

Supplemental information

Primer sequences:

N2-fwd: TTACAAACATTGGCCGCAAA

N2-rev: GCGCGACATTCCGAAGAA

Crassphage-fwd: CAGAAGTACAAACTCCTAAAAAACGTAGAG

Crassphage-rev: GATGACCAATAAACAAGCCATTAGC

MHV-fwd: GCCAAATAATCGCGCTAGAA

MHV-rev: CCGAGCTTAGCCAAAACAAG

qRT-PCR standard details:

Y-intercept: 36.55

Slope: 2.923

LOD: 850 copies/L

LOQ: 1705 copies/L