

Table S1. List of the mitogenomes of species analyzed in this study and their GenBank accession numbers.

Species	Family	Genus	GenBank No.
<i>Alytes obstetricans pertinax</i>	Alytidae	<i>Alytes</i>	AY585337
<i>Discoglossus galganoi</i>	Alytidae	<i>Discoglossus</i>	AY585339
<i>Leiopelma archeyi</i>	Leiopelmatidae	<i>Leiopelma</i>	HM142901
<i>Leiopelma hochstetteri</i>	Leiopelmatidae	<i>Leiopelma</i>	KJ792087
<i>Bombina orientalis</i>	Bombinatoridae	<i>Bombina</i>	AY585338
<i>Bombina bombina</i>	Bombinatoridae	<i>Bombina</i>	EU115993
<i>Bombina pachypus</i>	Bombinatoridae	<i>Bombina</i>	JX893179
<i>Bombina microdeladigitora</i>	Bombinatoridae	<i>Bombina</i>	JX893182
<i>Pipa pipa</i>	Pipidae	<i>Pipa</i>	GQ244477
<i>Hymenochirus boettgeri</i>	Pipidae	<i>Hymenochirus</i>	HM991331
<i>Pipa carvalhoi</i>	Pipidae	<i>Pipa</i>	HM991332
<i>Pseudhymenochirus merlini</i>	Pipidae	<i>Pseudhymenochirus</i>	HM991333
<i>Scaphiopus couchii</i>	Scaphiopodidae	<i>Scaphiopus</i>	JX564894
<i>Spea bombifrons</i>	Scaphiopodidae	<i>Spea</i>	JX564896
<i>Scaphiopus holbrookii</i>	Scaphiopodidae	<i>Scaphiopus</i>	KY962390
<i>Pelodytes ibericus</i>	Pelodytidae	<i>Pelodytes</i>	JX564882
<i>Pelodytes punctatus</i>	Pelodytidae	<i>Pelodytes</i>	JF703231
<i>Pelobates cultripes</i>	Pelobatidae	<i>Pelobates</i>	AJ871086
<i>Atympanophrys shapingsensis</i>	Megophryidae	<i>Atympanophrys</i>	JX458090
<i>Leptobrachium boringii</i>	Megophryidae	<i>Leptobrachium</i>	KJ630505
<i>Leptobrachium leishanense</i>	Megophryidae	<i>Leptobrachium</i>	KU760082
<i>Scutiger ningshanensis</i>	Megophryidae	<i>Scutiger</i>	KX619450
<i>Xenophrys omeimontis</i>	Megophryidae	<i>Xenophrys</i>	KP728257
<i>Megophrys pingjiangensis</i>	Megophryidae	<i>Megophrys</i>	KT601071
<i>Oreolalax lichuanensis</i>	Megophryidae	<i>Oreolalax</i>	KU096847
<i>Oreolalax major</i>	Megophryidae	<i>Oreolalax</i>	KU127230
<i>Oreolalax rhodostigmatus</i>	Megophryidae	<i>Oreolalax</i>	MF770485
<i>Oreolalax jingdongensis</i>	Megophryidae	<i>Oreolalax</i>	MF953479
<i>Oreolalax multipunctatus</i>	Megophryidae	<i>Oreolalax</i>	MF966382
<i>Oreolalax xiangchengensis</i>	Megophryidae	<i>Oreolalax</i>	MH727696
<i>Oreolalax omeimontis</i>	Megophryidae	<i>Oreolalax</i>	OP722573
<i>Pelomedusa subrufa</i>	Pelomedusidae	<i>Pelomedusa</i>	AF039066
<i>Chelonia mydas</i>	Cheloniidae	<i>Chelonia</i>	AB012104
<i>Testudo graeca</i>	Testudinidae	<i>Testudo</i>	DQ080050

Table S2. Best partitioning schemes selected by ModelFinder (13PCGS - ML) and PartitionFinder2 (13PCGS - BI), respectively.

Data Matrix	Subset Partitions	Best Model
13PCGS - BI	1: <i>nad3_</i> pos1, <i>atp6_</i> pos1, <i>nad4_</i> pos1	GTR+I+G
	2: <i>atp6_</i> pos2, <i>nad1_</i> pos2	GTR+I+G
	3: <i>nad3_</i> pos3, <i>atp6_</i> pos3	GTR +G
	4: <i>atp8_</i> pos1	HKY+I+G
	5: <i>atp8_</i> pos2	GTR+I+G
	6: <i>atp8_</i> pos3	HKY+G
	7: <i>cox1_</i> pos1	SYM +G
	8: <i>cox1_</i> pos2	GTR+I+G
	9: <i>cox1_</i> pos3	GTR+I+G
	10: <i>cox2_</i> pos1	GTR+I+G
	11: <i>cox2_</i> pos2	HKY+I+G
	12: <i>cox2_</i> pos3	GTR+I+G
	13: <i>cox3_</i> pos1	SYM +G
	14: <i>cox3_</i> pos2, <i>cob_</i> pos2	GTR+I+G
	15: <i>cox3_</i> pos3	GTR+G
	16: <i>cob_</i> pos1, <i>nad1_</i> pos1	GTR+I+G
	17: <i>cob_</i> pos3	GTR+G
	18: <i>nad1_</i> pos3, <i>nad5_</i> pos3, <i>nad4_</i> pos3	GTR+I+G
	19: <i>nad2_</i> pos1, <i>nad5_</i> pos1	GTR+I+G
	20: <i>nad2_</i> pos2	GTR+I+G
	21: <i>nad2_</i> pos3	GTR+G
	22: <i>nad3_</i> pos2, <i>nad4_</i> pos2	GTR+I+G
	23: <i>nad4l_</i> pos1	SYM+I+G
	24: <i>nad4l_</i> pos2	GTR+G
	25: <i>nad4l_</i> pos3	HKY +G
	26: <i>nad5_</i> pos2	GTR+I+G
	27: <i>nad6_</i> pos1	GTR+G
	28: <i>nad6_</i> pos2	GTR+G
	29: <i>nad6_</i> pos3	GTR+I+G

Table S2. *Cont.*

Data Matrix	Subset Partitions	Best Model
13PCGS - ML	1: <i>nad1_</i> pos1, <i>cob_</i> pos1	GTR+I+G
	2: <i>nad4_</i> pos2, <i>nad1_</i> pos2, <i>atp6_</i> pos2	GTR+I+G
	3: <i>nad3_</i> pos3, <i>nad1_</i> pos3, <i>nad4l_</i> pos3, <i>nad4_</i> pos3, <i>atp6_</i> pos3	GTR+I+G
	4: <i>nad2_</i> pos1, <i>nad5_</i> pos1	GTR+I+G
	5: <i>nad2_</i> pos2, <i>atp8_</i> pos2	GTR+G
	6: <i>nad2_</i> pos3	GTR+G
	7: <i>cox1_</i> pos1, <i>cox3_</i> pos1	GTR+I+G
	8: <i>cox3_</i> pos2, <i>cox1_</i> pos2	GTR+I+G
	9: <i>cox1_</i> pos3	GTR+G
	10: <i>cox2_</i> pos1	GTR+I+G
	11: <i>cox2_</i> pos2	GTR+G
	12: <i>atp8_</i> pos3, <i>cox2_</i> pos3, <i>cox3_</i> pos3	GTR+G
	13: <i>atp8_</i> pos1	GTR+G
	14: <i>atp6_</i> pos1, <i>nad4_</i> pos1	GTR+I+G
	15: <i>nad3_</i> pos1, <i>nad4l_</i> pos1	GTR+G
	16: <i>nad4l_</i> pos2, <i>nad3_</i> pos2	GTR +G
	17: <i>nad5_</i> pos2	GTR+I+G
	18: <i>nad5_</i> pos3	GTR+G
	19: <i>nad6_</i> pos1	GTR+G
	20: <i>nad6_</i> pos2	GTR+G
	21: <i>nad6_</i> pos3	GTR+G
	22: <i>cob_</i> pos2	GTR+I+G
	23: <i>cob_</i> pos3	GTR+G

Table S3. Usage of start and stop codons in the mitogenomes of seven species of *Oreolalax*.

Species	<i>nad1</i>		<i>nad2</i>		<i>cox1</i>		<i>cox2</i>		<i>atp8</i>		<i>atp6</i>		<i>cox3</i>	
	Start	Stop	Start	Stop	Start	Stop	Start	Stop	Start	Stop	Start	Stop	Start	Stop
<i>O. omeimontis</i>	ATG	TAA	ATG	TAA	GTG	AGG	ATG	T(AA)	ATG	TAA	ATG	TA(A)	ATG	TA(A)
<i>O. lichuanensis</i>	ATG	TA(A)	ATG	TAA	GTG	AGA	ATG	T(AA)	ATG	TAA	ATG	TA(A)	ATA	TAA
<i>O. jingdongensis</i>	ATG	TA(A)	ATG	TAG	GTG	AGG	GTG	TAA	ATG	TAA	ATG	TA(A)	ATG	TA(A)
<i>O. xiangchengensis</i>	ATG	TA(A)	ATG	TAA	GTG	AGG	GTG	T(AA)	ATG	TAA	ATG	TA(A)	ATG	TA(A)
<i>O. rhodostigmatus</i>	ATG	TA(A)	ATG	TAA	GTG	AGA	ATG	T(AA)	GTG	TGA	ATG	TA(A)	ATG	TA(A)
<i>O. multipunctatus</i>	ATG	TA(A)	ATG	TAA	GTG	AGG	ATG	T(AA)	ATG	TAA	ATG	TA(A)	ATG	TA(A)
<i>O. major</i>	ATG	TA(A)	ATG	TAA	ATG	AGG	GTG	T(AA)	ATG	TAA	ATG	TA(A)	ATG	TA(A)

Species	<i>nad3</i>		<i>nad4l</i>		<i>nad4</i>		<i>nad5</i>		<i>nad6</i>		<i>Cob</i>	
	Start	Stop	Start	Stop	Start	Stop	Start	Stop	Start	Stop	Start	Stop
<i>O. omeimontis</i>	ATG	T(AA)	ATG	TAA	ATG	TA(A)	ATT	AGG	GTG	AGG	ATG	T(AA)
<i>O. lichuanensis</i>	ATT	T(AA)	ATG	TAA	ATG	TA(A)	GTG	AGA	GTG	AGG	ATG	T(AA)
<i>O. jingdongensis</i>	ATA	TAA	ATG	TAA	ATG	T(AA)	ATG	TAA	GTG	AGG	ATG	T(AA)
<i>O. xiangchengensis</i>	ATG	TA(A)	ATG	TAA	ATG	T(AA)	ATG	AGA	GTG	AGG	ATG	T(AA)
<i>O. rhodostigmatus</i>	ATA	TAA	ATG	TAA	ATG	T(AA)	ATA	AGG	ATG	AGG	ATG	T(AA)
<i>O. multipunctatus</i>	ATA	TAA	ATG	TA(A)	ATG	TA(A)	ATG	AGA	ATG	AGG	ATG	T(AA)
<i>O. major</i>	ATA	TAA	ATG	TAA	ATG	T(AA)	ATG	AGG	GTG	AGG	ATG	T(AA)

Table S4. Condon number and RSCU of seven *Oreolalax* species mitochondrial PCGs. The asterisk in parentheses indicates the stop codon.

Species	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU
<i>O. omeimontis</i>	UUU(F)	177	1.31	UCU(S)	100	1.87	UAU(Y)	59	1	UGU(C)	9	0.6
	UUC(F)	94	0.69	UCC(S)	70	1.31	UAC(Y)	59	1	UGC(C)	21	1.4
	UUA(L)	172	1.65	UCA(S)	81	1.51	UAA (*)	4	2.29	UGA(W)	95	1.79
	UUG(L)	28	0.27	UCG(S)	23	0.43	UAG (*)	0	0	UGG(W)	11	0.21
	CUU(L)	153	1.47	CCU(P)	58	1.18	CAU(H)	39	0.76	CGU(R)	14	0.81
	CUC(L)	91	0.88	CCC(P)	71	1.44	CAC(H)	64	1.24	CGC(R)	17	0.99
	CUA(L)	141	1.36	CCA(P)	48	0.97	CAA(Q)	73	1.59	CGA(R)	31	1.8
	CUG(L)	39	0.38	CCG(P)	20	0.41	CAG(Q)	19	0.41	CGG(R)	7	0.41
	AUU(I)	198	1.17	ACU(T)	82	1.23	AAU(N)	67	1.11	AGU(S)	22	0.41
	AUC(I)	140	0.83	ACC(T)	95	1.43	AAC(N)	54	0.89	AGC(S)	25	0.47
	AUA(M)	102	1.39	ACA(T)	76	1.14	AAA(K)	69	1.77	AGA (*)	0	0
	AUG(M)	45	0.61	ACG(T)	13	0.2	AAG(K)	9	0.23	AGG (*)	3	1.71
	GUU(V)	47	1.07	GCU(A)	104	1.46	GAU(D)	27	0.84	GGU(G)	47	0.8
	GUC(V)	35	0.8	GCC(A)	107	1.51	GAC(D)	37	1.16	GGC(G)	78	1.33
	GUA(V)	66	1.5	GCA(A)	52	0.73	GAA(E)	72	1.5	GGA(G)	56	0.96
	GUG(V)	28	0.64	GCG(A)	21	0.3	GAG(E)	24	0.5	GGG(G)	53	0.91
<i>O. lichuanensis</i>	UUU(F)	179	1.31	UCU(S)	105	2.03	UAU(Y)	69	1.29	UGU(C)	18	1.24
	UUC(F)	95	0.69	UCC(S)	54	1.05	UAC(Y)	38	0.71	UGC(C)	11	0.76
	UUA(L)	185	1.77	UCA(S)	90	1.74	UAA (*)	4	2.67	UGA(W)	95	1.7
	UUG(L)	39	0.37	UCG(S)	12	0.23	UAG (*)	0	0	UGG(W)	17	0.3
	CUU(L)	148	1.42	CCU(P)	60	1.22	CAU(H)	41	0.83	CGU(R)	12	0.69
	CUC(L)	82	0.78	CCC(P)	67	1.37	CAC(H)	58	1.17	CGC(R)	15	0.86
	CUA(L)	133	1.27	CCA(P)	49	1	CAA(Q)	73	1.64	CGA(R)	37	2.11
	CUG(L)	40	0.38	CCG(P)	20	0.41	CAG(Q)	16	0.36	CGG(R)	6	0.34
	AUU(I)	223	1.35	ACU(T)	102	1.47	AAU(N)	67	1.06	AGU(S)	33	0.64
	AUC(I)	107	0.65	ACC(T)	76	1.09	AAC(N)	60	0.94	AGC(S)	16	0.31
	AUA(M)	102	1.4	ACA(T)	81	1.17	AAA(K)	65	1.6	AGA (*)	1	0.67
	AUG(M)	44	0.6	ACG(T)	19	0.27	AAG(K)	16	0.4	AGG (*)	1	0.67
	GUU(V)	52	1.05	GCU(A)	88	1.25	GAU(D)	30	0.9	GGU(G)	45	0.8
	GUC(V)	49	0.99	GCC(A)	116	1.65	GAC(D)	37	1.1	GGC(G)	64	1.14
	GUA(V)	63	1.27	GCA(A)	63	0.9	GAA(E)	71	1.56	GGA(G)	66	1.17
	GUG(V)	34	0.69	GCG(A)	14	0.2	GAG(E)	20	0.44	GGG(G)	50	0.89

Table S4. *Cont.*

Species	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU
<i>O. jingdongensis</i>	UUU(F)	182	1.4	UCU(S)	96	1.89	UAU(Y)	71	1.25	UGU(C)	17	1.13
	UUC(F)	78	0.6	UCC(S)	49	0.96	UAC(Y)	43	0.75	UGC(C)	13	0.87
	UUA(L)	200	1.93	UCA(S)	100	1.97	UAA (*)	5	2.5	UGA(W)	98	1.77
	UUG(L)	26	0.25	UCG(S)	12	0.24	UAG (*)	1	0.5	UGG(W)	13	0.23
	CUU(L)	157	1.51	CCU(P)	79	1.6	CAU(H)	52	1.07	CGU(R)	21	1.14
	CUC(L)	60	0.58	CCC(P)	35	0.71	CAC(H)	45	0.93	CGC(R)	12	0.65
	CUA(L)	144	1.39	CCA(P)	66	1.34	CAA(Q)	77	1.69	CGA(R)	38	2.05
	CUG(L)	36	0.35	CCG(P)	17	0.35	CAG(Q)	14	0.31	CGG(R)	3	0.16
	AUU(I)	213	1.31	ACU(T)	110	1.57	AAU(N)	74	1.14	AGU(S)	25	0.49
	AUC(I)	113	0.69	ACC(T)	70	1	AAC(N)	56	0.86	AGC(S)	23	0.45
	AUA(M)	129	1.54	ACA(T)	85	1.21	AAA(K)	71	1.8	AGA (*)	0	0
	AUG(M)	39	0.46	ACG(T)	15	0.21	AAG(K)	8	0.2	AGG (*)	2	1
	GUU(V)	58	1.25	GCU(A)	117	1.64	GAU(D)	32	0.96	GGU(G)	55	0.98
	GUC(V)	42	0.9	GCC(A)	92	1.29	GAC(D)	35	1.04	GGC(G)	58	1.03
	GUA(V)	62	1.33	GCA(A)	60	0.84	GAA(E)	76	1.71	GGA(G)	71	1.26
	GUG(V)	24	0.52	GCG(A)	16	0.22	GAG(E)	13	0.29	GGG(G)	41	0.73
<i>O. xiangchengensis</i>	UUU(F)	185	1.43	UCU(S)	106	2.07	UAU(Y)	72	1.25	UGU(C)	17	1.17
	UUC(F)	74	0.57	UCC(S)	46	0.9	UAC(Y)	43	0.75	UGC(C)	12	0.83
	UUA(L)	209	2.04	UCA(S)	102	1.99	UAA (*)	3	2	UGA(W)	100	1.8
	UUG(L)	23	0.22	UCG(S)	7	0.14	UAG (*)	0	0	UGG(W)	11	0.2
	CUU(L)	171	1.67	CCU(P)	85	1.74	CAU(H)	49	0.99	CGU(R)	18	1
	CUC(L)	51	0.5	CCC(P)	29	0.59	CAC(H)	50	1.01	CGC(R)	15	0.83
	CUA(L)	135	1.31	CCA(P)	74	1.52	CAA(Q)	80	1.76	CGA(R)	31	1.72
	CUG(L)	27	0.26	CCG(P)	7	0.14	CAG(Q)	11	0.24	CGG(R)	8	0.44
	AUU(I)	240	1.49	ACU(T)	111	1.55	AAU(N)	80	1.2	AGU(S)	25	0.49
	AUC(I)	82	0.51	ACC(T)	76	1.06	AAC(N)	53	0.8	AGC(S)	21	0.41
	AUA(M)	130	1.51	ACA(T)	88	1.23	AAA(K)	73	1.83	AGA (*)	1	0.67
	AUG(M)	42	0.49	ACG(T)	11	0.15	AAG(K)	7	0.18	AGG (*)	2	1.33
	GUU(V)	69	1.43	GCU(A)	113	1.63	GAU(D)	36	1.11	GGU(G)	52	0.92
	GUC(V)	33	0.68	GCC(A)	92	1.32	GAC(D)	29	0.89	GGC(G)	55	0.98
	GUA(V)	70	1.45	GCA(A)	59	0.85	GAA(E)	73	1.64	GGA(G)	73	1.3
	GUG(V)	21	0.44	GCG(A)	14	0.2	GAG(E)	16	0.36	GGG(G)	45	0.8

Table S4. *Cont.*

Species	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU
<i>O. rhodostigmatus</i>	UUU(F)	178	1.37	UCU(S)	91	1.8	UAU(Y)	60	1.1	UGU(C)	17	1.06
	UUC(F)	81	0.63	UCC(S)	58	1.14	UAC(Y)	49	0.9	UGC(C)	15	0.94
	UUA(L)	184	1.75	UCA(S)	86	1.7	UAA (*)	3	2	UGA(W)	90	1.59
	UUG(L)	33	0.31	UCG(S)	19	0.38	UAG (*)	0	0	UGG(W)	23	0.41
	CUU(L)	168	1.6	CCU(P)	70	1.39	CAU(H)	45	0.9	CGU(R)	13	0.73
	CUC(L)	73	0.7	CCC(P)	62	1.23	CAC(H)	55	1.1	CGC(R)	12	0.68
	CUA(L)	138	1.31	CCA(P)	59	1.17	CAA(Q)	76	1.63	CGA(R)	44	2.48
	CUG(L)	34	0.32	CCG(P)	11	0.22	CAG(Q)	17	0.37	CGG(R)	2	0.11
	AUU(I)	214	1.37	ACU(T)	92	1.32	AAU(N)	69	1.05	AGU(S)	22	0.43
	AUC(I)	99	0.63	ACC(T)	83	1.19	AAC(N)	62	0.95	AGC(S)	28	0.55
	AUA(M)	124	1.49	ACA(T)	90	1.29	AAA(K)	69	1.73	AGA (*)	1	0.67
	AUG(M)	42	0.51	ACG(T)	14	0.2	AAG(K)	11	0.28	AGG (*)	2	1.33
	GUU(V)	56	1.16	GCU(A)	109	1.55	GAU(D)	30	0.95	GGU(G)	47	0.83
	GUC(V)	49	1.02	GCC(A)	102	1.45	GAC(D)	33	1.05	GGC(G)	64	1.13
	GUA(V)	56	1.16	GCA(A)	52	0.74	GAA(E)	71	1.56	GGA(G)	61	1.07
	GUG(V)	32	0.66	GCG(A)	19	0.27	GAG(E)	20	0.44	GGG(G)	55	0.97
<i>O. multipunctatus</i>	UUU(F)	162	1.27	UCU(S)	105	2.01	UAU(Y)	70	1.21	UGU(C)	21	1.31
	UUC(F)	93	0.73	UCC(S)	54	1.04	UAC(Y)	46	0.79	UGC(C)	11	0.69
	UUA(L)	203	1.93	UCA(S)	94	1.8	UAA (*)	2	1.6	UGA(W)	98	1.77
	UUG(L)	35	0.33	UCG(S)	10	0.19	UAG (*)	0	0	UGG(W)	13	0.23
	CUU(L)	159	1.51	CCU(P)	77	1.56	CAU(H)	50	1.03	CGU(R)	13	0.73
	CUC(L)	85	0.81	CCC(P)	53	1.08	CAC(H)	47	0.97	CGC(R)	15	0.85
	CUA(L)	118	1.12	CCA(P)	56	1.14	CAA(Q)	82	1.74	CGA(R)	35	1.97
	CUG(L)	30	0.29	CCG(P)	11	0.22	CAG(Q)	12	0.26	CGG(R)	8	0.45
	AUU(I)	224	1.42	ACU(T)	106	1.5	AAU(N)	70	1.08	AGU(S)	25	0.48
	AUC(I)	91	0.58	ACC(T)	77	1.09	AAC(N)	60	0.92	AGC(S)	25	0.48
	AUA(M)	113	1.53	ACA(T)	81	1.15	AAA(K)	75	1.81	AGA (*)	1	0.8
	AUG(M)	35	0.47	ACG(T)	18	0.26	AAG(K)	8	0.19	AGG (*)	2	1.6
	GUU(V)	63	1.28	GCU(A)	112	1.58	GAU(D)	36	1.11	GGU(G)	48	0.85
	GUC(V)	32	0.65	GCC(A)	96	1.36	GAC(D)	29	0.89	GGC(G)	61	1.07
	GUA(V)	71	1.44	GCA(A)	54	0.76	GAA(E)	75	1.63	GGA(G)	73	1.29
	GUG(V)	31	0.63	GCG(A)	21	0.3	GAG(E)	17	0.37	GGG(G)	45	0.79

Table S4. *Cont.*

Species	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU
<i>O. major</i>	UUU(F)	162	1.25	UCU(S)	110	2.17	UAU(Y)	69	1.19	UGU(C)	14	0.97
	UUC(F)	97	0.75	UCC(S)	46	0.91	UAC(Y)	47	0.81	UGC(C)	15	1.03
	UUA(L)	201	1.93	UCA(S)	87	1.72	UAA (*)	4	2.29	UGA(W)	97	1.75
	UUG(L)	26	0.25	UCG(S)	14	0.28	UAG (*)	0	0	UGG(W)	14	0.25
	CUU(L)	171	1.64	CCU(P)	78	1.6	CAU(H)	48	0.99	CGU(R)	18	0.99
	CUC(L)	58	0.56	CCC(P)	40	0.82	CAC(H)	49	1.01	CGC(R)	15	0.82
	CUA(L)	141	1.35	CCA(P)	65	1.33	CAA(Q)	83	1.8	CGA(R)	35	1.92
	CUG(L)	28	0.27	CCG(P)	12	0.25	CAG(Q)	9	0.2	CGG(R)	5	0.27
	AUU(I)	207	1.31	ACU(T)	96	1.32	AAU(N)	78	1.17	AGU(S)	26	0.51
	AUC(I)	109	0.69	ACC(T)	93	1.28	AAC(N)	55	0.83	AGC(S)	21	0.41
	AUA(M)	129	1.54	ACA(T)	93	1.28	AAA(K)	76	1.9	AGA (*)	0	0
	AUG(M)	38	0.46	ACG(T)	8	0.11	AAG(K)	4	0.1	AGG (*)	3	1.71
	GUU(V)	68	1.4	GCU(A)	102	1.48	GAU(D)	33	1.03	GGU(G)	51	0.91
	GUC(V)	40	0.82	GCC(A)	99	1.43	GAC(D)	31	0.97	GGC(G)	62	1.1
	GUA(V)	65	1.34	GCA(A)	62	0.9	GAA(E)	76	1.67	GGA(G)	66	1.17
	GUG(V)	21	0.43	GCG(A)	13	0.19	GAG(E)	15	0.33	GGG(G)	46	0.82