

**Table S1.** The list of sample information of bark beetles.

<b>Species</b>	<b>Accession no.</b>	<b>Species</b>	<b>Accession no.</b>
<i>Hylates brunneus</i>	NC_036262.1	Scolytinae BMNH 1039855	X035164.1
<i>Hylates attenuatus</i>	NC_036290.1	Scolytinae BMNH1274287	KT696206.1
<i>Pityophthorus pubescens</i>	NC_036288.1	Scolytinae BMNH1040341	KX035192.1
<i>Pityogenes bidentatus</i>	NC_036289.1	Scolytinae BMNH1039965	KX035170.1
<i>Ips acuminatus</i>	MK988441	Scolytinae BMNH1043104	KX035197.1
<i>Ips sexdentatus</i>	NC_036281.1	Scolytinae BMNH1040075	KX035181.1
<i>Orthotomicus laricis</i>	NC_036291.1	Scolytinae BMNH1040174	KX035185.1
<i>Dryocoetes autographus</i>	NC_036287.1	Scolytinae BMNH1040327	KX035189.1
<i>Dryocoetes villosus</i>	NC_036282.1	Scolytinae BMNH1040118	KX035183.1
<i>Xylosandrus morigerus</i>	NC_036283.1	Scolytinae BMNH1040002	KX035174.1
<i>Xylosandrus germanus</i>	NC_036280.1	Scolytinae BMNH1039905	KX035168.1
<i>Xylosandrus crassiusculus</i>	NC_036284.1	<i>Hypothenemus</i> BMNH1040235	KX035186.1
<i>Anisandrus dispar</i>	NC_036293.1	<i>Hypothenemus</i> BMNH1039837	KX035163.1
<i>Cyclorhipidion bodoanum</i>	NC_036295	<i>Hypothenemus</i> BMNH1040003	KX035175.1
<i>Gnathotrichus materiarius</i>	NC_036294.1	<i>Hypothenemus</i> BMNH1039866	KX035165.1
<i>Trypophloeus asperatus</i>	NC_036285.1	Scolytinae BMNH1040351	KX035193.1
<i>Trypodendron signatum</i>	NC_036292.1	Scolytinae BMNH1039994	KX035172.1
<i>Trypodendron domesticum</i>	NC_036286.1	Scolytinae BMNH1039990	KX035171.1
<i>Sitophilus oryzae</i>	KX373615	Scolytinae BMNH1040265	KX035187.1
<i>Sitophilus zeamais</i>	KX373614	Scolytinae BMNH10403133	KX035199.1
<i>Xyleborus</i> BMNH1040067	KX035179.1	Scolytinae BMNH1040331	KX035190.1

**Table S2.** Annotation of the mitogenome of *Orthotomicus erosus*.

Gene	Direction	Start position	Stop position	Length	Anticodon	Start Codon	Stop Codon	IGS
trnQ	R	1	70	70	CAT			
trnM	F	116	183	68	TTG			45
ND2	F	202	1191	990		ATT	TAA	18
trnW	F	1211	1278	68	TCA			19
trnC	R	1298	1363	66	GCA			19
trnY	R	1394	1459	66	GTA			30
COI	F	1506	3050	1545		ATA	TAA	46
trnL2	F	3046	3112	67	TAA			-5
COII	F	3068	3796	729		ATG	TAA	-45
trnK	F	3804	3874	71	CTT			7
trnD	F	3887	3954	68	GTC			12
ATP8	F	3964	4125	162		ATA	TAG	9
ATP6	F	4119	4802	684		ATG	TAA	-7
COIII	F	4807	5601	795		ATG	TAA	4
trnG	F	5639	5704	66	TCC			37
ND3	F	5705	6058	354		ATT	TAG	0
trnA	F	6106	6173	68	TGC			47
trnR	F	6184	6249	66	TCG			10
trnN	F	6325	6389	65	GTT			75
trnS1	F	6390	6456	67	GCT			0
trnE	F	6457	6523	67	TTC			0
trnF	R	6548	6616	69	GAA			24
ND5	R	6617	8326	1710		ATT	TAA	0
trnH	R	8342	8406	65	GTG			15
ND4	R	8469	9815	1347		ATG	TAA	62
ND4L	R	9809	10096	288		ATG	TAG	-7
trnT	F	10114	10180	67	TGT			17
trnP	R	10181	10248	68	TGG			0
ND6	F	10266	10772	507		ATA	TAA	17
CytB	F	10781	11920	1140		ATG	TAA	8
trnS2	F	11945	12012	68	TGA			24
ND1	R	12031	12957	927		ATT	TAA	18
trnL1	R	12976	13043	68	TAG			18
rrnL	R	13082	14390	1309				38
trnV	R	14421	14485	65	TAC			30
rrnS	R	14484	15269	786				-2
trnI	F	16687	16753	67	GAT			1417

**Table S3.** Annotation of the mitogenome of *Dryocoetes hectographus*.

Gene	Direction	Start Position	Stop Position	Length	Anticodon	Start Codon	Stop Codon	IGS
trnQ	R	1	69	69	CAT			
trnM	F	69	139	71	TTG			-1
ND2	F	113	1132	1020		ATG	TAA	-27
trnW	F	1132	1197	66	TCA			-1
trnC	R	1197	1258	62	GCA			-1
trnY	R	1262	1325	64	GTA			3
COI	F	1318	2865	1548		ATT	TAA	-8
trnL2	F	2861	2925	65	TAA			-5
COII	F	2926	3612	687		ATT	TAA	0
trnK	F	3613	3683	71	CTT			0
trnD	F	3684	3751	68	GTC			0
ATP8	F	3752	3907	156		ATT	TAG	0
ATP6	F	3901	4572	672		ATG	TAA	-7
COIII	F	4573	5355	783		ATG	TAA	0
trnG	F	5362	5424	63	TCC			6
ND3	F	5425	5778	354		ATA	TAG	0
trnA	F	5777	5838	62	TGC			-2
trnR	F	5840	5907	68	TCG			1
trnN	F	5909	5972	64	GTT			1
trnS1	F	5973	6040	68	GCT			0
trnE	F	6041	6103	63	TTC			0
trnF	R	6127	6189	63	GAA			23
ND5	R	6143	7858	1716		ATT	TAG	-47
trnH	R	7898	7963	66	GTG			39
ND4	R	7944	9290	1347		ATG	TAA	-20
ND4L	R	9294	9587	294		ATG	TAG	3
trnT	F	9589	9652	64	TGT			1
trnP	R	9653	9715	63	TGG			0
ND6	F	9718	10227	510		ATT	TAA	2
CytB	F	10227	11369	1143		ATG	TAG	-1
trnS2	F	11368	11435	68	TGA			-2
ND1	R	11453	12379	927		ATA	TAA	17
trnL1	R	12405	12470	66	TAG			25
rrnL	R	12472	13756	1285				1
trnV	R	13758	13822	65	TAC			1
rrnS	R	13821	14596	776				-2
trnI	F	15432	15495	64	GAT			835

**Table S4.** Annotation of the mitogenome of *Polygraphus poligraphus*.

Gene	Direction	Start Position	Stop Position	Length	Anticodon	Start Codon	Stop Codon	IGS
trnI	F	1	63	63	GAT			
trnQ	R	1025	1092	68	CAT			961
trnM	F	1092	1160	69	TTG			-1
ND2	F	1161	2165	1005		ATT	TAA	0
trnW	F	2168	2235	68	TCA			2
trnC	R	2236	2302	67	GCA			0
trnY	R	2307	2371	65	GTA			4
COI	F	2364	3908	1545		ATT	TAA	-8
trnL2	F	3911	3973	63	TAA			2
COII	F	3995	4687	693		ATA	TAA	21
trnK	F	4653	4723	71	CTT			-35
trnD	F	4723	4786	64	GTC			-1
ATP8	F	4787	4945	159		ATT	TAG	0
ATP6	F	4939	5613	675		ATG	TAA	-7
COIII	F	5613	6398	786		ATG	TAA	-1
trnG	F	6405	6468	64	TCC			6
ND3	F	6469	6822	354		ATA	TAA	0
trnA	F	6831	6894	64	TGC			8
trnR	F	6895	6958	64	TCG			0
trnN	F	6960	7024	65	GTT			1
trnS1	F	7024	7083	60	GCT			-1
trnE	F	7085	7145	61	TTC			1
ND5	R	7155	8831	1677		ATG	TAA	9
trnH	R	8907	8973	67	GTG			75
ND4	R	8973	10301	1329		ATG	TAA	-1
ND4L	R	10295	10588	294		ATG	TAG	-7
trnT	F	10592	10656	65	TGT			3
trnP	R	10657	10720	64	TGG			0
ND6	F	10723	11229	507		ATG	TAA	2
CytB	F	11230	12369	1140		ATG	TAA	0
trnS2	F	12369	12434	66	TGA			-1
ND1	R	12444	13379	936		ATT	TAA	9
trnL1	R	13399	13465	67	TAG			19
rrnL	R	13426	14759	1334				-40
trnV	R	14748	14815	68	TAC			-12
rrnS	R	14815	15586	772				-1

**Table S5.** Annotation of the mitogenome of *Dendroctonus micans*.

Gene	Direction	Start Position	Stop Position	Length	Anticodon	Start Codon	Stop Codon	IGS
trnM	F	1	66	66	TTG			
ND2	F	88	1089	1002		ATT	TAA	21
trnW	F	1088	1151	64	TCA			-2
trnC	R	1151	1212	62	GCA			-1
trnY	R	1216	1278	63	GTA			3
COI	F	1271	2815	1545		ATT	TAA	-8
trnL2	F	2811	2875	65	TAA			-5
COII	F	2876	3559	684		ATT	TAA	0
trnK	F	3561	3631	71	CTT			1
trnD	F	3632	3695	64	GTC			0
ATP8	F	3696	3851	156		ATA	TAA	0
ATP6	F	3845	4516	672		ATG	TAA	-7
COIII	F	4522	5304	783		ATG	TAA	5
trnG	F	5311	5374	64	TCC			6
ND3	F	5375	5728	354		ATT	TAG	0
trnA	F	5727	5787	61	TGC			-2
trnR	F	5786	5852	67	TCG			-2
trnN	F	5851	5916	66	GTT			-2
trnS1	F	5917	5981	65	GCT			0
trnE	F	5981	6043	63	TTC			-1
trnF	R	6042	6104	63	GAA			-2
ND5	R	6061	7770	1710		ATT	TAG	-44
trnH	R	7813	7873	61	GTG			42
ND4	R	7857	9203	1347		ATG	TAA	-17
ND4L	R	9197	9493	297		ATG	TAA	-7
trnT	F	9497	9559	63	TGT			3
trnP	R	9560	9622	63	TGG			0
ND6	F	9625	10128	504		ATT	TAA	2
CytB	F	10128	11267	1140		ATG	TAA	-1
trnS2	F	11270	11334	65	TGA			2
ND1	R	11352	12281	930		ATA	TAG	17
trnL1	R	12301	12362	62	TAG			19
rrnL	R	12325	13629	1305				-38
trnV	R	13657	13722	66	TAC			27
rrnS	R	13720	14486	767				-3
trnI(gat)	F	16053	16117	65	GAT			1566
trnQ	R	16738	16807	70	CAT			620

**Table S6** Annotation of the mitogenome of *Ips hauseri*

Gene	Direction	Start Position	Stop Position	Length	Anticodon	Start Codon	Stop Codon	IGS
trnQ	R	1	70	70	CAT			
trnM	F	123	193	71	TTG			52
ND2	F	194	1204	1011		ATA	TAA	0
trnW	F	1226	1292	67	TCA			21
trnC	R	1309	1373	65	GCA			16
trnY	R	1439	1506	68	GTA			65
COI	F	1470	3050	1581		ATT	TAA	-37
trnL2	F	3046	3113	68	TAA			-5
COII	F	3114	3794	681		ATT	TAA	0
trnK	F	3835	3905	71	CTT			40
trnD	F	3951	4019	69	GTC			45
ATP8	F	4020	4190	171		ATC	TAG	0
ATP6	F	4184	4864	681		ATG	TAA	-7
COIII	F	4876	5658	783		ATG	TAA	11
trnG	F	5714	5783	70	TCC			55
ND3	F	5784	6137	354		ATT	TAA	0
trnA	F	6150	6218	69	TGC			12
trnR	F	6317	6386	70	TCG			98
trnN	F	6418	6483	66	GTT			31
trnS1	F	6484	6551	68	GCT			0
trnE	F	6554	6621	68	TTC			2
trnF	R	6656	6723	68	GAA			34
ND5	R	6781	8488	1708		ATC	T-	57
trnH	R	8489	8557	69	GTG			0
ND4	R	8570	9907	1338		ATG	TAA	12
ND4L	R	9921	10214	294		ATA	TAG	13
trnT	F	10231	10297	67	TGT			16
trnP	R	10298	10365	68	TGG			0
ND6	F	10377	10874	498		ATT	TAA	11
CytB	F	10924	12063	1140		ATG	TAA	49
trnS2	F	12172	12240	69	TGA			108
ND1	R	12276	13212	937		TTG	T-	35
trnL1	R	13214	13283	70	TAG			1
rrnL	R	13300	14660	1361				16
trnV	R	14654	14720	67	TAC			-7
rrnS	R	14719	15516	798				-2

**Table S7.** Annotation of the mitogenome of *Ips subelongatus*.

Gene	Direction	Start Position	Stop Position	Length	Anticodon	Start Codon	Stop Codon	IGS
trnQ	R	1	71	71	CAT			
trnM	F	140	210	71	TTG			68
ND2	F	214	1221	1008		ATA	TAA	3
trnW	F	1223	1289	67	TCA			1
trnC	R	1296	1359	64	GCA			6
trnY	R	1373	1440	68	GTA			13
COI	F	1452	2999	1548		ATT	TAA	11
trnL2	F	3012	3079	68	TAA			12
COII	F	3080	3760	681		ATC	TAA	0
trnK	F	3804	3874	71	CTT			43
trnD	F	3880	3947	68	GTC			5
ATP8	F	3948	4121	174		ATT	TAG	0
ATP6	F	4115	4795	681		ATG	TAA	-7
COIII	F	4820	5602	783		ATG	TAA	24
trnG	F	5630	5700	71	TCC			27
ND3	F	5704	6054	351		ATC	TAA	3
trnA	F	6064	6128	65	TGC			9
trnR	F	6147	6215	69	TCG			18
trnN	F	6248	6314	67	GTT			32
trnS1	F	6315	6381	67	GCT			0
trnE	F	6384	6448	65	TTC			2
trnF	R	6456	6524	69	GAA			7
ND5	R	6534	8276	1743		ATT	TAA	9
trnH	R	8277	8348	72	GTG			0
ND4	R	8373	9710	1338		ATG	TAA	24
ND4L	R	9726	10019	294		ATA	TAA	15
trnT	F	10067	10133	67	TGT			47
trnP	R	10134	10199	66	TGG			0
ND6	F	10202	10711	510		ATT	TAA	2
CytB	F	10761	11897	1137		ATG	TAA	49
trnS2	F	11912	11981	70	TGA			14
ND1	R	12001	12948	948		TTG	TAA	19
trnL1	R	12950	13018	69	TAG			1
rrnL	R	13004	14367	1364				-15
trnV	R	14383	14448	66	TAC			15
rrnS	R	14447	15259	813				-2

**Table S8.** Annotation of the mitogenome of *Ips typographus*.

Gene	Direction	Start Position	Stop Position	Length	Anticodon	Start Codon	Stop Codon	IGS
trnQ	R	1	71	71	CAT			
trnM	F	89	160	72	TTG			17
ND2	F	164	1171	1008		ATA	TAA	3
trnW	F	1172	1239	68	TCA			0
trnC	R	1269	1338	70	GCA			29
trnY	R	1344	1410	67	GTA			5
COI	F	1439	3007	1569		ATT	TAA	28
trnL2	F	3031	3099	69	TAA			23
COII	F	3100	3780	681		ATC	TAA	0
trnK	F	3811	3882	72	CTT			30
trnD	F	3898	3965	68	GTC			15
ATP8	F	3966	4130	165		ATT	TAG	0
ATP6	F	4127	4804	678		ATA	TAA	-4
COIII	F	4810	5592	783		ATG	TAA	5
trnG	F	5618	5683	66	TCC			25
ND3	F	5687	6037	351		ATT	TAA	3
trnA	F	6049	6117	69	TGC			11
trnR	F	6139	6208	70	TCG			21
trnN	F	6241	6306	66	GTT			32
trnS1	F	6307	6374	68	GCT			0
trnE	F	6376	6445	70	TTC			1
trnF	R	6450	6520	71	GAA			4
ND5	R	6551	8293	1743		ATT	TAA	30
trnH	R	8294	8359	66	GTG			0
ND4	R	8392	9729	1338		ATG	TAA	32
ND4L	R	9736	10113	378		ATT	TAA	6
trnT	F	10050	10116	67	TGT			-64
trnP	R	10117	10183	67	TGG			0
ND6	F	10195	10692	498		ATT	TAA	11
CytB	F	10785	11927	1143		ATA	TAA	92
trnS2	F	12019	12088	70	TGA			91
ND1	R	12108	13055	948		TTG	TAA	19
trnL1	R	13057	13125	69	TAG			1
rrnL	R	13144	14509	1366				18
trnV	R	14502	14566	65	TAC			-8
rrnS	R	14565	15376	812				-2

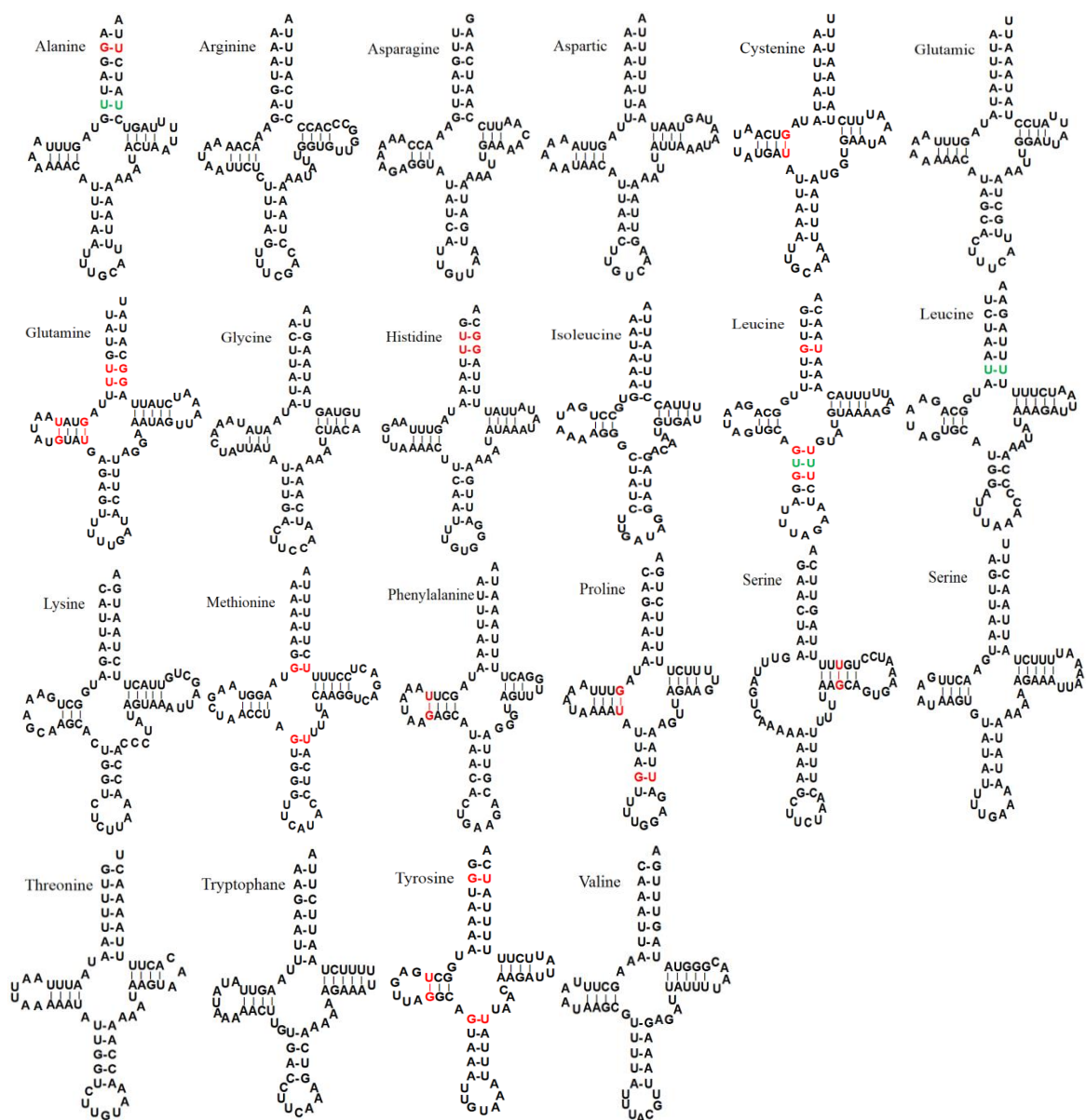


**Table S9.** Annotation of the mitogenome of *Ips nitidus*.

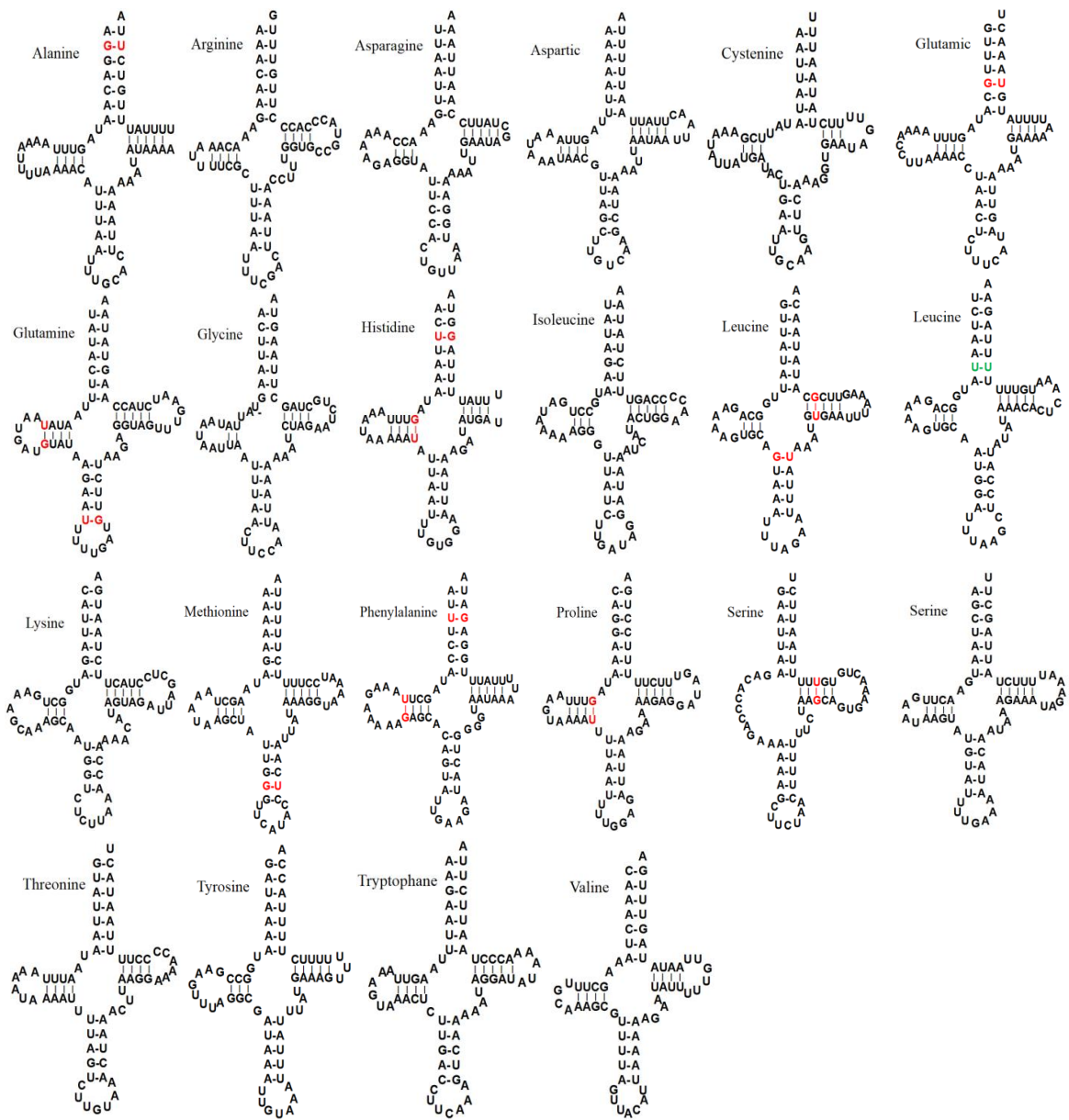
Gene	Direction	Start Position	Stop Position	Length	Anticodon	Start Codon	Stop Codon	IGS
trnQ	R	1	71	71	CAT			
trnM	F	87	158	72	TTG			15
ND2	F	159	1169	1011		ATT	TAA	0
trnW	F	1170	1237	68	TCA			0
trnC	R	1263	1333	71	GCA			25
trnY	R	1342	1408	67	GTA			8
COI	F	1446	3002	1557		ATT	TAA	37
trnL2	F	3022	3090	69	TAA			19
COII	F	3091	3771	681		ATC	TAA	0
trnK	F	3802	3873	72	CTT			30
trnD	F	3890	3957	68	GTC			16
ATP8	F	3958	4122	165		ATT	TAG	0
ATP6	F	4119	4796	678		ATA	TAA	-4
COIII	F	4802	5584	783		ATG	TAA	5
trnG	F	5610	5675	66	TCC			25
ND3	F	5676	6029	354		ATT	TAA	0
trnA	F	6041	6109	69	TGC			11
trnR	F	6131	6200	70	TCG			21
trnN	F	6233	6298	66	GTT			32
trnS1	F	6299	6366	68	GCT			0
trnE	F	6368	6438	71	TTC			1
trnF	R	6443	6513	71	GAA			4
ND5	R	6535	8280	1746		ATC	TAA	21
trnH	R	8281	8346	66	GTG			0
ND4	R	8387	9724	1338		ATG	TAA	40
ND4L	R	9731	10018	288		ATT	TAG	6
trnT	F	10045	10111	67	TGT			26
trnP	R	10112	10178	67	TGG			0
ND6	F	10190	10687	498		ATT	TAA	11
CytB	F	10778	11920	1143		ATA	TAA	90
trnS2	F	12000	12069	70	TGA			79
ND1	R	12089	13036	948		TTG	TAA	19
trnL1	R	13038	13106	69	TAG			1
rrnL	R	13124	14486	1363				17
trnV	R	14480	14544	65	TAC			-7
rrnS	R	14543	15359	817				-2

**Table S10.** Investigation of nucleotide composition in the mitochondrial genomes of eight bark beetles.

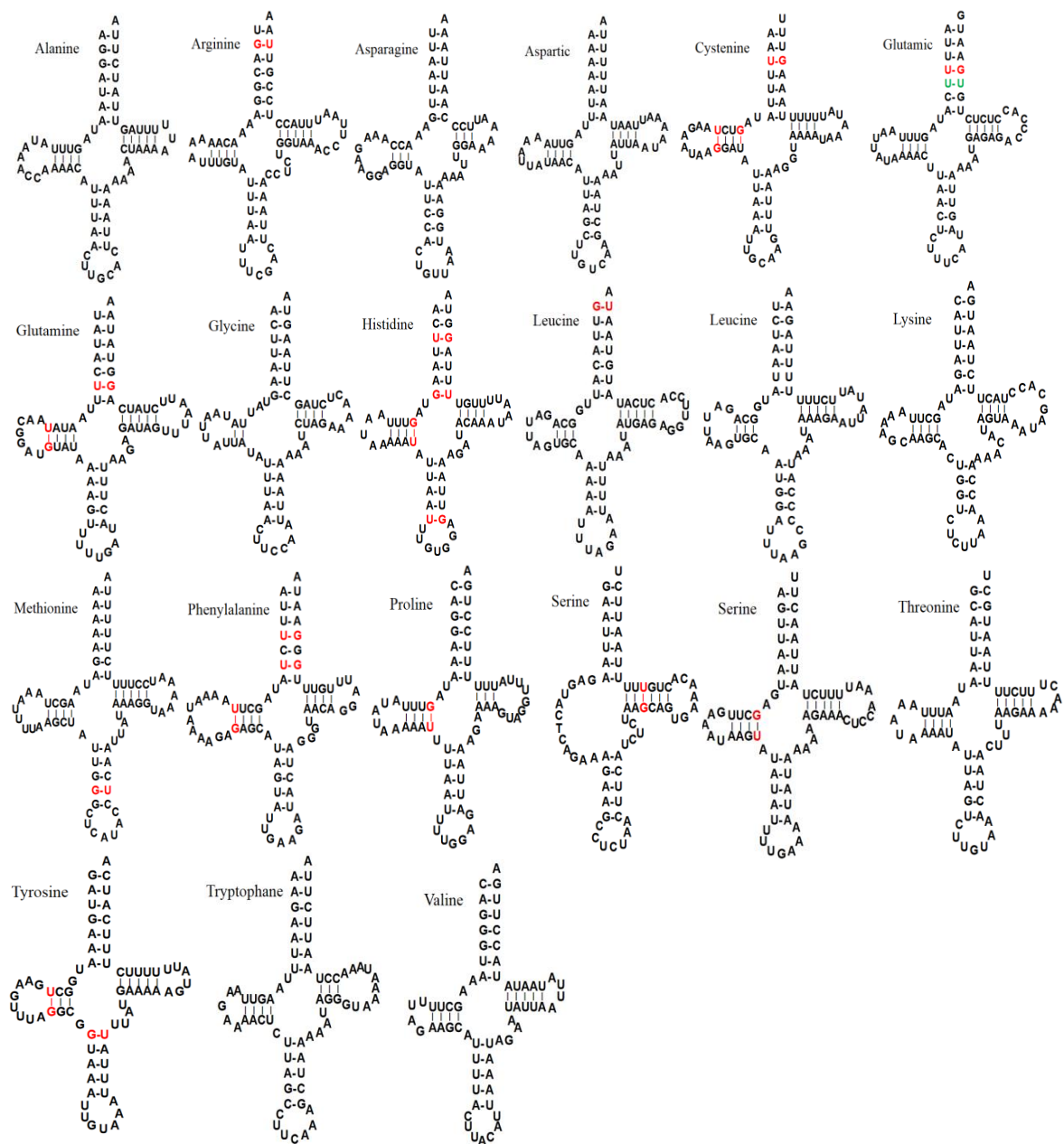
<b>Species</b>	<b>Length</b>	<b>T %</b>	<b>C %</b>	<b>A %</b>	<b>G %</b>	<b>A+T</b>	<b>C+G</b>	<b>AT-ske</b>	<b>GC-ske</b>
<b>Whole genome</b>									
<i>Orthotomicus erosus</i>	16753	33.48	18.64	37.21	10.67	70.69	29.31	0.0528	-0.2722
<i>Dryocoetes hectographus</i>	15495	35.39	15.88	39.14	9.60	74.52	25.48	0.0503	-0.2467
<i>Polygraphus poligraphus</i>	15586	33.37	17.46	37.69	11.49	71.06	28.95	0.0608	-0.2458
<i>Dendroctonus micans</i>	16807	34.57	15.08	41.16	9.20	75.72	24.28	0.0870	-0.2421
<i>Ips hauseri</i>	15516	35.45	16.87	37.90	9.78	73.35	26.65	0.0335	-0.2662
<i>Ips subelongatus</i>	15259	35.92	15.80	38.79	9.50	74.70	25.30	0.0384	-0.2489
<i>Ips typographus</i>	15376	35.18	16.63	38.22	9.97	73.40	26.60	0.0414	-0.2501
<i>Ips nitidus</i>	15359	35.92	15.80	38.79	9.50	74.70	25.30	0.0384	-0.2489
Average ( <i>Ips</i> )	15425	34.78	16.61	38.55	10.06	73.33	26.67	0.0514	-0.2463
<b>PCGs</b>									
<i>Orthotomicus erosus</i>	11162	40.09	17.31	27.78	14.82	67.87	32.13	-0.1814	-0.0775
<i>Dryocoetes hectographus</i>	11157	41.76	13.62	31.50	13.12	73.25	26.75	-0.1401	-0.0188
<i>Polygraphus poligraphus</i>	11091	40.24	17.05	28.78	13.93	69.02	30.98	-0.1660	-0.1007
<i>Dendroctonus micans</i>	11124	41.68	14.43	31.57	12.32	73.25	26.75	-0.1379	-0.0786
<i>Ips hauseri</i>	11177	41.06	15.95	29.14	13.85	70.20	29.80	-0.1698	-0.0705
<i>Ips subelongatus</i>	11196	42.43	14.22	30.44	12.92	72.87	27.13	-0.1645	-0.0481
<i>Ips typographus</i>	11196	41.94	14.83	30.16	13.07	72.10	27.90	-0.1634	-0.0629
<i>Ips nitidus</i>	11190	41.36	15.39	29.85	13.40	71.21	28.79	-0.1616	-0.0689
Average ( <i>Ips</i> )	11162	41.32	15.35	29.90	13.43	71.22	28.78	-0.1606	-0.0658
<b>rRNA</b>									
<i>Orthotomicus erosus</i>	2095	39.62	7.64	36.13	16.61	75.75	24.25	-0.0460	0.3701
<i>Dryocoetes hectographus</i>	2061	37.99	7.96	36.68	17.37	74.67	25.33	-0.0175	0.3716
<i>Polygraphus poligraphus</i>	2016	39.08	8.02	35.80	17.09	74.88	25.12	-0.0438	0.3611
<i>Dendroctonus micans</i>	2072	43.29	6.71	36.34	13.66	79.63	20.37	-0.0873	0.3412
<i>Ips hauseri</i>	2159	39.97	6.67	38.72	14.64	78.69	21.31	-0.0159	0.3739
<i>Ips subelongatus</i>	2177	40.24	6.66	38.31	14.79	78.55	21.45	-0.0246	0.3790
<i>Ips typographus</i>	2178	40.22	6.80	38.06	14.92	78.28	21.72	-0.0276	0.3742
<i>Ips nitidus</i>	2180	39.86	7.16	37.98	15.00	77.84	22.16	-0.0242	0.3540
Average ( <i>Ips</i> )	2117	40.03	7.20	37.25	15.51	77.29	22.71	-0.0358	0.3656
<b>tRNA</b>									
<i>Orthotomicus erosus</i>	1480	35.34	11.62	39.73	13.31	75.07	24.93	0.0585	0.0678
<i>Dryocoetes hectographus</i>	1443	37.35	9.70	39.29	13.65	76.65	23.35	0.0253	0.1691
<i>Polygraphus poligraphus</i>	1443	35.47	12.67	36.85	15.00	72.32	27.68	0.0191	0.0842
<i>Dendroctonus micans</i>	1419	37.56	10.50	39.18	12.76	76.74	23.26	0.0211	0.0970
<i>Ips hauseri</i>	1438	37.48	9.94	38.73	13.84	76.22	23.78	0.0164	0.1637
<i>Ips subelongatus</i>	1431	37.32	9.92	40.39	12.37	77.71	22.29	0.0396	0.1097
<i>Ips typographus</i>	1441	35.60	10.96	40.67	12.77	76.27	23.73	0.0664	0.0760
<i>Ips nitidus</i>	1443	36.17	10.46	40.12	13.24	76.30	23.70	0.0518	0.1170
Average ( <i>Ips</i> )	1442	36.54	10.72	39.37	13.37	75.91	24.09	0.0373	0.1106



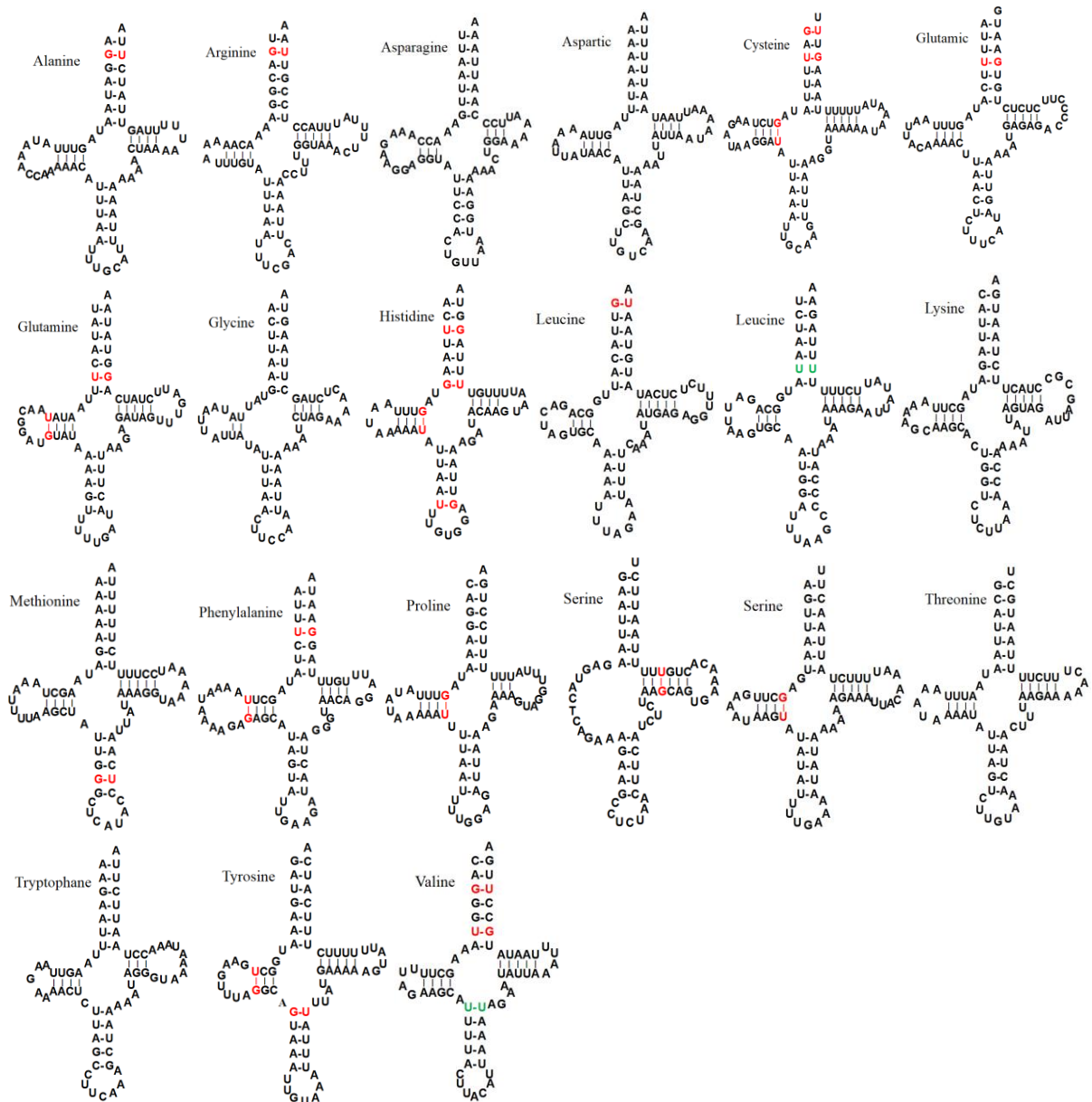
**Figure S1.** Secondary structures for tRNA genes from the mtDNA of *Dryocoetes hectographus*



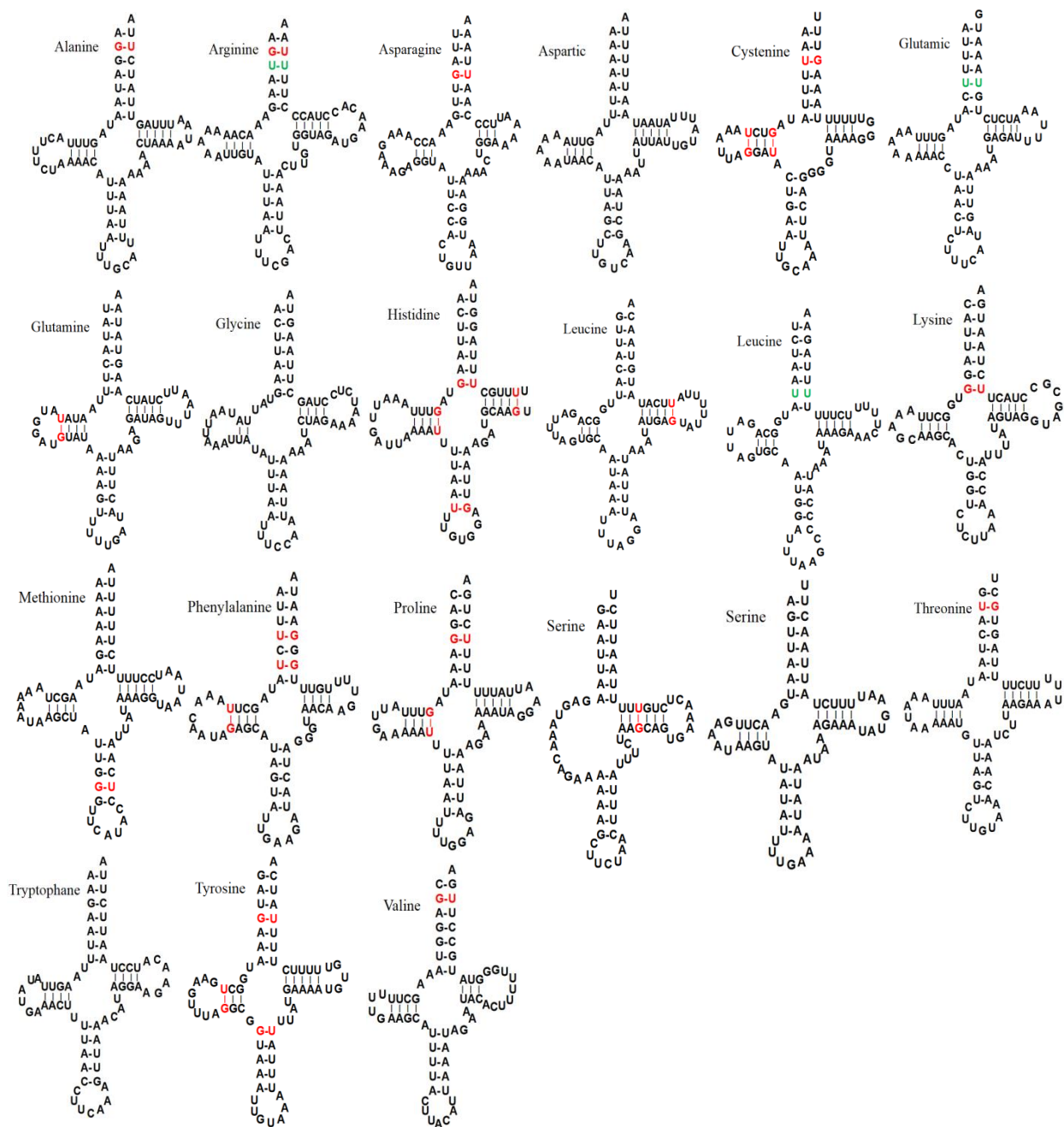
**Figure S2.** Secondary structures for tRNA genes from the mtDNA of *Orthotomicus erosus*



**Figure S3.** Secondary structures for tRNA genes from the mtDNA of *Ips typographus*

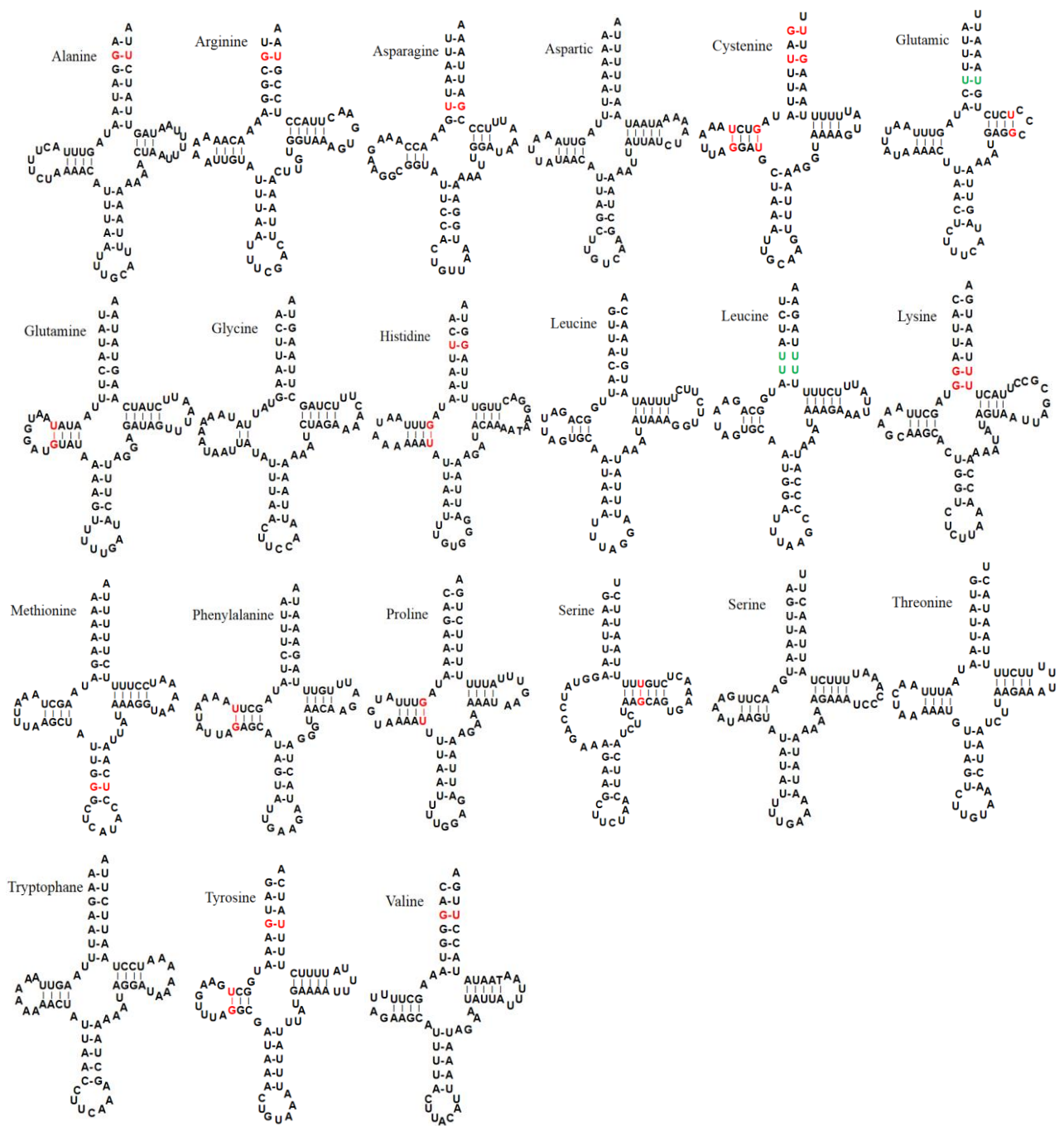


**Figure S4.** Secondary structures for tRNA genes from the mtDNA of *Ips nitidus*



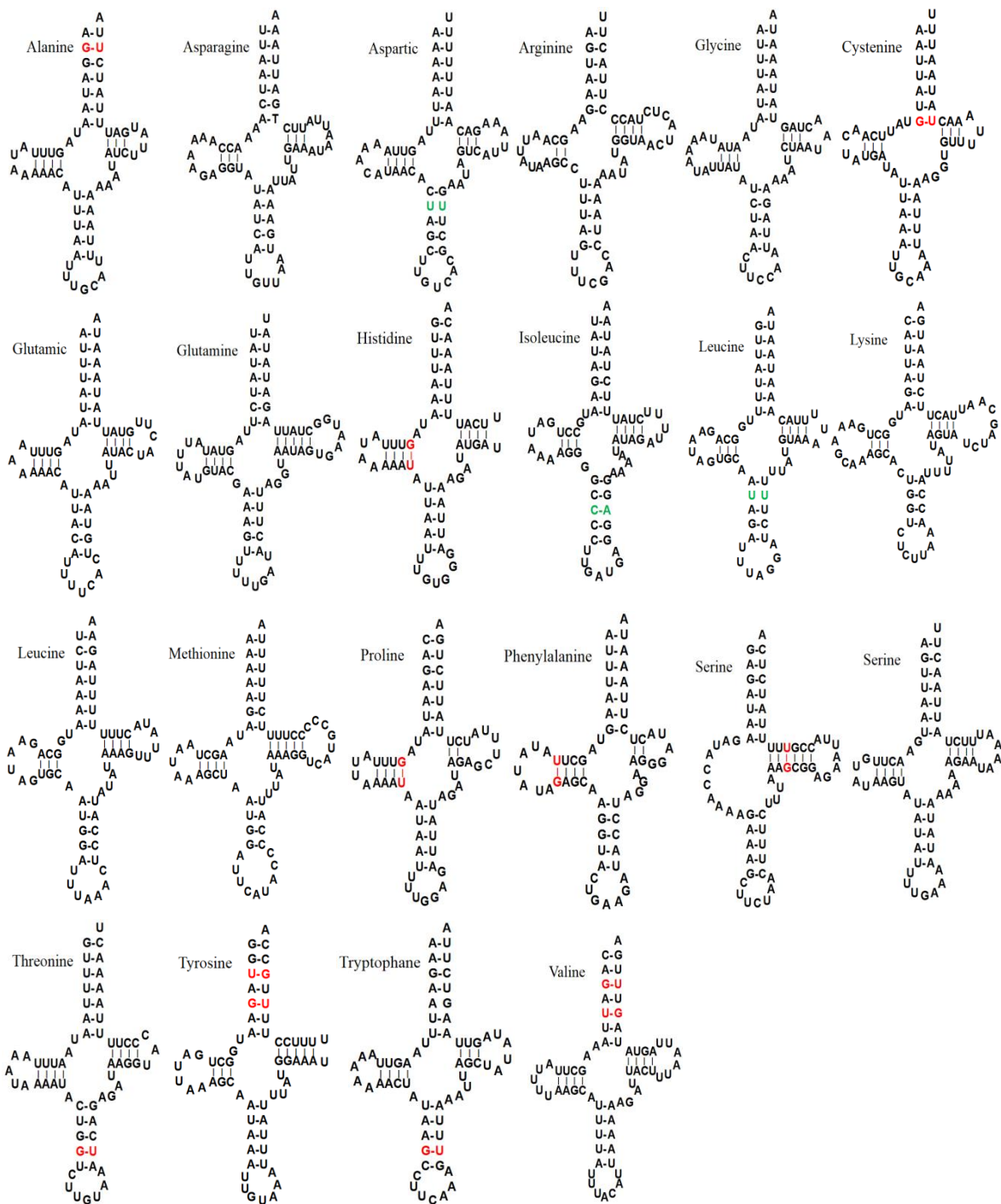
**Figure S5.** Secondary structures for tRNA genes from the mtDNA of *Ips hauseri*



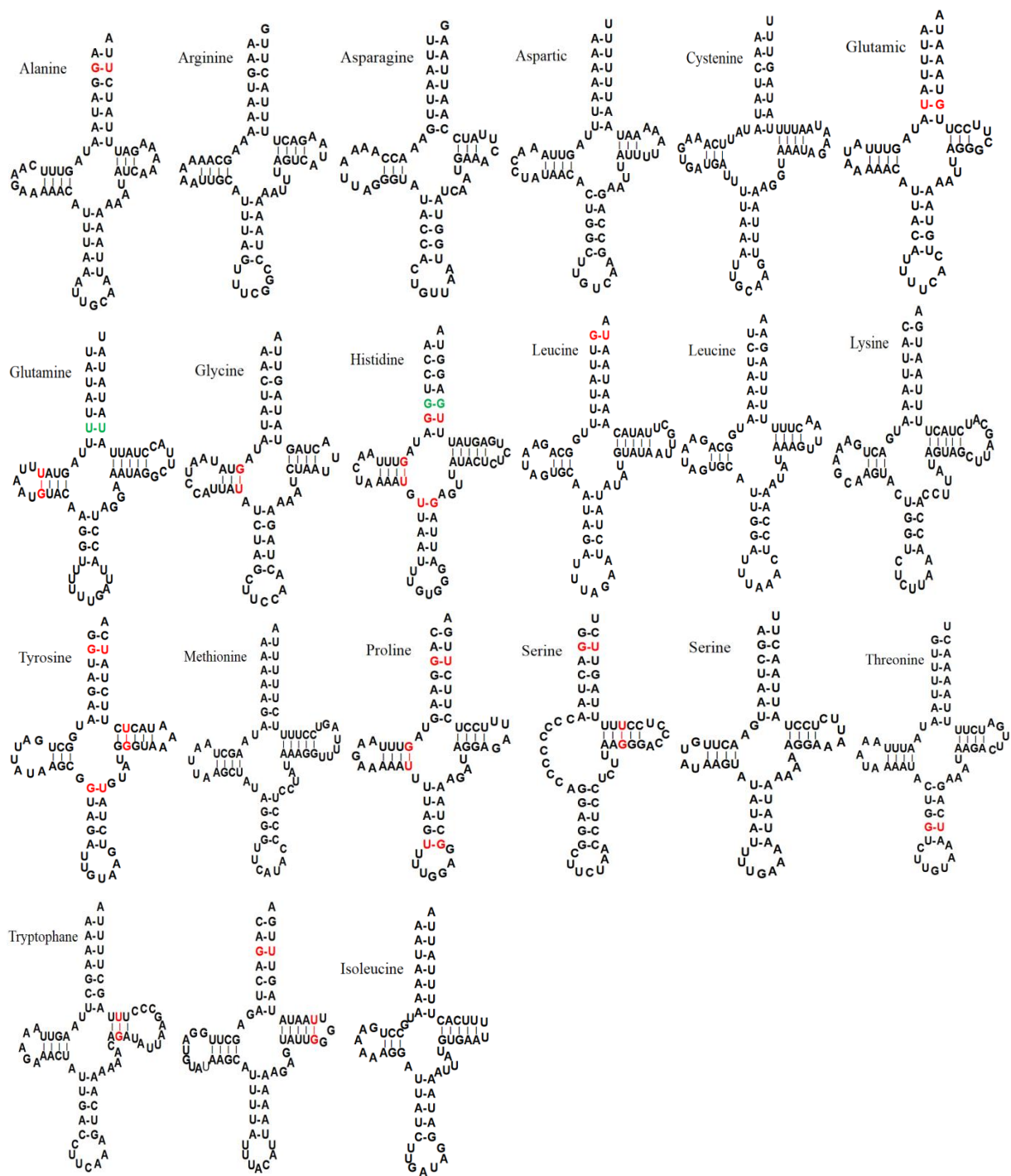


**Figure S6.** Secondary structures for tRNA genes from the mtDNA of *Ips subelongatus*





**Figure S7.** Secondary structures for tRNA genes from the mtDNA of *Dendroctonus micans*



**Figure S8.** Secondary structures for tRNA genes from the mtDNA of *Polygraphus poligraphus*

