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SUPPORTING INFORMATION

Additional supporting information may be found in the online version of this article:

Supplement 1. Diversity (min-max%) between 12 MuV genotypes based on 73 whole genomes, 120 SH, 94 HN and 98 F sequences (Neighbour-joining, P-distant, MEGA5.1-nt)

Supplement 2. The HN gene alignment of MuV strains and the Bat-MuV

Supplement 3. The F gene alignment of MuV strains and the Bat-MuV

