Programmed Frameshift in RitaG

Here are my recommendations:

1. Read the literature. I have attached a review article that describes a bunch of different frameshifts associated with the tail assembly chaperones in bacteriophages. You can use the bibliography of that one to find others to read.
2. There are 2 genes involved. In the literature they are named G and G/T. In your genome you will find them as 2 sequential genes upstream of the tapemeasure. You could think of those 2 genes as G and T, but that is not technically correct. There is no gene product made called T. Instead the ribosome slips near the end of G into the frame of t, hence the protein G/T is made.
3. The programmed frame shifts of the tail assembly chaperones is due to a slippery sequence. Meaning that as the transcript is in the ribosome, it slips backwards or forwards and the translation is shifted into a different reading frame.
4. Open up the six-frame translation in DNA Master, click the ORF button to find the 2 genes called, and look to see if the sequence has to slip forwards (+ frame shift) or backwards (-) frameshift to get from the first frame to the second.
5. In the case of RitaG you are looking at a +1 (or a -2 - \_2 is not as likely, so we will see if the +1 works.
6. Check to see that there are no stops in the way, once the ribosome slips.
7. Now look for a run of one kind of nucleotide – 4 or 5 Gs or As are most common.
8. At position 9001-9004 there are 4 As in a row. So the last nucleotide in the G part of the frameshift is 9002. To get to the reading from of the T portion of the G/T gene, the slip could go forward one, or reverse 2. Forward 1 is more common, so that is what we will do. So the T portion start at bp 9004.
9. This G/T gen is recorded with 2 regions. The coordinates of the 2 regions are 8532-9002; 9004 – 9441.
10. The product is:

MSVKKPENNGAAAREQATEFDSPFADRVLRFDDGSTMTIPPHPNLRMLDDDALEAYEAYLEEIETYDREPDLYIPDEMVLPAETRPGAVKGPPYFKDGKRVSPPREVRIVQVVLGMDSYEVLRSKQINGRPAGARDVWRAWTEQGFTIAERAESDSKVMEAQWFWRLYPRQIASDLRRFFGLSVADWHQGRLSSLELLDLFGVRFVDNAEERVRELYVDFAPVNGAVARAVRGGRWSESELIAAETYNEIARFRASFHASRSRKAAYEPFAFEDPVDRLEKARASVEAHELQREVEADLFGWZ