Table S1. Primers used for the amplification of full-length genomes of the GAstV strain ZJCX.

Primers	Sequences (5′-3′)	Amplicon size (bp)	Purpose
GAstV 1F	CCGAAACAGCGATATGGCGGCCGGTG	2266	Genome sequencing
GAstV 2246R	GTCCTCTCGCAATTCCTCAA		
GAstV 1976F	CTGGCTGGTGTATTATTGATG	1198	Genome sequencing
GAstV 3154R	GACCATCAAACAATGAGTGCAT		
GAstV 3049F	GAGCAGCGCAAAAGGATCTG	1498	Genome sequencing
GAstV 4529R	TAAGACCACAGAAAGTCATA		
GAstV 4440F	GACACGAATGTCGTCATAG	2698	Genome sequencing
GAstV 7119R	CTTAAAAATCACATTTGATTC		
GAstV 6795F	GACTTCCACCTAGCAGTCTC	NA	3′RACE
GAstV 6838F	AAGAAGAGGCTGAGTACTGGA		nest PCR
GAstV 412R	GTTGGACAAGAGCTCCACATCG	NA	5′RACE
GAstV 204R	GCATTACACTTCATGAGAGCA		nest PCR
GAstV II-F	GAGCAGGACCAGAATGAGAAA		qRT-PCR
GAstV II-R	CACCACCAATGAGCCTAGATAC		
β-actin-F	ACATCAGGAAGGACCTGTACG		qRT-PCR
β-actin-R	GGGGCGATGATCTTGATC		
OASL-F	CAGCGTGTGGTGGTTCTC		qRT-PCR
OASL-R	AACCAGACGATGACATACAC		
TLR-3-F	CTCTCTGGAAAAAAATAAGCAATTTG		qRT-PCR
TLR-3-R	CTCAAGCAAAGTGCATGATTGC		
TLR-7-F	CACAGAAAAATGGTACCTC		qRT-PCR
TLR-7-R	TACATCGCAGGGTAAACT		
IFN-α-F	CAGCACCACATCCACCAC		qRT-PCR
IFN-α-R	TACTTGTTGATGCCGAGGT		
Mx2-F	TTCACAGCAATGGAAAGGGA		qRT-PCR
Mx2-R	ATTAGTGTCGGGTCTGGGA		
IL-6-F	AAGTTGAGTCGCTGTGCT		qRT-PCR
IL-6-R	GCTTTGTGAGGAGGGATT		
IL-8-F	GCTGTCCTGGCTCTTCTCCTGATT		qRT-PCR
IL-8-R	GGGTCCAAGCACACCTCTCTGTTG		
IL-10-F	TGCCTCCACTTGTCTGACC		qRT-PCR
IL-10-R	TCCTCCATGTAGAACCGCATC		
IFITM1-F	ATCAAGGCCCGAGATAGGA		qRT-PCR
IFITM1-R	AGAGTATCACCAGGACCAGAA		
TRIM25-F	CTGGATTTCAACACAGCTCATAAC		qRT-PCR
TRIM25-R	CCCAGCACTTGGGAACAATA		

Table S2. Analysis of the main functional amino acid sites between ZJCX and other GAstV II ORFs.

Protein	Position	Isolates							
		ZJCX	AH02	GD	JSCZ15	JSW10	ZJLD	G576	Others
ORF1a	175	M	I	M	I	M	M	M	M/I
	188	A	T	T	T	T	T	T	T
	265	T	T	S	S	S	S	S	S
	355	I	I	V	V	V	I	V	V/I
	428	N	N	T	T	N	N	T	N/T
	520	T	T	A	A	T	T	A	T/A
	527	V	A	A	A	A	A	A	A
	528	T	T	I	I	T	T	I	T/I
	535	R	R	S	S	R	R	S	R/S
	555	V	V	V	V	I	I	V	I/V
	890	V	A	A	A	A	A	A	V/A
	910	P	Q	Q	Q	Q	Q	Q	Q
	911	K	E	E	E	E	E	E	E
	912	G	V	V	V	V	V	V	V
	918	G	D	D	D	D	D	D	D
	927	V	A	A	A	A	A	A	A
ORF1b	30	T	I	I	I	I	I	I	I
	167	R	K	K	K	K	K	K	K/R
	415	R	K	K	K	K	K	K	K
ORF2	229	P	Q	Q	Q	P	P	P	P/Q
	289	A	A	A	T	T	A	T	A/T
	456	E	E	E	E	D	D	D	D/E
	464	N	N	A	A	N	N	N	A/N
	498	L	L	I	I	I	I	I	L/I
	540	L	L	L	L	Q	Q	Q	L/Q
	586	T	S	S	T	S	S	S	T/S
	587	D	N	N	N	N	N	N	N
	610	G	E	E	E	E	E	D	E/D
	614	A	A	A	A	T	A	N	A/N/S/T
	634	D	E	E	D	E	E	E	D/E
	695	T	A	A	A	A	A	A	A

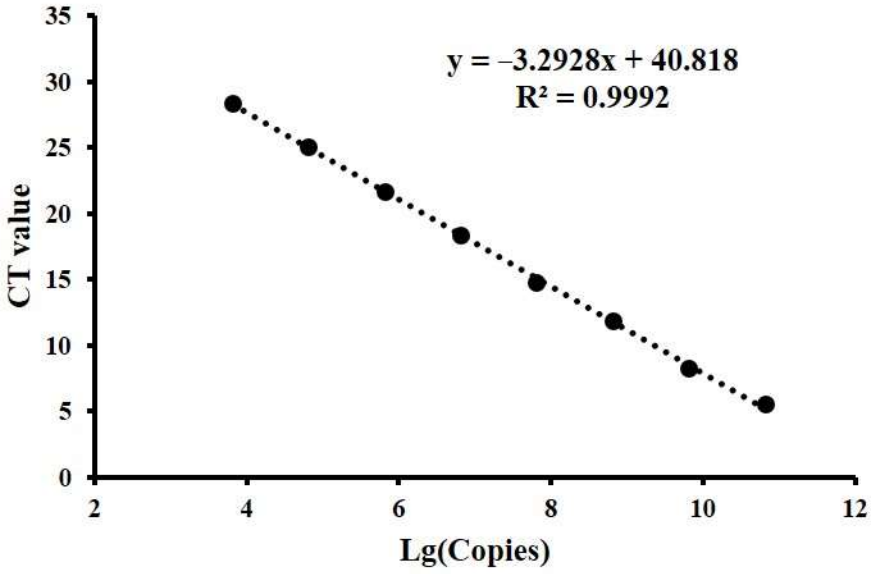

Figure S1. Establishment of a standard curve for the Duplex RT-qPCR assay. The RdRp gene fragment was amplified by PCR using GAstV-II cDNA template. The PCR product was purified and linked to the pEASY–T5 vector. DNA concentrations were determined and the copy number per μL was calculated according to the formula: 6.02×10^{23} copies/mol × Concentration/Average molecular weight. The recombinant standard plasmid with 6.49×10^{10}copies/μL was 10-fold diluted before use. One Step PrimeScript III RT-qPCR Mix was used according to instruction. The standard curve was obtained according to the average threshold cycle (Ct) and the logarithm of the initial copy number.

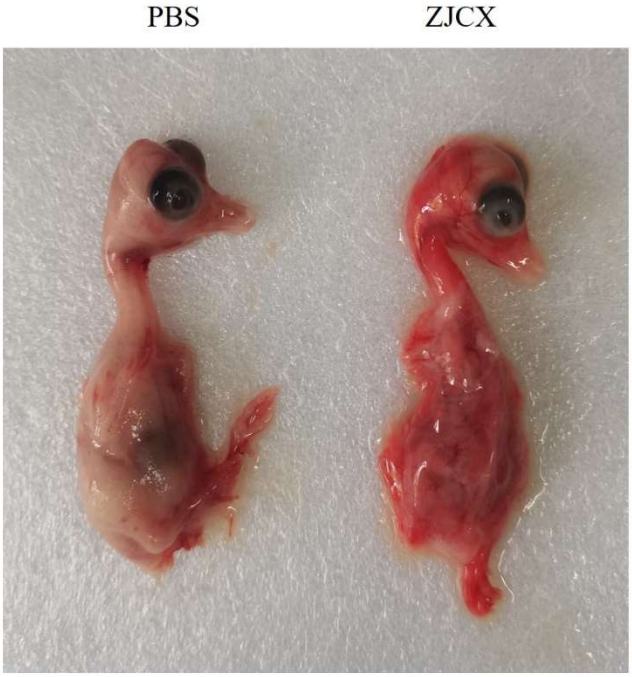

Figure S2. Isolation and identification of GAstV in goose embryos. The pathological changes in goose embryos infected with GAstV in the presence of haemorrhage and oedema.

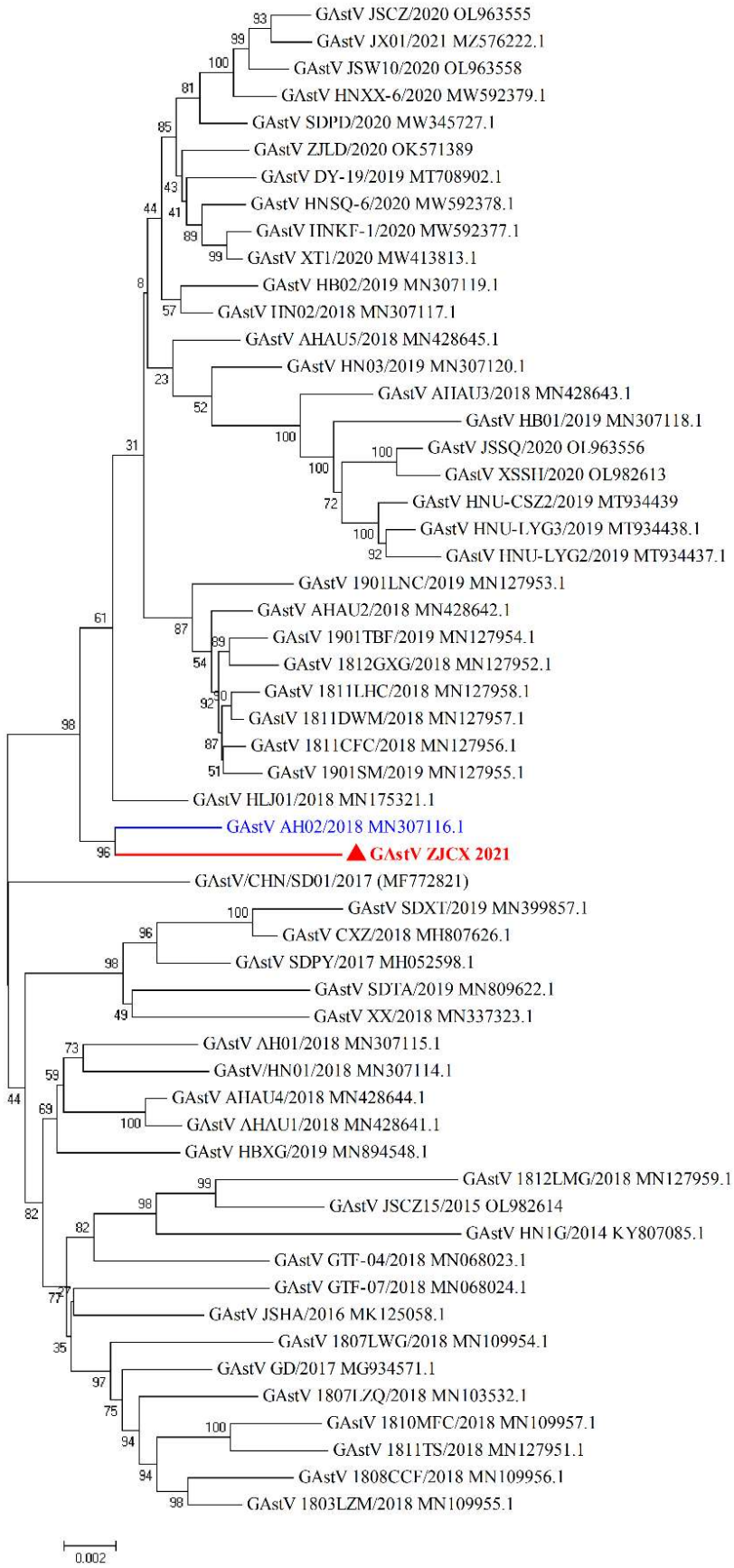

Figure S3. Phylogenetic tree of most GAstV II strains in China based on whole-genome sequences. Phylogeny-based genotyping of GAstV strains, constructed based on ClustalW alignment as a neighbor-joining tree via the neighbor-joining method (1,000 bootstrap replicates). The ZJCX (red color) strain get close to AH02 (blue color) in genetic relationships.