

Additional file 1. Coverage of newly designed primers set and probe in 135 HMPV genomes.

Primer/ Probe	Name*	Sequence 5' to 3'	Genetic region	%Coverage (n = 135)	
				100% identity	One mismatch
Forward	4730f	CGYAARGCTCCRTGCAAATATGAAG	<i>M2</i>	99.3	99.3
Reverse	4919r	CTTCTCTRCCTGDCCTGATATTATTG	<i>M2</i>	100.0	100.0
Probe	4796fp	FAM-CACAAYTACTGGAGYTGGC-MGB	<i>M2</i>	99.3	99.3

* Nucleotide location was determined based on NC_004148.2.