

Table S1. Mtgenome organization of *N. tuberculus*.

Name	Location		Size(bp)	Intergenic	Codon		Strand
	From	To			nucleotides Start	Stop	
<i>trnI</i>	1	67	67				J
<i>trnQ</i>	65	135	71	-3			N
<i>trnM</i>	136	206	71	-			J
<i>nad2</i>	207	1181	975	-	ATT	TAG	J
<i>trnW</i>	1180	1247	68	-2			J
<i>trnC</i>	1240	1302	63	-8			N
<i>trnY</i>	1303	1370	68	-			N
<i>cox1</i>	1369	2902	1534	-2	ATG	T	J
<i>trnL2(UUR)</i>	2903	2966	64	-			J
<i>cox2</i>	2967	3645	679	-	ATA	T	J
<i>trnK</i>	3647	3715	69	1			J
<i>trnD</i>	3715	3776	62	-1			J
<i>atp8</i>	3777	3929	153	-	ATA	TAA	J
<i>atp6</i>	3917	4573	657	-13	ATG	TAA	J
<i>cox3</i>	4576	5355	780	2	ATG	TAA	J
<i>trnG</i>	5355	5415	61	-1			J
<i>nad3</i>	5416	5769	354	-	ATT	TAA	J
<i>trnA</i>	5770	5830	61	-			J
<i>trnR</i>	5829	5892	64	-2			J
<i>trnN</i>	5895	5960	66	2			J
<i>trnS1(ACN)</i>	5960	6021	62	-1			J
<i>trnE</i>	6022	6082	61	-			J
<i>trnF</i>	6085	6150	66	2			N
<i>nad5</i>	6151	7813	1663	-	TTG	T	N
<i>trnH</i>	7814	7874	61	-			N
<i>nad4</i>	7878	9225	1348	3	ATT	T	N
<i>nad4L</i>	9206	9472	267	-20	ATT	TAG	N
<i>trnT</i>	9475	9537	63	2			J
<i>trnP</i>	9538	9605	68	-			N
<i>nad6</i>	9608	10091	484	2	ATT	T	J
<i>cytb</i>	10092	11228	1137	-	ATG	TAG	J
<i>trnS2(UCN)</i>	11227	11289	63	-2			J
<i>nad1</i>	11280	12203	924	-10	ATT	TAA	N
<i>trnL1(CUN)</i>	12204	12270	67	-			N
<i>rrnL</i>	12271	13465	1195	-			N
<i>trnV</i>	13466	13528	63	-			N
<i>rrnS</i>	13529	14258	730	-			N
CR	14259	15737	1479	-			J

Table S2. Mtgenome organization of *H. paradoxa*.

Name	Location		Size(bp)	Intergenic	Codon		Strand
	From	To			nucleotides Start	Stop	
<i>trnI</i>	1	64	64				J
<i>trnQ</i>	62	131	70	-3			N
<i>trnM</i>	131	200	70	-1			J

<i>nad2</i>	201	1172	972	-	ATC	TAG	J
<i>trnW</i>	1171	1235	65	-2			J
<i>trnC</i>	1228	1291	64	-8			N
<i>trnY</i>	1292	1357	66	-			N
<i>cox1</i>	1356	2892	1537	-2	ATG	T	J
<i>trnL2(UUR)</i>	2893	2957	65	-			J
<i>cox2</i>	2958	3636	679	-	ATT	T	J
<i>trnK</i>	3637	3704	68	-			J
<i>trnD</i>	3704	3764	61	-1			J
<i>atp8</i>	3765	3917	153	-	ATA	TAA	J
<i>atp6</i>	3905	4561	657	-13	ATG	TAA	J
<i>cox3</i>	4569	5346	778	7	ATG	T	J
<i>trnG</i>	5347	5408	62	-			J
<i>nad3</i>	5409	5762	354	-	ATA	TAA	J
<i>trnA</i>	5763	5823	61	-			J
<i>trnR</i>	5826	5889	64	2			J
<i>trnN</i>	5891	5957	67	1			J
<i>trnS1(ACN)</i>	5957	6017	61	-1			J
<i>trnE</i>	6017	6078	62	-1			J
<i>trnF</i>	6078	6143	66	-1			N
<i>nad5</i>	6144	7803	1660	-	TTG	T	N
<i>trnH</i>	7804	7866	63	-			N
<i>nad4</i>	7870	9190	1321	3	ATT	T	N
<i>nad4L</i>	9171	9434	264	-20	ATT	TAG	N
<i>trnT</i>	9437	9502	66	2			J
<i>trnP</i>	9503	9567	65	-			N
<i>nad6</i>	9570	10053	484	2	ATT	T	J
<i>cytb</i>	10054	11190	1137	-	ATG	TAG	J
<i>trnS2(UCN)</i>	11194	11255	62	3			J
<i>nad1</i>	11246	12187	942	-10	ATA	TAA	N
<i>trnL1(CUN)</i>	12188	12250	63	-			N
<i>rrnL</i>	12251	13438	1188	-			N
<i>trnV</i>	13439	13499	61	-			N
<i>rrnS</i>	13500	14231	732	-			N
CR	14232	14762	531	-			J

Table S3. Mtgenome organization of *B. fujiana*.

Name	Location		Size(bp)	Intergenic nucleotides	Codon		Strand
	From	To			Start	Stop	
<i>trnI</i>	1	63	63				J
<i>trnQ</i>	61	128	68	-3			N
<i>trnM</i>	135	202	68	6			J
<i>nad2</i>	203	1177	975	-	ATA	TAA	J
<i>trnW</i>	1176	1236	61	-2			J
<i>trnC</i>	1229	1289	61	-8			N
<i>trnY</i>	1290	1356	67				N
<i>cox1</i>	1355	2888	1534	-2	ATG	T	J
<i>trnL2(UUR)</i>	2889	2958	70	-			J
<i>cox2</i>	2959	3637	679	-	ATA	T	J
<i>trnK</i>	3638	3706	69	-			J

<i>trnD</i>	3706	3766	61	-1			J
<i>atp8</i>	3767	3919	153	-	ATT	TAA	J
<i>atp6</i>	3907	4563	657	-13	ATG	TAA	J
<i>cox3</i>	4569	5346	778	5	ATG	T	J
<i>trnG</i>	5347	5409	63	-			J
<i>nad3</i>	5410	5763	354	-	ATA	TAA	J
<i>trnA</i>	5764	5825	62	-			J
<i>trnR</i>	5824	5888	65	-2			J
<i>trnN</i>	5889	5953	65	-			J
<i>trnS1(ACN)</i>	5953	6015	63	-1			J
<i>trnE</i>	6016	6077	62	-			J
<i>trnF</i>	6080	6148	69	2			N
<i>nad5</i>	6149	7811	1663	-	TTG	T	N
<i>trnH</i>	7812	7875	64	-			N
<i>nad4</i>	7879	9226	1348	3	ATT	T	N
<i>nad4L</i>	9207	9476	270	-20	ATT	TAA	N
<i>trnT</i>	9479	9541	63	2			J
<i>trnP</i>	9542	9604	63	-			N
<i>nad6</i>	9607	10090	484	2	ATA	T	J
<i>cytb</i>	10091	11227	1137	-	ATG	TAG	J
<i>trnS2(UCN)</i>	11226	11290	65	-2			J
<i>nad1</i>	11281	12201	921	-10	ATT	TAA	N
<i>trnL1(CUN)</i>	12202	12263	62	-			N
<i>rrnL</i>	12264	13443	1180	-			N
<i>trnV</i>	13444	13505	62	-			N
<i>rrnS</i>	13506	14245	740	-			N
CR	14246	16221	1,976	-			J

Table S4. Mtgenome organization of and *K. nativa*.

Name	Location		Size(bp)	Intergenic nucleotides	Codon		Strand
	From	To			Start	Stop	
<i>trnI</i>	1	66	66				J
<i>trnQ</i>	64	132	69	-3			N
<i>trnM</i>	135	205	71	2			J
<i>nad2</i>	206	1180	975	-	ATT	TAG	J
<i>trnW</i>	1179	1240	62	-2			J
<i>trnC</i>	1233	1295	63	-8			N
<i>trnY</i>	1296	1363	68	-			N
<i>cox1</i>	1362	2895	1534	-2	ATG	T	J
<i>trnL2(UUR)</i>	2896	2962	67	-			J
<i>cox2</i>	2963	3641	679	-	ATG	T	J
<i>trnK</i>	3642	3711	70	-			J
<i>trnD</i>	3711	3772	62	-1			J
<i>atp8</i>	3774	3926	153	1	ATC	TAA	J
<i>atp6</i>	3914	4570	657	-13	GTG	TAA	J
<i>cox3</i>	4574	5353	780	3	ATG	TAA	J
<i>trnG</i>	5352	5414	63	-2			J
<i>nad3</i>	5415	5765	351	-	ATT	TAA	J
<i>trnA</i>	5766	5826	61	-			J
<i>trnR</i>	5826	5888	63	-1			J
<i>trnN</i>	5890	5954	65	1			J
<i>trnS1(ACN)</i>	5954	6014	61	-1			J
<i>trnE</i>	6014	6076	63	-1			J
<i>trnF</i>	6077	6139	63	-			N
<i>nad5</i>	6140	7799	1660	-	ATT	T	N
<i>trnH</i>	7801	7863	63	1			N
<i>nad4</i>	7867	9214	1348	3	ATT	T	N
<i>nad4L</i>	9195	9464	270	-20	ATT	TAG	N
<i>trnT</i>	9467	9528	62	2			J
<i>trnP</i>	9529	9599	71	-			N
<i>nad6</i>	9602	10082	481	2	ATA	T	J
<i>cytb</i>	10083	11219	1137	-	ATG	TAG	J
<i>trnS2(UCN)</i>	11218	11285	68	-2			J
<i>nad1</i>	11276	12217	942	-10	ATT	TAA	N
<i>trnL1(CUN)</i>	12218	12280	63	-			N
<i>rrnL</i>	12281	13487	1207	-			N
<i>trnV</i>	13488	13548	61	-			N
<i>rrnS</i>	13549	14287	739	-			N
CR	14288	15716	1429	-			J

Table S5. Nucleotide composition and skewness comparison of different elements of four Hylicinae mtgenomes.

Species	Feature	Size(bp)	T%	C%	A%	G%	A+ T%	AT-skew	GC-skew
<i>N. tuberculatus</i>	PCGs	10950	42.8	12.0	33.2	12.0	76.0	-0.126	-0.003
	Control region	1479	37.8	11.0	41.0	10.1	78.8	0.041	-0.042
	tRNAs	1429	38.5	8.7	40.4	12.5	78.9	0.024	0.179
	rRNAs	1925	54.7	7.2	26.3	11.8	81.0	-0.351	0.240
	Whole genome	15737	38.1	15.2	47.1	9.5	77.1	0.222	-0.166
<i>H. paradoxa</i>	PCGs	10932	41.5	12.9	32.8	12.8	74.3	-0.118	-0.002
	Control region	531	40.3	7.2	46.3	6.2	76.6	0.070	-0.017
	tRNAs	1416	37.4	9.5	40.4	12.7	77.8	0.038	0.146
	rRNAs	1920	58.7	6.5	23.9	11.0	82.6	-0.307	0.312
	Whole genome	14762	28.1	15.2	47.7	9.1	75.8	0.259	-0.251
<i>B. fujiana</i>	PCGs	10947	43.2	11.3	34.0	11.5	77.2	-0.119	0.006
	Control region	1976	38.2	14.5	35.3	11.7	73.5	-0.039	0.104
	tRNAs	1416	37.6	9.2	40.5	12.8	78.0	0.037	0.164
	rRNAs	1920	58.7	6.5	23.8	11	82.5	-0.423	0.26
	Whole genome	16221	30.1	13.4	47.3	9.2	77.4	0.223	-0.185
<i>K. nativa</i>	PCGs	10962	40.3	13.5	32.7	13.5	73.0	-0.104	0.002
	Control region	1429	40.0	13.3	36.7	10.1	76.6	-0.043	-0.138
	tRNAs	1425	36.6	10.8	38.8	13.8	75.4	0.029	0.120
	rRNAs	1946	55.8	7.3	24.3	12.6	80.1	-0.394	0.268
	Whole genome	15716	27.1	15.8	47.3	9.8	74.4	0.272	-0.235

Table S6. Best partitioning schemes and models based on different datasets for Bayesian inference (BI) analysis.

Dataset	Partitioning scheme	Models
P123	P1: (<i>atp8_pos2, atp6_pos1</i>)	GTR+I+G
	P2: (<i>nad2_pos2, atp6_pos2, nad6_pos2, nad3_pos2</i>)	GTR+I+G
	P3: (<i>nad6_pos3, nad3_pos3, atp8_pos3, atp6_pos3</i>)	GTR+I+G
	P4: (<i>nad3_pos1, nad2_pos1, nad6_pos1, atp8_pos1</i>)	GTR+I+G
	P5: (<i>cox1_pos1</i>)	GTR+I+G
	P6: (<i>cox1_pos2, cox3_pos2, cytb_pos2, cox2_pos2</i>)	GTR+I+G
	P7: (<i>cox1_pos3</i>)	GTR+ G
	P8: (<i>cytb_pos1, cox3_pos1, cox2_pos1</i>)	GTR+I+G
	P9: (<i>cytb_pos3, cox2_pos2, cox3_pos3</i>)	GTR +G
	P10: (<i>nad1_pos1, nad4l_pos1, nad4_pos1, nad5_pos1</i>)	GTR+I+G
	P11: (<i>nad5_pos2, nad4_pos2, nad1_pos2, nad4L_pos2</i>)	GTR+I+G
	P12: (<i>nad1_pos3</i>)	GTR +G
	P13: (<i>nad2_pos3</i>)	GTR +G
	P14: (<i>nad5_pos3, nad4l_pos3, nad4_pos3</i>)	GTR +G
P123R	P1: (<i>atp6_pos1</i>)	GTR+I+G
	P2: (<i>cox2_pos2, atp6_pos2, cox3_pos2,</i>	GTR+I+G

	<i>nad3_pos2, cytb_pos2)</i>	
	P3: (<i>nad6_pos3, nad3_pos3, atp8_pos3, atp6_pos3</i>)	GTR+I+G
	P4: (<i>nad2_pos1, nad3_pos1, nad6_pos1, atp8_pos1</i>)	GTR+I+G
	P5: (<i>atp8_pos2, nad6_pos2, nad2_pos2</i>)	GTR+I+G
	P6: (<i>cox1_pos1</i>)	GTR+I+G
	P7: (<i>cox1_pos2</i>)	GTR+I+G
	P8: (<i>cox1_pos3</i>)	GTR+G
	P9: (<i>cytb_pos1, cox3_pos1, cox2_pos1</i>)	GTR+I+G
	P10: (<i>cytb_pos3, cox2_pos3, cox3_pos3</i>)	GTR+G
	P11: (<i>nad1_pos1, nad4l_pos1, nad4_pos1, nad5_pos1</i>)	GTR+I+G
	P12: (<i>nad5_pos2, nad4_pos2, nad1_pos2, nad4L_pos2</i>)	GTR+I+G
	P13: (<i>nad1_pos3</i>)	GTR+G
	P14: (<i>nad2_pos3</i>)	GTR+G
	P15: (<i>nad5_pos3, nad4l_pos3, nad4_pos3</i>)	GTR+G
	P16: (<i>rrnS, rrnL</i>)	GTR+I+G
AA	P1: (<i>atp8, nad3, nad6, cox3, nad2, cox2, cytb, atp6</i>)	MTREV+ I+G
	P2: (<i>cox1</i>)	MTART+ I+G
	P3: (<i>nad4l, nad4, nad5, nad1</i>)	MTART+ I+G

Table S7. Best partitioning schemes and models based on different datasets for maximum likelihood (ML) analysis.

Dataset	Partitioning scheme	Models
P123	P1: (<i>atp8_pos2, atp6_pos1</i>)	GTR+I+G
	P2: (<i>nad2_pos2, atp6_pos2, nad6_pos2, nad3_pos2</i>)	TVM+I+G
	P3: (<i>nad6_pos3, nad3_pos3, atp8_pos3, atp6_pos3</i>)	TRN+I+G
	P4: (<i>nad3_pos1, nad2_pos1, nad6_pos1, atp8_pos1</i>)	GTR+I+G
	P5: (<i>cox1_pos1</i>)	GTR+I+G
	P6: (<i>cox1_pos2, cox3_pos2, cytb_pos2, cox2_pos2</i>)	TVM+I+G
	P7: (<i>cox1_pos3</i>)	TIM+G
	P8: (<i>cytb_pos1, cox3_pos1</i>)	GTR+I+G
	P9: (<i>cytb_pos3, cox2_pos3, cox3_pos3</i>)	GTR+G

P123R	P10: (<i>nad1_pos1, nad4l_pos1, nad4_pos1, nad5_pos1</i>)	GTR+I+G
	P11: (<i>nad5_pos2, nad4_pos2, nad1_pos2, nad4L_pos2</i>)	GTR+I+G
	P12: (<i>nad1_pos3</i>)	TIM+G
	P13: (<i>nad2_pos3</i>)	TRN+G
	P14: (<i>nad5_pos3, nad4l_pos3, nad4_pos3</i>)	K81UF+G
	P1: (<i>atp6_pos1</i>)	GTR+I+G
	P2: (<i>cox2_pos2, atp6_pos2, cox3_pos2, nad3_pos2</i>)	TVM+I+G
	P3: (<i>nad6_pos3, nad3_pos3, atp8_pos3, atp6_pos3</i>)	TRN+I+G
	P4: (<i>nad2_pos1, nad3_pos1, nad6_pos1, atp8_pos1</i>)	GTR+I+G
	P5: (<i>atp8_pos2, nad6_pos2, nad2_pos2</i>)	TVM+I+G
	P6: (<i>cox1_pos1</i>)	GTR+I+G
	P7: (<i>cox1_pos2</i>)	TVM+I+G
	P8: (<i>cox1_pos3</i>)	TVM+G
	P9: (<i>cytb_pos1, cox3_pos1, cox2_pos1</i>)	GTR+I+G
	P10: (<i>cytb_pos3, cox2_pos3, cox3_pos3</i>)	GTR+G
AA	P11: (<i>nad1_pos1, nad4l_pos1, nad4_pos1, nad5_pos1</i>)	GTR+I+G
	P12: (<i>nad5_pos2, nad4_pos2, nad1_pos2, nad4L_pos2</i>)	GTR+I+G
	P13: (<i>nad1_pos3</i>)	K81UF+G
	P14: (<i>nad2_pos3</i>)	TRN+G
	P15: (<i>nad5_pos3, nad4l_pos3, nad4_pos3</i>)	K81UF+G
	P16: (<i>rrn5, rrnL</i>)	GTR+I+G
	P1: (<i>atp8, nad3, nad6, cox3, nad2, cox2, cytb, atp6</i>)	MTART+I+G +F
	P2: (<i>cox1</i>)	MTART+I+G
	P3: (<i>nad4l, nad4, nad5, nad1</i>)	MTART+I+G +F

Table S8. Detail of software and kit.

Software/ Kit	Resource
Easy Pure Genomic DNA Kit	TransGen Biotech Co., Ltd, Beijing, China
NGS company	Illumina HiSeq Xten; Biomarker Technologies Corporation, Beijing, China
Geneious10.0.5	Biomatters, Auckland, New Zealand, http://www.geneious.com/
MITOS WebServer	http://mitos.bioinf.uni-leipzig.de/index.py
tRNAscan-SE Search Server v1.21	http://lowelab.ucsc.edu/tRNAscan-SE/
Tandem Repeats Finder server	http://tandem.bu.edu/trf/trf.html
CGView	http://stothard.afns.ualberta.ca/cgview_server
MEGA v 7.313	Penn State University, State College, PA, USA

Prism 6.01	GraphPad Software, San Diego, USA
MAFFT v 7.313 online service	https://mat.cbrc.jp/alignment/server/
GBlocks v 0.91b	http://molevol.cmima.csic.es/castresana/Gblocks/Gblocks_documentation.html
PartitionFinder 2.1.1	www.phylo.org
IQ-TREE v 1.6.8	http://www.iqtree.org/
MrBayes 3.2.6	www.phylo.org

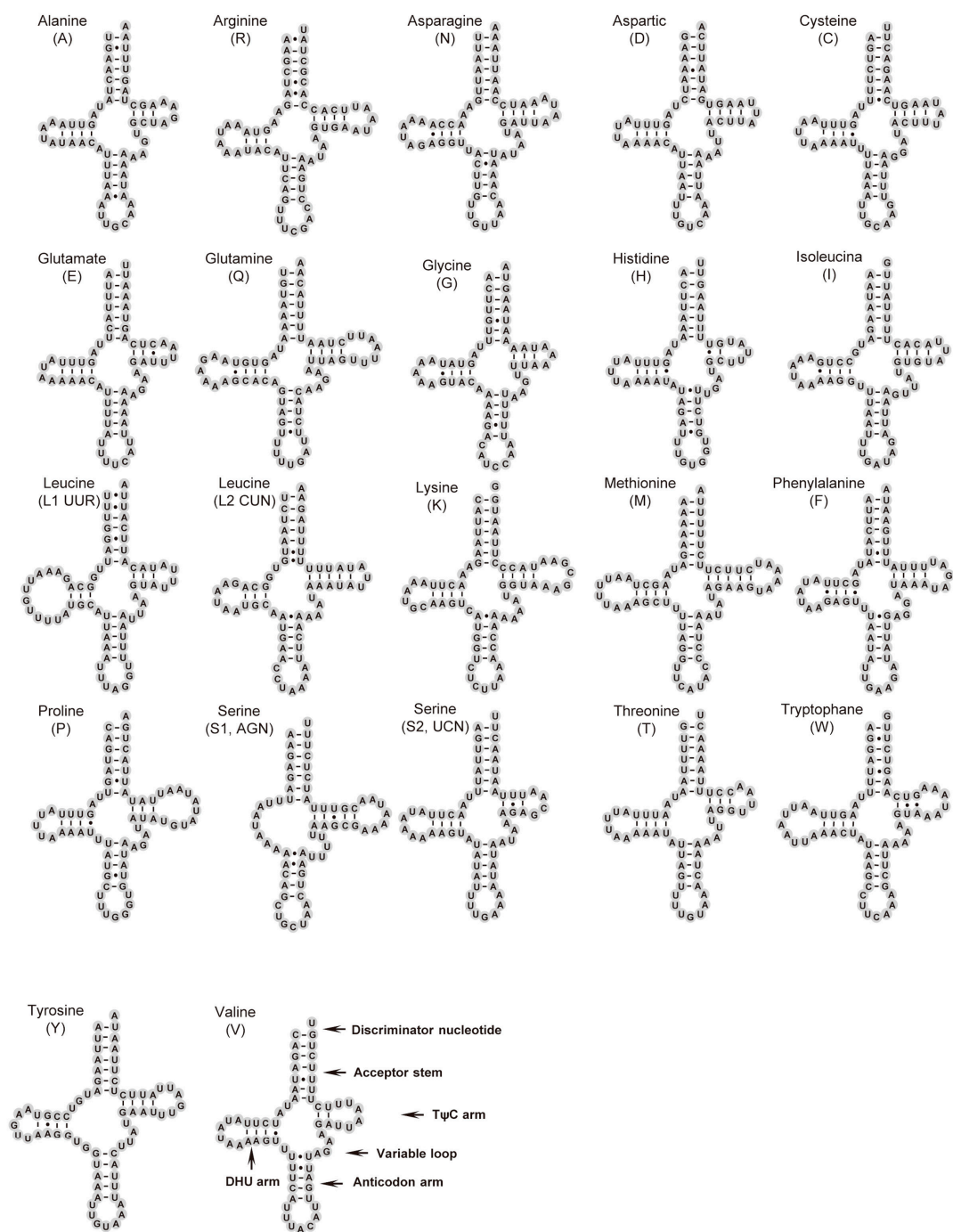


Figure S1. Predicted secondary cloverleaf structure for the tRNAs of *N. tuberculosis*.

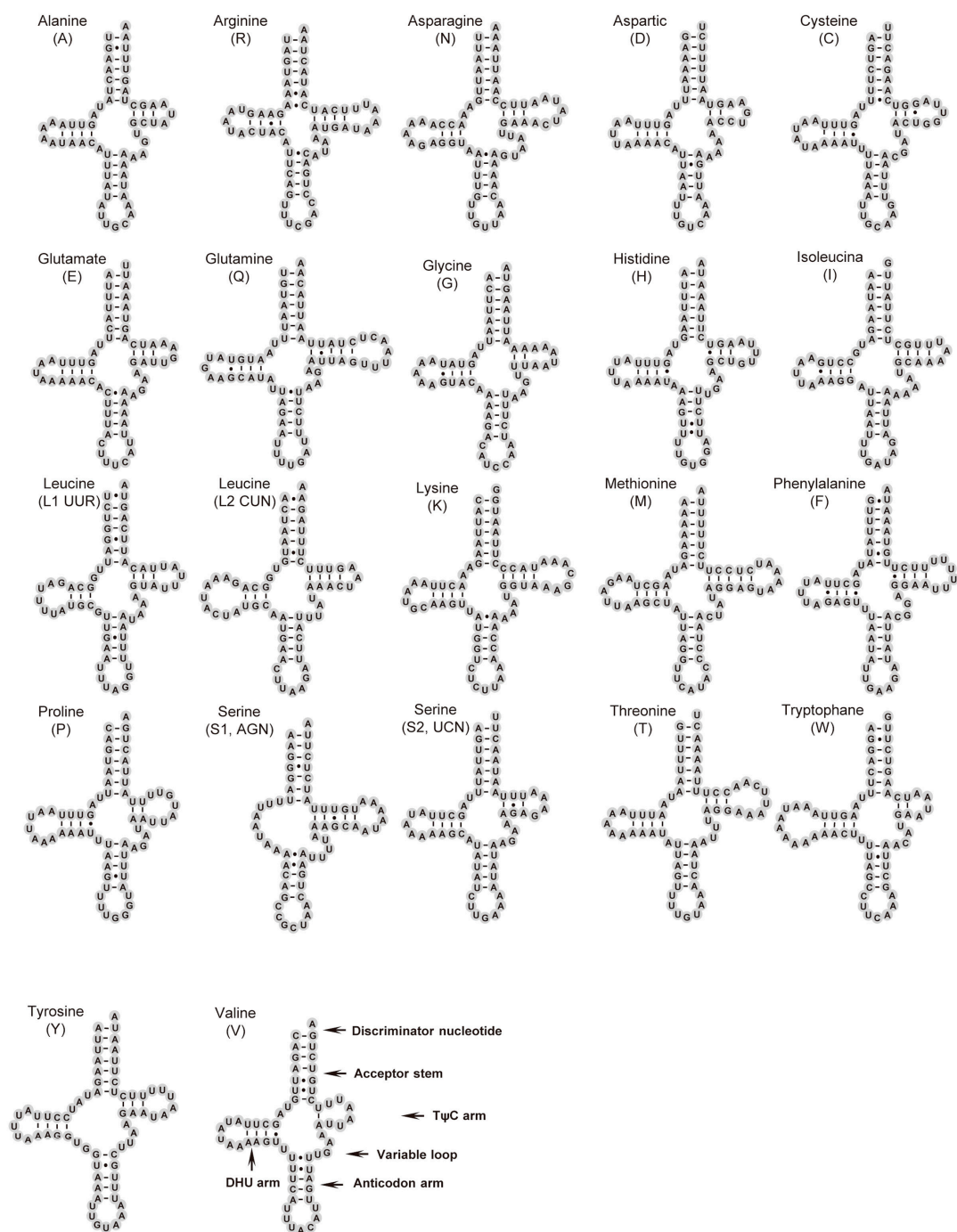


Figure S2. Predicted secondary cloverleaf structure for the tRNAs of *H. paradoxa*.

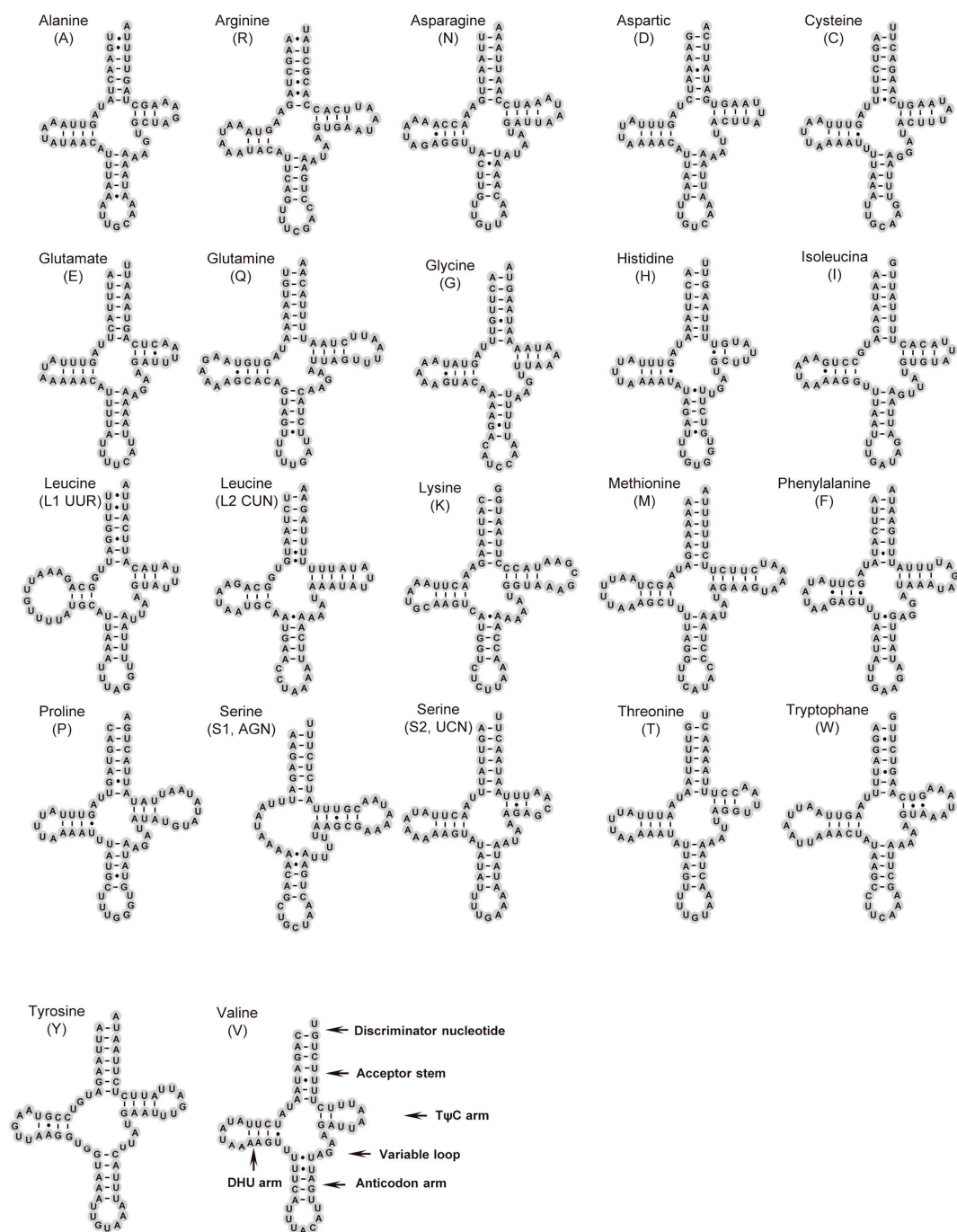


Figure S3. Predicted secondary cloverleaf structure for the tRNAs of *B. fujiana*.

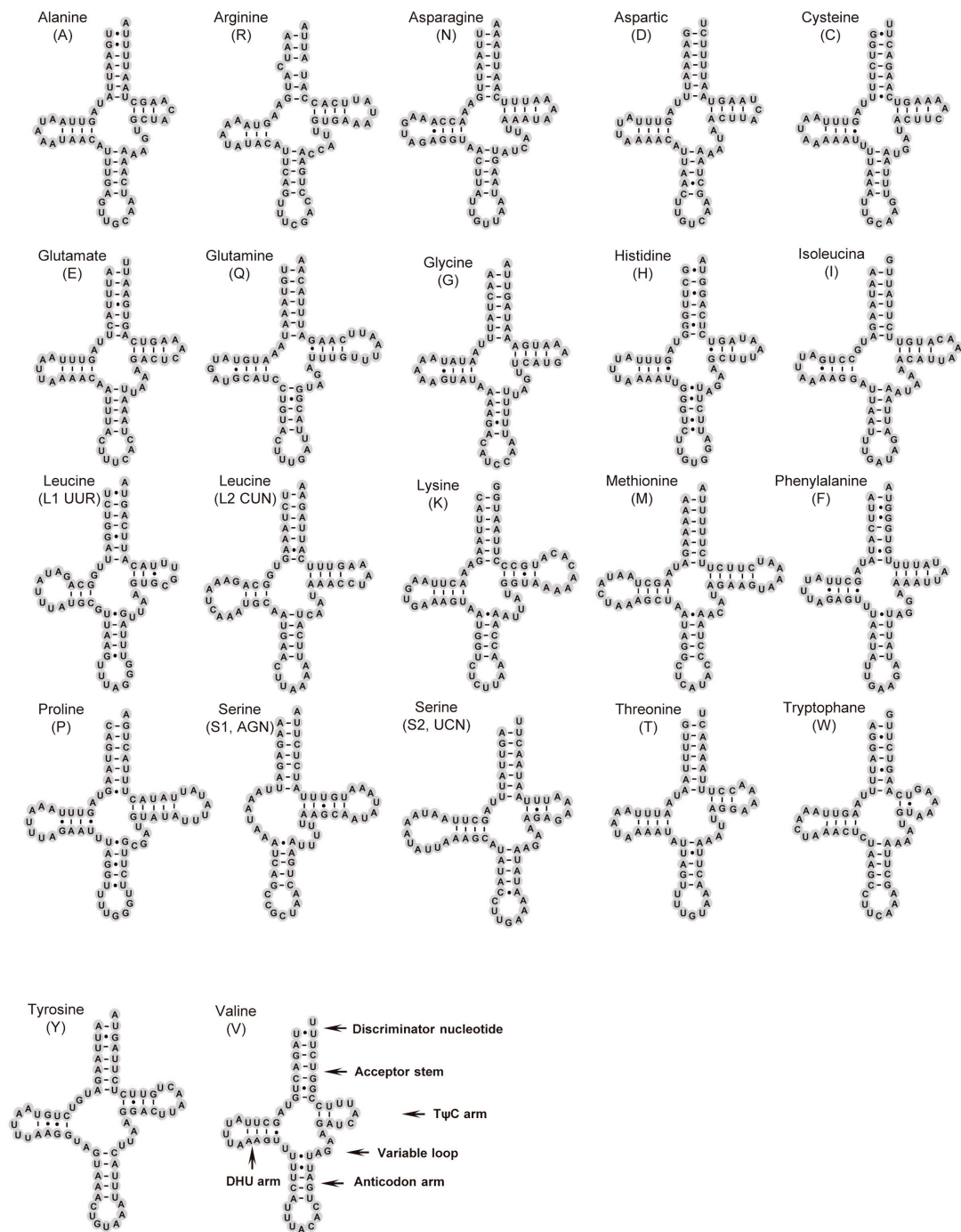


Figure S4. Predicted secondary cloverleaf structure for the tRNAs of *K. nativa*.