Table S1. Mitogenomic organization of *Scintilla strigiferalis* (Hampson, 1900) comb. nov.

Start	End	Length	Strand	Gene
1	67	67	+	trnM-CAU
66	134	69	+	trnI-GAU
131	201	71	-	trnQ-UUG
250	1263	1014	+	ND2
1273	1341	69	+	trnW-UCA
1332	1400	69	-	trnC-GCA
1400	1467	68	-	trnY-GUA
1470	3005	1536	+	COX1
3000	3067	68	+	trnL-UAA
3068	3749	682	+	COX2
3749	3821	73	+	trnK-CUU
3824	3891	68	+	trnD-GUC
3892	4049	158	+	ATP8
4044	4712	669	+	ATP6
4712	5500	789	+	COX3
5502	5571	70	+	trnG-UCC
5571	5924	354	+	ND3
5950	6016	67	+	trnA-UGC
6015	6081	67	+	trnR-UCG
6080	6146	67	+	trnN-GUU
6148	6216	69	+	trnS-GCU
6235	6299	65	+	trnE-UUC
6298	6366	69	-	trnF-GAA
6349	8091	1743	-	ND5
8095	8159	65	-	trnH-GUG
8167	9505	1339	-	ND4
9505	9795	291	-	ND4L
9798	9865	68	+	trnT-UGU
9865	9931	67	-	trnP-UGG
9933	10466	534	+	ND6
10466	11617	1152	+	CYTB
11621	11687	67	+	trnS-UGA
11705	12643	939	-	ND1
12645	12712	68	-	trnL-UAG
12713	14107	1395	-	rrn16
14108	14175	68	-	trnV-UAC
14176	14991	816	-	rrn12
14992	15351	360	+	control region