Supplemental Figure 1. The deduced amino acid sequences of the gp38 domain of nine nairoviruses aligned in ClustalX and adjusted visually. Cysteine residues are shaded in black and other conserved residues are shaded in gray. Predicted N-glycosylation sites are underlined. Predicted proteolytic cleavage sites that may define the N-terminus gp38 (furin-like or SKI-1) and N-terminus of Gn (R[R/K]LL) are shaded in black and underlined.
SUPPLEMENTAL FIGURE 2. ClustalX alignment of the deduced amino acid sequences of the Gn proteins of nine nairoviruses. Conserved cysteine residues are shaded in black and two predicted transmembrane domains are shaded in gray. Predicted N-glycosylation sites are underlined. Identical (*), strongly conserved (:) and weakly conserved (.) residues as assigned in the Gronnet Pam250 matrix are indicated below the alignment.
SUPPLEMENTAL FIGURE 3. ClustalX alignment of the deduced amino acid sequences of the Gc proteins of nine nairoviruses. Conserved cysteine residues are shaded in black and one predicted transmembrane domain is shaded in gray. Identical (*), strongly conserved (:) and weakly conserved (.) residues as assigned in the Gronnet Pam250 matrix are indicated below the alignment. Potential SKI-1 proteolytic cleavage sites near the N-terminus that may generate the fully processed glycoprotein are shaded in black and underlined. Predicted N-glycosylation sites are underlined. Identical (*), strongly conserved (:) and weakly conserved (.) residues as assigned in the Gronnet Pam250 matrix are indicated below the alignment.

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**Figure Details:**
- The alignment highlights conserved cysteine residues in black and a predicted transmembrane domain in gray.
- Identical, strongly conserved, and weakly conserved residues are indicated using the Gronnet Pam250 matrix.
- Potential SKI-1 proteolytic cleavage sites are shaded in black and underlined.
- Predicted N-glycosylation sites are underlined.

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**Legend:**
- **KEOV**
- **LHNV**
- **YOG**
- **IVK**
- **KTRV**
- **GPSV**
- **ERVV**
- **ITAV**
- **CCHF**

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**Supplemental**: The figure shows an alignment of Gc protein sequences from nine nairoviruses, highlighting conserved cysteine residues in black and a predicted transmembrane domain in gray. Residues are classified as identical (*), strongly conserved (:) or weakly conserved (.) based on the Gronnet Pam250 matrix. Potential SKI-1 proteolytic cleavage sites are shaded in black and underlined, while predicted N-glycosylation sites are underlined. This alignment provides insights into the evolutionary relationships and conserved regions among these viruses.
SUPPLEMENTAL FIGURE 4. ClustalX alignment of the deduced amino acid sequences of the OTU-like protease domain in the L proteins of nine nairoviruses. Identical (*), strongly conserved (:) and weakly conserved (.) residues as assigned in the Gronnet Pam250 matrix are indicated below the alignment. Fully conserved residues that may be critical in the active site fold are shaded in gray.