Table

Table S1, related to Figure 2. Summary of viruses identified in rhesus macaques at the NEPRC.

Virus family	Virus name[1]	Name of most closely related virus[2]	Percent identity nt or aa[3] (length, nt or aa)	Animal(s) in which viruses were detected[4]			
				24 weeks		64 weeks	
				SIV -	SIV +	SIV -	SIV +
Adenoviridae	WUHARV Adenovirus 1	Simian adenovirus 1 ATCC VR-195	79-99% nt	-	40[5]*	-	23
	WUHARV Adenovirus 2	Human adenovirus G	36-100% nt	-	44*	-	-
	WUHARV Adenovirus 3	Human adenovirus G	36-100% nt	-	44*	-	-
	WUHARV Adenovirus 4	Human adenovirus G	87-93% nt	-	30	-	-
	WUHARV Adenovirus 5	Human adenovirus G	48-100% nt	-	-	-	27
Caliciviridae	WUHARV Calicivirus 1	Tulane virus	75% nt (4839/6489)	-	25, 26, 31, 33, 34*, 35*, 37, 38, 39*, 40*, 41, 44*	-	23, 25
	WUHARV Calicivirus 2	Tulane virus	88-93% nt (4463/5082, 753/812)	-	37	-	30, 37, 41
	WUHARV Calicivirus 3	Rhesus macaque recovirus strain FT437	0-81% nt (50/64, 288/413, 216/268)	-	23, 28*, 32, 39*	-	-
Papillomaviridae	WUHARV Papillomavirus 1	Human papillomavirus	69% nt (300/432)	15	25	-	32
Parvoviridae	WUHARV Bocavirus 1	Human bocavirus isolate KU3	73% nt (118/160)	-	-	-	29
	WUHARV Dependovirus 1	Adeno-associated virus 11	93% nt (3812/4090)	-	40*	-	29
	WUHARV Dependovirus 2	Adeno-associated virus 10	92% nt (3680/4020)	-	23, 30, 31, 32, 34*, 38, 39*, 40*, 44*	-	27, 29
	WUHARV Dependovirus 3	Adeno-associated virus isolate rh.31	94% nt (1680/1793)	-	40*	-	-
	WUHARV Dependovirus 4	Adeno-associated virus isolate rh.8R	86% nt (988/1145)	-	37, 40*	-	-
	WUHARV Dependovirus 5	Adeno-associated virus 7	86% nt (264/307)	-	26	-	-
	WUHARV Parvovirus 1	Bufavirus 2	77% nt (1626/2111)	7	24*, 31, 33, 38, 39*	-	25, 37
	WUHARV Parvovirus 2	Bufavirus 2	75-79% nt (522/698, 139/175)	-	35*	-	27

Picobirnaviridae	WUHARV Picobirnavirus 1	Human picobirnavirus	26% aa (147/574)	-	26, 36*	-	-
	WUHARV Picobirnavirus 2	Otarine picobirnavirus	29% aa (119/415)	14, 17	-	-	-
	WUHARV Picobirnavirus 3	Human picobirnavirus	29% aa (102/354)	8, 15	-	-	-
	WUHARV Picobirnavirus 4	Human picobirnavirus	36% aa (94/260)	-	27	-	-
	WUHARV Picobirnavirus 5	Human picobirnavirus	34% aa (63/187)	22	37	-	-
	WUHARV Picobirnavirus 6	Human picobirnavirus	37% aa (55/149)	-	36*	-	-
	WUHARV Picobirnavirus 7	Human picobirnavirus	33% aa (101/302)	-	27	-	-
Picornaviridae	WUHARV Enterovirus 1	Human enterovirus 92 strain RJG7	86% nt (6228/7268)	-	41, 44*	-	-
	WUHARV Enterovirus 2	Simian enterovirus SV19 strain M19s	83% nt (5879/7100)	-	23, 25, 26, 27, 29, 31, 35*, 38, 39*	-	25, 29, 30, 32, 33, 38, 41
	WUHARV Enterovirus 3	Simian enterovirus SV19 strain M19s	84% nt (5854/6961)	-	-	-	25, 26, 27, 29, 30, 33, 37, 41
	WUHARV Picornavirus 1	Simian picornavirus 6	85% nt (284/335)	-	26	-	-
	WUHARV Sapelovirus 1	Simian sapelovirus 1	81% nt (6558/8087)	19	25, 26, 29, 30, 31, 32, 34*, 35*, 38, 39*, 42*, 43*	1, 11, 17, 19, 22	23, 25, 26, 30, 31, 32, 33, 37, 38
	WUHARV Sapelovirus 2	Simian sapelovirus 1	81% nt (6510/8076)	-	25, 28*, 35*, 37, 41	-	29, 41
	WUHARV Sapelovirus 3	Simian sapelovirus 1	79% nt (5476/6919)	-	23, 37, 40*	-	27
Polyomaviridae	WUHARV Polyomavirus 1	Polyomavirus HPyV6 isolate 601a	76% nt (242/318)	-	-	-	29

[1] Viruses with 98% nt identity over the full length of aligned regions are the "same" virus.

[2] Most closely related viruses were identified as the top hit using a NCBI web-based BLAST search against the NCBI nr database on 8/31/2012.

[3] Percent aa identity is reported for viruses for which no known virus had nt identity.

[4] As determined by 454 sequencing.

[5] Underlined numbers indicate animals from which virus contigs were assembled.

* Euthanized for progressive AIDS 24 to 64 weeks after SIV infection.

Table S2, related to Figure 3. Primers used for PCR screen.

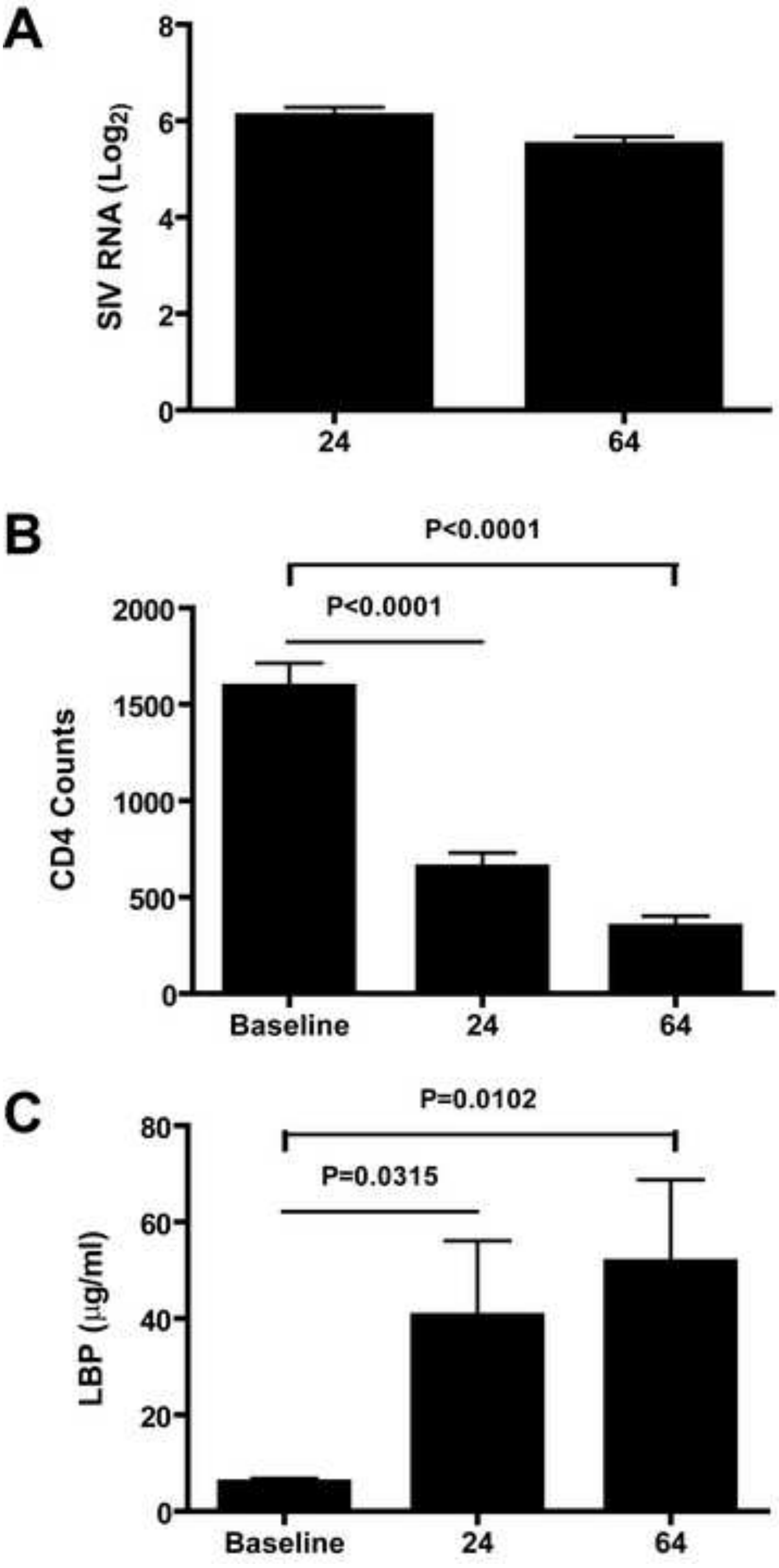
WUHARV Virus	Primer name	Targeted region	Sequence (5’-3’)	Orientation
Adenovirus 1	4302c3f	Hexon	GGCAATCATGATGGACACCTT	F
Adenovirus 1	4302c3r	Hexon	TTAATCACCACCGCAACGC	R
Adenovirus 1	4302c1f	Hexon	CAATGGAACATTAATCCCACG	F
Adenovirus 1	4302c1r	Hexon	CCTGCCAACACTCCCATATTT	R
Adenovirus 1	4302c18f	E1B	AGAGCTATCACACAGCGTTCA	F
Adenovirus 1	4302c18r	E1B	ACCGAGTGGTGGAGGAGAA	R
Adenovirus 2	4310ac18f	pIIIa	TAACGTTCAGACCAATCTGGA	F
Adenovirus 2	4310ac18r	pIIIa	CGGCAATAGTGCTACTGTTGG	R
Adenovirus 2	4310ac16f	Hexon	CGGGACAACTTCATTGGACT	F
Adenovirus 2	4310ac16r	Hexon	GCGCCAATGTTTACAAAGGT	R
Adenovirus 3	4310bc18f	pIIIa	TAACGTTCAGACCAATCTGGA	F
Adenovirus 3	4310bc18r	pIIIa	CGGCAATAGTGCTACTGTTGG	R
Adenovirus 3	4310bc21f	Hexon	ACGACAGCACCAGTTCAAAAC	F
Adenovirus 3	4310bc21r	Hexon	TTTTCTGGCAGCGTGATGTT	R
Adenovirus 3	4310bc28r	E3	CTCTTGGCAACCCCTTATTG	F
Adenovirus 3	4310bc28f	E3	TGGGTGAAACCATTCCTGTT	R
Adenovirus 4	4312u11r	E3	CCGTCCTCTCCTGGTAGAAA	F
Adenovirus 4	4312u11f	E3	CGTCGACTGTTGGAGAAACA	R
Adenovirus 4	4312u10r	DBP	GCCGTTACATCCAGATCCTC	F
Adenovirus 4	4312u10f	DBP	TACACCGAGGGAATGAAAGC	R
Adenovirus 4	4312u7r	NCR[1] between E1a and E1b	CTTGTGCCTGTGCTTTTCAT	F
Adenovirus 4	4312u7f	NCR between E1a and E1b	GTGCAAAGAGAACTAGTATGG	R
Adenovirus 5	4287u7f	Iva	GGATGTTCAAGTACATGGGCA	F
Adenovirus 5	4287u7r	Iva	GATGCATGACAAGTTCCCCAA	R
Adenovirus 5	4287c5f	E3	GAATGGTAGCTGCTTTCTTCA	F
Adenovirus 5	4287c5r	E3	TGTTGGGTGATTGTGATGGA	R
Adenovirus 5	4287c11f	Fiber-1	CTGAAAAAAACGAATTGGTGG	F
Adenovirus 5	4287c11r	Fiber-1	TTGACAACAATGGTGCGTTG	R
Adenovirus (1-5)	AdV-a	pIIIa	ACTAACGTKCAGACCAATCTGG	F
Adenovirus (1-5)	AdV-b	pIIIa	GTACAGRCTCACGGACTGC	R
Calicivirus (1-2)	CV-a	NS[2] polyprotein	GTACGAYGTCGGAGGGACC	F
Calicivirus (1-2)	CV-b	NS polyprotein	GRTCACAAGCCATGACACTCAG	R
Calicivirus 3	CV-c	NS polyprotein	TTATGTTATGGACAACCCAAAGG	F
Calicivirus 3	CV-d	NS polyprotein	GGTCAAGAGACAATAGCTCCAT	R
Parvovirus (1-3)	PV-a	capsid	ACCAGACTAACWCAAGGCGC	F
Parvovirus (1-3)	PV-b	capsid	GGTASGTGTTCCATTGTCTTGG	R
Enterovirus (1-3)	EV-a	5’ UTR[3]	GCACAACCCCAGTGTAGTTC	F
Enterovirus (1-3)	EV-b	5’ UTR	CCAATCCAATMGCTATATGATGAC	R
Sapelovirus (1-3)	SV-a	5’ UTR	CCAGKMTAAAAGGCAATTGTGG	F
Sapelovirus (1-3)	SV-b	5’ UTR	CCTGTCAGGTAGCACTAGACT	R

[1] NCR = non-coding region

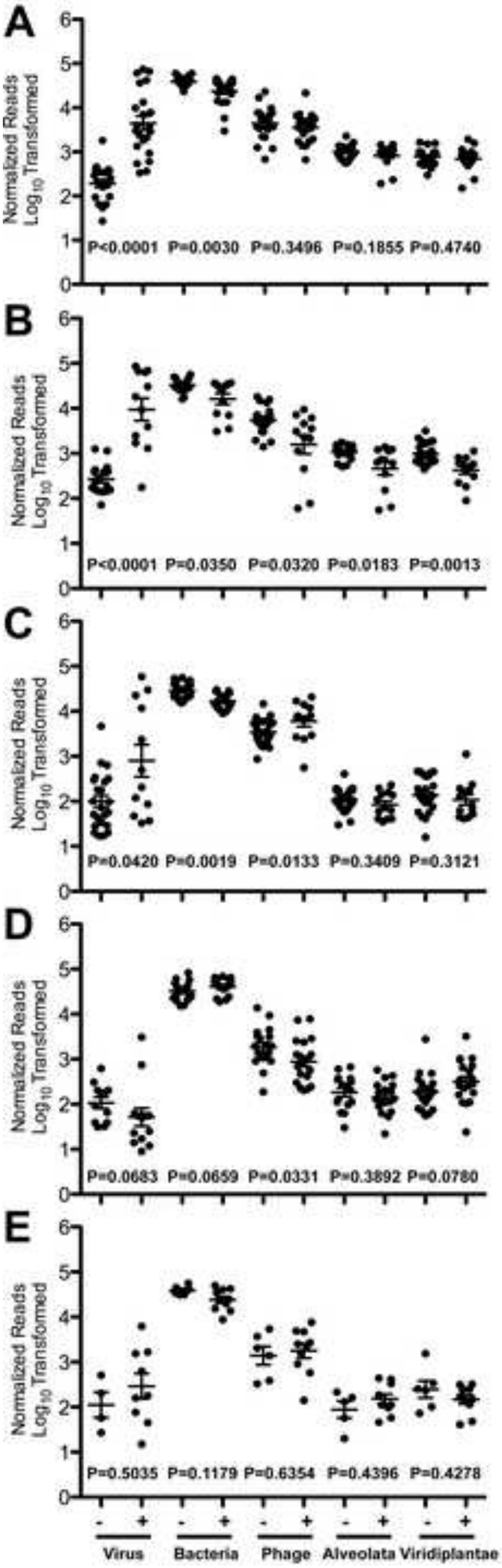
[2] NS = non-structural

[3] UTR = untranslated region

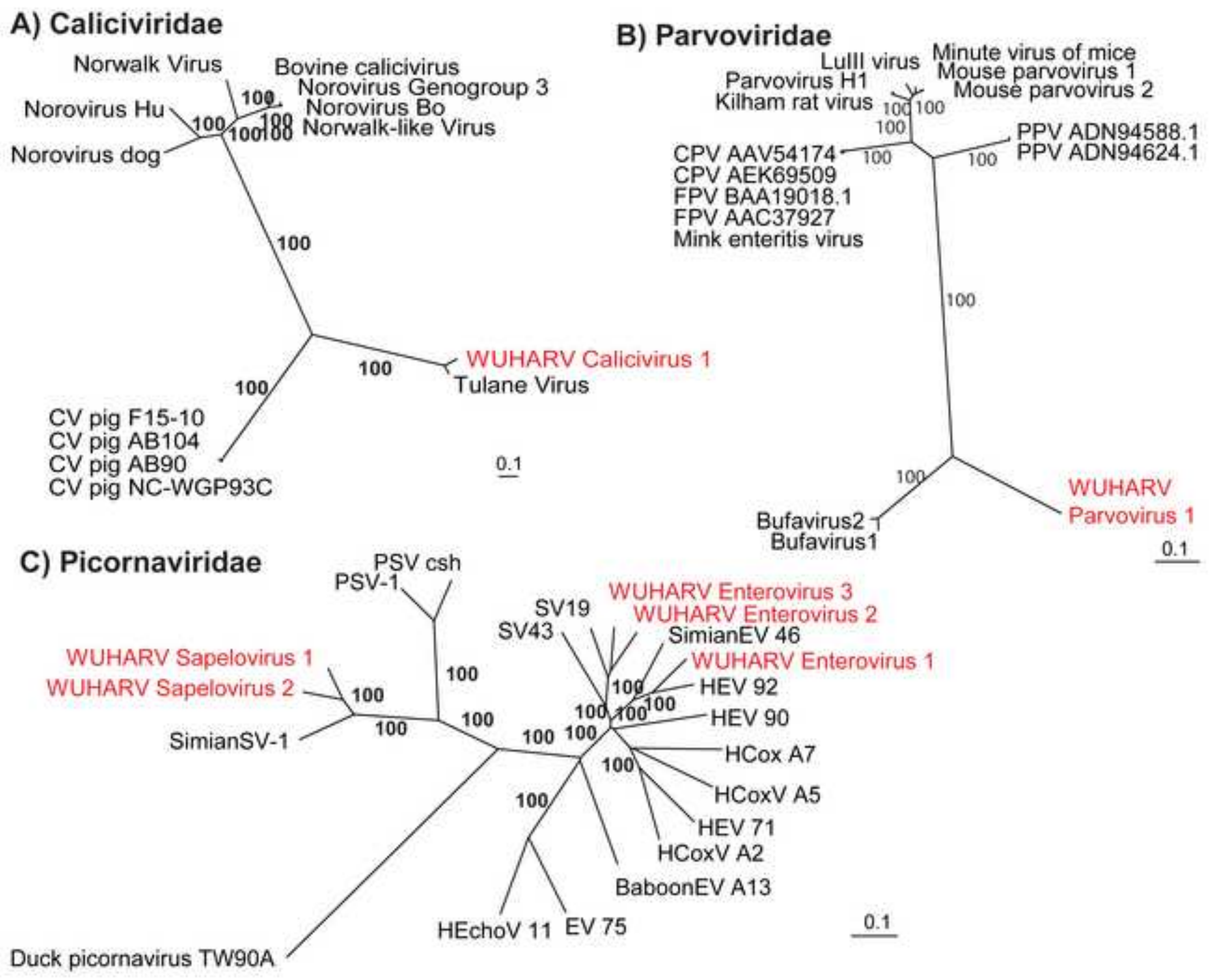
Supplemental Figure



Supplemental Figure



Supplemental Figure



Supplemental Figure