Table S3. The base composition of 13 PCGs in ten mitogenomes.

Species	Region	whole genome	PCGs		tRNA		rRNA
	Strand	Heavy	Heavy	Light	Heavy	Light	Light
Allopsontus tibetensis	length(bp)	15437	6888	4305	946	537	2123
	AT%	70	66.8	70.2	74.4	71.9	74.2
	AT-skew	0.031	-0.102	-0.233	0.031	0.01	-0.048
	GC-skew	-0.222	-0.198	0.254	-0.008	0.338	0.296
Allopsontus sp.	length(bp)	15511	6885	4323	935	540	2121
	AT%	67	63.7	68.3	70.1	69.3	69.4
	AT-skew	0.059	-0.067	-0.252	0.047	-0.011	-0.075
	GC-skew	-0.222	-0.195	0.257	-0.05	0.301	0.311
Pedetontus elegans	length(bp)	15612	6891	4335	946	548	2154
	AT%	74.9	71.6	77.2	77.6	73.9	76.6
	AT-skew	0.036	-0.072	-0.208	0.03	0.032	-0.044
	GC-skew	-0.209	-0.165	0.275	0	0.245	0.324
Machilontus medogensis	length(bp)	15625	6852	4317	947	549	2183
	AT%	70	66.4	70.8	71.4	72.1	74.3
	AT-skew	0.09	-0.029	-0.274	0.056	-0.071	-0.139
	GC-skew	-0.217	-0.153	0.305	-0.041	0.412	0.346
Pedetontus xanthospilus	length(bp)	15707	6906	4329	953	557	2210
	AT%	70.4	66.7	72.7	74	69.5	73.4
	AT-skew	0.05	-0.062	-0.25	0.035	0.034	-0.03
	GC-skew	-0.207	-0.162	0.277	-0.016	0.212	0.299
Pedetontus jinxiuensis	length(bp)	15720	6903	4329	957	550	2221
	AT%	69.4	65.9	70.6	73.3	68	73.3
	AT-skew	0.043	-0.068	-0.238	0.028	0	-0.029
	GC-skew	-0.179	-0.146	0.227	-0.02	0.227	0.269
Pedetontus hezhouensis	length(bp)	15751	6906	4323	956	557	2235
	AT%	69.6	66.1	71.1	74.3	67.5	72.4
	AT-skew	0.052	-0.06	-0.263	0.02	0.021	-0.032
	GC-skew	-0.215	-0.169	0.279	-0.008	0.282	0.335
Pedetontus nanningensis	length(bp)	15789	6885	4326	942	563	2116
	AT%	72.2	69.3	73.5	74.3	71.2	74.6
	AT-skew	0.061	-0.045	-0.269	0.02	0.002	-0.013
	GC-skew	-0.215	-0.157	0.317	0	0.247	0.285
Pedetontus shenzhenensis	length(bp)	15814	6903	4329	964	575	2272
	AT%	72.8	69.9	74	74.8	73.2	75.1
	AT-skew	0.047	-0.056	-0.265	0.029	0.05	0.015
	GC-skew	-0.224	-0.165	0.327	0.021	0.299	0.32
Pedetontus sp.	length(bp)	15827	6906	4329	961	574	2281
	AT%	71.2	68.3	72.8	73.5	68.5	73.2
	AT-skew	0.053	-0.072	-0.272	0.045	-0.028	-0.022
	GC-skew	-0.245	-0.197	0.315	-0.027	0.359	0.346