Supplementary Information
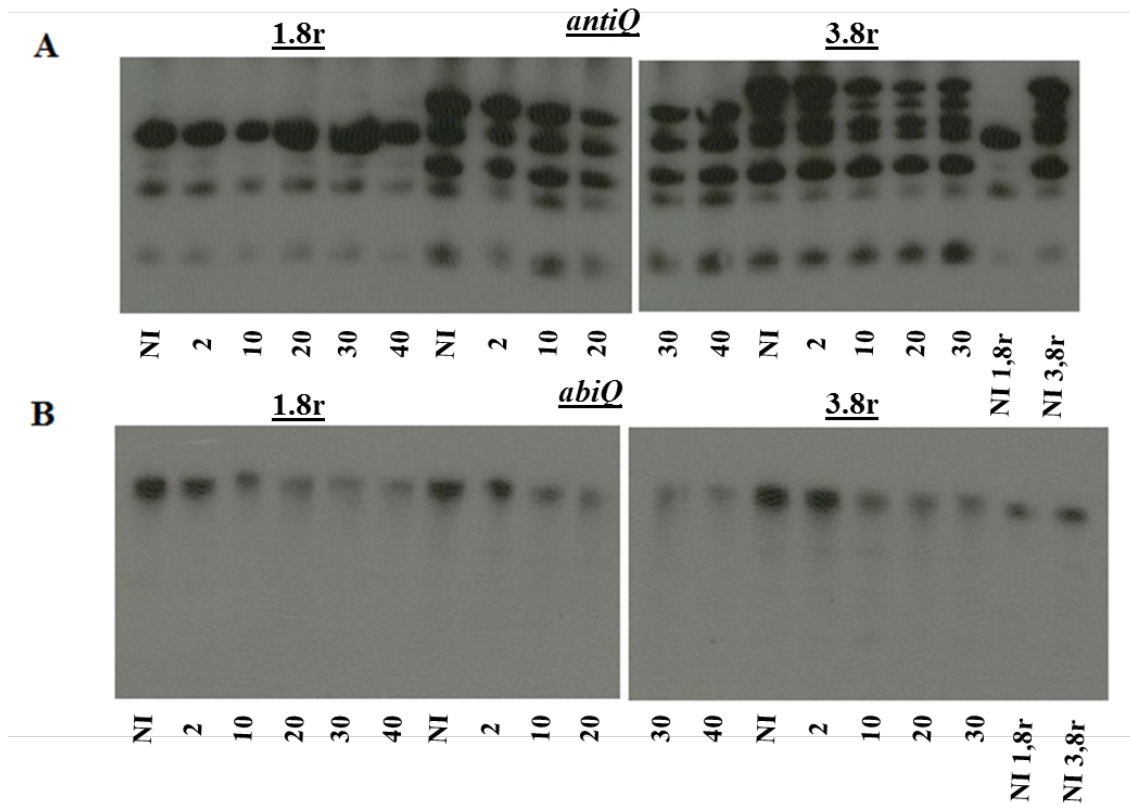
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3   **Table S1.** Primers used in this study.

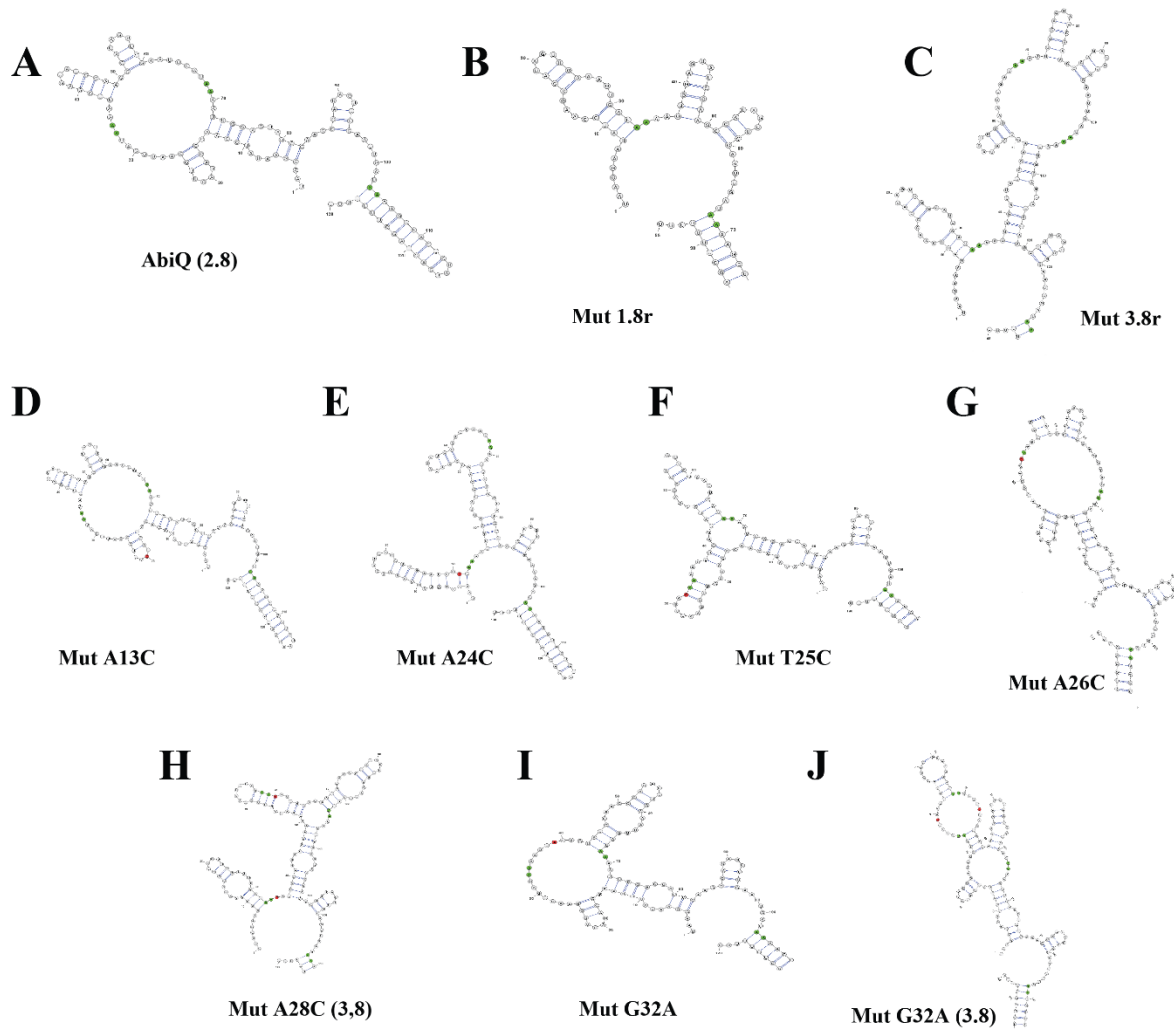| Function	Primers	Sequence (5'-3')[a]	Tm (°C)	Notes
5'RACE PCR				
	JS2	ccatctttttcatgagcagctt	53,9	cDNA of AbiQ$_{op}$ trancripts
	AbiQFwd	ttttacgaatgacgttaagattc	49,3	Control+, cDNA
	AbiQRev	CAGAATTCGAATTCccaagaggattatttatattgcca	50,9	Control+/-, cDNA
	PolyC	GACTCGAGTCGACATCGAcccccccccccccccccc	73,8	PCR RACE-AbiQ
	M13Fwd	gtaaaacgacggccagt	52,6	MCS of pBS-KS
	M13Rev	caggaaacagctatgac	47	MCS of pBS-KS
Revertant (*antiQ* repeats)				
	Mut1.8Fwd	attacttttataccttt**gtca**agctacaaaaaggggaa	59,6	Revertant 1.8R
	Mut1.8Rev	ttcccctttttgtagct**tga**caaaggtataaagtaat	59,6	Revertant 1.8R
	Mut3.8Fwd	attactttataccttt gtca**agc**tacaaaaaggggaacc	61	Revertant 3.8R
	Mut3.8Rev	ggttccccttttgta**gct**tgacaaaggtataaagtaat	61	Revertant 3.8R
Point mutant (*antiQ*)				
	antiQ(A13C)Fwd	gatattataattgtaaggaa<u>tatccaagccatc</u>**g**ttggaattgataaaattggagtatcc	63,5	Mutant A13C
	antiQ(A13C)Rev	ggatactccaattttatcaattccaac**g**atggcttggatattccttacaattataatatc	63,5	Mutant A13C
	antiQ(A24C)Fwd	gatattataattgtaaggaa<u>tatccaagccatagttggaatt**g**c</u>taaaattggagtatcc	63,5	Mutant A24C
	antiQ(A24C)Rev	ggatactccaatttta**g**caattccaactatggcttggatattccttacaattataatatc	63,5	Mutant A24C
	antiQ(T25C)Fwd	gatattataattgtaaggaa<u>tatccaagccatagttggaattga</u>**c**aaaattggagtatcc	63,5	Mutant T25C
	antiQ(T25C)Rev	ggatactccaatttt**g**tcaattccaactatggcttggatattccttacaattataatatc	63,5	Mutant T25C
	antiQ(A26C)Fwd	gatattataattgtaaggaa<u>tatccaagccatagttggaattgatc</u>**c**aaattggagtatccaagccatagttgg	65	Mutant A26C
	antiQ(A26C)Rev	ccaactatggcttggatactccaattt**g**atcaattccaactatggcttggatattccttacaattataatatc	65	Mutant A26C
	antiQ(A28C)Fwd	gatattataattgtaaggaa<u>tatccaagccatagttggaattgataa</u>**c**attggagtatccaagccatagttgg	65	Mutant A28C
	antiQ(A28C)Rev	ccaactatggcttggatactccaat**g**ttatcaattccaactatggcttggatattccttacaattataatatc	65	Mutant A28C
	antiQ(G32A)Fwd	gatattataattgtaaggaa<u>tatccaagccatagttggaattgataaaatt**a**</u>gagtatccaagccatagttgg	65	Mutant G32A
	antiQ(G32A)Rev	ccaactatggcttggatactc**t**aattttatcaattccaactatggcttggatattccttacaattataatatc	65	Mutant G32A
Vector (MCS)				
	pNZ-F	aatgtcactaacctgccccg	57,4	MCS of pNZ123
	pNZ-R	cattgaacatgctgaagagc	52,1	MCS of pNZ123

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5   [a] Capital letters, 5' flanking region. <u>Dotted underline</u>, recognition site of restriction enzyme. Solid

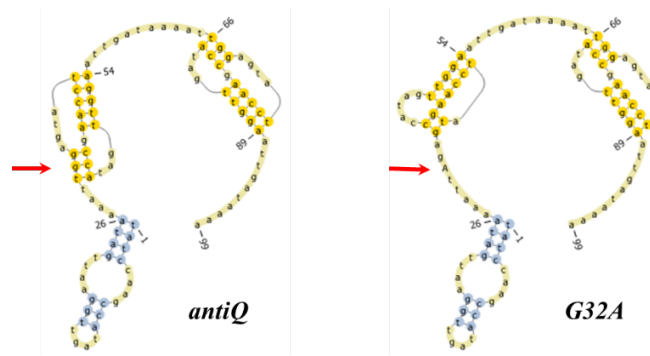6   underline, first repetition of *antiQ* (35nt). Bold letters, mutated nucleotides.

Figure S1. Northern blot experiment targeting *antiQ* (Panel A) and *abiQ* (Panel B) transcripts from *L. lactis* IL1403 AbiQ wild-type and mutants (1.8 and 3.8 repetitions) during phage infection by P008.

A AbiQ (2.8)

B Mut 1.8r

C Mut 3.8r

D Mut A13C

E Mut A24C

F Mut T25C

G Mut A26C

H Mut A28C (3,8)

I Mut G32A

J Mut G32A (3.8)

Figure S2. Comparison of the secondary structure of *antiQ* non-coding RNA (A), mutants with variable numbers of repeats (B, C) and point mutations mutants (D-J). RNAfold software (mode: mfe-partition function) has been used in combination with VARNA visualization software to characterize all the complete *antiQ* RNA structures (1, 2). Green nucleotides surround the ABIQ cleavage site and the specifically mutated nucleotides are shown in red.

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20 **Figure S3.** Comparison of pseudoknot structure of *antiQ* non-coding RNA (left) and the G32A

21 mutants (right). Pseudoknot structure analysis was performed using pKnotsRG software and the

22 visualization software Pseudovoewer 3.0 (3-5). To simplify analysis, only the nucleotides of the

23 repeats (99 nt) were used as the sequence and uracil was replaced by thymine.

References

1. **Gruber AR, Lorenz R, Bernhart SH, Neuböck R, Hofacker IL.** 2008. The Vienna RNA websuite. Nucleic Acids Res. **36:**W70-74.

2. **Darty K, Denise A, Ponty Y.** 2009. VARNA: Interactive drawing and editing of the RNA secondary structure. Bioinformatics **25:**1974-1975.

3. **Reeder J, Steffen P, Giegerich R.** 2007. pknotsRG: RNA pseudoknot folding including near-optimal structures and sliding windows. Nucleic Acids Res. **35:**W320-324.

4. **Byun Y, Han K.** 2006. PseudoViewer: web application and web service for visualizing RNA pseudoknots and secondary structures. Nucleic Acids Res. **34:**W416-422.

5. **Byun Y, Han K.** 2009. PseudoViewer3: generating planar drawings of large-scale RNA structures with pseudoknots. Bioinformatics **25:**1435-1437.