SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Temporal distribution of food samples tested positive for hepatitis E virus RNA. Numbers shown in boxes denote monthly number of positive samples.

Figure S2. Comparison of cycle threshold (Ct) value of hepatitis E virus (HEV) RNA in one-step quantitative reverse transcription-polymerase chain reaction assay between pig liver and other food samples. All pig liver samples are labelled with purple dots and those successfully genotyped are shown in a dark purple color. Red and blue dots denote oyster and pig intestine samples, respectively. Grey horizontal lines indicate median values.

Figure S3. Neighbor-joining phylogenetic tree of human and swine hepatitis E virus (HEV) obtained in this study from 2014—2016 in Hong Kong. The trees were constructed using Kimura 2-parameter distance method with 1,000 bootstrap replicates. Sequences used were **(A)** partial open reading frame 1 (ORF1) 133 nucleotides in length and **(B)** partial ORF2/3 junction 97 nucleotides in length. Sequences obtained in this study are shown in bold. Magenta squares denote pig liver samples and those collected in supermarket and wet market are labelled with a suffix S and W, respectively. Purple squares indicate human serum samples. Best three hits in BLAST search are included. Green triangle refers to the World Health Organization HEV RNA standard 6329/10 (subtype 3a). Proposed reference sequences of HEV subtypes are shown in brown and labelled in the following format: genotype and subtype, followed by GenBank accession number (*1*). Bootstrap values above a cut-off value of 70% are shown at nodes on the

phylogenetic tree. The tree is mid-point rooted. Scale bar indicates the number of nucleotide substitutions per site.

REFERENCES

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2. **Jothikumar N, Cromeans TL, Robertson BH, Meng XJ, and Hill VR.** 2006. A broadly reactive one-step real-time RT-PCR assay for rapid and sensitive detection of hepatitis E virus. J Virol Methods **131:**65-71.
3. **La Rosa G, Fratini M, Muscillo M, Iaconelli M, Taffon S, Equestre M, Chionne P, Madonna E, Pisani G, Bruni R, and Ciccaglione AR.** 2014. Molecular characterisation of human hepatitis E virus from Italy: comparative analysis of five reverse transcription-PCR assays. Virol J **11:**72.

Table S1. Food sampling strategy.

Food Item	Sampling Frequency	Number of District	Supermarket	Wet Market	Duration (mo)	Total Sample Number
Lamb	Twice monthly	5	+		24	240
Oyster	Twice monthly	5	+	+	24	479
Pig blood curd	Twice monthly	5		+	24	240
Pig intestine	Twice monthly	5		+	24	240
Pig liver	Twice monthly	5	+	+	24	479

+ indicates food item was purchased in that market setting. mo, month.

Table S2. Primers used in virus detection and genotyping.

Primer Name	Target Region	Function	Nucleotide Sequence (5'-3')	Positions*	Reference
Virus detection					
JVHEV-F	ORF3	Detection	GGTGGTTTCTGGGGTGAC	5261-5278	(*2*)
JVHEV-R			AGGGGTTGGTTGGATGAA	5313-5330	
JVHEV-P			6FAM-TGATTCTCAGCCCTTCGC-BHQ1	5284-5301	
Virus genotyping					
HEV-1679-F	ORF1	Outer PCR	CCAYCAGTTYATHAAGGCTCC	36-56	(*3*)
HEV-1680-R			TACCAVCGCTGRACRTC	383-367	
HEV-1681-F		Inner PCR and Sanger sequencing	CTCCTGGCRTYACWACTGC	53-71	
HEV-1682-R			GGRTGRTTCCANARVACYTC	224-205	
HEV-1847-F	ORF2/3	Outer PCR	GCRGTGGTTTCTGGGGTGAC	5259-5278	

HEV-1848-R			CTGGGMYTGGTCDCGCCAAG	5422-5403	
HEV-1849-F		Inner PCR and Sanger sequencing	GYTGATTCTCAGCCCTTCGC	5282-5301	
HEV-1850-R			GMYTGGTCDCGCCAAGHGGA	5418-5399	

*Primer positions are with reference to GenBank accession number M73218.

ORF, open reading frame; PCR, polymerase chain reaction.

	2014									2015										2016		
	Q2			Q3			Q4			Q1			Q2			Q3			Q4			Q1		
	A	M	J	J	A	S	O	N	D	J	F	M	A	M	J	J	A	S	O	N	D	J	F	M
Pig liver		1		1				1	1				1			1		1						
Pig intestine			1																					
Pig blood curd																								
Oyster		1																						
Lamb																								

Supermarket

Wet market

Figure S1

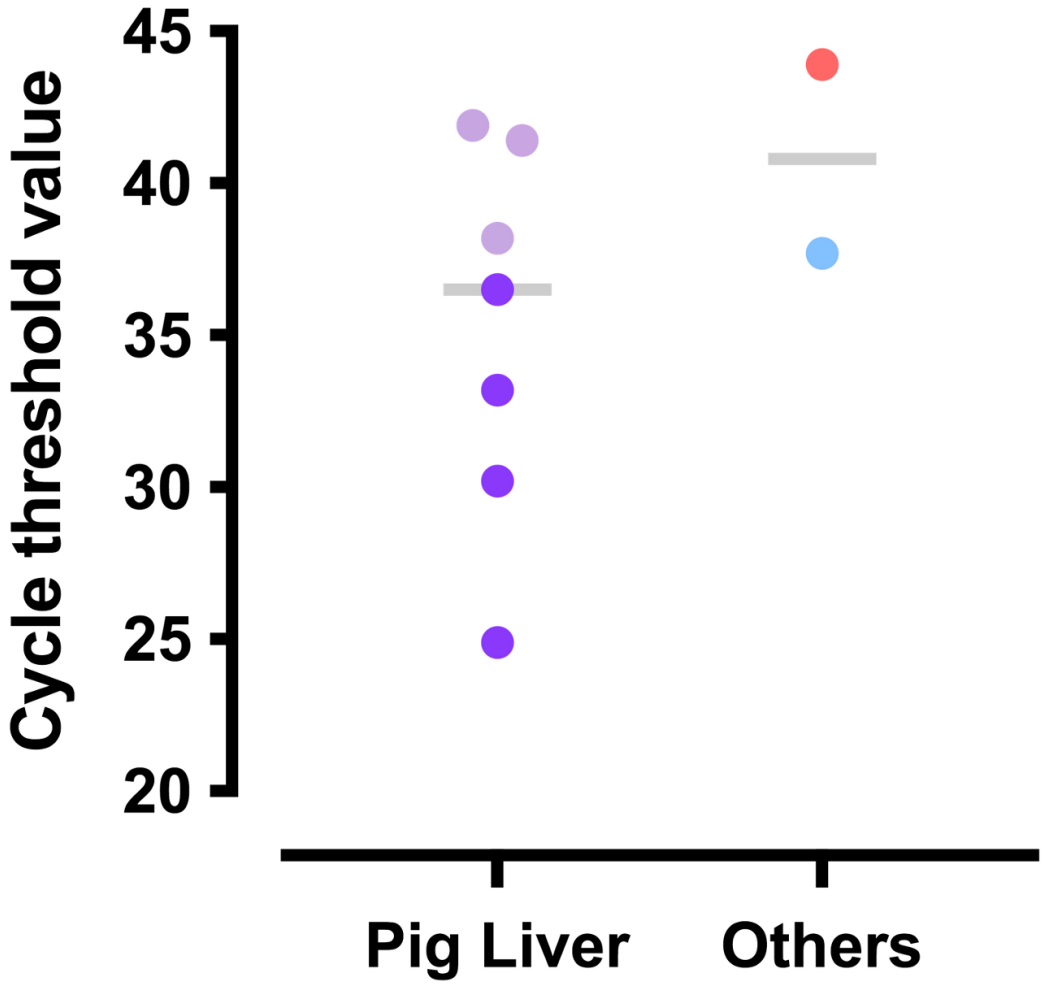
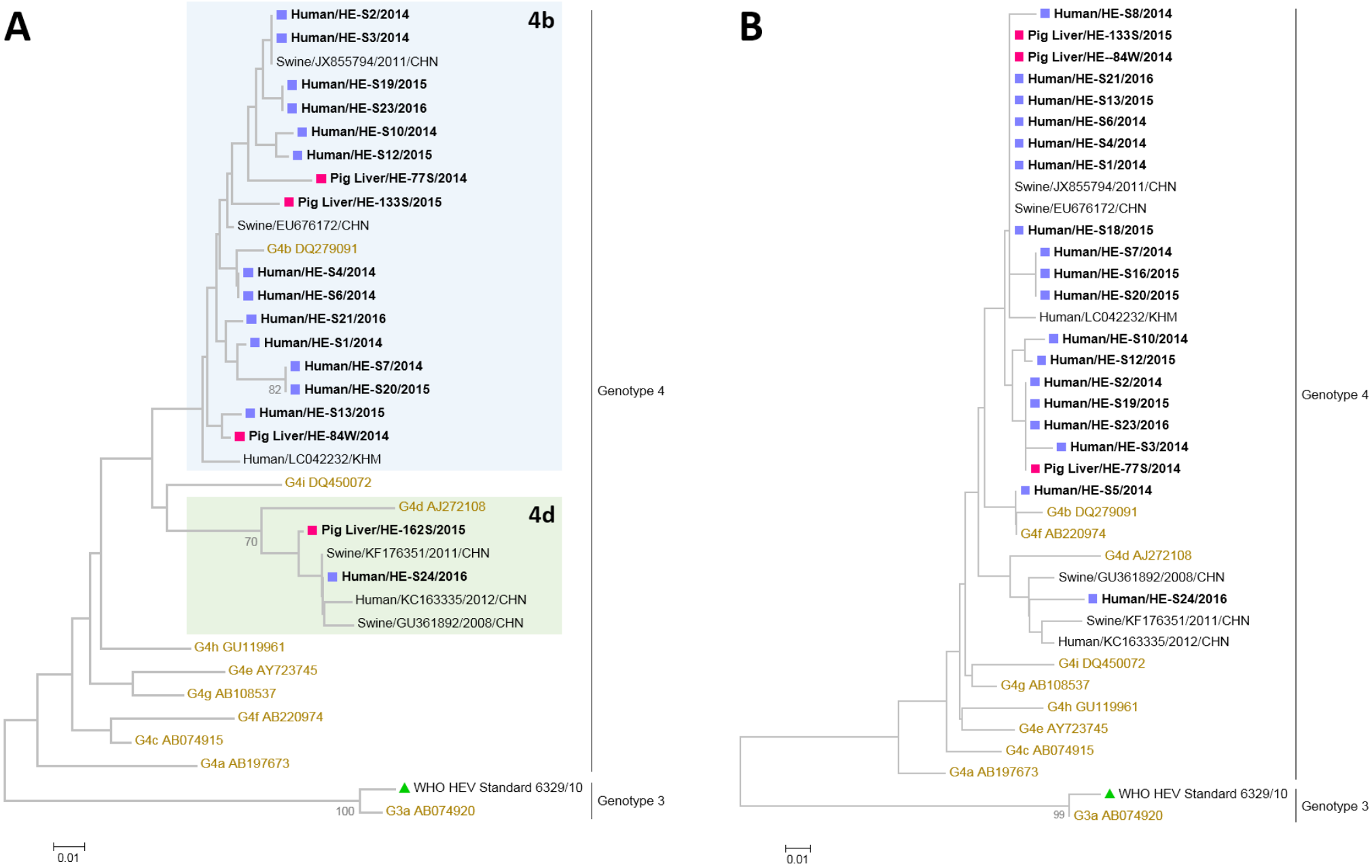


Figure S2


A
4b
Human/HE-S2/2014
Human/HE-S3/2014
Swine/JX855794/2011/CHN
Human/HE-S19/2015
Human/HE-S23/2016
Human/HE-S10/2014
Human/HE-S12/2015
Pig Liver/HE-77S/2014
Pig Liver/HE-133S/2015
Swine/EU676172/CHN
G4b DQ279091
Human/HE-S4/2014
Human/HE-S6/2014
Human/HE-S21/2016
Human/HE-S1/2014
Human/HE-S7/2014
82
Human/HE-S20/2015
Human/HE-S13/2015
Pig Liver/HE-84W/2014
Human/LC042232/KHM
G4i DQ450072
4d
G4d AJ272108
Pig Liver/HE-162S/2015
70
Swine/KF176351/2011/CHN
Human/HE-S24/2016
Human/KC163335/2012/CHN
Swine/GU361892/2008/CHN
G4h GU119961
G4e AY723745
G4g AB108537
G4f AB220974
G4c AB074915
G4a AB197673
WHO HEV Standard 6329/10
100
G3a AB074920
Genotype 4
Genotype 3
0.01
B
Human/HE-S8/2014
Pig Liver/HE-133S/2015
Pig Liver/HE--84W/2014
Human/HE-S21/2016
Human/HE-S13/2015
Human/HE-S6/2014
Human/HE-S4/2014
Human/HE-S1/2014
Swine/JX855794/2011/CHN
Swine/EU676172/CHN
Human/HE-S18/2015
Human/HE-S7/2014
Human/HE-S16/2015
Human/HE-S20/2015
Human/LC042232/KHM
Human/HE-S10/2014
Human/HE-S12/2015
Human/HE-S2/2014
Human/HE-S19/2015
Human/HE-S23/2016
Human/HE-S3/2014
Pig Liver/HE-77S/2014
Human/HE-S5/2014
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G4f AB220974
G4d AJ272108
Swine/GU361892/2008/CHN
Human/HE-S24/2016
Swine/KF176351/2011/CHN
Human/KC163335/2012/CHN
G4i DQ450072
G4g AB108537
G4h GU119961
G4e AY723745
G4c AB074915
G4a AB197673
WHO HEV Standard 6329/10
99
G3a AB074920
Genotype 4
Genotype 3
0.01

Figure S3