

A

Exon_orf20 _{NK-198-1}	CACTGGAAAG	AGAGATTAAT	CACCATGAAC	TCGAACTCGA	ACTCGAAAGA	GATGAAACTT	557
Exon_orf20 _{NK-198-2}	CACTGGAAAG	AGAGATTAAT	CACCATGAAC	TCGAACTCGA	A-----AGA	GATGAAACTT	551
Exon_orf20 _{NK-198-3}	CACTGGAAAG	AGAGATTAAT	CACCATGAAC	TCGAACTCGA	A-----AGA	GATGAAACTT	542
Exon_orf20 _{NK-198-4}	CACTGGAAAG	AGAGATTAAT	CACCATGAAC	TCGAACTCGA	ACTCGAAAGA	GATGAAACTT	557
consensus	CACTGGAAAG	AGAGATTAAT	CACCATGAAC	TCGAACTCGA	ACTCGAAAGA	GATGAAACTT	
▼							
Exon_orf20 _{NK-198-1}	TCAAGGAGAA	AACCATTG	AAGGAGGAGA	CAGTTGATGA	TAAAGATAGT	A	609
Exon_orf20 _{NK-198-2}	TCAAGGAGAA	AACCATTG	AAGGAGGAGA	CAGTTGATGA	TAAAGATAGT	A	603
Exon_orf20 _{NK-198-3}	TCAAGGAGAA	AACCATTG	AAGGAGGAGA	CAGTTGATGA	TAAAGATAGT	A	594
Exon_orf20 _{NK-198-4}	TCAAGGAGAA	AACCATTG	AAGGAGGAGA	CAGTTGATGA	TAAAGATAGT	A	609
consensus	TCAAGGAGAA	AACCATTG	AAGGAGGAGA	CAGTTGATGA	TAAAGATAGT	A	

B

3'UTR_orf20 _{NK-198-1}	CCATTTACCA	ACCAGCATCT	TCTTTTAGCA	GCTTCGCCTG	TTTATGAATT	GTGGTAATCA	1926
3'UTR_orf20 _{NK-198-2}	CCATTTACCA	ACCAGCATCT	TCTTTTAGCA	GCTTCGCCTG	TTTATGAATT	GTGGTAATCA	1920
3'UTR_orf20 _{NK-198-3}	CCATTTACCA	ACCAGCATCT	TCTTTTAGCA	GCTTCGCCTG	TTTATGAATT	GTGGTAATCA	1943
3'UTR_orf20 _{NK-198-4}	CCATTTACCA	ACCAGCATCT	TCTTTTAGCA	GCTTCGCCTG	TTTATGAATT	ATGGTAATCA	1926
consensus	CCATTTACCA	ACCAGCATCT	TCTTTTAGCA	GCTTCGCCTG	TTTATGAATT	*TGGAATCA	
▼							
3'UTR_orf20 _{NK-198-1}	AAATTAAACA	GCTCATCGAT	CATTATATTG	TCGTTATATT	TCATCTGTTT	GACAAAGTTT	1986
3'UTR_orf20 _{NK-198-2}	AAATTAAACA	GCTCATCGAT	CATTATATTG	TCGTTATATT	TCATCTGTTT	GACAAAGTTT	1980
3'UTR_orf20 _{NK-198-3}	AAATTAAACA	GCTCATGGAT	CATTATATTG	TCGTTATATT	TCATCTGTTT	GACAAAGTTT	2003
3'UTR_orf20 _{NK-198-4}	AAATTAAACA	GCTCATGGAT	CATTATATTG	TCGTTATATT	TCGTCTGTTT	GACAAAGTTT	1986
consensus	AAATTAAACA	GCTCAT*GAT	CATTATATTG	TCGTTATATT	TC*TCTGTTT	GACAAAGTTT	

Fig. S1. Alignments of reference sequences derived from each *RF-Oma1* in NK-198 *Rf1*. Nucleotide residues are numbered from the from the translational initiation codon. Exon and 3' trailer regions are shown (A and B, respectively). Dashes indicate gaps inserted for maximum matching. The nucleotide positions for read-number counting are shown with black triangles.