

Table S1. Annotation of *Dicyrtomina saundersi* mitogenome. Nucleotide composition is calculated on the coding strand; spacers and overlaps (positive and negative numbers, respectively) are calculated with respect to the following gene.

Gene	A%	C%	G%	T%	Length (bp)	Strand	Position	Spacers/ overlaps	Star/Stop codons
<i>trnI</i>	30.3	9.1	19.7	40.9	66	J	1-66	4	
<i>trnQ</i>	39.7	5.9	14.7	39.7	68	N	138-71	6	
<i>trnM</i>	38.8	13.4	11.9	35.8	67	J	145-211	0	
<i>nad2</i>	33.2	17.5	11.1	38.2	994	J	212-1,205	0	ATG (Met) / T--
<i>trnW</i>	43.5	10.1	7.2	39.1	69	J	1,206-1,274	5	
<i>trnC</i>	31.7	15.0	16.7	36.7	60	N	1,339-1,280	-1	
<i>trnY</i>	35.8	9.4	17.0	37.7	52	N	1,391-1,339	8	
<i>cox1</i>	29.1	18.3	16.8	35.8	1,542	J	1,400-2,941	4	CTT (Leu) / TAA
<i>trnLuua</i>	40.4	12.3	15.8	31.6	57	J	2,946-3,002	-1	
<i>cox2</i>	32.9	17.9	14.2	34.9	684	J	3,002-3,685	0	ATA (Met) / TAA
<i>trnK</i>	35.7	20.0	14.3	30.0	70	J	3,686-3,755	0	
<i>trnD</i>	43.8	7.8	12.5	35.9	64	J	3,756-3,819	0	
<i>atp8</i>	40.9	15.7	12.6	30.8	162	J	3,820-3,981	-7	ATT (Ile) / TAA
<i>atp6</i>	32.6	16.7	12.5	38.2	680	J	3,975-4,654	0	ATG (Met) / TA-
<i>cox3</i>	30.0	16.3	16.3	37.4	789	J	4,655-5,443	3	ATG (Met) / TA-
<i>trnG</i>	38.7	12.9	11.3	37.1	62	J	5,447-5,508	0	
<i>nad3</i>	27.8	18.1	13.7	40.4	343	J	5,509-5,851	0	ATT (Ile) / T--
<i>trnA</i>	40.3	8.1	12.9	38.7	62	J	5,852-5,913	0	
<i>trnR</i>	33.9	19.4	14.5	32.3	62	J	5,914-5,975	7	
<i>trnN</i>	35.8	10.4	14.9	38.8	67	J	5,983-6,049	1	
<i>trnSgcu</i>	34.3	17.9	16.4	31.3	67	J	6,051-6,117	-2	
<i>trnE</i>	48.6	2.9	4.3	44.3	70	J	6,116-6,185	-1	
<i>trnF</i>	36.9	7.7	15.4	40.0	65	N	6,249-6,185	0	
<i>nad5</i>	26.3	13.2	15.0	45.5	1,685	N	7,934-6,250	0	ATT (Ile) / TA-
<i>trnH</i>	37.5	4.7	17.2	40.6	64	N	7,998-7,935	1	
<i>nad4</i>	22.3	12.8	16.4	48.6	1,335	N	9,334-8,000	0	ATG (Met) / TAA
<i>nad4L</i>	23.2	10.9	16.1	49.8	269	N	9,603-9,335	2	ATT (Ile) / TA-
<i>trnT</i>	49.2	6.2	7.7	36.9	65	J	9,606-9,670	0	
<i>trnP</i>	40.0	6.2	13.8	40.0	65	N	9,735-9,671	5	
<i>nad6</i>	35.1	16.8	10.6	37.5	455	J	9,741-10,195	0	ATA (Met) / TA-
<i>cob</i>	30.2	17.9	16.4	35.5	1,132	J	10,196-11,327	0	ATG (Met) / T--
<i>trnSuga</i>	33.8	11.3	15.5	39.4	71	J	11,328-11,398	1	
<i>nad1</i>	24.0	12.0	17.3	46.6	967	N	12,366-11,400	1	ATT (Ile) / T--
<i>trnLuag</i>	33.3	4.5	13.6	48.5	66	N	12,433-12,368	1	
<i>rrnL</i>	34.7	8.7	12.9	43.7	1,232	N	13,666-12,435	0	
<i>trnV</i>	37.7	7.2	11.6	43.5	69	N	13,735-13,667	0	
<i>rrnS</i>	42.8	13.8	9.5	33.9	747	N	14,482-13,736	0	
A+T-rich	40.0	8.2	11.2	40.7	563		14,483-15,045		
total	38.5	15.7	12.8	33.1	15,045				