

**Table S2. Predicted initiation and termination codons distribution of the 13 mitochondrial PCGs among Nymphalidae species in this study.**

Species	Start codon						Stop codon			
	ATA	ATT	ATC	ATG	CGA	TTG	TAA	TAG	TA	T
<i>Apatura ilia</i>	2	3	0	7	1	0	6	2	0	5
<i>Apatura metis</i>	1	4	0	7	1	0	9	1	0	3
<i>Sasakia charonda</i>	6	2	0	5	0	0	10	1	0	2
<i>Sasakia funebris</i>	3	3	0	6	1	0	8	1	0	4
<i>Timelaea maculata</i>	1	3	1	7	1	0	8	1	0	4
<i>Ariadne ariadne</i>	0	5	0	7	1	0	7	0	2	4
<i>Cyrestis thyodamas</i>	3	2	1	6	1	0	8	0	0	5
<i>Kallima inachus</i>	1	3	0	8	1	0	8	2	1	2
<i>Melitaea cinxia</i>	0	5	0	7	1	0	9	0	2	2
<i>Hypolimnas bolina</i>	0	4	1	7	1	0	7	1	1	4
<i>Junonia orithya</i>	0	4	1	7	1	0	9	0	2	2
<i>Dichorragia nesimachus</i> ▼	3	1	0	7	1	0	10	1	0	2
<i>Argyreus hyperbius</i>	3	3	0	6	1	0	11	0	0	2
<i>Acraea issoria</i>	2	2	0	8	0	1	12	0	0	1
<i>Fabriciana nerippe</i>	1	5	0	6	0	1	8	0	2	3
<i>Issoria lathonia</i>	0	5	0	7	1	0	8	0	2	3
<i>Heliconius melpomene</i>	1	5	0	6	0	1	10	3	0	0
<i>Cethosia biblis</i>	1	4	1	6	1	0	6	1	3	3
<i>Parathyma sulpitia</i>	1	4	0	7	1	0	9	0	0	4
<i>Libythea celtis</i>	0	4	1	7	1	0	8	1	0	4
<i>Eumenis autonoe</i>	0	2	3	7	1	0	10	0	0	3
<i>Melanitis leda</i>	0	2	2	8	1	0	8	0	0	5
<i>Elymnias hypermnestra</i>	1	2	2	7	1	0	8	0	0	5
<i>Lethe dura</i>	2	4	0	6	1	0	7	0	0	6
<i>Callerebia suroia</i>	2	3	1	6	1	0	7	1	0	5
<i>Stichopthalma howqua</i> ▼	1	3	1	6	1	0	11	0	1	1
<i>Polyura nepenthes</i>	1	4	1	6	1	0	10	0	1	2
<i>Calinaga davidis</i>	0	4	1	7	0	1	11	0	1	1
<i>Euploea mulciber</i>	1	4	0	7	1	0	8	1	0	4
<i>Danaus plexippus</i>	1	4	0	7	1	0	9	0	0	4
<i>Danaus chrysippus</i>	0	5	0	7	1	0	9	0	0	4
<i>Ideopsis similes</i>	2	4	0	6	1	0	8	1	0	4
<i>Parantica aglea</i>	2	2	2	6	1	0	7	2	0	4

▼ indicates lack of initiation codon for *nad2* gene in the mitogenome.