

Table S1. Primers used to obtain the complete/nearly complete DNA-dependent DNA polymerase and hexon coding sequences, and partial penton base coding sequences of simian adenovirus (SAdV) strains KNA-S6 and KNA-08975 detected in African green monkeys from St. Kitts. Primers employed in semi-nested PCR assays to amplify a region of the putative hexon that is genetically divergent between SAdV-17, -18 and *Human mastadenovirus-F* strains (HAdV-F) are highlighted with yellow. Forward primers (used in combination with 2 reverse primers designed from partial penton base sequences of KNA-S6 and KNA-08975) that failed to amplify the 5'- region of the penton base are shown with red font.

Target gene	Primer name	Primer sequence ¹ (5'-3')	Primer position ²
DNA-dependent DNA polymerase	NHP-pol-5ENDF	TCTACGGCATCTCGATCCAGCAG	nt 5228-nt 5250
	NHP-pol-5ENDR	AAGCTCTACGCCCTCAAGTGCCTC	nt 5591-nt 5569
	NHP-pol-5261F	TGCGGGGGTTGGGRCGGCTTT	nt 5261-nt 5281
	NHP-pol-5283F	GCTGTASGGBACCAGBCGGTG	nt 5283-nt 5303
	NHP-pol-5946R	GGTGGATCCCCCTGGTGGAGAACG	nt 5946-nt 5924
	NHP-pol-5800F	GATTTGAGCGCGCGCTGCTCCAG	nt 5800-nt 5822
	NHP-pol-6954R	CTCCAACTCSCACGCCATCTT	nt 6954-nt 6934
	NHP-pol-6976R	TCTTYCAGCGSCCCACCATCTC	nt 6976-nt 6955
	NHP-pol-6721F	CCCCAGGGCATGGRTGGGT	nt 6721-nt 6740
	NHP-pol-6742F	AGGGCCGAGGCGTACATGCC	nt 6742-nt 6761
	NHP-pol-7983R	CACCTACGACGTGARGACCTACAC	nt 7983-nt 7960
	NHP-pol-7751F	TCTGGAGGCGGTGCGGTAGT	nt 7751-nt 7771
	NHP-pol-7774F	CGGAACTTTTTGCCACCGCCA	nt 7774-nt 7795
	NHP-pol-8817R	CTGTGAACTCTCTTTCAGGTTC	nt 8817-nt 8795
	NHP-pol-8752R	CAGGACCTCAACCGCCGCGT	nt 8752-nt 8733
Hexon	NHP-hex-18098F	AACAGCATYGTGGGYCTGGG	nt 18098-nt 18117
	NHP-hex-18582R	CGGTCCAGCACGCCGCGGATGTC	nt 18582-nt 18560
	NHP-hex-18625R	GGAGTTGTAAGCGGTGCCGGAGTA	nt 18625-nt 18602
	NHP-hex-18253F	CAAGATGGCCACCCCCTCSATGATGC	nt 18253-nt 18278
	NHP-hex-18308F	CAGGACGCCTCGAGTACCTGAGC	nt 18308-nt 18331
	NHP-hex-18837R ³	TCTCCGGCTTCGCTGTCCACTG ³	nt 18837-nt 18815
	NHP-hex-18836R ⁴	GCGTGGGATCAATATTCCATTGCG ⁴	nt 18836-nt 18813
	NHP-hex-18494F	TACAAAGTGCCTTCACGCTGG	nt 18494-nt 18515
	NHP-hex-18524F	GACAACCGCGTGCTGGACATG	nt 18524-nt 18544
	NHP-hex-19337R	GGTCATAGCTGTCYACGGCCTG	nt 19337-nt 19316
	NHP-hex-19100F ³	CAGCAGCGCGCTCCCAACAGAC ³	nt 19100-nt 19117
	NHP-hex-19177F ³	TGGAATATGGGAGTTCTTGCGGG ³	nt 19177-nt 19200
	NHP-hex-19174F ⁴	CACCTGGTAATATGGGGTCTTGCG ⁴	nt 19174-nt 19197
	NHP-hex-19192F ⁴	CTTGGCAGGTCAGGCTTCGCAAC ⁴	nt 19192-nt 19213
	NHP-hex-20006R	AGTTGGCGTAVAGGTTRATGCTGTC	nt 20006-nt 19982
	NHP-hex-19883F	TCCTACACCTACGAGTGAACCTT	nt 19883-nt 19905
	NHP-hex-20887R	CTCATCCATGGGGTCCACCTC	nt 20887-nt 20867
	NHP-hex-20946R	TGCGGCTGGTGGATGCGCAC	nt 20946-nt 20927
	NHP-hex-20783F	AACCTCATGTCCATGGGGGC	nt 20783-nt 20802
	NHP-hex-21114R	AAGCGYTTGTCRAASGTGCCCA	nt 21114-nt 21093
	NHP-hex-21162R	GTGTTACRATGGCGCASGCCA	nt 21162-nt 21141
Penton base	NHP-pen-13461	TGGARAGCCTRGTRGAYAAGATGAA	nt 13461- nt 13485
	NHP-pen-13496	ACSTACGCSCAGGAGCAGCGGG	nt 13496- nt 13517
	NHP-pen-13610	AGCGTGTGGACTTGGGGGG	nt 13610-nt 13629
	NHP-pen-13658	GCYCACTGCGSCCKCAGGG	nt 13658-nt 13677
	NHP-pen-14407F	GAAGTTYGACACGCGCAACTCCG	nt 14407-nt 14430
	NHP-pen-14462F	ATGCCSGCGGTGTACACCAACGAG	nt 14462-nt 14485
	NHP-pen-15243R	GCGTCRGTGATGGTCACGCGC	nt 15243-nt 15223
	NHP-pen-15210R	ATRCTGCTGCGCAGCGGCAGGG	nt 15210-nt 15189
	NHP-pen-15036F	ACGAGCAGGCCGTCTACTCGCAGC	nt 15036-nt 15059
	NHP-pen-15446R	CGGTAGTGGCCGCGGACGCG	nt 15446-nt 15427

NHP-pen-15404R	CGCTTGGCGCCGCGGTACAT	nt 15404-nt 15385
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¹ The primers were designed following multiple alignment of the complete genomic sequences of SAdV-18 strain C676 (GenBank accession number FJ025931), SAdV-17 strain B-105 (KP329566), and HAdV-F strains (HAdV-40 isolates Dugan (L19443) and SA12680 (MK883611), and HAdV-41 isolate Tak (DQ315364)).

² Nucleotide positions are those of SAdV-18 (FJ025931).

^{3,4} Primers specific to SAdV strain KNA-08975 ³ and KNA-S6 ⁴ (designed from partial hexon sequences of respective virus strains), respectively.

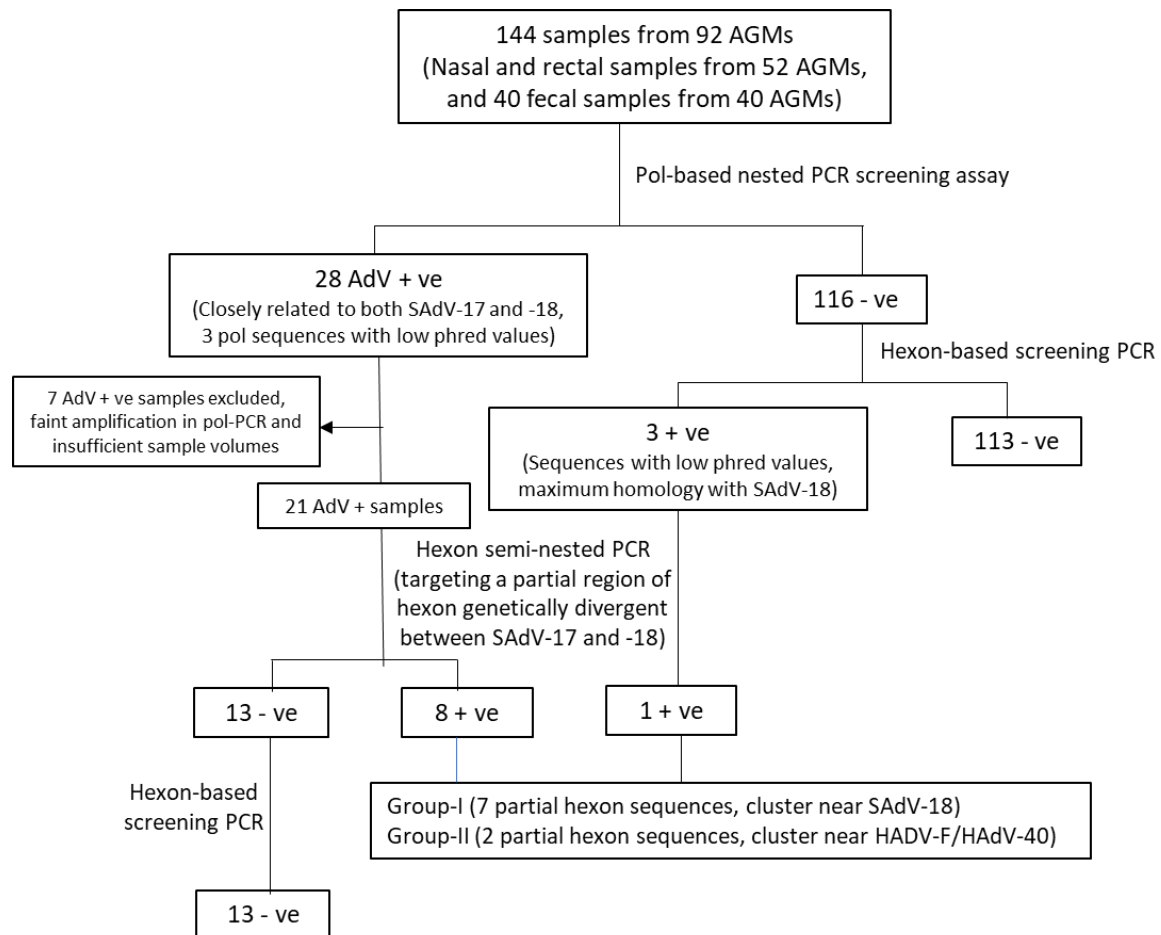


Figure S1. Flow chart summarizing the work pipeline and PCR results from the present study.

KNA-S6 54	-----PGAGGLHAAEAHPGTQPPRRRARQSAASPAPAAAGAPRRRAVAAAAGGTRTPAA
KNA-08975 54	-----PGAGGLHAAEAHPGTQPPRRRARQSAASPAPAAAGAPRRRAVAAAAGGTRTPAA
SAdV-F/SAdV-18 60	MALVPSPGTGGLHAAEAHPGPQPPRRRARQSAASSAPAAAGAPRRRAAAAHAGGTRTPAA
SAdV-F/SAdV-17 60	MALVPSPGTGGLHAEKAHPGPQPPRRRARQSAASPAPAAAGAPRRRAAGAHAGGSRTTPAA
HAdV-F/HAdV-40 60	MALVPSPRAGGFLPAETHSGPQPPRRRVQSTAGAAAPTATRAPRRRAATASPGEPPSTTA
HAdV-F/HAdV-41 60	MALVPSPGTGLGLHSTKTYPGTQPPRCRARQSAAGSASTATRAPGQRASTSSSGGSRTATA
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KNA-S6 109	ARRPTAANHVS-----PAYRRHRGTIVAGRGHALLYAVDTSTNEPLEFKYHQRLAPALTR
KNA-08975 109	ARRPTAANHVS-----PAYRRHRGTIVAGRGHALLYAVDTSTNEPLEFKYHQRLAPALTR
SAdV-F/SAdV-18 120	ARRQAQAGDVTSPPEYATYRRHRGTIVAARGQALLYAIDTSTNEPLEIKYHQRLAPALTR
SAdV-F/SAdV-17 118	ARRQAAADV--PPEHATYRRHRGTIVAARGHGLLYAIDTSTNEPLEIKYHQRLAPALTR
HAdV-F/HAdV-40 116	SGRPPAANNVS----LTPNSRLRGTIVAPRGQGLLYAIDTATNSPMEIKFHRRLASALTR
HAdV-F/HAdV-41 116	PRRPSASNDVN----PPSTFRLRGTIVASRGQGLLYAIDTSTNSPLEIKFHQRLASALTR
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KNA-S6 169	LLQVHRRTLTPVDLNEAFLNSLDAAQIRALALRLRPPRVDIWTGSRGVVTPSVLHPQQER
KNA-08975 169	LLQVHRRTLTPVDLNEAFLNSLDAAQIRALALRLRPPRVDIWTGSRGVVTPSVLHPQQER
SAdV-F/SAdV-18 180	LLQVHRRTLTPVDLSEAFDLSLDAAQIRTLALSLRPPRVDIWTGSRGVVTPSVLHPQQER
SAdV-F/SAdV-17 178	LLQVHRRTLTPVDLDEAFDLSLDAAHIRTLALRLRPPRVDIWTGSLRGIVTPSVLHPQQER
HAdV-F/HAdV-40 176	LLQVNLRSVPADLNEAFLDLSLSSQIRTLALKLKVPRVEVWTCGSRGVVPSIIHPQQER
HAdV-F/HAdV-41 176	LLQVNLRLSLPAGLSEAFDLSLSSQIRSLALRLQPPRVEVWTCASRGIVTPSVILPQQER
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KNA-S6 229	AGAEEHDEAEGQRAEAPLDCPLRFLVGRGRRVHLVQEVQSVQRCEHCARFYKYQHECTVRR
KNA-08975 229	AGAEEHDEAEGQRAEAPLDCPLRFLVGRGRRVHLVQEVQSVQRCEHCARFYKYQHECTVRR
SAdV-F/SAdV-18 240	AGAEEHDEAEGQRAEAPLDCPLRLLVGRGRRVHLVQEVQSVQRCEYCARFYKYQHECTVRR
SAdV-F/SAdV-17 238	AGAEEHDEAEGQHAELPLNCPRLLLVGRGRRVHLVQEVQSVQRCEYCARFYKHQHECTVRR
HAdV-F/HAdV-40 236	AGAEEGDEGERQDTEDFLNFLPLRFLVGRQVHLIQEMQSVQRCEYCARFYKYQHECTVRR
HAdV-F/HAdV-41 236	AGAEENNEGERQSAQEPLNFLPLRFLVGRQVHLIQEVQNVQRCEYCARFYKYQHECTVRR
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KNA-S6 289	RDFYFHHVNAHSSGWWQEINFFPLGSHPRTERLFVITYDVETYTWMGAFGKQLVPFMLVMH
KNA-08975 289	RDFYFHHVNAHSSGWWQEINFFPLGSHPRTERLFVITYDVETYTWMGAFGKQLVPFMLVMH
SAdV-F/SAdV-18 300	RDFYFHHVNAHSSGWWQEINFFPLGSHPRTERLFVITYDVETYTWMGAFGKQLVPFMLVMH
SAdV-F/SAdV-17 298	RDFYFHHVNAHSSGWWQQINFFPLGSHPRTERLFVITYDVETYTWMGAFGKQLVPFMLVMH
HAdV-F/HAdV-40 296	RDFYFHHINAHSSGWWQKINFFPIGSHPRVERLFVITYDVETYTWMGAFGKQLVPFMLVMH
HAdV-F/HAdV-41 296	RNFYFHHINAQSSGWWQEINFFPIGSHPRVERLFVITYDVETYTWMGAFGKQLVPFMLVMH
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KNA-S6 349	LSGEEALVEEACRLAREQSWDAWGEGDGRTFYVVVTPEKMAVGKKFRDYRDLQTALALQLW
KNA-08975 349	LSGEEALVEEACRLAREQSWDAWGEGDGRTFYVVVTPEKMAVGKKFRDYRDLQTALALQLW
SAdV-F/SAdV-18 360	LSGEEALVEEACRLAREQNWDAGQDGRTFYVVVTPEKMAVGKKFRDYRDLQTQLALQLW
SAdV-F/SAdV-17 358	LSGEETLVEEACRLAREQSWDAWGEGDGRTFYVVVTPEKMAVGKKFRDYRDLQTALALQLW
HAdV-F/HAdV-40 356	LSGEEALVKEACRLACELQWDWTGNDERTFYVVVTPEKLAVGKKFREYRNRLQAHFALQLW
HAdV-F/HAdV-41 356	LSGDDTLVEEACRLAHELQWDAGNDGHTFYVVVTPEKMAVGKKFRNYRDLQTHFATQLW
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KNA-S6 409	RGFLQANPQVADWARQELGLYSPDCLTYEELKKAPKLQGRPRFVELYIVGHNINGFDEIV
KNA-08975 409	RGFLQANPQVADWARQELGLYSPDCLTYEELKKAPKLQGRPRFVELYIVGHNINGFDEIV
SAdV-F/SAdV-18 420	RGFLQANPQVAEWARQELGLYSPDCLTYEELKKAPKLQGRPRFVELYIVGHNINGFDEIV
SAdV-F/SAdV-17 418	RGFLQANPQVAEWARQELGLYSPDCLTYEELKKAPKLQGRPRFVELYIVGHNINGFDEIV
HAdV-F/HAdV-40 416	RGFLAANPQLAEWACLEMGLFSPDYLTYEELQKAPKLQGRPRFLELYIVGHNINGFDEIV
HAdV-F/HAdV-41 416	QAFLAANPQVAEWARLEMGLFSPDNLTYEELKKAPKLQGTPRFVELYIVGHNINGFDEIV
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KNA-S6 469	LAAQVINNRSDVPGPFRI TRNFMPRAGKILFNDVTFALPNPRSQKRTDYGLWERGACDDT
KNA-08975 469	LAAQVINNRSDVPGPFRI TRNFMPRAGKILFNDVTFALPNPRSQKRTDYGLWERGACDDT
SAdV-F/SAdV-18 480	LAAQVINNRSDVPGPFRI TRNFMPRAGKILFNDVTFALPNPRSQKRTDYGLWERGACDDT
SAdV-F/SAdV-17 478	LAAQVINNRSDVPGPFRI TRNFMPRAGKILFNDVTFALPNPRSQKRTDYGLWERGACDDT
HAdV-F/HAdV-40 476	LAAQVINNRSDVPGPFKITRNFMPRAGKILFNDITFALPNPSSKKRTDYRLWEQGACDDS
HAdV-F/HAdV-41 476	LAAQVINNRSDVPGPFKITRNFMPRAGKILFNDITFALPNPLSKKRTDYHLWEQGACDDT
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KNA-S6 529	DFRFQFLKVMVRDTFALHTHTSLRKAQAAYALPVEKGCCPYRAVNRFYMLGSYLADERGFP
KNA-08975 529	DFRFQFLKVMVRDTFALHTHTSLRKAQAAYALPVEKGCCPYRAVNRFYMLGSYLADERGFP
SAdV-F/SAdV-18 540	DFRFQFLKVMVRDTFALHTHTSLRKAQAAYSLPVEKGCCPYRAVNRFYMLGSYLADERGFP
SAdV-F/SAdV-17 538	DFRFQFLKVMVRDTFALHTHTSLRKAQAAYSLPVEKGCCPYRAVNRFYMLGSYLADERGFP
HAdV-F/HAdV-40 536	DFKYQFLKVMVRDTFALHTHTSLRKAQAAYTLPVEKGCCPYKAVNEFYMLGSYRADERGFP
HAdV-F/HAdV-41 536	DFKHQFLKVMVRDTFALHTHTSLRKAQAAYALPVEKGCCPYKAVNQFYMLGSYRADERGFP
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KNA-S6 589	AEFYWKDREEYLLNRELWEKKQEPYDLVRETLDYCALDVLVTAALVQKLRESYAQFIHD
KNA-08975 589	AEFYWKDREEYLLNRELWEKKQEPYDLVRETLDYCALDVLVTAALVQKLRESYAQFIHD
SAdV-F/SAdV-18 600	AEFYWKDREEYLLNRELWEKKQEPYDLVRETLDYCALDVLVTAALVQKL RDSYAQFVHD
SAdV-F/SAdV-17 598	AEFYWKDREEYLLNRELWEKKQEPYDLVRETLDYCALDVLVTAALVQKL RDSYAQFVHD
HAdV-F/HAdV-40 596	AEDYWKDREEYLLNRELWEKKQCPHYDLVRETLDYCALDVLVTAALVQKLRESYAQFIRD
HAdV-F/HAdV-41 596	AEDYWKDREEYLLNRELWEKKQQSRDYDLIRETLDYCALDVLVTAALVQKLRESYAQFICD
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KNA-S6 649	AVGLPEASFNIFQRPTISSNSHAIFRQVTYRAVRPQRADLGGGLLAPSHEMYDYVRASIR
KNA-08975 649	AVGLPEASFNIFQRPTISSNSHAIFRQVTYRAVRPQRADLGGGLLAPSHEMYDYVRASIR
SAdV-F/SAdV-18 660	AVGLPEASFNIFQRPTISSNSHAIFRQVTYRAVRPQRGDLGGGLLAPSHEMYDYVRASIR
SAdV-F/SAdV-17 658	AVGLPEASFNIFQRPTISSNSHAIFRQVTYRAVKPQRGDLGGGLLAPSHEMYDYVRASIR
HAdV-F/HAdV-40 656	AVGLPEASFNVFQRPTISSNSHAIFRQILYRTVKPQRSDLGGGLLAPSHEMYDYVRASIR
HAdV-F/HAdV-41 656	AVGLPEAKFNVFQRPTISSNSHAIFRQILYRSVKPKRSDLGNLLAPSHEMYDYVRASIR
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KNA-S6 709	GGRCYPTYLGVLREPLYVYDICGMYASALTHMPWGAPLNPYERALAVRDWERALADPAV
KNA-08975 709	GGRCYPTYLGVLREPLYVYDICGMYASALTHMPWGAPLNPYERALAVRDWERALADPAV
SAdV-F/SAdV-18 720	GGRCYPTYLGVLREPLYVYDICGMYASALTHMPWGAPLNPYERALAVRDWERALADPAV
SAdV-F/SAdV-17 718	GGRCYPTYLGVLREPLYVYDICGMYASALTHMPWGAPLNPYERALAVRDWERALADPAV
HAdV-F/HAdV-40 716	GGRCYPTYIGVLREPLYVYDICGMYASALTHMPWGFPLNPYERALAVRDWEHALLQVGT
HAdV-F/HAdV-41 716	GGRCYPTYIGVLREPLYVYDICGMYASALTHMPWGSPLNPYERALAVRDWERRALLQVDT
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KNA-S6 769	SIDYFDRQLLPGIFTIDADPPAEDQLDVLPPFCSRKGGRCLCWTNEPLRGEVATSVDLITL
KNA-08975 769	SIDYFDRQLLPGIFTIDADPPAEDQLDVLPPFCSRKGGRCLCWTNEPLRGEVATSVDLITL
SAdV-F/SAdV-18 780	AIDYFDRHLLPGIFTIDADPPAEDQLDVLPPFCSRKGGRCLCWTNEPLRGEVATSVDLITL
SAdV-F/SAdV-17 778	AIDYFDRHLLPGIFTIDADPPAEDQLDVLPPFCSRKGGRCLCWTNEPLRGEVATSVDLITL
HAdV-F/HAdV-40 776	PIDYFNRTLPGIFTIDADPPENLLDVLPPPLCSRKGGRCLCWTNEPLRGEVVTSDVLITL
HAdV-F/HAdV-41 776	PIDYFNHVLLPGIFTIDADPPSENLLDVLPPYCSRKGGRCLCWTNEPLRGEVATSIDLITL
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KNA-S6 829	HNRGWRVRLLPDERATVFPEWRCVAREYVQLNIAAKERADREKNQTLRSIAKLLSNALYG
KNA-08975 829	HNRGWRVRLLPDERATVFPEWRCVAREYVQLNIAAKERADREKNQTLRSIAKLLSNALYG
SAdV-F/SAdV-18 840	HNRGWRVRLLPDERATVFPEWRCVAREYVQLNIAAKERADREKNQTLRSIAKLLSNALYG
SAdV-F/SAdV-17 838	HNRGWRVRLLPDERATVFPEWRCVAREYVQLNIAAKERADREKNQTLRSIAKLLSNALYG
HAdV-F/HAdV-40 836	HNRGWHVRLLPDERATVFPEWRCVAKEYVHLNITAKERADREKNQTLRSIAKLLSNALYG
HAdV-F/HAdV-41 836	HNRGWQVRLLPDERTTVFPEWRCVARKYVQLNIAAKERADREKNQTLRSIAKLLSNALYG
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KNA-S6 889	SFATKLDNKKIVFSDQMDPATVKSIAAGQVNIKSTSFVETDTLSAEVMPAFQRAYSPPEQL
KNA-08975 889	SFATKLDNKKIVFSDQMDPATVKSIAAGQVNIKSTSFVETDTLSAEVMPAFQRAYSPPEQL
SAdV-F/SAdV-18 900	SFATKLDNKKIVFSDQMDPATVKSIAAGQVNIKSTSFVETDTLSAEVMPAFQRAYSPPEQL

SADV-F/SAdV-17 898	SFATKLDNKKIVFSDQMDPATVKSIAAGQVNIKSTSFVETDTLSAEVMPAFQRAYSPEQL
HAdV-F/HAdV-40 896	SFATKLDNKKIVFSDQMDSATIKSIAAGQINIKSTSFVETDTLSAEVMPTFQRAYSPEQL
HAdV-F/HAdV-41 896	SFATKLDNKKIVFSDQMDPATIKSIAAGQIKIKSTSFVETDTLSAEVMPAFQRAYSPEQL
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KNA-S6 949	DLVHSDAEESDGETGHAPFYKPTRDPDGHVTTYTYKPITFMDAEEDDLCLHLEKVDPLVE
KNA-08975 949	DLVHSDAEESDGETGHAPFYKPTRDPDGHVTTYTYKPITFMDAEEDDLCLHLEKVDPLVE
SAdV-F/SAdV-18 960	DLVHSDAEESDGEAGHAPFYKPTRDPDGHVTTYTYKPITFMDAEEDDLCLHLEKVDPLVE
SADV-F/SAdV-17 958	DLVHSDAEESDGEAGHAPFYKPTRDPDGHVTTYTYKPITFMDAEEDDLCLHLEKVDPLVE
HAdV-F/HAdV-40 956	AVVHSDAEESDEEPGHAPFYTPTHKPNDHVTTYTYKPITFMDAEEDDLCLHLEKVDPLVE
HAdV-F/HAdV-41 955	ALAHSDAEESDEERGA-LYTPTQDPKGHVTTYTYKPITFMDAEEDDLCLHLEKVDPLVE
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KNA-S6 1009	NDRYPSQIASFVLAWTRAFVSEWSEFLHAEDRGIPLEQRALKSVYGDTSLSFVTEAGRRL
KNA-08975 1009	NDRYPSQIASFVLAWTRAFVSEWSEFLHAEDRGIPLEQRALKSVYGDTSLSFVTEAGRRL
SAdV-F/SAdV-18 1020	NDRYPSQIASFVLAWTRAFVSEWSEFLHAEDRGIPLEQRALKSVYGDTSLSFVTEAGRRL
SADV-F/SAdV-17 1018	NDRYPSQIASFVLAWTRAFVSEWSEFLHAEDRGIPLEQRALKSVYGDTSLSFVTEAGRRL
HAdV-F/HAdV-40 1016	NNRYPSQIASFVLAWTRAFVSEWSEILYAEDRGTPLEQRTLKSVYGDTSLSFVTEAGYRL
HAdV-F/HAdV-41 1015	NDRYPSQIASFVLAWTRAFVSEWSEFLYAEDRGTPLEQRTLKSVYGDTSLSFVTEAGHRL
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KNA-S6 1069	METRGGKRIKKHGGQLVFDPQRPELTWLVECETTCAQCGADAFSPESVFLAPKLYALKCL
KNA-08975 1069	METRGGKRIKKHGGQLVFDPQRPELTWLVECETTCAQCGADTFSPETVFLAPKLYALKCL
SAdV-F/SAdV-18 1080	METRGGKRIKKHGGQLVFDPQHPELTWLVECETTCAQCGADAYSPESVFLAPKLYALKCL
SADV-F/SAdV-17 1078	METRGGKRIKKHGGQLVFDPQRPELTWLVECETTCAQCGADAYSPESVFLAPKLYALKCL
HAdV-F/HAdV-40 1076	METRGGKRIKKHGGNLVFDPKHPELAWLVECETVCAQCGADAYSPESVFLAPKLYALKCL
HAdV-F/HAdV-41 1075	METRGGKRIKKHGGSLVFDKPNPELTWLVECETTCAQCGANAYSPESVFLAPKLYALKCL
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KNA-S6 1129	QCPACGHVSKGKLRAKGHAAEALSYDLMLRCYLADSQGEDARFHTSRMSLKRTLASAQPG
KNA-08975 1129	QCPACGHVSKGKLRAKGHAAEALSYDLMLRCYLADSQGEDARFHTSRMSLKRTLASAQPG
SAdV-F/SAdV-18 1140	HCPACGHVSKGKLRAKGHAAEALSYDLMLKCYLADSQGEDARFHTSRMSLKRTLASAQPG
SADV-F/SAdV-17 1138	QCPACGHVSKGKLRAKGHAAEALSYDLMLKCYLADSQGEDARFHTSRMSLKRTLASAQPG
HAdV-F/HAdV-40 1136	RCPSCQQISKGKLRAKGHAAETLNYDLMLKCYLADFQGEDARFHTSRMSLKRTLASAQPG
HAdV-F/HAdV-41 1135	YCPSCQHISKGKLRAKGHAAEALSYELMLKCYLADSQGEDARFHTSRMSLKRTLASAQPG
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KNA-S6	AHPFTVTETTLTRTLRPWRDVT LAPLDAHRLVPYSQSRPNPRNQEVCI--- 1178
KNA-08975	AHPFTVTETTLTRTLRPWRDVT LAPLDAHRLVPYSQSRPNPRNQEVCI--- 1178
SAdV-F/SAdV-18	AHPFTVTETTLTRTLRPWKDVT LASLDAHRLVPYSQSRPNPRNQEVCIEMP 1192
SADV-F/SAdV-17	AHPFTVTETTLTRTLRPWRDVT LAPLDAHRLVPYSQSRPNPRNQEVCIEMP 1190
HAdV-F/HAdV-40	ARPFTVTETNLTRTLRPWKDIT LAPLDAHRLVPYSQSRPNPRNQEVCIEMP 1188
HAdV-F/HAdV-41	AHPFTVTETTLTRTLRPWKDIT LAPLDAHRLVPYSQSRPNPRNQEVCIEMP 1187

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Figure S3. Multiple alignment of the nearly complete deduced amino acid (aa) sequences of the putative DNA-dependent DNA polymerase (Pol) of simian adenovirus (SAdV) strains KNA-S6 and KNA-08975 with cognate sequences of SAdV-F/SAdV-17 strain B-105 (GenBank accession number KP329566), SAdV-F/SAdV-18 strain C676 (FJ025931), Human AdV-F (HAdV-F)/HAdV-40 isolate Dugan (L19443), and HAdV-F/HAdV-41 isolate Tak (DQ315364). Numbers to the right indicate the positions of the aa for respective AdV strains.

KNA-S6	MATPSMMPQWSYMHIAQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR	
60		
HAdV-F/HAdV-40	MATPSMMPQWSYMHIAQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR	
60		
SAdV-F/SAdV-17	MATPSMMPQWSYMHIAQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR	
60		
KNA-08975	MATPSMMPQWSYMHIAQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR	
60		
SAdV-F/SAdV-18	MATPSMMPQWSYMHIAQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR	
60		
HAdV-F/HAdV-41	MATPSMMPQWSYMHIAQDASEYLSPLGVQFARATDTYFSLGNKFRNPTVAPTHDVTDDR	
60		

KNA-S6	SQRLTLRFVPVDREDTAYSYKVRFTLAVGDNRVLDMASTYFDIRGVLDRGPSFK	PYSGTA
120		
HAdV-F/HAdV-40	SQRLTLRFVPVDREETAYSYKVRFTLAVGDNRVLDMASTYFDIRGVLDRGPSFK	PYSGTA
120		
SAdV-F/SAdV-17	SQRLTLRFVPVDREDTAYSYKVRFTLAVGDNRVLDMASTYFDIRGVLDRGPSFK	PYSGTA
120		
KNA-08975	SQRLTLRFVPVDREDTAYSYKVRFTLAVGDNRVLDMASTYFDIRGVLDRGPSFK	PYSGTA
120		
SAdV-F/SAdV-18	SQRLTLRFVPVDREDTAYSYKVRFTLAVGDNRVLDMASTYFDIRGVLDRGPSFK	PYSGTA
120		
HAdV-F/HAdV-41	SQRLTLRFVPVDREDTAYSYKVRFTLAVGDNRVLDMASTYFDIRGVLDRGPSFK	PYSGTA
120		
*****:*****		
KNA-S6	YNSLAPKGAPNPSQWTNSVTNTKTSSFGQAPFIGEKITNE-GVQVGTD--SGGDVFADK	
177		
HAdV-F/HAdV-40	YNSLAPKGAPNPSQWTN---QNKTNSFGQAPYIGQKITNQ-GVQVGSDS--NNRDVFADK	
174		
SAdV-F/SAdV-17	YNSLAPKNA PNACQWTSTTNGNKTNTFAQAPFIGLSITKD-GVQVGVDTSQTQQAVYADK	
179		
KNA-08975	YNSLAPKGAPNPSEWK--TDSKVNVRGQAPFFSTSISKD-GIQVGTDSTPTQAIYADK	
177		
SAdV-F/SAdV-18	YNSLAPKGAPNPSEWK--SDNKISVRGQAPFFSTSITKD-GIQVATDTSS--GAVYAKK	
175		
HAdV-F/HAdV-41	YNSLAPKTAPNPCEWK---DNNKIKVRGQAPFIGTNINKDNGIQIGTDTTN--QPIYADK	
175		
***** **..:*. .*. .***:..*.::*:..*: :*:.*		
KNA-S6	TFQPEPQVGQTQWNIDPTQN--AAGRILKKTTPMQPCYGSYARPTNEQGGQAKLVVNG-G	
234		
HAdV-F/HAdV-40	TYQPEPQVGQTQWNINPMQN--AAGRILKQTTPMQPCYGSYARPTNEKGGQAKLVKNDN	
232		
SAdV-F/SAdV-17	SFQPEPQVGESQWNSNPTTN--AAGRVLPKTTAMLPCYGSYAYPTNEKGG-----	
227		
KNA-08975	TYQPEPQVGQEQWNSEAGDNDKVAGRVLDSTPMFPCYGSYAKPTNEHGGQCTNSTVDLQ	
237		
SAdV-F/SAdV-18	EYQPEPQVGQEQWNSEASDSKIVAGRVLDSTPMFPCYGSYAKPTNEQGGQGTN-TVVDLQ	
234		
HAdV-F/HAdV-41	TYQPEPQVGQTQWNSEVGAAQKVAGRVLDSTPMLPCYGSYAKPTNEKGGQASLITNGTD	
235		
:*****: *** : .***:* :*. * ***** ***:**		
KNA-S6	QTQTTDVSLNFFTASESSSFTPKVVLVYGEDVNLEAPDTHLVFKPDTND--TSAEILLGQ	
292		

[illegible]

KNA-S6	PFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMILQSSSLGNDLRVDGASVKFDSINLY
589	
HAdV-F/HAdV-40	PFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMILQSSSLGNDLRVDGASVRFDSINLY
587	
SAdV-F/SAdV-17	PFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMILQSSSLGNDLRVDGASVRFDSINLY
581	
KNA-08975	PFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMILQSSSLGNDLRVDGASVRFDSINLY
586	
SAdV-F/SAdV-18	PFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMILQSSSLGNDLRVDGASVRFDSINLY
581	
HAdV-F/HAdV-41	PFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMILQSSSLGNDLRVDGASVRFDSINLY
589	*****:*****
KNA-S6	ANFFPMAHNTASTLEAMLRNDTNDQSFNDYLCAANMLYPIPANATSVPISSIPSRNWAAFR
649	
HAdV-F/HAdV-40	ANFFPMAHNTASTLEAMLRNDTNDQSFNDYLCAANMLYPIPANATSVPISSIPSRNWAAFR
647	
SAdV-F/SAdV-17	ANFFPMAHNTASTLEAMLRNDTNDQSFNDYLCAANMLYPIPANATSVPISSIPSRNWAAFR
641	
KNA-08975	ANFFPMAHNTASTLEAMLRNDTNDQSFNDYLCAANMLYPIPANATSVPISSIPSRNWAAFR
646	
SAdV-F/SAdV-18	ANFFPMAHNTASTLEAMLRNDTNDQSFNDYLCAANMLYPIPANATSVPISSIPSRNWAAFR
641	
HAdV-F/HAdV-41	ANFFPMAHNTASTLEAMLRNDTNDQSFNDYLCAANMLYPIPSNATSVPISSIPSRNWAAFR
649	*****:*****
KNA-S6	GWSFTRLKTKETPSLGS GFDPYFTYSGSIPYLDGTFYLNHTFKKVSVMFDSVSWPGNDR
709	
HAdV-F/HAdV-40	GWSFTRLKTKETPSLGS GFDPYFTYSGSVPYLDGTFYLNHTFKKVSVMFDSVSWPGNDR
707	
SAdV-F/SAdV-17	GWSFTRLKTKETPSLGS GFDPYFTYSGSIPYLDGTFYLNHTFKKVSIMFDSVSWPGNDR
701	
KNA-08975	GWSFTRLKTRETPSLGS GFDPYFTYSGSIPYLDGTFYLNHTFKKVSIMFDSVSWPGNDR
706	
SAdV-F/SAdV-18	GWSFTRLKTKETPSLGS GFDPYFTYSGSIPYLDGTFYLNHTFKKVSIMFDSVSWPGNDR
701	
HAdV-F/HAdV-41	GWSFTRLKTKETPSLGS GFDPYFTYSGSVPYLDGTFYLNHTFKKVSIMFDSVSWPGNDR
709	*****:*****:*****:*****
KNA-S6	LLTPNEFEIKRTVDGEGYNVAQCNMTKDWFLIQMLSHYNIGYQGFYVPEGYKDRMYSFFR
769	
HAdV-F/HAdV-40	LLTPNEFEIKRTVDGEGYNVAQCNMTKDWFLIQMLSHYNIGYQGFHPESYKDRMYSFFR
767	
SAdV-F/SAdV-17	LLTPNEFEIKRTVDGEGYNVAQCNMTKDWFLIQMLSHYNIGYQGFYVPEGYKDRMYSFFR
761	
KNA-08975	LLTPNEFEIKRTVDGEGYNVAQCNMTKDWFLIQMLSHYNIGYQGFYVPEGYKDRMYSFFR
766	
SAdV-F/SAdV-18	LLTPNEFEIKRTVDGEGYNVAQCNMTKDWFLIQMLSHYNIGYQGFYVPEGYKDRMYSFFR
761	
HAdV-F/HAdV-41	LLTPNEFEIKRTVDGEGYNVAQCNMTKDWFLIQMLSHYNIGYQGFYVPESYKDRMYSFFR
769	*****:***.*****
KNA-S6	NFQPM SRQVVD TTSYSDYKNVTLPFQHNNSGFVG YMGPTMREGQAYPANYPYPLIGKTAV
829	
HAdV-F/HAdV-40	NFQPM SRQVVD TTTYTEYQNVTLPFQHNNSGFVG YMGPAIREGQAYPANYPYPLIGQTAV
827	
SAdV-F/SAdV-17	NFQPM SRQVVD SVNYANYKEVKLPFQHNNSGFVG YMGPTMREGQAYPANYPYPLIGKTAV
821	
KNA-08975	NFQPM SRQVVD TTTYSDYQNVTLPFQHNNSGFVG YMGPTMREGQAYPANYPYPLIGKTAV
826	
SAdV-F/SAdV-18	NFQPM SRQVVD TTTYTDYKNVTLPFQHNNSGFVG YMGPTMREGQAYPANYPYPLIGKTAV
821	
HAdV-F/HAdV-41	NFQPM SRQVVD TTTYKEYQNVTLPFQHNNSGFVG YMGPTMREGQAYPANYPYPLIGQTAV
829	*****:..* :*:*.*****:*****:***

KNA-S6	PSLTQKKFLCDRTMWRIPFSSNFMSMGALTDLGQNMLYANSAHALDMTFEVDPMDEPTLL
889	
HAdV-F/HAdV-40	PSLTQKKFLCDRTMWRIPFSSNFMSMGALTDLGQNMLYANSAHALDMTFEVDPMDEPTLL
887	
SAdV-F/SAdV-17	DSLTQKKFLCDRTMWRIPFSSNFMSMGALTDLGQNMLYANSAHALDMTFEVDPMDEPTLL
881	
KNA-08975	PSLTQKKFLCDRTMWRIPFSSNFMSMGALTDLGQNMLYANSAHALDMTFEVDPMDEPTLL
886	
SAdV-F/SAdV-18	PSLTQKKFLCDRTMWRIPFSSNFMSMGALTDLGQNMLYANSAHALDMTFEVDPMDEPTLL
881	
HAdV-F/HAdV-41	PSLTQKKFLCDRTMWRIPFSSNFMSMGALTDLGQNMLYANSAHALDMTFEVDPMDEPTLL
889	

KNA-S6	YVLFEVFDVVRIHQPHRGVIEAVYLRTPFSAAGNATT	925
HAdV-F/HAdV-40	YVLFEVFDVVRIHQPHRGVIEAVYLRTPFSAAGNATT	923
SAdV-F/SAdV-17	YVLFEVFDVVRIHQPHRGVIEAVYLRTPFSAAGNATT	917
KNA-08975	YVLFEVFDVVRIHQPHRGVIEAVYLRTPFSAAGNATT	922
SAdV-F/SAdV-18	YVLFEVFDVVRIHQPHRGVIEAVYLRTPFSAAGNATT	917
HAdV-F/HAdV-41	YVLFEVFDVVRIHQPHRGVIEAVYLRTPFSAAGNATT	925

Figure S4. Multiple alignment of the complete deduced amino acid (aa) sequences of the putative hexons of simian adenovirus (SAdV) strains KNA-S6 and KNA-08975 with those of SAdV-F/SAdV-17 strain B-105 (GenBank accession number KP329566), SAdV-F/SAdV-18 strain C676 (FJ025931), Human AdV-F (HAdV-F)/HAdV-40 isolate Dugan (L19443), and HAdV-F/HAdV-41 isolate Tak (DQ315364). The region of the putative hexon (genetically divergent between the hexons of SAdV-17, -18, and HAdV-F) that formed the basis of classification of the AdV strains from African green monkeys into group-I and group-II viruses is highlighted with blue. Numbers to the right indicate the positions of the aa for respective AdV strains.

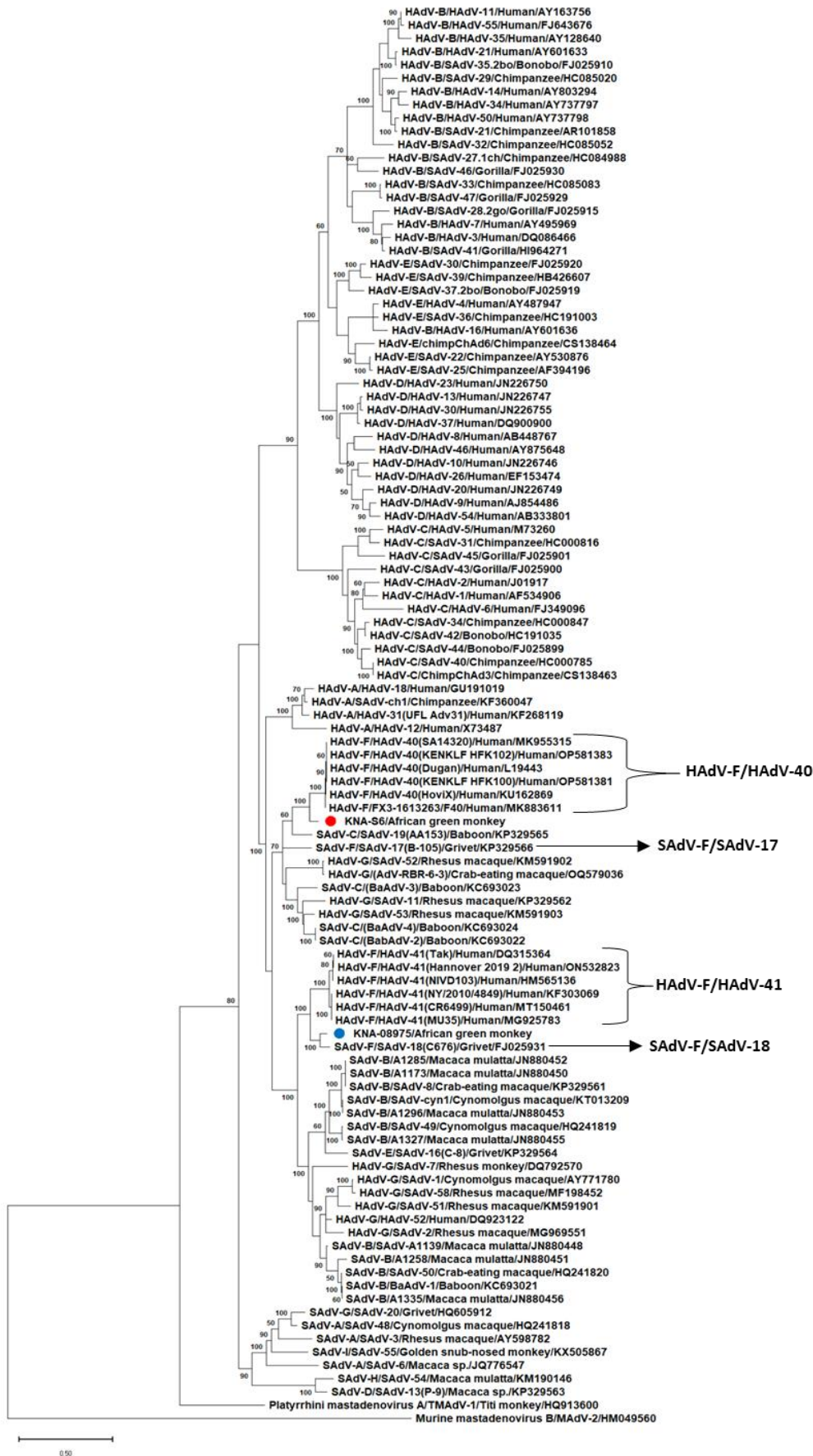


Figure S5. Expanded version of figure 4.

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KNA-S6      NFRLGWDPVTKLVMPGVYTNEAFHPDIVLLPGCGVDFTQSRLSNLLGIRKRMPPQEGFQI
SAdV-F/SAdV-17 NFRLGWDPVTKLVMPGVYTNEAFHPDIVLLPGCGVDFTQSRLSNLLGIRKRMPPQAGFQI
KNA-08975   NFRLGWDPVTKLVMPGVYTNEAFHPDIVLLPGCGVDFTQSRLSNLLGIRKRMPPQEGFQI
SAdV-F/SAdV-18 NFRLGWDPVTKLVMPGVYTNEAFHPDIVLLPGCGVDFTQSRLSNLLGIRKRMPPQAGFQI
HAdV-F/HAdV-40 NFRLGWDPVTKLVMPGVYTNEAFHPDIVLLPGCGVDFTQSRLSNLLGIRKRMPPQKGFQI
HAdV-F/HAdV-41 NFRLGWDPVTKLVMPGVYTNEAFHPDIVLLPGCGVDFTQSRLSNLLGIRKRLPFQEGFQI
*****.*****:*** ****

KNA-S6      MYNDLEGGNIPALLDVAKYEASITEAQQQGKEIRGDTFAVSPQDLVIEPVANDSKNRSYN
SAdV-F/SAdV-17 MYEDLEGGNIPALLDVAKYEASITQAQQQGKEIRGDTFAVSPQDLVIEPVANDSKNRSYN
KNA-08975   MYEDLEGGNIPALLDVAKYEASIQQAREQGQEIIRGDNFTVIPRDVEIVPVEQDSKGRSYN
SAdV-F/SAdV-18 MYEDLEGGNIPALLDVAKYEASIQKAREQGQEIIRGDNFTVIPRDVEIVPVEKDSKDRSYN
HAdV-F/HAdV-40 MYEDLEGGNIPALLDVAKYEASIKEA----QEIRGADFKPNPQDLEIVPVEKDSKERSYN
HAdV-F/HAdV-41 MYEDLEGGNIPALLDVAKYEASIQKAKEEGKEIGDDTFATRPQDLVIEPVAKDSKNRSYN
*:*****:*****:*****:*****:*****:*****:*****:*****

KNA-S6      LLPDDKNNTAYRSWFLAYNYGDPEKGVRSWTLLTTTDDVTCGQQQVYWSLPDMMQDPVTFR
SAdV-F/SAdV-17 LLPDDKNNTAYRSWFLAYNYGDPEKGVRSWTLLTTTDDVTCGQQQVYWSLPDMMQDPVTFR
KNA-08975   LIPTDKTNTAYRSWFLAYNYGDPEKGVRSWTLLTTTDDVTCGQQQVYWSLPDMMQDPVTFR
SAdV-F/SAdV-18 LLPGDQNTAYRSWFLAYNYGDPEKGVRSWTLLTTTDDVTCGQQQVYWSLPDMMQDPVTFR
HAdV-F/HAdV-40 LLEGDKNNTAYRSWFLAYNYGDAEKGVKSWTLLTTTDDVTCGQQQVYWSLPDMMQDPVTFR
HAdV-F/HAdV-41 LLPNDQNNTAYRSWFLAYNYGDPKKGVSWTLLTTADVTCGQQQVYWSLPDMMQDPVTFR
*:*.***:*****:*****:*****:*****:*****:*****:*****

KNA-S6      PSSQVSNYPVVGVELLPVHAKSFYNEQAVYSQLIRQSTALTHVFNRFPENQILVRPPAPT
SAdV-F/SAdV-17 PSSQVSNYPVVGVELLPVHAKSFYNEQAVYSQLIRQSTALTHVFNRFPENQILVRPPAPT
KNA-08975   PSSQVSNYPVVGVELLPVHAKSFYNEQAVYSQLIRQSTALTHVFNRFPENQILVRPPAPT
SAdV-F/SAdV-18 PSSQVSNYPVVGVELLPVHAKSFYNEQAVYSQLIRQSTALTHVFNRFPENQILVRPPAPT
HAdV-F/HAdV-40 PSTQVSNYPVVGVELLPVHAKSFYNEQAVYSQLIRQSTALTHVFNRFPENQILVRPPAPT
HAdV-F/HAdV-41 PSTQVSNYPVVGVELLPVHAKSFYNEQAVYSQLIRQSTALTHVFNRFPENQILVRPPAPT
*:*****:*****:*****:*****:*****:*****:*****:*****

KNA-S6      ITTVSENVPALTDHGTLPRLSSISGVQRVTITDARRRTCYPVHKALGIVAPKVLSSRTF
SAdV-F/SAdV-17 ITTVSENVPALTDHGTLPRLSSISGVQRVTITDARRRTCYPVHKALGIVAPKVLSSRTF
KNA-08975   ITTVSENVPALTDHGTLPRLSSISGVQRVTITDARRRTCYPVHKALGIVAPKVLSSRTF
SAdV-F/SAdV-18 ITTVSENVPALTDHGTLPRLSSISGVQRVTITDARRRTCYPVHKALGIVAPKVLSSRTF
HAdV-F/HAdV-40 ITTVSENVPALTDHGTLPRLSSISGVQRVTITDARRRTCYPVHKALGIVAPKVLSSRTF
HAdV-F/HAdV-41 ITTVSENVPALTDHGTLPRLSSISGVQRVTITDARRRTCYPVHKALGIVAPKVLSSRTF
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508

Figure S7. Multiple alignment of the partial deduced amino acid (aa) sequences of the putative penton bases of simian adenovirus (SAdV) strains KNA-S6 and KNA-08975 with cognate sequences of SAdV-F/SAdV-17 strain B-105 (GenBank accession number KP329566), SAdV-F/SAdV-18 strain C676 (FJ025931), Human AdV-F (HAdV-F)/HAdV-40 isolate Dugan (L19443), and HAdV-F/HAdV-41 isolate Tak (DQ315364). The putative 'RGD' motif is highlighted with green and was absent in HAdV-F strains. The aa numbers shown here correspond to those of the complete deduced aa sequence of penton base of SAdV-F/SAdV-18.

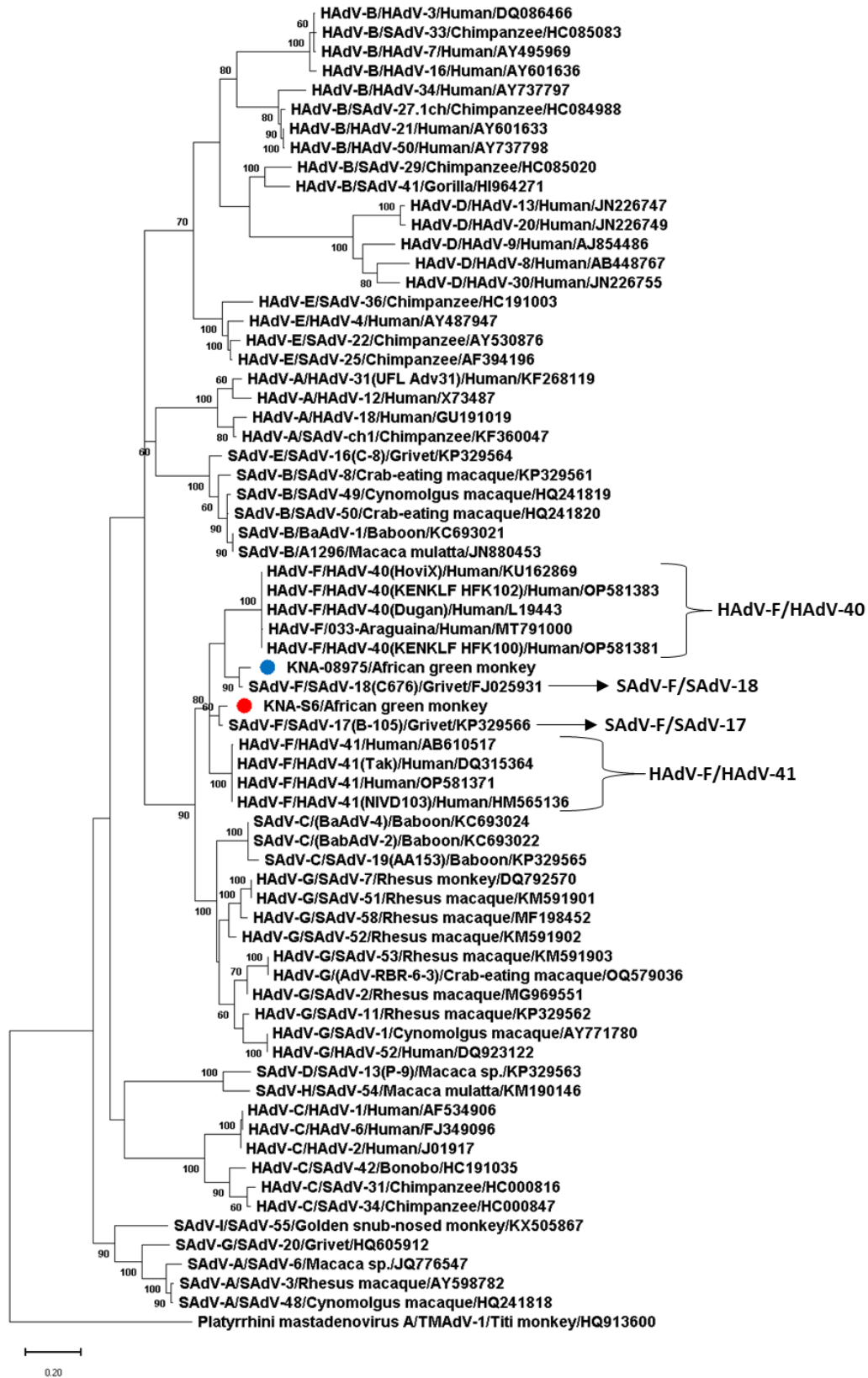


Figure S8. Expanded version of figure 5.

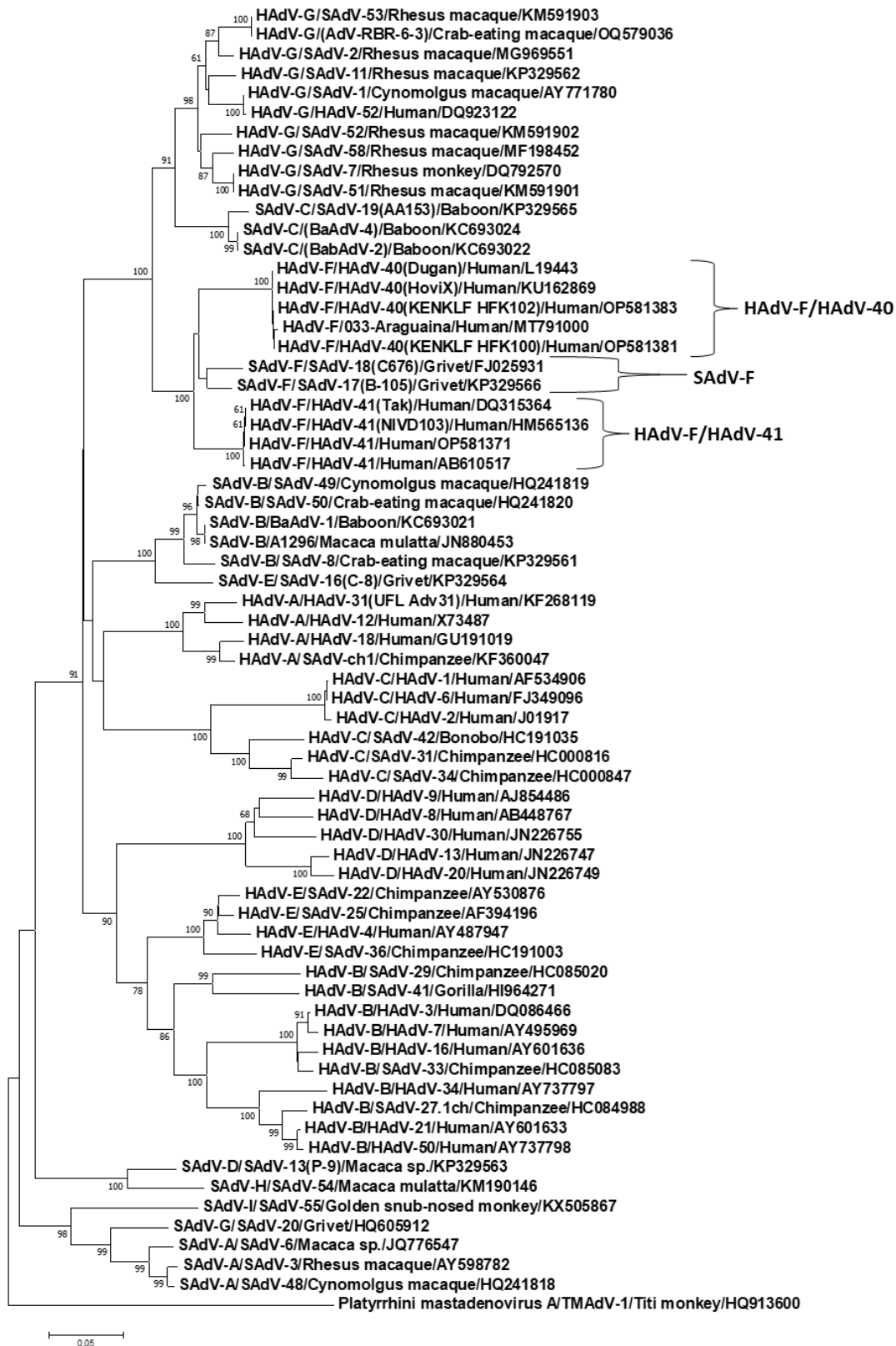


Figure S9. Phylogenetic analysis of the complete deduced amino acid (aa) sequences of the putative penton bases of simian adenoviruses (SAdVs) and human adenoviruses (HAdVs). The phylogenetic analysis was performed as described under 'Materials and Methods' section. Bootstrap values < 60% are not shown. Scale bar, 0.05 substitutions per aa residue.