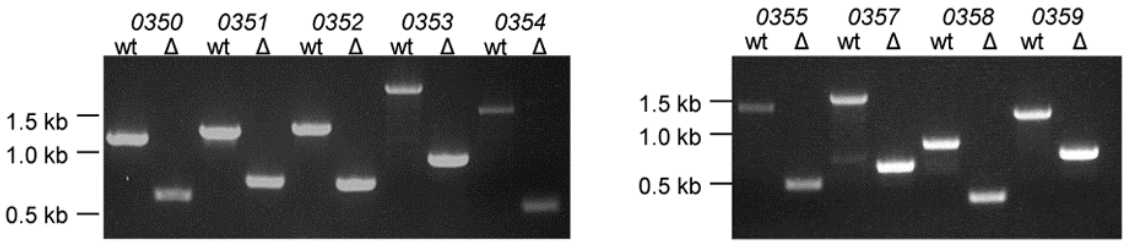

Figure S1. **Confirmation of in-frame deletions of targeted genes.** PCR screens of *M. maripaludis* wild type cells (wt) and in-frame deletion mutants for each targeted gene (Δ) using gene-specific primer pairs. The size of the PCR products for both the wildtype and the deleted versions of each gene are the predicted sizes using the sequencing primers listed in Supplemental Table S3.

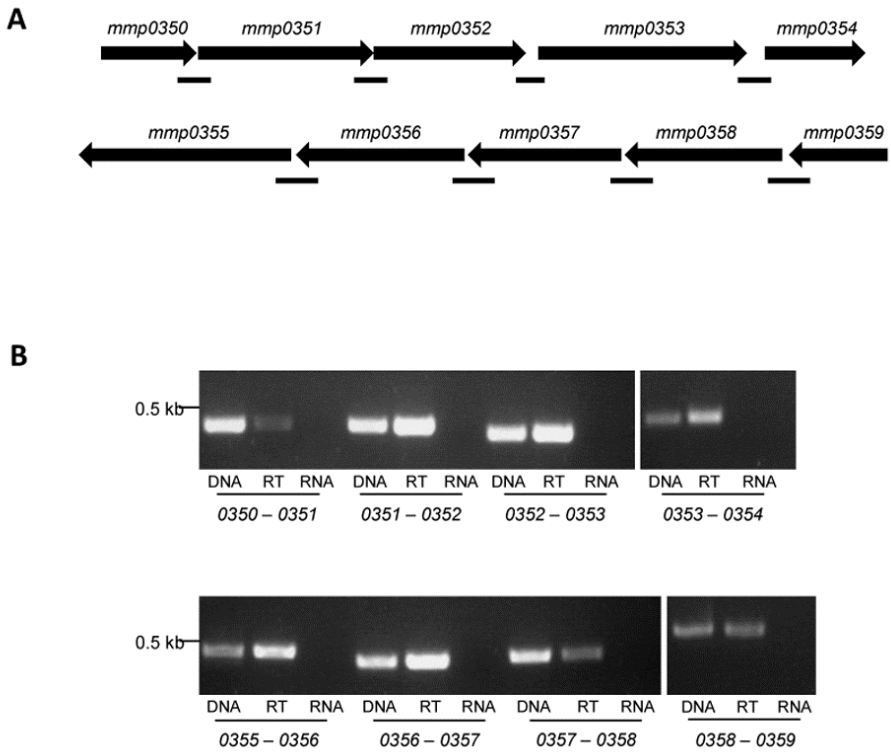

Figure S2. *mmp0350-mmp0354* and *mmp0355-mmp0359* are each transcribed as an operon. A. Depiction of the gene cluster targeted for RT-PCR analysis to determine co-transcription. The black lines indicate the intergenic regions that were targeted for amplification. B. RT-PCR experiments indicate the co-transcription of *mmp0350-mmp0354*, and *mmp0355-mmp0359*. Primer sets were used for standard PCR with Mm900 genomic DNA to confirm product sizes (DNA). RT-PCR was done using the same primer sets with purified Mm900 RNA to determine co-transcription of genes (RT). A standard PCR was also run using the purified RNA as template as a negative control against DNA contamination of the RNA (RNA).

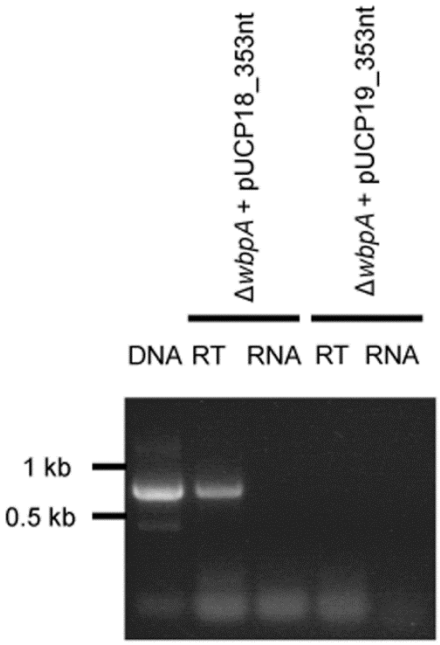

Figure S3.

Detection of PA353nt transcript by RT-PCR. RT-PCR primers were designed to amplify an internal fragment of *mmp0353*, synthesized using the codon preferences of *P. aeruginosa* (PA353nt). Plasmid pUCP18_PA353nt was used as template for a standard PCR reaction to confirm the amplicon size (DNA). RT-PCR was conducted using RNA isolated from either *P. aeruginosa* ΔwbpI + pUCP18_PA353nt or *P. aeruginosa* ΔwbpI + pUCP19_PA353nt (RT). PCR reactions using the same primers and RNA not subjected to the reverse transcription step as template were also performed as a control against DNA contamination of the RNA samples (RNA).