Supplementary

Table S1. Information on collecting samples.

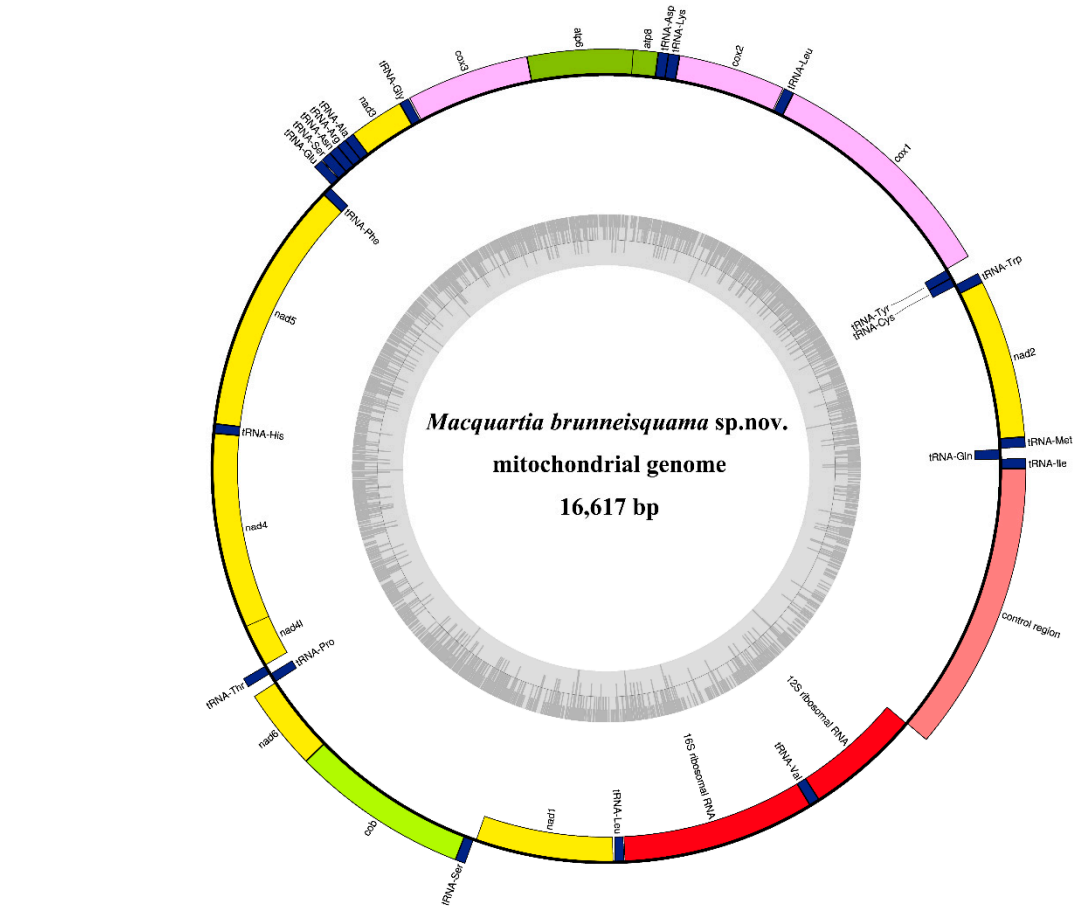
Species	Specimen numbers	Collecting sites	Distribution
M. brunneisquama	6♂	Hubei	China (Hubei, Qinghai)
	1♀	Qinghai	
M. chinensis	7♂2♀	Hubei	China (Hubei, Liaoning, Yunnan)
	3♂	Liaoning	
	1♀	Yunnan	
M. flavipedicel	19♂1♀	Hubei	China (Hubei)
M. flavifemorata	1♂9♀	Hubei	China (Hubei)
M. dispar	19♂	Liaoning	Austria, Belgium, Britain, China (Liaoning, Ningxia, Qinghai), France, Hungary, Mongolia, Russia (East Siberia, North European Part), Sweden, Transcaucasus.
	1♂1♀	Nei Mongolia	
M. macularis	1♀	Liaoning	Albania, China (Liaoning, Ningxia, Shanxi, Sichuan), Mongolia, Morocco, Switzerland, Tunisia.
M. nudigena	60♂11♀	Liaoning	China (Liaoning, Nei Mongolia, Ningxia), Europe (northwards to Scotland, Sweden), Russia.
M. pubiceps	1♀	Anhui	China **(**Anhui, Fujian, Guizhou, Guangdong, Guangxi, Hainan, Hebei, Hubei, Liaoning, Nei Mongolia, Ningxia, Shaanxi, Shanxi), Europe (northwards to Scotland and Lapland), Japan, Russia, Transcaucasus.
	1♀	Fujian	
	5♂	Guangdong	
	3♂1♀	Guangxi	
	5♂5♀	Guizhou	
	1♂2♀	Hubei	
	4♂2♀	Liaoning	
	2♂1♀	Ningxia	
	1♂3♀	Shanxi	
M. tenebricosa	13♂1♀	Gansu	China (Beijing, Gansu, Hebei, Heilongjiang, Jilin, Liaoning, Nei Mongolia, Ningxia, Qinghai, Shanxi), Europe, Israel, Middle East, Mongolia, Russia, Transcaucasus.
	2♂	Hebei	
	6♂	Heilongjiang	
	2♂	Jilin	
	52♂3♀	Liaoning	
	1♂	Nei Mongolia	
	7♂1♀	Ningxia	
	13♂	Qinghai	
M. viridana	5♂1♀	Liaoning	China **(**Liaoning, Nei Mongolia, Zhejiang), Europe (Austria, Britain, France, Germany, Hungary, Spain, Switzerland), Russia.

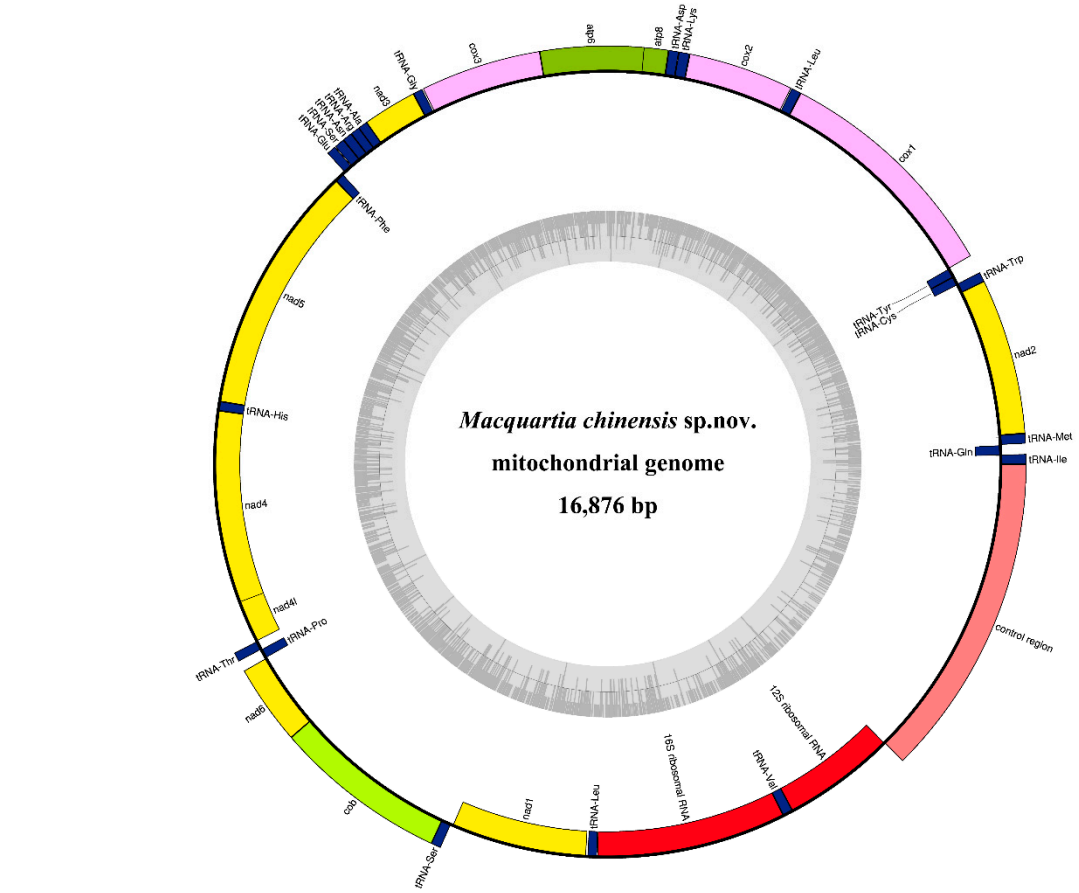
Table S2. Annotations for the four species of *Macquartia*.

Gene	Direction	Size (bp)	Start Codons	Stop Codons	Anticodon	Intergenic Nucleotides
trnI	F	66			GAT	
trnQ	R	69			TTG	-5
trnM	F	66-68			CAT	3-5
nad2	F	1017	ATT	TAA		0
trnW	F	66			TCA	-2
trnC	R	62-64			GCA	-8
trnY	R	64			GTA	0
cox1	F	1539	TCG	TAA		-2
trnL2	F	66			TAA	-5
cox2	F	688	ATG	T		4
trnK	F	71			CTT	0
trnD	F	65-66			GTC	-1-0
atp8	F	162	ATT	TAA		0
atp6	F	678	ATG	TAA		-7
cox3	F	789	ATG	TAA		-1
trnG	F	63			TCC	6
nad3	F	354	ATC	TAG		0
trnA	F	64			TGC	-2
trnR	F	62-63			TCG	-1
trnN	F	64-65			GTT	0
trnS1	F	67-68			GCT	0
trnE	F	63-64			TTC	2-3
trnF	R	64-65			GAA	18
nad5	R	1735	ATT	T		0
trnH	R	63-64			GTG	0
nad4	R	1339	ATG	T		0
nad4l	R	294	ATG	TAA		-7
trnT	F	63			TGT	2
trnP	R	66			TGG	0
nad6	F	525	ATT	TAA		2
cob	F	1137	ATG	TAG		-1
trnS2	F	66-67			TGA	-2
nad1	R	939	ATA	TAA		15
trnL1	R	65			TAG	10
rrnL	R	1312-1316				2
trnV	R	71			TAC	0
rrnS	R	783-811				-1

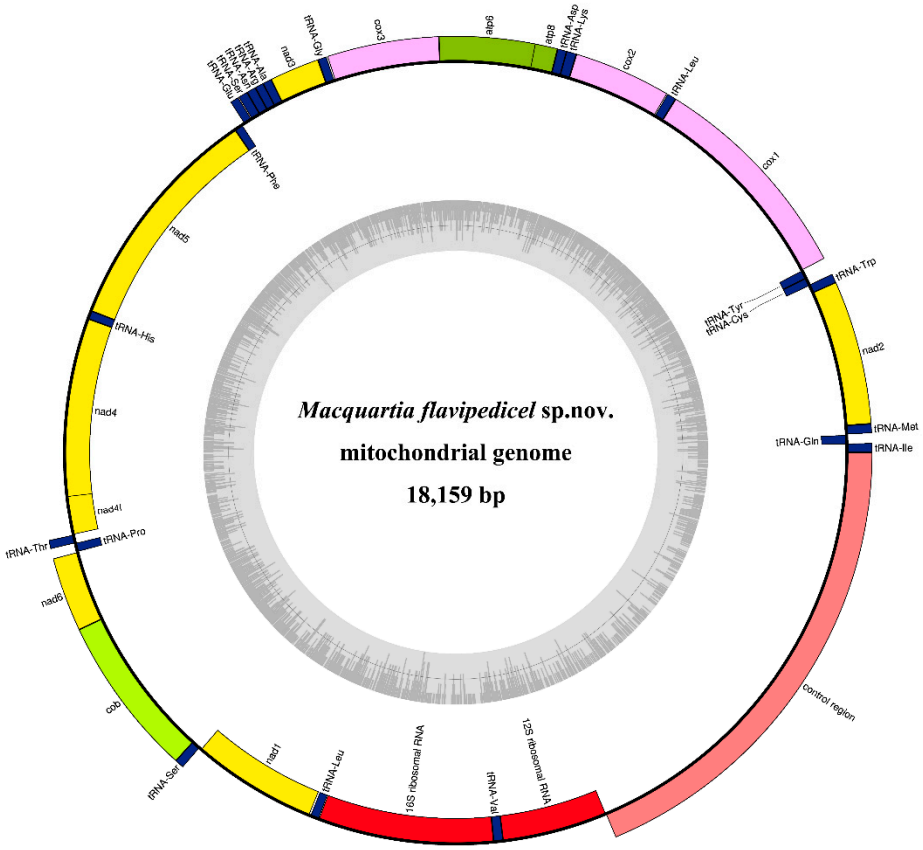
Table S3. Nucleotide composition features of the four species of *Macquartia*.

Species	Regions	T(U)	C	A	G	A+T(%)	G+C(%)	AT-Skew	GC-Skew
Macquartia	Whole genome	38.1	12.3	40.8	8.7	79.0	21.0	0.034	-0.170
brunneisquama	PCGs	44.0	11.5	32.8	11.7	76.8	23.2	-0.145	0.010
sp. nov.	1st codon	42.7	9.4	37.2	10.7	79.9	20.1	-0.070	0.061
	2nd codon	43.5	12.7	29.9	13.8	73.4	26.6	-0.185	0.041
	3rd codon	45.6	12.3	31.4	10.7	77.0	23.0	-0.185	-0.070
	tRNAs	38.9	9.6	38.7	12.8	77.6	22.4	-0.002	0.143
	rRNAs	42.4	6.4	39.2	12.0	81.6	18.4	-0.040	0.304
	Control region	42.4	6.3	45.5	5.8	87.9	12.1	0.035	-0.044
Macquartia	Whole genome	38.1	12.3	40.8	8.7	79.0	21.0	0.034	-0.170
chinensis	PCGs	44.0	11.4	32.7	11.8	76.7	23.3	-0.147	0.016
sp. nov.	1st codon	42.8	9.4	37.2	10.6	79.9	20.1	-0.070	0.061
	2nd codon	43.6	12.7	29.8	13.9	73.4	26.6	-0.187	0.044
	3rd codon	45.7	12.2	31.2	10.9	76.9	23.1	-0.189	-0.057
	tRNAs	39.0	9.5	38.7	12.8	77.7	22.3	-0.004	0.146
	rRNAs	42.8	6.3	39.1	11.9	81.9	18.1	-0.045	0.307
	Control region	40.5	6.2	47.8	5.5	88.4	11.6	0.082	-0.061
Macquartia	Whole genome	38.6	12.4	40.3	8.7	78.9	21.1	0.022	-0.177
flavifemorata	PCGs	44.0	11.3	32.8	11.8	76.8	23.2	-0.146	0.022
sp. nov.	1st codon	42.7	9.3	37.3	10.8	80.0	20.0	-0.068	0.074
	2nd codon	43.5	12.6	29.9	14.1	73.4	26.6	-0.186	0.056
	3rd codon	45.8	12.2	31.4	10.7	77.1	22.9	-0.187	-0.063
	tRNAs	38.8	10.4	38.8	11.9	77.6	22.4	0.000	0.068
	rRNAs	42.6	6.1	39.7	11.6	82.3	17.7	-0.035	0.312
	Control region	43.8	6.3	45.4	4.5	89.2	10.8	0.018	-0.174
Macquartia	Whole genome	38.1	12.5	41.0	8.3	79.1	20.9	0.037	-0.203
flavipedicel sp.	PCGs	43.6	12.0	32.6	11.9	76.2	23.8	-0.144	-0.003
nov.	1st codon	42.0	10.3	37.0	10.7	79.0	21.0	-0.064	0.020
	2nd codon	43.1	13.1	29.6	14.2	72.7	27.3	-0.185	0.041
	3rd codon	45.5	12.5	31.2	10.8	76.7	23.3	-0.187	-0.075
	tRNAs	38.3	10.0	38.6	13.2	76.9	23.1	0.005	0.139
	rRNAs	42.6	6.5	38.6	12.3	81.2	18.8	-0.050	0.310
	Control region	41.7	7.7	46.6	4.0	88.3	11.7	0.055	-0.322


Macquartia brunneisquama sp.nov.
mitochondrial genome
16,617 bp
cox3
atp6
tRNA-Asp
tRNA-Lys
cox2
tRNA-Leu
cox1
tRNA-Trp
nad2
tRNA-Met
tRNA-Ile
control region
12S ribosomal RNA
tRNA-Val
16S ribosomal RNA
tRNA-Leu
nad1
tRNA-Ser
cob
nad6
tRNA-Pro
tRNA-Thr
nad4l
nad4
tRNA-His
nad5
tRNA-Phe
tRNA-Glu
tRNA-Ser
tRNA-Arg
tRNA-Ala
nad3
tRNA-Gly
tRNA-Gln
tRNA-Cys
tRNA-Tyr
complex I (NADH dehydrogenase)
complex III (ubichinol cytochrome c reductase)
complex IV (cytochrome c oxidase)
ATP synthase
transfer RNAs
ribosomal RNAs
origin of replication



- complex I (NADH dehydrogenase)
- complex III (ubichinol cytochrome c reductase)
- complex IV (cytochrome c oxidase)
- ATP synthase
- transfer RNAs
- ribosomal RNAs
- origin of replication



complex I (NADH dehydrogenase)
complex III (ubichinol cytochrome c reductase)
complex IV (cytochrome c oxidase)
ATP synthase
transfer RNAs
ribosomal RNAs
origin of replication

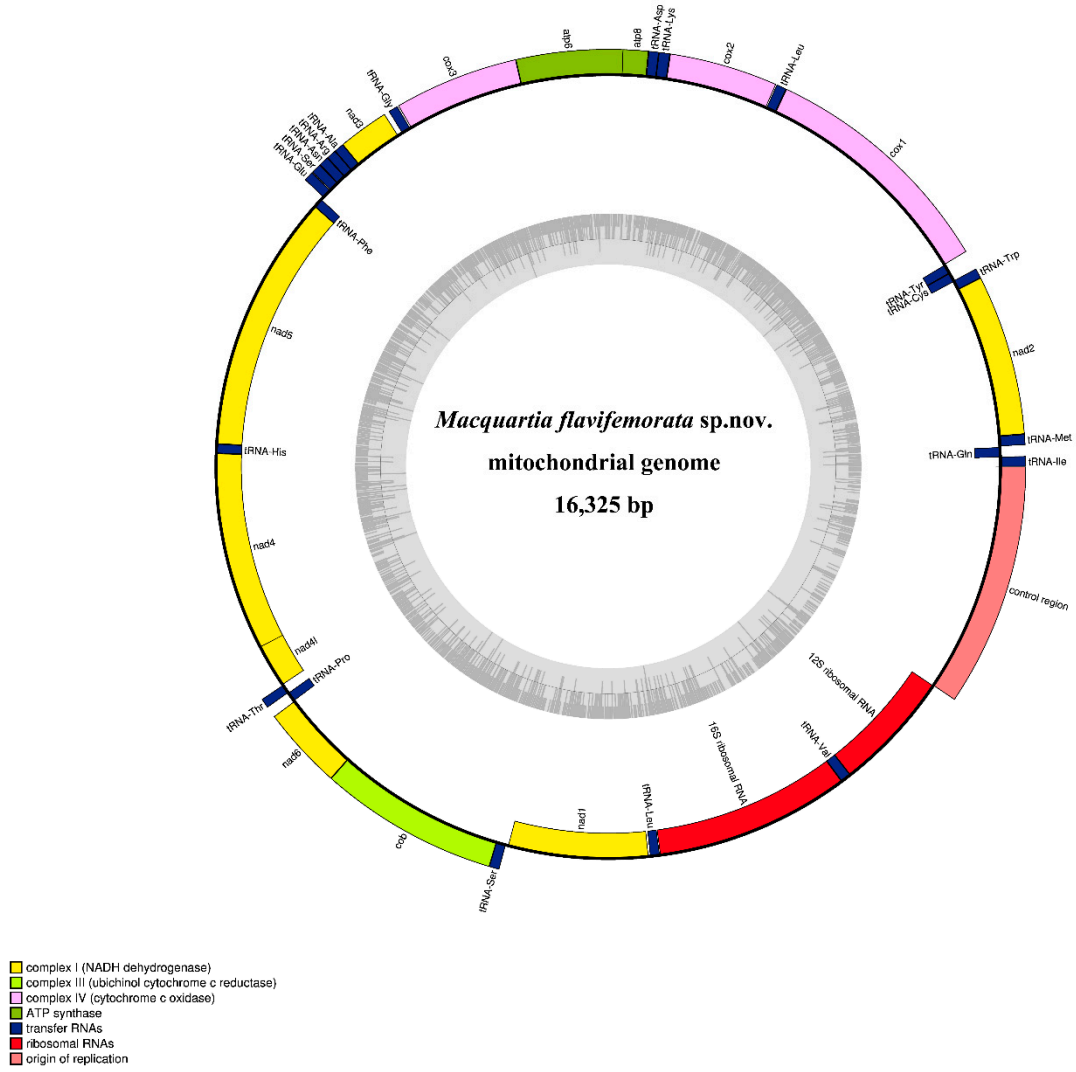


Figure S1. Circular maps of mitogenomes of four species in *Macquartia*.

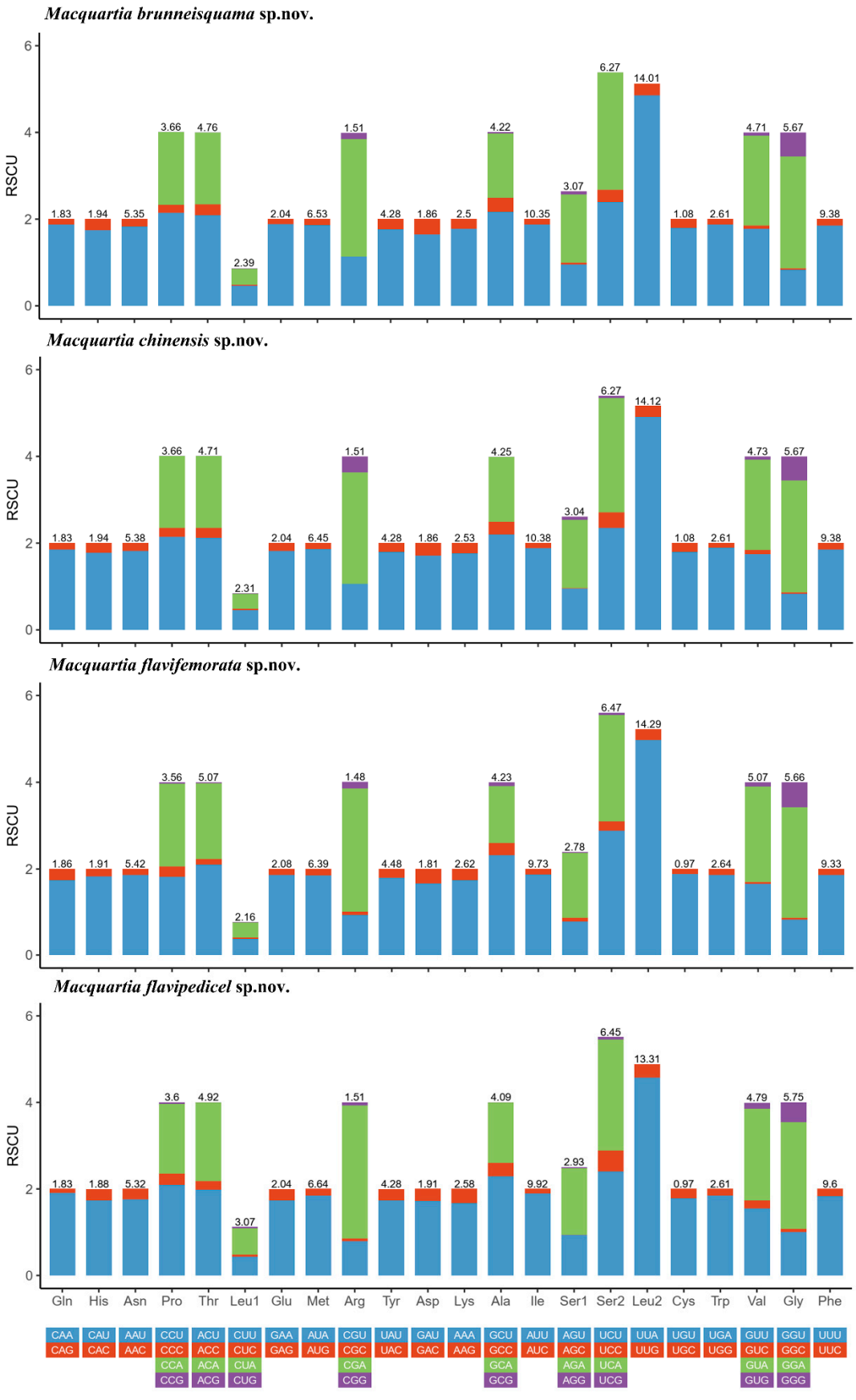
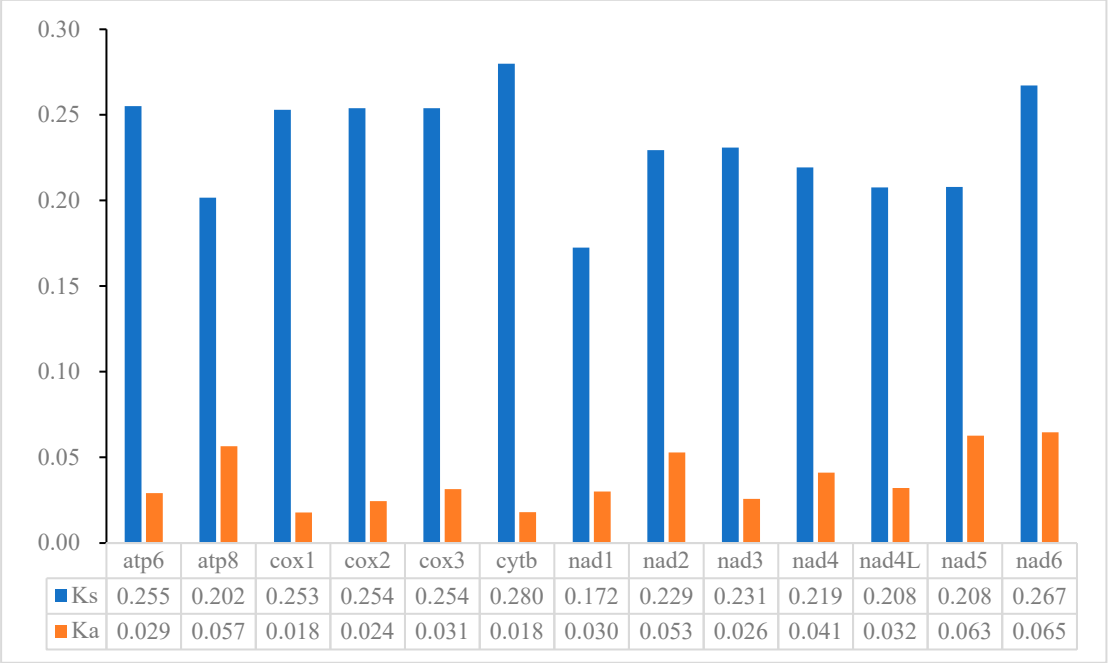


Figure S2. Relative synonymous codon usage (RSCU) in the mitogenomes of four *Macquartia* species.



	atp6	atp8	cox1	cox2	cox3	cytb	nad1	nad2	nad3	nad4	nad4L	nad5	nad6
Ks	0.255	0.202	0.253	0.254	0.254	0.280	0.172	0.229	0.231	0.219	0.208	0.208	0.267
Ka	0.029	0.057	0.018	0.024	0.031	0.018	0.030	0.053	0.026	0.041	0.032	0.063	0.065

Figure S3. Synonymous and non-synonymous substitutional rates of four *Macquartia* species for each PCG. Ks, synonymous substitutional rate; Ka, non-synonymous substitutional rate.