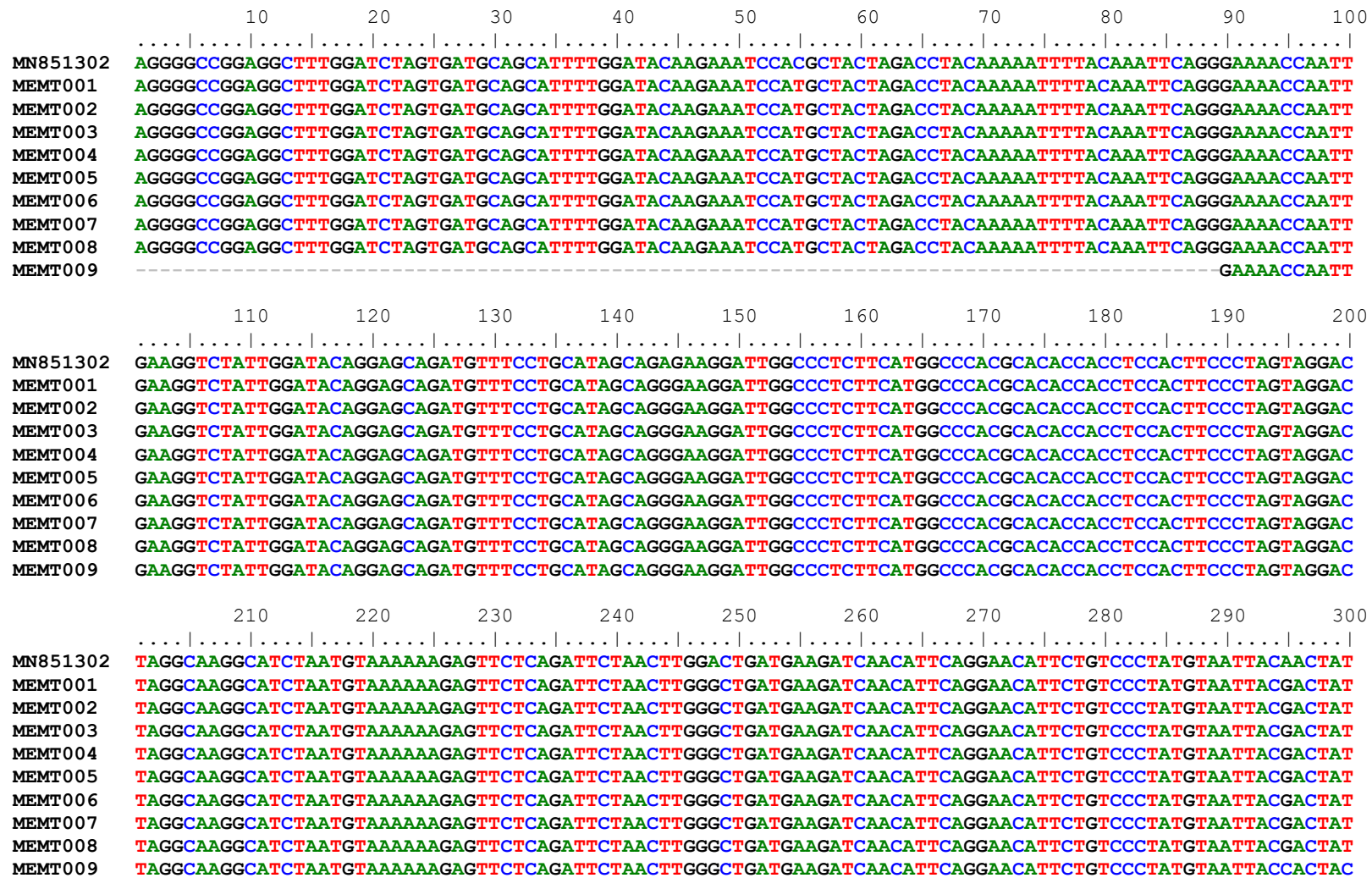


Supplementary Figure S4: Alignment of the *Myotis myotis* endogenous retrovirus (MMER) (A), *Myotis ricketti* endogenous retrovirus (MRER) (B) and *Myotis daubentonii* endogenous retrovirus (MDER) (C) sequences identified in bat samples. Identical nucleotides with the reference sequence are shown as colored dots. Positions are numbered according to the reference sequence in each alignment

A: MN851302. Myotis myotis endogenous retrovirus isolate EuB-RV1



	610	620	630	640	650	660
					
MN851302	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAGAAATCAGGCAAT					
MEMT001	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAGAAATCAGGCAA					
MEMT002	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAGAAATCAGGCAA-					
MEMT003	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAGAAATCAGGCAA-					
MEMT004	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAGAAATCAGGCAA-					
MEMT005	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAGAAATCAGGCAA-					
MEMT006	-----					
MEMT007	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAGAAATCAGGCAA-					
MEMT008	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAGAAATCAGGCAA-					
MEMT009	TATAGAGCCATCAAATAGTCCCTGGAACACACCCATATTTGTAATAAGAAAG-----					

B: MN851303. Myotis daubentonii endogenous retrovirus isolate EuB-RV3

	10	20	30	40	50	60	70	80	90	100
									
MN851303	GCCCTCAATTATTTTCATTTTGATGAGCATGGATTAAACCCCTATGTATAAACATTGGGGAGGACTCCGGGACATAGCAACACCTCTTCCCTTGGTCCGGT									
MEMT007	-----AAACATTGGGGAGGTCTCAGGGACATACCAACACCTCTCCCTTGGTCCGGT									
	110	120	130	140	150	160	170	180	190	200
									
MN851303	GGAGAGACCCACTTACCGAAGCCTGGAAGGCCCCGACCCACTCTTAACCCAGGGGAGAGGGTTTGCTTGTTATTTTTCCAGAAGCGCAAAAGTCCCGC									
MEMT007	GGAGAGATCCACTAACCGGGGCTTGAAAGGGCCCCGACCCACTCTTAACCCAGGGGAGAGGGTTTGCTTGTTATTTTTCCAGAAGATGAGAAAAATCCCGC									
	210	220	230	240						
									
MN851303	ATGGATCCCTGCTCGTGACATCAAACCCACACACCAGCGATGAGCCG									
MEMT007	TTGGATTCTACCCGTAACATCAAACCCTGCAACCACAGTGATGACCCG									

C: JQ292912. Myotis ricketti retrovirus isolate MrRV

	310	320	330	340	350	360	370	380	390	400
									
JQ292912	GAGACAGAAGAAATTGCCTTTAATCAGATAAAGAAAGCTCTTTTGGCTGCTCCAGCCCTGGGCCTACCAGACATTACAAAACCCCTTTCGCCCTCTTTGTAG									
MEMT001	-----CTCCAGCCCTGGGCCTACCAGACATTACAAAACCCCTTTCGCCCTCTTTGTAG									
	410	420	430	440	450	460	470	480	490	500
									
JQ292912	ACGAGCGCAAAGGAGTAGCAAAAGGAGTTTAAACCCAGGCTTTAGGCCCTTGAGTCGCCAGTAGCATATTTGTCTAAAAAGCTGGATCCCGTAGCTGC									
MEMT001	ATGAGTGCAAAATGAGTAGCAAGAGGGGTTTAAACCCAGGCTTTAGGCCCTTGAGTCGCCAGTAGCATATTTGTCTAAAAAGCTGGATCCTGTAGCTGC									

510 520 530 540 550 560 570 580 590 600

JQ292912
MEMT001

CGGCCTGGCCACCGTGCCTAAGAATCATTGCAGCAACTGCGCTCTTAGTCAAGGATGCCGACAAACTAACCCCTGGGACAGGAGATCTGGATCACAACCCCG
CGGCCTGGCCACCGTGCCTAAGAATCGTTGCAGCAACCGCGCTCTTAGTCAAGGATGCCAACAACCTGACCCCTGGGACAGGAGATATGGATCACAACACCG

610 620 630 640 650 660 670 680

JQ292912
MEMT001

CATGCCATTGAGGGGGTCCATAAAGCAGCCTCGTAGATGGAATGAGCAATGCTCGCATGACCCACTATCAAAGCTTGCTGCTC
CATGCCATTGAGGGGGTCCATAAAGCAGCCTCCTAATAGGTGGATGAGCAATGCTCG-----