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Table S5. Nucleotide composition of mitogenomes of the eight *Parupeneus* species.

Table S1. Detailed information of collection and voucher numbers of specimens.

Family	Gene	Species	Voucher No.	Location	Accession No.	Source
Callionymidae	<i>Synchiropus</i>	<i>Synchiropus sycorax</i>	BGERL20191101	Seto Inland Sea of Hiroshima Prefecture, Japan	NC047299	Genbank
Callionymidae	<i>Synchiropus</i>	<i>Synchiropus splendidus</i>			NC024195	Genbank
Callionymidae	<i>Repomucenus</i>	<i>Repomucenus curvicornis</i>	NSMTP96286		NC018567	Genbank
Callionymidae	<i>Neosynchiropus</i>	<i>Neosynchiropus moyeri</i>			NC024193	Genbank
Callionymidae	<i>Foetorepus</i>	<i>Foetorepus altivelis</i>			AP006027	Genbank
Dactylopteridae	<i>Dactylopterus</i>	<i>Dactylopterus volitans</i>		East China Sea, China Xisha Islands, China Japan Zhanjiang, Guangdong, China Haikou, Hainan, China Sansha, Hainan, China Xisha Islands, China Guangdong, China East China Sea, China Zhanjiang, Guangdong, China Sansha, Hainan, China Haikou, Hainan, China	LC512458	Genbank
Dactylopteridae	<i>Dactyloptena</i>	<i>Dactyloptena tiltoni</i>			NC004402	Genbank
Dactylopteridae	<i>Dactyloptena</i>	<i>Dactyloptena peterseni</i>			NC003194	Genbank
Dactylopteridae	<i>Dactyloptena</i>	<i>Dactyloptena orientalis</i>			NC024189	Genbank
Dactylopteridae	<i>Callionymus</i>	<i>Callionymus olidus</i>			NC046750	Genbank
Dactylopteridae	<i>Callionymus</i>	<i>Callionymus enneactis</i>			NC024194	Genbank
Draconettidae	<i>Draconetta</i>	<i>Draconetta xenica</i>			NC024185	Genbank
Mullidae	<i>Upeneus</i>	<i>Upeneus tragula</i>			NC061030	Genbank
Mullidae	<i>Upeneus</i>	<i>Upeneus sulphureus</i>	S120		NC063690	Genbank
Mullidae	<i>Upeneus</i>	<i>Upeneus japonicus</i>	FIORBF02		NC063704	Genbank
Mullidae	<i>Parupeneus</i>	<i>Parupeneus multifasciatus</i>	GOU104145		OP718221	This study
Mullidae	<i>Parupeneus</i>	<i>Parupeneus multifasciatus</i>			NC024192	Genbank
Mullidae	<i>Parupeneus</i>	<i>Parupeneus indicus</i>	GOU100526		NC060686	Genbank
Mullidae	<i>Parupeneus</i>	<i>Parupeneus heptacanthus</i>	MuHK005		OL890693	This study
Mullidae	<i>Parupeneus</i>	<i>Parupeneus cyclostomus</i>	MuSS001		OP718223	This study
Mullidae	<i>Parupeneus</i>	<i>Parupeneus crassilabris</i>	MuXS010		OP718225	This study
Mullidae	<i>Parupeneus</i>	<i>Parupeneus chrysopleuron</i>	GOU101720		OP718219	This study
Mullidae	<i>Parupeneus</i>	<i>Parupeneus chrysopleuron</i>			NC029247	Genbank
Mullidae	<i>Parupeneus</i>	<i>Parupeneus biaculeatus</i>	GOU104532		OP718222	This study
Mullidae	<i>Parupeneus</i>	<i>Parupeneus barberinus</i>	MuSS002		OP718224	This study
Mullidae	<i>Parupeneus</i>	<i>Parupeneus barberinoides</i>	GOU102093		OP718220	This study
Mullidae	<i>Mullus</i>	<i>Mullus surmuletus</i>	DM358	China	NC052759	Genbank
Mullidae	<i>Mulloidichthys</i>	<i>Mulloidichthys vanicolensis</i>			NC024188	GenBank
Pegasidae	<i>Pegasus</i>	<i>Pegasus volitans</i>			NC010271	Genbank
Pegasidae	<i>Eurypegasus</i>	<i>Eurypegasus draconis</i>			NC010264	Genbank
Syngnathidae	<i>Syngnathus</i>	<i>Syngnathus pelagicus</i>		China	NC065498	Genbank
Syngnathidae	<i>Hippocampus</i>	<i>Hippocampus kuda</i>			NC010272	Genbank
Syngnathidae	<i>Hippocampus</i>	<i>Hippocampus abdominalis</i>			NC028181	Genbank

Table S2. Best-fit model selections of ML and BI in all datasets

Model	Method	
	ML	BI
TIM2+F+R4	ATP6_C1+ATP6_C3+ATP8_C1+ATP8_C2+ND4_C1+ND5_C1+ND5_C2+12S rRNA+16S rRNA	
TIM3+F+R4	ATP6_C2+ATP8_C3+COI_C3+COII_C3+COIII_C3+cytb_C3+ND1_C3+ND2_C3+ND3_C3+ND4L_C3+ND5_C3	
SYM+R3	COI_C1+COII_C1+COII_C2+COIII_C1+cytb_C1+ND1_C1+ND3_C1+ND4L_C1+22 tRNAs	
TVM+F+R3	COI_C2+COIII_C2+cytb_C2+ND1_C2+ND3_C2+ND4L_C2	
TIM3+F+I+G4	ND2_C1+ND2_C2	
TN+F+I+G4	ND4_C2+ND4_C3	
TIM+F+I+G4	ND6_C1+ND6_C2+ND6_C3	
GTR+F+I+G4		ATP6_C1+COI_C2+COII_C2+COIII_C2+cytb_C2+ND1_C2+ND3_C2+ND4L_C2+ATP6_C2+ATP8_C3+COI_C3+COII_C3+COIII_C3+cytb_C3+ND1_C3+ND2_C3+ND3_C3+ND4L_C3+ND5_C3+ATP6_C3+ATP8_C1+ATP8_C2+ND5_C1+ND5_C2+12S rRNA+16S rRNA+ ND2_C1+ND2_C2+ ND6_C1+ND6_C2+ND6_C3
SYM+I+G4		COI_C1+COII_C1+COIII_C1+cytb_C1+ND1_C1+ND3_C1+ND4L_C1+ND4_C1+22 tRNAs
HKY+F+I+G4		ND4_C2+ND4_C3

C1: first codon position; C2: second codon position; C3: third codon position

Table S3. Features of the complete mitogenomes of *P. barberinoides*, *P. multifasciatus*, *P. biaculeatus*, *P. heptacanthus*, *P. cyclostomus*, *P. barberinus*, *P. crassilabris*.

Gene	Position		Size	Intergenic nucleotides	Codon		Anti-Codon	Strand
	From	To			Start	Stop		
tRNA-Phe	1/1/1/1/1/1	68/68/69/69/72/69/68	68/68/69/69/72/69/68	0/0/0/0/0/0			GAA	H
12S rRNA	69/69/70/70/73/70/69	1028/1023/1023/1023/1029/1024/1022	960/955/954/954/957/955/954	0/0/0/0/0/0				H
tRNA-Val	1029/1027/1026/1025/1030/1025/1024	1100/1098/1097/1096/1101/1096/1095	72/72/72/72/72/72/72	0/3/2/1/0/0/1			TAC	H
16S rRNA	1124/1122/1121/1120/1125/1121/1119	2795/2797/2789/2787/2790/2789/2790	1672/1676/1669/1668/1666/1669/1672	23/23/23/23/23/24/23				H
tRNA-Leu	2796/2798/2790/2788/2791/2790/2791	2869/2871/2863/2861/2864/2863/2864	74/74/74/74/74/74/74	0/0/0/0/0/0/0			TAA	H
ND1	2870/2872/2864/2862/2865/2864/2865	3844/3846/3838/3836/3839/3838/3839	975/975/975/975/975/975/975	0/0/0/0/0/0/0	ATG/ATG/ATG/ATG/ATG/ATG/ATG	TAG/TAA/TAG/TAG/TAG/TAA/TAG		H
tRNA-Ile	3849/3851/3843/3841/3844/3843/3845	3919/3922/3913/3911/3914/3913/3916	71/72/71/71/71/71/72	4/4/4/4/4/4/5			GAT	H
tRNA-Gln	3920/3924/3915/3913/3916/3914/3918	3989/3994/3985/3983/3986/3984/3988	70/71/71/71/71/71/71	0/1/1/1/1/0/1			TTG	L
tRNA-Met	3989/3994/3985/3983/3986/3984/3988	4059/4064/4055/4053/4056/4054/4058	71/71/71/71/71/71/71	-1/-1/-1/-1/-1/-1/-1			CAT	H
ND2	4064/4066/4057/4055/4058/4056/4060	5115/5112/5103/5101/5104/5102/5106	1052/1047/1047/1047/1047/1047/1047	4/1/1/1/1/1/1	ATG/GTG/GTG/ATG/GTG/GTG/GTG	TA/TAA/TAA/TAA/TAA/TAA/TAA		H
tRNA-Trp	5116/5112/5103/5101/5104/5102/5106	5186/5182/5173/5171/5174/5172/5176	71/71/71/71/71/71/71	0/-1/-1/-1/-1/-1/-1			TCA	H
tRNA-Ala	5188/5183/5174/5172/5175/5173/5177	5256/5251/5242/5240/5243/5241/5245	69/69/69/69/69/69/69	1/0/0/0/0/0/0			TGC	L
tRNA-Asn	5258/5253/5244/5242/5245/5243/5247	5330/5325/5316/5314/5317/5315/5319	73/73/73/73/73/73/73	1/1/1/1/1/1/1			GTT	L
OL	5334/5329/5320/5318/5321/5319/5323	5363/5359/5349/5347/5351/5347/5352	30/31/30/30/31/29/30	3/3/3/3/3/3/3				L
tRNA-Cys	5363/5359/5349/5347/5351/5347/5352	5429/5424/5415/5413/5417/5413/5418	67/66/67/67/67/67/67	-1/33/32/-1/33/31/32			GCA	L
tRNA-Tyr	5430/5434/5415/5414/5418/5414/5419	5499/5503/5484/5483/5487/5483/5488	70/70/70/70/70/70/70	0/9/-1/0/0/0/0			GTA	L
COI	5492/5505/5486/5485/5489/5485/5490	7051/7055/7036/7041/7066/7035/7040	1560/1551/1551/1557/1578/1551/1551	-8/1/1/1/1/1/1	ATC/GTG/GTG/GTG/GTG/GTG/GTG	TAA/TAA/TAG/TAA/TAA/TAG/TAA		H
tRNA-Ser	7070/7076/7058/7062/7068/7056/7061	7140/7146/7128/7132/7138/7126/7131	71/71/71/71/71/71/71	18/20/21/20/1/20/20			TGA	L
tRNA-Asp	7143/7149/7138/7135/7158/7129/7134	7215/7221/7210/7207/7231/7201/7206	73/73/73/73/74/73/73	2/2/9/2/19/2/2			GTC	H
COII	7217/7229/7218/7215/7234/7209/7214	7907/7919/7905/7907/7917/7899/7904	691/691/688/693/684/691/691	1/7/7/2/7/7	ATG/ATG/ATG/ATG/ATG/ATG/ATG	T/T/T/TAA/TAG/T/T		H
tRNA-Lys	7908/7920/7909/8077/7993/7900/7905	7981/7993/7982/8150/8066/7973/7978	74/74/74/74/74/74/74	0/0/3/169/75/0/0			TTT	H
ATP8	7984/7995/7984/8152/8070/7975/7980	8151/8162/8151/8319/8258/8142/8147	168/168/168/168/189/168/168	2/1/1/1/3/1/1	ATG/ATG/ATG/ATG/ATG/ATG/ATG	TAG/TAG/TAG/TAG/TAA/TAG/TAG		H
ATP6	8142/8180/8142/8310/8228/8133/8138	8824/8836/8825/8993/8911/8816/8821	689/684/684/684/684/684/684	-10/17/-10/-10/-31/-10/-10	ATC/ATA/ATG/GTG/ATG/ATG/ATG	TA/TAA/TAA/TAA/TAA/TAA/TAA		H
COIII	8825/8836/8825/8993/8911/8816/8821	9610/9621/9610/9778/9696/9601/9606	786/786/786/786/786/786/786	0/-1/-1/-1/-1/-1/-1	ATG/ATG/ATG/ATG/ATG/ATG/ATG	TAA/TAA/TAA/TAA/TAA/TAA/TAA		H
tRNA-Gly	9610/9621/9610/9778/9696/9601/9606	9680/9691/9680/9847/9766/9671/9676	71/71/71/70/71/71/71	-1/-1/-1/-1/-1/-1/-1			TCC	H
ND3	9681/9692/9681/9848/9767/9672/9677	10031/10042/10031/10198/10117/10022/10027	351/351/351/351/351/351/351	0/0/0/0/0/0/0	ATG/ATG/ATG/ATG/ATG/ATG/ATG	TAA/TAA/TAA/TAA/TAA/TAA/TAA		H

Gene	Position		Size	Intergenic nucleotides	Codon		Anti-Codon	Strand
	From	To			Start	Stop		
tRNA-Arg	10031/10042/10031/10119/10022/10027	10099/10110/10099/10266/10188/10090/10095	69/69/69/69/70/69/69	-1/-1/-1/-1/-1/-1			TCG	H
ND4L	10100/10111/10100/10268/10189/10091/10096	10396/10407/10396/10564/10485/10387/10392	297/297/297/297/297/297/297	0/0/0/1/0/0/0	ATG/ATG/ATG/ATG/ATG/ATG/ATG	TAA/TAA/TAA/TAA/TAA/TAA/TAA		H
ND4	10390/10401/10390/10558/10479/10381/10386	11769/11781/11770/11938/11859/11761/11766	1380/1381/1381/1381/1381/1381/1381	-7/-7/-7/-7/-7/-7/-7	ATG/GTG/ATG/ATG/ATG/ATG/ATG	AGA/T/T/T/T/T/T		H
tRNA-His	11771/11782/11771/11939/11860/11762/11767	11840/11851/11841/12008/11932/11831/11836	70/70/71/70/73/70/70	1/0/0/0/0/0/0			GTG	H
tRNA-Ser	11841/11852/11842/12009/11933/11832/11837	11908/11919/11909/12076/12000/11899/11904	68/68/68/68/68/68/68	0/0/0/0/0/0/0			GCT	H
tRNA-Leu	11913/11923/11913/12080/12004/11903/11908	11985/11995/11985/12152/12076/11975/11980	73/73/73/73/73/73/73	4/3/3/3/3/3/3			TAG	H
ND5	11986/11996/11986/12153/12079/11976/11981	13824/13834/13824/13991/13923/13814/13819	1839/1839/1839/1839/1845/1839/1839	0/0/0/0/2/0/0	ATG/ATG/ATG/ATG/ATG/ATG/ATG	TAG/TAA/TAA/TAA/TAA/TAA/TAA		H
ND6	13821/13831/13821/13988/13920/13811/13816	14342/14352/14342/14509/14441/14332/14337	522/522/522/522/522/522/522	-4/-4/-4/-4/-4/-4/-4	ATG/ATG/ATG/ATG/ATG/ATG/ATG	TAG/TAG/TAG/TAG/TAG/TAG/TAG		L
tRNA-Glu	14343/14353/14343/14510/14442/14333/14338	14411/14421/14411/14578/14510/14401/14406	69/69/69/69/69/69/69	0/0/0/0/0/0/0			TTC	L
Cytb	14417/14426/14416/14584/14558/14406/14411	15557/15566/15556/15724/15698/15546/15551	1141/1141/1141/1141/1141/1141/1141	5/4/4/5/47/4/4	ATG/ATG/ATG/ATG/ATG/ATG/ATG	T/T/T/T/T/T/T		H
tRNA-Thr	15558/15567/15557/15725/15699/15547/15552	15629/15638/15628/15796/15770/15618/15623	72/72/72/72/72/72/72	0/0/0/0/0/0/0			TGT	H
tRNA-Pro	15629/15638/15628/15796/15770/15618/15623	15698/15708/15698/15865/15839/15687/15693	70/71/71/70/70/70/71	-1/-1/-1/-1/-1/-1/-1			TGG	L
D-Loop	15699/15709/15699/15866/15840/15688/15694	16530/16537/16536/16707/16721/16518/16529	832/829/838/842/882/831/836	0/0/0/0/0/0/0				H

Table S4. Features of the complete mitogenomes of *Parupeneus chrysopleuron*.

Gene	Position		Size	Intergenic nucleotides	Codon		Anti-Codon	Strand
	From	To			Start	Stop		
tRNA- <i>Phe</i>	1	69	69	0			GAA	H
12S rRNA	70	1021	952	0				H
tRNA- <i>Val</i>	1022	1093	72	0			UAC	H
16S rRNA	1116	2780	1665	22				H
tRNA- <i>Leu</i>	2781	2854	74	0			UAA	H
<i>ND1</i>	2855	3829	975	0	ATG	TAA		H
tRNA- <i>Met</i>	3949	4019	71	119			CAU	H
<i>ND2</i>	4021	5067	1047	1	ATG	TAA		H
tRNA- <i>Trp</i>	5067	5137	71	-1			UCA	H
tRNA- <i>Ala</i>	5138	5206	69	0			UGC	L
tRNA- <i>Asn</i>	5207	5279	73	0			GUU	L
OL	5283	5312	30	3				L
tRNA- <i>Cys</i>	5313	5379	67	0			GCA	L
tRNA- <i>Tyr</i>	5380	5449	70	0			GUA	L
<i>COI</i>	5451	7001	1551	1	GTG	TAA		H
tRNA- <i>Ser</i>	7022	7092	71	20			UGA	L
tRNA- <i>Asp</i>	7095	7167	73	2			GUC	H
<i>COII</i>	7174	7864	691	6	ATG	T		H
tRNA- <i>Lys</i>	7865	7938	74	0			UUU	H
<i>ATP8</i>	7940	8107	168	1	ATG	TAG		H
<i>ATP6</i>	8092	8781	690	-16	ATG	TAA		H
<i>COIII</i>	8781	9566	786	-1	ATG	TAA		H
tRNA- <i>Gly</i>	9566	9636	71	-1			UCC	H
<i>ND3</i>	9637	9987	351	0	ATG	TAA		H
tRNA- <i>Arg</i>	9987	10055	69	-1			UCG	H
<i>ND4L</i>	10056	10352	297	0	ATG	TAA		H
<i>ND4</i>	10346	11726	1381	-7	ATG	T		H
tRNA- <i>His</i>	11727	11796	70	0			GUG	H
tRNA- <i>Ser</i>	11797	11864	68	0			GCU	H
tRNA- <i>Leu</i>	11868	11940	73	3			UAG	H
<i>ND5</i>	11941	13779	1839	0	ATG	TAA		H
<i>ND6</i>	13772	14293	522	-8	ATG	TAG		L
tRNA- <i>Glu</i>	14294	14362	69	0			UUC	L
<i>Cytb</i>	14368	15508	1141	5	ATG	T		H
tRNA- <i>Thr</i>	15509	15579	71	0			UGU	H
tRNA- <i>Pro</i>	15579	15648	70	-1			UGG	L
D-Loop	15649	16465	817	0				H
tRNA- <i>Gln</i>	16466	16536	71	0			UUG	L
tRNA- <i>Ile</i>	16871	16940	70	334			GAU	H

Table S5. Nucleotide composition of mitogenomes of the eight *Parupeneus* species.

Species	Regions	Size (bp)	T	C	A	G	AT(%)	GC(%)	AT skew	GC skew
<i>Parupeneus chrysopleuron</i>	Full genome	17402	25.1	30.2	26	18.7	51.1	48.9	0.017	-0.234
	PCGs	11436	26.4	32	24.1	17.4	50.5	49.4	-0.046	-0.296
	tRNAs	1627	24.2	25.3	28.7	21.7	52.9	47	0.085	-0.077
	rRNAs	2617	19.8	26.5	31	22.7	50.8	49.2	0.22	-0.077
	1st codon position	3812	19.3	29.4	25.4	25.9	44.7	55.3	0.136	-0.063
	2nd codon position	3812	38.9	27.9	19.5	13.7	58.4	41.6	-0.332	-0.341
	3rd codon position	3812	21.2	38.6	27.5	12.7	48.7	51.3	0.129	-0.505
	CR	817	28	25.8	28.9	17.3	56.9	43.1	0.016	-0.197
<i>Parupeneus barberinoides</i>	Full genome	16581	24.7	30.8	26	18.4	50.7	49.2	0.025	-0.251
	PCGs	11436	25.5	33.3	24	17.3	49.5	50.6	-0.03	-0.316
	tRNAs	1556	24.4	25.2	29.1	21.4	53.5	46.6	0.088	-0.082
	rRNAs	2632	20.6	25.8	31.1	22.5	51.7	48.3	0.203	-0.068
	1st codon position	3812	19.3	29.1	25.3	26.5	44.6	55.6	0.135	-0.047
	2nd codon position	3812	38.7	28.2	19.3	13.8	58	42	-0.334	-0.343
	3rd codon position	3812	18.2	42.7	27.3	11.9	45.5	54.6	0.2	-0.564
	CR	882	29.4	22.4	32.8	15.4	62.2	37.8	0.055	-0.185
<i>Parupeneus multifasciatus</i>	Full genome	16607	25	30.3	26.4	18.3	51.4	48.6	0.027	-0.247
	PCGs	11205	25.6	32.7	24.7	17.1	50.3	49.8	-0.018	-0.313
	tRNAs	1558	24.5	24.9	29.4	21.2	53.9	46.1	0.091	-0.08
	rRNAs	2631	20.8	25.8	30.7	22.8	51.5	48.6	0.192	-0.062
	1st codon position	3735	19	29.3	25.8	25.8	44.8	55.1	0.152	-0.064
	2nd codon position	3735	38.7	27.8	19.7	13.7	58.4	41.5	-0.325	-0.34
	3rd codon position	3735	18.8	40.8	28.6	11.7	47.4	52.5	0.207	-0.554
	CR	899	30.3	22.9	31	15.8	61.3	38.7	0.011	-0.183
<i>Parupeneus biaculeatus</i>	Full genome	16579	25.3	30	26.2	18.5	51.5	48.5	0.017	-0.239
	PCGs	11346	25.9	32.4	24.4	17.3	50.3	49.7	-0.03	-0.304
	tRNAs	1560	24.7	24.9	29.2	21.1	53.9	46	0.083	-0.083
	rRNAs	2623	21.3	25.2	30.6	22.8	51.9	48	0.179	-0.05
	1st codon position	3782	19	29.2	25.8	25.9	44.8	55.1	0.152	-0.06
	2nd codon position	3782	38.8	27.8	19.7	13.7	58.5	41.5	-0.326	-0.34
	3rd codon position	3782	19.6	40.1	27.9	12.5	47.5	52.6	0.175	-0.525
	CR	881	30.4	22.2	31.6	15.8	62	38	0.019	-0.168
<i>Parupeneus cyclostomus</i>	Full genome	16777	24.9	30.6	26.5	18	51.4	48.6	0.031	-0.258
	PCGs	11475	25.8	32.5	24.9	16.8	50.7	49.3	-0.018	-0.318
	tRNAs	1566	24.1	26.2	28.7	21.1	52.8	47.3	0.087	-0.108
	rRNAs	2623	19.9	26.4	30.6	23.1	50.5	49.5	0.212	-0.067
	1st codon position	3825	19.5	29	25.9	25.6	45.4	54.6	0.141	-0.062
	2nd codon position	3825	38.8	27.7	19.6	13.8	58.4	41.5	-0.329	-0.335
	3rd codon position	3825	18.9	40.9	29.2	11.1	48.1	52	0.214	-0.573
	CR	938	29.6	24	31.4	14.9	61	38.9	0.03	-0.234
<i>Parupeneus barberinus</i>	Full genome	16570	24.7	30.5	26.7	18.1	51.4	48.6	0.039	-0.255
	PCGs	11340	25.1	32.9	25.1	16.8	50.2	49.7	0	-0.324
	tRNAs	1558	24.7	25	29.2	21.2	53.9	46.2	0.083	-0.082
	rRNAs	2624	21	25.6	30.8	22.7	51.8	48.3	0.189	-0.06
	1st codon position	3780	18.6	29.4	25.9	26	44.5	55.4	0.164	-0.061
	2nd codon position	3780	38.9	27.8	19.8	13.4	58.7	41.2	-0.325	-0.35

Species	Regions	Size (bp)	T	C	A	G	AT(%)	GC(%)	AT skew	GC skew
	3rd codon position	3780	17.8	41.5	29.7	11	47.5	52.5	0.251	-0.581
	CR	883	29.8	22.9	31.7	15.6	61.5	38.5	0.031	-0.19
<i>Parupeneus crassilabris</i>	Full genome	16580	25	30.4	26.1	18.5	51.1	48.9	0.023	-0.243
	PCGs	11340	25.4	32.8	24.5	17.3	49.9	50.1	-0.018	-0.309
	tRNAs	1559	24.7	25	28.7	21.6	53.4	46.6	0.075	-0.073
	rRNAs	2626	20.7	26	30.5	22.8	51.2	48.8	0.191	-0.066
	1st codon position	3780	18.9	29.4	25.6	26	44.5	55.4	0.151	-0.061
	2nd codon position	3780	38.8	27.7	19.7	13.7	58.5	41.4	-0.326	-0.338
	3rd codon position	3780	18.5	41.1	28.2	12.2	46.7	53.3	0.208	-0.542
	CR	887	31.3	21.8	31.2	15.7	62.5	37.5	-0.002	-0.163
<i>Parupeneus heptacanthus</i>	Full genome	16749	24.1	31.5	26.1	18.4	50.2	49.9	0.039	-0.263
	PCGs	11439	24.5	34.1	24.3	17.2	48.8	51.3	-0.004	-0.329
	tRNAs	1557	24	25.5	28.7	21.9	52.7	47.4	0.089	-0.076
	rRNAs	2622	19.8	26.5	31	22.7	50.8	49.2	0.22	-0.077
	1st codon position	3813	18.8	29.8	25.5	25.9	44.3	55.7	0.151	-0.07
	2nd codon position	3813	38.7	28.2	19.2	13.8	57.9	42	-0.337	-0.343
	3rd codon position	3813	15.9	44.2	28.1	11.7	44	55.9	0.277	-0.581
	CR	884	31.6	22.2	30.7	15.6	62.3	37.8	-0.014	-0.175