



## Supplementary Material

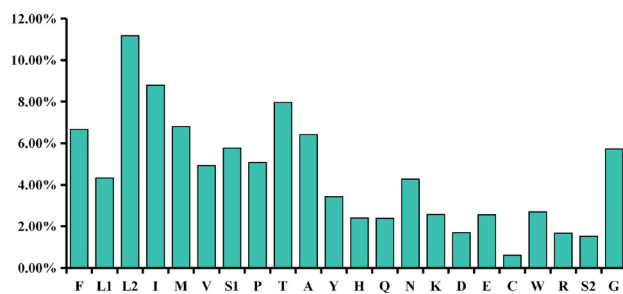
# Sequencing and Characterization of the Complete Mitochondrial Genome of Tufted Deer, *Elaphodus cephalophus* (Artiodactyla: Cervidae) and its Phylogenetic Position within the Family Cervidae

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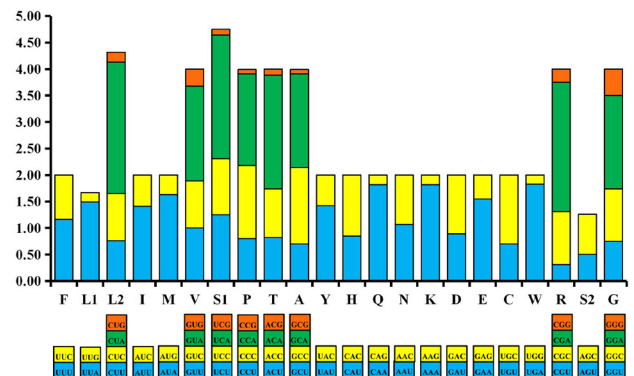
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Supplementary Fig. S1. Percentages of amino acid usage in *Elaphodus cephalophus* mitogenome. Each amino acid is represented by the one-letter abbreviation. Codon families are provided on the X-axis. Note that leucine (L1, L2) and serine (S1, S2) are each coded by two different genetic codons, and listed separately.



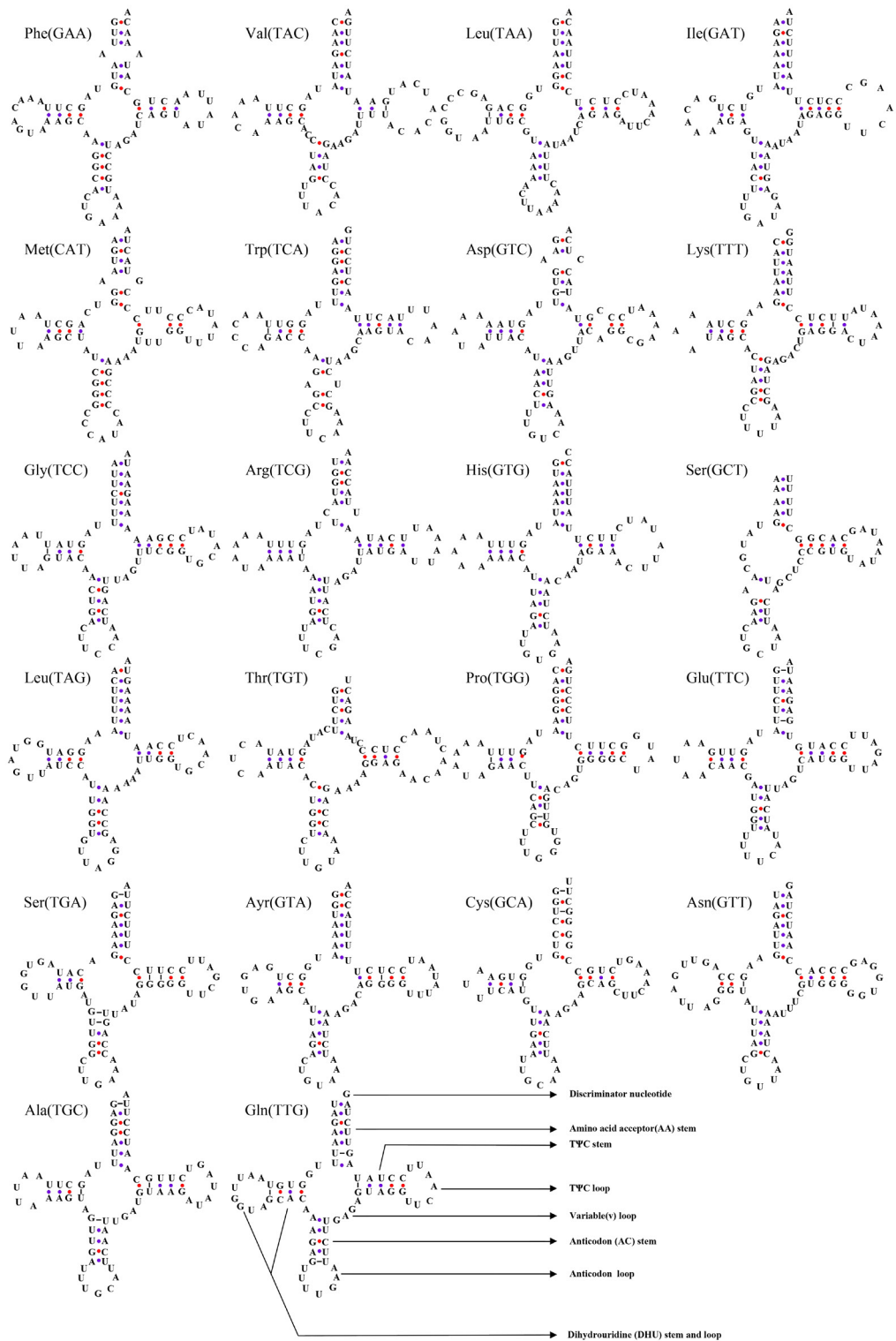
Supplementary Fig. S2. The relative synonymous codon usage (RSCU) in the mitogenome of *Elaphodus cephalophus*. Codon families are provided on the X-axis.

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0030-9923/2023/0005-2019 \$ 9.00/0

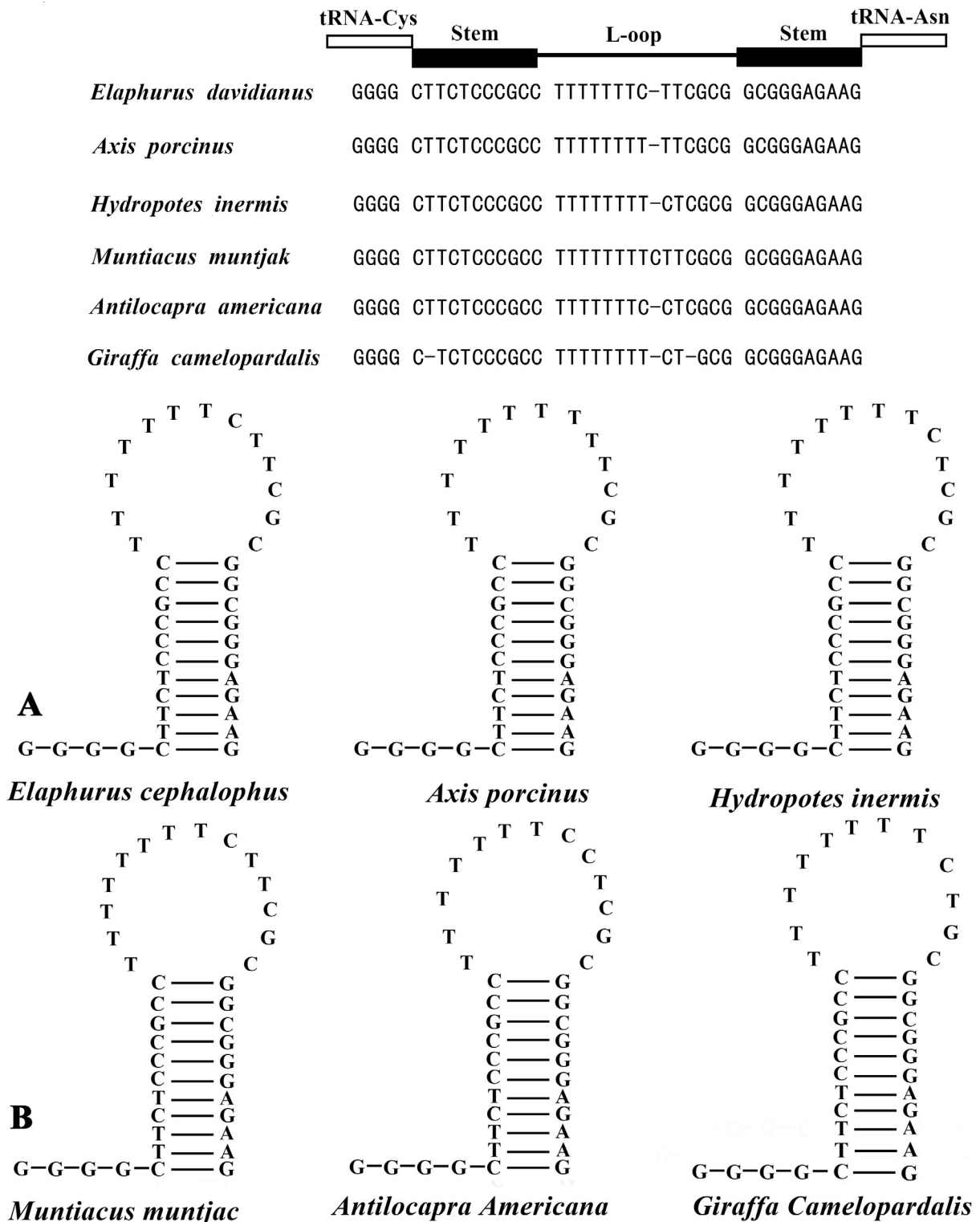


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Supplementary Fig. S3. Inferred secondary structures for 22 tRNA genes of *Elaphodus cephalophus*. 22 tRNA genes are labeled with the abbreviations of corresponding amino acids. a dot indicate Watson- Crick base pairing and dashes represents an unmatched base (G-U).



Supplementary Fig. S4. Alignment of the light strand replication origin (OL) between tRNA-Cys and tRNA-Asn of *Elaphodus cephalophus* (A) and the putative stem-loop structure found in the OL region (B). The tRNAs are shown with white blocks whereas stem regions are shown in black blocks.

**Supplementary Table SI. Species mentioned in the present study with their GenBank accession number.**

No.	Family/ SubFamily	Tribe	Genus	Species	Size	Accession no.		
1	Cervidae/ Cervinae	Muntiacini	<i>Elaphodus</i>	<i>Elaphodus cephalophus</i>	16,196	MN248532		
2				<i>E. cephalophus</i>	16,347	DQ873526		
3			<i>Muntiacus</i>	<i>Muntiacus crinifrons</i>	16,357	AY239042		
4				<i>M. muntjak</i>	16,354	AY225986		
5				<i>M. reevesi micrurus</i>	16,353	EF035447		
6				<i>M. putaoensis</i>	16,349	NC_036430		
7				<i>M. vuquangensis</i>	16,361	NC_016920		
8				<i>M. sp. JAV10</i>	16,351	KY052152		
9				<i>M. sp. IND8</i>	16,355	KY052107		
10				<i>M. sp. LAO1</i>	16,352	KY052082		
11		<i>M. reevesi</i>	16,354	NC_004069				
12		Cervini	<i>Cervus</i>	<i>Cervus elaphus hippelaphus</i>	16,354	KT290948		
13				<i>C. nippon hortulorum</i>	16,434	KX689229		
14				<i>C. albirostris</i>	16,478	HM049636		
15				<i>C. unicolor swinhoei</i>	16,505	DQ989636		
16				<i>C. elaphus songaricus</i>	16,419	KJ025072		
17				<i>C. nippon kopschi</i>	16,429	HQ832482		
18				<i>C. nippon yakushimae</i>	16,440	NC_007179		
19				<i>C. nippon sichuanicus</i>	16,429	JN389443		
20				<i>Elaphurus</i>	<i>Elaphurus davidianus</i>	16,355	JN399997	
21				<i>Axis</i>	<i>Axis</i>	<i>Axis porcinus</i>	16,351	MF435989
22		<i>A. axis</i>	16,439			JN632599		
23		<i>Rucervus</i>	<i>Rucervus eldii eldii</i>			16,357	KU133959	
24			<i>R. duvaucelii</i>			16,342	JN632696	
25		<i>Przewalskium</i>	<i>Przewalskium albirostris</i>			16,478	NC_016707	
26		<i>Dama</i>	<i>Dama mesopotamica</i>			16,355	JN632630	
27			<i>D. dama</i>			16,300	JN632629	
28		<i>Rusa</i>	<i>Rusa</i>			<i>Rusa alfredi</i>	16,355	NC_020744
29						<i>R. unicolor hainana</i>	16,436	KY946815
30						<i>R. unicolor</i>	16,437	NC_031835
31				<i>R. unicolor swinhoei</i>	16,505	NC_008414		
32	Capreolinae			Odocoileini	<i>Hippocamelus</i>	<i>Hippocamelus antisensis</i>	16,410	JN632646
33					<i>Mazama</i>	<i>Mazama rufina</i>	16,429	JN632661
34		<i>M. gouazoupira</i>	16,355			JN632658		
35		<i>M. nemorivaga</i>	16,361		NC_024812			
36		<i>M. americana</i>	16,473		JN632657			
37		<i>Ozotoceros</i>	<i>Ozotoceros bezoarticus</i>		16,357	NC_020766		
38		<i>Odocoileus</i>	<i>Odocoileus hemionus</i>		16,482	JN632670		
39			<i>O. virginianus</i>		16,477	KM612278		
40			<i>Pudu</i>		<i>Pudu mephistophiles</i>	16,426	NC_020739	
41		<i>P. puda</i>			16,347	JN632692		
42	Capreolini	<i>Rangifer</i>	<i>Rangifer tarandus</i>	16,357	KM506758			
43			<i>Hydropotes</i>	<i>Hydropotes inermis argyropus</i>	16,355	KP203884		
44		<i>H. inermis</i>		16,335	EU315254			
45		<i>Capreolus</i>	<i>Capreolus capreolus</i>	16,354	KJ681484			
46			<i>C. pygargus</i>	16,355	KJ681495			
47			Alceini	<i>Alces</i>	<i>Alces alces</i>	16,418	KP405229	
48		Giraffidae		<i>Giraffa</i>	<i>Giraffa camelopardalis</i>	16,433	AP003424	
49			<i>Okapia</i>	<i>Okapia johnstoni</i>	16,422	JN632674		
50	Antilocapridae		<i>Antilocapra</i>	<i>Antilocapra americana</i>	16,352	NC_020679		

**Supplementary Table SII. Nucleotide composition and skews rate in the forward strand of *Elaphodus cephalophus* mitochondrial DNA by regions.**

Gene/region	Nucleotide frequency (%)				A+T(%)	AT-skew	GC-skew
	A	T	C	G			
Total	33.37	29.33	23.94	13.36	62.70	0.06	-0.28
L-strand	37.34	25.69	25.79	11.18	63.03	0.18	-0.40
H-strand	33.08	29.65	23.80	13.47	62.73	0.05	-0.28
tRNA	35.88	28.96	20.05	15.11	64.84	0.11	-0.14
rRNA	37.32	24.37	20.88	17.43	61.69	0.21	-0.09
13 Protein-coding genes	31.54	31.26	24.20	13.00	62.80	0.00	-0.30
1st	31.98	23.83	22.80	21.38	55.81	0.15	-0.03
2nd	19.67	42.79	25.28	12.26	62.47	-0.37	-0.35
3rd	42.95	27.17	24.51	5.37	70.12	0.23	-0.64
Protein-coding genes-H strand	31.95	30.81	24.97	12.28	62.75	0.02	-0.34
1st	32.21	23.61	23.61	20.57	55.82	0.15	-0.07
2nd	19.72	42.66	25.76	11.86	62.38	-0.37	-0.37
3rd	43.91	26.14	25.54	4.41	70.05	0.25	-0.71
Protein-coding genes-L strand	23.11	40.72	8.33	27.84	63.83	-0.28	0.54
1st	27.27	28.41	6.25	38.07	55.68	-0.02	0.72
2nd	18.75	45.45	15.34	20.45	64.20	-0.42	0.14
3rd	23.30	48.30	3.41	25.00	71.59	-0.35	0.76
ATP6	31.28	32.45	24.08	12.19	63.73	-0.02	-0.33
ATP8	40.30	33.83	19.90	5.97	74.13	0.09	-0.54
COX1	29.13	32.30	22.46	16.12	61.42	-0.05	-0.16
COX2	35.23	28.51	23.25	13.01	63.74	0.11	-0.28
COX3	26.50	32.23	26.24	15.03	58.73	-0.10	-0.27
ND1	31.56	30.20	26.54	11.70	61.76	0.02	-0.39
ND2	36.30	29.21	25.67	8.81	65.52	0.11	-0.49
ND3	31.99	29.68	26.80	11.53	61.67	0.04	-0.40
ND4	31.28	30.84	26.27	11.61	62.12	0.01	-0.39
ND4L	31.65	31.99	23.91	12.46	63.64	-0.01	-0.31
ND5	33.55	30.81	24.93	10.71	64.36	0.04	-0.40
ND6	40.72	23.11	27.84	8.33	63.83	0.28	-0.54
Cytb	31.15	29.75	26.07	13.04	60.89	0.02	-0.33
12S rRNA	36.68	22.78	22.68	17.87	59.46	0.23	-0.12
16S rRNA	37.72	25.34	19.78	17.17	63.05	0.20	-0.07
Control region	30.33	30.72	24.44	14.51	61.05	-0.01	-0.26
Overall	32.08	31.00	22.28	14.64	63.08	0.02	-0.22

Note; AT skew= (A% - T%)/(A% + T%); GC skew = (G% - C%)/(G% + C%).

**Supplementary Table SIII. The RSCU of 13 protein-coding genes of *Elaphodus cephalophus* mitogenome.**

Amino acid	Codon	Count	RSCU	Frequency (%)	Amino acid	Codon	Count	RSCU	Frequency (%)
Phe	UUU(F)	147	1.16	3.86%	Tyr	UAU(Y)	93	1.42	2.44%
Phe	UUC(F)	107	0.84	2.81%	Tyr	UAC(Y)	38	0.58	0.99%
Leu	UUA(L)	147	1.49	3.86%	*	UAA	8	3.20	0.21%
Leu	UUG(L)	18	0.18	0.47%	*	UAG	2	0.80	0.05%
Leu	CUU(L)	75	0.76	1.97%	His	CAU(H)	39	0.85	1.02%
Leu	CUC(L)	88	0.89	2.31%	His	CAC(H)	53	1.15	1.39%
Leu	CUA(L)	244	2.48	6.41%	Gln	CAA(Q)	83	1.82	2.18%
Leu	CUG(L)	19	0.19	0.49%	Gln	CAG(Q)	8	0.18	0.21%
Ile	AUU(I)	237	1.41	6.23%	Asn	AAU(N)	87	1.07	2.28%
Ile	AUC(I)	98	0.59	2.57%	Asn	AAC(N)	76	0.93	1.99%
Met	AUA(M)	211	1.63	5.54%	Lys	AAA(K)	89	1.82	2.34%
Met	AUG(M)	48	0.37	1.26%	Lys	AAG(K)	9	0.18	0.23%
Val	GUU(V)	47	1.00	1.23%	Asp	GAU(D)	29	0.89	0.76%
Val	GUC(V)	42	0.89	1.10%	Asp	GAC(D)	36	1.11	0.94%
Val	GUA(V)	84	1.79	2.20%	Glu	GAA(E)	76	1.55	1.99%
Val	GUG(V)	15	0.32	0.39%	Glu	GAG(E)	22	0.45	0.57%
Ser	UCU(S)	58	1.25	1.52%	Cys	UGU(C)	8	0.70	0.21%
Ser	UCC(S)	49	1.06	1.28%	Cys	UGC(C)	15	1.30	0.39%
Ser	UCA(S)	108	2.33	2.84%	Trp	UGA(W)	94	1.83	2.47%
Ser	UCG(S)	5	0.11	0.13%	Trp	UGG(W)	9	0.17	0.23%
Pro	CCU(P)	39	0.80	1.02%	Arg	CGU(R)	5	0.31	0.13%
Pro	CCC(P)	67	1.38	1.76%	Arg	CGC(R)	16	1.00	0.42%
Pro	CCA(P)	84	1.73	2.20%	Arg	CGA(R)	39	2.44	1.02%
Pro	CCG(P)	4	0.08	0.10%	Arg	CGG(R)	4	0.25	0.10%
Thr	ACU(T)	62	0.82	1.63%	Ser	AGU(S)	23	0.50	0.60%
Thr	ACC(T)	70	0.92	1.84%	Ser	AGC(S)	35	0.76	0.92%
Thr	ACA(T)	162	2.14	4.26%	*	AGA	0	0.00	0.00%
Thr	ACG(T)	9	0.12	0.23%	*	AGG	0	0.00	0.00%
Ala	GCU(A)	43	0.70	1.13%	Gly	GGU(G)	41	0.75	1.07%
Ala	GCC(A)	88	1.44	2.31%	Gly	GGC(G)	54	0.99	1.42%
Ala	GCA(A)	108	1.77	2.84%	Gly	GGA(G)	96	1.76	2.52%
Ala	GCG(A)	5	0.08	0.13%	Gly	GGG(G)	27	0.50	0.71%

Note: RSCU, Relative Synonymous Codon Usage.