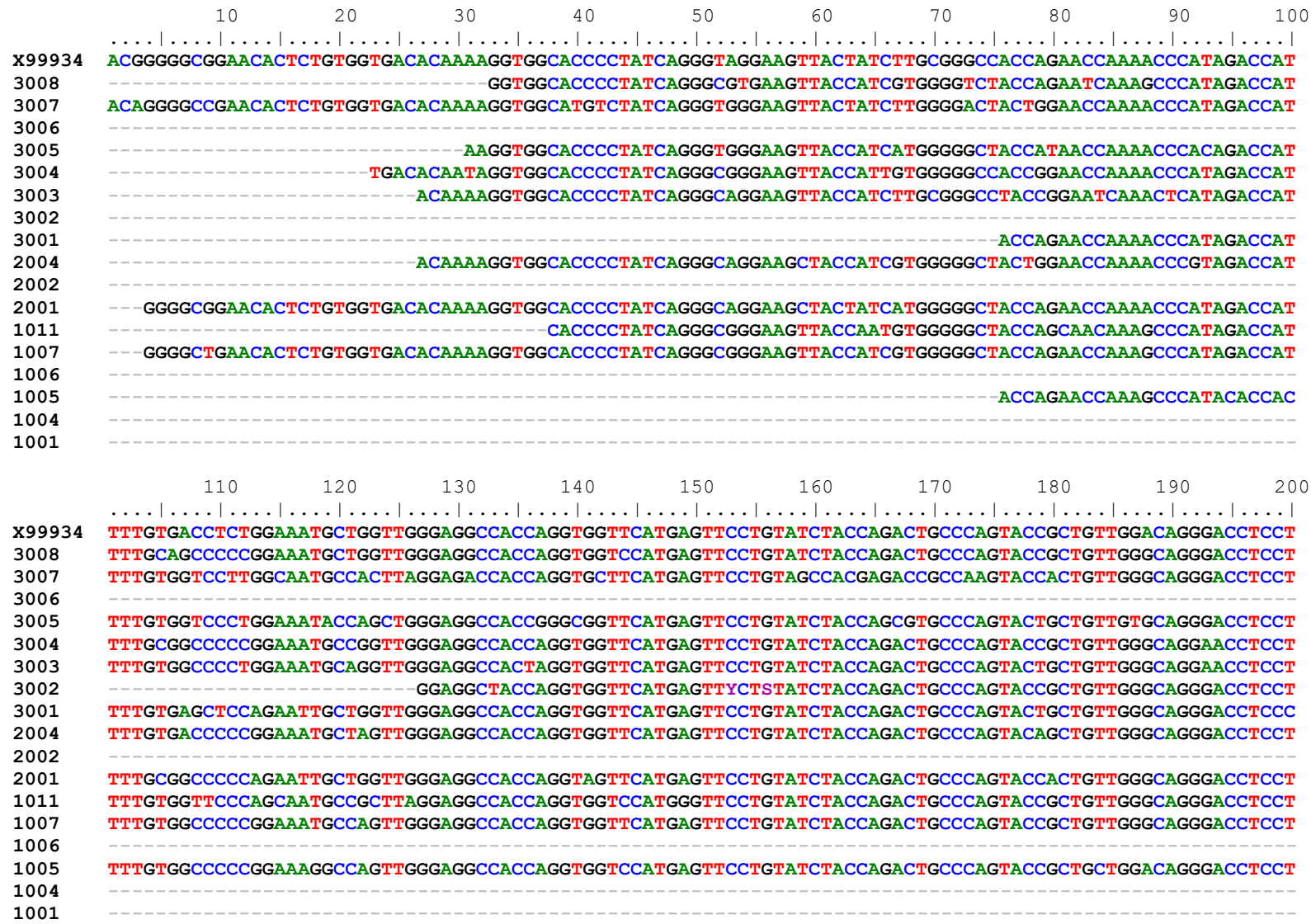


**Supplementary Figure S7:** Alignment of the murine leukemia virus-related virus (MLRV) sequences detected in bats. Positions are indicated according to the MLRV strain TaEV (GenBank accession: X99934).





3005 CCCC**TGGTCTGGGCAAAAACCATGCCCCGATACTGATTGACCTGAAGCCTTGAGCCCAGCCTGTCAAAATACGCCAGTACATGGTTCCGCGGGAAGCAC**A  
 3004 -----  
 3003 CCCC**TGGC**----**CAAAAACCATGCCCCAATCCTGATTGACCTGAAGCCTGGAGCCCAACCTGTCAAAATATGCCAGTACATGGTTCCGCGGGAAGCACG**  
 3002 CCCC**TGGTCTGGCCAAAACCCACACCCCGATCCTGATTGACCTGAAGCCTGGAGCCCAGCCTGTGAAAATACACCAGTACATGGTTCTATGGGAAGCGTG**  
 3001 -----  
 2004 CCCC**TGGC**--**GCCAAAACCATGCCCCAATCCTGATTGACCTGAAGCCTGGAGCCCAACCTGTCAAAATACGCCAGTACATGGTTCCACGGGAAGCACG**  
 2002 -----  
 2001 CCCC**TGGTATGGCCAAAACCATACCCCAATCCTGATTGACCTGAAGCCTGGAGCCCAGCCTGTCAAAATATGCCAGTACATGGTTCTGTGGGAAGCAC**A  
 1011 CCCC**TGGTCTGGCCAAAACCATGCCCCGATACTGAATGACCTGAAGCCTGGAGCCTGGCCTGTCAAAATACGCCAGTACATGGTTCTGCGGGAAGTGC**G  
 1007 CCCC**TGGC**----**CAAAAACCCACACCCCAATACTGATTGACCTGAAGCCTGGAGCCCAACCTGTCAAAATACGCCAGTACATGGTTCCGCGGGAAGTGC**G  
 1006 -----  
 1005 CCCC**AGGTC****AATCAGGAGTGGGGC**--**ATGGTTTTTGGCCAGAAGCCTGGGGGGCAACCTGTCCAAATACACCAGTACATGGTTCCATGGGAAGCACG**  
 1004 -----  
 1001 -----**CAATAACCATGTCCCAATCCTGTTTGACCTGAAGCCTGGAGCCTAACCTGTATAAATGCGCCAGTACATGGTTCCGCAGGAAGCAC**A

510 520 530 540 550 560 570 580 590 600

X99934 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|  
 3008 TCTAGGGATCCAGATTCACCTAGACCGATTACTCAAGTGGGAC**TTTTTAAAGCAATGCCAGTCCCCATGGAAACACCCCTCTGCTGCCCATAAAGAAACCT**  
 3007 TCTAGGGATCCAGATTCACCTAGACCGATTACTCAAGTGGGGAC**TTTTTAAAGCAATGCCAGTCCCCATGGAAACACCTCCTTGCTGCCTGTAAAGAAACCT**  
 3006 TCTAGGGATCCAGATTCACCTAGACCAAGTACTCAAGTGGGGAC**TTTTTAAAGCGATGCCAGTCCCCATGGAAACACCCCTCTGCTGCCCATAAAGAAACCT**  
 3005 TCTAGTGATCCAGATTCACCTAGACCAACTACTCAGTGGGGAC**TTTTTAAAGTCAATGTCAGTCCCCATGGAAACACCCCTGCTGCCTGTAAAGAAACCTG**  
 3004 -----  
 3003 TCTAGGGATCCAGATTCACCTAGACCGACTACTCAAGTGGGGAC**TTTTTAAAGCGATGCCAGTCCCCATGGAAACACCCCTCTGCTGCCCATAAAGAAACCT**  
 3002 TCTAGGGATCCAGATTCACCTAAACTGACTACTCAAGTGGGGAC**TTTCAAAGC**-----  
 3001 -----  
 2004 TCTAGGGATCCAGATTCACCTAGACCGACTACTCAAGTGGGGAC**TTTTTAAAGCAATGCCAGTCCCCATGGAAACACCCCTCTGCTGCCGTAAAGAAACCT**  
 2002 -----**TGCCAGTCCCCATGGAAACACCCCTCTGCTGCCTGAAAAGAAACCT**  
 2001 TCTAGGGATCCAGATTCACCTAGACCGACTACTCAAGTGGGGAC**TTTTTAAAGCGATGCCAGTCCCCATGGAAACACCCCTCTGCTGCCCATAAAGAAACCT**  
 1011 TCTAGGGATCCAGATTCACCTATACCAAGAACTCAAGTAGGAAC**TTTCAAAGCAATGCCAGTCTTCGTGGAAACATCCACCTGCTGCCCGTAAAGAAACCT**  
 1007 TCTAGGGATCCAGATTCACCTAGACCAACTACTCAAGTGGGGAC**TTTTTAAAGCAATGCCAGTCCCTGTGGAAACACCCCTCTGCTGCCCATAAAGAAACCT**  
 1006 -----**CACCTAGACCAACTACTCAGTGGGGACTTTTAAGTCAATGTCAGTCCCCATGGAAACACCCCTCTGCTGCCCATAAAGAAACCT**  
 1005 TCTAGGGATCCAGATTCACCTAGACTGACTACTCAAGTGGGGAC**TTTTTAAAGCGATGCCAGTCCCTGTGGAAACACCCCTCTGCTGCCCATAAAGAAACCTG**  
 1004 -----**AGTCCCCGAGGGACACACCCCTGCTGCCTGTAAAGAAACCT**  
 1001 TCTAGGGATCCAGATTCACCTAGACTGACTACTCATATGGGGAC**TGGTAAAGCAATGCAAGTCCCCATGGAAACACCCCTCTGCTGCCCATAAAGAAACCT**

610 620 630 640 650 660 670 680 690 700

X99934 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|  
 3008 GGGACAAAC**GACTACCGCCCGTACAAGACTTAAGGGCCATTAATGAAGTGGTCATCATGTTGCATTTGACACTGCCTAACCCTACACTCTATTAGGAC**  
 3007 GGGACAAAT**GACTACCGCCCGGTATAAGACTTAAGGGCCATTAATGAAGTGGTCATCATGTTGCATTTCGGCACTGCCTAACCCTACACTCTATTAGGAC**  
 3006 GGGACAAAC**GACTACCGCCCGGTACAAGACTTAAGGGCCATTAATGAAGCGGTCAATCACGTTGCATTTCGGCACTGCCTAACCCTACACTCTGTATTGGAC**  
 3005 GGACAAA-----  
 3004 -----  
 3003 GGGACAAAC**GACTACCGCCTGGTACAAGACTTAAGGGCCATTAATGAAGTGGTCATCACGTTGCATTTGGCACTGCCTAACCCTACACTCTATTAGGAC**  
 3002 -----  
 3001 -----  
 2004 GGGACAAAC**GACTACCGCCCGGTACAAGACTTAAGGGCCATTAATGAAGTGGTCATCACGTTGCATTTCGGCACTGCCTAACCCTACACTCTATTAGGAC**

2002 GACATAAAATGACTACCTCTCAGTACAACACTTAACAGCCATTAAAGGCGGTTCATCACGTTGCATTTCAGCACTGCCTAACCCATACACTCTATTAGGAC  
2001 GGGACAAATGACTACCGCCTGGTACAAGACTTAAGGGCCATTAAATGAAGCGGTCAATACGTTGCATTTCGGCACTGCCTAACCCATACACTCTATTAGGAC  
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1001 GGGACAAATGACTACCGCCCCGGTACAAGACTTAAGGGCCATTAAATGAAGCGGTTCATCACGTTGCATTTCGGCACTGCCTAACCCATACACTCTATTAGGAC

710 720 730 740 750 760 770 780 790 800  
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3006 TTATTGTTCTGTGGCAGGGTGGTTTACATGCCTGGGCTTAAAGGATGCCCTCTTCTGCCTCCAACCTAGCGCCCAATAGCCAGCCTCTGTTGCGCTTGA  
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3004 -----  
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810 820 830 840 850 860 870 880 890 900  
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|  
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1001 ATGGGAAAATCCCACCATAGGAACAAAGGAACAATTACACTTGGACTCAACTACCCCAAGGATTCAAGAATTCACCAGCTTTGTTAGCAAGACACTGGCG

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....|....|....|....|....|....|....|....|....|....|....|...  
x99934 TCTGACTTAGCCAAGTTCCCGGGACTGAACGTAGGATGTGTCTCCTCCAGTACGTC  
3008 TCTGACTTAGCCAAGTTCCCGGGCTGGAACTTAGGATGTGTCTC-----  
3007 TC-----  
3006 TCTGACTTAGCCAAGTTCTTGGGACAGAACTTAGGATGTGTCTCCTCCAATATGT-  
3005 -----  
3004 -----  
3003 TCTGACTTAGCCAAGTTCCCGGGACAGAACTTAGGATGTGTCTCCTCCAATATGT-  
3002 -----  
3001 -----  
2004 TCTGACTTAGCCAAGTTCCAGGACGGAACTTAGGATGTGTCTCCTCCAATACGT-  
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