newly generated in this study.

Table S2. Annotation of the four newly sequenced mitogenomes.1. Annotation of the mitogenome of *Euwallacea fornicatus*

Gene	Direction	Location	Size	Anticodon	Start/Stop codon	Intergenic Nucleotides
<i>trnI</i>	F	1-62	62	GAU		
<i>trnQ</i>	R	570-638	69	UUG		507
<i>trnM</i>	F	638-705	68	CAU		-1
<i>nad2</i>	F	706-1701	996		ATA/TAA	0
<i>trnW</i>	F	1702-1767	66	UCA		0
<i>trnC</i>	R	1767-1828	62	GCA		-1
<i>trnY</i>	R	1835-1899	65	GUA		6
<i>cox1</i>	F	1892-3439	1548		ATT/TAA	-8
<i>trnL2^(UUR)</i>	F	3435-3499	65	UAA		-5
<i>cox2</i>	F	3500-4179	680		TTG/TA-	0
<i>trnK</i>	F	4180-4249	70	CUU		0
<i>trnD</i>	F	4250-4315	66	GUC		0
<i>atp8</i>	F	4316-4471	156		ATT/TAA	0
<i>atp6</i>	F	4465-5136	672		ATG/TAA	-7
<i>cox3</i>	F	5136-5918	783		ATG/TAA	-1
<i>trnG</i>	F	5921-5984	64	UCC		2
<i>nad3</i>	F	5985-6338	354		ATA/TAA	0
<i>trnA</i>	F	6338-6402	65	UGC		-1
<i>trnR</i>	F	6402-6469	68	UCG		-1

<i>trnN</i>	F	6512-6575	64	GUU		42
<i>trnS1^(AGN)</i>	F	6576-6642	67	UCU		0
<i>trnE</i>	F	6643-6705	63	UUC		0
<i>trnF</i>	R	6710-6772	63	GAA		4
<i>nad5</i>	R	6773-8477	1705		ATT/T--	0
<i>trnH</i>	R	8478-8540	63	GUG		0
<i>nad4</i>	R	8541-9873	1333		GTG/T--	0
<i>nad4l</i>	R	9867-10166	300		ATG/TAA	-7
<i>trnT</i>	F	10168-10231	64	UGU		1
<i>trnP</i>	R	10232-10295	64	UGG		0
<i>nad6</i>	F	10298-10786	489		ATT/TAA	2
<i>cytb</i>	F	10786-11922	1137		ATG/TAG	-1
<i>trnS2^(UCN)</i>	F	11921-11987	67	UGA		-2
<i>nad1</i>	R	12047-12977	951		TTG/TAA	59
<i>trnL1^(CUN)</i>	R	12999-13063	65	UAG		21
<i>rrnL</i>	R	13064-14523	1460			0
<i>trnV</i>	R	14524-14587	64	UAC		0
<i>rrnS</i>	R	14588-15371	784			0
<i>Control</i>		15372-16265	894			0
<i>region</i>						

2. Annotation of the mitogenome of *Euwallacea interjectus*

Gene	Direction	Location	Size	Anticodon	Start/Stop codon	Intergenic Nucleotides
<i>trnI</i>	F	1-63	63	GAU		
<i>trnQ</i>	R	343-411	69	UUG		279
<i>trnM</i>	F	411-480	70	CAU		-1
<i>nad2</i>	F	481-1473	993		ATA/TAA	0
<i>trnW</i>	F	1472-1537	66	UCA		-2
<i>trnC</i>	R	1537-1597	61	GCA		-1
<i>trnY</i>	R	1598-1662	65	GUA		0
<i>cox1</i>	F	1655-3202	1548		ATT/TAA	-8
<i>trnL2^(UUR)</i>	F	3198-3262	65	UAA		-5
<i>cox2</i>	F	3263-3945	683		TTG/TA-	0
<i>trnK</i>	F	3946-4016	71	CUU		0
<i>trnD</i>	F	4019-4082	64	GUC		2
<i>atp8</i>	F	4083-4238	156		ATT/TAA	0
<i>atp6</i>	F	4232-4903	672		ATG/TAA	-7
<i>cox3</i>	F	4903-5685	783		ATG/TAA	-1
<i>trnG</i>	F	5688-5750	63	UCC		2
<i>nad3</i>	F	5751-6104	354		ATT/TAA	0
<i>trnA</i>	F	6109-6172	64	UGC		4
<i>trnR</i>	F	6173-6240	68	UCG		0
<i>trnN</i>	F	6368-6430	63	GUU		127

<i>trnS1</i> ^(AGN)	F	6431-6497	67	UCU		0
<i>trnE</i>	F	6498-6563	66	UUC		0
<i>trnF</i>	R	6562-6626	65	GAA		-2
<i>nad5</i>	R	6627-8331	1705		ATT/T--	0
<i>trnH</i>	R	8332-8397	66	GUG		0
<i>nad4</i>	R	8398-9730	1327		GTG/T--	0
<i>nad4l</i>	R	9724-10023	300		ATG/TAA	-7
<i>trnT</i>	F	10025-10087	63	UGU		1
<i>trnP</i>	R	10088-10151	64	UGG		0
<i>nad6</i>	F	10154-10654	501		ATA/TAA	2
<i>cytb</i>	F	10654-11790	1137		ATG/TAA	-1
<i>trnS2</i> ^(UCN)	F	11793-11859	67	UGA		2
<i>nad1</i>	R	11922-12875	954		TTG/TAG	62
<i>trnL1</i> ^(CUN)	R	12877-12941	65	UAG		1
<i>rrnL</i>	R	12942-14418	1477			0
<i>trnV</i>	R	14419-14482	64	UAC		0
<i>rrnS</i>	R	14483-15317	835			0
<i>Control</i>		15318-16179	862			0
<i>region</i>						

3. Annotation of the mitogenome of *Euwallacea similis*

Gene	Direction	Location	Size	Anticodon	Start/Stop codon	Intergenic Nucleotides
<i>trnQ</i>	R	1-69	69	UUG		
<i>trnM</i>	F	69-138	70	CAU		-1
<i>nad2</i>	F	139-1134	996		ATA/TAA	0
<i>trnW</i>	F	1133-1196	64	UCA		-2
<i>trnC</i>	R	1196-1257	62	GCA		-1
<i>trnY</i>	R	1258-1322	65	GUA		0
<i>cox1</i>	F	1315-2862	1548		ATT/TAA	-8
<i>trnL2^(UUR)</i>	F	2858-2921	64	UAA		-5
<i>cox2</i>	F	2922-2602	681		ATG/TAA	0
<i>trnK</i>	F	3610-3680	71	CUU		7
<i>trnD</i>	F	3682-3746	65	GUC		1
<i>atp8</i>	F	3747-3902	156		ATT/TAG	0
<i>atp6</i>	F	3896-4567	672		ATG/TAA	-7
<i>cox3</i>	F	4567-5349	783		ATG/TAA	-1
<i>trnG</i>	F	5352-5415	64	UCC		2
<i>nad3</i>	F	5416-5769	354		ATA/TAG	0
<i>trnA</i>	F	5768-5831	64	UGC		-2
<i>trnR</i>	F	5832-5896	65	UCG		0
<i>trnN</i>	F	5981-6045	65	GUU		84
<i>trnS1^(AGN)</i>	F	6046-6112	67	UCU		0

<i>trnE</i>	F	6114-6178	65	UUC		1
<i>trnF</i>	R	6177-6241	65	GAA		-2
<i>nad5</i>	R	6242-7952	1711		ATT/T--	0
<i>trnH</i>	R	7953-8017	65	GUG		0
<i>nad4</i>	R	8018-9350	1333		GTG/T--	0
<i>nad4l</i>	R	9344-9643	300		ATG/TAA	-7
<i>trnT</i>	F	9645-9707	63	UGU		1
<i>trnP</i>	R	9708-9771	64	UGG		0
<i>nad6</i>	F	9774-10271	498		ATT/TAA	2
<i>cytb</i>	F	10271-11413	1143		ATG/TAA	-1
<i>trnS2^(UCN)</i>	F	11413-11479	67	UGA		-1
<i>nad1</i>	R	11530-12480	951		TTG/TAA	50
<i>trnL1^(CUN)</i>	R	12482-12547	66	UAG		1
<i>rrnL</i>	R	12548-13831	1284			0
<i>trnV</i>	R	13832-13896	65	UAC		0
<i>rrnS</i>	R	13897-14738	842			0
<i>Control</i>		14739-15419	681			0
<i>region</i>						

4. Annotation of the mitogenome of *Xylosandrus* sp.

Gene	Direction	Location	Size	Anticodon	Start/Stop codon	Intergenic Nucleotides
<i>trnI</i>	F	1-63	63	GAU		
<i>trnQ</i>	R	394-462	69	UUG		279
<i>trnM</i>	F	462-533	72	CAU		-1
<i>nad2</i>	F	534-1529	996		ATA/TAA	0
<i>trnW</i>	F	1528-1593	66	UCA		-2
<i>trnC</i>	R	1593-1657	65	GCA		-1
<i>trnY</i>	R	1658-1724	67	GUA		0
<i>cox1</i>	F	1717-3264	1548		ATT/TAA	-8
<i>trnL2^(UUR)</i>	F	3260-3327	68	UAA		-5
<i>cox2</i>	F	3328-4014	687		ATC/TAA	0
<i>trnK</i>	F	4015-4084	70	CUU		0
<i>trnD</i>	F	4085-4150	66	GUC		2
<i>atp8</i>	F	4151-4306	156		ATT/TAG	0
<i>atp6</i>	F	4300-4971	672		ATG/TAA	-7
<i>cox3</i>	F	4971-5753	783		ATG/TAA	-1
<i>trnG</i>	F	5762-5826	65	UCC		2
<i>nad3</i>	F	5827-6180	354		ATT/TAA	0
<i>trnA</i>	F	6181-6245	65	UGC		4
<i>trnR</i>	F	6246-6312	67	UCG		0
<i>trnN</i>	F	6331-6396	66	GUU		127

<i>trnS1^(AGN)</i>	F	6397-6462	66	UCU		0
<i>trnE</i>	F	6465-6529	65	UUC		0
<i>trnF</i>	R	6528-6592	65	GAA		-2
<i>nad5</i>	R	6593-8288	1696		ATT/T--	0
<i>trnH</i>	R	8289-8356	68	GUG		0
<i>nad4</i>	R	8357-9695	1338		GTG/T--	0
<i>nad4l</i>	R	9689-9994	306		ATT/TAA	-7
<i>trnT</i>	F	10002-10065	64	UGU		1
<i>trnP</i>	R	10066-10132	67	UGG		0
<i>nad6</i>	F	10135-10638	504		ATC/TAA	2
<i>cytb</i>	F	10638-11772	1135		ATG/T--	-1
<i>trnS2^(UCN)</i>	F	11773-11839	67	UGA		2
<i>nad1</i>	R	11902-12855	954		TTG/TAA	62
<i>trnL1^(CUN)</i>	R	12856-12922	67	UAG		1
<i>rrnL</i>	R	12923-14209	1287			0
<i>trnV</i>	R	14210-14276	67	UAC		0
<i>rrnS</i>	R	14277-15053	777			0
<i>Control</i>		15054-16057	1004			0
<i>region</i>						

Table S3. Base composition and skewness of the newly sequenced mitogenomes.**1. Base composition and skewness of the *Euwallacea fornicatus* mitogenome**

Dataset	Size(bp)	A%	C%	G%	T%	A+T%	AT-Skew	GC-Skew
Whole genome	16,265	39.3	16.5	10.1	34.1	73.4	0.071	-0.024
PCGs	11,105	39.4	17.7	10.7	32.2	71.6	0.101	-0.246
tRNA genes	1,500	39.3	13.8	9.9	37.0	76.3	0.030	-0.165
rRNA genes	2,244	39.8	16.8	8.1	35.3	75.1	0.060	-0.349
Control Region	894	40.0	6.5	5.6	47.9	87.9	-0.090	-0.074

2. Base composition and skewness of the *Euwallacea interjectus* mitogenome

Dataset	Size(bp)	A%	C%	G%	T%	A+T%	AT-Skew	GC-Skew
Whole genome	16,179	38.6	17.5	10.5	33.4	72.0	0.072	-0.250
PCGs	11,112	38.7	18.6	11.2	31.7	70.4	0.099	-0.250
tRNA genes	1,439	39.1	14.9	10.7	35.3	74.4	0.051	-0.164
rRNA genes	2,312	39.4	17.9	8.7	34.0	73.4	0.074	-0.346
Control Region	862	38.6	6.7	7.1	47.6	86.2	-0.104	0.029

3. Base composition and skewness of the *Euwallacea similis* mitogenome

Dataset	Size(bp)	A%	C%	G%	T%	A+T%	AT-Skew	GC-Skew
Whole genome	15,419	39.5	19.4	9.9	31.2	70.7	0.117	-0.324
PCGs	11,125	39.6	20.6	10.6	29.2	68.8	0.151	-0.321
tRNA genes	1,376	39.5	14.9	9.5	36.1	75.6	0.045	-0.221
rRNA genes	2,126	39.7	19.5	7.7	33.1	72.8	0.091	-0.434
Control Region	681	40.8	5.9	8.8	44.5	85.3	-0.043	0.197

4. Base composition and skewness of the *Xylosandrus* sp. mitogenome

Dataset	Size(bp)	A%	C%	G%	T%	A+T%	AT-Skew	GC-Skew
Whole genome	16,056	39.6	18.1	10.1	32.3	71.8	0.102	-0.284
PCGs	11,131	39.7	19.3	10.6	30.4	70.1	0.133	-0.291
tRNA genes	1,465	39.9	13.7	10.5	35.9	75.8	0.053	-0.132
rRNA genes	2,064	39.4	18.8	8.1	33.6	73.1	0.079	-0.398
Control Region	1004	41.4	7.5	7.1	43.7	85.8	-0.027	-0.028

Table S4. Cross-validation analyses of the homogeneous and heterogeneous models implemented in PhyloBayes based on PCRG and PCG12R datasets.

Dada set	Model1	Model2	Cross-validation score	Standard deviation
PCGR	GTR	GTR+CAT	1472.85	±76.68
PCG12R	GTR	GTR+CAT	684.41	±40.22

Model 1 is the reference model in cross-validation analysis; negative cross-validation score correspond to a better fit of reference model