

SUPPLEMENTARY MATERIAL

Table S1. Summary of structural probing data

A	WT Leader + 84nt 16S						C3 Leader + 84nt 16S					
	DMS	KE	DEPC	CVE	S1	T1	DMS	KE	DEPC	CVE	S1	T1
L- C40				+						++		
L- U43				+						++		
L- U45				+						++		
L- U47				+						++		
L- C48				+						++		
L- G50		++						+				
L- A51				+						++		
L- C52				+						++		
L- U65				+						++		
L- C56				+						++		
L- U57				+						++		
L- U59				nd						+		
L- G63		nd						++				
L- A66	++			++			++			+		
L- A71/72	+		+				+		++			
L- U82				+						++		
L- G92					+						nd	
L- C93	+				++		++				+	
L- A94	+				++		++				+	
L- A95	+						++					
L- A100	++		++				++		nd			
L- A102	+		+				++		++			
L- A103	+		nd				++		+			
L- A110	+		++				++		++			
L- A121	+		++				nd		++			
L- A123	+			nd			+			+		
L- G124		++		+				++		++		
L- A127	++		+				+		nd			
L- A128	++						+					
L- A130	++			++			+			++		
L- U140				+						++		
L- C143				++						+		
L- U149				++						+		
L- C155	nd						+					
L- U170				+						++		
A3			nd		++				+		++	
U12				++						+		
A19	+		+		+		++		nd		nd	
U24				++						+		
G38		++			+	+		++			nd	+
G41		++			+			++			nd	
G42		++			++	++		++			+	+
C43					++	+					nd	nd
C47				nd						+		
C48				+						nd		
U49				nd						+		
A51				+						nd		
C52					nd						+	
A53				+						nd		
C54					nd						+	
A55				+						nd		
C58					nd						+	
A59	+			+			++			+		
A60	+						++					
B	WT Leader + complete 16S						C3 Leader + complete 16S					
	DMS	KE	DEPC	CVE	S1	T1	DMS	KE	DEPC	CVE	S1	T1
U813				nd						++		
C862				nd						++		
A892				nd						++		
A906				nd						++		
C	WT Leader + 84nt 16S						WT Leader + complete 16S					
	DMS	KE	DEPC	CVE	S1	T1	DMS	KE	DEPC	CVE	S1	T1
L- G144					nd	nd					++	+
L- G147					nd	nd					++	+
G15					nd	nd					++	+
G22					nd	nd					++	+
G27					nd	nd					++	+
G31		nd		++	nd	nd		++		nd	++	++
G39		++			+	+		nd			+	+
G41		++			+			nd			nd	
A44				nd						+		
G46		nd						++				
G57		nd			nd			++			++	
G61						nd						++

Different transcript regions are presented in (A), (B) and (C). The length of the respective transcripts and the probes used are given in the top rows, with sequence positions indicated in the left column. Relative accessibilities are indicated by: +, accessible; ++, highly accessible; nd, not detected. Only those positions where differences in modification or cleavage were detected are listed.