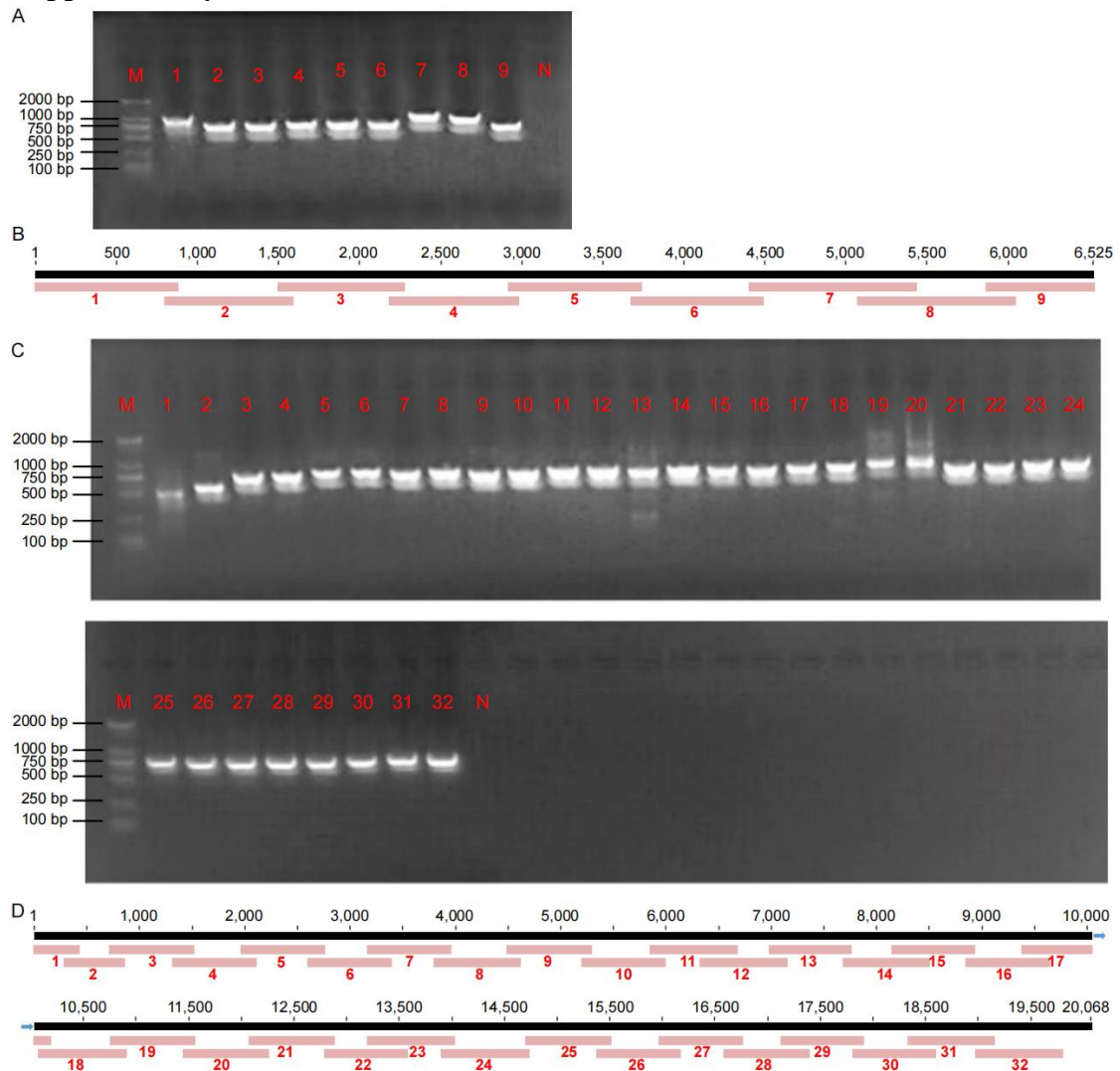




Supplementary Materials



Supplementary Figure S1. Sequence confirmation by RT-PCR and Sanger sequencing. (A) Gel electrophoresis result showing overlapping RT-PCR confirmation for GeAstV genome. The amplicons for each pair primers have been run in sequential order. (B) Graphical view of each amplicon assembly obtained from Sanger methods for GeAstV genome. (C) Gel electrophoresis result showing overlapping RT-PCR confirmation for GePV genome. The amplicons for each pair primers have been run in sequential order. (D) Graphical view of each amplicon assembly obtained from Sanger methods for GePV genome.

A

	ORF1a	RdRp	ORF2	
AVX29490 Marmot astrovirus 3	37.94	68.77	29.73	
QJF11791 Grey squirrel astrovirus	36.05	67.95	28.82	
QOE77535 Murine astrovirus	36.47	70.14	32.39	
APA19822 Rodent astrovirus	41.07	68.49	30.89	
APA19831 Rodent astrovirus	38.68	68.22	30.08	
APA19843 Rodent astrovirus	39.51	70.96	31.09	
 QNJ35016 Rodent astrovirus	42.14	69.32	35.94	Rodent
 ART85572 Mamastrovirus 4	38.83	75.07	30.60	Porcine
ARU76986 Mamastrovirus 4	38.47	72.05	32.12	
QPM92607 Pig astrovirus CX1	38.80	72.60	31.41	
QNJ99354 Rodent astrovirus	38.47	72.34	30.42	
QDH76153 Bovine astrovirus	38.19	71.51	30.76	

B

	N	P	M	F	SH	TM	G	L
Beilong virus	58.74	54.25	82.35	72.43	50.00	28.57	60.17	76.26
Tailam virus	59.56	53.04	81.18	71.79	56.58	27.80	61.29	77.04
Rodent paramyxovirus	59.02	56.35	80.00	73.13	39.24	24.32	60.03	75.39
Pohorje myodes paramyxovirus 1	52.59	45.42	74.12	69.30	22.62	22.31	55.96	72.64
Jun jeilongvirus	45.63	46.56	79.12	69.67	16.05	23.85	46.69	72.37
Mount Mabu Lophuromys virus 2	49.87	36.23	77.06	59.60		21.35	41.14	67.76
Mount Mabu Lophuromys virus 1	37.12	29.18	69.23	51.56		15.04	31.48	60.61
Feline paramyxovirus	44.81	31.28	69.14	54.24		14.13	28.04	60.77
Ruloma virus	41.84	21.16	66.47	51.63		11.71	29.90	55.74

Supplementary Figure S2. Pairwise amino acid similarities between representative strains and GeAstV and GePV, respectively. (A) Pairwise amino acid similarities between GeAstV and representative strains. (B) Comparison of sequence similarity based on amino acid sequences of the eight ORFs between GePV and nine paramyxoviruses from the genus *Jeilongvirus*.

Supplementary Table S1. Summary of the meta-transcriptomic sequence libraries used in this study.

Group ID	Library ID	Organ	Individuals	Total raw reads	Reads(RPM)	
					GeAstV	GePV
DB01	CL100105264_L01_68	Lung	10	113,817,000	1,629(14)	
DB01	CL100105264_L01_69	Kidney	10	78,417,434		
DB01	CL100105264_L01_70	Brain	10	123,766,012		
DB02	CL100105264_L01_1	Kidney	10	140,534,218		
DB02	CL100105264_L01_71	Liver	10	136,371,344		
DB02	CL100105264_L01_72	Lung	10	136,369,758		
DB02	CL100105270_L02_2	Brain	10	150,142,220		
DB03	CL100105264_L02_74	Liver	10	175,355,292		
DB03	CL100105264_L02_75	Lung	10	154,954,496	43,472(281)	
DB03	CL100105264_L02_76	Kidney	10	129,071,668	1,630(13)	
DB03	CL100105264_L02_77	Brain	10	162,219,268		
DB04	CL100105264_L02_1	Brain	10	168,271,754		
DB04	CL100105264_L02_78	Liver	10	148,987,300		
DB04	CL100105264_L02_79	Lung	10	168,931,082		
DB04	CL100105264_L02_80	Kidney	10	137,583,002	11,778(86)	
*SX04	CL100125473_L01_43	Kidney		62,583,426	16,486(263)	
*SX07	CL100125473_L01_2	Kidney		64503350	798(12.37)	
*SX10	CL100105270_L02_3	Kidney		128785198	2349(18.24)	
*SX11	CL100105270_L02_58	Kidney		148714314	856(5.76)	

*From previous meta-transcriptomic library [BioSample accession: SAMN20352314, SAMN20352323, SAMN20352335 and SAMN20352338, respectively].

Supplementary Table S2. Overlapping primer sequences used for genome confirmation

Virus	Order	Primer ID	Primer sequence(5'-3')	Size (bp)
GeAstV	1	GeAstV-1F	CAGCAGGATGGTGCCTGCT	872
		GeAstV-908R	GGCAGATTGTAAGCACTGGTTC	
		GeAstV-1089R	GCTATCCGCCAGACAGCAAG	
	2	LA-642F_1K1	TTGGTGGACACCGTTTGGAT	780
		LA-1693R_1K1	TCGAACAGCACCACCAGTAT	
		LA-787F_2K1	TGCTGTGAGTGGTGCTAAGTT	
		LA-1596R_2K1	GTGGGCGTTGCATATGAGTA	
	3	LA-1319F_1K2	TACATTGTTACTGCGGGGCA	771
		LA-2397R_1K2	ACAAGTGCACGATCCATTGC	
		LA-1483F_2K2	AAAGAGGGACTGCACTTGGG	
		LA-2283R_2K2	TGAAGCAATTGGCGAACGTC	
	4	LA-2077F_1K3	TCGTAGGTTAGCGGAGGAGA	787
		LA-3084R_1K3	GCAAGCACCAATACGAGCAT	
		LA-2161F_2K3	TGAGGAGGATTGGTTTGGGAAG	
		LA-2986R_2K3	AGCAATACCACAAAACAGGAGG	
	5	LA-2845F_1K4	GTTCAATCAACACCTGCTTATCCA	812
		LA-3883R_1K4	GCACCGATGTTGTAGCAAGAC	
		LA-2906F_2K4	ACCATTTTGGTTGGCTTCCC	
		LA-3746R_2K4	AACCCAGCAAACAACCTTTTCACA	
	6	LA-3608F_1K5	AGGATGTCTTTGGTATGTGGGT	805
		LA-4616R_1K5	AGCCACCCATACAATCTGCT	
		LA-3665F_2K5	TTGGTCTCACCTTTTGTGGC	
		LA-4498R_2K5	AGCATGTTTCCTAGCACCCAA	
	7	LA-4363F_1K6	TGAGCGGCTTTCCATTAGGT	1023
		LA-5457R_1K6	AGCTGATAAGTGGTGGCTGAG	
	8	LA-5050F_1K7	AGGCTCCATTGTTTACCGTGT	967
		LA-6086R_1K7	AGAGAGCCAGACGCTCAATC	
9	As-5,728 F	CATGGTTATGGAGAGGGATG	657	
	As-5,826 F	CCCAGGGTGCTTACTATATTAC		
GePV	1	pv-RT2	GGGATAATTGAGCCGTAGTCACT	412
		pv-RT3	TGTCCAGATGAACCCTGAGATG	
		pv-R1	GCCACCTTCTGCCATTCTGATGATCTCT	
		pv-R2	CCATGTCTCTCCCTCGAGCAACAAGC	
	2	PV-5-1K34F	GCAGCGCTTTCATTTATGACA	555
		PV-5-2K34F	CTTGCATGGTCAGTTCGTTTTCAT	
		PV-5-1K34R	AGTTAAGAAGAAGCCTGCGAGAC	
		PV-5-2K34R	ATCAGCTCCAAGATTCTGGCT	
	3	KP-516F_1K1	AGTGACTACGGCTCAATTATCCC	784
		KP-1531R_1K1	GCTGGTTTCCCTTTGTCTGC	

	KP-679F_2K1	GAGCAGACGCTGATTACAAGC	
	KP-1488R_2K1	CTCTGAGAGGTGTGTACGGG	
4	KP-1152F_1K2	TACAACCTAGGCGTTGGGATG	771
	KP-2175R_1K2	CTCCTTCGCTCTCGCTTTTG	
	KP-1277F_2K2	TCAAACAAGTGGAGGACCGA	
	KP-2079R_2K2	ACGCGTGCATCCTGTTTCT	
5	KP-1777F_1K3	CCAAGCTCAATTAACACCTCCA	784
	KP-2816R_1K3	TGCAGACGAGTCACTTTGGT	
	KP-1924F_2K3	TCTCCATGACAAGCTACAGCA	
	KP-2734R_2K3	GAACTGGGCTGGTGTAAACAGTA	
6	KP2484F_1K4-2	GCTGTTAACATCCGGAACGC	779
	KP3540R_1K4-2	ATAAGAAGTCTGCGGTGCCA	
	KP2552F_2K4-2	GCATCGTAGACTTCGAGGGA	
	KP3373R_2K4-2	GAGCTTCGGAGGATCCTGTA	
7	KP-3002F_1K5	ACCTGGTTCAGGGAAAAATGAGA	780
	KP-4036R_1K5	TTGTAAATCCCGGCGTCTGT	
	KP-3121F_2K5	TGGAAGACCTGAACATTGATAACC	
	KP-3933R_2K5	TTGCTGGAAAGATTGCTCCTG	
8	KP-3654F_1K6	GAACAGCAGGAAATCAGCAGG	799
	KP-4699R_1K6	TCGTGTTCAATTGTGTTCCGT	
	KP-3760F_2K6	TTGGCAAATCAACCTCTGCC	
	KP-4588R_2K6	ACTTTTGGGCAATGTACAGGT	
9	KP-4301F_1K7	GTGGGCTTAGCCTTCATGTG	785
	KP-5337R_1K7	ATTCTCTACGACCCCAGTTGT	
	KP-4449F_2K7	GTGTTGCAGCCATCTGTTCC	
	KP-5263R_2K7	ACAATATGCTGATATGTCACCTGAG	
10	KP-4986F_1K8	CTGGCTTACATCTGAAATCCTCA	775
	KP-6074R_1K8	CCCCGAACTAACAACCTGGAGA	
	KP-5159F_2K8	TGTCACGCCTCAGTTAGCAT	
	KP-5963R_2K8	AGTAAGCAAAGACGGGTACTCT	
11	KP-5758F_1K9	GGGCCAAATTTAAGAGACCCC	819
	KP-6760R_1K9	AGCCTTAACCCAAGAAACCAGA	
	KP-5810F_2K9	TGGAGATTTTGACTCCATGTTGA	
	KP-6655R_2K9	AGATAACAAGCCAAACAAGCGT	
12	KP-6144F_1K10	CACCAGCACCCCATTAGTT	812
	KP-7181R_1K10	CTCGTGTATATGCTGGTGGGT	
	KP-6279F_2K10	CGGTGCCAAGATCCACAATATAA	
	KP-7128R_2K10	ATTTGTAAGTGTCTGTTCCCTGCAA	
13	KP-6804F_1K11	CTTAACCCTGTACGGTACTGCT	760
	KP-7873R_1K11	ACTTGTCTCCAATCTTATCCCCT	
	KP-6932F_2K11	AAATCAGGATCATGGAACGGGA	
	KP-7731R_2K11	TGAGTAATAAATCCCTGCCTCTCT	
14	KP-7491F_1K12	TAGGAGGGAGTTAGGTCGCA	804

	KP-8530R_1K12	GGTTGTGTGCTGCTAACTGG	
	KP-7641F_2K12	GGCTTGTGACAAGGGATCA	
	KP-8476R_2K12	CAATGGACGACCCTTTGAGC	
	KP8070F_1K13-2	TCAAGCGACACTTCAGTTGC	
15	KP9072R_1K13-2	AGCTACCTGGTTTTGTTGATCCT	773
	KP8105F_2K13-2	AACAAAGAACAGTGCTCCCAC	
	KP8927R_2K13-2	ATTCTCTGCAATTGGACAAATGGT	
	KP8720F_1K14-2	TCAAGAATCACTCGCTGGCT	
16	KP9723R_1K14-2	CGAATGGTCCCTTGTGAGGT	775
	KP8806F_2K14-2	TGGTAAGTTACAACATCCCTGC	
	KP9612R_2K14-2	GGGGTTTTTGTGCCTGGTTAC	
	KP-9200F_1K15	GGGTGGCCGACAGTAATCAT	
17	KP-10282R_1K15	AATCACCCTGTCCCCTGTT	793
	KP-9342F_2K15	GTGAACTCGGAGGGTACTAGC	
	KP-10166R_2K15	TGTAGCAGGGCTTAACTCGAT	
	KP-9924F_1K16	TCCAAGAGAATGTGTCCTGGAG	
18	KP-10934R_1K16	CTTGTCCCTCAGGTTGGGACT	819
	KP-10033F_2K16	TCAATTCCACTTCTAGACTGACAGA	
	KP-10875R_2K16	TCTTCCGTTTCTAGTGTTTCATCG	
	KP-10612F_1K17	CCGGAAGATCCTGGGATGAC	
19	KP-11622R_1K17	AGTGCTGGAGATGGGATTCCG	786
	KP-10720F_2K17	TGATTGACAACATGAGTCACCAAA	
	KP-11537R_2K17	GGTCTGGCTATTTTGGGGGT	
	KP-11293F_1K18	CTCAAACCCACGGCAACAAA	
20	KP-12304R_1K18	ATACTGATTCATCCCCGTCCC	795
	KP-11413F_2K18	CCCAAATATGCACATCCGCC	
	KP-12244R_2K18	CCTTCGCCTATAACCTTCGAATC	
	KP-12053F_1K19	CATGTGACGGGGTAGTGTC	
21	KP-13086R_1K19	GGACCAGTCTTGTGTCCTAAGT	794
	KP-12053F_2K19	CATGTGACGGGGTAGTGTC	
	KP-13086R_2K19	ACCAGTTCCAAACACCTATCCA	
	KP-12625F_1K20	GACGGGAATTACGCAAGTTGG	
22	KP-13632R_1K20	TGCTAAAGACAGGACAGAGGT	769
	KP-12748F_2K20	GTGCAACAGTTCCTCATTGG	
	KP-13549R_2K20	GCATAGGGATAAGGGACTGGA	
	KP-13069F_1K21	AGGACACAAGACTGGTCCTAATC	
23	KP-14081R_1K21	TACCCACGAGTCCTAAAATTGGT	805
	KP-13165F_2K21	ATTGATGTAGAGCCCTGATCACC	
	KP-13996R_2K21	CAGACATCACAGAACATGAGCAC	
	KP-13769F_1K22	TCATGGAAGGGAGTAACTGGTAT	
24	KP-14809R_1K22	ACACCTCAACAAGTCTACGGG	818
	KP-13165F_2K22	CACAGAGGTGATTGCTGATACA	
	KP-13996R_2K22	AGGTGCAATCGCAGCTAAAG	

	KP-14573F_1K23	CTTGCGCAGCAAACCTGTGA	
25	KP-15595R_1K23	CTTGACTACGGCAGCGATCT	793
	KP-14655F_2K23	ACACTTGATGAAGACCTCACTATG	
	KP-15491R_2K23	ACCTTCTATTCCACCCATTGGA	
26	KP-15336F_2K24	CCAGGTTTCTTCTCGTGGCT	774
	KP-16145R_2K24	TGCTGTTACAGGGTCACCAA	
	KP-15244F_1K24	ACAATGAGCACATTTTTAACCACTG	
	KP-16282R_1K24	TAGAGTATGGGTCGCTTGCC	
27	KP-15911F_2K25	AGGTTTTAGTCGGTGGGTCG	775
	KP-16732R_2K25	TAAATGGGACGACCCTGTGT	
	KP-158721F_1K25	CAAGATCAGCTTGACGCAACA	
	KP-16946R_1K25	TCACTCCTCTCCTCTGTTGTAGA	
28	KP-16547F_2K26	AGGACTGAGGCCTAGATTGGT	795
	KP-17368R_2K26	TGCTCAACATGCAAGTGGTAT	
	KP-16447F_1K26	ATACCTAGAGCAGCTCATGAAATC	
	KP-17452R_1K26	CCCTAAGTACTGGTGGTGGC	
29	KP-17086F_2K27	AGTTGAAGGCCATAACACCCAT	767
	KP-17891R_2K27	TCTCCTGAACACTCTTGGATGA	
	KP-16927F_1K27	ACAACAGAGGAGAGGAGTGAGA	
	KP-18000R_1K27	ACAGCTCCTTGTGACGCAAATC	
30	KP-17767F_2K28	ATTACAGGAGGCCACAAGGG	764
	KP-19238R_2K28	AATGTTCCCTGGCTATGTTGTGAT	
	KP-17590F_1K28	GCTCAATCCTTGGCTATGACA	
	KP-18659R_1K28	GCACCTGATCCCTCTCCAAG	
31	KP18172F_1K29-1	GTGCTGTTCTGCATAATGCTCT	799
	KP19238R_1K29-1	AATGTTCCCTGGCTATGTTGTGAT	
	KP18172F_2K29-2	CAGAAGGGGTGCTGTAAAACAT	
	KP19238R_2K29-2	ACAAGGATTGCTATATGCCGGA	
32	KP-18933F_2K30	TCACTCGAGAAAACACCCGA	812
	KP-19778R_2K30	TGAGAGCTGATATGACCAATCCA	
	KP-18832F_1K30	AGCCTGAATGCACATGGGT	
	KP-19916R_1K30	TCGTATCCCCTGTGTGTATGT	
33	1K35R	ATCCCCTGTGTGTATGTCCAAT	496
	2K35R	TCCACCAGATCTTAACTTCTGC	
	1K35F	ATCCACAAAGAGGAGACTGA	
	2K35F	GAGGAGACTGATAACAGATGTC	
