

**Supplementary Figure 1.** Sequence alignment of the complete hexon genes of HAdV-1 (D11) and FeAdV.

HAdV-1	1	GCTACCCCTTCGATGATGCCGCAGTGGTCTTACATGCACATCTCGGGCCA	50
FeAdV	1	GCTACCCCTTCGATGATGCCGCAGTGGTCTTACATGCACATCTCGGGCCA	50
	51	GGACGCCTCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTCGCCCCGCGCCA	100
	51	GGACGCCTCGGAGTACCTGAGCCCCGGGCTGGTGCAGTTCGCCCCGCGCCA	100
	101	CCGAGACGTACTTCAGCCTGAATAACAAGTTTAGAAACCCACGGTGGCG	150
	101	CCGAGACGTACTTCAGCCTGAATAACAAGTTTAGAAACCCACGGTGGCG	150
	151	CCTACGCACGACGTGACCACAGACCGGTCTCAGCGTTTGACGCTGCGGTT	200
	151	CCTACGCACGACGTGACCACAGACCGGTCTCAGCGTTTGACGCTGCGGTT	200
	201	TATCCCCGTGGACCGCGAGGATAACCGCATACTCGTACAAGGCGCGGTTTA	250
	201	TATCCCCGTGGACCGCGAGGATAACCGCATACTCGTACAAGGCGCGGTTTA	250
	251	CCCTGGCTGTGGGTGACAACCGTGTGCTTGACATGGCTTCCACATACTTT	300
	251	CCCTGGCTGTGGGTGACAACCGTGTGCTTGACATGGCTTCCACATACTTT	300
	301	GACATTTCGCGGCGTGCTGGACCGGGGCCCACTTTTAAGCCCTACTCCGG	350
	301	GACATTTCGCGGCGTGCTGGACCGGGGCCCACTTTTAAGCCCTACTCCGG	350
	351	CACTGCCTACAACGCTCTAGCCCCCAAGGGCGCTCCCAATTCTGCGAGT	400
	351	CACTGCCTACAACGCTCTAGCCCCCAAGGGCGCTCCCAATTCTGCGAGT	400
	401	GGGAACAAGAAGAACCAACTCAGGAAATGGCTGAAGAACTTGAAGATGAG	450
	401	GGGAACAAGAAGAACCAACTCAGGAAATGGCTGAAGAACTTGAAGATGAG	450
	451	GAGGAGGCAGAGGAGGAGGAGGCAGAGGAGGAGGCAGAAGCACCACAAGC	500
	451	GAGGAGGCAGAGGAGGAGGAGGCAGAGGAGGAGGCAGAAGCACCACAAGC	500
	501	TGATCAGAAGGTTAAGAAGACTCATGTATATGCTCAGGCTCCTTTGGCAG	550
	501	TGATCAGAAGGTTAAGAAGACTCATGTATATGCTCAGGCTCCTTTGGCAG	550
	551	GGGAAAAAATTACCGCCAATGGCTTACAAATAGTTTCTGATACCCAAACT	600
	551	GGGAAAAAATTACCGCCAATGGCTTACAAATAGTTTCTGATACCCAAACT	600
	601	GAAGGCAATCCAGTTTTTGGCGATCCCACTTATCAACCTGAACCTCAGGT	650
	601	GAAGGCAATCCAGTTTTTGGCGATCCCACTTATCAACCTGAACCTCAGGT	650

651	TGGAGAATCTCAGTGAATGAAGCTGAAGCAACTGCATCTGGAGGCAGAG	700
651	TGGAGAATCTCAGTGAATGAAGCTGAAGCAACTGCATCTGGAGGCAGAG	700
701	TACTAAAAAAGACTACTCCCATGAAACCATGCTACGGATCGTATGCCAGA	750
701	TACTAAAAAAGACTACTCCCATGAAACCATGCTACGGATCGTATGCCAGA	750
751	CCTACAAATAAAAATGGGGGTCAAGGTATACTAGTAGCAAACAACCAAGG	800
751	CCTACAAATAAAAATGGGGGTCAAGGTATACTAGTAGCAAACAACCAAGG	800
801	TGCTCTAGAGTCTAAAGTTGAAATGCAGTTTTTTGCCCCCTCTGGCACTG	850
801	TGCTCTAGAGTCTAAAGTTGAAATGCAGTTTTTTGCCCCCTCTGGCACTG	850
851	CCATGAATGAAAGAAATGCTGTTCAGCCAAGTATTGTTTTGTACAGTGAG	900
851	CCATGAATGAAAGAAATGCTGTTCAGCCAAGTATTGTTTTGTACAGTGAG	900
901	GATGTTAATATGGAAACTCCTGATACTCACATTTTCATACAAACCAAGCAA	950
901	GATGTTAATATGGAAACTCCTGATACTCACATTTTCATACAAACCAAGCAA	950
951	AACTGATGAAAACCTCTAAGGCTATGTTGGGTCAACAAGCAATGCCAAACA	1000
951	AACTGATGAAAACCTCTAAGGCTATGTTGGGTCAACAAGCAATGCCAAACA	1000
1001	GACCCAATTACATCGCTTTTAGGGACAATTTTATTGGCCTTATGTATTAC	1050
1001	GACCCAATTACATCGCTTTTAGGGACAATTTTATTGGCCTTATGTATTAC	1050
1051	AACAGCACTGGTAACATGGGTGTCCTTGCTGGACAAGCATCACAGCTAAA	1100
1051	AACAGCACTGGTAACATGGGTGTCCTTGCTGGACAAGCATCACAGCTAAA	1100
1101	TGCCGTGGTAGACTTGCAGGACAGAAACACAGAGCTGTCATATCAACTTT	1150
1101	TGCCGTGGTAGACTTGCAGGACAGAAACACAGAGCTGTCATATCAACTTT	1150
1151	TGCTTGATTCTATTGGCGATAGAACCAGATACTTTTCCATGTGGAATCAG	1200
1151	TGCTTGATTCTATTGGCGATAGAACCAGATACTTTTCCATGTGGAATCAG	1200
1201	GCTGTAGACAGCTATGATCCAGATGTCAGAATCATTGAAAATCATGGAAC	1250
1201	GCTGTAGACAGCTATGATCCAGATGTCAGAATCATTGAAAATCATGGAAC	1250
1251	TGAGGATGAGTTGCCAAATTACTGCTTCCCACTTGGCGGTATAGGGGTAA	1300
1251	TGAGGATGAGTTGCCAAATTACTGCTTCCCACTTGGCGGTATAGGGGTAA	1300
1301	CTGACACCTACCAAGGTATAAAATCAAACGGAAACGGTAATCCTCAAAAC	1350
1301	CTGACACCTACCAAGGTATAAAATCAAACGGAAACGGTAATCCTCAAAAC	1350

1351	TGGACCAAAAATGACGATTTTGCGGCACGTAATGAAATAGGTGTGGGAAA	1400
1351	TGGACCAAAAATGACGATTTTGCGGCACGTAATGAAATAGGTGTGGGAAA	1400
1401	CAACTTTGCCCTGGAGATTAACCTTAATGCCAACCTATGGAGAAATTTCC	1450
1401	CAACTTTGCCCTGGAGATTAACCTTAATGCCAACCTATGGAGAAATTTCC	1450
1451	TCTACTCCAACATTGCACTGTACCTGCCTGACAAGCTAAAATACACTCCT	1500
1451	TCTACTCCAACATTGCACTGTACCTGCCTGACAAGCTAAAATACACTCCT	1500
1501	ACAAATGTGGAAATATCTCCCAACCCTAATTCATACGATTATATGAACAA	1550
1501	ACAAATGTGGAAATATCTCCCAACCCTAATTCATACGATTATATGAACAA	1550
1551	GCGAGTGGTGGCTCCCGGGTTGGTGGATTGCTACATTAACCTTGGAGCGC	1600
1551	GCGAGTGGTGGCTCCCGGGTTGGTGGATTGCTACATTAACCTTGGAGCGC	1600
1601	GTTGGTCATTGGACTACATGGACAACGTCAACCCCTTTAACCATCACCGC	1650
1601	GTTGGTCATTGGACTACATGGACAACGTCAACCCCTTTAACCATCACCGC	1650
1651	AATGCGGGCCTACGCTACCGCTCCATGTTGCTGGGCAACGGTCGCTACGT	1700
1651	AATGCGGGCCTACGCTACCGCTCCATGTTGCTGGGCAACGGTCGCTACGT	1700
1701	GCCCTTTTACATCCAGGTTCCCTCAGAAGTTTTTTGCCATTAAGAACCTCC	1750
1701	GCCCTTTTACATCCAGGTTCCCTCAGAAGTTTTTTGCCATTAAGAACCTCC	1750
1751	TACTCTTGCCGGGCTCATACACCTACGAGTGGAACCTCAGGAAAGATGTT	1800
1751	TACTCTTGCCGGGCTCATACACCTACGAGTGGAACCTCAGGAAAGATGTT	1800
1801	AACATGGTCCTGCAAAGCTCCCTAGGAAACGACCTAAGAGTTGACGGAGC	1850
1801	AACATGGTCCTGCAAAGCTCCCTAGGAAACGACCTAAGAGTTGACGGAGC	1850
1851	CAGCATTAAGTTTGACAGCATTTGCCTCTACGCCACCTT <b>Y</b> TTTCCGATGG	1900
1851	CAGCATTAAGTTTGACAGCATTTGCCTCTACGCCACCTT <b>T</b> TTTCCGATGG	1900
1901	CCCACAACACCGCCTCAACGCTTGAAGCCATGCTTAGAAACGACACCAAC	1950
1901	CCCACAACACCGCCTCAACGCTTGAAGCCATGCTTAGAAACGACACCAAC	1950
1951	GACCAGTCCTTTAACGACTACCTATCCGCCGCCAACATGCTTTACCCCAT	2000
1951	GACCAGTCCTTTAACGACTACCTATCCGCCGCCAACATGCTTTACCCCAT	2000
2001	ACCCGCCAACGCCACCAACGTGCCCATCTCTATCCCCTCGCGCAACTGGG	2050
2001	ACCCGCCAACGCCACCAACGTGCCCATCTCTATCCCCTCGCGCAACTGGG	2050

2051	CGGCTTTCCGAGGCTGGGCCTTTACGCGCCTTAAGACTAAGGAAACCCCA	2100
2051	CGGCTTTCCGAGGCTGGGCCTTTACGCGCCTTAAGACTAAGGAAACCCCA	2100
2101	TCCCTGGGTTCCGGCTACGACCCTTACTATACCTACTCTGGCTCCATACC	2150
2101	TCCCTGGGTTCCGGCTACGACCCTTACTATACCTACTCTGGCTCCATACC	2150
2151	CTACCTAGACGGAACCTTTTACCTTAATCACACCTTCAAAAAGGTGGCCA	2200
2151	CTACCTAGACGGAACCTTTTACCTTAATCACACCTTCAAAAAGGTAGCCA	2200
2201	TCACCTTTGACTCTTCTGTAGCTGGCCTGGCAATGACCGTCTGCTTACC	2250
2201	TCACCTTTGACTCTTCTGTAGCTGGCCTGGCAATGACCGTCTGCTTACC	2250
2251	CCCAACGAGTTTGAGATCAAGCGTTCAGTTGACGGAGAGGGCTACAACGT	2300
2251	CCCAACGAGTTTGAGATCAAGCGTTCAGTTGACGGAGAGGGCTACAACGT	2300
2301	TGCCCCAATGCAACATGACCAAAGACTGGTTCTTGGTACAGATGCTAGCCA	2350
2301	TGCCCCAATGCAACATGACCAAAGACTGGTTCTTGGTACAGATGCTAGCCA	2350
2351	ACTACAACATAGGCTACCAGGGCTTTTATATCCCAGAAAGCTATAAGGAC	2400
2351	ACTACAACATAGGCTACCAGGGCTTTTATATCCCAGAAAGCTATAAGGAC	2400
2401	CGCATGTACTCCTTCTTTAGAAACTTCCAGCCCATGAGCCGTCAGGTGGT	2450
2401	CGCATGTACTCCTTCTTTAGAAACTTCCAGCCCATGAGCCGTCAGGTGGT	2450
2451	GGACGATACCAAATACAAGGACTACCAACAGGTGGGCATCCTCCACCAGC	2500
2451	GGACGATACCAAATACAAGGACTACCAACAGGTGGGCATCCTCCACCAGC	2500
2501	ACAATAACTCTGGCTTTGTTGGTTACCTCGCTCCCACCATGCGAGAGGGA	2550
2501	ACAATAACTCTGGCTTTGTTGGTTACCTCGCTCCCACCATGCGAGAGGGA	2550
2551	CAGGCCTACCCCGCCAACTTCCCCTACCCGCTTATAGGCAAGACCGCGGT	2600
2551	CAGGCCTACCCCGCCAACTTCCCCTACCCGCTTATAGGCAAGACCGCGGT	2600
2601	TGACAGTATTACCCAGAAAAAGTTTCTTTGCGACCGCACCCCTTTGGCGCA	2650
2601	TGACAGTATTACCCAGAAAAAGTTTCTTTGCGACCGCACCCCTTTGGCGCA	2650
2651	TTCCATTCTCCAGTAACTTTATGTCCATGGGTGCACTCACAGACCTGGGC	2700
2651	TTCCATTCTCCAGTAACTTTATGTCCATGGGTGCACTCACAGACCTGGGC	2700
2701	CAAAACCTTCTCTATGCAAACCTCCGCCCACGCGCTAGATATGACTTTTGA	2750
2701	CAAAACCTTCTCTATGCAAACCTCCGCCCACGCGCTAGATATGACTTTTGA	2750

2751	GGTGGATCCCATGGACGAGCCCACCCTTCTTTATGTTTTGTTTGAAGTCT	2800
2751	GGTGGATCCCATGGACGAGCCCACCCTTCTTTATGTTTTGTTTGAAGTCT	2800
2801	TTGACGTGGTCCGTGTGCACCAGCCGCACCGCGGCGTCATCGAGACCGTG	2850
2801	TTGACGTGGTCCGTGTGCACCAGCCGCACCGCGGCGTCATCGAGACCGTG	2850
2851	TACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACAA.....	2900
2851	TACCTGCGCACGCCCTTCTCGGCCGGCAACGCCACAACAA.....	2900

Mismatched sequences are printed in bold. The r-strands are shown.