Table S2. Mitogenomic organization of *Melanoleuca luteamacula* sp. nov.

Start	End	Length	Strand	Gene
1	68	68	+	trnM-CAU
69	132	64	+	trnI-GAU
130	198	69	-	trnQ-UUG
260	1273	1014	+	ND2
1275	1341	67	+	trnW-UCA
1334	1401	68	-	trnC-GCA
1432	1497	66	-	trnY-GUA
1502	3032	1531	+	COX1
3032	3100	69	+	trnL-UAA
3100	3781	682	+	COX2
3781	3853	73	+	trnK-CUU
3852	3918	67	+	trnD-GUC
3919	4080	162	+	ATP8
4074	4748	675	+	ATP6
4748	5536	789	+	COX3
5538	5606	69	+	trnG-UCC
5606	5959	354	+	ND3
6040	6107	68	+	trnA-UGC
6115	6179	65	+	trnR-UCG
6179	6243	65	+	trnN-GUU
6244	6311	68	+	trnS-GCU
6310	6378	69	+	trnE-UUC
6375	6444	70	-	trnF-GAA
6427	8184	1758	-	ND5
8184	8252	69	-	trnH-GUG
8261	9599	1339	-	ND4
9631	9924	294	-	ND4L
9926	9995	70	+	trnT-UGU
9993	10060	68	-	trnP-UGG
10062	10598	537	+	ND6
10611	11759	1149	+	CYTB
11758	11823	66	+	trnS-UGA
11839	12777	939	-	ND1
12779	12852	74	-	trnL-UAG
12853	14228	1376	-	rrn16
14229	14294	66	-	trnV-UAC
14295	15109	815	-	rrn12
15110	15443	334	+	control region