CHAPTER FIVE

PAPER THREE

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Short communication

Whole genome sequence analyses of three African bovine rotaviruses reveal that they emerged through multiple reassortment events between rotaviruses from different mammalian species

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ABSTRACT

Animal-to-human interspecies transmission is one of the evolutionary mechanisms driving rotavirus strain diversity in humans. Although quite a few studies emanating from Africa revealed evidence of bovine-to-human rotavirus interspecies transmission, whole genome data of African bovine rotavirus strains are not yet available. To gain insight into the complete genome constellation of African bovine rotaviruses, the full genomes of three bovine rotavirus strains were extracted from stool samples collected from calves, amplified using a sequence-independent procedure, followed by 454® pyrosequencing. Strains RVA/Cow-wt/ZAF/1603/2007/G6P[5] and RVA/Cow-wt/ZAF/1605/2007/G6P[5] were both genotyped as G6-P[5]-I2-R2-C2-M2-A3-N2-T6-E2-H3 and were probably two variants of the same rotavirus due to their close nucleotide sequence similarity. The genotype constellation of strain RVA/Cow-wt/ZAF/1604/2007/G8P[1] was G8-P[1]-I2-R2-C2-M2-A3-N2-T6-E2-H3. The genetic relationships and phylogenetic analyses suggested that these three bovine rotavirus strains may have emerged through multiple reassortment events between bovine, giraffe and antelope rotaviruses. Due to the close relatedness of genome segments 1 (encoding VP1), 7 (NSP2), 9 (VP7) and 10 (NSP4) of strain RVA/Cow-wt/ZAF/1604/2007/G8P[1] to those of the corresponding segments of human rotaviruses, RVA strain 1604 may represent bovine strains that were transmitted to humans and possibly reassorted with human rotaviruses previously. The complete nucleotide sequences of the bovine rotavirus strains reported in this study represent the first whole genome data of bovine rotaviruses from Africa.

1. Introduction

Rotaviruses are some of the primary invaders of the intestinal epithelial of young animals and birds and often cause severe diarrhoea (Mebus et al., 1969; Wani et al., 2003). The mature rotavirus particle consists of a triple layer of capsid proteins that encloses its genomic material. The genome of rotavirus contains 11 segments of double-stranded RNA (dsRNA). Each genome segment encodes a single viral protein, except for segment 11 which encodes two proteins (NSP5 and NSP6). In total, there are six structural (VP) and six non-structural (NSP) proteins (Estes and Kapikian, 2007). Based on the properties of its proteins and genome segments, individual rotaviruses can be classified in several ways. According to immunological epitopes, rotaviruses are subdivided into species A–G

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which are commonly named groups that are further classified into serotypes and genotypes (Estes and Kapikian, 2007). A dual classification system that uses genotypes assigned to the genome segments encoding the protease-sensitive VP4 (P types) and the glycoprotein VP7 (G types) is commonly used to distinguish rotavirus strains (Estes and Kapikian, 2007). However, the *Rotavirus Classification Working Group* recommends a whole genome classification system that assigns genotypes to all 11 genome segments (Matthijnssens et al., 2008b). Compared to the dual typing system, the whole genome classification is superior in elucidating the evolutionary mechanisms through which the strain under study has emerged because it uses the genotypes assigned to each genome segment (Ghosh et al., 2011a; Jere et al., 2011a; Matthijnssens et al., 2008a).

A wide genomic and antigenic diversity exists amongst group A rotaviruses. To date, at least 35 G and 27 P genotypes have been identified in both animals and humans (Matthijnssens et al., 2011a). Some rotavirus strains seem to be well adapted in several species, whilst others are species-specific. For instance, strains bearing G1, G2, G3, G4, G9 and G12 in combination with P[4], P[6] or P[8] genotypes are commonly isolated from humans, whilst strains containing G3, G4, G5, G9 and G11 genotypes in association with P[6], P[7], P[13], P[19], P[23], P[26], P[27] are most common in swine, whereas strains with G6, G8 and G10 in association with P[1], P[5], P[11], P[15], and P[21] have been detected in bovine species (Martella et al., 2010). Some studies from Africa have reported on the detection of rotaviruses from cattle (Adah et al., 2002; da Costa Mendes et al., 1993). However, only a few of these studies managed to genotype the circulating bovine strains. One example is the report of Fodha et al. (2005) on the prevalence of G6 and G8 strains. The ability of distinct rotavirus strains to exchange their cognate genome segments through reassortment, and to accumulate point mutations due to lack of proof-reading activity of their RNA-dependent RNA polymerase (RdRp) are the major contributors to the broad rotavirus strain diversity (Desselberger et al., 2001). Animals also play a crucial role in driving rotavirus strain diversity in human communities through animal-to-human interspecies transmission (Martella et al., 2010). This hypothesis is supported by the wide diversity of rotavirus strains characterised from most developing countries (Ahmed et al., 1991; Arguelles et al., 2000; Mwenda et al., 2010) where close proximity exist between human and animal dwellings (Cunliffe et al., 2000) compared to developed countries (Gray et al., 2008).

In order to understand the impact which animal rotaviruses have on the evolution of strains circulation in humans, knowledge of the sequence of the full genome of animal rotaviruses is necessary. However, the genomes of only a few animal rotavirus strains have been fully characterised. Of these, only three strains, RVA/Cat-wt/ITA/BA222/2005/G3P[9] (Martella et al., 2011), RVA/Antelope-wt/ZAF/RC-18-08/G6P[14] (Matthijnssens et al., 2009) and RVA/Horse-wt/ZAF/ EqRV-SA1/2006/G14P[12] (Matthijnssens et al., 2011b) have been sequenced on a mass parallel sequencing platform. Studies on human African rotavirus strains have revealed evidence of bovine-to-human interspecies transmission (Ghosh et al., 2011b; Martella et al., 2011), reassortment between bovine and human strains (Esona et al., 2009; Todd et al., 2010), and a common origin between bovine and some strains circulating in humans, for instance DS-1-like rotaviruses (Jere et al., 2011a; Matthijnssens et al., 2008a). The complete consensus sequence of the genome of bovine rotavirus strains isolated from African countries where several human rotavirus strains are known to share common ancestry with bovine rotaviruses have not yet been reported. Although G6P[5] and G8P[1] strains are often isolated from calves (Martella et al., 2010), Ghosh et al. (2011b) recently isolated a G8P[1] strain in an asymptomatic Kenyan child that revealed evidence for *artiodactyl*-to-human interspecies transmission. In most African communities, reassortment and/or interspecies transmission events between human and animal strains seems to be common due to poor hygienic conditions and close contact between human settlements and livestock (Cunliffe et al., 2000; Esona et al., 2009; Ghosh et al., 2011b; Matthijnssens et al., 2008a). Therefore, determination of the full genome sequence of animal rotavirus strains in this region is important to better understand the genetic diversity and zoonotic aspects of rotavirus strains circulating in humans. These and other mechanisms impact on the global burden of diseases through generation of zoonotic strains (Banyai et al., 2009) or human–animal reassortant strains (Ghosh et al., 2011b; Jere et al., 2011a). In this study, the whole genome of three bovine African rotavirus strains from stools of calves in South Africa were pyrosequenced. The strains were used for no reason other than that they were the only bovine samples available to us at the time. Their genome constellation and relatedness to rotaviruses of human and other mammals were investigated to understand their evolutionary relationships. The genetic diversity in the nine non-G and non-P genome segments of strains carrying similar genome segment 4 (VP4) and 9 (VP7) genotypes (G6P[5]) was also investigated to better understand their genetic relationships.

2. Materials and methods

2.1. Bovine rotavirus samples

Rotavirus strains RVA/Cow-wt/ZAF/1603/2007/G6P[5], RVA/Cow-wt/ZAF/1604/2007/G8P[1] and RVA/Cow-wt/ZAF/1605/2007/G6P[5] were characterised from stools collected in 2007 from three calves presenting with diarrhoea on a farm in Malmesbury, Western Cape Province, South Africa. The stool samples were screened for the presence of rotaviruses at the Onderspoort Veterinary Institute (OVI), South Africa. Making use of the dual RT-PCR based genotyping system (Gentsch et al., 1992; Gouvea et al., 1990), genome segment 4 (VP4) and 9 (VP7) genotypes were assigned to these strains at the Diarrhoeal Pathogens Research Unit (DPRU), South Africa.

2.2. Nucleotide sequencing, genotyping, distance matrices and phylogenetic analyses

The rotavirus dsRNA was extracted from the stool specimens, purified and ligated to the PC3-T7loop oligonucleotide as described previously (Potgieter et al., 2009).

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The sequence-independent cDNA synthesis and PCR amplification procedure described by Jere et al. (2011a) was followed to generate and amplify cDNA of the whole genomes of the study bovine rotavirus strains. 454® pyrosequencing (Margulies et al., 2005) with the GS/FLX Titanium (Roche, Mannheim, Germany) technology was performed at Inqaba Biotec (PTY), Pretoria, South Africa. DNASTAR® Lasergene™ software, version 8.1.2 was used to generate consensus nucleotide sequences as described previously (Jere et al., 2011a). The nucleotide sequences reported in this study were submitted to the NCBI GenBank under the accession numbers listed in Supplement 1.

The web-based automated rotavirus genotyping tool, RotaC (http://rotac.regatools.be; Maes et al., 2009) was used to assign genotypes to all 11 genome segments of the study strains. The nucleotide sequences of the selected rotavirus strains characterised elsewhere used for comparison were acquired from GenBank (accession numbers listed in Supplement 2). BioEdit (Hall, 1999) and MEGA software, version 4.0 (Tamura et al., 2007) were used to generate distance matrices and perform phylogenetic and molecular evolutionary analyses.

3. Results

3.1. Genetic constellation and phylogenetic analyses of the genome segments of rotavirus strains RVA/Cow-wt/ZAF/1603/2007/G6P[5] and RVA/Cow-wt/ZAF/1605/2007/G6P[5]

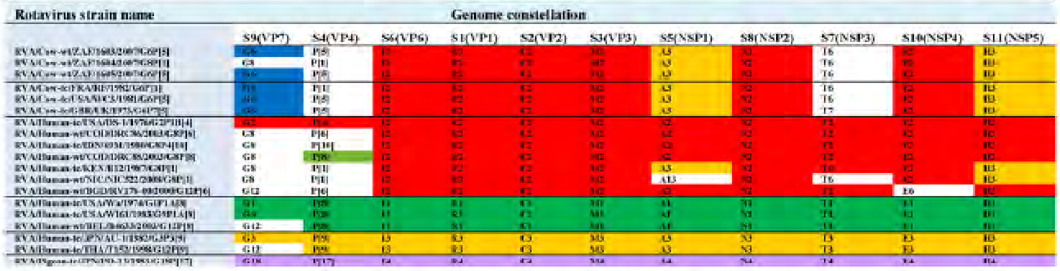
A high sequence coverage rate was achieved for all the genome segments of the three rotaviruses (Supplement 3). The sizes of the complete nucleotide and deduced amino acid sequences for each genome segment of the three bovine study strains are listed in Supplement 4. Based on the genotypes that were assigned to all the nucleotide sequences of the 11 genome segments of RVA strains 1603 and 1605, an identical descriptor, namely G6-P[5]-I2-R2-C2-M2-A3-N2-T6-E2-H3, was assigned to both strains (Fig. 1). This genome constellation suggest that the two strains are typical G6P[5] bovine rotaviruses that are on a genetic backbone comprised of DS-1-like, AU-like and T6 genotypes. These strains may have emerged through multiple reassortment events.

Phylogenetic analysis revealed that all the genome segments of RVA strains 1603 and 1605 were very closely related (Supplement 5). Based on the clusters formed in the phylograms, the closest strains listed in the GenBank to RVA strains 1603 and 1605 are summarised in Table 1. Although genome segments 3 (VP3), 4 (VP4), 5 (NSP1), 6 (VP6), 8 (NSP2) and 9 (VP7) of the G6P[5] study bovine rotavirus strains share a common ancestry with the cognate genome segments of other bovine rotaviruses, their genome segments 1 (VP1) and 2 (VP2) share a common origin with that of a *Hippotragus niger* (sable antelope) RVA strain RC-18-08, genome segments 7 (NSP3) and 11 (NSP5) are most closely related to that of a bovine-like RVA strain UCD identified from a giraffe, whereas segment 10 (NSP4) shares a common origin with that of animal–human reassortant strains such as the human RVA strain PAH136 (De Grazia et al., 2010).

3.2. Genetic constellation and phylogenetic analyses of the genome segments of strain RVA/Cow-wt/ZAF/1604/2007/G8P[1]

Based on genotypes assigned to all the genome segments of RVA strain 1604, it was assigned a unique complete genotype descriptor G8-P[1]-I2-R2-C2-M2-A3-N2-T6-E2-H3. Although RVA strain 1604 has a similar genetic backbone as the two G5P[6] study bovine strains, it contains completely different genome segment 4 (VP4, P[1]) and 9 (VP7, G8) genotypes. Furthermore, there were several nucleotide sequences variations in the genome segments encoding NSP1, NSP2, NSP3, NSP4, NSP5, VP1, VP3, VP3 and VP6 when all the genome segments of the G8P[1] strain were aligned against the other two G6P[5] bovine study strains (data not shown).

Phylogenetic analysis of each of the 11 genome segments of the RVA strain 1604 (Supplement 5) revealed that its genome segments 3 (VP3), 4 (VP4), 5 (NSP1) and 8 (NSP2) were most closely related to those of other bovine rotaviruses. Genome segment 4 (VP4) of the simian RVA strain SA11-4F, which is most closely related to that of RVA strain 1604, is of bovine origin (Mattion and Estes, 1991). The following genetic relationships were observed for the other genome segments: segment 6 (VP6) was most closely related to that of the *H. niger* RVA strain RC-18-08; segments 2 (VP2) and 11 (NSP5) were most closely related to a bovine-like RVA strain UCD characterised from a giraffe; segments 1 (VP1) and 7 (NSP3) were most closely



Rotavirus strain name	Genome constellation										
	S9(VP7)	S4(VP4)	S6(VP6)	S1(VP1)	S2(VP2)	S3(VP3)	S5(NSP1)	S8(NSP2)	S7(NSP3)	S10(NSP4)	S11(NSP5)
RVA/Cow-wt/ZAF/1603/2007/G6P[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3
RVA/Cow-wt/ZAF/1604/2007/G8P[1]	G8	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3
RVA/Cow-wt/ZAF/1605/2007/G6P[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3
RVA/Cow-tc/FRA/RF/1982/G6P[1]	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3
RVA/Cow-tc/USA/WC3/1981/G6P[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3
RVA/Cow-tc/GBR/UK/1975/G6P[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T7	E2	H3
RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
RVA/Human-wt/COD/DRC86/2003/G8P[6]	G8	P[6]	I2	R2	C2	M2	A2	N2	T2	E2	H2
RVA/Human-tc/IDN/69M/1980/G8P4[10]	G8	P[10]	I2	R2	C2	M2	A2	N2	T2	E2	H2
RVA/Human-wt/COD/DRC88/2003/G8P[8]	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
RVA/Human-tc/KEN/B12/1987/G8P[1]	G8	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3
RVA/Human-wt/NIC/NIC522/2008/G8P[1]	G8	P[1]	I2	R2	C2	M2	A13	N2	T6	E2	H3
RVA/Human-wt/BGD/RV176-00/2000/G12P[6]	G12	P[6]	I2	R2	C2	M2	A2	N2	T2	E6	H2
RVA/Human-tc/USA/Wa/1974/G1P1A[8]	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
RVA/Human-tc/USA/WI61/1983/G9P1A[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
RVA/Human-wt/BEL/B4633/2003/G12P[8]	G12	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	G3	P[9]	I3	R3	C3	M3	A3	N3	T3	E3	H3
RVA/Human-tc/THA/T152/1998/G12P[9]	G12	P[9]	I3	R3	C3	M3	A3	N3	T3	E3	H3
RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	G18	P[17]	I4	R4	C4	M4	A4	N4	T4	E4	H4

Fig. 1. Whole genome classification of the three African bovine rotaviruses analysed in this study compared to well-characterised rotavirus strains listed in the GenBank. Colours were added to visualise patterns of genome constellations as follows: green (Wa-like), red (DS-1-like), orange (AU-like), purple (PO-13-like) and blue (some typical animal rotavirus genotypes). S, genome segment; VP, viral structural protein; NSP, viral non-structural protein.

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Table 1
Percentage identities of the most closely related nucleotide sequences of the complete genome segments of rotavirus strains listed in the GenBank compared to the three study bovine strains.

Genome segment	RVA/Cow-wt/ZAF/1603/2007/G6P[5]	RVA/Cow-wt/ZAF/1604/2007/G8P[1]	RVA/Cow-wt/ZAF/1605/2007/G6P[5]
1 (VP1)	RVA/Antelope-wt/ZAF/ RC-18-08/G6P[14] (97.5%)	RVA/Human-wt/KEN/B12/1987/G8P[1] (95.4%)	RVA/Antelope-wt/ZAF/ RC-18-08/G6P[14] (96.3%)
2 (VP2)	RVA/Antelope-wt/ZAF/ RC-18-08/G6P[14] (98.5%)	RVA/giraffe-wt/IRL/UCD/2007/ G10P[11] (95.1%)	RVA/Antelope-wt/ZAF/ RC-18-08/G6P[14] (98.4%)
3 (VP3)	RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29] (95.5%)	RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29] (95.4%)	RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29] (95.6%)
4 (VP4)	RVA/Cow-wt/THA/61A/XXXX/G10P[5] (95.7%)	RVA/Vervet monkey-tc/ZAF/SA11-4F/1958/ G3P6[1] (95.4%)[a]	RVA/Cow-wt/THA/61A/XXXX/G10P[5] (95.7%)
5 (NSP1)	RVA/Cow-tc/USA/NCDV/1967/G6P6[1] (97.2%)	RVA/Cow-tc/FRA/RF/1982/G6P[1] (97.5%)	RVA/Cow-wt/ZAF/1603/2007/G6P[5] (97%)
6 (VP6)	RVA/Bovine-tc/JPN/22R/XXXX/GXP[X] (96.5%)	RVA/Antelope-wt/ZAF/ RC-18-08/G6P[14] (98.8%)	RVA/Bovine-tc/JPN/22R/XXXX/GXP[X] (96.5%)
7 (NSP3)	RVA/Giraffe/UCD/IRL/2007/G10P[11] (96.7%)	RVA/Human-wt/ITA/111-05-27/2005/ G6P[14] (96.8%)	RVA/Giraffe/UCD/IRL/2007/G10P[11] (96.6%)
8 (NSP2)	RVA/Cow-lab/USA/UKg9ST3/ 1986/G4P[5] (98%)	RVA/Cow-wt/ARG/B383/1998/G15P[11] (94.9)	RVA/Cow-lab/USA/UKg9ST3/ 1986/G4P[5] (98%)
9 (VP7)	RVA/Cow-tc/GBR/UK/1973/G6P7[5] (95%)	RVA/Human-wt/AUS/MG8/ 1997/G8P[14] (91.7%)	RVA/Cow-tc/GBR/UK/1973/G6P7[5] (95%)
10 (NSP4)	RVA/Human-wt/ITA/PAH136/1996/G3P[9] (94.3%)	RVA/Human-wt/COD/DRC86/2003/G8P[6] (97.3%)	RVA/Human-wt/ITA/PAH136/1996/G3P[9] (94.1%)
11 (NSP5/NSP6)	RVA/giraffe-wt/IRL/UCD/2007/ G10P[11] (98.8%)	RVA/giraffe-wt/IRL/UCD/2007/ G10P[11] (98.2%)	RVA/giraffe-wt/IRL/UCD/2007/ G10P[11] (98.8%)

The table summarises the closest related rotavirus strains to each study bovine strain as shown in the phylograms of all 11 rotavirus genome segments (Supplement 5). The percentages in parenthesis were generated with the basic local alignment search tool (BLAST). Accession numbers of each reference strains are provided in Supplement 2. The strain nomenclature represents the rotavirus group/species of origin/country of identification/common name/year of identification/G- and P-type. The unique 3-letter abbreviation code used for each country are as listed on the website https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html (Matthijnssens et al., 2011a,b).

[a] RVA/Vervet monkey-tc/ZAF/SA11-4F/1958/G3P6[1] contains a genome segment 4 (VP4) of bovine origin (Mattion and Estes, 1991).

related to zoonotic-human reassortant rotaviruses like RVA strains B12 and 111-05-27 identified in humans; whereas segments 9 (VP7) and 10 (NSP4) were most closely related to human rotavirus strains that have been suggested to originate from cattle, for instance, RVA strain MG8 collected in Australia (Cooney et al., 2001).

3.3. *Distance matrix analyses*

Since the nine genome segments encoding VP6, VP1, VP2, VP3, NSP1, NSP2, NSP3, NSP4 and NSP5 of the three study bovine rotaviruses were assigned identical genotypes (I2-R2-C2-M2-A3-N2-T6-E2-H3), the relationships between their genetic backbones were analysed further. Distance matrix analyses were estimated with MEGA 4 software using the Maximum Composite Likelihood method (Tamura et al., 2007) (Supplement 6). As expected, all the genome segments of RVA strain 1604 were distantly related to those of both RVA strain 1603 [up to 0.12 variance in genome segment 8 (NSP2) and 10 (NSP4)] and RVA strain 1605 [up to 1.64 variance in genome segment 7 (NSP3)]. By contrast, no evolutionary distances (variance of 0.00) was estimated between all the genome segments of the G6P[5] strains. Furthermore, multiple sequence alignment of all the genome segments of the three bovine rotaviruses reported here revealed some nucleotide variations that appeared not to affect the amino acid sequences of the deduced proteins (data not shown). Although the nucleotide sequences of the two G6P[5] rotaviruses were remarkably conserved in general, they did show minor nucleotide variations at the following positions: genome segment 1 (VP1) [3123 G → A]; 2 (VP2) [1445 A → G], 3 (VP3) [1279C → T]; 4 (VP4) [336 G → A]; 5 (NSP1) [T deletion at nt position 11 and TA deletion at nt position 68–69]; and 8 (NSP3) [212–213 AT → TA and 210–212 ACT → CTC] (data not shown).

4. Discussion and conclusion

Previously, the robustness and versatility of the sequence-independent whole genome dsRNA amplification (Potgieter et al., 2009) coupled with next generation sequencing was reported. 454® pyrosequencing (Margulies et al., 2005) and RotaC (Maes et al., 2009) were used to obtain and characterise the consensus nucleotide sequence of the full genome of the prototype rotavirus DS-1 strain (Mlera et al., 2011), African human rotaviruses (Jere et al., 2011a) and to dissect the classification of genome segments of multiple rotavirus strains simultaneously infecting a single patient (Jere et al., 2011b). In this study, the same approach was used to determine the sequences of full genomes of three African bovine rotavirus strains genotyped as G8P[1] and G6P[5]. As often reported for most bovine rotavirus strains (Gerna et al., 1990), both the dsRNA and cDNA of the three study bovine rotavirus strains also displayed long electropherotype profiles. All three study strains had a conserved I2-R2-C2-M2-A3-N2-T6-E2-H3 genetic backbone which is common in some of the well characterised bovine strains (Matthijnssens et al., 2011a).

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Numerous studies have illustrated the evidence of animal-to-human interspecies transmission of rotavirus strains (reviewed by Martella et al., 2010). G8P[1] strains RVA/Human-wt/KEN/B12/1987/G8P[1] and RVA/Human-wt/NIC/NIC522/2008/G8P[1] represent two of the few human rotavirus strains that are believed to have been directly transmitted from cattle or other *artiodactyla* species to humans (Banyai et al., 2009; Ghosh et al., 2011b). Comparing the genetic constellation of these only two zoonotic G8P[1] human rotavirus strains to the G8P[1] bovine strain presented in the current study, RVA strain B12 and 1604 shared identical genotype constellations despite nine of their genome segments clustering separately within the phylograms (Supplement 5). This suggests that these two G8P[1] strains were distantly related despite having identical segmental genotypes and genotype constellation. The genotypes assigned to strain RVA/Human-wt/NIC/NIC522/2008/G8P[1] differed only in genome segment 5 (NSP1) to those of the bovine RVA strain 1604 (Fig. 1). Since the nucleotide sequences of strain RVA/Human-wt/NIC/NIC522/2008/G8P[1] were not available from GenBank, the phylogenetic comparisons to the study bovine strains could not be made.

The genetic constellations and the phylogenies of the complete genomes of the three bovine rotavirus strains reported in this study imply that multiple reassortment and interspecies transmission within the *artiodactyla* species most likely led to the emergence of these strains. RVA strains 1603 and 1605 might be the result of multiple reassortment events between bovine, giraffe and antelope rotaviruses. This is hypothesized based on the close similarity of their genome segments to the cognate genome segments of rotaviruses characterised from these *artiodactyla* species. The close similarity between the nucleotide sequences of RVA strains 1603 and 1605 suggests that the two calves carrying them may have been infected by a single rotavirus strain, which then generated quasispecies. Although these isolates have an identical genotype constellation, G6-P[5]-I2-R2-C2-M2-A3-N2-T6-E2-H3, and showed remarkable conservation in five genome segments, some nucleotide variations were obtained in genome segments 1 (VP1), 2 (VP2), 3 (VP3), 4 (VP4), 5 (NSP1) and 7 (NSP3). This may illustrate some minor diversity of the G6P[5] strains that were circulating on the South African farm in 2007. The fact that nucleotide variations were observed between six of the genome segments of the two G6P[5] strains warrants further research to understand whether and how these variations may affect the strain virulence in bovine species or when these strains were transmitted to other species.

RVA strain 1604 potentially emerged through multiple reassortment events between bovine, giraffe and antelope rotaviruses due to the close relationship of its genome segments to the corresponding genome segments of rotaviruses identified from these mammalian species. Evidence suggest that G8 rotaviruses, which are common in cattle, that are frequently detected from infants and young children in Africa potentially originated from or shared a common origin with bovine rotavirus strains (Cunliffe et al., 2000; Esona et al., 2009; Jere et al., 2011a; Matthijnssens et al., 2008a). RVA strain 1604 might be considered an example of such a bovine rotavirus strain due to the close similarity of its genome segments 4 (VP4), 7 (NSP3), 9 (VP7) and 10 (NSP4) to cognate genes of human rotavirus strains. This correlates with the hypothesis made by Esona et al. (2009) and Matthijnssens et al. (2006) that G8 human rotavirus strains detected from several African countries share a common origin with bovine rotavirus strains.

In conclusion, zoonotic studies are hampered by lack of whole genome sequence data of rotavirus strains circulating in animals. Although the full genomes of only two *artiodactyla* rotavirus strains have been characterised from Africa, one from an antelope (Matthijnssens et al., 2009), and one from a horse (Matthijnssens et al., 2011b), no complete nucleotide sequences of the whole genome of African bovine rotavirus strains have been characterised. Accumulation of more sequence data of animal strains using massive parallel next generation sequencing is important to accurately understand the ecology, epidemiology and evolution of rotaviruses. This will also enable deciphering of the true origin of the zoonotic strains circulating in humans. The fact that wide strain diversities have been reported from African countries where interspecies transmission has been implicated as one of the main cause resulting from the close proximity between livestock and human settlement clearly calls for more understanding of rotavirus strains circulating in various animal species from this region.

Competing interests

The author(s) declare that they have no competing interests.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.vetmic.2012.03.040.

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Supplementary Data

Supplement 1: Accession numbers of the complete consensus nucleotide and amino acid sequences of the three African bovine rotaviruses analysed in this study.

Study bovine rotaviruses	**GenBank accession numbers**										
	S9(VP7)	**S4(VP4)**	**S6(VP6)**	**S1(VP1)**	**S2(VP2)**	**S3(VP3)**	**S5(NSP1)**	**S8(NSP2)**	**S7(NSP3)**	**S10(NSP4)**	**S11(NSP5)**
RVA/Cow-wt/ZAF/1603/2007/G6P[5]	JN831209	JN831210	JN831211	JN831212	JN831213	JN831214	JN831204	JN831205	JN831206	JN831207	JN831208
RVA/Cow-wt/ZAF/1604/2007/G8P[1]	JN831220	JN831221	JN831222	JN831223	JN831224	JN831225	JN831215	JN831216	JN831217	JN831218	JN831219
RVA/Cow-wt/ZAF/1605/2007/G6P[5]	JN831231	JN831232	JN831233	JN831234	JN831235	JN831236	JN831226	JN831227	JN831228	JN831229	JN831230

Supplement 2: Accession numbers for the selected nucleotide sequences acquired from the GenBank.

Genome segment 1 (VP1)

RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]: FJ495126; RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627542; RVA/Cow-tc/FRA/RF/1982/G6P[1]: J04346; RVA/USA/Rotashield-ST3xRRV/XXXX/G4P[3]: HQ846876; RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]: GU565041; RVA/Human-tc/USA/Se584/1998/G6P[9]: EF583041; RVA/Human-wt/ITA/PAI58/1996/G3P[9]: GU296421; RVA/Human-tc/AUS/MG6/1993/G6P[14]: EF554093; RVA/Cow-tc/USA/WC3/1981/G6P[5]: EF560615; RVA/Cow-tc/VEN/BRV033/1990/G6P6[1]: EF560612; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009629; RVA/Human-tc/USA/DS-1/1976/G2P[4]: HQ650116; RVA/Human-wt/ZAF/3203WC/2009/G2P[4]: HQ657166; RVA/Human-wt/ZAF/GR10924/1999/ G9P[6]: FJ183353; RVA/Human-wt/MWI/1473/2001/G8P[4: HQ657133; RVA/Human-wt/COD/DRC86/2003/G8P[6]: DQ005125; RVA/Human-wt/COD/DRC88/2003/G8P[8]: DQ005114; RVA/Human-wt/USA/ LB2764/2006/G2P[4]: HM467926; RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]: AY78765.

Genome segment 2 (VP2)

RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]: FJ495127; RVA/Human-wt/ITA/ PAH136/1996/G3P[9]: GU296422; RVA/Human-wt/HUN/Hun5/1997/G6P[14]: EF554105; RVA/Human-wt/EGY/Egy3399/2004/G6P[14]: HM113526; RVA/Human-wt/BGD/RV176/2000/G12P[6]: DQ490552; RVA/giraffe/IRL/UCD/2007/G10P[11]: GQ428142; RVA/Human-tc/JPN/S2/1980/G2P1B[4]: DQ870486; RVA/Human-tc/USA/DS-1/1976/G2P1B[4]: DQ870506; RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]; AY787652; RVA/Cow-tc/USA/NCDV/1967/G6P6[1]: DQ870494; RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]: GU565064; RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]: GU565042; RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]: GU565053; RVA/Human-tc/USA/DS-1/1976/G2P[4]: HQ650117; RVA/Human-wt/MWI/1473/2001/G8P[4]: HQ657134; RVA/Human-wt/ZAF/3203WC/2009/G2P[4]; HQ657167; RVA/Human-wt/ZAF/GR10924/ 1999/G9P[6]: FJ183354; RVA/Human-wt/USA/LB2744/2006/G2P[4]: HM467931; RVA/Human-wt/BGD/RV161/2000/G12P[6]: DQ490546; RVA/Human-wt/DEU/GER1H-09/2009/G8P[4]: GQ414541; RVA/Human-wt/COD/DRC86/2003/G8P[6]: DQ005124; RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]: AY787652; RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627543; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009630; RVA/Human-tc/ITA/PA169/1988/G6P[14]: EF554127.

Genome segment 3 (VP3)

RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29]: AB573081; RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5]: GU565076; RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7[5]: GU565087; RVA/Human-tc/IDN/69M/1980/G8P4[10]: AY277916; RVA/Cow-tc/USA/NCDV/1967/G6P6[1]: DQ870495; RVA/Cow-tc/USA/WC3/1981/G6P[5]: EF560617; RVA/Guanaco-wt/ARG/Rio-Negro/1998/G8P[1]: FJ347124; RVA/Cow-tc/GBR/UK/1973/G6P7[5]: AY300923; RVA/Cow-wt/KOR/KJ9-1/XXXX/G6P[7]: HM988964; RVA/Cow-tc/FRA/RF/1982/G6P[1]: AY116592; RVA/Human-tc/USA/Se584/1998/G6P[9]: EF583043; VA/Cat-wt/ITA/BA222/2005/G3P[9]: GU827408; RVA/Human-wt/BEL/B1711/2002/G6P[6]: EF554084; RVA/Cow-tc/VEN/BRV033/1990/G6P6[1]: EF560614; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009631; RVA/Human-tc/USA/DS-1/1976/G2P[4]: HQ650118; RVA/Human-wt/MWI/1473/2001/G8P[4]: HQ657135; RVA/Human-wt/ZAF/3203WC/2009/G2P[4]: HQ657168; RVA/Human-wt/ZAF/GR10924/1999/G9P[6]: FJ183355; RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]: AY787654; RVA/Human-wt/BGD/MMC88/2005/G2P[4]: HQ641366; RVA/Human-wt/BGD/RV176-00/2000/G12P[6]: DQ490553; RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627544.

Genome segment 4 (VP4)

RVA/Cow-wt/THA/61A/XXXX/G10P[5]: D13396; RVA/Pig-wt/THA/P343/XXX/G10P[5]: U35851; RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]: GU565055; RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5]: GU565077; RVA/Human-tc/THA/CJN-M/XXXX/G1P[5]: D16351; RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]: GU565066; RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7[5]: GU565088; RVA/Cow-tc/FRA/RF/1982/G6P[1]: U65924; RVA/Velvet monkey-tc/ZAF/SA11-4F/1958/G3P6[1]: X57319; RVA/Rhesus-tc/USA/PTRV/1990/G8P[1]: FJ422134; RVA/Labstr/USA/SA11g4Oagent/XXXX/G3P[1]: DQ838602; RVA/Labstr/USA/SA11-30/1A/1958/G3P[1]: DQ838605; RVA/Cow-tc/USA/VMRI/XXXX/G6P[5]: U53923; RVA/Labstr/USA/UKg9D/1984/G1P[5]: GQ496215; RVA/Labstr/USA/UKg9P/1984/G3P[5]: GQ496246; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009632; RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627545; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009631; RVA/Cow-wt/CHN/CHLY/XXXX/G6P[1]: FJ969816; RVA/Cow-tc/USA/NCDV/1967/G6P6[1]: AB119636.

Genome segment 6 (VP6)

RVA/Cow-tc/USA/WC3/1981/G6P[5]: AF411322; RVA/Cow-wt/KOR/KJ9-1/XXXX/G6P[7]: HM988974; RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5]: GU565078; RVA/Bovine-tc/JPN/22R/XXXX/GXP[X]: AB040055; RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]: GU565067; RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]: GU565056; RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]: FJ495131; RVA/Cow-tc/USA/NCDV/1967/G6P6[1]: DQ870496; RVA/Sheep-tc/ESP/OVR762/2002/G8P[14]: EF554152; RVA/Labstr/USA/Rotashield-DS1xRRV/XXXX/G2P[3]: HQ846870: RVA/Cow-tc/CHN/DQ-75/2008/G10P[11]: GU384194; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: D16329; RVA/Human-wt/COD/DRC88/2003/G8P[8]: DQ005110; RVA/Human-tc/USA/DS-1/1976/G2P[4]: HQ650121; RVA/Human-wt/MWI/1473/2001/G8P[4]: HQ657137; RVA/Human-wt/ZAF/GR10924/1999/G9P[6]: FJ183358; RVA/Human-wt/ZAF/3203WC/2009/G2P[4]: HQ657170; RVA/Human-wt/USA/LB2744/2006/G2P[4]: HM467947; RVA/Human-wt/BGD/MMC6/2005/G2P[4]: HQ641358; RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]: AY787645; RVA/Human-tc/JPN/S2/1980/G2P1[4]: DQ870488.

Genome segment 9 (VP7)

RVA/Cow-tc/GBR/UK/1973/G6P7[5]: X00896; RVA/Cow-wt/KOR/KJ69-1/XXXX/G6P[7]: FJ206066; RVA/Foal-wt/IND/Erv99/XXXX/G6P[1]: DQ981478; RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]: GU565046; RVA/Human-wt/ITA/PA169/1988/G6P[14]: L20883; RVA/Human-wt/AUS/MG8/1997/G8P[14]: AF207061; RVA/Human-tc/IDN/69M/1980/G8P4[10]: EF672560; RVA/Human-wt/GBR/QEH14262/1990/G8P[X]: AF143689; RVA/Human-wt/KEN/B12/1987/G8P[1]: RVA/Cow-wt/CHN/CHLY/XXXX/G6P[1]: DQ195152; RVA/Cow-wt/KOR/KV0426/XXXX/G6P[X]: EU873015; RVA/Cow-tc/USA/IND/XXXX/G6P[X]: U15000; RVA/Human-wt/MWI/MW1479/2001/G8P[4]: FJ386441: RVA/Human-wt/ZAF/GR570-85/1985/G8P[X]: RVA/Human-wt/ZAF/GR570-85/1985/G8P[X]: FJ386441; RVA/Human-wt/MW4103/2000/G8P[8]: FJ386443; RVA/Human-wt/NGA/HMG035/XXXX/G8P[1]: AF359359; RVA/Human-wt/KEN/1290/1991/G8P[X]: EU488721; RVA/Human-wt/COD/DRC88/2003/G8P[8]: DQ005109: RVA/Human-wt/COD/DRC86/2003/G8P[6]: DQ005120; RVA/Swine-wt/KOR/C-1/2006/G8P[7]: FJ807868; RVA/Human-wt/AUS/WAG8.3/2007/G8P[8][14]: GQ398018; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: D82979.

Genome segment 5 (NSP1)

RVA/Human-tc/KEN/B12/1987/G8P[1]: HM627548; RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]: GU565069; RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]: GU565047; RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5]: GU565080; RVA/Cow-tc/USA/NCDV/1967/G6P6[1]: GU808570; RVA/Cow-tc/USA/WC3/1981/G6P[5]: EF990699; RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7[5]: GU565091; RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]: GU565058; RVA/Human-wt/ITA/111-05-27/2005/G6P[14]: EF554143; RVA/Rhesus-tc/USA/PTRV/1990/G8P[1]: FJ422135; RVA/Cow-wt/THA/A44/1989/G10P[11]: U23726; RVA/giraffe-wt/IRL/UCD/2007/G10P[11]: GQ428136; RVA/Cow-tc/GBR/UK/1973/G6P7[5]: HQ186289; RVA/Human-wt/BEL/B10925/1997/G6P[14]: EF554121; RVA/Cow-tc/USA/WC3/1981/G6P[5]: EF990699; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009633; RVA/Human-tc/JPN/AU-1/1982/G3P3[9]: D45244; RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627548; RVA/Cow-tc/USA/NCDV/1967/G6P6[1]: GU808570; RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7[5]: GU565091; RVA/Cow-tc/FRA/RF/1982/G6P[1]: M22308; RVA/Human-wt/ITA/111-05-27/2005/G6P[14]: EF554143.

Genome segment 8 (NSP2)

RVA/Cow-tc/USA/WC3/1981/G6P[5]: EF990700; RVA/Human-wt/JPN/KF17/2010/G6P[9]: JF421982; RVA/Simian-tc/USA/RRV/1975/G3P[3]: EU636931; RVA/Dog-tc/ITA/RV52-96/1996/G3P[3]: HQ661130; RVA/Human-tc/ITA/PA260-97/1997/G3P[3]: HQ661119; RVA/Simian-tc/USA/RRV/1975/G3P[3]: EU636931; RVA/Cow-tc/CHN/DQ-75/2008/G10P[11]: GU384196; RVA/Rhesus-tc/USA/PTRV/1990/ G8P[1]: FJ422139; RVA/Cow-wt/ARG/B383/1998/G15P[11]: FJ347118; RVA/Sheep-tc/CHN/Lamb-NT/XXXX/G10P[15]: FJ031020; RVA/Cow-wt/ARG/B383/1998/G15P[11]: FJ347118; RVA/Goat-tc/BGD/GO34/1999/G6P[1]: GU937884; RVA/Labstr/USA/UKg9ST3/1986/G4P[5]: GQ225816; RVA/Human-wt/KEN/D205/1989/G2P[4]: JF304922; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009625; RVA/Human-wt/COD/DRC86/2003/G8P[6]: DQ005118; RVA/Human-tc/IDN/69M/1980/G8P4[10]: EF672559; RVA/Human-wt/MWI/1473/2001/G8P[4]: HQ657140; RVA/Human-wt/ZAF/3203WC/2009/G2P[4]: HQ657173; RVA/Human-wt/ZAF/GR10924/1999/G9P[6]: FJ183361; RVA/Human-tc/USA/DS-1/1976/G2P1B[4]: EF672580; RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627549; RVA/Cow-tc/GBR/UK/1973/G6P7[5]: J02420.

Genome segment 7 (NSP3)

RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5] NSP3: GU565060; RVA/Vaccine/ USA/RotaTeq-WI78-8/1992/G3P7[5]: GU565082; RVA/Cow-tc/FRA/RF/1982/G6P[1]: Z21639; strain RVA/Cow-tc/USA/WC3/1981/G6P[5]: EF990701; RVA/Human-tc/ITA/PA169/1988/G6P[14]: EF554134; RVA/Sheep-wt/CHN/CC0812-1/2008/G10P[15]: HQ834204; RVA/Human-wt/ITA/PAH136/1996/G3P[9]: GU296415; RVA/Vaccine/USA/ RotaTeq-SC2-9/1992/G2P7[5]: GU565071; RVA/giraffe/UCD/IRL/2007/G10P[11]: GQ428138; RVA/Human-wt/ITA/PAI58/1996/G3P[9]: GU296414; RVA/Human-tc/AUS/MG6/1993/G6P[14]: EF554101; RVA/Cow-tc/CHN/DQ-75/2008/G10P[11]: GU384196; RVA/Labstr/USA/UKg9D/1984/G1P[5]: GQ496199; RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]: FJ495134; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009626; RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1]: FJ347130; RVA/Human-wt/BEL/B10925/1997/G6P[14]: EF554123; RVA/Cow-wt/ARG/B383/1998/G15P[11]: FJ347119; RVA/Human-wt/ITA/111-05-27/2005/G6P[14]: EF554145; RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627550; RVA/Human-wt/MWI/1473/2001/G8P[4]: HQ657141; RVA/Human-wt/ZAF/3203WC/2009/G2P[4]: HQ657174.

Genome segment 10 (NSP4)

RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627551; RVA/giraffe-wt/IRL/UCD/2007/ G10P[11]: GQ428139; strain RVA/Human-wt/HUN/Hun5/1997/G6P[14]: EF554113; RVA/Human-wt/ITA/111-05-27/2005/G6P[14]: EF554146; RVA/Human-wt/ITA/PAI58/ 1996/G3P[9]: GU296417; RVA/Cat-wt/ITA/BA222/2005/G3P[9]: GU827415; RVA/Human-tc/ITA/PA169/1988/G6P[14]: EF554135; RVA/Human-wt/ITA/PAH136/1996/ G3P[9]: GU296416; RVA/Human-wt/COD/DRC88/2003/G8P[8]: DQ005105; RVA/Human-wt/ESP/RV1019/SAG/2009/G8P[6]: RVA/Human-tc/USA/DS-1/1976/G2P[4]: HQ650125; RVA/Human-wt/FRA/R1853/2007/G8/P[6]: HM035536; RVA/Human-wt/COD/DRC86/2003/ G8P[6]: DQ005116; RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]: FJ495135; RVA/Human-wt/ESP/RV902/VLC/2008/G8P[6]: HQ674766; RVA/Human-Wt/ITA/PA43/2003/G6P[9]: JF793928; RVA/Human-Wt/THA/CMH134/2005/G2P[4]: GU288649; RVA/Cat-wt/ITA/BA222/2005/G3P[9]: GU827415; RVA/Human-wt/BGD/MMC88/2005/G2P[4]: HQ641371; RVA/Human-wt/USA/LB2764/2006/G2P[4]: HM467980; RVA/Human-wt/ZAF/3203WC/2009/G2P[4]: HQ657175; RVA/Human-wt/ZAF/GR10924/1999/G9P[6]: FJ183363; RVA/Human-wt/MWI/1473/2001/G8P[4]:

HQ657142; RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]: AY787650; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009627; RVA/Cow-tc/GBR/UK/1973/G6P7[5]: J02420; RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]: FJ495135.

Genome segment 11 (NSP5)

RVA/Cat-wt/ITA/BA222/2005/G3P[9]: GU827416; RVA/Human-wt/BEL/B10925/1997/G6P[14]: EF554125; RVA/Goat-tc/BGD/GO34/1999/G6P[1]: GU937887; RVA/Cow-wt/KOR/KJ19-2/XXXX/G6P[7]: FJ206054; RVA/Cow-tc/USA/WC3/1981/G6P[5]: EF990702; RVA/giraffe-wt/IRL/UCD/2007/G10P[11]: RVA/giraffe-wt/ IRL/UCD/2007/G10P[11]: GQ428140; RVA/Human-wt/ITA/PAH136/1996/G3P[9]: GU296418; RVA/Human-wt/JPN/KF17/2010/G6P[9]: JF421985; RVA/Cow-tc/CHN/DQ-75/2008/G10P[11]: GU384198; RVA/Cow-wt/ARG/B383/1998/G15P[11]: FJ347121; RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1]: FJ347132; RVA/Guanaco-wt/ARG/Chubut/1999/G8P[14]: FJ347110; RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]: GU565051; RVA/Sheep-tc/ESP/OVR762/2002/G8P[14]: EF554158; RVA/Sheep-wt/CHN/CC0812-1/2008/G10P[15]: HQ834206; RVA/Rhesus-tc/USA/PTRV/1990/G8P[1]: FJ422141; RVA/Human-tc/USA/Se584/1998/G6P[9]: EF672611; RVA/Dog-tc/ITA/RV198-95/1995/G3P[3]: HQ661144; RVA/Human-wt/THA/CMH079/2005/G3P[10]: EU791926; RVA/Cow-tc/USA/NCDV/1967/G6P6[1]: GU937876; RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]: AB009628; RVA/Human-tc/JPN/AU-1/1982/G3P3[9]: AB008656; RVA/Human-wt/BEL/B10925/1997/G6P[14]: EF554125; RVA/Sheep-tc/CHN/Lamb-NT/XXXX/G10P[15]: FJ031023; RVA/Human-wt/KEN/B12/1987/G8P[1]: HM627552.

Supplement 3. Average sequence coverage for all genome segments of the three bovine rotaviruses characterised in this study.

Genome segment	Average depth of sequence coverage		
	RVA/Cow-wt/ZAF/1603/2007/G6P[5]	RVA/Cow-wt/ZAF/1604/2007/G8P[1]	RVA/Cow-wt/ZAF/1605/2007/G6P[5]
1 (VP1)	58	147	136
2 (VP2)	124	219	101
3(VP3)	191	317	136
4(VP4)	107	399	114
5 (NSP1)	191	355	151
6 (VP6)	473	374	136
7 (NSP3)	678	210	435
8 (NSP2)	628	399	323
9 (VP7)	499	623	112
10 (NSP4)	182	132	174
11 (NSP5/NSP6)	361	216	142

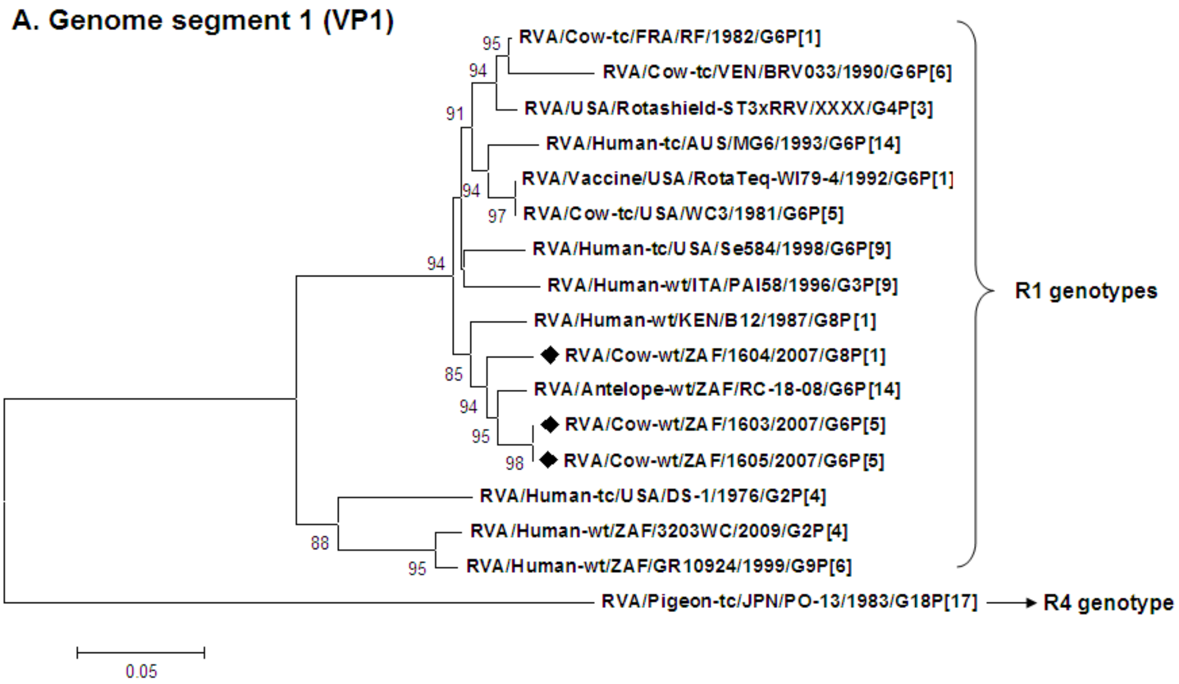
Supplement 4. Size of the complete nucleotide and deduced amino acid sequence of all 11 genome segments of the three study bovine rotaviruses.

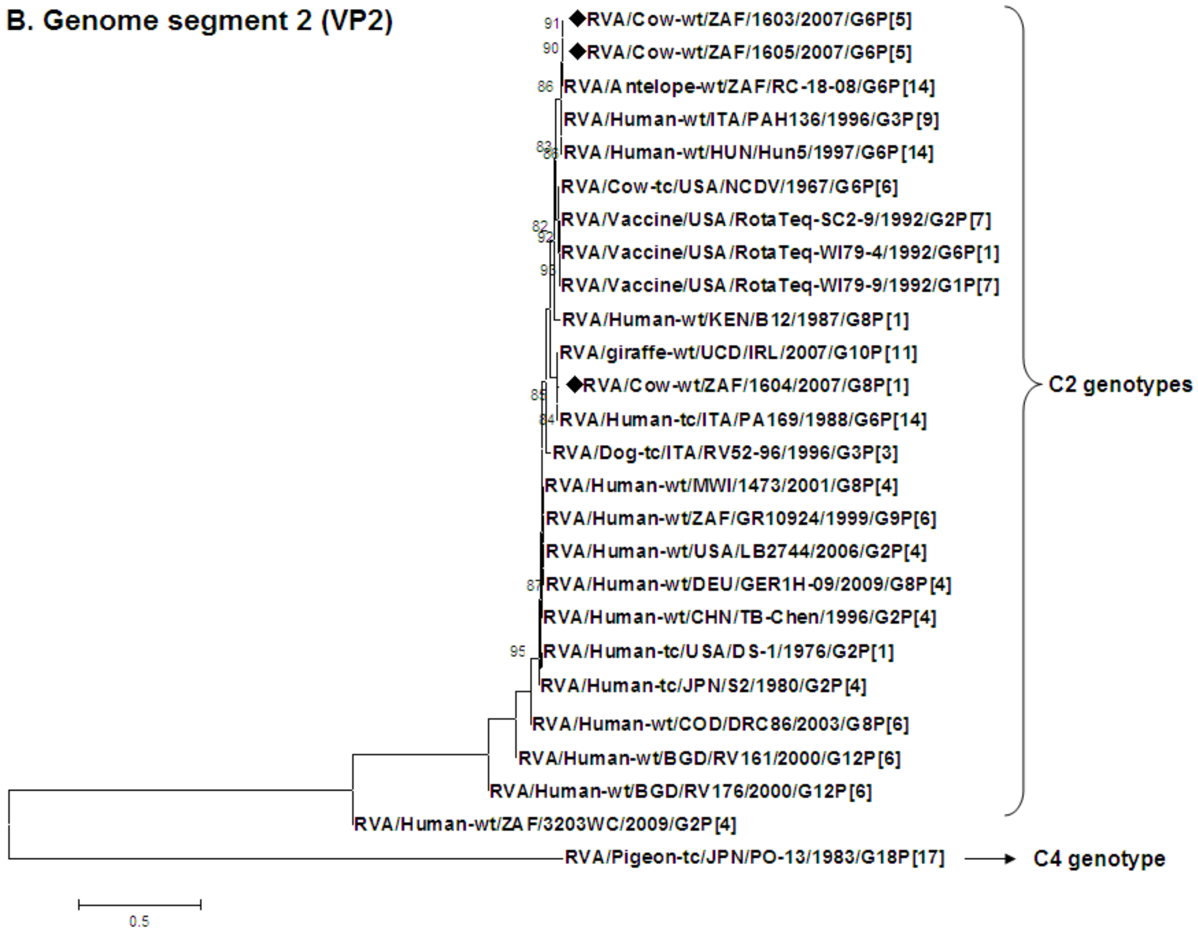
Study bovine rotavirus strains	**Genome segments**										
	Nucleotides (nt)										
	S9(VP7)	**S4(VP4)**	**S6(VP6)**	**S1(VP1)**	**S2(VP2)**	**S3(VP3)**	**S5(NSP1)**	**S8(NSP2)**	**S7(NSP3)**	**S10(NSP4)**	**S11(NSP5)**
RVA/Cow-wt/ZAF/1603/2007/G6P[5]	1062	2362	1356	3302	2687	2591	1579[a]	1059	1074[b]	751	667
RVA/Cow-wt/ZAF/1604/2007/G8P[1]	1062	2362	1356	3302	2687	2591	1578	1059	1078	751	667
RVA/Cow-wt/ZAF/1605/2007/G6P[5]	1062	2362	1356	3302	2687	2591	1579[a]	1059	1074[b]	751	667
	Deduced amino acids (aa)										
	(VP7)S9	**(VP4)S4**	**(VP6)S6**	**(VP1)S1**	**(VP2)S2**	**(VP3)S3**	**(NSP1)S5**	**(NSP2)S8**	**(NSP3)S7**	**(NSP4)S10**	**(NSP5)S11**
RVA/Cow-wt/ZAF/1603/2007/G6P[5]	326	776	397	1088	880	835	491	317	313	175	198
RVA/Cow-wt/ZAF/1604/2007/G8P[1]	326	776	397	1088	880	835	491	317	313	175	198
RVA/Cow-wt/ZAF/1605/2007/G6P[5]	326	776	397	1088	880	835	491	317	313	175	198

[a] NSP1 polypeptide was translated from nt 26 – 967. RVA strains 1603 and 1605 contains nucleotide ‘A’ insertion at position 18.

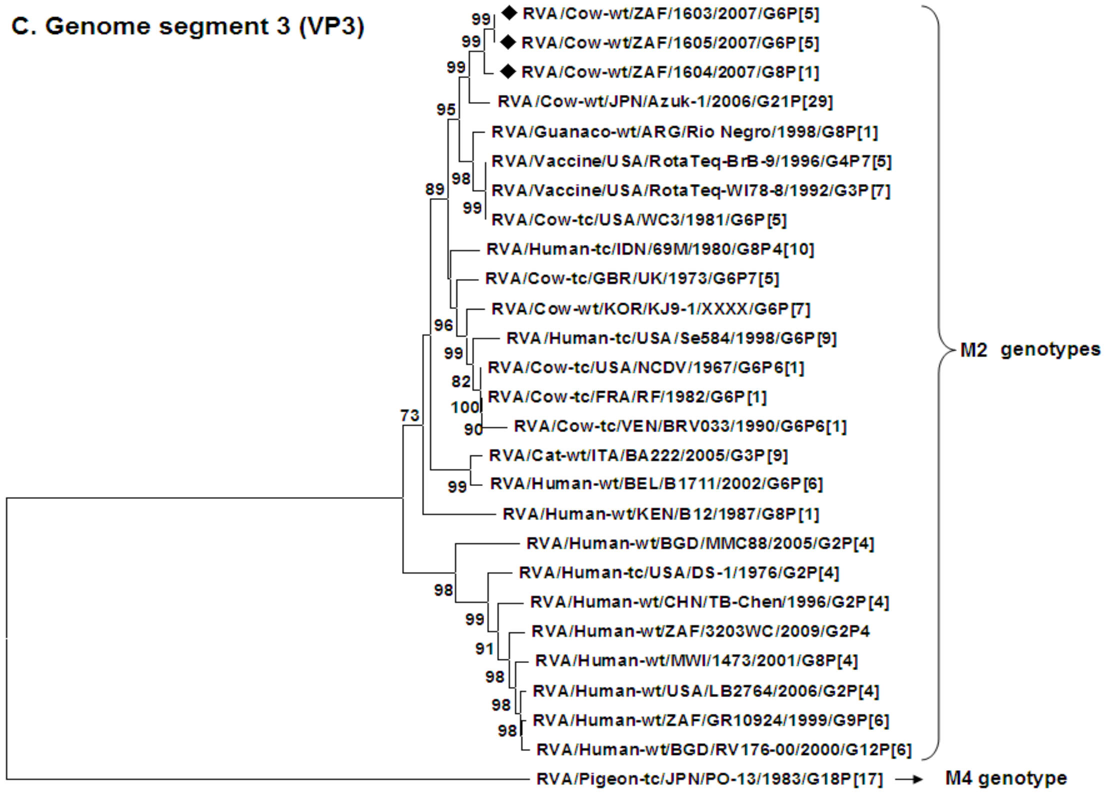
[b] NSP3 polypeptide for RVA strains 1603 and 1605 was translated from nt 32 – 1507, whereas NSP3 polypeptide for RVA strains 1604 was translated from nt 33 – 1508. RVA strains 1603 and 1605 contains nucleotides ‘GACT’ insertions from position 983 – 986.

Supplement 5. Phylogenetic trees

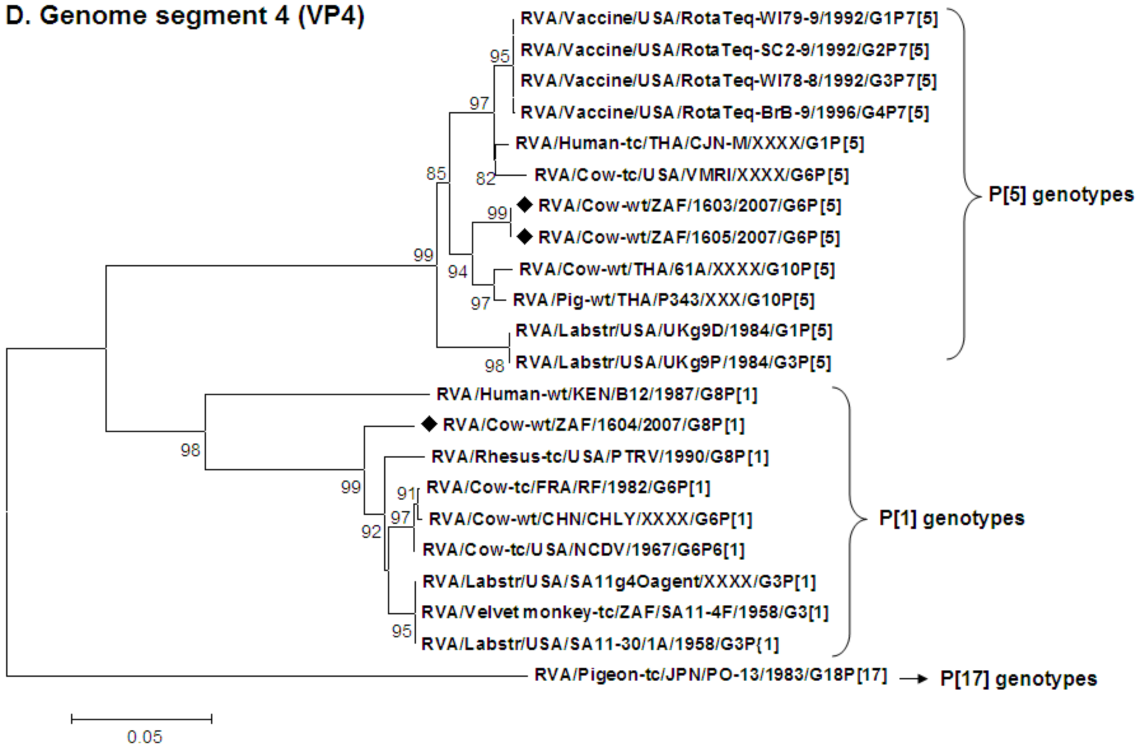

A. Genome segment 1 (VP1)

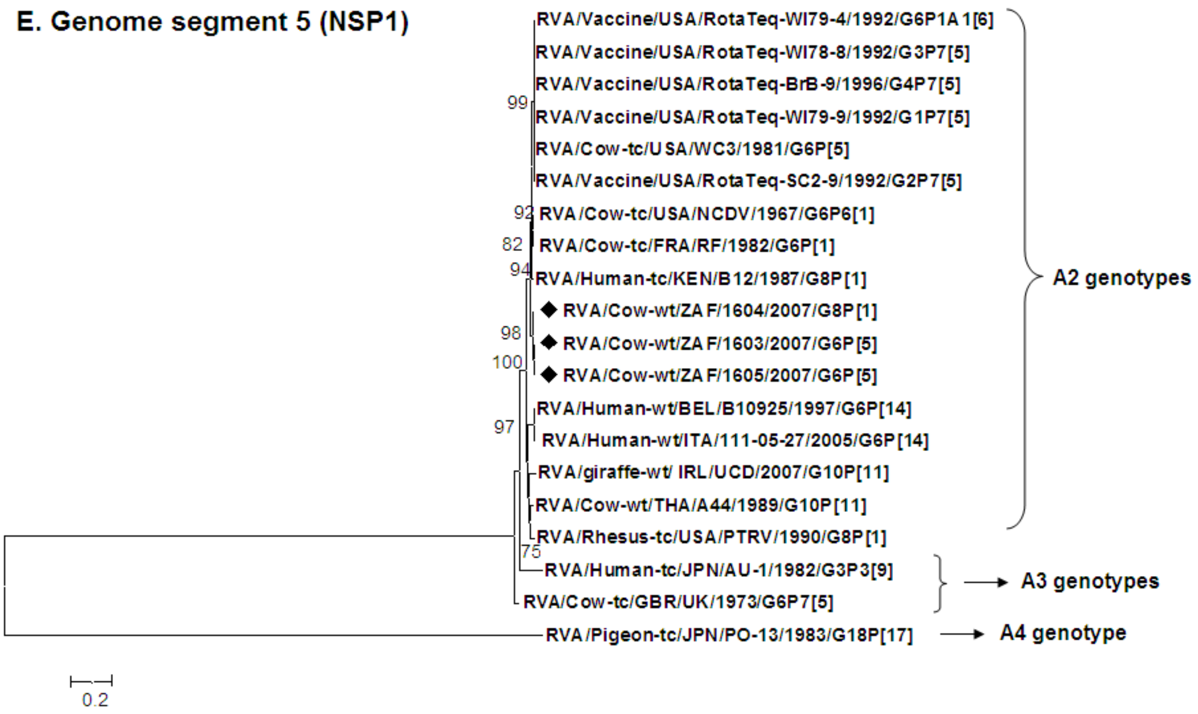

B. Genome segment 2 (VP2)

C. Genome segment 3 (VP3)

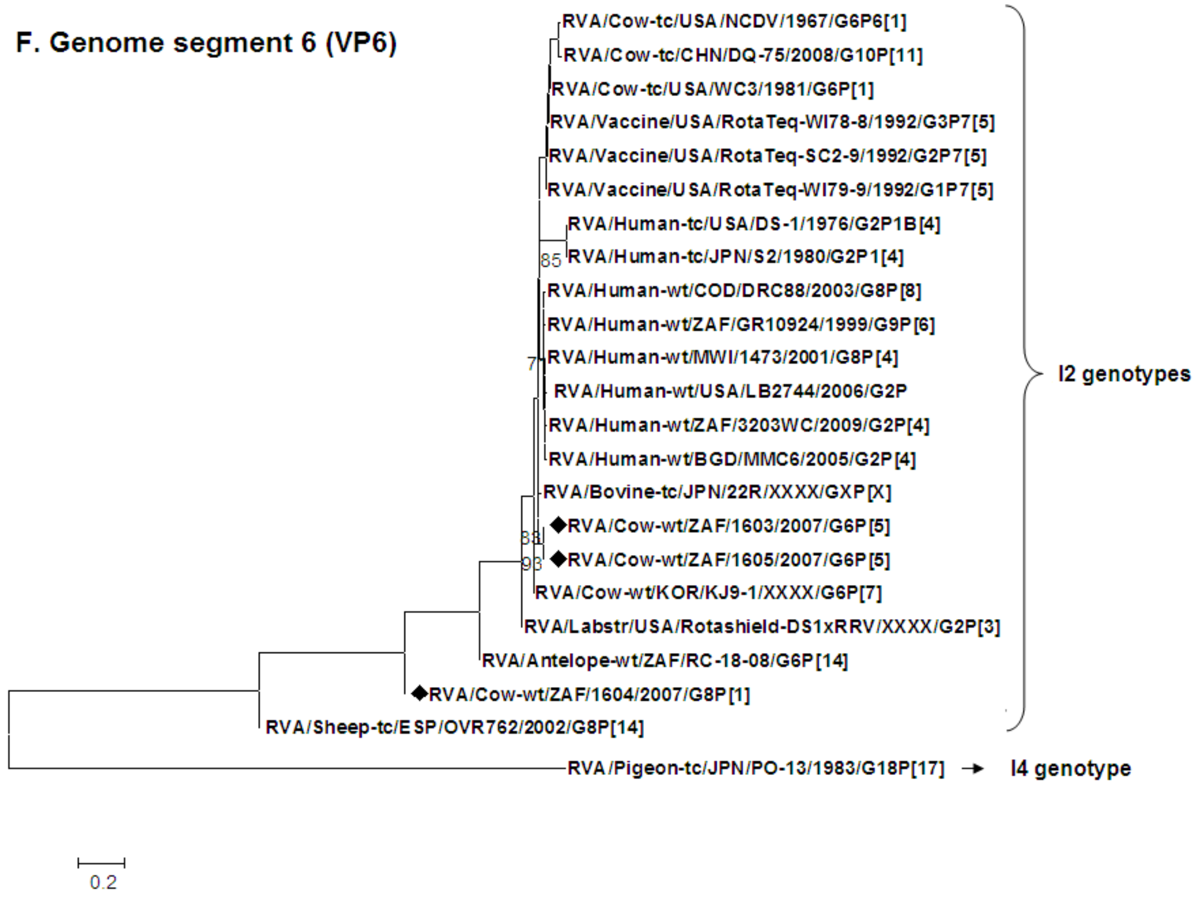


D. Genome segment 4 (VP4)



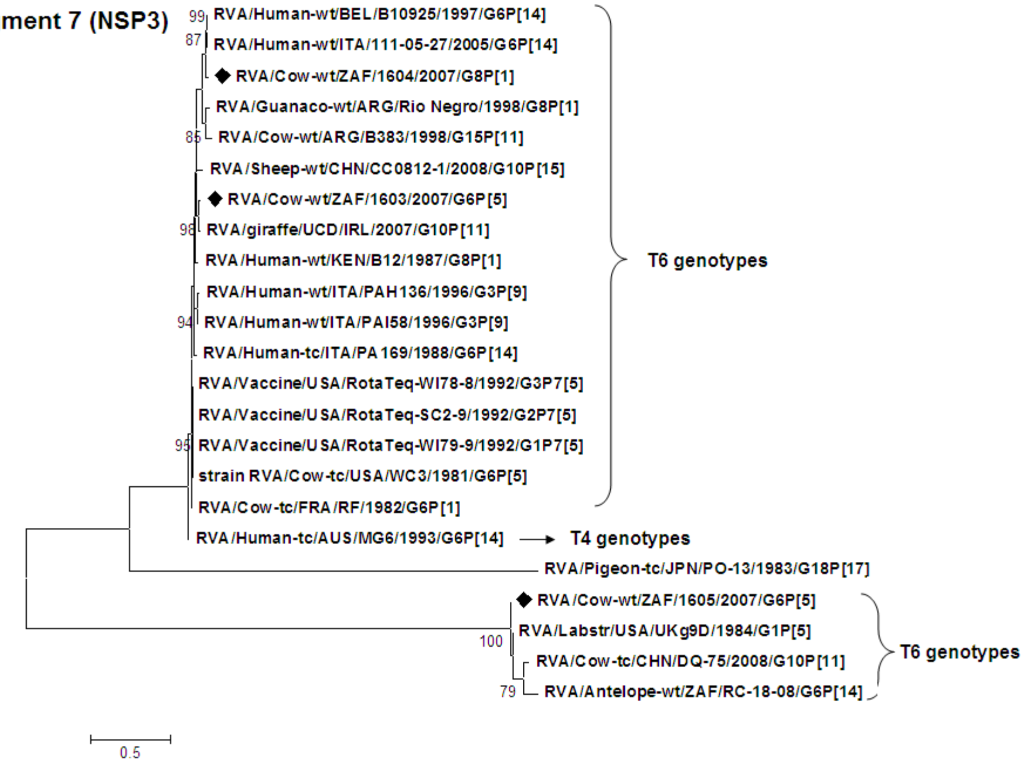


E. Genome segment 5 (NSP1)

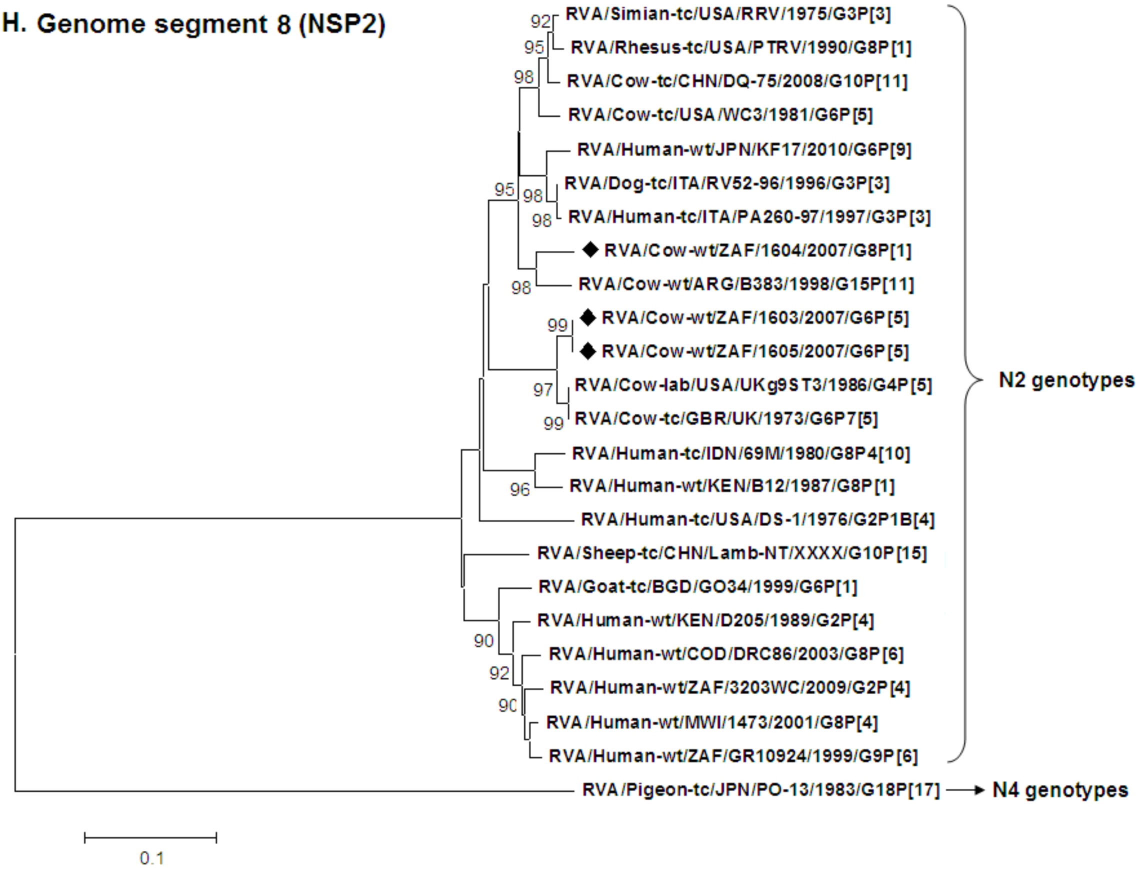


F. Genome segment 6 (VP6)

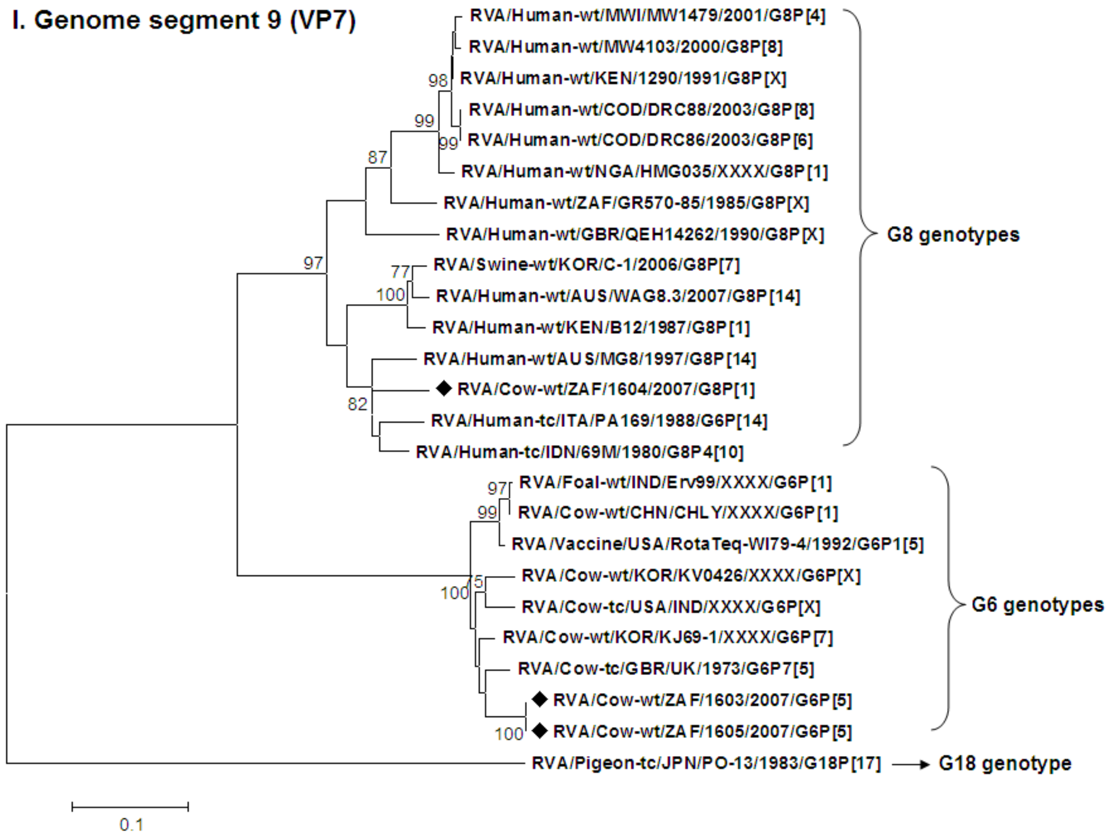
G. genome segment 7 (NSP3)



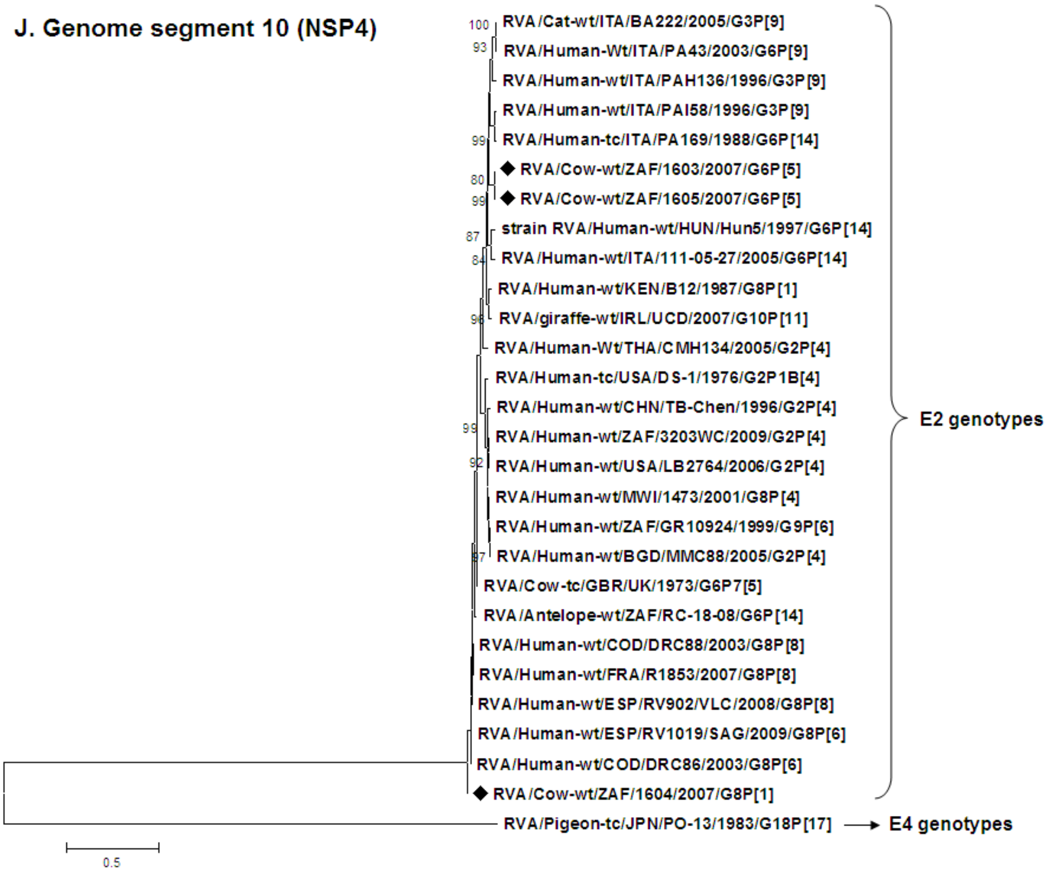
H. Genome segment 8 (NSP2)

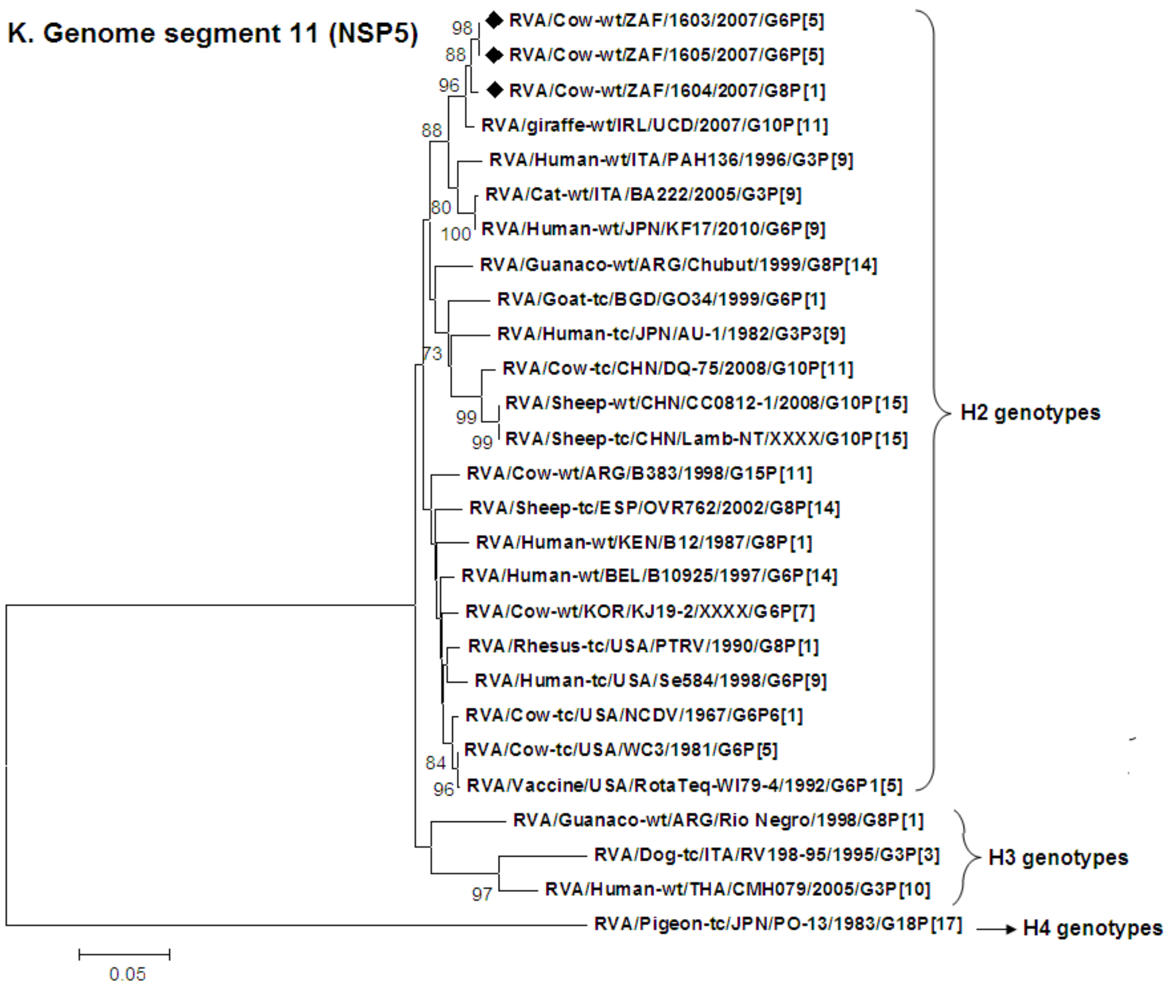


I. Genome segment 9 (VP7)



J. Genome segment 10 (NSP4)

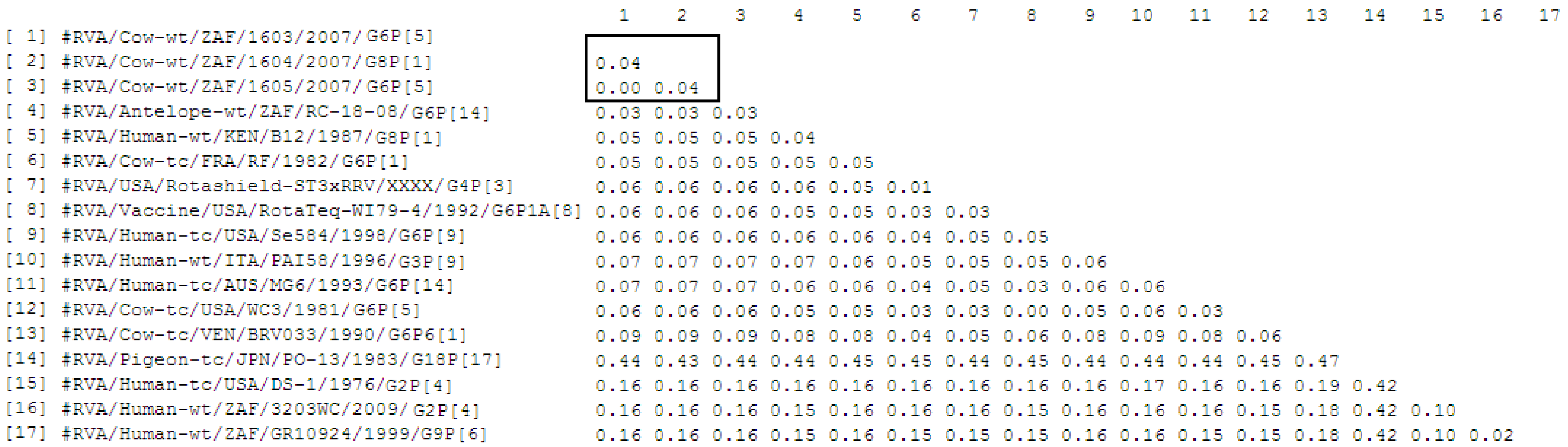



K. Genome segment 11 (NSP5)

Supplement 5. Phylogenetic trees based on the full-length consensus nucleotide sequence of rotavirus genome segments 1–11 encoding structural (VP1–VP4, VP6 and VP7) and non-structural (NSP1–NSP5) proteins. The nomenclature of all the rotavirus strains included in the trees indicate the rotavirus group/species of origin-(wild type or tissue culture sample)/country of identification (unique 3-letter abbreviation code for each country)/common name of the sample/year of isolation/G- and P-type of each strain as proposed by the RCWG (Matthijnssens et al., 2011). Accession numbers of all the nucleotide sequences of the strains used for comparison in the phylogenetic trees are listed in Supplement 2. The study strains are marked with a black diamond. The horizontal branch lengths are proportional to the genetic distance calculated by the Neighbour-Joining method. The numbers adjacent to the nodes represent the bootstrap value of 1,000 replicates, and values less than 70% were not shown. The scale bars represent nucleotide substitutions per site.

Supplement 6. Distance matrices.

A. Genome segment 1 (VP1)



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                                                      1    2    3    4    5    6    7    8    9   10   11   12   13   14   15   16   17
[ 1] #RVA/Cow-wt/ZAF/1603/2007/G6P[5]
[ 2] #RVA/Cow-wt/ZAF/1604/2007/G8P[1]                0.04
[ 3] #RVA/Cow-wt/ZAF/1605/2007/G6P[5]                0.00 0.04
[ 4] #RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]           0.03 0.03 0.03
[ 5] #RVA/Human-wt/KEN/B12/1987/G8P[1]               0.05 0.05 0.05 0.04
[ 6] #RVA/Cow-tc/FRA/RF/1982/G6P[1]                  0.05 0.05 0.05 0.05 0.05
[ 7] #RVA/USA/Rotashield-ST3xRRV/XXXX/G4P[3]         0.06 0.06 0.06 0.06 0.05 0.01
[ 8] #RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]   0.06 0.06 0.06 0.05 0.05 0.03 0.03
[ 9] #RVA/Human-tc/USA/Se584/1998/G6P[9]             0.06 0.06 0.06 0.06 0.06 0.04 0.05 0.05
[10] #RVA/Human-wt/ITA/PAI58/1996/G3P[9]             0.07 0.07 0.07 0.07 0.06 0.05 0.05 0.05 0.06
[11] #RVA/Human-tc/AUS/MG6/1993/G6P[14]              0.07 0.07 0.07 0.06 0.06 0.04 0.05 0.03 0.06 0.06
[12] #RVA/Cow-tc/USA/WC3/1981/G6P[5]                 0.06 0.06 0.06 0.05 0.05 0.03 0.03 0.00 0.05 0.06 0.03
[13] #RVA/Cow-tc/VEN/BRV033/1990/G6P6[1]             0.09 0.09 0.09 0.08 0.08 0.04 0.05 0.06 0.08 0.09 0.08 0.06
[14] #RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]          0.44 0.43 0.44 0.44 0.45 0.45 0.44 0.45 0.44 0.44 0.44 0.45 0.47
[15] #RVA/Human-tc/USA/DS-1/1976/G2P[4]              0.16 0.16 0.16 0.16 0.16 0.16 0.16 0.16 0.16 0.17 0.16 0.16 0.19 0.42
[16] #RVA/Human-wt/ZAF/3203WC/2009/G2P[4]            0.16 0.16 0.16 0.15 0.16 0.16 0.16 0.15 0.16 0.16 0.16 0.15 0.18 0.42 0.10
[17] #RVA/Human-wt/ZAF/GR10924/1999/G9P[6]           0.16 0.16 0.16 0.15 0.16 0.15 0.15 0.15 0.16 0.16 0.15 0.15 0.18 0.42 0.10 0.02
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B. Genome segment 2 (VP2)

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                                                      1    2    3    4    5    6    7    8    9    10   11   12   13   14   15   16   17   18   19   20   21   22   23   24   25   26   27
[ 1] #RVA/Cow-wt/ZAF/1603/2007/G6P[5]               
[ 2] #RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]         1.90
[ 3] #RVA/Cow-wt/ZAF/1604/2007/G8P[1]               0.08 1.10
[ 4] #RVA/Cow-wt/ZAF/1605/2007/G6P[5]               0.00 1.92 0.08
[ 5] #RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]          0.01 1.77 0.08 0.01
[ 6] #RVA/Human-wt/ITA/PAH136/1996/G3P[9]           0.02 1.78 0.08 0.02 0.02
[ 7] #RVA/Human-wt/HUN/Hun5/1997/G6P[14]            0.02 1.34 0.08 0.02 0.02 0.01
[ 8] #RVA/Human-wt/EGY/Egy3399/2004/G6P[14]         0.02 1.41 0.08 0.02 0.02 0.01 0.01
[ 9] #RVA/Human-wt/BGD/RV176/2000/G12P[6]           0.08 1.00 0.07 0.08 0.08 0.08 0.08 0.08
[10] #RVA/giraffe-wt/UCD/IRL/2007/G10P[11]          0.08 1.41 0.02 0.08 0.08 0.08 0.08 0.08 0.07
[11] #RVA/Dog-tc/ITA/RV52-96/1996/G3P[3]            0.08 1.21 0.07 0.08 0.08 0.08 0.08 0.08 0.04 0.07
[12] #RVA/Human-tc/JPN/S2/1980/G2P1B[4]             0.08 1.29 0.07 0.08 0.08 0.08 0.08 0.08 0.01 0.07 0.04
[13] #RVA/Human-tc/USA/DS-1/1976/G2P[4]             0.08 1.65 0.07 0.08 0.08 0.08 0.08 0.08 0.03 0.07 0.04 0.02
[14] #RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]          0.08 1.43 0.07 0.08 0.08 0.09 0.08 0.09 0.01 0.07 0.04 0.00 0.02
[15] #RVA/Cow-tc/USA/NCDV/1967/G6P6[1]              0.04 2.05 0.08 0.04 0.04 0.04 0.04 0.04 0.07 0.08 0.08 0.07 0.08 0.07
[16] #RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]    0.05 2.24 0.08 0.05 0.05 0.04 0.04 0.04 0.07 0.08 0.08 0.07 0.08 0.08 0.01
[17] #RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]  0.05 2.23 0.08 0.05 0.05 0.04 0.04 0.04 0.07 0.08 0.08 0.07 0.08 0.08 0.01 0.00
[18] #RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]   0.05 2.23 0.08 0.05 0.05 0.04 0.04 0.04 0.07 0.08 0.08 0.07 0.08 0.08 0.01 0.00 0.00
[19] #RVA/Human-tc/USA/DS-1/1976/G2P[4]             0.08 1.63 0.07 0.08 0.08 0.08 0.08 0.08 0.03 0.07 0.04 0.02 0.00 0.02 0.08 0.08 0.08 0.08
[20] #RVA/Human-wt/MWI/1473/2001/G8P[4]             0.08 1.09 0.08 0.08 0.08 0.08 0.08 0.08 0.01 0.07 0.04 0.01 0.03 0.01 0.07 0.07 0.07 0.07 0.03
[21] #RVA/Human-wt/ZAF/3203WC/2009/G2P[4]           0.08 0.86 0.08 0.08 0.08 0.08 0.08 0.08 0.01 0.07 0.04 0.01 0.03 0.02 0.07 0.08 0.08 0.08 0.03 0.01
[22] #RVA/Human-wt/ZAF/GR10924/1999/G9P[6]          0.08 1.08 0.07 0.08 0.08 0.08 0.08 0.08 0.01 0.07 0.04 0.01 0.03 0.01 0.08 0.07 0.07 0.07 0.03 0.01 0.01
[23] #RVA/Human-wt/USA/LB2744/2006/G2P[4]           0.08 1.65 0.08 0.08 0.08 0.08 0.08 0.08 0.01 0.07 0.05 0.01 0.03 0.02 0.08 0.08 0.08 0.08 0.03 0.01 0.01 0.01
[24] #RVA/Human-wt/BGD/RV161/2000/G12P[6]           0.08 1.02 0.07 0.08 0.08 0.08 0.08 0.08 0.00 0.07 0.04 0.01 0.03 0.01 0.07 0.07 0.07 0.07 0.03 0.01 0.01 0.00 0.01
[25] #RVA/Human-wt/DEU/GER1H-09/2009/G8P[4]         0.08 1.10 0.07 0.08 0.08 0.08 0.08 0.08 0.01 0.07 0.04 0.01 0.03 0.02 0.08 0.08 0.08 0.08 0.03 0.01 0.01 0.01 0.01 0.01
[26] #RVA/Human-wt/COD/DRC86/2003/G8P[6]            0.08 1.00 0.08 0.08 0.08 0.08 0.08 0.08 0.01 0.07 0.04 0.01 0.03 0.01 0.07 0.07 0.07 0.07 0.03 0.01 0.01 0.01 0.01 0.01 0.01
[27] #RVA/Human-wt/KEN/B12/1987/G8P[1]              0.06 1.36 0.08 0.06 0.06 0.05 0.05 0.05 0.08 0.08 0.08 0.08 0.08 0.08 0.05 0.05 0.05 0.05 0.08 0.07 0.08 0.08 0.08 0.08 0.08 0.07
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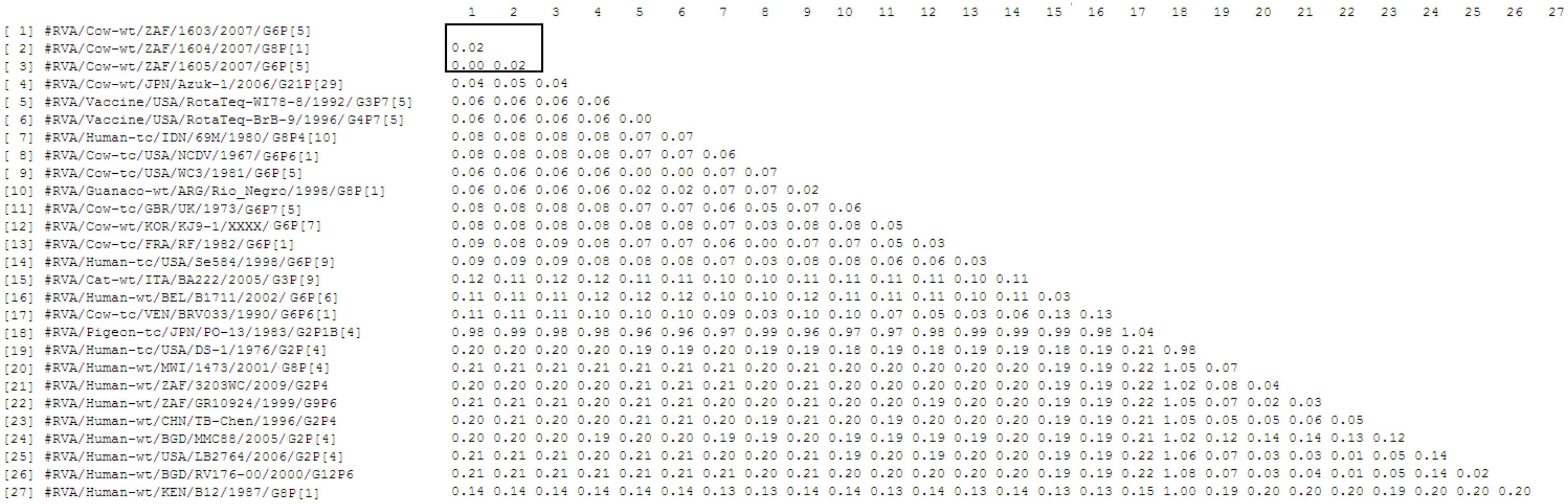
C. Genome segment 3 (VP3)



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
[1] #RVA/Cow-wt/ZAF/1603/2007/G6P[5]																											
[2] #RVA/Cow-wt/ZAF/1604/2007/G8P[1]	0.02																										
[3] #RVA/Cow-wt/ZAF/1605/2007/G6P[5]	0.00	0.02																									
[4] #RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29]	0.04	0.05	0.04																								
[5] #RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5]	0.06	0.06	0.06	0.06																							
[6] #RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7[5]	0.06	0.06	0.06	0.06	0.00																						
[7] #RVA/Human-tc/IDN/69M/1980/G8P4[10]	0.08	0.08	0.08	0.08	0.07	0.07																					
[8] #RVA/Cow-tc/USA/NCDV/1967/G6P6[1]	0.08	0.08	0.08	0.08	0.07	0.07	0.06																				
[9] #RVA/Cow-tc/USA/WC3/1981/G6P[5]	0.06	0.06	0.06	0.06	0.00	0.00	0.07	0.07																			
[10] #RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1]	0.06	0.06	0.06	0.06	0.02	0.02	0.07	0.07	0.02																		
[11] #RVA/Cow-tc/GBR/UK/1973/G6P7[5]	0.08	0.08	0.08	0.08	0.07	0.07	0.06	0.05	0.07	0.06																	
[12] #RVA/Cow-wt/KOR/KJ9-1/XXXX/G6P[7]	0.08	0.08	0.08	0.08	0.08	0.08	0.07	0.03	0.08	0.08	0.05																
[13] #RVA/Cow-tc/FRA/RF/1982/G6P[1]	0.09	0.08	0.09	0.08	0.07	0.07	0.06	0.00	0.07	0.07	0.05	0.03															
[14] #RVA/Human-tc/USA/Se584/1998/G6P[9]	0.09	0.09	0.09	0.08	0.08	0.08	0.07	0.03	0.08	0.08	0.06	0.06	0.03														
[15] #RVA/Cat-wt/ITA/BA222/2005/G3P[9]	0.12	0.11	0.12	0.12	0.11	0.11	0.10	0.10	0.11	0.11	0.11	0.11	0.10	0.11													
[16] #RVA/Human-wt/BEL/B1711/2002/G6P[6]	0.11	0.11	0.11	0.12	0.12	0.12	0.10	0.10	0.12	0.11	0.11	0.11	0.10	0.11	0.03												
[17] #RVA/Cow-tc/VEN/BRV033/1990/G6P6[1]	0.11	0.11	0.11	0.10	0.10	0.10	0.09	0.03	0.10	0.10	0.07	0.05	0.03	0.06	0.13	0.13											
[18] #RVA/Pigeon-tc/JPN/PO-13/1983/G2P1B[4]	0.98	0.99	0.98	0.98	0.96	0.96	0.97	0.99	0.96	0.97	0.97	0.98	0.99	0.99	0.99	0.98	1.04										
[19] #RVA/Human-tc/USA/DS-1/1976/G2P[4]	0.20	0.20	0.20	0.20	0.19	0.19	0.20	0.19	0.19	0.18	0.19	0.18	0.19	0.19	0.18	0.19	0.21	0.98									
[20] #RVA/Human-wt/MWI/1473/2001/G8P[4]	0.21	0.21	0.21	0.21	0.21	0.21	0.21	0.20	0.21	0.20	0.20	0.20	0.20	0.20	0.19	0.19	0.22	1.05	0.07								
[21] #RVA/Human-wt/ZAF/3203WC/2009/G2P4	0.20	0.20	0.20	0.20	0.21	0.21	0.21	0.20	0.21	0.20	0.20	0.20	0.20	0.20	0.19	0.19	0.22	1.02	0.08	0.04							
[22] #RVA/Human-wt/ZAF/GR10924/1999/G9P6	0.21	0.21	0.21	0.20	0.21	0.21	0.20	0.20	0.21	0.20	0.20	0.19	0.20	0.20	0.19	0.19	0.22	1.05	0.07	0.02	0.03						
[23] #RVA/Human-wt/CHN/TB-Chen/1996/G2P4	0.20	0.21	0.20	0.20	0.21	0.21	0.20	0.19	0.21	0.20	0.19	0.20	0.20	0.20	0.19	0.19	0.21	1.05	0.05	0.05	0.06	0.05					
[24] #RVA/Human-wt/BGD/MMC88/2005/G2P[4]	0.20	0.20	0.20	0.19	0.20	0.20	0.19	0.19	0.20	0.19	0.19	0.19	0.19	0.20	0.19	0.19	0.21	1.02	0.12	0.14	0.14	0.13	0.12				
[25] #RVA/Human-wt/USA/LB2764/2006/G2P[4]	0.21	0.21	0.21	0.20	0.21	0.21	0.20	0.20	0.21	0.19	0.20	0.19	0.20	0.20	0.19	0.19	0.22	1.06	0.07	0.03	0.03	0.01	0.05	0.14			
[26] #RVA/Human-wt/BGD/RV176-00/2000/G12P6	0.21	0.21	0.21	0.21	0.21	0.21	0.21	0.20	0.21	0.20	0.20	0.20	0.20	0.20	0.19	0.19	0.22	1.08	0.07	0.03	0.04	0.01	0.05	0.14	0.02		
[27] #RVA/Human-wt/KEN/B12/1987/G8P[1]	0.14	0.14	0.14	0.14	0.14	0.14	0.13	0.13	0.14	0.14	0.13	0.14	0.13	0.14	0.13	0.13	0.15	1.00	0.19	0.20	0.20	0.20	0.19	0.20	0.20	0.20	

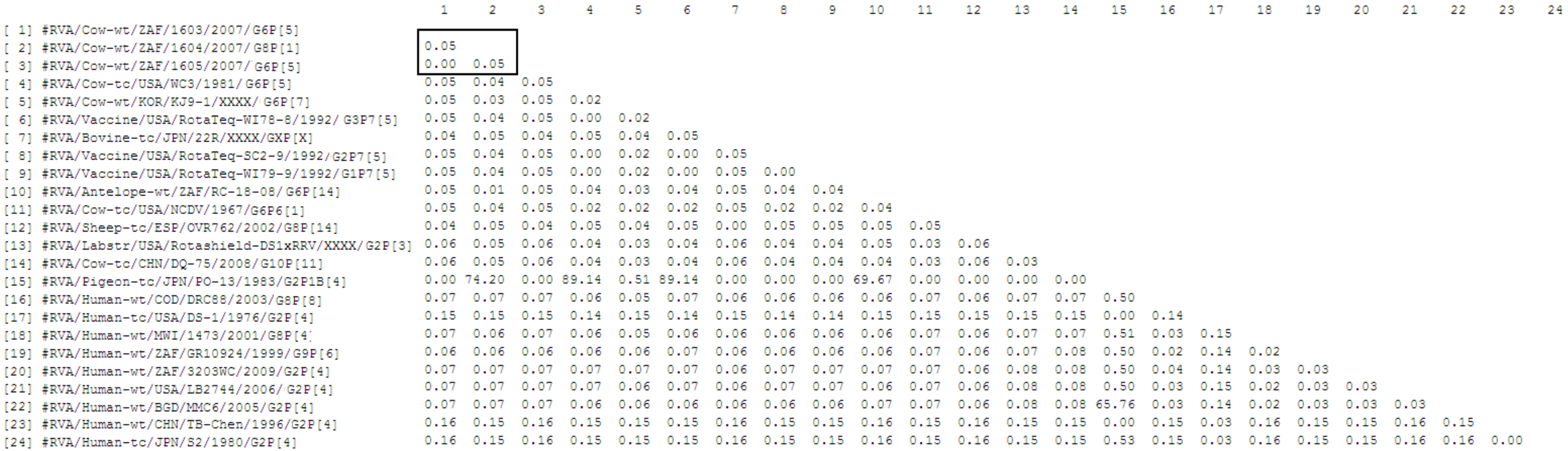
D. Genome segment 1 (VP4)

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
[1]	#RVA/Cow-wt/ZAF/1603/2007/G6P[5]																				
[2]	#RVA/Cow-wt/ZAF/1604/2007/G8P[1]	0.25																			
[3]	#RVA/Cow-wt/ZAF/1605/2007/G6P[5]	0.00	0.25																		
[4]	#RVA/Cow-wt/THA/61A/XXXX/G10P[5]	0.03	0.25	0.03																	
[5]	#RVA/Pig-wt/THA/P343/XXX/G10P[5]	0.02	0.25	0.03	0.01																
[6]	#RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]	0.04	0.25	0.04	0.05	0.04															
[7]	#RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7	0.04	0.25	0.04	0.05	0.04	0.00														
[8]	#RVA/Human-tc/THA/CJN-M/XXXX/G1P[5]	0.04	0.25	0.04	0.04	0.04	0.01	0.01													
[9]	#RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]	0.04	0.25	0.04	0.05	0.04	0.00	0.00	0.01												
[10]	#RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7	0.04	0.25	0.04	0.05	0.04	0.00	0.00	0.01	0.00											
[11]	#RVA/Cow-tc/FRA/RF/1982/G6P[1]	0.25	0.04	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25										
[12]	#RVA/Velvet_monkey-tc/ZAF/_SA11-4F/1958/G3P6[1]	0.25	0.03	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.02									
[13]	#RVA/Rhesus-tc/USA/PTRV/1990/G8P[1]	0.25	0.04	0.25	0.26	0.26	0.25	0.25	0.26	0.25	0.25	0.03	0.03								
[14]	#RVA/Labstr/USA/SA11g4Oagent/XXXX/G3P[1]	0.25	0.03	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.02	0.00	0.03							
[15]	#RVA/Labstr/USA/SA11-30/1A/1958/G3P[1]	0.25	0.03	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.02	0.00	0.03	0.00						
[16]	#RVA/Cow-tc/USA/VMRI/XXXX/G6P[5]	0.05	0.25	0.05	0.05	0.05	0.02	0.02	0.02	0.02	0.02	0.26	0.25	0.26	0.25	0.25					
[17]	#RVA/Labstr/USA/UKg9D/1984/G1P	0.05	0.25	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.26	0.25	0.26	0.25	0.25	0.06				
[18]	#RVA/Labstr/USA/UKg9P/1984/G3P[1]	0.05	0.25	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.26	0.25	0.26	0.25	0.25	0.06	0.00			
[19]	#RVA/Pigeon-tc/JPN/PO-13/1983/G2P1B[4]	0.36	0.32	0.36	0.36	0.36	0.36	0.36	0.36	0.36	0.36	0.32	0.32	0.32	0.32	0.32	0.37	0.36	0.36		
[20]	#RVA/Human-wt/KEN/B12/1987/G8P[1]	0.25	0.15	0.25	0.25	0.25	0.25	0.25	0.26	0.25	0.25	0.15	0.15	0.15	0.15	0.15	0.26	0.26	0.26	0.33	

E. Genome segment 5 (NSP1)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
[1] #RVA/Cow-wt/ZAF/1603/2007/G6P[5]																			
[2] #RVA/Cow-wt/ZAF/1604/2007/G8P[1]	0.02																		
[3] #RVA/Cow-wt/ZAF/1605/2007/G6P[5]	0.00	0.02																	
[4] #RVA/Human-tc/KEN/B12/1987/G8P[1]	0.04	0.04	0.04																
[5] #RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]	0.04	0.04	0.04	0.03															
[6] #RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]	0.04	0.04	0.04	0.03	0.00														
[7] #RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7	0.04	0.04	0.04	0.03	0.00	0.00													
[8] #RVA/Cow-tc/USA/NCDV/1967/G6P6[1]	0.03	0.03	0.03	0.02	0.01	0.02	0.02												
[9] #RVA/Cow-tc/USA/WC3/1981/G6P[5]	0.04	0.04	0.04	0.03	0.00	0.00	0.00	0.01											
[10] #RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7[5]	0.04	0.04	0.04	0.03	0.00	0.00	0.00	0.01	0.00										
[11] #RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]	0.04	0.04	0.04	0.03	0.00	0.00	0.00	0.01	0.00	0.00									
[12] #RVA/Cow-wt/THA/A44/1989/G10P[11]	0.08	0.08	0.08	0.08	0.07	0.07	0.07	0.06	0.07	0.07	0.07								
[13] #RVA/Human-wt/ITA/111-05-27/2005/G6P[14]	0.09	0.09	0.09	0.08	0.07	0.08	0.08	0.07	0.07	0.07	0.07	0.06							
[14] #RVA/Rhesus-tc/USA/PTRV/1990/G8P[1]	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.07	0.08	0.08	0.08	0.04	0.06						
[15] #RVA/giraffe-wt/_IRL/UCD/2007/G10P[11]	0.09	0.09	0.09	0.09	0.08	0.09	0.08	0.08	0.08	0.08	0.08	0.06	0.09	0.07					
[16] #RVA/Cow-tc/GBR/UK/1973/G6P7[5]	0.13	0.13	0.13	0.13	0.13	0.14	0.13	0.13	0.13	0.13	0.13	0.14	0.14	0.14	0.14				
[17] #RVA/Human-wt/BEL/B10925/1997/G6P[14]	0.09	0.08	0.09	0.08	0.08	0.08	0.08	0.07	0.08	0.08	0.08	0.06	0.01	0.06	0.08	0.15			
[18] #RVA/Pigeon-tc/JPN/PO-13/1983/G2P1B[4]	5.30	5.30	5.30	5.29	5.32	5.33	5.32	5.28	5.32	5.32	5.32	5.27	5.33	5.35	5.29	5.24	5.31		
[19] #RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	0.19	0.18	0.19	0.19	0.19	0.19	0.19	0.18	0.19	0.19	0.19	0.20	0.20	0.20	0.19	0.18	0.20	5.36	

F. Genome segment 6 (VP6)



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
[1] #RVA/Cow-wt/ZAF/1603/2007/G6P[5]																								
[2] #RVA/Cow-wt/ZAF/1604/2007/G8P[1]	0.05																							
[3] #RVA/Cow-wt/ZAF/1605/2007/G6P[5]	0.00	0.05																						
[4] #RVA/Cow-tc/USA/WC3/1981/G6P[5]	0.05	0.04	0.05																					
[5] #RVA/Cow-wt/KOR/KJ9-1/XXXX/G6P[7]	0.05	0.03	0.05	0.02																				
[6] #RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5]	0.05	0.04	0.05	0.00	0.02																			
[7] #RVA/Bovine-tc/JPN/22R/XXXX/GXP[X]	0.04	0.05	0.04	0.05	0.04	0.05																		
[8] #RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]	0.05	0.04	0.05	0.00	0.02	0.00	0.05																	
[9] #RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]	0.05	0.04	0.05	0.00	0.02	0.00	0.05	0.00																
[10] #RVA/Antelope-wt/ZAF/RC-18-08/G6P[14]	0.05	0.01	0.05	0.04	0.03	0.04	0.05	0.04	0.04															
[11] #RVA/Cow-tc/USA/NCDV/1967/G6P6[1]	0.05	0.04	0.05	0.02	0.02	0.02	0.05	0.02	0.02	0.04														
[12] #RVA/Sheep-tc/ESP/OVR762/2002/G8P[14]	0.04	0.05	0.04	0.05	0.04	0.05	0.00	0.05	0.05	0.05	0.05													
[13] #RVA/Labstr/USA/Rotashield-DS1xRRV/XXXX/G2P[3]	0.06	0.05	0.06	0.04	0.03	0.04	0.06	0.04	0.04	0.05	0.03	0.06												
[14] #RVA/Cow-tc/CHN/DQ-75/2008/G10P[11]	0.06	0.05	0.06	0.04	0.03	0.04	0.06	0.04	0.04	0.04	0.03	0.06	0.03											
[15] #RVA/Pigeon-tc/JPN/PO-13/1983/G2P1B[4]	0.00	74.20	0.00	89.14	0.51	89.14	0.00	0.00	0.00	69.67	0.00	0.00	0.00	0.00										
[16] #RVA/Human-wt/COD/DRC88/2003/G8P[8]	0.07	0.07	0.07	0.06	0.05	0.07	0.06	0.06	0.06	0.06	0.07	0.06	0.07	0.07	0.50									
[17] #RVA/Human-tc/USA/DS-1/1976/G2P[4]	0.15	0.15	0.15	0.14	0.15	0.14	0.15	0.14	0.14	0.15	0.15	0.15	0.15	0.15	0.00	0.14								
[18] #RVA/Human-wt/MWI/1473/2001/G8P[4]	0.07	0.06	0.07	0.06	0.05	0.06	0.06	0.06	0.06	0.06	0.07	0.06	0.07	0.07	0.51	0.03	0.15							
[19] #RVA/Human-wt/ZAF/GR10924/1999/G9P[6]	0.06	0.06	0.06	0.06	0.06	0.07	0.06	0.06	0.06	0.06	0.07	0.06	0.07	0.08	0.50	0.02	0.14	0.02						
[20] #RVA/Human-wt/ZAF/3203WC/2009/G2P[4]	0.07	0.07	0.07	0.07	0.07	0.07	0.06	0.07	0.07	0.07	0.07	0.06	0.08	0.08	0.50	0.04	0.14	0.03	0.03					
[21] #RVA/Human-wt/USA/LB2744/2006/G2P[4]	0.07	0.07	0.07	0.07	0.06	0.07	0.06	0.07	0.07	0.06	0.07	0.06	0.08	0.08	0.50	0.03	0.15	0.02	0.03	0.03				
[22] #RVA/Human-wt/BGD/MMC6/2005/G2P[4]	0.07	0.07	0.07	0.06	0.06	0.06	0.06	0.06	0.06	0.07	0.07	0.06	0.08	0.08	65.76	0.03	0.14	0.02	0.03	0.03	0.03			
[23] #RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]	0.16	0.15	0.16	0.15	0.15	0.15	0.16	0.15	0.15	0.16	0.15	0.16	0.15	0.15	0.00	0.15	0.03	0.16	0.15	0.15	0.16	0.15		
[24] #RVA/Human-tc/JPN/S2/1980/G2P[4]	0.16	0.15	0.16	0.15	0.15	0.15	0.16	0.15	0.15	0.16	0.15	0.16	0.15	0.15	0.53	0.15	0.03	0.16	0.15	0.15	0.16	0.16	0.00	

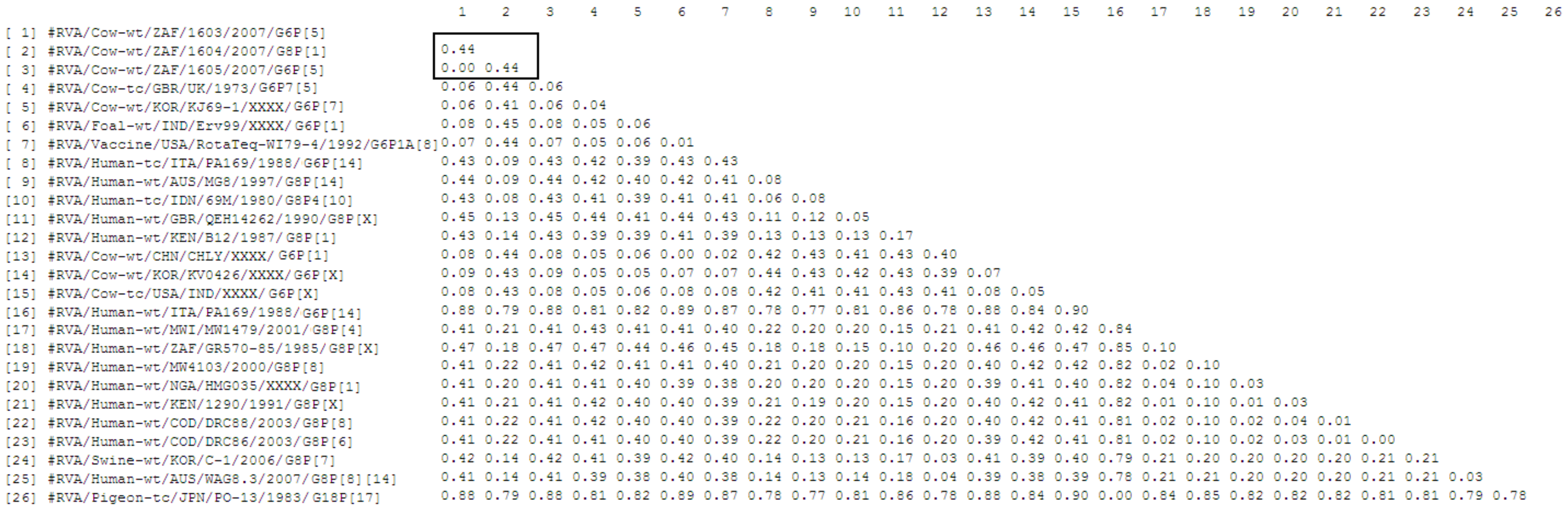
G. Genome segment 7 (NSP3)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
[1] #RVA/Cow-tc/FRA/RF/1982/G6P[5]																						
[2] #RVA/Cow-wt/ARG/B383/1998/G15P[11]	0.13																					
[3] #RVA/Cow-wt/ZAF/1603/2007/G6P[5]	0.06	0.12																				
[4] #RVA/Cow-wt/ZAF/1604/2007/G8P[1]	0.10	0.09	0.10																			
[5] #RVA/Cow-wt/ZAF/1605/2007/G6P[5]	0.06	0.12	0.00	0.10																		
[6] #RVA/giraffe/UCD/IRL/2007/ G10P[11]	0.05	0.13	0.03	0.10	0.04																	
[7] #RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1]	0.11	0.06	0.11	0.10	0.11	0.11																
[8] #RVA/Human-tc/AUS/MG6/1993/G6P[14]	0.03	0.13	0.07	0.10	0.07	0.07	0.11															
[9] #RVA/Human-tc/ITA/PA169/1988/G6P[14]	0.04	0.12	0.06	0.10	0.06	0.05	0.11	0.05														
[10] #RVA/Human-wt/BEL/B10925/1997/ G6P[14]	0.10	0.08	0.09	0.03	0.09	0.10	0.08	0.10	0.09													
[11] #RVA/Human-wt/ITA/111-05-27/2005/ G6P[14]	0.10	0.08	0.09	0.03	0.10	0.10	0.08	0.10	0.09	0.01												
[12] #RVA/Human-wt/ITA/PAH136/1996/ G3P[9]	0.05	0.15	0.07	0.11	0.07	0.06	0.13	0.07	0.06	0.11	0.11											
[13] #RVA/Human-wt/ITA/PAI58/1996/G3P[9]	0.04	0.13	0.07	0.10	0.07	0.06	0.12	0.06	0.04	0.10	0.10	0.02										
[14] #RVA/Human-wt/KEN/B12/1987/ G8P[1]	0.04	0.11	0.07	0.11	0.07	0.06	0.11	0.06	0.05	0.09	0.10	0.07	0.05									
[15] #RVA/Human-wt/MWI/1473/2001/G8P[4]	0.25	0.27	0.26	0.25	0.26	0.25	0.26	0.26	0.25	0.25	0.25	0.27	0.26	0.26								
[16] #RVA/Human-wt/ZAF/3203WC/2009/G2P[4]	0.25	0.27	0.26	0.25	0.27	0.26	0.25	0.26	0.25	0.25	0.24	0.27	0.25	0.26	0.02							
[17] #RVA/Pigeon-tc/JPN/PO-13/1983/G2P1B[4]	0.91	0.92	0.94	0.88	0.95	0.94	0.91	0.93	0.95	0.94	0.93	0.92	0.93	0.93	0.97	0.99						
[18] #RVA/Sheep-wt/CHN/CC0812-1/2008/G10P[15]	0.08	0.13	0.07	0.11	0.07	0.07	0.12	0.09	0.08	0.11	0.11	0.09	0.08	0.07	0.26	0.26	0.94					
[19] #RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5]	0.01	0.13	0.06	0.10	0.06	0.05	0.11	0.03	0.04	0.10	0.10	0.06	0.04	0.05	0.25	0.25	0.93	0.08				
[20] #RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5]	0.01	0.13	0.06	0.10	0.06	0.05	0.11	0.03	0.04	0.10	0.10	0.06	0.04	0.05	0.25	0.25	0.93	0.08	0.00			
[21] #RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5]	0.01	0.13	0.06	0.10	0.06	0.05	0.12	0.03	0.04	0.10	0.10	0.06	0.04	0.05	0.26	0.26	0.94	0.08	0.00	0.00		
[22] #strain_RVA/Cow-tc/USA/WC3/1981/ G6P[5]	0.01	0.13	0.06	0.10	0.06	0.05	0.11	0.03	0.04	0.10	0.10	0.06	0.04	0.05	0.25	0.25	0.93	0.08	0.00	0.00	0.00	

H. Genome segment 8 (NSP2)

	1	2	3	4	5	6	7	8	9	10	11	12	13			16	17	18	19	20	21	22	23
[1] #RVA/Cow-wt/ZAF/1603/2007/G6P[5]																							
[2] #RVA/Cow-wt/ZAF/1604/2007/G8P[1]	0.12																						
[3] #RVA/Cow-wt/ZAF/1605/2007/G6P[5]	0.00	0.12																					
[4] #RVA/Cow-tc/USA/WC3/1981/G6P[5]	0.12	0.08	0.12																				
[5] #RVA/Human-wt/JPN/KF17/2010/G6P[9]	0.13	0.09	0.13	0.07																			
[6] #RVA/Simian-tc/USA/RRV/1975/G4P[3]	0.12	0.08	0.12	0.03	0.07																		
[7] #RVA/Dog-tc/ITA/RV52-96/1996/G3P[3]	0.12	0.08	0.12	0.06	0.03	0.06																	
[8] #RVA/Human-tc/ITA/PA260-97/1997/G3P[3]	0.12	0.08	0.12	0.07	0.03	0.06	0.01																
[9] #RVA/Cow-tc/CHN/DQ-75/2008/G10P[11]	0.13	0.08	0.13	0.03	0.07	0.02	0.06	0.06															
[10] #RVA/Rhesus-tc/USA/PTRV/1990/G8P[1]	0.13	0.07	0.13	0.04	0.08	0.01	0.06	0.07	0.02														
[11] #RVA/Cow-wt/ARG/B383/1998/G15P[11]	0.13	0.06	0.13	0.07	0.09	0.07	0.07	0.07	0.07	0.07													
[12] #RVA/Sheep-tc/CHN/Lamb-NT/XXXX/G10P[15]	0.13	0.14	0.13	0.13	0.14	0.13	0.13	0.14	0.13	0.13	0.13												
[13] #RVA/Goat-tc/BGD/GO34/1999/G6P[1]	0.13	0.15	0.13	0.13	0.13	0.14	0.13	0.13	0.13	0.14	0.14	0.10											
[14] #RVA/Cow-lab/USA/UKg9ST3/1986/G4P[5]	0.02	0.12	0.02	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.13	0.13	0.12										
[15] #RVA/Human-wt/KEN/D205/1989/G2P[4]	0.14	0.15	0.14	0.14	0.13	0.13	0.12	0.13	0.13	0.13	0.14	0.11	0.05	0.13									
[16] #RVA/Pigeon-tc/JPN/PO-13/1983/G2P1B[4]	0.84	0.88	0.84	0.82	0.83	0.82	0.81	0.82	0.86	0.84	0.85	0.82	0.82	0.84	0.80								
[17] #RVA/Human-wt/COD/DRC86/2003/G8P[6]	0.14	0.15	0.14	0.14	0.15	0.14	0.14	0.14	0.14	0.14	0.14	0.11	0.06	0.14	0.04	0.82							
[18] #RVA/Human-tc/IDN/69M/1980/G8P[4]	0.13	0.14	0.13	0.12	0.13	0.12	0.13	0.13	0.12	0.13	0.13	0.14	0.14	0.13	0.15	0.83	0.15						
[19] #RVA/Human-wt/MWI/1473/2001/G8P[4]	0.14	0.15	0.14	0.14	0.14	0.13	0.13	0.13	0.13	0.14	0.14	0.11	0.06	0.14	0.03	0.83	0.03	0.16					
[20] #RVA/Human-wt/ZAF/3203WC/2009/G2P[4]	0.15	0.15	0.15	0.15	0.15	0.14	0.14	0.15	0.14	0.15	0.15	0.11	0.06	0.14	0.03	0.81	0.03	0.16	0.03				
[21] #RVA/Human-wt/ZAF/GR10924/1999/G9P[6]	0.14	0.16	0.14	0.15	0.15	0.14	0.14	0.14	0.14	0.14	0.15	0.11	0.06	0.14	0.03	0.81	0.03	0.16	0.02	0.02			
[22] #RVA/Human-tc/USA/DS-1/1976/G2P[4]	0.15	0.15	0.15	0.14	0.15	0.14	0.14	0.15	0.14	0.13	0.14	0.14	0.14	0.14	0.14	0.85	0.15	0.14	0.15	0.14	0.16		
[23] #RVA/Human-wt/KEN/B12/1987/G8P[1]	0.14	0.14	0.14	0.12	0.13	0.12	0.13	0.13	0.13	0.13	0.13	0.14	0.13	0.13	0.14	0.84	0.15	0.05	0.15	0.15	0.15	0.14	

I. Genome segment 9 (VP7)



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                                                   1    2    3    4    5    6    7    8    9   10   11   12   13   14   15   16   17   18   19   20   21   22   23   24   25   26
[ 1] #RVA/Cow-wt/ZAF/1603/2007/G6P[5]
[ 2] #RVA/Cow-wt/ZAF/1604/2007/G8P[1]               0.44
[ 3] #RVA/Cow-wt/ZAF/1605/2007/G6P[5]               0.00 0.44
[ 4] #RVA/Cow-tc/GBR/UK/1973/G6P7[5]                0.06 0.44 0.06
[ 5] #RVA/Cow-wt/KOR/KJ69-1/XXXX/ G6P[7]            0.06 0.41 0.06 0.04
[ 6] #RVA/Foal-wt/IND/Erv99/XXXX/ G6P[1]            0.08 0.45 0.08 0.05 0.06
[ 7] #RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]0.07 0.44 0.07 0.05 0.06 0.01
[ 8] #RVA/Human-tc/ITA/PA169/1988/ G6P[14]          0.43 0.09 0.43 0.42 0.39 0.43 0.43
[ 9] #RVA/Human-wt/AUS/MG8/1997/G8P[14]             0.44 0.09 0.44 0.42 0.40 0.42 0.41 0.08
[10] #RVA/Human-tc/IDN/69M/1980/G8P4[10]            0.43 0.08 0.43 0.41 0.39 0.41 0.41 0.06 0.08
[11] #RVA/Human-wt/GBR/QEH14262/1990/G8P[X]         0.45 0.13 0.45 0.44 0.41 0.44 0.43 0.11 0.12 0.05
[12] #RVA/Human-wt/KEN/B12/1987/ G8P[1]             0.43 0.14 0.43 0.39 0.39 0.41 0.39 0.13 0.13 0.13 0.17
[13] #RVA/Cow-wt/CHN/CHLY/XXXX/ G6P[1]              0.08 0.44 0.08 0.05 0.06 0.00 0.02 0.42 0.43 0.41 0.43 0.40
[14] #RVA/Cow-wt/KOR/KV0426/XXXX/ G6P[X]            0.09 0.43 0.09 0.05 0.05 0.07 0.07 0.44 0.43 0.42 0.43 0.39 0.07
[15] #RVA/Cow-tc/USA/IND/XXXX/ G6P[X]               0.08 0.43 0.08 0.05 0.06 0.08 0.08 0.42 0.41 0.41 0.43 0.41 0.08 0.05
[16] #RVA/Human-wt/ITA/PA169/1988/ G6P[14]          0.88 0.79 0.88 0.81 0.82 0.89 0.87 0.78 0.77 0.81 0.86 0.78 0.88 0.84 0.90
[17] #RVA/Human-wt/MWI/MW1479/2001/ G8P[4]          0.41 0.21 0.41 0.43 0.41 0.41 0.40 0.22 0.20 0.20 0.15 0.21 0.41 0.42 0.42 0.84
[18] #RVA/Human-wt/ZAF/GR570-85/1985/G8P[X]         0.47 0.18 0.47 0.47 0.44 0.46 0.45 0.18 0.18 0.15 0.10 0.20 0.46 0.46 0.47 0.85 0.10
[19] #RVA/Human-wt/MW4103/2000/G8P[8]               0.41 0.22 0.41 0.42 0.41 0.41 0.40 0.21 0.20 0.20 0.15 0.20 0.40 0.42 0.42 0.82 0.02 0.10
[20] #RVA/Human-wt/NGA/HMG035/XXXX/G8P[1]           0.41 0.20 0.41 0.41 0.40 0.39 0.38 0.20 0.20 0.20 0.15 0.20 0.39 0.41 0.40 0.82 0.04 0.10 0.03
[21] #RVA/Human-wt/KEN/1290/1991/G8P[X]             0.41 0.21 0.41 0.42 0.40 0.40 0.39 0.21 0.19 0.20 0.15 0.20 0.40 0.42 0.41 0.82 0.01 0.10 0.01 0.03
[22] #RVA/Human-wt/COD/DRC88/2003/G8P[8]            0.41 0.22 0.41 0.42 0.40 0.40 0.39 0.22 0.20 0.21 0.16 0.20 0.40 0.42 0.41 0.81 0.02 0.10 0.02 0.04 0.01
[23] #RVA/Human-wt/COD/DRC86/2003/G8P[6]            0.41 0.22 0.41 0.41 0.40 0.40 0.39 0.22 0.20 0.21 0.16 0.20 0.39 0.42 0.41 0.81 0.02 0.10 0.02 0.03 0.01 0.00
[24] #RVA/Swine-wt/KOR/C-1/2006/G8P[7]              0.42 0.14 0.42 0.41 0.39 0.42 0.40 0.14 0.13 0.13 0.17 0.03 0.41 0.39 0.40 0.79 0.21 0.20 0.20 0.20 0.20 0.21 0.21
[25] #RVA/Human-wt/AUS/WAG8.3/2007/G8P[8][14]       0.41 0.14 0.41 0.39 0.38 0.40 0.38 0.14 0.13 0.14 0.18 0.04 0.39 0.38 0.39 0.78 0.21 0.21 0.20 0.20 0.20 0.21 0.21 0.03
[26] #RVA/Pigeon-tc/JPN/PO-13/1983/ G18P[17]        0.88 0.79 0.88 0.81 0.82 0.89 0.87 0.78 0.77 0.81 0.86 0.78 0.88 0.84 0.90 0.00 0.84 0.85 0.82 0.82 0.82 0.81 0.81 0.79 0.78
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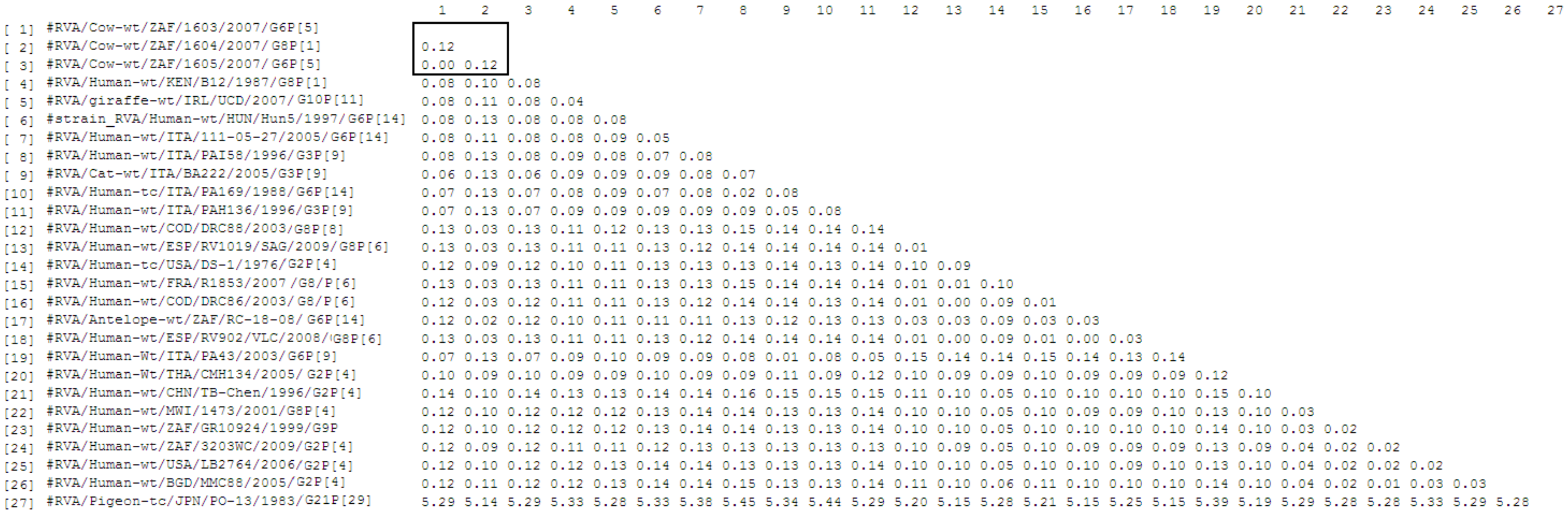
J. Genome segment 10 (NSP4)



		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
[1]	#RVA/Cow-wt/ZAF/1603/2007/G6P[5]																											
[2]	#RVA/Cow-wt/ZAF/1604/2007/G8P[1]	0.12																										
[3]	#RVA/Cow-wt/ZAF/1605/2007/G6P[5]	0.00	0.12																									
[4]	#RVA/Human-wt/KEN/B12/1987/G8P[1]	0.08	0.10	0.08																								
[5]	#RVA/giraffe-wt/IRL/UCD/2007/G10P[11]	0.08	0.11	0.08	0.04																							
[6]	#strain_RVA/Human-wt/HUN/Hun5/1997/G6P[14]	0.08	0.13	0.08	0.08	0.08																						
[7]	#RVA/Human-wt/ITA/111-05-27/2005/G6P[14]	0.08	0.11	0.08	0.08	0.09	0.05																					
[8]	#RVA/Human-wt/ITA/PAI58/1996/G3P[9]	0.08	0.13	0.08	0.09	0.08	0.07	0.08																				
[9]	#RVA/Cat-wt/ITA/BA222/2005/G3P[9]	0.06	0.13	0.06	0.09	0.09	0.09	0.08	0.07																			
[10]	#RVA/Human-tc/ITA/PA169/1988/G6P[14]	0.07	0.13	0.07	0.08	0.09	0.07	0.08	0.02	0.08																		
[11]	#RVA/Human-wt/ITA/PAH136/1996/G3P[9]	0.07	0.13	0.07	0.09	0.09	0.09	0.09	0.09	0.05	0.08																	
[12]	#RVA/Human-wt/COD/DRC88/2003/G8P[8]	0.13	0.03	0.13	0.11	0.12	0.13	0.13	0.15	0.14	0.14	0.14																
[13]	#RVA/Human-wt/ESP/RV1019/SAG/2009/G8P[6]	0.13	0.03	0.13	0.11	0.11	0.13	0.12	0.14	0.14	0.14	0.14	0.01															
[14]	#RVA/Human-tc/USA/DS-1/1976/G2P[4]	0.12	0.09	0.12	0.10	0.11	0.13	0.13	0.13	0.14	0.13	0.14	0.10	0.09														
[15]	#RVA/Human-wt/FRA/R1853/2007 /G8/P[6]	0.13	0.03	0.13	0.11	0.11	0.13	0.13	0.15	0.14	0.14	0.14	0.01	0.01	0.10													
[16]	#RVA/Human-wt/COD/DRC86/2003/G8/P[6]	0.12	0.03	0.12	0.11	0.11	0.13	0.12	0.14	0.14	0.13	0.14	0.01	0.00	0.09	0.01												
[17]	#RVA/Antelope-wt/ZAF/RC-18-08/ G6P[14]	0.12	0.02	0.12	0.10	0.11	0.11	0.11	0.13	0.12	0.13	0.13	0.03	0.03	0.09	0.03	0.03											
[18]	#RVA/Human-wt/ESP/RV902/VLC/2008/G8P[6]	0.13	0.03	0.13	0.11	0.11	0.13	0.12	0.14	0.14	0.14	0.14	0.01	0.00	0.09	0.01	0.00	0.03										
[19]	#RVA/Human-Wt/ITA/PA43/2003/G6P[9]	0.07	0.13	0.07	0.09	0.10	0.09	0.09	0.08	0.01	0.08	0.05	0.15	0.14	0.14	0.15	0.14	0.13	0.14									
[20]	#RVA/Human-Wt/THA/CMH134/2005/ G2P[4]	0.10	0.09	0.10	0.09	0.09	0.10	0.09	0.09	0.11	0.09	0.12	0.10	0.09	0.09	0.10	0.09	0.09	0.09	0.12								
[21]	#RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]	0.14	0.10	0.14	0.13	0.13	0.14	0.14	0.16	0.15	0.15	0.15	0.11	0.10	0.05	0.10	0.10	0.10	0.10	0.15	0.10							
[22]	#RVA/Human-wt/MWI/1473/2001/G8P[4]	0.12	0.10	0.12	0.12	0.12	0.13	0.14	0.14	0.13	0.13	0.14	0.10	0.10	0.05	0.10	0.09	0.09	0.10	0.13	0.10	0.03						
[23]	#RVA/Human-wt/ZAF/GR10924/1999/G9P	0.12	0.10	0.12	0.12	0.12	0.13	0.14	0.14	0.13	0.13	0.14	0.10	0.10	0.05	0.10	0.10	0.10	0.10	0.14	0.10	0.03	0.02					
[24]	#RVA/Human-wt/ZAF/3203WC/2009/G2P[4]	0.12	0.09	0.12	0.11	0.11	0.12	0.13	0.13	0.13	0.13	0.13	0.10	0.09	0.05	0.10	0.09	0.09	0.09	0.13	0.09	0.04	0.02	0.02				
[25]	#RVA/Human-wt/USA/LB2764/2006/G2P[4]	0.12	0.10	0.12	0.12	0.13	0.14	0.14	0.13	0.13	0.13	0.14	0.10	0.10	0.05	0.10	0.10	0.09	0.10	0.13	0.10	0.04	0.02	0.02	0.02			
[26]	#RVA/Human-wt/BGD/MMC88/2005/G2P[4]	0.12	0.11	0.12	0.12	0.13	0.14	0.14	0.15	0.13	0.13	0.14	0.11	0.10	0.06	0.11	0.10	0.10	0.10	0.14	0.10	0.04	0.02	0.01	0.03	0.03		
[27]	#RVA/Pigeon-tc/JPN/PO-13/1983/G21P[29]	5.29	5.14	5.29	5.33	5.28	5.33	5.38	5.45	5.34	5.44	5.29	5.20	5.15	5.28	5.21	5.15	5.25	5.15	5.39	5.19	5.29	5.28	5.28	5.33	5.29	5.28	

K. Genome segment 11 (NSP5)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
[1] #RVA/Cow-wt/ZAF/1603/2007/ G6P[5]																											
[2] #RVA/Cow-wt/ZAF/1604/2007/ G8P[1]	0.01																										
[3] #RVA/Cow-wt/ZAF/1605/2007/ G6P[5]	0.00	0.01																									
[4] #RVA/Cat-wt/ITA/BA222/2005/G3P[9]	0.04	0.04	0.04																								
[5] #RVA/Human-wt/BEL/B10925/1997/G6P[14]	0.05	0.05	0.05	0.05																							
[6] #RVA/Goat-tc/BGD/GO34/1999/ G8P[1]	0.05	0.05	0.05	0.06	0.06																						
[7] #RVA/Cow-wt/KOR/KJ19-2/XXXX/ G6P[7]	0.05	0.05	0.05	0.05	0.02	0.06																					
[8] #RVA/Cow-tc/USA/WC3/1981/ G6P[5]	0.05	0.05	0.05	0.04	0.02	0.06	0.02																				
[9] #RVA/giraffe-wt/IRL/UCD/2007/G10P[11]	0.01	0.01	0.01	0.03	0.05	0.05	0.05	0.05																			
[10] #RVA/Human-wt/ITA/PAH136/1996/ G3P[9]	0.03	0.04	0.03	0.03	0.05	0.07	0.06	0.05	0.03																		
[11] #RVA/Human-wt/JPN/KF17/2010/G6P[9]	0.04	0.04	0.04	0.00	0.05	0.06	0.05	0.04	0.03	0.02																	
[12] #RVA/Cow-tc/CHN/DQ-75/2008/ G10P[11]	0.05	0.05	0.05	0.07	0.06	0.05	0.06	0.06	0.05	0.07	0.06																
[13] #RVA/Cow-wt/ARG/B383/1998/ G15P[11]	0.05	0.05	0.05	0.04	0.03	0.06	0.03	0.03	0.05	0.05	0.04	0.06															
[14] #RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1]	0.08	0.08	0.08	0.08	0.08	0.08	0.07	0.08	0.07	0.08	0.08	0.08	0.08														
[15] #RVA/Guanaco-wt/ARG/Chubut/1999/ G8P[14]	0.05	0.05	0.05	0.06	0.04	0.05	0.05	0.05	0.05	0.06	0.06	0.05	0.05	0.07													
[16] #RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8]	0.05	0.06	0.05	0.05	0.02	0.06	0.02	0.00	0.05	0.05	0.04	0.07	0.03	0.08	0.05												
[17] #RVA/Sheep-tc/ESP/OVR762/2002/G8P[14]	0.06	0.06	0.06	0.06	0.03	0.07	0.03	0.03	0.05	0.05	0.05	0.06	0.03	0.08	0.05	0.03											
[18] #RVA/Sheep-wt/CHN/CC0812-1/2008/G10P[15]	0.06	0.06	0.06	0.07	0.06	0.05	0.07	0.07	0.06	0.07	0.07	0.02	0.06	0.08	0.05	0.07	0.06										
[19] #RVA/Rhesus-tc/USA/PTRV/1990/ G8P[1]	0.05	0.05	0.05	0.05	0.02	0.07	0.02	0.02	0.05	0.05	0.05	0.06	0.03	0.08	0.05	0.02	0.03	0.07									
[20] #RVA/Human-tc/USA/Se584/1998/ G6P[9]	0.05	0.05	0.05	0.05	0.02	0.07	0.02	0.02	0.05	0.05	0.05	0.06	0.04	0.08	0.05	0.02	0.04	0.07	0.02								
[21] #RVA/Dog-tc/ITA/RV198-95/1995/G3P[3]	0.12	0.12	0.12	0.12	0.13	0.15	0.12	0.12	0.12	0.13	0.12	0.15	0.12	0.13	0.13	0.13	0.13	0.15	0.13	0.12							
[22] #RVA/Human-wt/THA/CMH079/2005/ G3P[10]	0.11	0.11	0.11	0.10	0.09	0.11	0.09	0.09	0.10	0.11	0.10	0.11	0.09	0.10	0.10	0.09	0.10	0.11	0.10	0.09	0.07						
[23] #RVA/Cow-tc/USA/NCDV/1967/ G6P6[1]	0.05	0.06	0.05	0.05	0.02	0.06	0.02	0.01	0.06	0.06	0.05	0.07	0.03	0.08	0.05	0.01	0.03	0.07	0.02	0.02	0.13	0.09					
[24] #RVA/Pigeon-tc/JPN/PO-13/1983/G21P[29]	0.59	0.60	0.59	0.60	0.58	0.59	0.56	0.58	0.59	0.60	0.60	0.61	0.59	0.61	0.60	0.58	0.58	0.60	0.59	0.59	0.63	0.65	0.58				
[25] #RVA/Human-tc/JPN/AU-1/1982/ G3P3[9]	0.06	0.06	0.06	0.06	0.05	0.05	0.06	0.06	0.06	0.07	0.06	0.05	0.06	0.08	0.06	0.06	0.06	0.05	0.06	0.06	0.14	0.11	0.06	0.60			
[26] #RVA/Sheep-tc/CHN/Lamb-NT/XXXX/ G10P[15]	0.06	0.06	0.06	0.07	0.06	0.05	0.07	0.07	0.06	0.07	0.07	0.02	0.06	0.08	0.05	0.07	0.06	0.00	0.07	0.07	0.15	0.11	0.07	0.60	0.05		
[27] #RVA/Human-wt/KEN/B12/1987/ G8P[1]	0.07	0.07	0.07	0.06	0.03	0.07	0.03	0.03	0.07	0.07	0.06	0.07	0.04	0.08	0.05	0.03	0.03	0.07	0.03	0.04	0.13	0.09	0.03	0.58	0.06	0.07	

Supplement 6. Estimates of the evolutionary divergence between the nucleotide sequences of 11 genome segments (1–11) of the study bovine rotaviruses compared to some closely related sequences acquired from the GenBank. The accession numbers of all the nucleotide sequences of the strains used for comparison are listed in Supplement 2. The number of base substitutions per site from analysis between sequences is shown as a variance estimated by a bootstrap approach. All results are based on the pairwise analysis of the number of sequences compared for each genome segment. Analyses were conducted using the Maximum Composite Likelihood method in MEGA4 (Tamura et al., 2007). Codon positions included were 1st+2nd+3rd+non-coding. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). The variances between the three study samples are boxed. The complete nomenclature for each strain is listed in Supplement 2.