

**Table S6. PCR to confirm viral gene presence in the genome assembly.**

<b>Primer</b>	<b>Sequence (5'-3')</b>	<b>Within gene?</b>	<b>Amplicon size (bp)</b>
mg96_3prime_overlap_F1	ATGCAACGCGGTCTATTACC	<i>mg96</i>	1283
mg96_3prime_overlap_R1	GTAGGCGCTTCACTGGTCTC	-	
mg96_5prime_overlap_R1	CCATATAGCAGCTTGCGTCA	-	1404
mg96_5prime_overlap_F1	CCTAAAGGGTGCCTCCTACC	-	
DNApolB_3prime_overlap_F1	ATCCCAACTTTTCAGCCTCCT	<i>DNA polB</i>	1334
DNApolB_3prime_overlap_R1	ACAGGAGGTGCGTCCATTAC	<i>hypothetical</i>	
DNApolB_5prime_overlap_R1	TTTCTCAGGACGAGGCAGTT	<i>DNA polB</i>	1678
DNApolB_5prime_overlap_F1	TGGTACCATGCGACTAACCA	<i>Predicted carbohydrate binding protein</i>	
MCP_Hist_3kb_F1	AAGACTGACCTCCGCTTTCA	<i>histone (intron)</i> <i>[confirms integration in host genome]</i>	2837
MCP_Hist_3kb_R1	GCTGGATGCCTGTACCTTGT	<i>mcp</i>	
MCP_Hist_3kb_F2	AGATCAACGGCTCCATCTCG	<i>hnh</i> <i>endonuclease</i>	Primer walking
MCP_Hist_3kb_R2	CTTCGATCAAACCCGCAGAG	Between <i>hnh</i> and <i>mcp</i>	Primer walking
MCP_3prime_overlap_F1	ACGCATCCAATCCTAACCAG	<i>mcp</i>	1299
MCP_3prime_overlap_R1	TCCGCTTTGGAGAAGACACT	<i>hypothetical</i>	