

Table S16. Annotation of mitogenome of *Dentimodiolus subsulcatus*

Gene	Position	Strand direction	Codon (Start)	Codon (Stop)	Anticodon	Intergenic spacers
<i>cox1</i>	1–1,659	+	ATT	TAG		
<i>atp6</i>	1,669–2,394	+	ATG	TAG		9
<i>trnT</i>	2,395–2,461	+			TGT	
<i>nad4l</i>	2,462–2,743	+	GTG	TAA		
<i>nad5</i>	2,736–4,463	+	GTG	TAA		–8
<i>nad6</i>	4,467–4,931	+	ATG	TAA		3
<i>trnF</i>	4,931–5,000	+			GAA	–1
<i>rrnS</i>	5,008–5,951	+				7
<i>trnG</i>	5,951–6,016	+			TCC	–1
<i>trnN</i>	6,017–6,081	+			GTT	
<i>trnE</i>	6,082–6,145	+			TTC	
<i>trnC</i>	6,152–6,216	+			GCA	6
<i>trnI</i>	6,217–6,284	+			GAT	
<i>trnQ</i>	6,286–6,356	+			TTG	1
<i>trnD</i>	6,361–6,427	+			GTC	4
<i>rrnL</i>	6,428–7,676	+				
<i>trnY</i>	7,677–7,739	+			GTA	
<i>cytb</i>	7,743–9,068	+	ATT	TAA		3
<i>cox2</i>	9,089–9,820	+	ATG	TAA		20
<i>trnK</i>	9,819–9,884	+			TTT	–2
<i>trnM</i>	9,919–9,981	+			TAT	34
<i>trnL2</i>	9,990–10,054	+			TAA	8
<i>nad1</i>	10,479–11,396	+	ATA	TAA		424
<i>trnV</i>	11,417–11,480	+			TAC	20
<i>nad4</i>	11,481–12,788	+	ATG	TAA		
<i>cox3</i>	12,793–13,734	+	ATG	TAG		4
<i>trnS1</i>	13,750–13,820	+			TGA	15
<i>nad2</i>	13,886–14,833	+	ATG	TAA		65
<i>trnR</i>	14,846–14,902	+			TCG	12
<i>trnL1</i>	15,364–15,428	+			TAG	461
<i>trnW</i>	15,513–15,579	+			TCA	84
<i>trnA</i>	15,580–15,644	+			TGC	
<i>trnS2</i>	15,645–15,711	+			GCT	
<i>trnH</i>	15,712–15,774	+			GTG	
<i>trnP</i>	15,778–15,842	+			TGG	3
<i>nad3</i>	15,843–16,193	+	ATG	TAA		
<i>trnM</i>	16,215–16,278	+			TAT	21