MR. HÉCTOR PUENTE (Orcid ID : 0000-0002-5847-9208)

DR. MARTI CORTEY (Orcid ID : 0000-0003-1126-3423)

DR. PEDRO JOSÉ GÓMEZ DE NOVA (Orcid ID : 0000-0001-9725-6747)

DR. IVAN DÍAZ (Orcid ID : 0000-0002-8090-1073)

DR. MARGA MARTÍN (Orcid ID : 0000-0003-4370-6700)

Article type : Rapid Communication

First identification and characterization of rotavirus H in swine in Spain

Running title

Rotavirus H in Spain

Authors

Héctor Puente[1], Marti Cortey[2], Pedro J.G. de Nova[1], Óscar Mencía-Ares[1], Manuel Gómez-García[1], Ivan Díaz[3], Héctor Arguello[1], Margarita Martín[2,3], Pedro Rubio[1], Ana Carvajal[1]

Affiliations

[1]Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, León, Spain.

[2]Departament de Sanitat i Anatomia Animals, Facultat de Veterinària, Universitat Autònoma de Barcelona, Bellaterra, Spain.

[3]IRTA, Centre de Recerca en Sanitat Animal (CReSA, IRTA-UAB), Universitat Autònoma de Barcelona, Bellaterra, Spain.

Correspondence

Héctor Puente, Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, 24071 León, Spain. Email: hpuef@unileon.es. Phone number: +34 987291306.

ABSTRACT

Rotaviruses (RVs) are classified into nine species or groups (RVA-RVD and RVF-RVJ). RVA, RVB and RVC are well-recognized as etiological agents of enteric disease on swine farms and have been identified in all countries with a relevant pork production. Contrarily, RVH has only been identified on swine farms from Japan and more recently from Brazil, USA, South Africa and Vietnam but not yet in Europe.

The occurrence of RVH was investigated in 103 Spanish pig herds. Nine farms were positive and we achieved a complete nucleotide sequences in three isolates while another RVH isolate was partially sequenced. Mean nucleotide identities with the RVH sequences available in GenBank ranged between 69.4 and 93.7 %. Phylogenetically, all genomic segments of Spanish RVH isolates clustered closely with other porcine RVH strains but were distantly related to human RVH as well as bat RVH strain. To the best of our knowledge this is the first report of RVH on swine farms in Europe including its characterization by means of complete genome sequencing.

KEYWORDS

Rotavirus H, swine, whole genome, genotype classification, NGS.

INTRODUCTION

Rotaviruses (RVs) are members of the family *Reoviridae* and major causative agents of gastroenteritis in humans and animals worldwide. Their genome consists of 11 segments of double-stranded RNA that encode six structural proteins (VP1–4, VP6, and VP7) and five nonstructural proteins (NSP1–5) (Estes & Kapikian, 2007). According to the International Committee on Taxonomy of Viruses, the *Rotavirus* genus is divided into nine antigenically distinct groups or species (RVA, RVB, RVC, RVD, RVF, RVG, RVH, RVI and RVJ) based on the diversity of their inner capsid protein (VP6) sequence (Matthijnssens et al., 2012; Mihalov-Kovács et al., 2015).

RV infections are very prevalent on swine farms, frequently linked to suckling and post-weaning diarrhea, which ends in large economic losses to the pork industry. Main RV groups associated with diarrhea in swine include RVA, RVB and RVC. RVA affects piglets between three and five weeks of age while RVC is much more common in young piglets (<7 days of age) (Vlasova, Amimo, & Saif, 2017).

In 1997, a new human RV tentatively named as novel adult diarrhea rotavirus (ADRV-N) which did not belong to any previously established group was described in China causing an outbreak of gastroenteritis among adults (Alam et al., 2007; Yang et al., 2004). The ADRV-N was subsequently classified as RVH based on VP6 sequence analysis (Matthijnssens et al., 2012). In total, three human RVH strains from Asia (ADRV-N and J19 from China and B219 from Bangladesh) as well as a porcine RVH strain from Japan (SKA-1) were identified between 1997-2002 (Jiang et al., 2008; Nagashima et al., 2008). Since then, RVH has been reported in pigs from Japan (Suzuki & Inoue, 2018; Wakuda et al., 2011), USA (Marthaler et al., 2014), Brazil (Molinari, Lorenzetti, Otonel, Alfieri, & Alfieri, 2014), South Africa (Nyaga et al., 2016) and Vietnam (Phan et al., 2016). Although RVH has been detected in diarrheic samples from pigs, coinfections with other pathogens are common and its role in the etiology of enteric disease has not been established (Shepherd, Freeman, Culhane, & Marthaler, 2019). More recently RVH has been also reported in bats in Cameroon (Yinda et al., 2018).

To the best of our knowledge there are no reports of porcine RVH in Europe. Here we introduce the first detection and characterization of RVH in pigs with diarrhea from Spanish pig farms, the main European pig producer.

MATERIAL AND METHODS

The study was performed on 103 Spanish swine commercial farms with diarrhea outbreaks in which a viral etiology was suspected between 2017-2019 (shadow area in Figure 1). Farms were distributed throughout the country and fecal samples (2 to 6 per farm) were submitted for diagnostic purposes to the Animal Health Department of the University of León. The diagnosis included nursing piglets (<21 days) (26 farms), postweaning-growing pigs (21-70 days) (11 farms) or fattening pigs (>70 days) (33 farms). The age of affected animals was unknown on 33 farms.

Total RNA was extracted from one pooled fecal sample (2-6 individual samples) per farm using QIAamp Viral RNA Mini Kit (Qiagen) following the manufacturer’s instructions. Then, we performed a reverse transcription PCR (RT-PCR) using a newly designed primer pair, based on the VP6 gene from reference sequences of porcine RVH strains obtained from GenBank (Table 1), and amplifying a 1240 nt fragment. The RT-PCR reactions were carried out with the Verso 1-Step RT-PCR ReddyMix Kit (Thermo Scientific), following the manufacturer's recommendations, with the following cycling conditions: an initial step of 50ºC for 30 min and 95ºC for 2 min; followed by 45 cycles of 95ºC for 20 s, 50ºC for 30 s and 72ºC for 1 min; with a final extension step at 72ºC for 10 min.

From each positive pooled sample by RT-PCR to RVH, total RNA was extracted using a TRIzol LS reagent (Thermo Scientific) protocol. The total RNA extraction was directly sequenced at the Genomics Bioinformatics Service (SGB) of the Autonomous University of Barcelona (UAB), without using any primer or amplification step. Next Generation Sequencing (NGS) was carried out using an Illumina Miseq Platform. RVH sequences were obtained from NGS outputs applying a tailor-made, virus-specific script developed by us (Cortey et al., 2019). We confirmed each segment identified by BLAST analyses on the assembled sequences using the NCBI GenBank online tool (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Sequences were aligned using CLUSTALW. The evolutionary relationships among sequences were analyzed with a phylogenetic analysis, using the Maximum-Likelihood method (ML) and the Tamura-Nei substitution model with MEGAX software (Kumar, Stecher, Li, Knyaz, & Tamura, 2018). Sequences were deposited in the NCBI GenBank with the accession numbers MT644949-MT644992.

RESULTS AND DISCUSSION

We detected RVH in nine out of the 103 pooled samples (8.7%), most of them from fattening pigs (6 positive samples out of 33) or postweaning-growing pigs (2 positive samples out of 11) while only one positive sample was detected in nursing piglets (1 out of 26) (Figure 1). A similar result was reported in commercially raised pigs in the USA (15% of positive fecal samples) being the odds of RVH positive 5.9 in the >55-day group as compared with odds for the 4-20-day piglets (Marthaler et al., 2014). However, in our research, the number of RVH outbreaks did not differ significantly between age groups when compared using Fisher exact test (p=0.139). Although no significant differences were demonstrated in the number of RVH outbreaks between age groups, clearance of maternal antibodies together with the mix of piglets after weaning may explain a higher percentage of positive outbreaks (18%, 8 out of 44) in postweaning pigs (>21 days-old) as compared with suckling piglets (4%, 1 out of 26). RVH was detected as co-infection with other

RVs (A, B or C) in five outbreaks (55.5%) and with porcine epidemic diarrhea virus (PEDV) in four farms (44.4%) (Figure 1). It was the only viral etiological agent identified in two of the outbreaks, both occurring in fattening pigs. However, its role as the causative agent of diarrhea in these two outbreaks cannot be determined since we did not investigate the presence of bacterial agents causing diarrhea such as *Brachyspira* spp, *Lawsonia intracellularis* or *Salmonella* spp.

Whole genome sequencing was attempted in all the strains and we achieved the complete genome (11 segments) in three of them (SP-VC18, SP-VC29 and SP-VC36). In another strain (SP-VC19) complete segment sequence was achieved for VP4, VP6, VP1, NSP1, NSP2, NSP4 and NSP5 while partial for VP7, VP2, VP3 and NSP3. The nucleotide identity among sequences varied between 82.0%–100% for VP7, 83.2%–100% for VP4, 86.1%–100% for VP6, 87.0%–100% for VP1, 84.4%–100% for VP2, 81.6%–100% for VP3, 84.0%–100% for NSP1, 91.0-%–100% for NSP2, 83.5%–100% for NSP3, 81.5%–100% for NSP4 and 92.3%–100% for NSP5. In concordance with our results, NSP5, NSP2 and VP1 which encode proteins directly related to viral replication and assembly (phosphoprotein, NTPase and RNA-dependent RNA polymerase, respectively) have been proposed as highly conserved segments among RVH while VP3 and NSP4, encoding guanylyltransferase and enterotoxin, respectively, have greater diversity (Estes & Kapikian, 2007).

The four sequences of porcine RVH strains recovered from Spanish farms were compared with those available in GenBank, including partial and complete genome sequences of porcine RVH isolates from Japan (n=11), USA (n=2), Brazil (n=3), South Africa (n=1) and Vietnam (n=5), as well as human (n=3) and bat (n=1) RVH strains.

Pairwise identities between 69.4 and 93.7% were observed when comparing all genomic segments of Spanish porcine RVH strains with the proposed porcine RVH genotypes (Appendix 1). Also, Spanish porcine RVH strains were distantly related to human RVH strains at the nucleotide levels (31.3–71.3%), as well as to the bat RVH strain (15.9-68.0%). Accordingly, the ML phylogenetic trees shown that Spanish porcine RVH strains were more closely related to the porcine RVH strains from Japan, USA, Brazil, South Africa and Vietnam, and more distantly related to human RVH strains from Bangladesh and China and were also distinct from a bat RVH strain from Cameroon (Figure 2 and Appendix 2). Phylogenetic analyses indicate that genomic sequences of RVH isolates recovered from different host species cluster in clearly distinct sub-groups (porcine, human and bat), suggesting the lack of recent interspecies transmission events. However, this observation is based on a very limited number of fully sequenced RVH strains recovered until now in these three different host species, particularly in humans and bats. More global whole genome RVH sequences are needed to conclusively determine the RVH evolutionary pathways and their zoonotic potential. Recently a full genome-base genotyping system for RVH has been proposed with cut-off nucleotide identity values among genotypes ranging between 67 and 89 % (Suzuki & Inoue, 2018). Based on the recommended cut-off values, the Spanish porcine RVH strains were classified into one or two different genotypes for each genomic segment (Table 2 and Figure 2). Interestingly, the observed pairwise identity for segment VP7 in strains SP-VC29 and SP-VC36 exceeded cut-off values proposed for the genomic segments (86%) when compared with the rest of the available strains (Appendix 1). However, this result should be taken with caution due to limited number of RVH sequences available. This is particularly obvious in the VP6 segment (Figure 2), where the ML tree clustering seems to point to a single – very diverse – group, but according to the proposed thresholds the isolate SP-VC36 might be considered a new genotype (Appendix 1). Since more RVH sequences should be added to the proposed genotyping system and cut-offs for each genome segment should be reviewed based on them, the VP7 genotype for those strains was provisionally labelled as GX (Figure 2 and Table 2).

Herein we report the first genome sequences of four porcine RVH strains (three complete sequences and one partial sequence) from Spain being the first RVH strains identified in Europe. Our data indicate that RVH is relatively widespread in Spanish swine population being identified in almost 9% of the herein investigated diarrhea outbreaks. In addition, full genome sequencing showed its usefulness in the characterization of the isolates, will facilitate further RVH surveillance in pigs globally as well as the development of improved diagnostic methods for RVH detection on swine farms.

ACKNOWLEDGMENT

This study was supported by the program of the National Institute of Agricultural and Food Research and Technology (INIA project E-RTA2015-0003-C02-01 and E-RTA2015-0003-C02-02) of Spanish Government. H. Puente, O. Mencía-Ares, M. Cortey and H. Argüello were supported by Spanish Government (FPU17/00466, FPU16/03485, RYC-2015-1715-4 and BEAGAL-18-106, respectively) and M. Gómez-García by Junta de Castilla y León (LE131-18).

CONFLICT OF INTEREST

None of the authors of this study has a financial or personal relationship with other people or organizations that could inappropriately influence or bias the content of the paper.

ETHICAL APPROVAL

The authors confirm that the ethical policies of the journal, as noted on the journal's author guidelines page, have been adhered to, and the appropriate ethical review committee approval has been received. The regional guidelines for the care and use of animals were followed.

DATA AVAILABILITY STATEMENT

Data are available in the GenBank database (MT644949-MT644992) and by direct contact with the correspondence author.

REFERENCES

Alam, M. M., Kobayashi, N., Ishino, M., Ahmed, M. S., Ahmed, M. U., Paul, S. K., … Naik, T. N. (2007). Genetic analysis of an ADRV-N-like novel rotavirus strain B219 detected in a sporadic case of adult diarrhea in Bangladesh. *Archives of Virology*, *152*, 199-208. https://doi.org/10.1007/s00705-006-0831-y

Cortey, M., Díaz, I., Vidal, A., Martín-Valls, G., Franzo, G., Gómez De Nova, P. J., … Mateu, E. (2019). High levels of unreported intraspecific diversity among RNA viruses in faeces of neonatal piglets with diarrhoea. *BMC Veterinary Research*, *15*, 1-13. https://doi.org/10.1186/s12917-019-2204-2

Estes, M., & Kapikian, A. (2007). Rotaviruses. En M. M. et al Knipe DM, Howley PM, Griffin DE, Lamb RA (Ed.), *Fields Virology* (5.ª ed., pp. 1917-1974). Philadelphia: Lippincott Williams & Wilkins.

Jiang, S., Ji, S., Tang, Q., Cui, X., Yang, H., Kan, B., & Gao, S. (2008). Molecular characterization of a novel adult diarrhoea rotavirus strain J19 isolated in China and its significance for the evolution and origin of group B rotaviruses. *Journal of General Virology*, *89*, 2622-2629. https://doi.org/10.1099/vir.0.2008/001933-0

Kumar, S., Stecher, G., Li, M., Knyaz, C., & Tamura, K. (2018). MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution*, *35*, 1547-1549. https://doi.org/10.1093/molbev/msy096

Marthaler, D., Rossow, K., Culhane, M., Goyal, S., Collins, J., Matthijnssens, J., … Ciarlet, M. (2014). Widespread rotavirus H in domesticated pigs, United States. *Emerging Infectious Diseases*, *20*, 1195-1198. https://doi.org/10.3201/eid2007.140034

Matthijnssens, J., Otto, P. H., Ciarlet, M., Desselberger, U., van Ranst, M., & Johne, R. (2012). VP6-sequence-based cutoff values as a criterion for rotavirus species demarcation. *Archives of Virology*, *157*, 1177-1182. https://doi.org/10.1007/s00705-012-1273-3

Mihalov-Kovács, E., Gellért, Á., Marton, S., Farkas, S. L., Fehér, E., Oldal, M., … Bányai, K. (2015). Candidate new Rotavirus species in sheltered Dogs, Hungary. *Emerging Infectious Diseases*, *21*, 660-663. https://doi.org/10.3201/eid2104.141370

Molinari, B. L. D., Lorenzetti, E., Otonel, R. A. A., Alfieri, A. F., & Alfieri, A. A. (2014). Rotavirus Detected in Piglets with. *Emerging Infectious Diseases*, *20*, 1019-1022. https://doi.org/http://dx.doi.org/10.3201/eid2006.130776

Nagashima, S., Kobayashi, N., Ishino, M., Alam, M. M., Ahmed, M. U., Shyamal Kumar Paul, S. K., … Wang, Y. H. (2008). Whole Genomic Characterization of a Human Rotavirus Strain B219 Belonging to a Novel Group of the Genus Rotavirus Shigeo. *Journal of Medical Virology*, *80*, 2023-2033. https://doi.org/10.1002/jmv

Nyaga, M. M., Peenze, I., Potgieter, C. A., Seheri, L. M., Page, N. A., Yinda, C. K., … Mphahlele, M. J. (2016). Complete genome analyses of the first porcine rotavirus group H identified from a South African pig does not provide evidence for recent interspecies transmission events. *Infection, Genetics and Evolution*, *38*, 1-7. https://doi.org/10.1016/j.meegid.2015.11.032

Phan, M. V. T., Anh, P. H., Cuong, N. Van, Munnink, B. B. O., Hoek, L. Vander, My, P. T., … Cotten, M. (2016). Unbiased whole-genome deep sequencing of human and porcine stool samples reveals circulation ofmultiple groups of rotaviruses and a putative zoonotic infection. *Virus Evolution*, *2*, 1-15. https://doi.org/10.1093/ve/vew027

Shepherd, F. K., Freeman, M. J., Culhane, M. R., & Marthaler, D. G. (2019). Diseases of swine. En J. J. Zimmerman, L. A. Karriker, A. Ramirez, K. J. Schwartz, G. W. Stevenson, & J. Zhang (Eds.), *Diseases of swine* (11th ed., pp. 715-727). Hoboken: Wiley-Blackwell.

https://doi.org/10.1017/CBO9781107415324.004

Suzuki, T., & Inoue, D. (2018). Full genome-based genotyping system for rotavirus H and detection of potential gene recombination in nonstructural protein 3 between porcine rotavirus H and rotavirus C. *Journal of General Virology*, *99*, 1582-1589. https://doi.org/10.1099/jgv.0.001162

Vlasova, A. N., Amimo, J. O., & Saif, L. J. (2017). Porcine rotaviruses: Epidemiology, immune responses and control strategies. *Viruses*, *9*, 1-27. https://doi.org/10.3390/v9030048

Wakuda, M., Ide, T., Sasaki, J., Komoto, S., Ishii, J., Sanekata, T., & Taniguchi, K. (2011). Porcine rotavirus closely related to novel group of human rotaviruses. *Emerging Infectious Diseases*, *17*, 1491-1493. https://doi.org/10.3201/eid1708.101466

Yang, H., Makeyev, E. V., Kang, Z., Ji, S., Bamford, D. H., & Van Dijk, A. A. (2004). Cloning and sequence analysis of dsRNA segments 5, 6 and 7 of a novel non-group A, B, C adult rotavirus that caused an outbreak of gastroenteritis in China. *Virus Research*, *106*, 15-26. https://doi.org/10.1016/j.virusres.2004.05.011

Yinda, C. K., Ghogomu, S. M., Conceição-Neto, N., Beller, L., Deboutte, W., Vanhulle, E., … Matthijnssens, J. (2018). Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. *Virus Evolution*, *4*, 1-15. https://doi.org/10.1093/ve/vey008

Table 1. Oligonucleotide primers based on the VP6 gene designed for the detection of porcine RVH in fecal samples using RT-PCR. The nucleotide position was based on VP6 complete gene of RVH strains SKA-1 (AB576626), MRC-DPRU1575 (KT962031), MN.9.65 (KU254587) and OK.5.68 (MH230121).

Primer	Sequence (5' →3')	Nucleotide position
RVH-VP6-F	GTGACCCACAAGGATGGATCTCAT	19-42
RVH-VP6-R	GAACACTGGATCCCAGTGCGTGAC	1234-1257

Table 2. Genotypes for individual genes of the four porcine Spanish RVH strains identified in this study according to the full genome-based genotyping system proposed by Suzuki and Inoue, 2018.

Strains	Gene Segment	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5
	Cut-off in percentage	86	86	87	85	87	86	84	67	87	83	89
Porcine RVH SP-VC18		G3	P1	I3	R1	C3	M1	A6	N1	T1	E4	H3
Porcine RVH SP-VC19		G3	P1	I3	R1	C1	M1	A6	N1	T1	E4	H3
Porcine RVH SP-VC29		GX	P3	I3	R3	C3	M3	A6	N1	T1	E3	H3
Porcine RVH SP-VC36		GX	P3	I3	R3	C1	M3	A5	N1	T1	E4	H3

Figure 1**.** Map showing distribution of RVH positive farms detected through the investigation together with the date of sampling, age of affected animals and other enteric pathogens detected (RVA, RVB, RVC, porcine epidemic diarrhea virus, PEDV, and transmissible gastroenteritis virus, TGEV). Sampling area is showed by shading.

Figure 2. Maximum Likelihood trees constructed with the Tamura-Nei model for the VP7, VP4 and VP6 RVH segments. Numbers along the tree represents the confidence value for a given internal branch based on 500 Bootstrap replicates, only values larger than 70 are shown. The symbols (filled circles) above the strains indicate the porcine Spanish RVH strains identified in

this study. GenBank accession number, country and year of collection of fecal sample are also shown below the strains. Genotypes are indicated on the right of the bracket. Scale bars indicate nucleotide substitutions per site.

	Genotipo (86%)	Pig_RVH-SP-VC18	Pig_RVH-SP-VC19H	Pig_RVH-SP-VC29H	Pig_RVH-SP-VC36	AB576627.1	DQ113905.1	DQ168034.1	KM359485.1	KM359482.1	KM359487.1	KT962032.1	KU254583.2	MH230124.1	LC348470.1	LC416263.1	KX362553.1	KX362542.1	LC348463.1	LC348466.1	LC416274.1	LC416254.1	LC348469.1	Bat_MG693162.1
Pig_RVH-SP-VC18	**G3**																							
Pig_RVH-SP-VC19H	**G3**	0,974																						
Pig_RVH-SP-VC29H	**G11**	0,820	0,825																					
Pig_RVH-SP-VC36	**G11**	0,834	0,821	0,882																				
AB576627.1_Porcine_rotavirus_gene_for_VP7_complete_cds_strain:_SKA-1	**G1**	0,778	0,781	0,824	0,802																			
DQ113905.1_Adult_diarrheal_rotavirus_strain_J19_VP7_gene_complete_cds	**G2**	0,491	0,439	0,539	0,486	0,508																		
DQ168034.1_Rotavirus_B219_outer_capsid_protein_VP7_gene_complete_cds	**G2**	0,487	0,438	0,541	0,498	0,500	0,939																	
KM359485.1_Porcine_rotavirus_H_strain_BR61_VP7_gene_complete_cds	**G3**	0,880	0,877	0,806	0,818	0,786	0,517	0,517																
KM359482.1_Porcine_rotavirus_H_strain_BR59_VP7_gene_partial_cds	**G3**	0,878	0,875	0,804	0,817	0,775	0,505	0,505																
KM359487.1_Porcine_rotavirus_H_strain_BR64_VP7_gene_partial_cds	**G4**	0,751	0,733	0,828	0,810	0,856	0,493	0,501	0,792	0,783														
KT962032.1_Rotavirus_H_viral_protein_7_gene_complete_cds	**G4**	0,780	0,765	0,844	0,842	0,845	0,499	0,494	0,793	0,789	0,870													
KU254583.2_Porcine_rotavirus_H_strain_MN.9.65_VP7_gene_complete_cds	**G5**	0,834	0,834	0,847	0,832	0,792	0,512	0,520	0,801	0,798	0,785	0,801												
MH230124.1_Porcine_rotavirus_H_strain_OK.5.68_VP7_gene_complete_cds	**G5**	0,822	0,817	0,826	0,805	0,786	0,495	0,501	0,801	0,798	0,779	0,786	0,935											
LC348470.1_Porcine_rotavirus_H_NGS-16_VP7_gene_for_Viral_protein_7_complete_cds	**G5**	0,831	0,818	0,850	0,832	0,788	0,495	0,506	0,799	0,799	0,784	0,801	0,925	0,912										
LC416263.1_Porcine_rotavirus_H_NGS-17_VP7_gene_for_viral_protein_7_complete_cds	**G5**	0,828	0,798	0,824	0,801	0,780	0,506	0,519	0,806	0,803	0,769	0,809	0,911	0,903	0,914									
KX362553.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14176_13/VP7_outer_capsid_glycoprotein_(VP7)_gene_complete_cds	**G6**	0,768	0,739	0,780	0,797	0,822	0,476	0,502	0,770	0,763	0,802	0,814	0,785	0,771	0,771	0,772								
KX362542.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14250_11/VP7_outer_capsid_glycoprotein_(VP7)_gene_complete_cds	**G6**	0,768	0,744	0,785	0,793	0,825	0,483	0,503	0,783	0,776	0,807	0,816	0,783	0,773	0,772	0,764	0,968							
LC348463.1_Porcine_rotavirus_H_NGS-5_VP7_gene_for_Viral_protein_7_complete_cds	**G7**	0,768	0,755	0,797	0,801	0,857	0,467	0,478	0,775	0,776	0,827	0,849	0,778	0,765	0,779	0,764	0,808	0,804						
LC348466.1_Porcine_rotavirus_H_NGS-8_VP7_gene_for_Viral_protein_7_partial_cds	**G8**	0,744	0,732	0,721	0,710	0,708	0,477	0,468	0,758	0,754	0,738	0,758	0,731	0,719	0,744	0,723	0,733	0,737	0,713					
LC416274.1_Porcine_rotavirus_H_NGS-18_VP7_gene_for_viral_protein_7_complete_cds	**G9**	0,752	0,742	0,797	0,799	0,828	0,502	0,500	0,785	0,782	0,815	0,823	0,776	0,759	0,771	0,751	0,813	0,809	0,823	0,714				
LC416254.1_Porcine_rotavirus_H_NGS-9_VP7_gene_for_viral_protein_7_complete_cds	**G9**	0,723	0,694	0,783	0,792	0,808	0,491	0,491	0,778	0,777	0,803	0,817	0,756	0,744	0,764	0,741	0,816	0,808	0,808	0,721	0,961			
LC348469.1_Porcine_rotavirus_H_NGS-14_VP7_gene_for_Viral_protein_7_complete_cds	**G10**	0,786	0,754	0,768	0,756	0,756	0,459	0,462	0,772	0,772	0,733	0,777	0,821	0,815	0,809	0,800	0,747	0,743	0,755	0,711	0,728	0,703		
Bat_RVH_CMR63_(2014)_MG693162.1	**G12?**	0,226	0,159	0,167	0,180	0,210	0,193	0,135	0,206	0,190	0,192	0,227	0,242	0,246	0,213	0,223	0,199	0,216	0,151	0,172	0,164	0,160	0,171	

	Genotipo (86%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230119.1	AB576625.1	KU254590.2	KM359488.1	KM359491	EF453358.1	DQ113899.1	KT962030.1	KX362516.1	KX362540.1	LC416252.1	LC416272.1	KX362551.1	LC348479.1	LC348481.1	Bat_MG693160.1
Pig_RVH-VC18H	**P1**																				
Pig_RVH-VC19H	**P1**	0,951																			
Pig_RVH-VC29	**P3**	0,834	0,840																		
Pig_RVH-VC36	**P3**	0,832	0,857	0,895																	
MH230119.1:16-2463_Porcine_rotavirus_H_strain_OK.5.68_VP4_gene_complete_cds	**P1**	0,827	0,836	0,817	0,832																
AB576625.1:16-2463_Porcine_rotavirus_gene_for_VP4_complete_cds_strain:_SKA-1	**P1**	0,822	0,823	0,841	0,817	0,854															
KU254590.2:16-2463_Porcine_rotavirus_H_strain_MN.9.65_VP4_gene_complete_cds	**P1**	0,868	0,873	0,829	0,829	0,909	0,861														
KM359488.1:1-2398_Porcine_rotavirus_H_strain_BR59_VP4_gene_partial_cds	**P1**	0,826	0,828	0,833	0,824	0,874	0,873	0,878													
KM359491.1:1-2398_Porcine_rotavirus_H_strain_BR61_VP4_gene_partial_cds	**P1**	0,827	0,829	0,832	0,824	0,874	0,872	0,878													
EF453358.1:830-2460_Human_rotavirus_B219_VP4_mRNA_complete_cds	**P2**	0,534	0,544	0,557	0,553	0,518	0,496	0,516	0,511	0,510											
DQ113899.1:813-2451_Adult_diarrheal_rotavirus_strain_J19_VP4_gene_complete_cds	**P2**	0,525	0,525	0,553	0,540	0,501	0,480	0,498	0,502	0,501	0,914										
KT962030.1:16-2463_Rotavirus_H_viral_protein_4_gene_complete_cds	**P3**	0,837	0,845	0,886	0,884	0,832	0,840	0,830	0,840	0,840	0,529	0,512									
KX362516.1:1-2448_Rotavirus_H_strain_RVH/Pig-wt/VNM/12089_8/VP4_outer_capsid_spike_protein_(VP4)_gene_complete_cds	**P4**	0,803	0,814	0,833	0,831	0,805	0,817	0,811	0,808	0,807	0,506	0,497	0,854								
KX362540.1:1-2448_Rotavirus_H_strain_RVH/Pig-wt/VNM/14250_11/VP4_outer_capsid_spike_protein_(VP4)_gene_complete_cds	**P4**	0,807	0,817	0,840	0,838	0,811	0,818	0,814	0,812	0,811	0,516	0,513	0,854	0,970							
LC416252.1:1-2421_Porcine_rotavirus_H_NGS-9_VP4_gene_for_viral_protein_4_partial_cds	**P5**	0,780	0,782	0,792	0,804	0,781	0,781	0,776	0,787	0,787	0,522	0,508	0,797	0,784	0,787						
LC416272.1:16-2463_Porcine_rotavirus_H_NGS-18_VP4_gene_for_viral_protein_4_complete_cds	**P5**	0,790	0,792	0,809	0,814	0,795	0,811	0,786	0,800	0,799	0,526	0,514	0,819	0,800	0,799	0,953					
KX362551.1:1-2448_Rotavirus_H_strain_RVH/Pig-wt/VNM/14176_13/VP4_outer_capsid_spike_protein_(VP4)_gene_complete_cds	**P5**	0,789	0,793	0,802	0,808	0,789	0,791	0,786	0,793	0,792	0,524	0,505	0,814	0,796	0,794	0,915	0,912				
LC348479.1:1-2412_Porcine_rotavirus_H_NGS-3_VP4_gene_for_Viral_protein_4_partial_cds	**P6**	0,803	0,793	0,828	0,822	0,800	0,805	0,799	0,818	0,818	0,502	0,488	0,829	0,799	0,800	0,790	0,805	0,800			
LC348481.1:1-2406_Porcine_rotavirus_H_NGS-7_VP4_gene_for_Viral_protein_4_partial_cds	**P6**	0,815	0,806	0,833	0,838	0,810	0,819	0,814	0,837	0,837	0,520	0,509	0,842	0,812	0,817	0,804	0,816	0,801	0,922		
Bat_RVH_CMR63_(2014)_MG693160.1	**P7?**	0,349	0,354	0,314	0,317	0,338	0,333	0,345	0,336	0,337	0,544	0,524	0,348	0,351	0,349	0,378	0,370	0,373	0,337	0,353	

	Genotipo (87%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230121.1	LC416253.1	LC416273.1	AB576626.1	KU254587.2	DQ113902.1	AY632080.1	DQ168033.1	KT962031.1	KF021619.1	KM359479.1	KX362517.1	KX362541.1	LC348474.1	LC348471.1	KX362552.1	KX362528.1	LC348478.1	Bat_MG693161.1
Pig_RVH-VC18H	**I3**																							
Pig_RVH-VC19H	**I3**	0,896																						
Pig_RVH-VC29	**I3**	0,874	0,881																					
Pig_RVH-VC36	**I3**	0,861	0,865	0,910																				
MH230121.1_Porcine_rotavirus_H_strain_OK.5.68_VP6_gene_complete_cds	**I1**	0,863	0,866	0,841	0,834																			
LC416253.1_Porcine_rotavirus_H_NGS-9_VP6_gene_for_viral_protein_6_partial_cds	**I1**	0,828	0,855	0,823	0,824	0,881																		
LC416273.1_Porcine_rotavirus_H_NGS-18_VP6_gene_for_viral_protein_6_complete_cds	**I1**	0,846	0,857	0,832	0,830	0,891	0,899																	
AB576626.1_Porcine_rotavirus_gene_for_VP6_complete_cds_strain:_SKA-1	**I1**	0,842	0,863	0,829	0,828	0,911	0,896	0,909																
KU254587.2_Porcine_rotavirus_H_strain_MN.9.65_VP6_gene_complete_cds	**I1**	0,868	0,874	0,841	0,835	0,953	0,881	0,897	0,916															
DQ113902.1_Adult_diarrheal_rotavirus_strain_J19_VP6_gene_complete_cds	**I2**	0,640	0,652	0,634	0,617	0,640	0,626	0,639	0,662	0,652														
AY632080.1_Human_rotavirus_ADRV-N_segment_6_complete_sequence	**I2**	0,640	0,652	0,634	0,617	0,638	0,626	0,636	0,659	0,649	0,998													
DQ168033.1_Rotavirus_B219_inner_capsid_protein_VP6_gene_complete_cds	**I2**	0,630	0,639	0,634	0,623	0,644	0,627	0,640	0,649	0,652	0,937	0,937												
KT962031.1_Rotavirus_H_viral_protein_6_gene_complete_cds	**I3**	0,876	0,882	0,861	0,861	0,859	0,841	0,856	0,854	0,860	0,654	0,652	0,638											
KF021619.1_Porcine_rotavirus_H_strain_BR59_VP6_gene_partial_cds	**I3**	0,872	0,883	0,865	0,862	0,841	0,834	0,839	0,835	0,837	0,632	0,632	0,630	0,938										
KM359479.1_Porcine_rotavirus_H_strain_BR61_VP6_gene_partial_cds	**I3**	0,872	0,883	0,866	0,862	0,842	0,833	0,839	0,836	0,837	0,631	0,631	0,630	0,937	0,835									
KX362517.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/12089_8/VP6_inner_capsid_protein_(VP6)_gene_partial_cds	**I4**	0,857	0,846	0,839	0,815	0,827	0,830	0,830	0,833	0,835	0,628	0,626	0,628	0,855	0,835	0,835								
KX362541.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14250_11/VP6_inner_capsid_protein_(VP6)_gene_complete_cds	**I4**	0,860	0,854	0,848	0,832	0,831	0,827	0,835	0,839	0,843	0,643	0,641	0,638	0,858	0,841	0,840	0,964							
LC348474.1_Porcine_rotavirus_H_NGS-7_VP6_gene_for_Viral_protein_6_partial_cds	**I5**	0,858	0,874	0,848	0,842	0,849	0,840	0,833	0,845	0,844	0,652	0,652	0,643	0,872	0,853	0,852	0,844	0,839						
LC348471.1_Porcine_rotavirus_H_NGS-3_VP6_gene_for_Viral_protein_6_partial_cds	**I5**	0,857	0,869	0,845	0,841	0,846	0,835	0,832	0,844	0,847	0,657	0,657	0,647	0,864	0,851	0,850	0,840	0,841	0,978					
KX362552.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14176_13/VP6_inner_capsid_protein_(VP6)_gene_complete_cds	**I5**	0,864	0,885	0,852	0,837	0,855	0,825	0,843	0,853	0,856	0,659	0,656	0,652	0,870	0,861	0,860	0,860	0,862	0,933	0,932				
KX362528.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/12087_40/VP6_inner_capsid_protein_(VP6)_gene_complete_cds	**I5**	0,864	0,883	0,848	0,839	0,848	0,821	0,837	0,848	0,852	0,653	0,652	0,648	0,864	0,859	0,858	0,857	0,861	0,930	0,929	0,995			
LC348478.1_Porcine_rotavirus_H_NGS-16_VP6_gene_for_Viral_protein_6_partial_cds	**I6**	0,851	0,861	0,855	0,840	0,838	0,845	0,827	0,842	0,844	0,618	0,618	0,619	0,848	0,837	0,836	0,840	0,844	0,853	0,854	0,850	0,845		
Bat_RVH_CMR63_(2014)_MG693161.1	**I8?**	0,459	0,481	0,471	0,465	0,491	0,475	0,475	0,491	0,491	0,527	0,523	0,528	0,477	0,449	0,451	0,464	0,490	0,479	0,475	0,480	0,474	0,467	

	Genotipo (85%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230116.1	LC416249.1	LC416269.1	AB576629.1	KU254592.2	EF453355.1	DQ113897.1	KT962027.1	KX362548.1	KX362537.1	Bat_MG693157.1
Pig_RVH-VC18H	**R1**															
Pig_RVH-VC19H	**R1**	0,954														
Pig_RVH-VC29	**R3**	0,900	0,870													
Pig_RVH-VC36	**R3**	0,904	0,874	0,936												
MH230116.1_Porcine_rotavirus_H_strain_OK.5.68_VP1_gene_complete_cds	**R1**	0,862	0,868	0,858	0,855											
LC416249.1_Porcine_rotavirus_H_NGS-9_VP1_gene_for_viral_protein_1_partial_cds	**R1**	0,829	0,825	0,833	0,827	0,864										
LC416269.1_Porcine_rotavirus_H_NGS-18_VP1_gene_for_viral_protein_1_complete_cds	**R1**	0,849	0,847	0,852	0,845	0,881	0,844									
AB576629.1_Porcine_rotavirus_genomic_RNA_segment_RNA1_complete_sequence_strain:_SKA-1	**R1**	0,856	0,855	0,847	0,843	0,897	0,859	0,874								
KU254592.2_Porcine_rotavirus_H_strain_MN.9.65_VP1_gene_complete_cds	**R1**	0,896	0,897	0,851	0,855	0,882	0,842	0,859	0,868							
EF453355.1_Human_rotavirus_B219_VP1_mRNA_complete_cds	**R2**	0,647	0,646	0,650	0,645	0,651	0,640	0,655	0,643	0,640						
DQ113897.1_Adult_diarrheal_rotavirus_strain_J19_VP1_gene_complete_cds	**R2**	0,632	0,634	0,637	0,633	0,648	0,631	0,649	0,642	0,632	0,927					
KT962027.1_Rotavirus_H_viral_protein_1_gene_complete_cds	**R3**	0,861	0,862	0,867	0,868	0,869	0,827	0,844	0,847	0,849	0,647	0,648				
KX362548.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14176_13/VP1_RNA-dependent_RNA_polymerase_(VP1)_gene_complete_cds	**R3**	0,850	0,847	0,853	0,845	0,856	0,823	0,838	0,836	0,842	0,648	0,643	0,870			
KX362537.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14250_11/VP1_RNA-dependent_RNA_polymerase_(VP1)_gene_complete_cds	**R3**	0,848	0,850	0,850	0,847	0,858	0,819	0,841	0,839	0,845	0,639	0,641	0,874	0,944		
Bat_RVH_CMR63_(2014)_MG693157.1	**R4?**	0,626	0,627	0,627	0,623	0,631	0,618	0,629	0,626	0,621	0,604	0,609	0,624	0,621	0,621	

	Genotipo (87%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230117.1	LC416241.1	LC416243.1	AB576630.1	KU254591.2	DQ113898.1	EF453356.1	LC416239.1	LC416242.1	KT962028.1	KX362549.1	KX362538.1	LC416260.1	LC416270.1	Bat_MG693158.1
Pig_RVH-VC18H	**C3**																			
Pig_RVH-VC19H	**C1**	0,889																		
Pig_RVH-VC29	**C3**	0,862	0,847																	
Pig_RVH-VC36	**C1**	0,844	0,844	0,856																
MH230117.1_Porcine_rotavirus_H_strain_OK.5.68_VP2_gene_complete_cds	**C1**	0,850	0,862	0,851	0,868															
LC416241.1_Porcine_rotavirus_H_NGS-5_VP2_gene_for_viral_protein_2_partial_cds	**C1**	0,846	0,851	0,846	0,866	0,896														
LC416243.1_Porcine_rotavirus_H_NGS-14_VP2_gene_for_viral_protein_2_partial_cds	**C1**	0,844	0,853	0,840	0,859	0,938	0,874													
AB576630.1_Porcine_rotavirus_genomic_RNA_segment_RNA2_complete_sequence_strain:_SKA-1	**C1**	0,858	0,857	0,856	0,855	0,893	0,872	0,878												
KU254591.2_Porcine_rotavirus_H_strain_MN.9.65_VP2_gene_complete_cds	**C1**	0,860	0,874	0,852	0,873	0,933	0,890	0,911	0,889											
DQ113898.1_Adult_diarrheal_rotavirus_strain_J19_VP2_gene_complete_cds	**C2**	0,663	0,713	0,657	0,664	0,666	0,683	0,665	0,658	0,668										
EF453356.1_Human_rotavirus_B219_VP2_mRNA_complete_cds	**C2**	0,655	0,708	0,661	0,664	0,672	0,675	0,664	0,658	0,671	0,930									
LC416239.1_Porcine_rotavirus_H_NGS-3_VP2_gene_for_viral_protein_2_partial_cds	**C3**	0,865	0,838	0,840	0,826	0,836	0,837	0,824	0,836	0,830	0,659	0,654								
LC416242.1_Porcine_rotavirus_H_NGS-7_VP2_gene_for_viral_protein_2_partial_cds	**C3**	0,870	0,844	0,847	0,828	0,842	0,837	0,831	0,840	0,838	0,659	0,657	0,967							
KT962028.1_Rotavirus_H_viral_protein_2_gene_complete_cds	**C3**	0,885	0,853	0,864	0,846	0,856	0,852	0,837	0,856	0,853	0,651	0,650	0,873	0,879						
KX362549.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14176_13/VP2_core_protein_(VP2)_gene_partial_cds	**C3**	0,889	0,853	0,871	0,848	0,854	0,860	0,840	0,860	0,855	0,702	0,700	0,929	0,934	0,894					
KX362538.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14250_11/VP2_core_protein_(VP2)_gene_partial_cds	**C3**	0,851	0,842	0,847	0,839	0,842	0,838	0,829	0,846	0,844	0,694	0,687	0,851	0,852	0,880	0,870				
LC416260.1_Porcine_rotavirus_H_NGS-17_VP2_gene_for_viral_protein_2_complete_cds	**C4**	0,835	0,839	0,834	0,842	0,866	0,864	0,854	0,864	0,867	0,673	0,666	0,819	0,822	0,832	0,848	0,833			
LC416270.1_Porcine_rotavirus_H_NGS-18_VP2_gene_for_viral_protein_2_complete_cds	**C4**	0,834	0,837	0,833	0,841	0,865	0,862	0,852	0,863	0,863	0,669	0,661	0,816	0,819	0,829	0,845	0,831	0,997		
Bat_RVH_CMR63_(2014)_MG693158.1	**C5?**	0,649	0,680	0,653	0,656	0,648	0,651	0,630	0,645	0,653	0,636	0,643	0,644	0,642	0,639	0,674	0,657	0,642	0,640	

	Genotipo (86%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230118.1	AB576631.1	KU254588.2	DQ113900.1	EF453357.1	KT962029.1	KX362550.1	KX362539.1	KX362515.1	LC416240.1	LC416261.1	LC416271.1	Bat_MG693159.1
Pig_RVH-VC18H	**M1**																	
Pig_RVH-VC19H	**M1**	0,901																
Pig_RVH-VC29	**M3**	0,826	0,868															
Pig_RVH-VC36	**M3**	0,816	0,870	0,884														
Pig_RVH_OK.5.68_(2008)_MH230118.1	**M1**	0,893	0,856	0,815	0,806													
Pig_RVH_SKA-1_(1999)_AB576631.1	**M1**	0,865	0,849	0,811	0,805	0,892												
Pig_RVH_MN.9.65_(2008)_KU254588.2	**M1**	0,937	0,885	0,823	0,815	0,941	0,893											
Human_RVH_J19_(1997)_DQ113900.1	**M2**	0,513	0,572	0,526	0,505	0,527	0,512	0,515										
Human_RVH_B219_(2002)_EF453357.1	**M2**	0,650	0,661	0,653	0,632	0,679	0,662	0,653	0,910									
Pig_RVH_MRC-DPRU1575_(2007)_KT962029.1	**M3**	0,822	0,853	0,858	0,859	0,816	0,819	0,820	0,532	0,669								
Pig_RVH_VNM/14176_13_(2012)_KX362550.1	**M4**	0,800	0,868	0,830	0,827	0,812	0,792	0,804	0,525	0,661	0,827							
Pig_RVH_VNM/14250_11_(2012)_KX362539.1	**M4**	0,781	0,845	0,808	0,805	0,795	0,778	0,782	0,514	0,658	0,804	0,976						
KX362515.1:14-2129_Rotavirus_H_strain_RVH/Pig-wt/VNM/12089_8/VP3_methyltransferase_(VP3)_gene_partial_cds	**M5**	0,808	0,850	0,829	0,827	0,814	0,803	0,809	0,511	0,657	0,846	0,819	0,800					
LC416240.1:1-2078_Porcine_rotavirus_H_NGS-3_VP3_gene_for_viral_protein_3_partial_cds	**M6**	0,819	0,841	0,835	0,810	0,798	0,805	0,809	0,494	0,634	0,818	0,854	0,834	0,813				
Pig_RVH_NGS-17_(2013)_LC416261.1	**M7**	0,836	0,856	0,808	0,800	0,850	0,848	0,857	0,525	0,661	0,808	0,793	0,779	0,796	0,809			
Pig_RVH_NGS-18_(2013)_LC416271.1	**M7**	0,839	0,855	0,808	0,801	0,851	0,850	0,861	0,522	0,667	0,807	0,791	0,777	0,796	0,809	0,995		
Bat_RVH_CMR63_(2014)_MG693159.1	**M8?**	0,540	0,582	0,524	0,510	0,533	0,523	0,533	0,527	0,602	0,528	0,551	0,541	0,547	0,520	0,545	0,542	

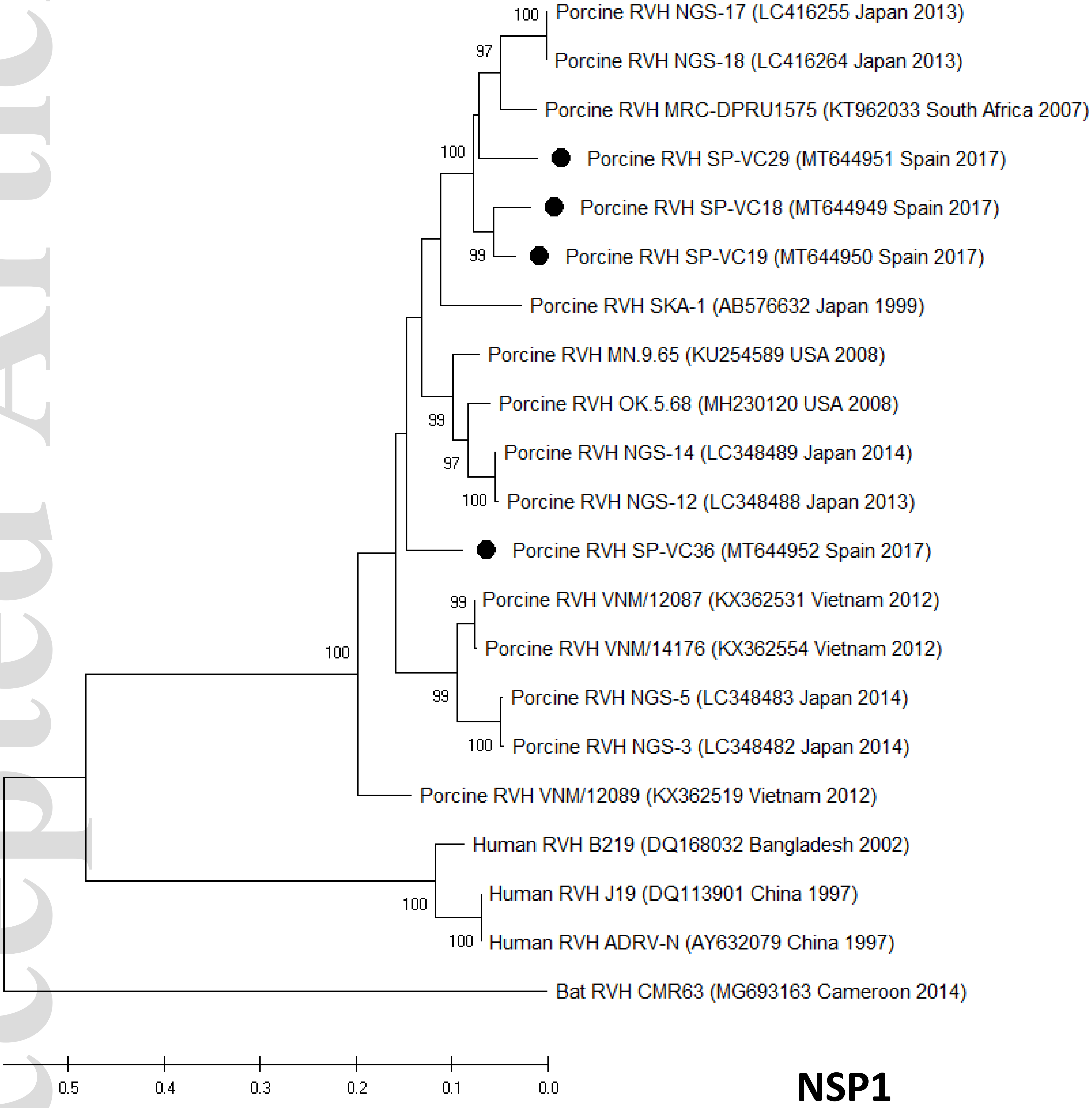
	Genotipo (84%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230120.1	AB576632.1	AY632079.1	DQ113901.1	DQ168032.1	KX362519.1	LC348482.1	LC348483.1	KX362531.1	KX362554.1	LC348488.1	LC348489.1	KU254589.2	LC416255.1	LC416264.1	KT962033.1	Bat_MG693163.1
Pig_RVH-VC18H	**A6**																					
Pig_RVH-VC19H	**A6**	0,935																				
Pig_RVH-VC29	**A6**	0,875	0,887																			
Pig_RVH-VC36	**A5**	0,841	0,853	0,839																		
MH230120.1_Porcine_rotavirus_H_strain_OK.5.68_NSP1_gene_complete_cds	**A5**	0,849	0,859	0,849	0,868																	
AB576632.1_Porcine_rotavirus_genomic_RNA_segment_RNA5_complete_sequence_strain:_SKA-1	**A1**	0,838	0,842	0,831	0,836	0,847																
AY632079.1_Human_rotavirus_ADRV-N_segment_5_complete_sequence	**A2**	0,369	0,403	0,371	0,410	0,408	0,436															
DQ113901.1_Adult_diarrheal_rotavirus_strain_J19_NSP1_gene_complete_cds	**A2**	0,369	0,403	0,371	0,410	0,408	0,436															
DQ168032.1_Rotavirus_B219_non-structural_protein_NSP1_gene_complete_cds	**A2**	0,377	0,394	0,365	0,404	0,398	0,434	0,918	0,918													
KX362519.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/12089_8/NSP1_non-structural_protein_1_(NSP1)_gene_partial_cds	**A3**	0,799	0,819	0,800	0,830	0,839	0,820	0,395	0,395	0,417												
LC348482.1_Porcine_rotavirus_H_NGS-3_NSP1_gene_for_Nonstructural_protein_1_complete_cds	**A4**	0,793	0,788	0,786	0,829	0,826	0,798	0,397	0,397	0,383	0,790											
LC348483.1_Porcine_rotavirus_H_NGS-5_NSP1_gene_for_Nonstructural_protein_1_complete_cds	**A4**	0,795	0,787	0,782	0,828	0,824	0,797	0,396	0,396	0,381	0,791	0,994										
KX362531.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/12087_40/NSP1_non-structural_protein_1_(NSP1)_gene_complete_cds	**A4**	0,819	0,823	0,793	0,848	0,845	0,830	0,415	0,415	0,402	0,824	0,931	0,932									
KX362554.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14176_13/NSP1_non-structural_protein_1_(NSP1)_gene_complete_cds	**A4**	0,814	0,818	0,787	0,844	0,831	0,815	0,417	0,417	0,403	0,810	0,930	0,930	0,998								
LC348488.1_Porcine_rotavirus_H_NGS-12_NSP1_gene_for_Nonstructural_protein_1_complete_cds	**A5**	0,844	0,848	0,839	0,866	0,942	0,839	0,403	0,403	0,403	0,822	0,810	0,809	0,826	0,818							
LC348489.1_Porcine_rotavirus_H_NGS-14_NSP1_gene_for_Nonstructural_protein_1_complete_cds	**A5**	0,844	0,850	0,842	0,869	0,946	0,841	0,403	0,403	0,399	0,823	0,812	0,811	0,828	0,822	0,994						
KU254589.2_Porcine_rotavirus_H_strain_MN.9.65_NSP1_gene_complete_cds	**A5**	0,858	0,867	0,855	0,871	0,932	0,848	0,434	0,434	0,420	0,845	0,827	0,826	0,846	0,835	0,927	0,928					
LC416255.1_Porcine_rotavirus_H_NGS-17_NSP1_gene_for_nonstructural_protein_1_complete_cds	**A6**	0,872	0,886	0,860	0,828	0,845	0,838	0,408	0,408	0,397	0,823	0,809	0,807	0,837	0,827	0,819	0,821	0,842				
LC416264.1_Porcine_rotavirus_H_NGS-18_NSP1_gene_for_nonstructural_protein_1_complete_cds	**A6**	0,871	0,885	0,861	0,827	0,844	0,839	0,411	0,411	0,400	0,822	0,807	0,806	0,836	0,826	0,818	0,820	0,841	0,998			
KT962033.1_Rotavirus_H_non-structural_protein_1_gene_complete_cds	**A6**	0,877	0,890	0,884	0,830	0,840	0,849	0,396	0,396	0,408	0,825	0,803	0,804	0,836	0,828	0,826	0,826	0,836	0,912	0,914		
Bat_RVH_CMR63_(2014)_MG693163.1	**A7?**	0,208	0,221	0,196	0,219	0,239	0,236	0,206	0,206	0,209	0,171	0,234	0,231	0,240	0,226	0,237	0,230	0,234	0,202	0,199	0,228	

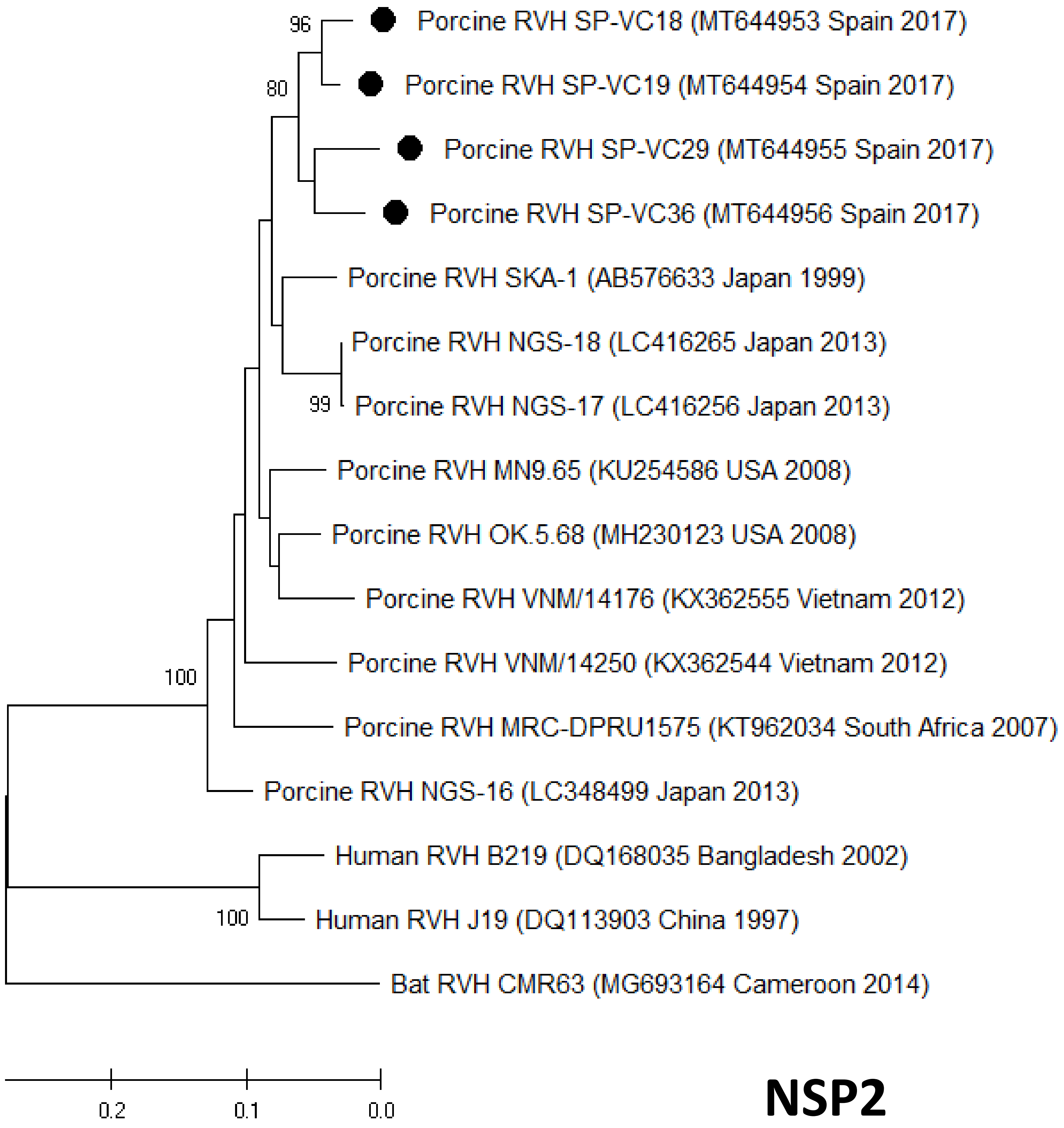
	Genotipo (67%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	AB576633.1	LC348499.1	LC416256.1	LC416265.1	KU254586.2	MH230123.1	KT962034.1	KX362555.1	KX362544.1	DQ168035.1	DQ113903.1	Bat_MG693164.1
Pig_RVH-VC18H	**N1**																
Pig_RVH-VC19H	**N1**	0,963															
Pig_RVH-VC29	**N1**	0,911	0,910														
Pig_RVH-VC36	**N1**	0,914	0,924	0,911													
Pig_RVH_SKA-1_(1999)_AB576633.1	**N1**	0,902	0,906	0,887	0,889												
Pig_RVH_NGS-16_(2013)_LC348499.1	**N1**	0,878	0,893	0,888	0,873	0,884											
Pig_RVH_NGS-17_(2013)_LC416256.1	**N1**	0,901	0,911	0,890	0,899	0,914	0,883										
Pig_RVH_NGS-18_(2013)_LC416265.1	**N1**	0,903	0,914	0,890	0,902	0,916	0,885	0,997									
Pig_RVH_USA/MN9.65-4_(2008)_KU254586.2	**N1**	0,898	0,910	0,891	0,886	0,911	0,891	0,900	0,903								
Pig_RVH_USA/OK.5.68_(2008)_MH230123.1	**N1**	0,896	0,907	0,894	0,900	0,915	0,893	0,902	0,904	0,927							
Pig_RVH_MRC-DPRU1575_(2007)_KT962034.1	**N1**	0,879	0,889	0,870	0,865	0,865	0,871	0,881	0,883	0,873	0,881						
Pig_RVH_VNM/14176_(2012)_KX362555.1	**N1**	0,893	0,907	0,888	0,884	0,887	0,884	0,895	0,899	0,903	0,911	0,875					
Pig_RVH_VNM/14250_(2012)_KX362544.1	**N1**	0,872	0,880	0,864	0,869	0,880	0,883	0,880	0,883	0,893	0,880	0,861	0,879				
Human_RVH_B219_(2002)_DQ168035.1	**N2**	0,641	0,653	0,653	0,643	0,648	0,648	0,644	0,642	0,649	0,656	0,640	0,640	0,635			
Human_RVH_J19_(1997)_DQ113903.1	**N2**	0,641	0,649	0,673	0,667	0,654	0,660	0,662	0,658	0,662	0,679	0,658	0,656	0,648	0,917		
Bat_RVH_CMR63_(2014)_MG693164.1	**N3?**	0,584	0,590	0,598	0,608	0,605	0,604	0,608	0,606	0,604	0,608	0,594	0,578	0,593	0,563	0,572	

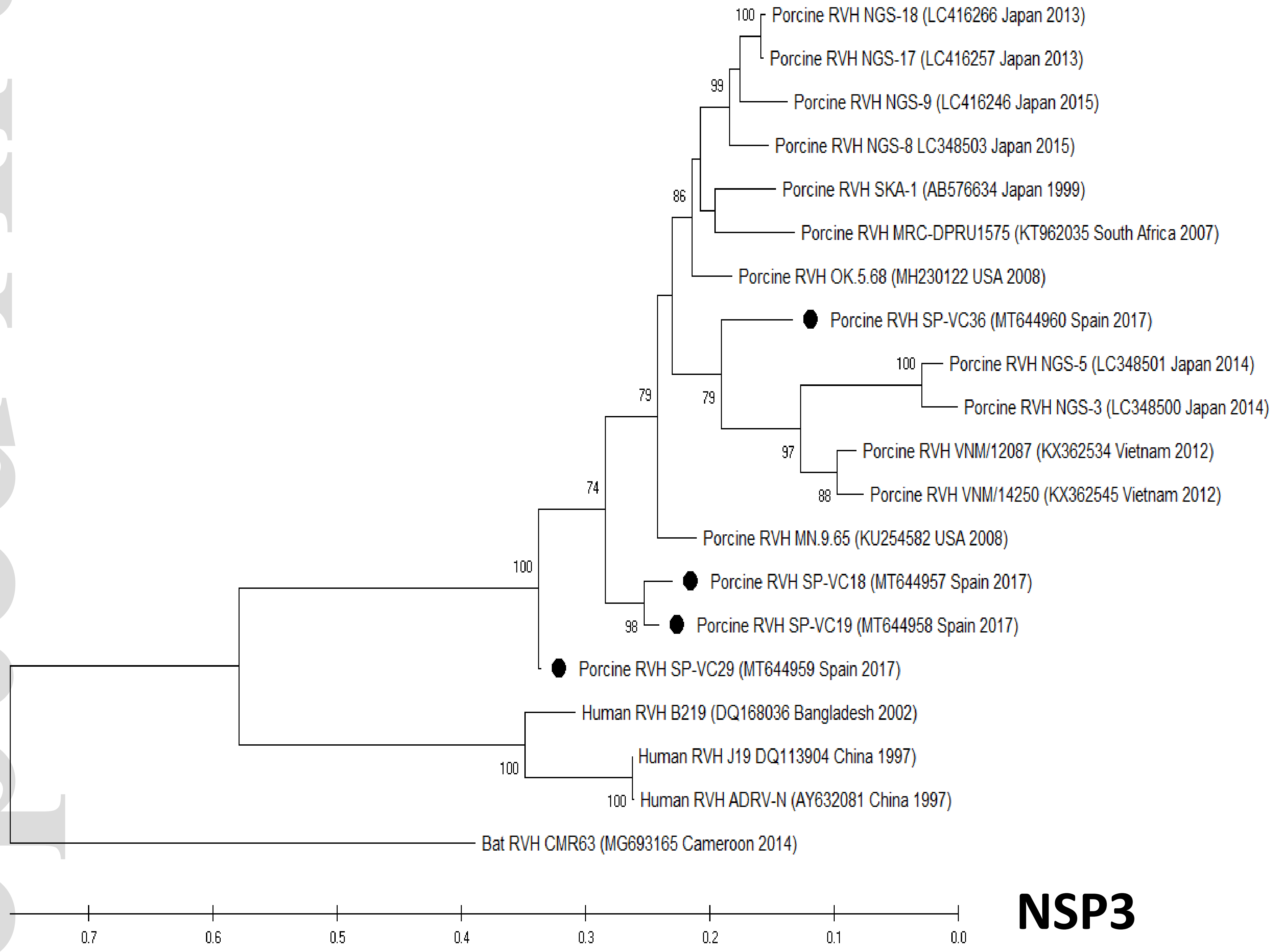
	Genotipo (87%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230122,1	AB576634.1	LC348503.1	LC416246.1	KU254582.2	KT962035.1	DQ113904.1	DQ168036.1	AY632081.1	KX362545.1	KX362534.1	LC348500.1	LC348501.1	LC416266.1	LC416257.1	Bat_MG693165.1
Pig_RVH-VC18H	**T1**																				
Pig_RVH-VC19H	**T1**	0,961																			
Pig_RVH-VC29	**T1**	0,901	0,921																		
Pig_RVH-VC36	**T1**	0,835	0,837	0,847																	
MH230122.1_Porcine_rotavirus_H_strain_OK.5.68_NSP3_gene_complete_cds	**T1**	0,863	0,862	0,879	0,871																
AB576634.1_Porcine_rotavirus_genomic_RNA_segment_RNA8_complete_sequence_strain:_SKA-1	**T1**	0,852	0,853	0,865	0,861	0,906															
LC348503.1_Porcine_rotavirus_H_NGS-8_NSP3_gene_for_Nonstructural_protein_3_complete_cds	**T1**	0,865	0,859	0,881	0,862	0,911	0,897														
LC416246.1_Porcine_rotavirus_H_NGS-9_NSP3_gene_for_nonstructural_protein_3_complete_cds	**T1**	0,867	0,847	0,871	0,856	0,902	0,891	0,930													
KU254582.2_Porcine_rotavirus_H_strain_MN.9.65_NSP3_gene_complete_cds	**T1**	0,896	0,889	0,881	0,881	0,909	0,894	0,891	0,888												
KT962035.1_Rotavirus_H_non-structural_protein_3_gene_complete_cds	**T1**	0,853	0,840	0,858	0,833	0,898	0,886	0,875	0,883	0,882											
DQ113904.1_Adult_diarrheal_rotavirus_strain_J19_NSP3_gene_complete_cds	**T2**	0,544	0,565	0,572	0,558	0,533	0,498	0,526	0,549	0,526	0,520										
DQ168036.1_Rotavirus_B219_non-structural_protein_NSP3_gene_complete_cds	**T2**	0,546	0,569	0,595	0,550	0,527	0,500	0,553	0,556	0,544	0,506	0,871									
AY632081.1_Human_rotavirus_ADRV-N_segment_7_complete_sequence	**T2**	0,544	0,565	0,572	0,558	0,543	0,503	0,528	0,551	0,532	0,524	0,999	0,865								
KX362545.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14250_11/NSP3_non-structural_protein_3_(NSP3)_gene_partial_cds	**T3**	0,863	0,841	0,840	0,854	0,864	0,837	0,860	0,860	0,870	0,830	0,567	0,541	0,567							
KX362534.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/12087_40/NSP3_non-structural_protein_3_(NSP3)_gene_partial_cds	**T3**	0,854	0,838	0,835	0,868	0,864	0,851	0,863	0,856	0,875	0,841	0,581	0,570	0,581	0,961						
LC348500.1_Porcine_rotavirus_H_NGS-3_NSP3_gene_for_Nonstructural_protein_3_complete_cds	**T3**	0,815	0,798	0,807	0,830	0,765	0,773	0,771	0,781	0,778	0,748	0,427	0,425	0,429	0,886	0,892					
LC348501.1_Porcine_rotavirus_H_NGS-5_NSP3_gene_for_Nonstructural_protein_3_complete_cds	**T3**	0,820	0,807	0,824	0,841	0,763	0,773	0,769	0,786	0,773	0,742	0,447	0,433	0,449	0,898	0,897	0,952				
LC416266.1_Porcine_rotavirus_H_NGS-18_NSP3_gene_for_nonstructural_protein_3_complete_cds	**T4**	0,867	0,853	0,871	0,864	0,912	0,898	0,942	0,939	0,895	0,897	0,527	0,543	0,529	0,862	0,866	0,772	0,770			
LC416257.1_Porcine_rotavirus_H_NGS-17_NSP3_gene_for_nonstructural_protein_3_complete_cds	**T4**	0,865	0,849	0,870	0,862	0,912	0,893	0,944	0,942	0,895	0,892	0,523	0,539	0,525	0,862	0,861	0,769	0,767	0,993		
Bat_RVH_CMR63_(2014)_MG693165.1	**T5?**	0,463	0,532	0,475	0,451	0,427	0,428	0,401	0,405	0,407	0,396	0,379	0,399	0,377	0,410	0,454	0,203	0,206	0,398	0,387	

	Genotipo (83%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230125.1	LC348512.1	AB576628.1	DQ113906.1	EF453359.1	KT962036.1	KM359494.1	KM359497.1	KU254585.2	KX362535.1	KX362546.1	LC348511.1	LC416258.1	KX362556.1	KX362522.1	Bat_MG693166.1
Pig_RVH-VC18H	**E4**																				
Pig_RVH-VC19H	**E4**	0,964																			
Pig_RVH-VC29	**E3**	0,815	0,819																		
Pig_RVH-VC36	**E4**	0,836	0,841	0,848																	
MH230125.1_Porcine_rotavirus_H_strain_OK.5.68_NSP4_gene_complete_cds	**E1**	0,787	0,786	0,784	0,785																
LC348512.1_Porcine_rotavirus_H_NGS-14_NSP4_gene_for_Nonstructural_protein_4_complete_cds	**E1**	0,744	0,750	0,766	0,764	0,883															
AB576628.1_Porcine_rotavirus_gene_for_NSP4_complete_cds_strain:_SKA-1	**E1**	0,762	0,763	0,777	0,796	0,876	0,861														
Human_RVH_J19_(1997)_DQ113906.1	**E2**	0,473	0,386	0,418	0,491	0,473	0,483	0,442													
EF453359.1_Human_rotavirus_B219_NSP4_mRNA_complete_cds	**E2**	0,351	0,329	0,313	0,340	0,418	0,339	0,413	0,900												
KT962036.1_Rotavirus_H_non-structural_protein_4_gene_complete_cds	**E3**	0,811	0,827	0,850	0,841	0,835	0,818	0,794	0,449	0,380											
KM359494.1_Porcine_rotavirus_H_strain_BR59_NSP4_gene_complete_cds	**E3**	0,807	0,819	0,819	0,836	0,802	0,769	0,777	0,511	0,386	0,919										
KM359497.1_Porcine_rotavirus_H_strain_BR61_NSP4_gene_complete_cds	**E3**	0,807	0,819	0,819	0,836	0,800	0,767	0,775	0,511	0,385	0,919	1,000									
KU254585.2_Porcine_rotavirus_H_strain_MN.9.65_NSP4_gene_complete_cds	**E4**	0,850	0,859	0,825	0,845	0,841	0,820	0,839	0,483	0,389	0,831	0,823	0,821								
KX362535.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/12087_40/NSP4_non-structural_protein_4_(NSP4)_gene_complete_cds	**E5**	0,750	0,757	0,812	0,801	0,798	0,779	0,770	0,512	0,372	0,860	0,843	0,842	0,804							
KX362546.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14250_11/NSP4_non-structural_protein_4_(NSP4)_gene_complete_cds	**E5**	0,752	0,759	0,814	0,808	0,787	0,776	0,754	0,502	0,353	0,844	0,841	0,840	0,793	0,979						
LC348511.1_Porcine_rotavirus_H_NGS-8_NSP4_gene_for_Nonstructural_protein_4_complete_cds	**E6**	0,788	0,786	0,809	0,798	0,767	0,782	0,764	0,501	0,424	0,817	0,819	0,818	0,796	0,791	0,788					
LC416258.1_Porcine_rotavirus_H_NGS-17_NSP4_gene_for_nonstructural_protein_4_complete_cds	**E6**	0,809	0,807	0,817	0,811	0,792	0,790	0,795	0,470	0,427	0,828	0,829	0,828	0,820	0,807	0,796	0,964				
KX362556.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14176_13/NSP4_non-structural_protein_4_(NSP4)_gene_complete_cds	**E6**	0,791	0,793	0,811	0,806	0,801	0,792	0,786	0,538	0,446	0,843	0,830	0,829	0,812	0,806	0,788	0,912	0,906			
KX362522.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/12089_8/NSP4_non-structural_protein_4_(NSP4)_gene_complete_cds	**E6**	0,780	0,785	0,809	0,807	0,782	0,782	0,762	0,530	0,420	0,840	0,835	0,834	0,795	0,814	0,805	0,927	0,919	0,910		
Bat_RVH_CMR63_(2014)_MG693166.1	**E7?**	0,199	0,195	0,238	0,231	0,222	0,233	0,219	-0,040	0,136	0,235	0,238	0,238	0,234	0,232	0,232	0,229	0,235	0,203	0,218	

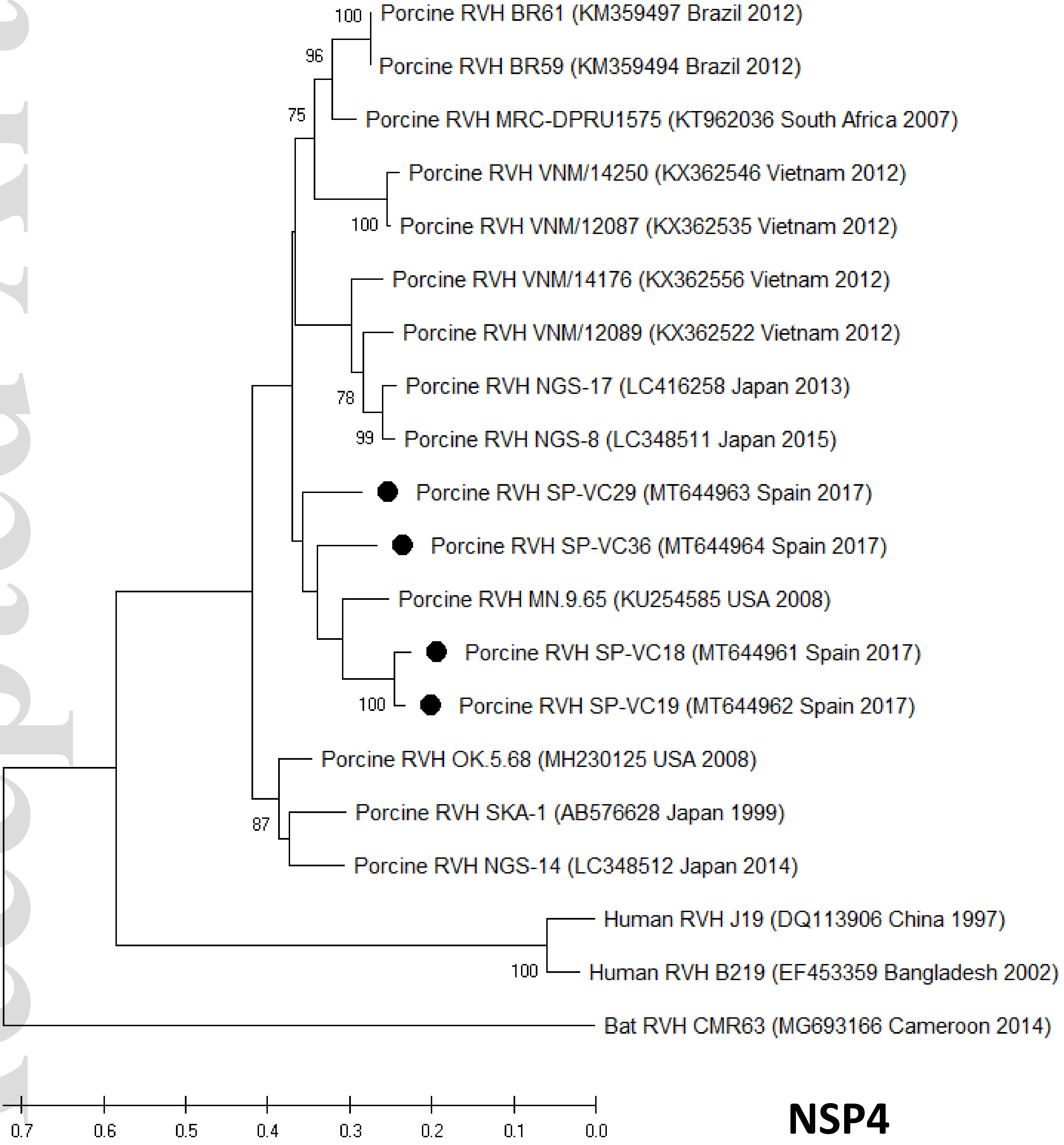
	Genotipo (89%)	Pig_RVH-VC18H	Pig_RVH-VC19H	Pig_RVH-VC29	Pig_RVH-VC36	MH230126.1	AB576635.1	LC416259.1	LC416268.1	KU254584.2	KT962037.1	KX362547.1	KX362523.1	EF453360.1	DQ113907.1	LC348513.1	LC348514.1	KX362557.1	KX362568.1	Bat_MG693167.1
Pig_RVH-VC18H	**H3**																			
Pig_RVH-VC19H	**H3**	0,936																		
Pig_RVH-VC29	**H3**	0,923	0,925																	
Pig_RVH-VC36	**H3**	0,952	0,946	0,940																
MH230126.1_Porcine_rotavirus_H_strain_OK.5.68_NSP5_gene_complete_cds	**H1**	0,895	0,890	0,899	0,915															
AB576635.1_Porcine_rotavirus_genomic_RNA_segment_RNA11_complete_sequence_strain:_SKA-1	**H1**	0,868	0,884	0,870	0,884	0,940														
LC416259.1_Porcine_rotavirus_H_NGS-17_NSP5_gene_for_nonstructural_protein_5_complete_cds	**H1**	0,870	0,875	0,875	0,882	0,939	0,920													
LC416268.1_Porcine_rotavirus_H_NGS-18_NSP5_gene_for_nonstructural_protein_5_complete_cds	**H1**	0,863	0,868	0,872	0,875	0,934	0,914	0,995												
KU254584.2_Porcine_rotavirus_H_strain_MN.9.65_NSP5_gene_complete_cds	**H1**	0,888	0,895	0,872	0,902	0,948	0,935	0,918	0,913											
KT962037.1_Rotavirus_H_non-structural_protein_5_gene_complete_cds	**H1**	0,879	0,883	0,869	0,890	0,943	0,946	0,940	0,935	0,941										
KX362547.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14250_11/NSP5_non-structural_protein_5_(NSP5)_gene_partial_cds	**H1**	0,889	0,889	0,912	0,917	0,944	0,935	0,939	0,939	0,909	0,934									
KX362523.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/12089_8/NSP5_non-structural_protein_5_(NSP5)_gene_complete_cds	**H1**	0,864	0,869	0,854	0,878	0,919	0,911	0,891	0,885	0,911	0,905	0,978								
EF453360.1_Human_rotavirus_B219_NSP5_mRNA_complete_cds	**H2**	0,567	0,549	0,554	0,571	0,614	0,609	0,585	0,588	0,604	0,619	0,673	0,602							
DQ113907.1_Adult_diarrheal_rotavirus_strain_J19_NSP5_gene_complete_cds	**H2**	0,587	0,581	0,568	0,585	0,646	0,652	0,622	0,625	0,631	0,656	0,701	0,643	0,933						
LC348513.1_Porcine_rotavirus_H_NGS-3_NSP5_gene_for_Nonstructural_protein_5_complete_cds	**H3**	0,910	0,908	0,910	0,925	0,907	0,895	0,887	0,883	0,896	0,890	0,914	0,882	0,630	0,643					
LC348514.1_Porcine_rotavirus_H_NGS-5_NSP5_gene_for_Nonstructural_protein_5_complete_cds	**H3**	0,914	0,908	0,905	0,925	0,910	0,895	0,892	0,887	0,894	0,897	0,904	0,881	0,624	0,645	0,980				
KX362557.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14176_13/NSP5_non-structural_protein_5_(NSP5)_gene_partial_cds	**H3**	0,915	0,907	0,907	0,926	0,880	0,867	0,864	0,855	0,863	0,865	0,851	0,845	0,513	0,554	0,941	0,943			
KX362568.1_Rotavirus_H_strain_RVH/Pig-wt/VNM/14254_1/NSP5_non-structural_protein_5_(NSP5)_gene_complete_cds	**H3**	0,925	0,918	0,916	0,936	0,918	0,900	0,893	0,887	0,904	0,902	0,915	0,888	0,619	0,649	0,960	0,965	0,970		
Bat_RVH_CMR63_(2014)_MG693167.1	**H4?**	0,392	0,402	0,401	0,417	0,383	0,426	0,349	0,323	0,399	0,408	#¡VALOR!	0,371	0,356	0,365	0,377	0,384	0,394	0,408	

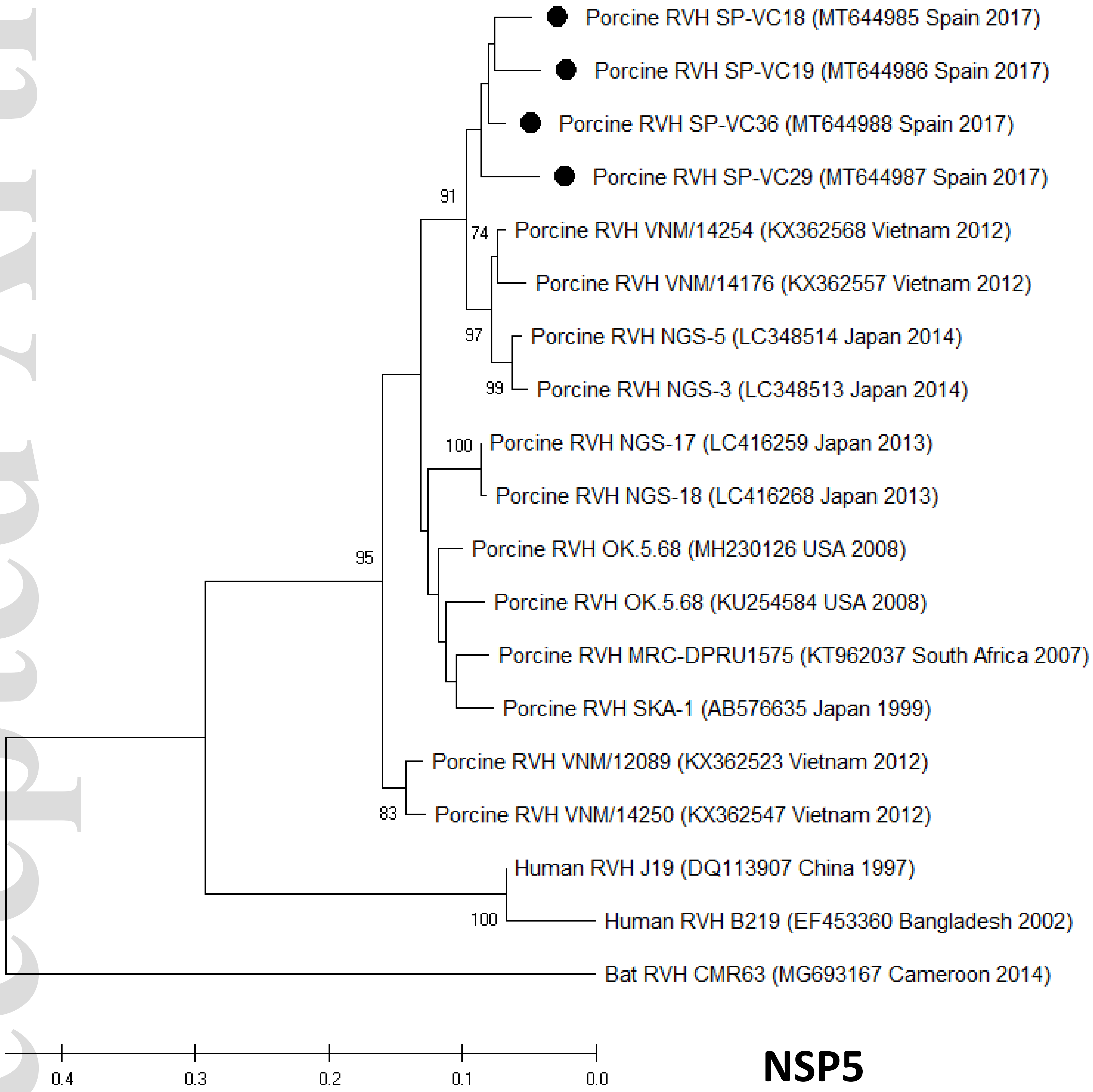

100
Porcine RVH NGS-17 (LC416255 Japan 2013)
97
Porcine RVH NGS-18 (LC416264 Japan 2013)
Porcine RVH MRC-DPRU1575 (KT962033 South Africa 2007)
100
● Porcine RVH SP-VC29 (MT644951 Spain 2017)
● Porcine RVH SP-VC18 (MT644949 Spain 2017)
99
● Porcine RVH SP-VC19 (MT644950 Spain 2017)
Porcine RVH SKA-1 (AB576632 Japan 1999)
Porcine RVH MN.9.65 (KU254589 USA 2008)
Porcine RVH OK.5.68 (MH230120 USA 2008)
99
97
Porcine RVH NGS-14 (LC348489 Japan 2014)
100
Porcine RVH NGS-12 (LC348488 Japan 2013)
● Porcine RVH SP-VC36 (MT644952 Spain 2017)
99
Porcine RVH VNM/12087 (KX362531 Vietnam 2012)
100
Porcine RVH VNM/14176 (KX362554 Vietnam 2012)
99
Porcine RVH NGS-5 (LC348483 Japan 2014)
100
Porcine RVH NGS-3 (LC348482 Japan 2014)
Porcine RVH VNM/12089 (KX362519 Vietnam 2012)
Human RVH B219 (DQ168032 Bangladesh 2002)
100
Human RVH J19 (DQ113901 China 1997)
100
Human RVH ADRV-N (AY632079 China 1997)
Bat RVH CMR63 (MG693163 Cameroon 2014)
0.5
0.4
0.3
0.2
0.1
0.0
NSP1

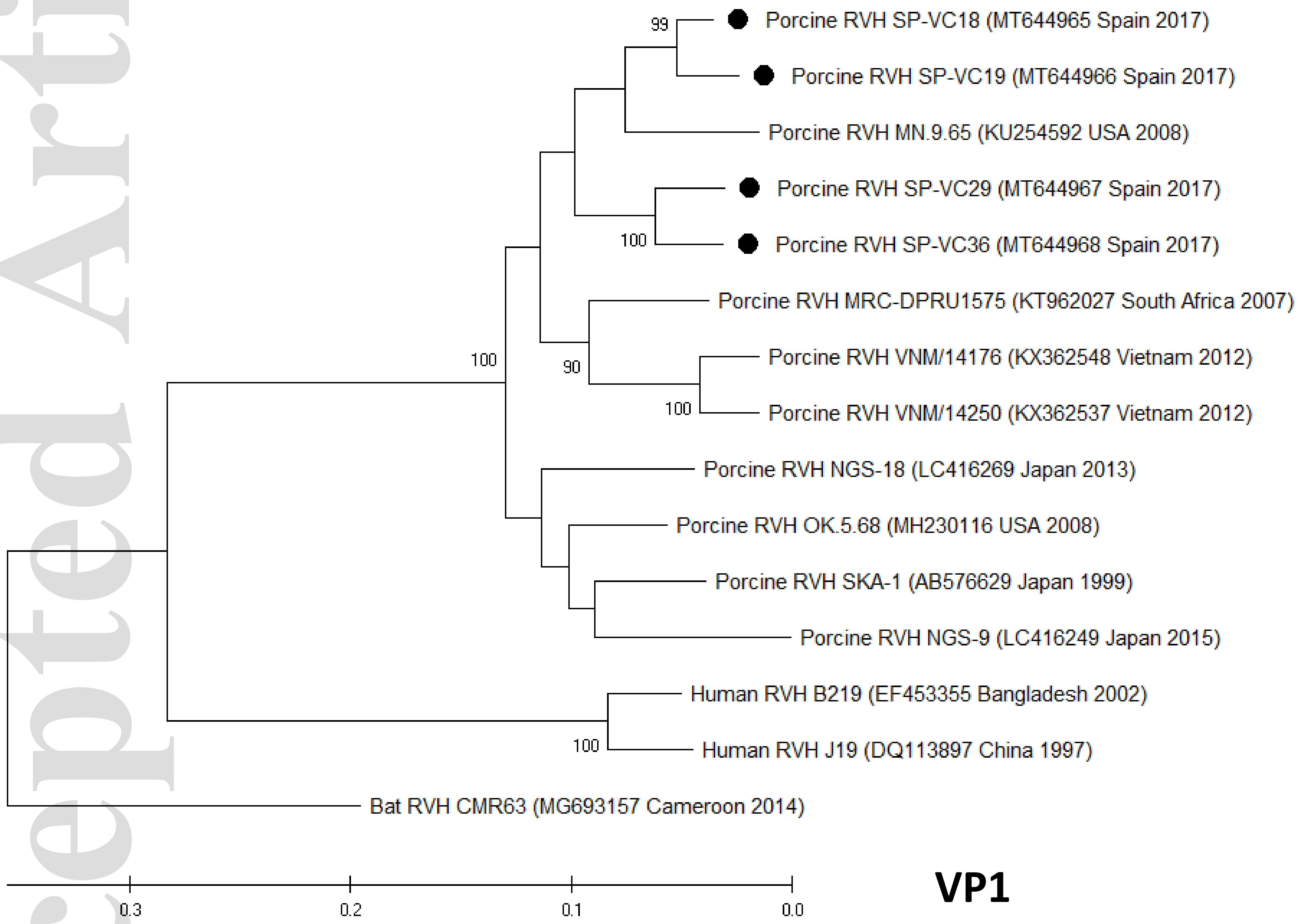

96
● Porcine RVH SP-VC18 (MT644953 Spain 2017)
80
● Porcine RVH SP-VC19 (MT644954 Spain 2017)
● Porcine RVH SP-VC29 (MT644955 Spain 2017)
● Porcine RVH SP-VC36 (MT644956 Spain 2017)
Porcine RVH SKA-1 (AB576633 Japan 1999)
Porcine RVH NGS-18 (LC416265 Japan 2013)
99
Porcine RVH NGS-17 (LC416256 Japan 2013)
Porcine RVH MN9.65 (KU254586 USA 2008)
Porcine RVH OK.5.68 (MH230123 USA 2008)
Porcine RVH VNM/14176 (KX362555 Vietnam 2012)
Porcine RVH VNM/14250 (KX362544 Vietnam 2012)
100
Porcine RVH MRC-DPRU1575 (KT962034 South Africa 2007)
Porcine RVH NGS-16 (LC348499 Japan 2013)
Human RVH B219 (DQ168035 Bangladesh 2002)
100
Human RVH J19 (DQ113903 China 1997)
Bat RVH CMR63 (MG693164 Cameroon 2014)
0.2
0.1
0.0
NSP2


100
Porcine RVH NGS-18 (LC416266 Japan 2013)
Porcine RVH NGS-17 (LC416257 Japan 2013)
99
Porcine RVH NGS-9 (LC416246 Japan 2015)
Porcine RVH NGS-8 LC348503 Japan 2015)
86
Porcine RVH SKA-1 (AB576634 Japan 1999)
Porcine RVH MRC-DPRU1575 (KT962035 South Africa 2007)
Porcine RVH OK.5.68 (MH230122 USA 2008)
● Porcine RVH SP-VC36 (MT644960 Spain 2017)
100
Porcine RVH NGS-5 (LC348501 Japan 2014)
79
79
Porcine RVH NGS-3 (LC348500 Japan 2014)
97
Porcine RVH VNM/12087 (KX362534 Vietnam 2012)
88
Porcine RVH VNM/14250 (KX362545 Vietnam 2012)
74
Porcine RVH MN.9.65 (KU254582 USA 2008)
100
● Porcine RVH SP-VC18 (MT644957 Spain 2017)
98
● Porcine RVH SP-VC19 (MT644958 Spain 2017)
● Porcine RVH SP-VC29 (MT644959 Spain 2017)
Human RVH B219 (DQ168036 Bangladesh 2002)
Human RVH J19 DQ113904 China 1997)
100
100
Human RVH ADRV-N (AY632081 China 1997)
Bat RVH CMR63 (MG693165 Cameroon 2014)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0

NSP3

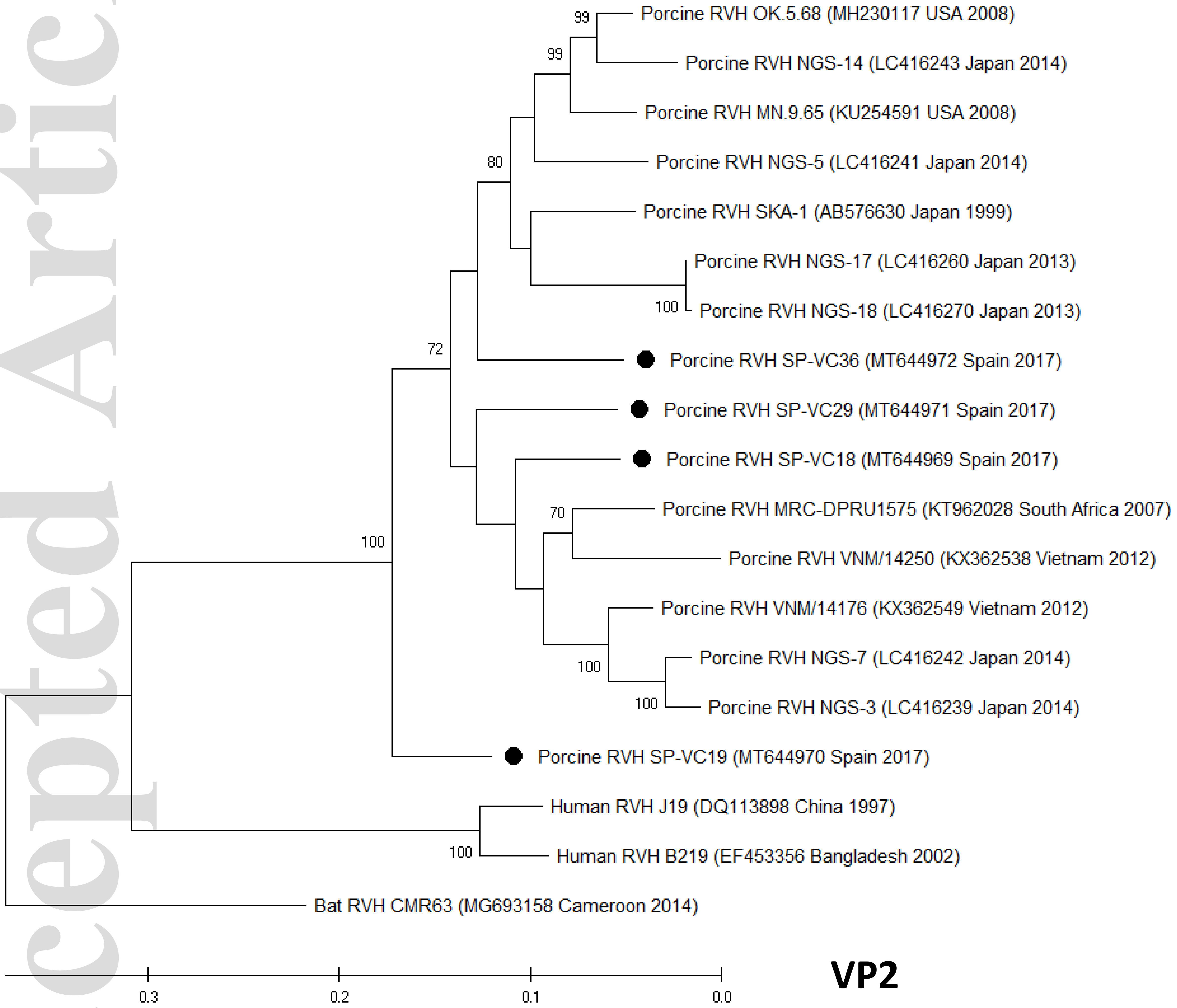

100
Porcine RVH BR61 (KM359497 Brazil 2012)
96
Porcine RVH BR59 (KM359494 Brazil 2012)
75
Porcine RVH MRC-DPRU1575 (KT962036 South Africa 2007)
Porcine RVH VNM/14250 (KX362546 Vietnam 2012)
100
Porcine RVH VNM/12087 (KX362535 Vietnam 2012)
Porcine RVH VNM/14176 (KX362556 Vietnam 2012)
Porcine RVH VNM/12089 (KX362522 Vietnam 2012)
78
Porcine RVH NGS-17 (LC416258 Japan 2013)
99
Porcine RVH NGS-8 (LC348511 Japan 2015)
● Porcine RVH SP-VC29 (MT644963 Spain 2017)
● Porcine RVH SP-VC36 (MT644964 Spain 2017)
Porcine RVH MN.9.65 (KU254585 USA 2008)
● Porcine RVH SP-VC18 (MT644961 Spain 2017)
100
● Porcine RVH SP-VC19 (MT644962 Spain 2017)
Porcine RVH OK.5.68 (MH230125 USA 2008)
87
Porcine RVH SKA-1 (AB576628 Japan 1999)
Porcine RVH NGS-14 (LC348512 Japan 2014)
Human RVH J19 (DQ113906 China 1997)
100
Human RVH B219 (EF453359 Bangladesh 2002)
Bat RVH CMR63 (MG693166 Cameroon 2014)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
NSP4

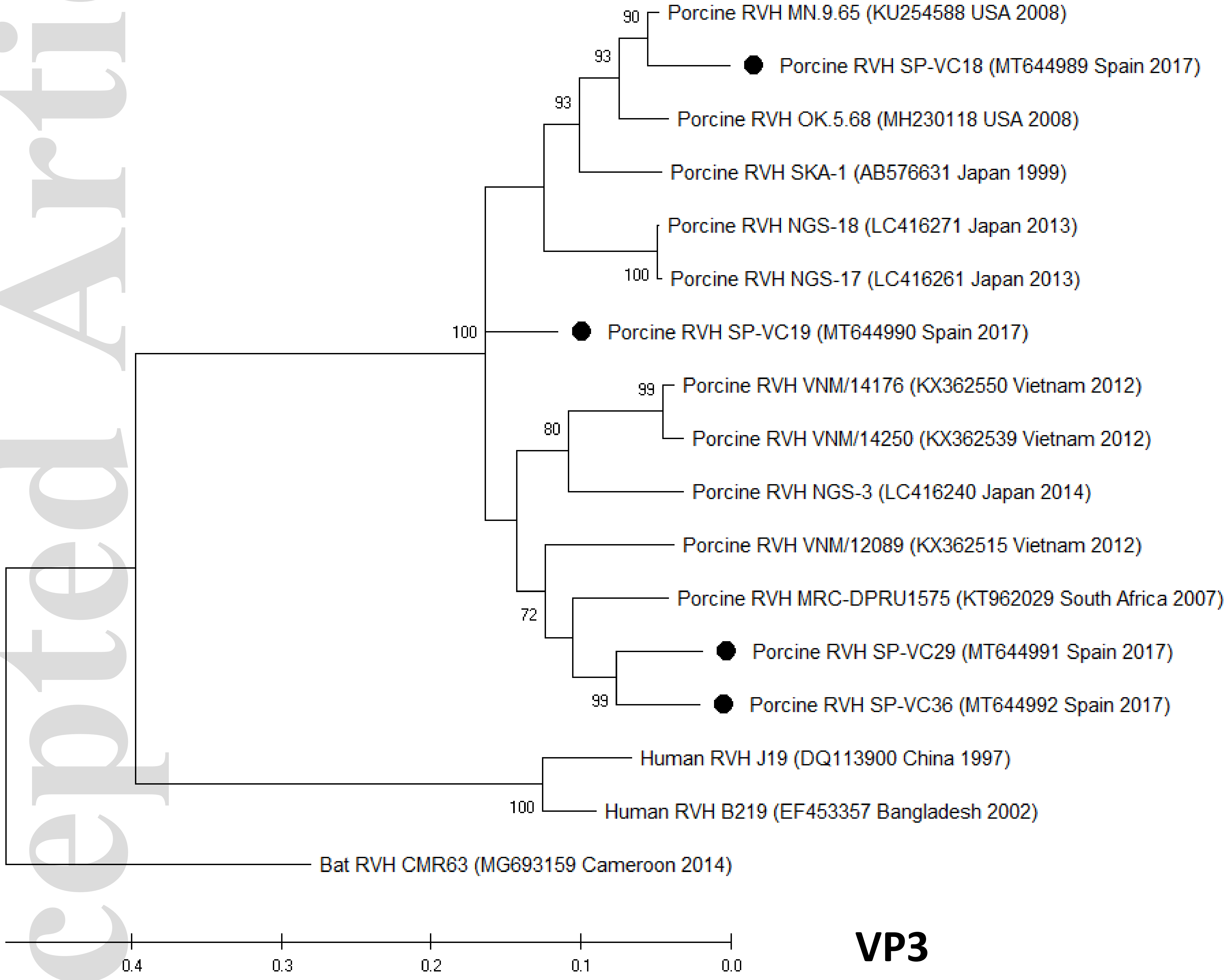

Porcine RVH SP-VC18 (MT644985 Spain 2017)
Porcine RVH SP-VC19 (MT644986 Spain 2017)
Porcine RVH SP-VC36 (MT644988 Spain 2017)
Porcine RVH SP-VC29 (MT644987 Spain 2017)
91
74
Porcine RVH VNM/14254 (KX362568 Vietnam 2012)
Porcine RVH VNM/14176 (KX362557 Vietnam 2012)
97
Porcine RVH NGS-5 (LC348514 Japan 2014)
99
Porcine RVH NGS-3 (LC348513 Japan 2014)
100
Porcine RVH NGS-17 (LC416259 Japan 2013)
Porcine RVH NGS-18 (LC416268 Japan 2013)
95
Porcine RVH OK.5.68 (MH230126 USA 2008)
Porcine RVH OK.5.68 (KU254584 USA 2008)
Porcine RVH MRC-DPRU1575 (KT962037 South Africa 2007)
Porcine RVH SKA-1 (AB576635 Japan 1999)
Porcine RVH VNM/12089 (KX362523 Vietnam 2012)
83
Porcine RVH VNM/14250 (KX362547 Vietnam 2012)
Human RVH J19 (DQ113907 China 1997)
100
Human RVH B219 (EF453360 Bangladesh 2002)
Bat RVH CMR63 (MG693167 Cameroon 2014)
0.4
0.3
0.2
0.1
0.0
NSP5

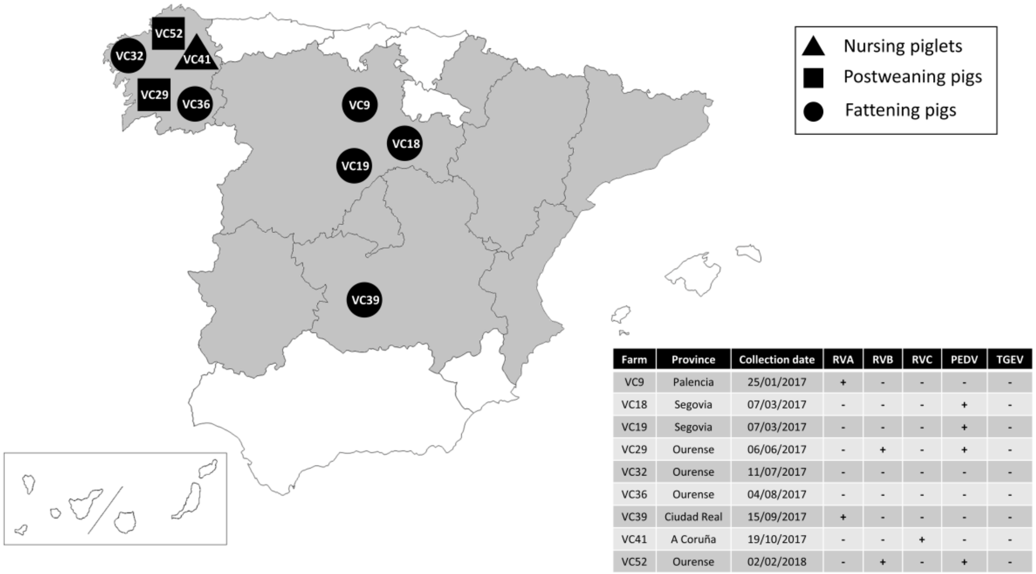


99
● Porcine RVH SP-VC18 (MT644965 Spain 2017)
● Porcine RVH SP-VC19 (MT644966 Spain 2017)
Porcine RVH MN.9.65 (KU254592 USA 2008)
● Porcine RVH SP-VC29 (MT644967 Spain 2017)
100
● Porcine RVH SP-VC36 (MT644968 Spain 2017)
Porcine RVH MRC-DPRU1575 (KT962027 South Africa 2007)
100
90
Porcine RVH VNM/14176 (KX362548 Vietnam 2012)
100
Porcine RVH VNM/14250 (KX362537 Vietnam 2012)
Porcine RVH NGS-18 (LC416269 Japan 2013)
Porcine RVH OK.5.68 (MH230116 USA 2008)
Porcine RVH SKA-1 (AB576629 Japan 1999)
Porcine RVH NGS-9 (LC416249 Japan 2015)
Human RVH B219 (EF453355 Bangladesh 2002)
100
Human RVH J19 (DQ113897 China 1997)
Bat RVH CMR63 (MG693157 Cameroon 2014)
0.3
0.2
0.1
0.0

VP1

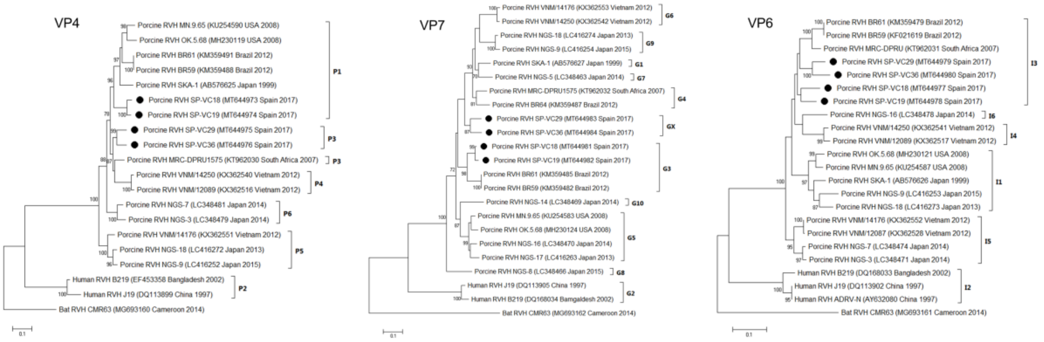

99
Porcine RVH OK.5.68 (MH230117 USA 2008)
99
Porcine RVH NGS-14 (LC416243 Japan 2014)
Porcine RVH MN.9.65 (KU254591 USA 2008)
80
Porcine RVH NGS-5 (LC416241 Japan 2014)
Porcine RVH SKA-1 (AB576630 Japan 1999)
Porcine RVH NGS-17 (LC416260 Japan 2013)
100
Porcine RVH NGS-18 (LC416270 Japan 2013)
72
● Porcine RVH SP-VC36 (MT644972 Spain 2017)
● Porcine RVH SP-VC29 (MT644971 Spain 2017)
● Porcine RVH SP-VC18 (MT644969 Spain 2017)
70
Porcine RVH MRC-DPRU1575 (KT962028 South Africa 2007)
100
Porcine RVH VNM/14250 (KX362538 Vietnam 2012)
Porcine RVH VNM/14176 (KX362549 Vietnam 2012)
100
Porcine RVH NGS-7 (LC416242 Japan 2014)
100
Porcine RVH NGS-3 (LC416239 Japan 2014)
● Porcine RVH SP-VC19 (MT644970 Spain 2017)
Human RVH J19 (DQ113898 China 1997)
100
Human RVH B219 (EF453356 Bangladesh 2002)
Bat RVH CMR63 (MG693158 Cameroon 2014)
0.3
0.2
0.1
0.0
VP2


90
Porcine RVH MN.9.65 (KU254588 USA 2008)
93
● Porcine RVH SP-VC18 (MT644989 Spain 2017)
93
Porcine RVH OK.5.68 (MH230118 USA 2008)
Porcine RVH SKA-1 (AB576631 Japan 1999)
Porcine RVH NGS-18 (LC416271 Japan 2013)
100
Porcine RVH NGS-17 (LC416261 Japan 2013)
100
● Porcine RVH SP-VC19 (MT644990 Spain 2017)
99
Porcine RVH VNM/14176 (KX362550 Vietnam 2012)
80
Porcine RVH VNM/14250 (KX362539 Vietnam 2012)
Porcine RVH NGS-3 (LC416240 Japan 2014)
Porcine RVH VNM/12089 (KX362515 Vietnam 2012)
Porcine RVH MRC-DPRU1575 (KT962029 South Africa 2007)
72
● Porcine RVH SP-VC29 (MT644991 Spain 2017)
99
● Porcine RVH SP-VC36 (MT644992 Spain 2017)
Human RVH J19 (DQ113900 China 1997)
100
Human RVH B219 (EF453357 Bangladesh 2002)
Bat RVH CMR63 (MG693159 Cameroon 2014)
0.4
0.3
0.2
0.1
0.0
VP3



Farm	Province	Collection date	RVA	RVB	RVC	PEDV	TGEV
VC9	Palencia	25/01/2017	+	-	-	-	-
VC18	Segovia	07/03/2017	-	-	-	+	-
VC19	Segovia	07/03/2017	-	-	-	+	-
VC29	Ourense	06/06/2017	-	+	-	+	-
VC32	Ourense	11/07/2017	-	-	-	-	-
VC36	Ourense	04/08/2017	-	-	-	-	-
VC39	Ciudad Real	15/09/2017	+	-	-	-	-
VC41	A Coruña	19/10/2017	-	-	+	-	-
VC52	Ourense	02/02/2018	-	+	-	+	-

tbed_13992_f1.tif



tbed_13992_f2.tif