



MuKV/XM34/CHN	7666	ATAGT	T	TAGGGAACAC	AGT	-G	CCTC	GGCACG	CTTAGTTAGT	TAGAACCT--	7715
Wencheng-Rt386-2	8030	ATAGT	T	TAGGGAACAT	AGT	-G	CCTC	GGCACG	CTTAGTTAGT	TAGAACCT--	8079
rat08/rAiA/HUN	8029	ATAGT	T	TAGGGAACAC	AGT	-G	CTTC	GGCACG	CTTAGTTAGT	TAGAACCT--	8078
MKV1/NYC/2014/M014/0146	7885	A-TAGT	T	TAGGGAACAC	AGT	G	CGGT	GAAACAC	CCGTCACG	CTTAGTTAGC--	7934
M-5/USA/2010	7931	T--AGT	T	TAGGGAACCC	AACC	A	CGGT	GGAATAC	CCGTGGT	GCT-AGTTAGTTA	7980
TF5WM	706	ATAGAT	-	AGGGAACAC	AGT	-G	CTTT	GGCACG	CATAGTTAG	CTAGAACCTC-	755

**Figure 5 Predicted barbell-like structure of partial 3'UTR of MuKV/XM34/CHN and sequence alignment of partial 3'UTRs of murine kobuvirus strains.** The sequence alignment in the 49-nt-long partial 3'UTRs begins after the stop codon, and the numbers on both sides of the sequences indicate the nucleotide position. The reference *Kobuvirus* strains include Wencheng-Rt386-2 (accession no.MF352432.1), rat08/rAiA/HUN (accession no.MN116647.1), MKV1/NYC/2014/M014/0146 (accession no.MF175074.1), M-5/USA/2010 (accession no.JF755427.1) and TF5WM (accession no.JQ408726.1).