

Table S11. Annotation of mitogenome of *Brachidontes* sp.

Gene	Position	Strand direction	Codon (Start)	Codon (Stop)	Anticodon	Intergenic spacers
<i>cox1</i>	1–1,605	+	ATG	TAG		
<i>nad2</i>	1,634–2,638	+	ATT	TAA		28
<i>trnI</i>	2,644–2,709	+			GAT	5
<i>trnF</i>	2,713–2,777	+			GAA	3
<i>rrnL</i>	2,807–3,964	+				29
<i>trnY</i>	3,982–4,045	+			GTA	17
<i>nad4l</i>	4,046–4,318	+	ATG	TAG		
<i>trnP</i>	4,325–4,388	+			TGG	6
<i>trnE</i>	4,389–4,454	+			TTC	
<i>trnC</i>	4,455–4,517	+			GCA	
<i>nad3</i>	4,518–4,868	+	ATG	TAA		
<i>trnM1</i>	4,869–4,931	+			TAT	
<i>trnW</i>	4,930–4,994	+			TCA	–2
<i>trnL1</i>	4,995–5,060	+			TAA	
<i>trnK</i>	5,061–5,127	+			TTT	
<i>trnL2</i>	5,130–5,193	+			TAG	2
<i>trnV</i>	5,195–5,259	+			TAC	1
<i>nad4</i>	5,260–6,555	+	ATG	TA-		
<i>trnA</i>	6,557–6,622	+			TGC	1
<i>trnR</i>	6,632–5,707	+			TCG	9
<i>trnM2</i>	6,711–6,782	+			CAT	3
<i>trnN</i>	6,783–6,846	+			GTT	
<i>cox3</i>	6,847–7,701	+	ATG	TAA		
<i>trnS2</i>	7,708–7,770	+			TGA	6
<i>nad5</i>	7,771–9,501	+	ATG	TAA		
<i>trnD</i>	9,841–9,908	+			GTC	139
<i>nad6</i>	10,008–10,493	+	ATG	TAA		99
<i>atp6</i>	11,539–12,278	+	ATG	TAA		33
<i>trnS1</i>	12,284–12,351	+			GCT	5
<i>nad1</i>	12,352–13,284	+	ATG	TAG		
<i>trnG</i>	12,384–13,349	+			TCC	–1
<i>rrnS</i>	13,360–13,897	+			TTG	10
<i>trnQ</i>	14,285–14,353	+				387
<i>cox2</i>	14,348–15,067	+	TTG	TAG		–5
<i>atp8</i>	15,087–15,227	+	GTG	TAG	TGT	19
<i>trnT</i>	15,233–15,303	+				5
<i>cytb</i>	15,306–16,460	+	GTG	TAA	GTG	2
<i>trnH</i>	16,473–16,540					12