

Table S8. Annotation of mitogenome of *Mytilisepta virgata*

Gene	Position	Strand direction	Codon (Start)	Codon (Stop)	Anticodon	Intergenic spacers
<i>cox3</i>	1–753	+	ATG	TAA		
<i>trnS2</i>	754–816	+			TGA	
<i>nad5</i>	823–2526	+	ATT	TAG		6
<i>nad6</i>	2,530–2,994	+	ATG	TAA		3
<i>trnI</i>	3,034–3,098	+			GAT	39
<i>trnT</i>	3,102–3,162	+			TGT	3
<i>cytb</i>	3,250–4,335	+	ATT	TAG		87
<i>cox2</i>	4,341–5,027	+	ATG	TAG		5
<i>trnR</i>	5,033–5,102	+			TCG	5
<i>atp8</i>	5,104–5,232	+	GTG	TAA		1
<i>atp6</i>	5,226–5,941	+	ATG	T--		–6
<i>trnS1</i>	5,942–6,008	+			TCT	
<i>cox1</i>	6,114–7,596	+	ATG	T--		105
<i>trnF</i>	7,597–7,663	+			GAA	
<i>rrnL</i>	7,664–8,815	+				
<i>trnY</i>	8,816–8,883	+			GTA	
<i>nad4l</i>	8,884–9,156	+	ATG	TAA		
<i>trnP</i>	9,157–9,222	+			TGG	
<i>trnE</i>	9,221–9,282	+			TTC	–2
<i>trnC</i>	9,282–9,345	+			GCA	–1
<i>nad3</i>	9,346–9,693	+	ATG	TAA		
<i>trnW</i>	9,699–9,763	+			TCA	5
<i>trnL2</i>	9,774–9,838	+			TAA	10
<i>trnK</i>	9,841–9,906	+			TTT	2
<i>trnL1</i>	9,907–9,972	+			TAG	
<i>trnG</i>	9,969–10,030	+			TCC	–3
<i>rrnS</i>	10,036–10,829	+				5
<i>trnQ</i>	10,833–10,900	+			TTG	3
<i>trnH</i>	10,901–10,961	+			GTG	
<i>trnN</i>	10,965–11,029	+			GTT	3
<i>trnM</i>	11,029–11,093	+			CAT	–1
<i>nad1</i>	11,109–12,036	+	ATG	T--		15
<i>trnD</i>	12,037–12,104	+			GTC	
<i>nad2</i>	12,166–13,146	+	ATT	TAA		61
<i>trnA</i>	13,152–13,218	+			TGC	5
<i>trnV</i>	13,218–13,280	+			TAC	–1
<i>nad4</i>	13,281–14,582	+	ATG	TAA		
<i>D-loop</i>	14,583–14,714	+				