

Table S13. Annotation of mitogenome of *Brachidontes variabilis*

Gene	Position	Strand direction	Codon (Start)	Codon (Stop)	Anticodon	Intergenic spacers
<i>atp6</i>	1–741	+	ATG	TAA		
<i>trnS1</i>	751–819	+			GCT	9
<i>nad1</i>	819–1,750	+	ATG	TA-		–1
<i>trnG</i>	1,751–1,816	+			TCC	
<i>rrnS</i>	1,824–2,724	+				7
<i>trnQ</i>	2,725–2,793	+			TTG	
<i>cox2</i>	2,836–3,504	+	ATG	TAA		42
<i>trnT</i>	3,678–3,747	+			TGT	173
<i>cytb</i>	3,752–4,906	+	ATG	TAA		4
<i>trnH</i>	4,972–5,035	+			GTG	65
<i>cox1</i>	5,036–6,640	+	ATG	TAG		
<i>nad2</i>	6,669–7,640	+	ATG	TAA		28
<i>trnI</i>	7,658–7,725	+			GAT	17
<i>trnF</i>	7,726–7,790	+			GAA	
<i>rrnL</i>	7,791–8,998	+				
<i>trnY</i>	8,999–9,063	+			GTA	
<i>nad4l</i>	9,082–9,336	+	ATG	TAG		18
<i>trnP</i>	9,345–9,410	+			TGG	8
<i>trnE</i>	9,409–9,472	+			TTC	–2
<i>trnC</i>	9,473–9,533	+			GCA	
<i>nad3</i>	9,534–9,883	+	ATG	TA-		
<i>trnM</i>	9,884–9,944	+			TAT	–2
<i>trnW</i>	9,943–10,007	+			TCA	
<i>trnL2</i>	10,008–10,074	+			TAA	
<i>trnK</i>	10,075–10,140	+			TTT	
<i>trnL1</i>	10,148–10,210	+			TAG	7
<i>trnV</i>	10,212–10,279	+			TAC	1
<i>nad4</i>	10,280–11,576	+	ATG	T--		
<i>trnA</i>	11,577–11,643	+			TGC	
<i>trnR</i>	11,645–11,709	+			TCG	1
<i>trnM</i>	11,724–11,796	+			CAT	14
<i>trnN</i>	12,037–12,099	+			GTT	240
<i>cox3</i>	12,100–12,957	+	ATG	TAA		
<i>trnS2</i>	13,006–13,068	+			TGA	48
<i>nad5</i>	13,480–15,177	+	ATG	TAA		411
<i>nad6</i>	15,235–15,702	+	ATG	TAA		57
<i>trnD</i>	15,726–15,794	+			GTC	23
<i>D-loop</i>	15,795–17,247	+				