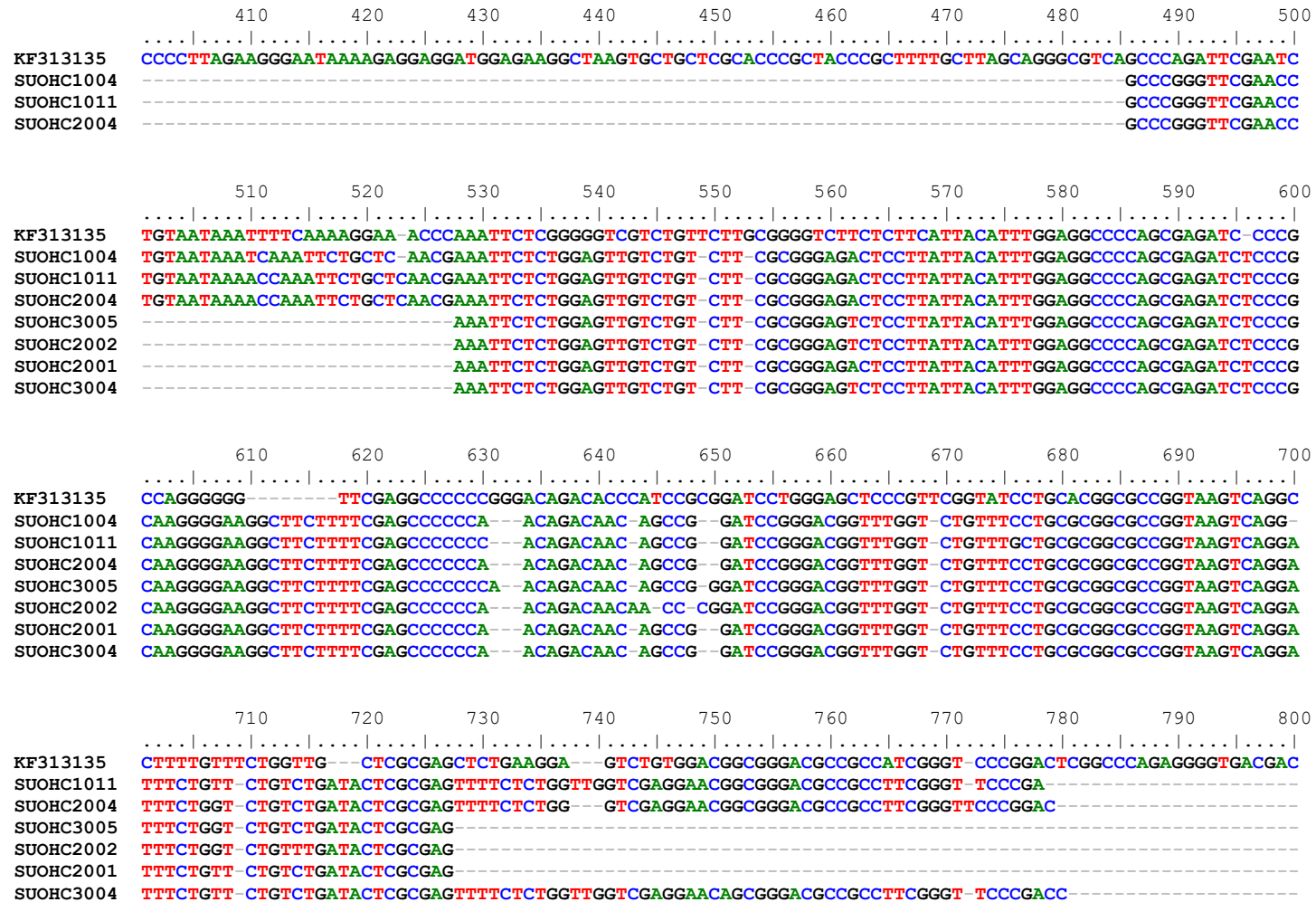


**Supplementary Figure S6:** Alignment of the Galidia endogenous retrovirus (GERV) sequences detected in bats. Positions are indicated according to the GERV strain AMNH-110064 (GenBank accession: KF313135).



	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
	.... ....									
KF313135	GATTTCTGCGCCTGCCGCGCCGCGCTGCGATACCTTAGAACCAAAAACAGGCCCTTCTAGCACTAAGTAAGGCGGGCTGCCCTCTCCCTCTTGGCCAAG									
SUOHC3003									GTCCCTCTCCCTCTCGGCCAAG	
SUOHC1003									CCTCTCCCTCTCGGCCAAG	
SUOHC1006									CCTCTCCCTCTCGGCCAAG	
SUOHC1014									CCTCTCCCTCTCGGCCAAG	
SUOHC1001									CCTCTCCCTCTCGGCCAAG	
SUOHC1002									CCTCTCCCTCTCGGCCAAG	
SUOHC3007									CTCCCTCTCGGCCAAG	
SUOHC3002									CAAG	

	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
	.... ....									
KF313135	ATGGGACAAGGCAGCTCTAAGGGCCCATTTGAGCCCATTTGGAATGTCTGATTAAAACTTCTCCGATTTTCGGAAATCGAGCCGCGGGATACGGGGCAACAG									
SUOHC3003	ATGGGACAGGGCGACTCAAAGGGCCCCCTTGAGCCCCCTTAGAATGCCTAATTAAGAATTTTGATGACTTCGCCGCCGCGCGGACGGGTACGGGGCGCCCCG									
SUOHC1003	ATGGGACAGGGCGACTCAAAGGGCCCCCTTGAGCCCCCTTAGAATGCCTAATTAAGAATTTTGATGACTTCGCCGCCGCGCGGACGGGTACGGGGCGCCCCG									
SUOHC1006	ATGGGACAGGGCGACTCAAAGGGCCCCCTTGAGCCCCCTTAGAATGCCTAATTAAGAATTTTGATGACTTCGCCGCCGCGCGGACGGGTACGGGGCGCCCCG									
SUOHC1014	ATGGGACAGGGCGACTCAAAGGGCCCCCTTGAGCCCCCTTAGAATGCCTAATTAAGAATTTTGATGACTTCGCCGCCGCGCGGACGGGTACGGGGCGCCCCG									
SUOHC1001	ATGGGACAGGGCGACTCAAAGGGCCCCCTTGAGCCCCCTTAGAATGCCTAATTAAGAATTTTGATGACTTCGCCGCCGCGCGGATGGGTACGGGGCGCCCCG									
SUOHC1002	ATGGGACAGGGCGACTCAAAGGGCCCCCTTGAGCCCCCTTAGAATGCCTAATTAAGAATTTTGATGACTTCGCCGCCGCGCGGACGGGTACGGGGCGCCCCG									
SUOHC3007	ATGGGATAGGGCGACTCAAAGGGCCCCCTTGAGCCCCCTTAGAATGCCTAATTAAGAATTTTGATGACTTCGCCGCCGCGCGGATGGGTACGGGGCGCCCCG									
SUOHC3002	ATGGGACAGGGCGACTCAAAGGGCCCCCTTGAGCCCCCTTAGAATGCCTAATTAAGAATTTTGATGACTTCGGCTGCCGCCGCGGACGGGTACGGGGCGCCCCG									

	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
	.... ....									
KF313135	TGAATGCTTTTCGACCTGCGAAAAATCTGTGAGTTGGAATGGCCACCTTTGGGGTCGGATGGCCAGGTGTGGGGACCCCTGGATGTAGGCACGG-CCAGTG									
SUOHC3003	TCAATGCTTTTGATTTGAGAAAAATCTGTGAGAGGGAGTGGCCACGTTTGGGGTCGGCTGGCCAGACATAGGGACCTTTGATCTGGCGACGGTCCAG-G									
SUOHC1003	TCAATGCTTTTCGATTTGAGAAAAATCTGTGAG- - - - -									
SUOHC1006	TCAATGCTTTTCGATTTGAGAAAAATCTGTGAGAGGGAGTGGCCACGTTTGGGGTCGGCTGGCCAGACATAGGGACCTTTGATCTGGCGACGG-TCCAGG									
SUOHC1014	TCAATGCTTTTGATTTGAGAAAAATCTGTGAGAGGGAGTGGCCACGTTTGGGGTCGGCTGGCCAGACATAGGGACCTTTGATCTGGCGACGG-TCCAGG									
SUOHC1001	TCAATGCTTTTGATTTGAGAAAAATCTGTGAGAGGGAGTGGCCACGTTTGGGGTCGGTTGGCCAGACATAGGGACCTTTGATCTGGCGACGG-TCCAGG									
SUOHC1002	TCAATGCTTTTGATTTGAGAAAAATCTGTGAGAGGGAGTGGCCACGTTTGGGGTCGGCTGGCCAGACATAGGGACCTTTGATCTGGTGACGG-TCCAGG									
SUOHC3007	TCAATGCTTTTGATTTGAGAAAAATCTGTGAGAGGGAGTGGCCACGTTTGGGGTCGGTTGGCCAGACATAGGGACCTTTGATCTGGCGACGGTCCAG-G									
SUOHC3002	TCAATGCTTTTGATTTGAGAAAAATCTGTGAGAGGGAGTGGCCACGTTTGGGGTCGGYTGGCCAGACATAGGGACCTTTGATCTGGCGACGGTCCAG-G									

	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
	.... ....									
KF313135	CGGTCCGTGCTGTT-TGCTACAGCACCCCTGGCCATCCTGACCAGGTCCCTTACATAGACATCTGGATTGACATCATCTGGGACAGGCCCGGTTATCTGA									
SUOHC3003	CGGTTCAG-GCGGACATGTTATGGAAATCCTGGGCACCCAGACCAATCCCGTA									
SUOHC1006	CGGTTC- - - - -									
SUOHC1014	CGGTTC- - - - -									
SUOHC1001	CGGTTC- - - - -									
SUOHC1002	CGGTTC- - - - -									
SUOHC3007	CGGTTCAG-GCGGACATGTTATGGAAATCCTGGGCACCCAGACC									
SUOHC3002	CGGTTCAG-GCGGACATGTTATGGAAATCCTGGGCACCCAGACCAAT									

	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC1005	ACCGCTCTAGGGAAGAACCAATGTGCCTACTGCAAGGAGGAAGGACATTGGAAGAGAGAAATATTCCTAAACGCCCTCGGGAGGGAGAGGGCCACCCCAACC									
SUOHC1007	-----GCTTATTGTCAGGAAGAAGGACACTGGAAGAGAGAGTGCCCAAAAAGACCCA--AGGCTGAGGCTCCGCCAGCCC									
	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC1005	CGGTCCCTGGTCAAAGAGACGGACTAGAGAACTCGGGGCTCCCTC-GCCCTCCAGGAACCCAGGCTAAAACTCTCGGTAGGAGGGCAACTGATTGATTTCT									
SUOHC1007	CAGTATTGGTAGAAGAGGAAGACTAGGGCCGCCGTGGGGCC-TCAGTCCTCCGGGAACCCAGGCTAAAACTCTCGGTAGGGGGACAAATGATTGACTTTT									
	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC1005	TGGTGGATACCGGGGCCACCCATTCTGTGTGACAGCGCCAGTTGGGCCC-CTCACCCCTGAGCGGGTCAGAAATTATAGGGGCCACTGGGATATCCAAA									
SUOHC1007	TAGTGGACACCGGGGCCACTCATTCGGTAGTTCAAGCCCTGTGGGCCCTACTCAGGCCAAAA--GGTGAGAATCGTAGGAGCCACTGGAACCTCCTCAG									
	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC1005	AGCTACCCCAAACTCGGAGGGTCGAAATCAGCGGACCTGGGTAAAGGACTCTTAACCCCACTCCTTCCTTGTGATACCCGAATGTCCTGACCCACTGCTGGGAA									
SUOHC1007	ACCTACCCCACTCTGAGGGCCGGATCACCAACTGAGCCAGGGTACTGTACCCCACTCCTTCCTCGTTATACCGGAATGCCCGGACCTCTCCTGGGTA									
	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC1005	GGGACCTCCTCCACAAGCTCAGGGCCACCATCACCTTCGATGGGGTAGGGACTCCAGAGGTAAAAACTGAAGGGAAGTCCCTCGTGACCTTTGCCCTTGGC									
SUOHC1007	GAGATTGTGTACACAAGTTACAGGCCACCAT-----GAGATTGTGTACACAAGTTGAGGCCACCAT-----									
	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC3006	GGGGAGTACGCGAGAATATCCGAAAACTAAGGGCGGGCCGCATCCTAGTTCCGTGCCACTCGCCCTGGAAACACCCCCCTACTCCCAGTTCGAAAGGCCGA									
	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC3006	GACTGGACAATACCGGATGGTCCAAGACTTAAGAGAGGTTGAATAAAAGGGTGGAAACCATTACCCCAACGGTTCTTAACCCCTTACACCTTCTTAGCCTC									
	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC3006	CTGCCCCCGGATCACATCTGGTATAGGCTACTCGACCTTAAGGACGCCCTTCTTCTGCCCTCCCTCTGGCCCCCTGGGAGTCAACCATTTGTTTGCCTTTGAAAT									
	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC3006	GGAGTGACCCAGAAAGAGGGGAGTCAGGACAATTAACATGGACCCGGCTGCCCAAGGGTTCAAAAACCTACCCACCCCTATTTGACGAGGCCCTCAGCCA									
	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900
KF313135	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
SUOHC3001	GGCTAAAAGGAGGGACTAGGACCCCTAACAGAAAGCCGAATAAAAGCGATCGTCCAGATTCCCTCTCCCCAAAACCAAGAGACAGGTACGCGAGTTCTTGGG									
	-----GGGAAGAGGACACTGGCTAACAGCCGGATCCAAGCCATTCTACAGATCCCCGCCCCCAACCACTAAGAGGCAAGTCAGGGAATTCTTAGG									

	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000
KF313135	.... ....									
SUOHC3001	CACGGTCGGGTACTGCAGGCTGTGGATCCCGGGGTTTCGCAGAACTAGCCGAAGCCCTGTCATGCAGTAGCCGGAGGGGGTGCCAGACCCCTGACATGGACT									
	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100
KF313135	.... ....									
SUOHC3001	AAGACCGAAGAAGAGGCATTCCAGGCCCTAAAGAGCGCTCTCCCTGCAAGCCCCAGCTCTCAGCCTCCCCGACCTTGAAAAGCCCTTCCAGTTATTTGTGG									
	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200
KF313135	.... ....									
SUOHC3001	CAGAGAACAAGGGGGTAGCAAAAGGGGTGCTCACCCAAAGGATAGGGCCCTGGAAAAGACCAGTAGCCTACCTCTCAAGAAAACTAGACCCAGTAGCTGC									
	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300
KF313135	.... ....									
SUOHC3001	TGGATGGCCTGGATGCCTACGGGCCATCGCAGCCGCTGCCCTCCTGGTCAAGGAAGCATCAAAACTCACCTTTGGACAAAACCTAGAGGTCACTTCGGCC									
	CGGATGGCCAGGTTGCTCCGAGCCATCGCGCGGCAGCCATTCTTGTAAGGAAGCCACTAAGCTGACCTTTGG-----									