

Table S1. Generated custom probe set for human adenovirus type 5

Gene	Targeted Region	Target Sequence
E1A	470-570	TCATTATCACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTCCTGTGTCTGAACCT
E1B_19K	131-231	GGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAGGTC
E1B_55K	741-841	GGTACGGTTTTCTGGCCAATACCAACCTTATCCTACACGGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCCTGGACCGATGTAAGGGTTC
IX	261-361	AGTGCAGCTTCCCGTTCATCCGCCCGCGATGACAAGTTGACGGCTCTTTGGCACAATTGGATTCTTTGACCCGGGAACCTAATGTCGTTTCTCAGCAGC
IVa2	688-788	GAACCATTATACCGCAGTCTGGCACCCCTCCGCCCGCGCTTTGTAAAAATGGCCTATGACGATCTCATCCTGGAACACAACCTATGACGTTAGTGATCCCAG
pol	1323-1423	CGCATCACACGCAACTTTATGCCTCGCGGGGAAAGATACTCTTCAACGATGTACCTTCGCCCTGCCAAATCCGCGTTCAAAAAGCGCACGGACTTTT
pTP	278-378	TTGCAACGACTACGTATTTGACTCGAGGGCTTACTCGCGTCTCAGGTACACCGAGCTCTCGCAGCCGGGTCACCAGACCGTTAACTGGTCCGTTATGGCC
VA1_RNA	24-124	ATAAATTCGCAAGGGTATCATGGCGGACGACCGGGGTTTCGAGCCCCGTATCCGGCCGTCCGCCGTGATCCATGCGGTTACCGCCCCGCGTGTCGAACCCAG
VA2_RNA	61-161	CGAGTCTCGGACCGGCCGACTGCGGGCAACGGGGGTTTGCCTCCCCGTATGCAAGACCCCGCTTGCAAATTCCTCCGAAACAGGGACGAGCCCCCTT
52K	787-887	ACAAGGTGGCCGCCATCAACTATTCCATGCTTAGCCTGGGCAAGTTTTACGCCCGCAAGATATAACCATACCCCTTACGTTCCCATAGACAAGGAGGTA
pIIIa	1178-1278	CCCTGGTTTCTACACCGGGGATTCGAGGTGCCCCGAGGGTAACGATGGATTCTCTGGGACGACATAGACGACAGCGTGTTTCCCCGCAACCGCAGACC

Table S1. (table continued).

Gene	Targeted Region	Target Sequence
III	362-462	CGACCTGAAAACCATCCTGCATACCAACATGCCAAATGTGAACGAGTTCATGTTTACCAATAAGTTTAAGGCGCGGGTGATGGTGTGCGCCTGCCTACT
pVII	217-317	CCACGCCGCCACCAGTGTCCACAGTGGACGCGGCCATTCAGACCGTGGTGC GCGGAGCCCGGCGCTATGCTAAAATGAAGAGACGGCGGAGGGCGGTAGC
V	186-286	CGGGTACAGTGAAAAGGTGACGCGTAAAACGTGTTTTGCGACCCGGCACCACCGTAGTCTTTACGCCCGGTGAGCGCTCCACCCGCACCTACAAGCGCG
pX	84-184	CTGACGGGCGGCATGCGTCGTGCGCACCCGCGCGGCGCGCGTGCACCGTCGCATGCGCGGCGGTATCCTGCCCTCCTTATTCCACTGATCGCCG
pVI	88-188	TGAGCGGTGGCGCCTTCAGCTGGGGCTCGCTGTGGAGCGGCATTA AAAAATTCGGTTCACCGTTAAGAACTATGGCAGCAAGGCTGGAACAGCAGCAC
hexon	2298-2398	CTGGTACAAATGCTAGCTAACTACAACATTGGCTACCAGGGCTTCTATATCCCAGAGAGCTACAAGGACCGCATGTACTCCTTCTTTAGAACTTCCAGC
protease	189-289	TCAAAAACATGCTACCTCTTTGAGCCCTTTGGCTTTTCTGACCAGCGACTCAAGCAGGTTTACCAGTTTGAGTACGAGTCACTCCTGCGCCGTAGCGCCA
DBP	1049-1149	TTCCGGCAAGTCTTGCGGCATGTTCTTCTCTGAAGGCGCAAAGGCTCAGGTGGCTTTTAAGCAGATCAAGGCTTTTATGCAGGGCGCTGTATCCTAACGCC
100K	1521-1621	TCAGGAATCTTGCCCGCCACCTGCTGTGCACTTCTTAGCGACTTTGTGCCATTAAGTACCGCGAATGCCCTCCGCCGCTTTGGGGCCACTGCTACCTTC
33K	460-560	CCAACGAACCCGTATCGACCCGCGAGCTTAGAAACAGGATTTTTCCACTCTGTATGCTATATTTCAACAGAGCAGGGGCCAAGAACAAGAGCTGAAAAT
22K	367-467	GCTACCGCTCATGGCGGGGCACAAGAACGCCATAGTTGCTTGCTTGCAAGACTGTGGGGGCAACATCTCCTTCGCCCGCGCTTTCTTCTTACCATCA

Table S1. (table continued).

Gene	Targeted Region	Target Sequence
pVIII	112-212	CCCACATGATATCCCGGGTCAACGGAATCCGCGCCACCGAAACCGAATTCTCTTGGAACAGGCGGCTATTACCACCACACCTCGTAATAACCTTAATCC
E3_12.5K	39-139	CTGGTCCACTGTCGCCGCCACAAGTGCTTTGCCCGGACTCCGGTGAGTTTTGCTACTTTGAATTGCCCGAGGATCATATCGAGGGCCCGCGCACGGCG
E3_CR1-alpha0	85-185	TCTTTATICTTATACTAACGCTTCTCTGCCTAAGGCTCGCCGCTGCTGTGTGCACATTTGCATTTATTGTCAGCTTTTTAAACGCTGGGGTCGCCACCC
E3_gp19K	0-100	ATGATTAGGTACATAATCCTAGGTTTACTCACCTTGCCTCAGCCACGGTACCACCCAAAAGGTGGATTTTAAGGAGCCAGCCTGTAATGTTACATTCG
10.5_kD	23-123	CGCCGCTACCGGACTTACATCTACCACAAAATACACCCCAAGTTTCTGCCCTTTGTCATAACTGGGATAACTTGGGCATGTGGTGGTTCTCCATAGCGCTT
E3_RID-alpha	158-258	CACTGTGGTCATCGCCTTTATCCAGTGCATTGACTGGGTCTGTGTGCGCTTTGCATATCTCAGACACCATCCCCAGTACAGGGACAGGACTATAGCTGAG
E3_RID-beta	145-245	CCGAAGCCTGGTTATATGCAATCATCTCTGTTATGGTGTCTGCAGTACCATCTTAGCCCTAGCTATATATCCCTACCTTGACATTGGCTGGAAACGAAT
E3_14.7K	87-187	CGCATGAATCAAGAGCTCCAAGACATGGTTAACTTGCACCAGTGCAAAAGGGGTATCTTTGTCTGGTAAAGCAGGCCAAAGTCACCTACGACAGTAATA
U_exon	5-105	GATAGTGGGTGCGGATGGACAGGAACAGGAGGAAACTGACATTCCATTTAGATTGTGGAGAAAGTTTGCAGCCAGGAGGAAGCTGCAATACCAGAGCTGG
fiber	592-692	CACAAAATGAAAACCTAGGACTAAAAGTACGGGGCTCCTTTCATGTAACAGACGACCTAAACACTTTGACCGTAGCAACTGGTCCAGGTGTGACTATTAA
E4_ORF6_7	321-421	GTGTGGAATATAACACCTAAGAATATGTCTGTTACCCATGATATGATGCTTTTTAAGGCCAGCCGGGGAGAAAGGACTGTGTACTCTGTGTGTTGGGAGG
ACTB	1062-1162	ATCAAGATCATTGCTCCTCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCCACCTTCCAGCAGATGTGGATCAGCAAGC
CLTC	290-390	GGGTATCAACCCAGCAAACATTGGCTTCAGTACCCTGACTATGGAGTCTGACAAATTCATCTGCATTAGAGAAAAAGTAGGAGAGCAGGCCAGGTGGTA
HPRT1	354-454	TAGCCCTCTGTGTGCTCAAGGGGGCTATAAATTCTTTGCTGACCTGCTGGATTACATCAAAGCACTGAATAGAAATAGTGATAGATCCATTCCTATGAC