

Table S12. Annotation of mitogenome of *Brachidontes mutabilis*

Gene	Position	Strand direction	Codon (Start)	Codon (Stop)	Anticodon	Intergenic spacers
<i>atp6</i>	1–738	+	ATG	TAG		
<i>trnS1</i>	753–822	+			GCT	14
<i>nad1</i>	822–1753	+	ATG	TA-		–1
<i>trnG</i>	1,754–1,819	+			TCC	
<i>rrnS</i>	1,827–2,737	+				7
<i>trnQ</i>	2,738–2,806	+			TTG	
<i>cox2</i>	2,820–3,518	+	TTG	TAA		13
<i>trnT</i>	3,672–3,743	+			TGT	153
<i>cytb</i>	3,746–4,897	+	ATG	TAA		2
<i>trnH</i>	4,912–4,978	+			GTG	32
<i>cox1</i>	4,979–6,583	+	ATG	TAG		
<i>nad2</i>	6,698–7,618	+	ATG	TAA		114
<i>trnI</i>	7,644–7,711	+			GAT	26
<i>trnF</i>	7,715–7,778	+			GAA	3
<i>rrnL</i>	7,825–9,031	+				46
<i>trnY</i>	9,032–9,096	+			GTA	
<i>nad4l</i>	9,097–9,369	+	ATG	TAA		
<i>trnP</i>	9,374–9,439	+			TGG	4
<i>trnE</i>	9,438–9,503	+			TTC	–2
<i>trnC</i>	9,504–9,566	+			GCA	
<i>nad3</i>	9,567–9,916	+	ATG	TA-		
<i>trnM</i>	9,917–9,978	+			TAT	
<i>trnW</i>	9,977–10,042	+			TCA	–2
<i>trnL2</i>	10,043–10,108	+			TAA	
<i>trnK</i>	10,109–10,175	+			TTT	
<i>trnL1</i>	10,178–10,241	+			TAG	2
<i>trnV</i>	10,242–10,307	+			TAC	
<i>nad4</i>	10,308–11,604	+	ATG	T--		
<i>trnA</i>	11,605–11,672	+			TGC	
<i>trnR</i>	11,691–11,755	+			TCG	18
<i>trnM</i>	11,757–11,830	+			CAT	1
<i>trnN</i>	11,831–11,893	+			GTT	
<i>cox3</i>	11,894–12,739	+	ATG	TAA		
<i>trnS2</i>	12,752–12,814	+			TGA	12
<i>nad5</i>	12,815–14,548	+	ATG	TAA		
<i>trnD</i>	14,963–15,033	+			GTC	414
<i>nad6</i>	15,136–15,603	+	ATG	TAA		102
<i>D-loop</i>	15,604–16,710	+				