

Figure 1 displays three panels (a, b, c) showing phylogenetic trees and sequence alignments for MBFV sequences. The sequences are aligned in a multiple sequence alignment format, with positions 1 to 1000 indicated at the bottom. The sequences are color-coded by position: positions 1-100 are red, 101-200 are green, 201-300 are blue, 301-400 are orange, 401-500 are yellow, 501-600 are light green, 601-700 are light blue, 701-800 are light orange, 801-900 are light yellow, and 901-1000 are light green.

Panel (a) shows a phylogenetic tree with 100% bootstrap support for the MBFV group. The tree is rooted with a human sequence (H1N1) as an outgroup. The MBFV sequences form a single, well-supported clade.

Panel (b) shows a phylogenetic tree with 100% bootstrap support for the MBFV group. The tree is rooted with a human sequence (H1N1) as an outgroup. The MBFV sequences form a single, well-supported clade.

Panel (c) shows a phylogenetic tree with 100% bootstrap support for the MBFV group. The tree is rooted with a human sequence (H1N1) as an outgroup. The MBFV sequences form a single, well-supported clade.