

A framework for using quantitative PCR as a non-culture based method to estimate virus infectivity

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SUPPORTING INFORMATION

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TABLE S1: Primer sets used for qPCR amplification of the MS2 genome.

Table S1. Primer sets used for qPCR amplification of the MS2 genome. The total genome size is 3569 nucleotides (NCBI accession number NC_001417).

Primer set	Direction	Primer sequence (5' to 3')	MS2 target location (nucleotide position)
2	Forward	AAGGTGCCTACAAGCGAAGT	344 to 678
	Reverse	TTCGTTTAGGGCAAGGTAGC	
3	Forward	CCGCTACCTTGCCCTAAAC	657 to 959
	Reverse	GACGACAACCATGCCAAAC	
6	Forward	CCTAAAGTGGCAACCCAGAC	1530 to 1818
	Reverse	AAAGATCGCGAGGAAGATCA	
7	Forward	CGCGATCTTTCTCTCGAAAT	1809 to 2125
	Reverse	GACGATCGGTAGCCAGAGAG	
10	Forward	ATAGTCAAAGCGACCCAAATC	2724 to 3033
	Reverse	GGCGTGGATCTGACATACCT	
12	Forward	GAAATCACCGACAGCATGAA	3285 to 3528
	Reverse	AATCCCGGGTCCTCTCTTTA	