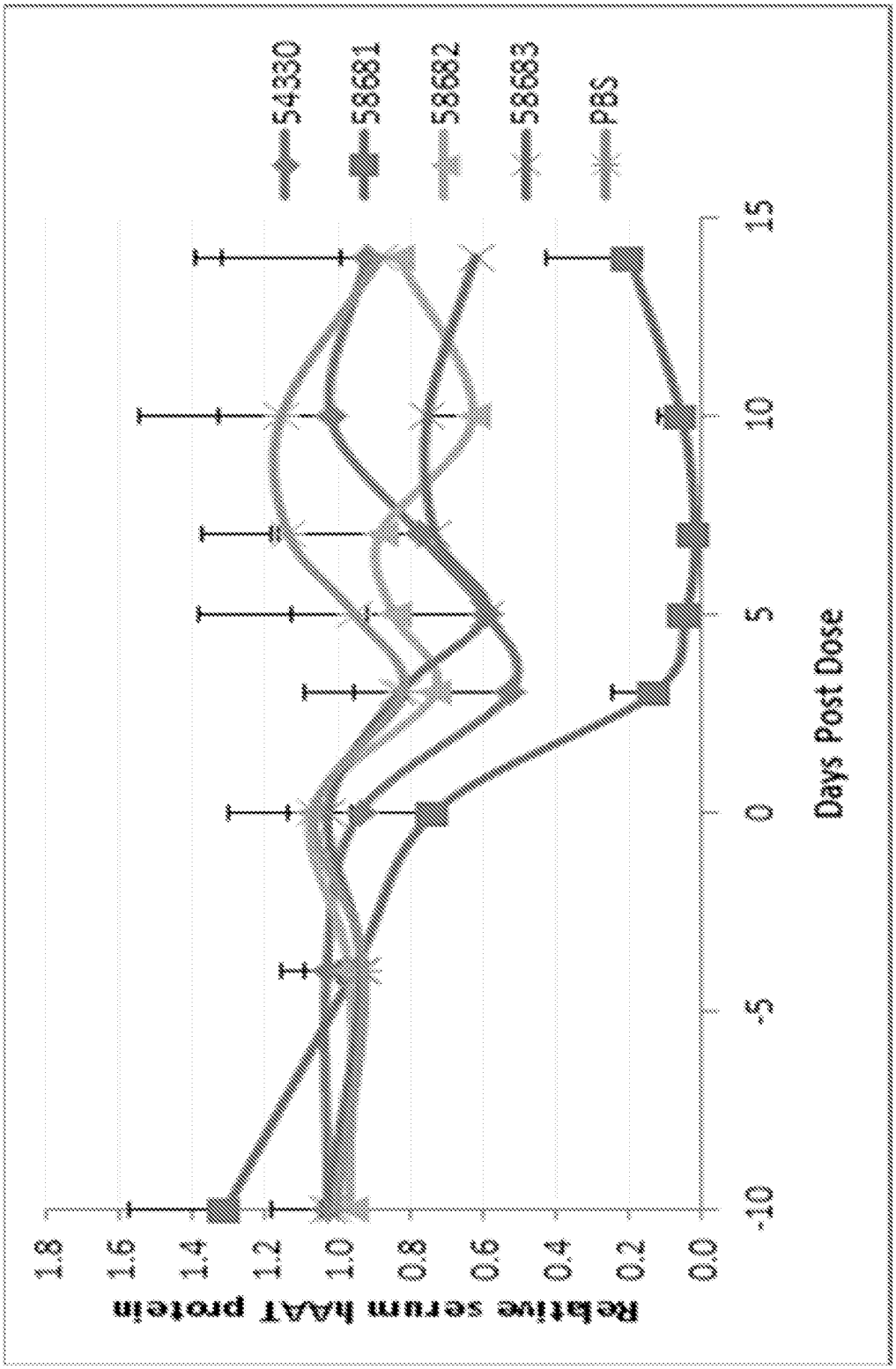

54330
58681
58682
58683
PBS
Relative serum hAAT protein
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-10
-5
0
5
10
15
Days Post Dose

Figure 1

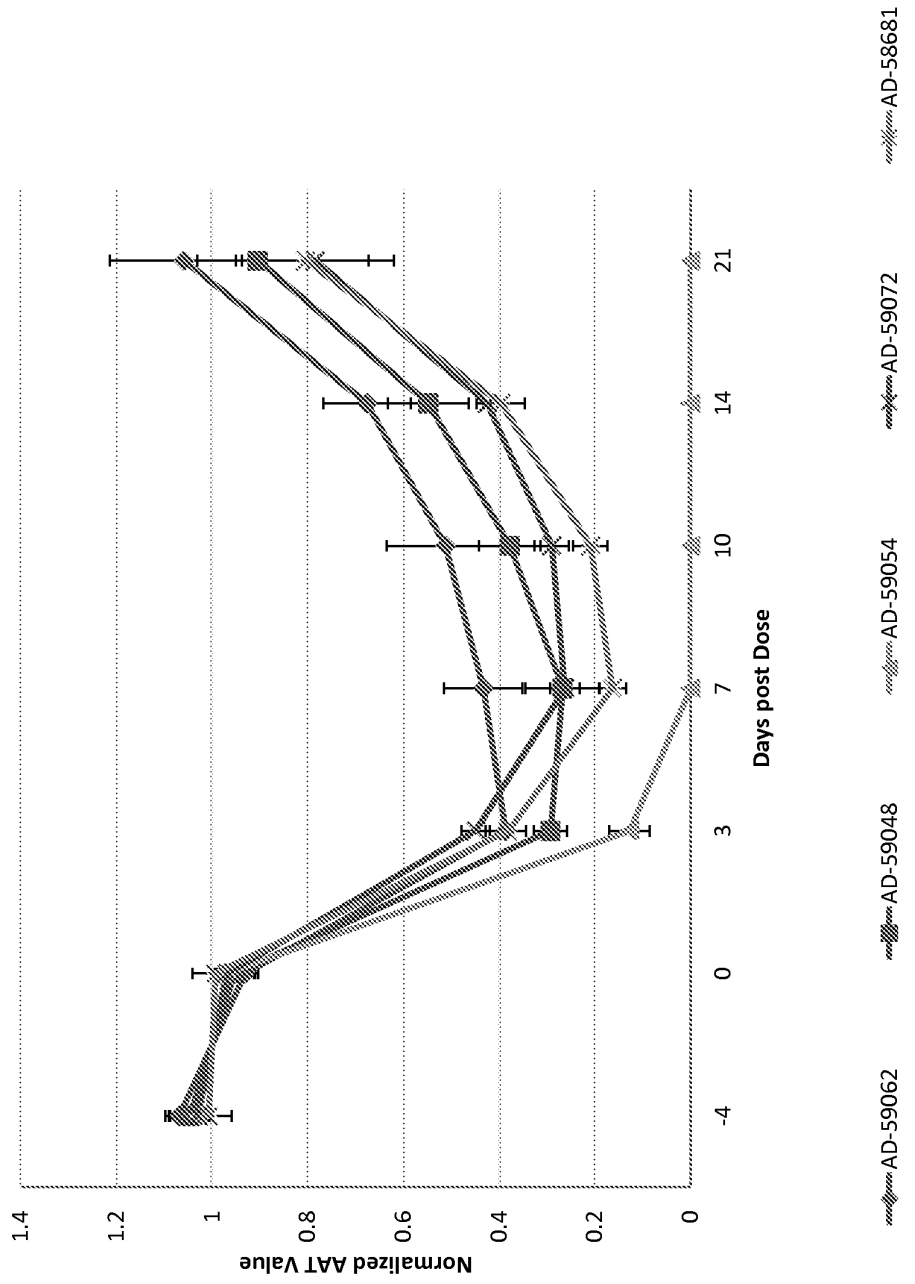

Normalized AAT Value
1.4
1.2
1
0.8
0.6
0.4
0.2
0
-4
0
3
7
10
14
21
Days post Dose
AD-59062
AD-59048
AD-59054
AD-59072
AD-58681

Figure 2A

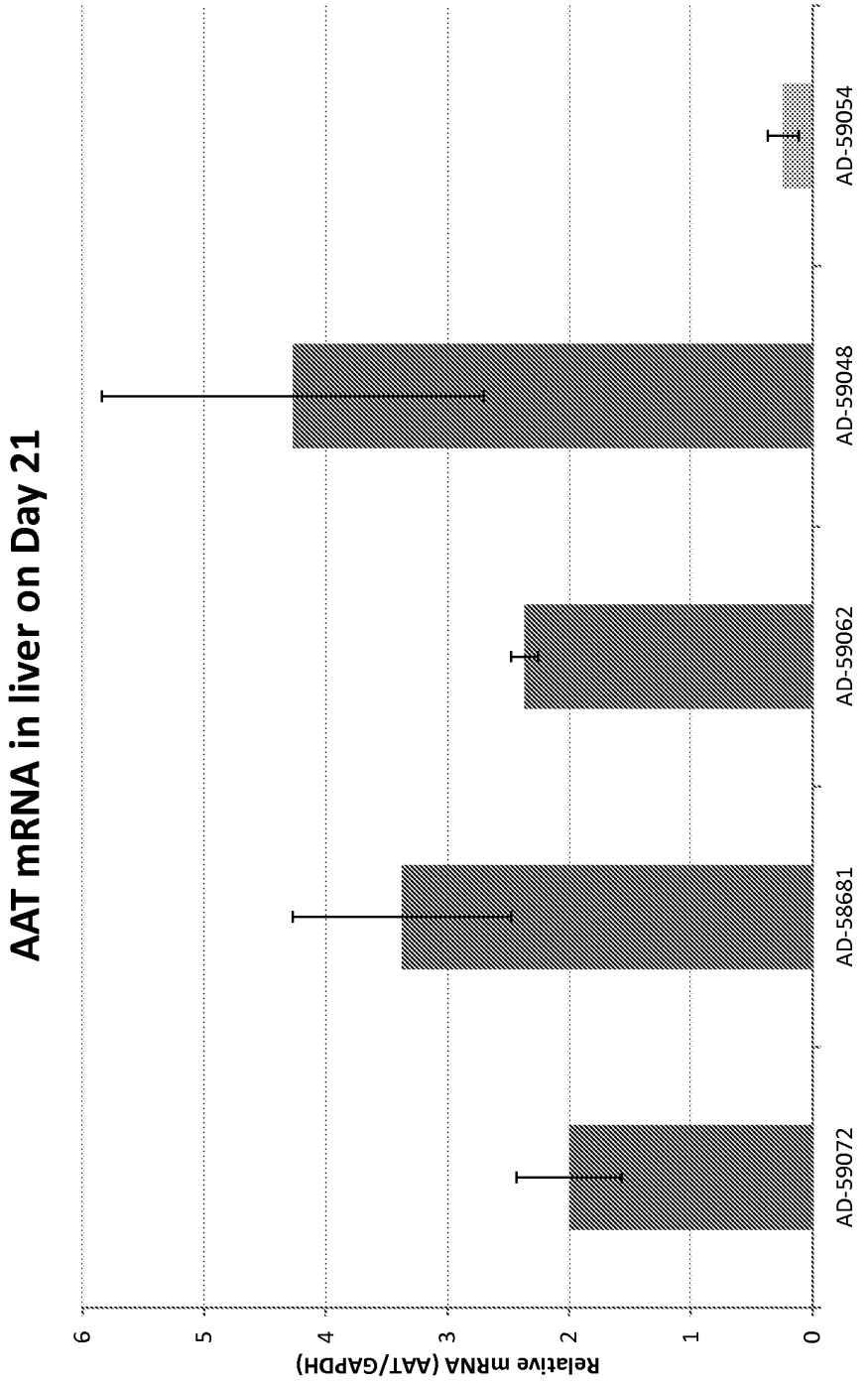

AAT mRNA in liver on Day 21
Relative mRNA (AAT/GAPDH)
0
1
2
3
4
5
6
AD-59072
AD-58681
AD-59062
AD-59048
AD-59054

Figure 2B

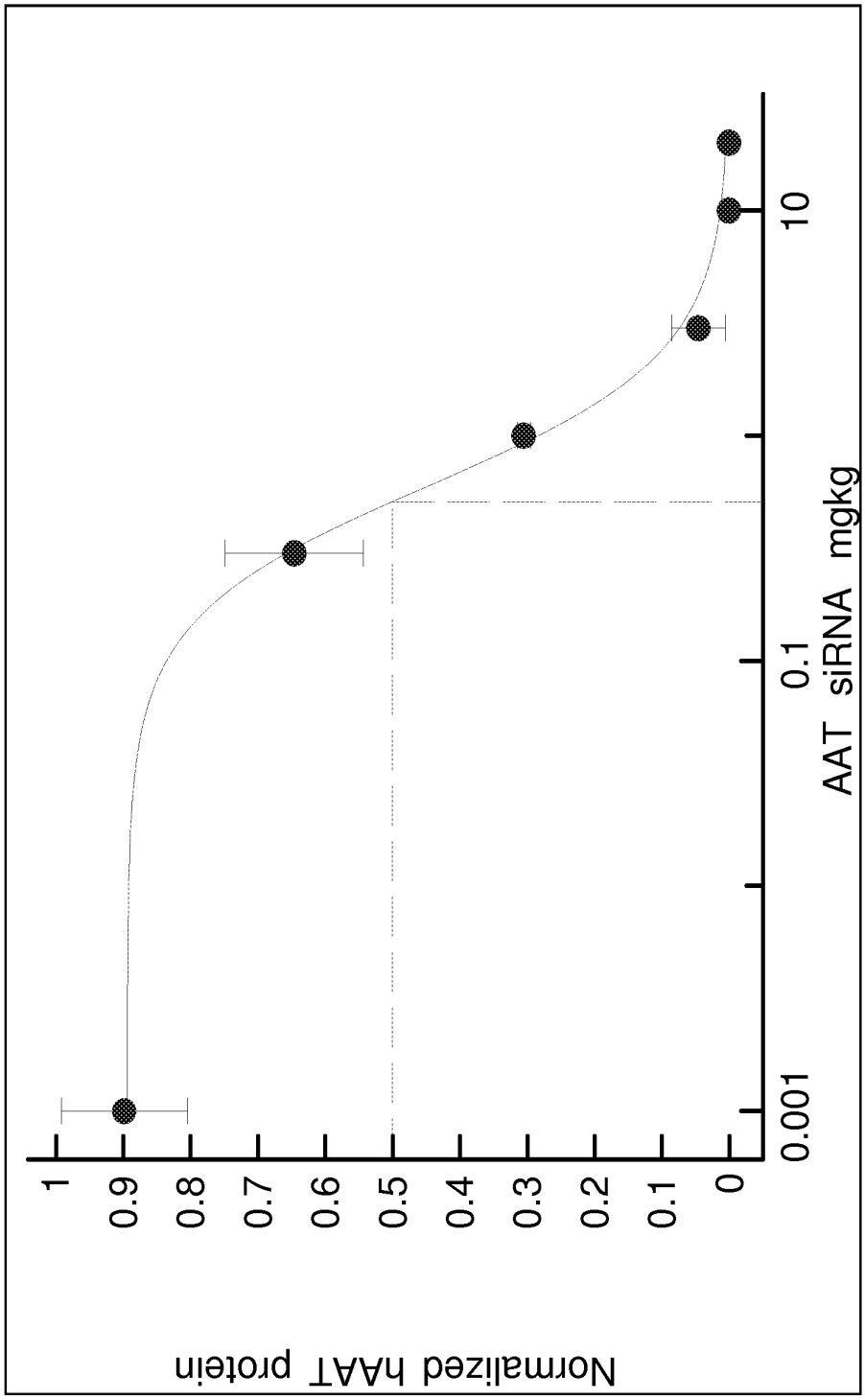

Normalized hAAT protein
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0.001
0.1
10
AAT siRNA mgkg

Figure 3A

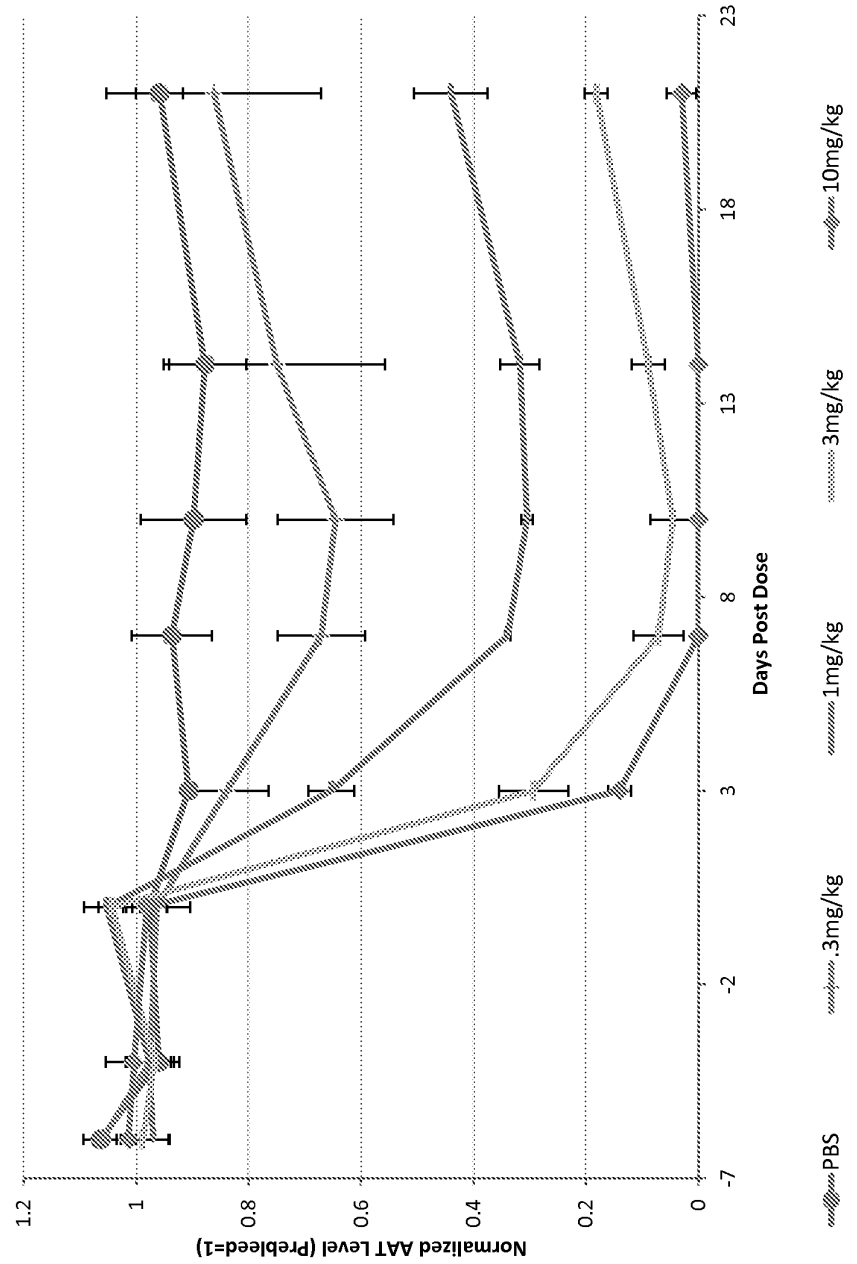

Normalized AAT Level (Prebleed=1)
1.2
1
0.8
0.6
0.4
0.2
0
-7
-2
3
8
13
18
23
Days Post Dose
PBS
.3mg/kg
1mg/kg
3mg/kg
10mg/kg

Figure 3B

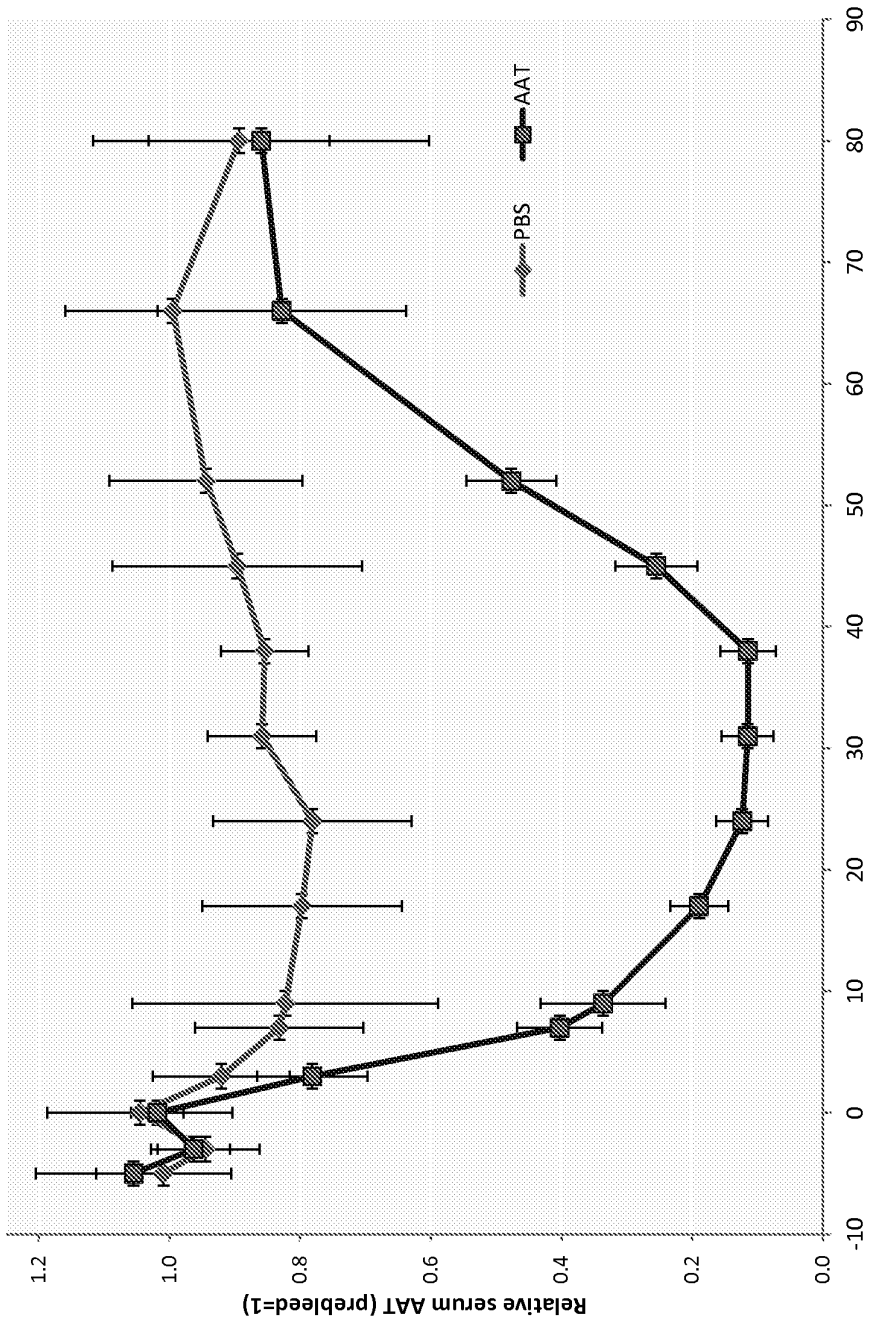

Relative serum AAT (prebleed=1)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-10
0
10
20
30
40
50
60
70
80
90
PBS
AAT

Figure 3C

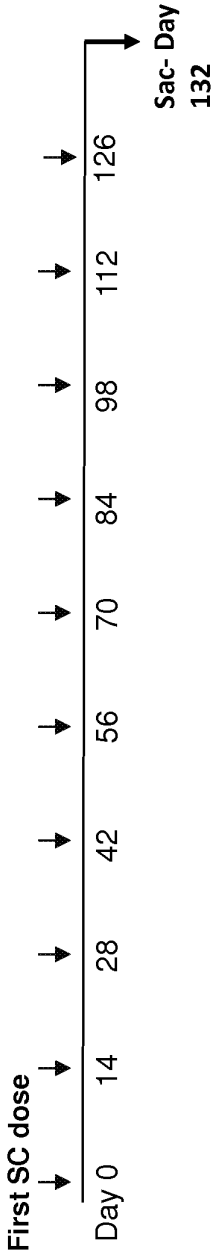


Figure 4A

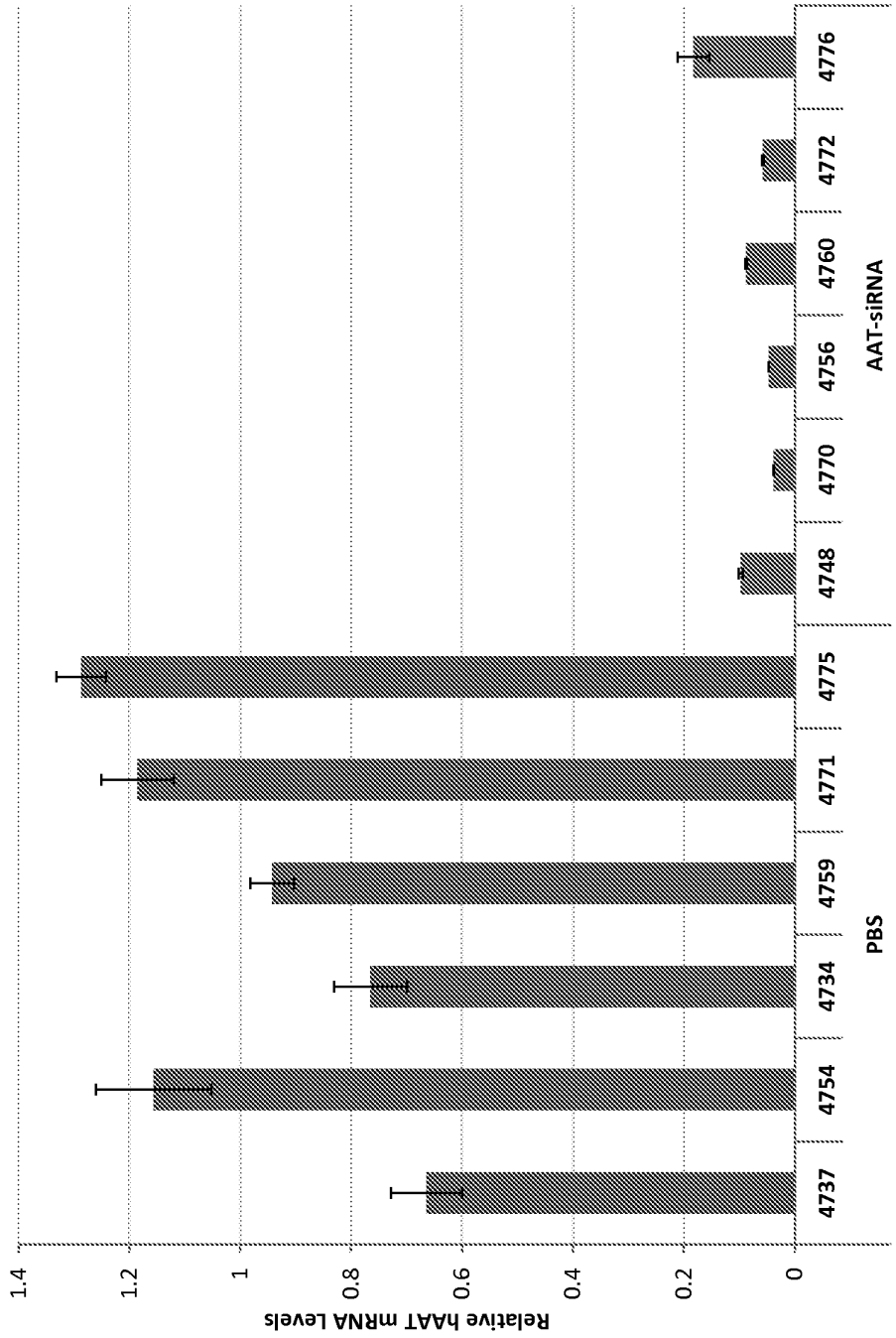

Relative hAAT mRNA Levels
1.4
1.2
1
0.8
0.6
0.4
0.2
0
PBS
4737
4754
4734
4759
4771
4775
4748
4770
4756
4760
4772
4776
AAT-siRNA

Figure 4B

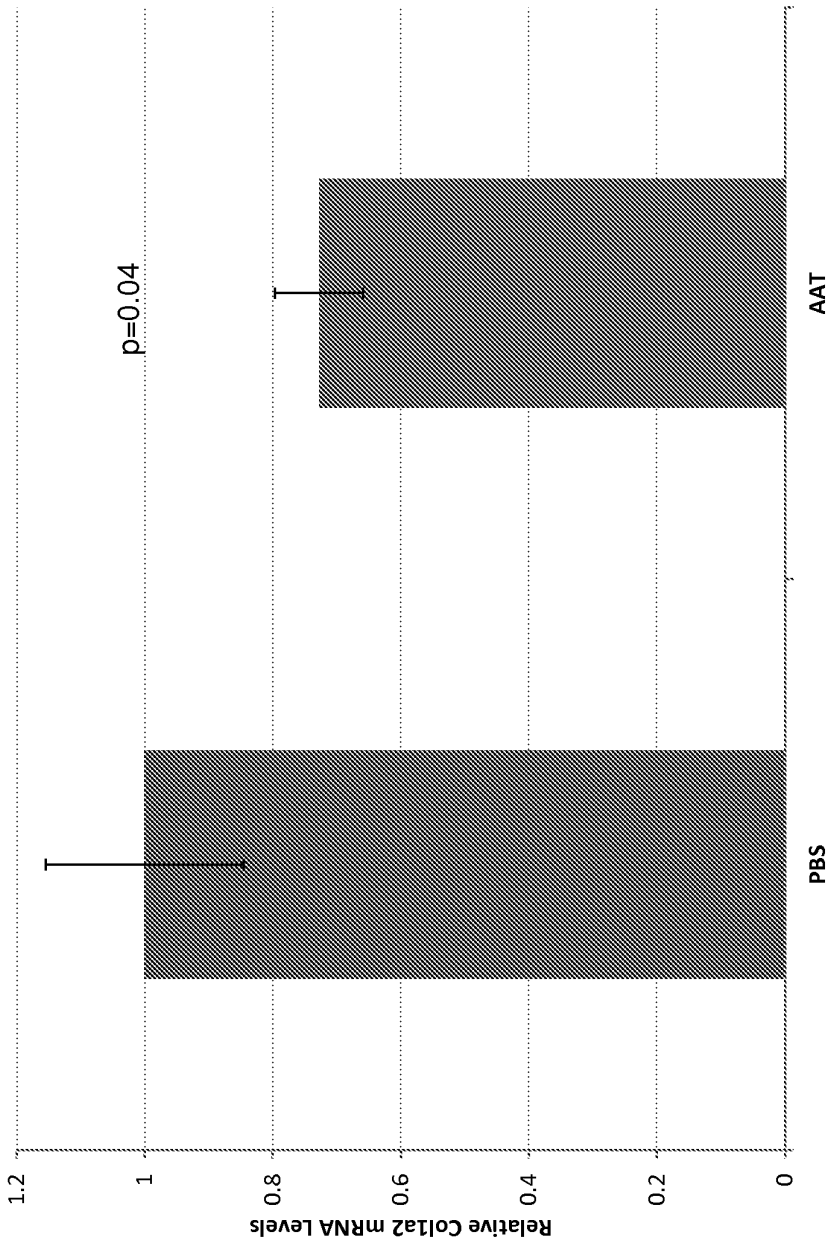


Figure 4C

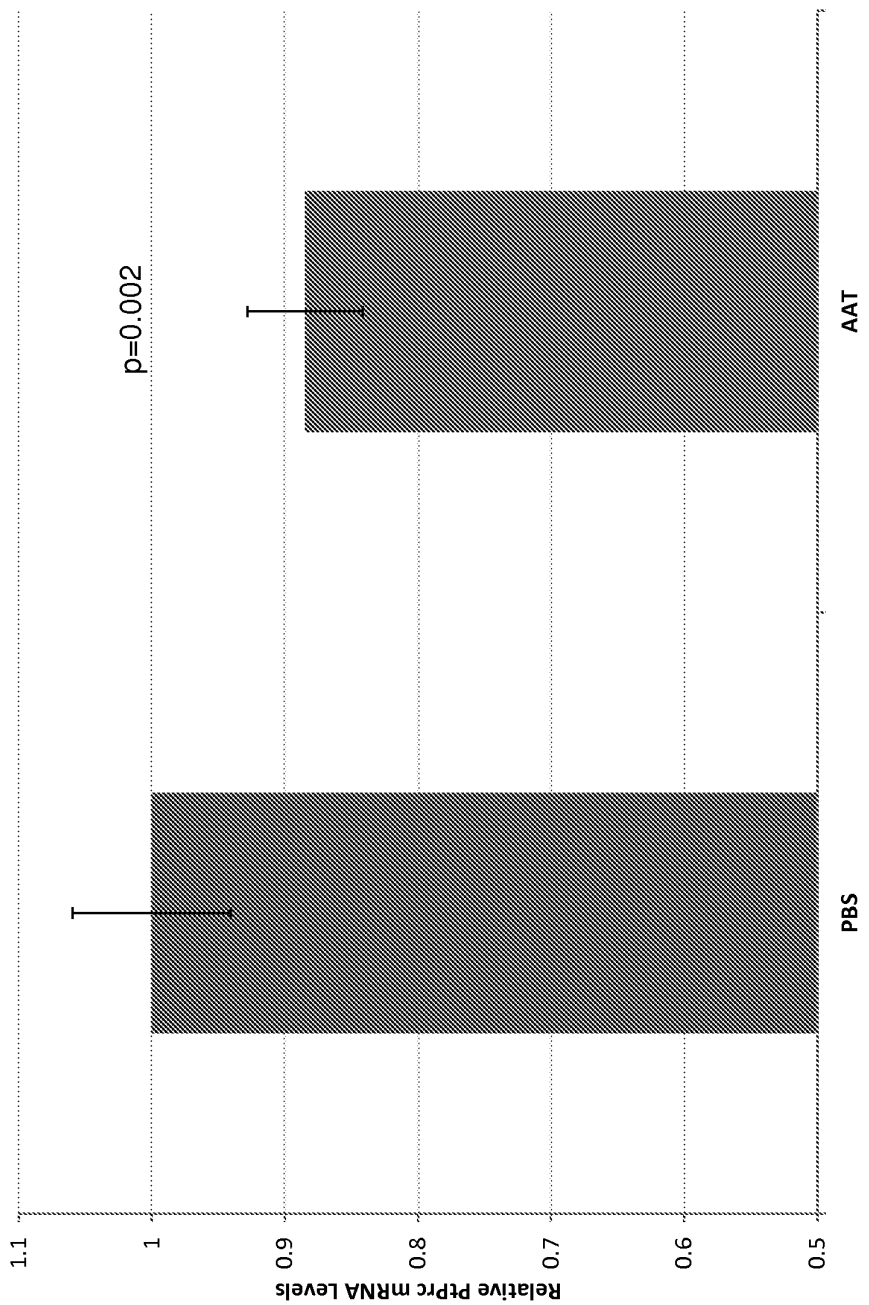


Figure 4D

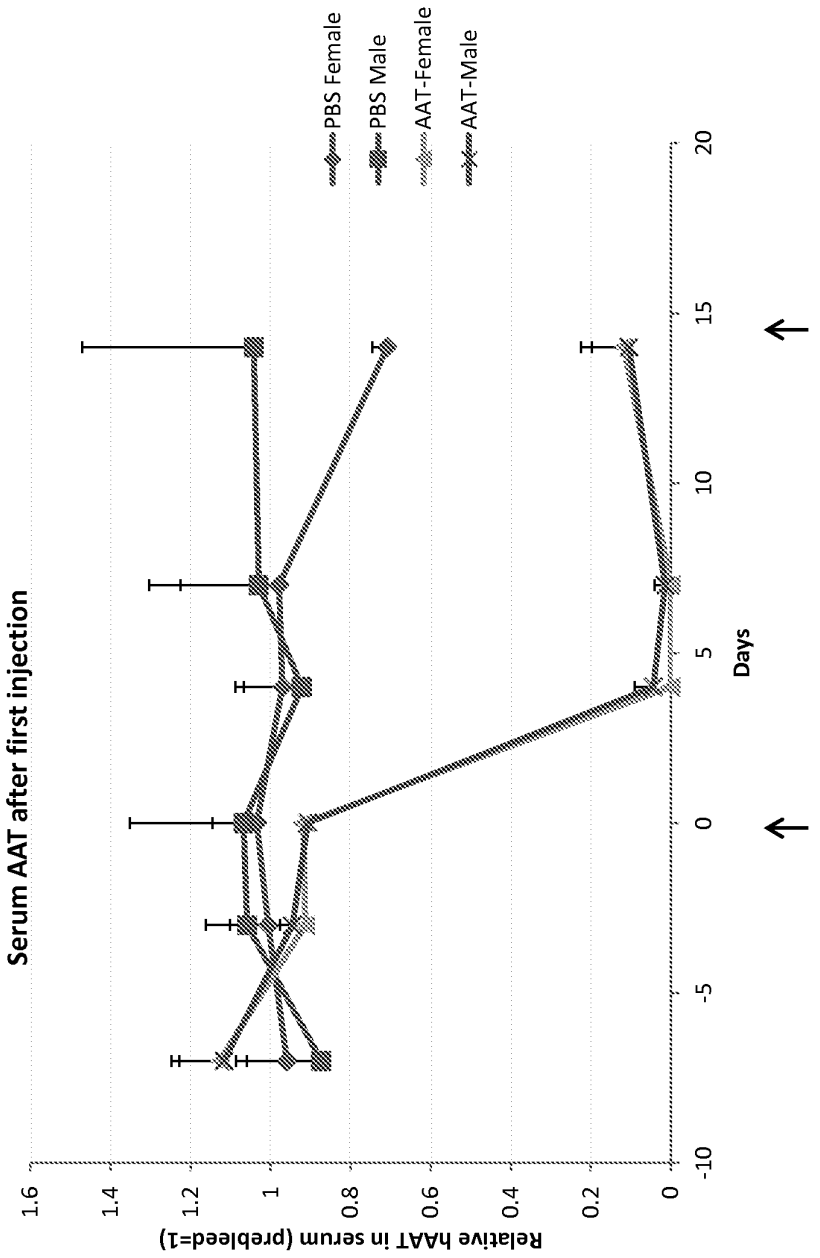

Serum AAT after first injection
Relative hAAT in serum (prebleed=1)
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
-10
-5
0
5
10
15
20
Days
PBS Female
PBS Male
AAT-Female
AAT-Male

Figure 5A

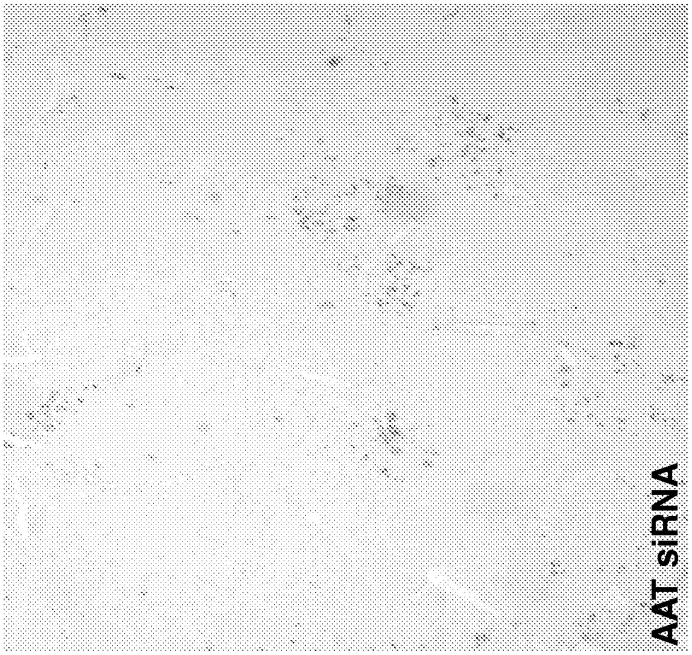


Figure 5C

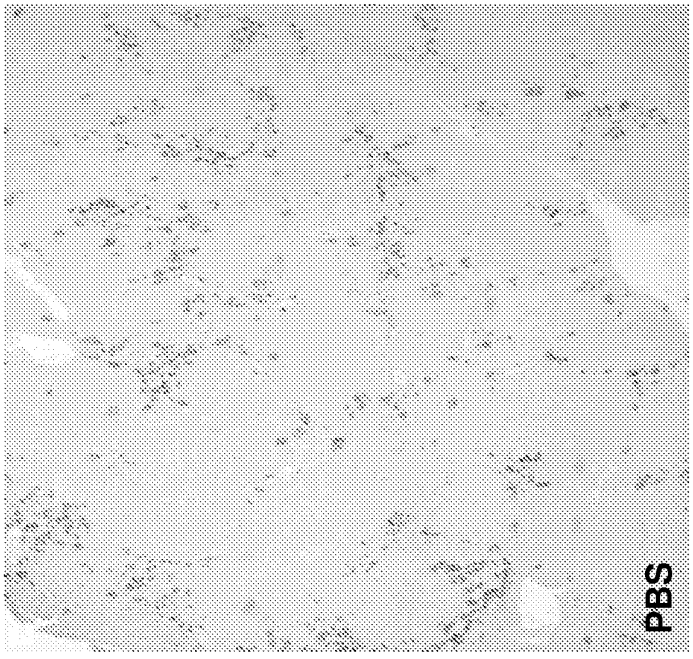


Figure 5B

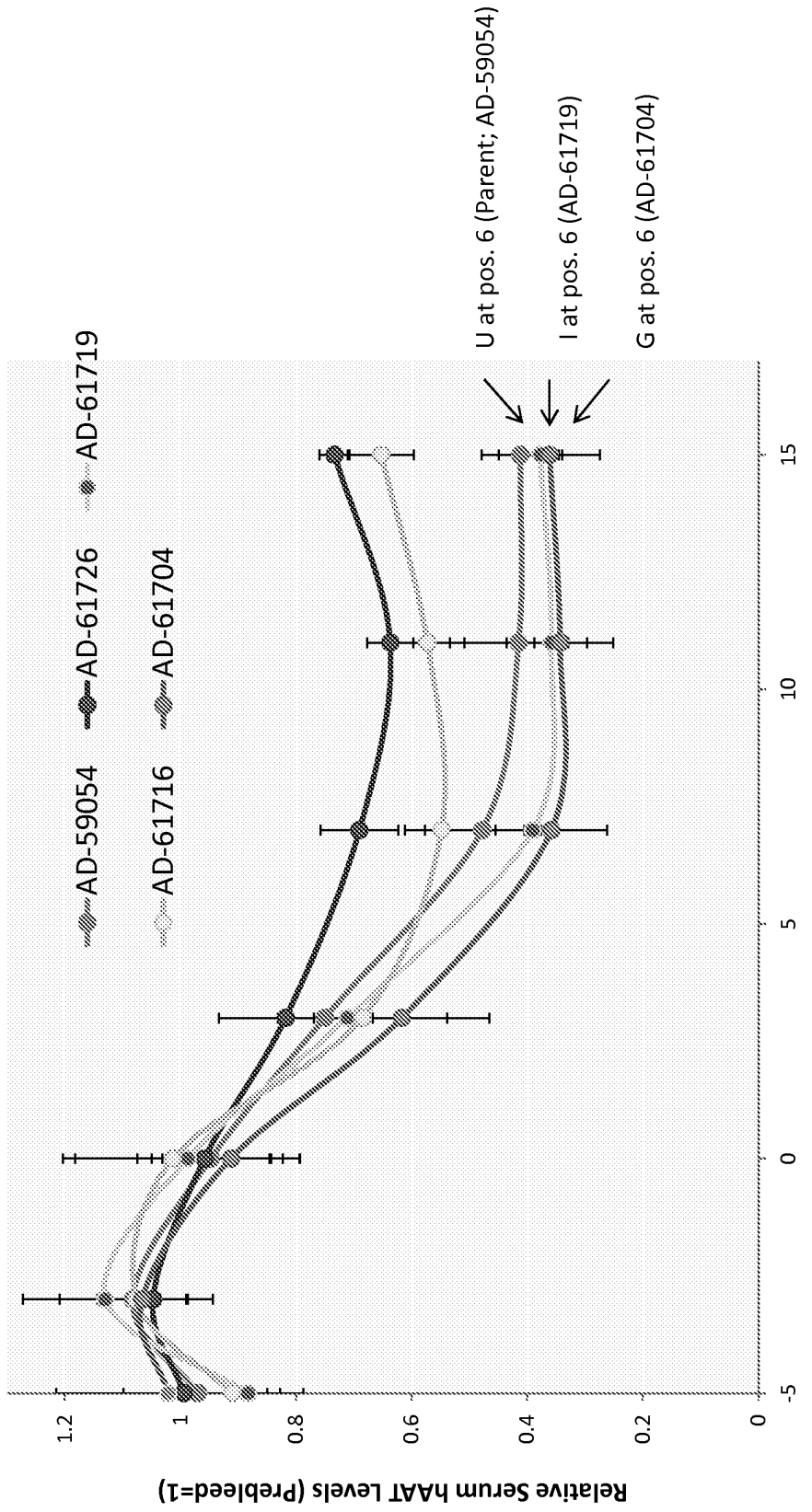

Relative Serum hAAT Levels (Prebleed=1)
1.2
1
0.8
0.6
0.4
0.2
0
-5
0
5
10
15
Day Post Dosing
AD-59054
AD-61726
AD-61719
AD-61716
AD-61704
U at pos. 6 (Parent; AD-59054)
I at pos. 6 (AD-61719)
G at pos. 6 (AD-61704)

Figure 6

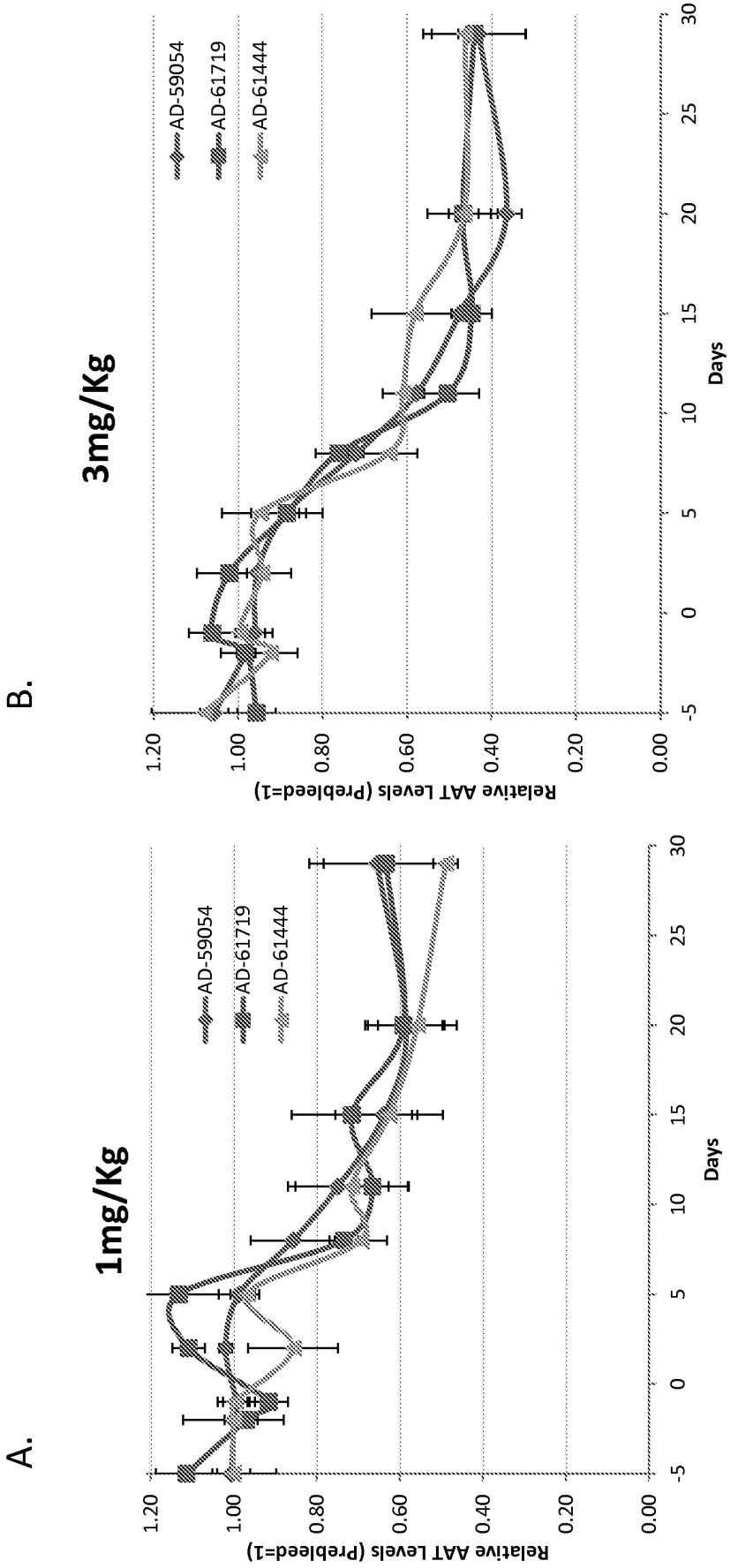

A.
1mg/Kg
B.
3mg/Kg
AD-59054
AD-61719
AD-61444
Relative AAT Levels (Prebleed=1)
Days
1.20
1.00
0.80
0.60
0.40
0.20
0.00
-5
0
5
10
15
20
25
30

Figure 7

>gi|189163524|ref|NM_000295.4| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 1, mRNA

ACAATGACTCCTTTCGGTAAGTGCAGTGGAAGCTGTACACTGCCCAGGCAAAGCGTCCGGGCAGCGTAGG
CGGGCGACTCAGATCCCAGCCAGTGGACTTAGCCCCTGTTTGCTCCTCCGATAACTGGGGTGACCTTGGT
TAATATTCACCAGCAGCCTCCCCCGTTGCCCCTCTGGATCCACTGCTTAAATACGGACGAGGACAGGGCC
CTGTCTCCTCAGCTTCAGGCACCACCACTGACCTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGT
GGGGCATCCTCCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGATCCCCAGGGAGA
TGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCCCCAAC
CTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAATATCTTCTTCT
CCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATGAAAT
CCTGGAGGGCCTGAATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTC
CTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTCCTCAGCGAGG
GCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTCACTGTCAA
CTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTACGTGGAGAAGGGTACTCAAGGGAAAATT
GTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTCTTTAAAGGCA
AATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAGAGGACTTCCACGTGGACCAGGTGACCACCGT
GAAGGTGCCTATGATGAAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAGCTGGGTG
CTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAACTACAGCACC
TGGAAAATGAACTCACCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGCCAGCTT
ACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTCCTGGGTCAACTGGGCATCACT
AAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAGGCCG
TGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCAT
ACCCATGTCTATCCCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACC
AAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAATAACTGCCTCTCGCTCCTCAACCCC
TCCCCTCCATCCCTGGCCCCCTCCCTGGATGACATTAAAGAAGGGTTGAGCTGGTCCCTGCCTGCATGTG
ACTGTAAATCCCTCCCATGTTTTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGTATGTGGGCTCCAGGTA
ACAGTGCTGTCTTCGGGCCCCCTGAACTGTGTTCATGGAGCATCTGGCTGGGTAGGCACATGCTGGGCTT
GAATCCAGGGGGGACTGAATCCTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAGGGCTCCAGTCTTC
CTTGTCCTGTCTTGGAGTCCCCAAGAAGGAATCACAGGGGAGGAACCAGATACCAGCCATGACCCCAGGC
TCCACCAAGCATCTTCATGTCCCCCTGCTCATCCCCCACTCCCCCCCACCCAGAGTTGCTCATCCTGCCA
GGGCTGGCTGTGCCCACCCCAAGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATCGTGCCGTGGCCCA
GTTTTGTGGCATCTGCAGCAACACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGCTGTCACCTAACCA
GACTCGGGCCCTGCACCTCTCAGGCACTTCTGGAAAATGACTGAGGCAGATTCTTCCTGAAGCCCATTCT
CCATGGGGCAACAAGGACACCTATTCTGTCCTTGTCCTTCCATCGCTGCCCCAGAAAGCCTCACATATCT
CCGTTTAGAATCAGGTCCCTTCTCCCCAGATGAAGAGGAGGGTCTCTGCTTTGTTTTCTCTATCTCCTCC
TCAGACTTGACCAGGCCCAGCAGGCCCCAGAAGACCATTACCCTATATCCCTTCTCCTCCCTAGTCACAT
GGCCATAGGCCTGCTGATGGCTCAGGAAGGCCATTGCAAGGACTCCTCAGCTATGGGAGAGGAAGCACAT
CACCCATTGACCCCCGCAACCCCTCCCTTTCCTCCTCTGAGTCCCGACTGGGGCCACATGCAGCCTGACT
TCTTTGTGCCTGTTGCTGTCCCTGCAGTCTTCAGAGGGCCACCGCAGCTCCAGTGCCACGGCAGGAGGCT
GTTCCTGAATAGCCCCTGTGGTAAGGGCCAGGAGAGTCCTTCCATCCTCCAAGGCCCTGCTAAAGGACAC
AGCAGCCAGGAAGTCCCCTGGGCCCCTAGCTGAAGGACAGCCTGCTCCCTCCGTCTCTACCAGGAATGGC
CTTGTCCTATGGAAGGCACTGCCCCATCCCAAACTAATCTAGGAATCACTGTCTAACCACTCACTGTCAT
GAATGTGTACTTAAAGGATGAGGTTGAGTCATACCAAATAGTGATTTCGATAGTTCAAAATGGTGAAATT
AGCAATTCTACATGATTCAGTCTAATCAATGGATACCGACTGTTTCCCACACAAGTCTCCTGTTCTCTTA
AGCTTACTCACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCATCACCAAGCCCCCTAG
GATGACACCAGACCTGAGAGTCTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCTGACAGCTGTGTGA
CCTTCGTGAAGTCGCCAAACCTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCTTTGAGTTGGTATG
ATGTTCAAGTTAGATAACAAAATGTTTATACCCATTAGAACAGAGAATAAATAGAACTACATTTCTTGCA

Figure 8A

SEQ ID NO:2
>gi|189163525|ref|NM_001002235.2| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 3, mRNA

TGGGCAGGAACTGGGCACTGTGCCCAGGGCATGCACTGCCTCCACGCAGCAACCCTCAGAGTCCTGAGCT
GAACCAAGAAGGAGGAGGGGGTCGGGCCTCCGAGGAAGGCCTAGCCGCTGCTGCTGCCAGGAATTCCAGG
TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
AGGAGAGCTTGAGGAGAGCAGGAAAGGACAATGCCGTCTTCTGTCTCGTGGGGCATCCTCCTGCTGGCAG
GCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGATCCCCAGGGAGATGCTGCCCAGAAGACAGATAC
ATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGC
CTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAG
CCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGAATTTCAA
CCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCCGTACCCTCAACCAGCCA
GACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTCCTCAGCGAGGGCCTGAAGCTAGTGGATAAGT
TTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTCACTGTCAACTTCGGGGACACCGAAGAGGC
CAAGAAACAGATCAACGATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTT
GACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGAAG
TCAAGGACACCGAGGAAGAGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATGAAGCG
TTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAGCTGGGTGCTGCTGATGAAATACCTGGGC
AATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACCCACG
ATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCAT
TACTGGAACCTATGATCTGAAGAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGGCT
GACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCA
TCGACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCGA
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCTCTTCATGGGA
AAAGTGGTGAATCCCACCCAAAAATAACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCC
TCCCTGGATGACATTAAAGAAGGGTTGAGCTGGTCCCTGCCTGCATGTGACTGTAAATCCCTCCCATGTT
TTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGTATGTGGGCTCCAGGTAACAGTGCTGTCTTCGGGCCCC
CTGAACTGTGTTCATGGAGCATCTGGCTGGGTAGGCACATGCTGGGCTTGAATCCAGGGGGGACTGAATC
CTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAGGGCTCCAGTCTTCCTTGTCCTGTCTTGGAGTCCC
CAAGAAGGAATCACAGGGGAGGAACCAGATACCAGCCATGACCCCAGGCTCCACCAAGCATCTTCATGTC
CCCCTGCTCATCCCCCACTCCCCCCCACCCAGAGTTGCTCATCCTGCCAGGGCTGGCTGTGCCCACCCCA
AGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATCGTGCCGTGGCCCAGTTTTGTGGCATCTGCAGCAA
CACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGCTGTCACCTAACCAGACTCGGGCCCTGCACCTCTC
AGGCACTTCTGGAAAATGACTGAGGCAGATTCTTCCTGAAGCCCATTCTCCATGGGGCAACAAGGACACC
TATTCTGTCCTTGTCCTTCCATCGCTGCCCCAGAAAGCCTCACATATCTCCGTTTAGAATCAGGTCCCTT
CTCCCCAGATGAAGAGGAGGGTCTCTGCTTTGTTTTCTCTATCTCCTCCTCAGACTTGACCAGGCCCAGC
AGGCCCCAGAAGACCATTACCCTATATCCCTTCTCCTCCCTAGTCACATGGCCATAGGCCTGCTGATGGC
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GCCCCTAGCTGAAGGACAGCCTGCTCCCTCCGTCTCTACCAGGAATGGCCTTGTCCTATGGAAGGCACTG
CCCCATCCCAAACTAATCTAGGAATCACTGTCTAACCACTCACTGTCATGAATGTGTACTTAAAGGATGA
GGTTGAGTCATACCAAATAGTGATTTCGATAGTTCAAAATGGTGAAATTAGCAATTCTACATGATTCAGT
CTAATCAATGGATACCGACTGTTTCCCACACAAGTCTCCTGTTCTCTTAAGCTTACTCACTGACAGCCTT
TCACTCTCCACAAATACATTAAAGATATGGCCATCACCAAGCCCCCTAGGATGACACCAGACCTGAGAGT
CTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCTGACAGCTGTGTGACCTTCGTGAAGTCGCCAAACC
TCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCTTTGAGTTGGTATGATGTTCAAGTTAGATAACAAA
ATGTTTATACCCATTAGAACAGAGAATAAATAGAACTACATTTCTTGCA

Figure 8B

SEQ ID NO:3
>gi|189163526|ref|NM_001002236.2| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 2, mRNA

TGGGCAGGAACTGGGCACTGTGCCCAGGGCATGCACTGCCTCCACGCAGCAACCCTCAGAGTCCTGAGCT
GAACCAAGAAGGAGGAGGGGGTCGGGCCTCCGAGGAAGGCCTAGCCGCTGCTGCTGCCAGGAATTCCAGG
TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
AGGAGAGCTTGAGGAGAGCAGGAAAGGGCGGCAGTAAGTCTTCAGCATCAGGCATTTTGGGGTGACTCAG
TAAATGGTAGATCTTGCTACCAGTGGAACAGCCACTAAGGATTCTGCAGTGAGAGCAGAGGGCCAGCTAA
GTGGTACTCTCCCAGAGACTGTCTGACTCACGCCACCCCCTCCACCTTGGACACAGGACGCTGTGGTTTC
TGAGCCAGGTACAATGACTCCTTTCGCAGCCTCCCCCGTTGCCCCTCTGGATCCACTGCTTAAATACGGA
CGAGGACAGGGCCCTGTCTCCTCAGCTTCAGGCACCACCACTGACCTGGGACAGTGAATCGACAATGCCG
TCTTCTGTCTCGTGGGGCATCCTCCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGG
ATCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAA
GATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACC
AATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACA
CTCACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGG
CTTCCAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTG
TTCCTCAGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAG
CCTTCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTACGTGGAGAAGGGTAC
TCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATC
TTCTTTAAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAGAGGACTTCCACGTGGACC
AGGTGACCACCGTGAAGGTGCCTATGATGAAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCT
GTCCAGCTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGG
AAACTACAGCACCTGGAAAATGAACTCACCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAA
GGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTCCTGGGTCA
ACTGGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAG
CTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTGCTGGGGCCATGT
TTTTAGAGGCCATACCCATGTCTATCCCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGAT
TGAACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAATAACTGCCTCTC
GCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCCCTGGATGACATTAAAGAAGGGTTGAGCTGGTCC
CTGCCTGCATGTGACTGTAAATCCCTCCCATGTTTTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGTATG
TGGGCTCCAGGTAACAGTGCTGTCTTCGGGCCCCCTGAACTGTGTTCATGGAGCATCTGGCTGGGTAGGC
ACATGCTGGGCTTGAATCCAGGGGGGACTGAATCCTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAG
GGCTCCAGTCTTCCTTGTCCTGTCTTGGAGTCCCCAAGAAGGAATCACAGGGGAGGAACCAGATACCAGC
CATGACCCCAGGCTCCACCAAGCATCTTCATGTCCCCCTGCTCATCCCCCACTCCCCCCCACCCAGAGTT
GCTCATCCTGCCAGGGCTGGCTGTGCCCACCCCAAGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATC
GTGCCGTGGCCCAGTTTTGTGGCATCTGCAGCAACACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGC
TGTCACCTAACCAGACTCGGGCCCTGCACCTCTCAGGCACTTCTGGAAAATGACTGAGGCAGATTCTTCC
TGAAGCCCATTCTCCATGGGGCAACAAGGACACCTATTCTGTCCTTGTCCTTCCATCGCTGCCCCAGAAA
GCCTCACATATCTCCGTTTAGAATCAGGTCCCTTCTCCCCAGATGAAGAGGAGGGTCTCTGCTTTGTTTT
CTCTATCTCCTCCTCAGACTTGACCAGGCCCAGCAGGCCCCAGAAGACCATTACCCTATATCCCTTCTCC
TCCCTAGTCACATGGCCATAGGCCTGCTGATGGCTCAGGAAGGCCATTGCAAGGACTCCTCAGCTATGGG
AGAGGAAGCACATCACCCATTGACCCCCGCAACCCCTCCCTTTCCTCCTCTGAGTCCCGACTGGGGCCAC
ATGCAGCCTGACTTCTTTGTGCCTGTTGCTGTCCCTGCAGTCTTCAGAGGGCCACCGCAGCTCCAGTGCC
ACGGCAGGAGGCTGTTCCTGAATAGCCCCTGTGGTAAGGGCCAGGAGAGTCCTTCCATCCTCCAAGGCCC
TGCTAAAGGACACAGCAGCCAGGAAGTCCCCTGGGCCCCTAGCTGAAGGACAGCCTGCTCCCTCCGTCTC
TACCAGGAATGGCCTTGTCCTATGGAAGGCACTGCCCCATCCCAAACTAATCTAGGAATCACTGTCTAAC
CACTCACTGTCATGAATGTGTACTTAAAGGATGAGGTTGAGTCATACCAAATAGTGATTTCGATAGTTCA
AAATGGTGAAATTAGCAATTCTACATGATTCAGTCTAATCAATGGATACCGACTGTTTCCCACACAAGTC
TCCTGTTCTCTTAAGCTTACTCACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCATCA
CCAAGCCCCCTAGGATGACACCAGACCTGAGAGTCTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCT
GACAGCTGTGTGACCTTCGTGAAGTCGCCAAACCTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCT
TTGAGTTGGTATGATGTTCAAGTTAGATAACAAAATGTTTATACCCATTAGAACAGAGAATAAATAGAAC
TACATTTCTTGCA

Figure 8C

SEQ ID NO:4
>gi|189163527|ref|NM_001127700.1| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 4, mRNA

TGGGCAGGAACTGGGCACTGTGCCCAGGGCATGCACTGCCTCCACGCAGCAACCCTCAGAGTCCTGAGCT
GAACCAAGAAGGAGGAGGGGGTCGGGCCTCCGAGGAAGGCCTAGCCGCTGCTGCTGCCAGGAATTCCAGG
TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
AGGAGAGCTTGAGGAGAGCAGGAAAGGTGGGACATTGCTGCTGCTGCTCACTCAGTTCCACAGGACAATG
CCGTCTTCTGTCTCGTGGGGCATCCTCCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTG
AGGATCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAA
CAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGC
ACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTG
ACACTCACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGA
AGGCTTCCAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAATGGC
CTGTTCCTCAGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAG
AAGCCTTCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTACGTGGAGAAGGG
TACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTAC
ATCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAGAGGACTTCCACGTGG
ACCAGGTGACCACCGTGAAGGTGCCTATGATGAAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAA
GCTGTCCAGCTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAG
GGGAAACTACAGCACCTGGAAAATGAACTCACCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACA
GAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTCCTGGG
TCAACTGGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTG
AAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTGCTGGGGCCA
TGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAAT
GATTGAACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAATAACTGCCT
CTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCCCTGGATGACATTAAAGAAGGGTTGAGCTGG
TCCCTGCCTGCATGTGACTGTAAATCCCTCCCATGTTTTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGT
ATGTGGGCTCCAGGTAACAGTGCTGTCTTCGGGCCCCCTGAACTGTGTTCATGGAGCATCTGGCTGGGTA
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GAGGGCTCCAGTCTTCCTTGTCCTGTCTTGGAGTCCCCAAGAAGGAATCACAGGGGAGGAACCAGATACC
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ATCGTGCCGTGGCCCAGTTTTGTGGCATCTGCAGCAACACAAGAGAGAGGACAATGTCCTCCTCTTGACC
CGCTGTCACCTAACCAGACTCGGGCCCTGCACCTCTCAGGCACTTCTGGAAAATGACTGAGGCAGATTCT
TCCTGAAGCCCATTCTCCATGGGGCAACAAGGACACCTATTCTGTCCTTGTCCTTCCATCGCTGCCCCAG
AAAGCCTCACATATCTCCGTTTAGAATCAGGTCCCTTCTCCCCAGATGAAGAGGAGGGTCTCTGCTTTGT
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TCCTCCCTAGTCACATGGCCATAGGCCTGCTGATGGCTCAGGAAGGCCATTGCAAGGACTCCTCAGCTAT
GGGAGAGGAAGCACATCACCCATTGACCCCCGCAACCCCTCCCTTTCCTCCTCTGAGTCCCGACTGGGGC
CACATGCAGCCTGACTTCTTTGTGCCTGTTGCTGTCCCTGCAGTCTTCAGAGGGCCACCGCAGCTCCAGT
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CTCTACCAGGAATGGCCTTGTCCTATGGAAGGCACTGCCCCATCCCAAACTAATCTAGGAATCACTGTCT
AACCACTCACTGTCATGAATGTGTACTTAAAGGATGAGGTTGAGTCATACCAAATAGTGATTTCGATAGT
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GTCTCCTGTTCTCTTAAGCTTACTCACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCA
TCACCAAGCCCCCTAGGATGACACCAGACCTGAGAGTCTGAAGACCTGGATCCAAGTTCTGACTTTTCCC
CCTGACAGCTGTGTGACCTTCGTGAAGTCGCCAAACCTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTG
CCTTTGAGTTGGTATGATGTTCAAGTTAGATAACAAAATGTTTATACCCATTAGAACAGAGAATAAATAG
AACTACATTTCTTGCA

Figure 8D

SEQ ID NO:5
>gi|189163529|ref|NM_001127701.1| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 5, mRNA

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GAACCAAGAAGGAGGAGGGGGTCGGGCCTCCGAGGAAGGCCTAGCCGCTGCTGCTGCCAGGAATTCCAGG
TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
AGGAGAGCTTGAGGAGAGCAGGAAAGGTGGGACATTGCTGCTGCTGCTCACTCAGTTCCACAGGGCGGCA
GTAAGTCTTCAGCATCAGGCATTTTGGGGTGACTCAGTAAATGGTAGATCTTGCTACCAGTGGAACAGCC
ACTAAGGATTCTGCAGTGAGAGCAGAGGGCCAGCTAAGTGGTACTCTCCCAGAGACTGTCTGACTCACGC
CACCCCCTCCACCTTGGACACAGGACGCTGTGGTTTCTGAGCCAGCAGCCTCCCCCGTTGCCCCTCTGGA
TCCACTGCTTAAATACGGACGAGGACAGGGCCCTGTCTCCTCAGCTTCAGGCACCACCACTGACCTGGGA
CAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCTCCTGCTGGCAGGCCTGTGCTGCCTGGTC
CCTGTCTCCCTGGCTGAGGATCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGG
ATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGC
ACACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCC
CTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTCCGG
AGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGCAATGGCCTGTTCCTCAGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAA
AAGTTGTACCACTCAGAAGCCTTCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG
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TGCTCTGGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAA
GAGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATGAAGCGTTTAGGCATGTTTAACA
TCCAGCACTGTAAGAAGCTGTCCAGCTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTT
CTTCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACCCACGATATCATCACCAAGTTC
CTGGAAAATGAAGACAGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATC
TGAAGAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCAC
AGAGGAGGCACCCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACT
GAAGCTGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCGAGGTCAAGTTCAACAAAC
CCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCAC
CCAAAAATAACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCCCTGGATGACATTAA
AGAAGGGTTGAGCTGGTCCCTGCCTGCATGTGACTGTAAATCCCTCCCATGTTTTCTCTGAGTCTCCCTT
TGCCTGCTGAGGCTGTATGTGGGCTCCAGGTAACAGTGCTGTCTTCGGGCCCCCTGAACTGTGTTCATGG
AGCATCTGGCTGGGTAGGCACATGCTGGGCTTGAATCCAGGGGGGACTGAATCCTCAGCTTACGGACCTG
GGCCCATCTGTTTCTGGAGGGCTCCAGTCTTCCTTGTCCTGTCTTGGAGTCCCCAAGAAGGAATCACAGG
GGAGGAACCAGATACCAGCCATGACCCCAGGCTCCACCAAGCATCTTCATGTCCCCCTGCTCATCCCCCA
CTCCCCCCCACCCAGAGTTGCTCATCCTGCCAGGGCTGGCTGTGCCCACCCCAAGGCTGCCCTCCTGGGG
GCCCCAGAACTGCCTGATCGTGCCGTGGCCCAGTTTTGTGGCATCTGCAGCAACACAAGAGAGAGGACAA
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GACTGAGGCAGATTCTTCCTGAAGCCCATTCTCCATGGGGCAACAAGGACACCTATTCTGTCCTTGTCCT
TCCATCGCTGCCCCAGAAAGCCTCACATATCTCCGTTTAGAATCAGGTCCCTTCTCCCCAGATGAAGAGG
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TACCCTATATCCCTTCTCCTCCCTAGTCACATGGCCATAGGCCTGCTGATGGCTCAGGAAGGCCATTGCA
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AGCCTGCTCCCTCCGTCTCTACCAGGAATGGCCTTGTCCTATGGAAGGCACTGCCCCATCCCAAACTAAT
CTAGGAATCACTGTCTAACCACTCACTGTCATGAATGTGTACTTAAAGGATGAGGTTGAGTCATACCAAA
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ACTGTTTCCCACACAAGTCTCCTGTTCTCTTAAGCTTACTCACTGACAGCCTTTCACTCTCCACAAATAC
ATTAAAGATATGGCCATCACCAAGCCCCCTAGGATGACACCAGACCTGAGAGTCTGAAGACCTGGATCCA
AGTTCTGACTTTTCCCCCTGACAGCTGTGTGACCTTCGTGAAGTCGCCAAACCTCTCTGAGCCCCAGTCA
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AACAGAGAATAAATAGAACTACATTTCTTGCA

Figure 8E

SEQ ID NO:6
>gi|189163531|ref|NM_001127702.1| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 6, mRNA

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GAACCAAGAAGGAGGAGGGGGTCGGGCCTCCGAGGAAGGCCTAGCCGCTGCTGCTGCCAGGAATTCCAGG
TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
AGGAGAGCTTGAGGAGAGCAGGAAAGGTGGGACATTGCTGCTGCTGCTCACTCAGTTCCACAGCAGCCTC
CCCCGTTGCCCCTCTGGATCCACTGCTTAAATACGGACGAGGACAGGGCCCTGTCTCCTCAGCTTCAGGC
ACCACCACTGACCTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCTCCTGCTGGCA
GGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGATCCCCAGGGAGATGCTGCCCAGAAGACAGATA
CATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAG
CCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACA
GCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGAATTTCA
ACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCCGTACCCTCAACCAGCC
AGACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTCCTCAGCGAGGGCCTGAAGCTAGTGGATAAG
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CCAAGAAACAGATCAACGATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCT
TGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGAA
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GATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCA
TTACTGGAACCTATGATCTGAAGAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGGC
TGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACC
ATCGACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCG
AGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCTCTTCATGGG
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CTCCCTGGATGACATTAAAGAAGGGTTGAGCTGGTCCCTGCCTGCATGTGACTGTAAATCCCTCCCATGT
TTTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGTATGTGGGCTCCAGGTAACAGTGCTGTCTTCGGGCCC
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CCTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAGGGCTCCAGTCTTCCTTGTCCTGTCTTGGAGTCC
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CCCCCTGCTCATCCCCCACTCCCCCCCACCCAGAGTTGCTCATCCTGCCAGGGCTGGCTGTGCCCACCCC
AAGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATCGTGCCGTGGCCCAGTTTTGTGGCATCTGCAGCA
ACACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGCTGTCACCTAACCAGACTCGGGCCCTGCACCTCT
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CAGGCCCCAGAAGACCATTACCCTATATCCCTTCTCCTCCCTAGTCACATGGCCATAGGCCTGCTGATGG
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CCCTCCCTTTCCTCCTCTGAGTCCCGACTGGGGCCACATGCAGCCTGACTTCTTTGTGCCTGTTGCTGTC
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GGCCCCTAGCTGAAGGACAGCCTGCTCCCTCCGTCTCTACCAGGAATGGCCTTGTCCTATGGAAGGCACT
GCCCCATCCCAAACTAATCTAGGAATCACTGTCTAACCACTCACTGTCATGAATGTGTACTTAAAGGATG
AGGTTGAGTCATACCAAATAGTGATTTCGATAGTTCAAAATGGTGAAATTAGCAATTCTACATGATTCAG
TCTAATCAATGGATACCGACTGTTTCCCACACAAGTCTCCTGTTCTCTTAAGCTTACTCACTGACAGCCT
TTCACTCTCCACAAATACATTAAAGATATGGCCATCACCAAGCCCCCTAGGATGACACCAGACCTGAGAG
TCTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCTGACAGCTGTGTGACCTTCGTGAAGTCGCCAAAC
CTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCTTTGAGTTGGTATGATGTTCAAGTTAGATAACAA
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Figure 8F

SEQ ID NO:7
>gi|189163533|ref|NM_001127703.1| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 7, mRNA

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TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
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GTGGTACTCTCCCAGAGACTGTCTGACTCACGCCACCCCCTCCACCTTGGACACAGGACGCTGTGGTTTC
TGAGCCAGCAGCCTCCCCCGTTGCCCCTCTGGATCCACTGCTTAAATACGGACGAGGACAGGGCCCTGTC
TCCTCAGCTTCAGGCACCACCACTGACCTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGC
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CCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGC
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GTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGG
AGGGCCTGAATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCCTCCG
TACCCTCAACCAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTCCTCAGCGAGGGCCTG
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TTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTCTTTAAAGGCAAATGG
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TACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTCCTGGGTCAACTGGGCATCACTAAGGT
CTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAGGCCGTGCAT
AAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCATACCCA
TGTCTATCCCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTC
TCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAATAACTGCCTCTCGCTCCTCAACCCCTCCCC
TCCATCCCTGGCCCCCTCCCTGGATGACATTAAAGAAGGGTTGAGCTGGTCCCTGCCTGCATGTGACTGT
AAATCCCTCCCATGTTTTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGTATGTGGGCTCCAGGTAACAGT
GCTGTCTTCGGGCCCCCTGAACTGTGTTCATGGAGCATCTGGCTGGGTAGGCACATGCTGGGCTTGAATC
CAGGGGGGACTGAATCCTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAGGGCTCCAGTCTTCCTTGT
CCTGTCTTGGAGTCCCCAAGAAGGAATCACAGGGGAGGAACCAGATACCAGCCATGACCCCAGGCTCCAC
CAAGCATCTTCATGTCCCCCTGCTCATCCCCCACTCCCCCCCACCCAGAGTTGCTCATCCTGCCAGGGCT
GGCTGTGCCCACCCCAAGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATCGTGCCGTGGCCCAGTTTT
GTGGCATCTGCAGCAACACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGCTGTCACCTAACCAGACTC
GGGCCCTGCACCTCTCAGGCACTTCTGGAAAATGACTGAGGCAGATTCTTCCTGAAGCCCATTCTCCATG
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CTTGACCAGGCCCAGCAGGCCCCAGAAGACCATTACCCTATATCCCTTCTCCTCCCTAGTCACATGGCCA
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CCTATGGAAGGCACTGCCCCATCCCAAACTAATCTAGGAATCACTGTCTAACCACTCACTGTCATGAATG
TGTACTTAAAGGATGAGGTTGAGTCATACCAAATAGTGATTTCGATAGTTCAAAATGGTGAAATTAGCAA
TTCTACATGATTCAGTCTAATCAATGGATACCGACTGTTTCCCACACAAGTCTCCTGTTCTCTTAAGCTT
ACTCACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCATCACCAAGCCCCCTAGGATGA
CACCAGACCTGAGAGTCTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCTGACAGCTGTGTGACCTTC
GTGAAGTCGCCAAACCTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCTTTGAGTTGGTATGATGTT
CAAGTTAGATAACAAAATGTTTATACCCATTAGAACAGAGAATAAATAGAACTACATTTCTTGCA

Figure 8G

SEQ ID NO:8
>gi|189163535|ref|NM_001127704.1| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 8, mRNA

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TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
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GTCTTCGGGCCCCCTGAACTGTGTTCATGGAGCATCTGGCTGGGTAGGCACATGCTGGGCTTGAATCCAG
GGGGGACTGAATCCTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAGGGCTCCAGTCTTCCTTGTCCT
GTCTTGGAGTCCCCAAGAAGGAATCACAGGGGAGGAACCAGATACCAGCCATGACCCCAGGCTCCACCAA
GCATCTTCATGTCCCCCTGCTCATCCCCCACTCCCCCCCACCCAGAGTTGCTCATCCTGCCAGGGCTGGC
TGTGCCCACCCCAAGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATCGTGCCGTGGCCCAGTTTTGTG
GCATCTGCAGCAACACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGCTGTCACCTAACCAGACTCGGG
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CCTGTTGCTGTCCCTGCAGTCTTCAGAGGGCCACCGCAGCTCCAGTGCCACGGCAGGAGGCTGTTCCTGA
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TACATGATTCAGTCTAATCAATGGATACCGACTGTTTCCCACACAAGTCTCCTGTTCTCTTAAGCTTACT
CACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCATCACCAAGCCCCCTAGGATGACAC
CAGACCTGAGAGTCTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCTGACAGCTGTGTGACCTTCGTG
AAGTCGCCAAACCTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCTTTGAGTTGGTATGATGTTCAA
GTTAGATAACAAAATGTTTATACCCATTAGAACAGAGAATAAATAGAACTACATTTCTTGCA

Figure 8H

SEQ ID NO:9
>gi|189163537|ref|NM_001127705.1| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 9, mRNA

TGGGCAGGAACTGGGCACTGTGCCCAGGGCATGCACTGCCTCCACGCAGCAACCCTCAGAGTCCTGAGCT
GAACCAAGAAGGAGGAGGGGGTCGGGCCTCCGAGGAAGGCCTAGCCGCTGCTGCTGCCAGGAATTCCAGG
TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
AGGAGAGCTTGAGGAGAGCAGGAAAGGGCGGCAGTAAGTCTTCAGCATCAGGCATTTTGGGGTGACTCAG
TAAATGGTAGATCTTGCTACCAGTGGAACAGCCACTAAGGATTCTGCAGTGAGAGCAGAGGGCCAGCTAA
GTGGTACTCTCCCAGAGACTGTCTGACTCACGCCACCCCCTCCACCTTGGACACAGGACGCTGTGGTTTC
TGAGCCAGGTACAATGACTCCTTTCGCCTCCCCCGTTGCCCCTCTGGATCCACTGCTTAAATACGGACGA
GGACAGGGCCCTGTCTCCTCAGCTTCAGGCACCACCACTGACCTGGGACAGTGAATCGACAATGCCGTCT
TCTGTCTCGTGGGGCATCCTCCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGATC
CCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGAT
CACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAAT
ATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTC
ACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTT
CCAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTC
CTCAGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCT
TCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTACGTGGAGAAGGGTACTCA
AGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTC
TTTAAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAGAGGACTTCCACGTGGACCAGG
TGACCACCGTGAAGGTGCCTATGATGAAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTC
CAGCTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAA
CTACAGCACCTGGAAAATGAACTCACCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGT
CTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTCCTGGGTCAACT
GGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTC
TCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTT
TAGAGGCCATACCCATGTCTATCCCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGA
ACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAATAACTGCCTCTCGCT
CCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCCCTGGATGACATTAAAGAAGGGTTGAGCTGGTCCCTG
CCTGCATGTGACTGTAAATCCCTCCCATGTTTTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGTATGTGG
GCTCCAGGTAACAGTGCTGTCTTCGGGCCCCCTGAACTGTGTTCATGGAGCATCTGGCTGGGTAGGCACA
TGCTGGGCTTGAATCCAGGGGGGACTGAATCCTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAGGGC
TCCAGTCTTCCTTGTCCTGTCTTGGAGTCCCCAAGAAGGAATCACAGGGGAGGAACCAGATACCAGCCAT
GACCCCAGGCTCCACCAAGCATCTTCATGTCCCCCTGCTCATCCCCCACTCCCCCCCCACCCAGAGTTGCT
CATCCTGCCAGGGCTGGCTGTGCCCACCCCAAGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATCGTG
CCGTGGCCCAGTTTTGTGGCATCTGCAGCAACACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGCTGT
CACCTAACCAGACTCGGGCCCTGCACCTCTCAGGCACTTCTGGAAAATGACTGAGGCAGATTCTTCCTGA
AGCCCATTCTCCATGGGGCAACAAGGACACCTATTCTGTCCTTGTCCTTCCATCGCTGCCCCAGAAAGCC
TCACATATCTCCGTTTAGAATCAGGTCCCTTCTCCCCAGATGAAGAGGAGGGTCTCTGCTTTGTTTTCTC
TATCTCCTCCTCAGACTTGACCAGGCCCAGCAGGCCCCAGAAGACCATTACCCTATATCCCTTCTCCTCC
CTAGTCACATGGCCATAGGCCTGCTGATGGCTCAGGAAGGCCATTGCAAGGACTCCTCAGCTATGGGAGA
GGAAGCACATCACCCATTGACCCCCGCAACCCCTCCCTTTCCTCCTCTGAGTCCCGACTGGGGCCACATG
CAGCCTGACTTCTTTGTGCCTGTTGCTGTCCCTGCAGTCTTCAGAGGGCCACCGCAGCTCCAGTGCCACG
GCAGGAGGCTGTTCCTGAATAGCCCCTGTGGTAAGGGCCAGGAGAGTCCTTCCATCCTCCAAGGCCCTGC
TAAAGGACACAGCAGCCAGGAAGTCCCCTGGGCCCCTAGCTGAAGGACAGCCTGCTCCCTCCGTCTCTAC
CAGGAATGGCCTTGTCCTATGGAAGGCACTGCCCCATCCCAAACTAATCTAGGAATCACTGTCTAACCAC
TCACTGTCATGAATGTGTACTTAAAGGATGAGGTTGAGTCATACCAAATAGTGATTTCGATAGTTCAAAA
TGGTGAAATTAGCAATTCTACATGATTCAGTCTAATCAATGGATACCGACTGTTTCCCACACAAGTCTCC
TGTTCTCTTAAGCTTACTCACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCATCACCA
AGCCCCCTAGGATGACACCAGACCTGAGAGTCTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCTGAC
AGCTGTGTGACCTTCGTGAAGTCGCCAAACCTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCTTTG
AGTTGGTATGATGTTCAAGTTAGATAACAAAATGTTTATACCCATTAGAACAGAGAATAAATAGAACTAC
ATTTCTTGCA

Figure 8I

SEQ ID NO:10
>gi|189163539|ref|NM_001127706.1| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 10, mRNA

TGGGCAGGAACTGGGCACTGTGCCCAGGGCATGCACTGCCTCCACGCAGCAACCCTCAGAGTCCTGAGCT
GAACCAAGAAGGAGGAGGGGGTCGGGCCTCCGAGGAAGGCCTAGCCGCTGCTGCTGCCAGGAATTCCAGG
TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
AGGAGAGCTTGAGGAGAGCAGGAAAGCAGCCTCCCCCGTTGCCCCTCTGGATCCACTGCTTAAATACGGA
CGAGGACAGGGCCCTGTCTCCTCAGCTTCAGGCACCACCACTGACCTGGGACAGTGAATCGACAATGCCG
TCTTCTGTCTCGTGGGGCATCCTCCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGG
ATCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAA
GATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACC
AATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACA
CTCACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGG
CTTCCAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTG
TTCCTCAGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAG
CCTTCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTACGTGGAGAAGGGTAC
TCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATC
TTCTTTAAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAGAGGACTTCCACGTGGACC
AGGTGACCACCGTGAAGGTGCCTATGATGAAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCT
GTCCAGCTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGG
AAACTACAGCACCTGGAAAATGAACTCACCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAA
GGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTCCTGGGTCA
ACTGGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAG
CTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTGCTGGGGCCATGT
TTTTAGAGGCCATACCCATGTCTATCCCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGAT
TGAACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAATAACTGCCTCTC
GCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCCCTGGATGACATTAAAGAAGGGTTGAGCTGGTCC
CTGCCTGCATGTGACTGTAAATCCCTCCCATGTTTTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGTATG
TGGGCTCCAGGTAACAGTGCTGTCTTCGGGCCCCCTGAACTGTGTTCATGGAGCATCTGGCTGGGTAGGC
ACATGCTGGGCTTGAATCCAGGGGGGACTGAATCCTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAG
GGCTCCAGTCTTCCTTGTCCTGTCTTGGAGTCCCCAAGAAGGAATCACAGGGGAGGAACCAGATACCAGC
CATGACCCCAGGCTCCACCAAGCATCTTCATGTCCCCCTGCTCATCCCCCACTCCCCCCCACCCAGAGTT
GCTCATCCTGCCAGGGCTGGCTGTGCCCACCCCAAGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATC
GTGCCGTGGCCCAGTTTTGTGGCATCTGCAGCAACACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGC
TGTCACCTAACCAGACTCGGGCCCTGCACCTCTCAGGCACTTCTGGAAAATGACTGAGGCAGATTCTTCC
TGAAGCCCATTCTCCATGGGGCAACAAGGACACCTATTCTGTCCTTGTCCTTCCATCGCTGCCCCAGAAA
GCCTCACATATCTCCGTTTAGAATCAGGTCCCTTCTCCCCAGATGAAGAGGAGGGTCTCTGCTTTGTTTT
CTCTATCTCCTCCTCAGACTTGACCAGGCCCAGCAGGCCCCAGAAGACCATTACCCTATATCCCTTCTCC
TCCCTAGTCACATGGCCATAGGCCTGCTGATGGCTCAGGAAGGCCATTGCAAGGACTCCTCAGCTATGGG
AGAGGAAGCACATCACCCATTGACCCCCGCAACCCCTCCCTTTCCTCCTCTGAGTCCCGACTGGGGCCAC
ATGCAGCCTGACTTCTTTGTGCCTGTTGCTGTCCCTGCAGTCTTCAGAGGGCCACCGCAGCTCCAGTGCC
ACGGCAGGAGGCTGTTCCTGAATAGCCCCTGTGGTAAGGGCCAGGAGAGTCCTTCCATCCTCCAAGGCCC
TGCTAAAGGACACAGCAGCCAGGAAGTCCCCTGGGCCCCTAGCTGAAGGACAGCCTGCTCCCTCCGTCTC
TACCAGGAATGGCCTTGTCCTATGGAAGGCACTGCCCCATCCCAAACTAATCTAGGAATCACTGTCTAAC
CACTCACTGTCATGAATGTGTACTTAAAGGATGAGGTTGAGTCATACCAAATAGTGATTTCGATAGTTCA
AAATGGTGAAATTAGCAATTCTACATGATTCAGTCTAATCAATGGATACCGACTGTTTCCCACACAAGTC
TCCTGTTCTCTTAAGCTTACTCACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCATCA
CCAAGCCCCCTAGGATGACACCAGACCTGAGAGTCTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCT
GACAGCTGTGTGACCTTCGTGAAGTCGCCAAACCTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCT
TTGAGTTGGTATGATGTTCAAGTTAGATAACAAAATGTTTATACCCATTAGAACAGAGAATAAATAGAAC
TACATTTCTTGCA

Figure 8J

SEQ ID NO:11
>gi|189163541|ref|NM_001127707.1| Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 11, mRNA

TGGGCAGGAACTGGGCACTGTGCCCAGGGCATGCACTGCCTCCACGCAGCAACCCTCAGAGTCCTGAGCT
GAACCAAGAAGGAGGAGGGGGTCGGGCCTCCGAGGAAGGCCTAGCCGCTGCTGCTGCCAGGAATTCCAGG
TTGGAGGGGCGGCAACCTCCTGCCAGCCTTCAGGCCACTCTCCTGTGCCTGCCAGAAGAGACAGAGCTTG
AGGAGAGCTTGAGGAGAGCAGGAAAGCCTCCCCCGTTGCCCCTCTGGATCCACTGCTTAAATACGGACGA
GGACAGGGCCCTGTCTCCTCAGCTTCAGGCACCACCACTGACCTGGGACAGTGAATCGACAATGCCGTCT
TCTGTCTCGTGGGGCATCCTCCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGATC
CCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGAT
CACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAAT
ATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTC
ACGATGAAATCCTGGAGGGCCTGAATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTT
CCAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAATGGCCTGTTC
CTCAGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCT
TCACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTACGTGGAGAAGGGTACTCA
AGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTC
TTTAAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAGAGGACTTCCACGTGGACCAGG
TGACCACCGTGAAGGTGCCTATGATGAAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTC
CAGCTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAA
CTACAGCACCTGGAAAATGAACTCACCCACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGT
CTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAGAGCGTCCTGGGTCAACT
GGGCATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTC
TCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTT
TAGAGGCCATACCCATGTCTATCCCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGA
ACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAATAACTGCCTCTCGCT
CCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCCCTGGATGACATTAAAGAAGGGTTGAGCTGGTCCCTG
CCTGCATGTGACTGTAAATCCCTCCCATGTTTTCTCTGAGTCTCCCTTTGCCTGCTGAGGCTGTATGTGG
GCTCCAGGTAACAGTGCTGTCTTCGGGCCCCCTGAACTGTGTTCATGGAGCATCTGGCTGGGTAGGCACA
TGCTGGGCTTGAATCCAGGGGGGACTGAATCCTCAGCTTACGGACCTGGGCCCATCTGTTTCTGGAGGGC
TCCAGTCTTCCTTGTCCTGTCTTGGAGTCCCCAAGAAGGAATCACAGGGGAGGAACCAGATACCAGCCAT
GACCCCAGGCTCCACCAAGCATCTTCATGTCCCCCTGCTCATCCCCCACTCCCCCCCCACCCAGAGTTGCT
CATCCTGCCAGGGCTGGCTGTGCCCACCCCAAGGCTGCCCTCCTGGGGGCCCCAGAACTGCCTGATCGTG
CCGTGGCCCAGTTTTGTGGCATCTGCAGCAACACAAGAGAGAGGACAATGTCCTCCTCTTGACCCGCTGT
CACCTAACCAGACTCGGGCCCTGCACCTCTCAGGCACTTCTGGAAAATGACTGAGGCAGATTCTTCCTGA
AGCCCATTCTCCATGGGGCAACAAGGACACCTATTCTGTCCTTGTCCTTCCATCGCTGCCCCAGAAAGCC
TCACATATCTCCGTTTAGAATCAGGTCCCTTCTCCCCAGATGAAGAGGAGGGTCTCTGCTTTGTTTTCTC
TATCTCCTCCTCAGACTTGACCAGGCCCAGCAGGCCCCAGAAGACCATTACCCTATATCCCTTCTCCTCC
CTAGTCACATGGCCATAGGCCTGCTGATGGCTCAGGAAGGCCATTGCAAGGACTCCTCAGCTATGGGAGA
GGAAGCACATCACCCATTGACCCCCGCAACCCCTCCCTTTCCTCCTCTGAGTCCCGACTGGGGCCACATG
CAGCCTGACTTCTTTGTGCCTGTTGCTGTCCCTGCAGTCTTCAGAGGGCCACCGCAGCTCCAGTGCCACG
GCAGGAGGCTGTTCCTGAATAGCCCCTGTGGTAAGGGCCAGGAGAGTCCTTCCATCCTCCAAGGCCCTGC
TAAAGGACACAGCAGCCAGGAAGTCCCCTGGGCCCCTAGCTGAAGGACAGCCTGCTCCCTCCGTCTCTAC
CAGGAATGGCCTTGTCCTATGGAAGGCACTGCCCCATCCCAAACTAATCTAGGAATCACTGTCTAACCAC
TCACTGTCATGAATGTGTACTTAAAGGATGAGGTTGAGTCATACCAAATAGTGATTTCGATAGTTCAAAA
TGGTGAAATTAGCAATTCTACATGATTCAGTCTAATCAATGGATACCGACTGTTTCCCACACAAGTCTCC
TGTTCTCTTAAGCTTACTCACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCATCACCA
AGCCCCCTAGGATGACACCAGACCTGAGAGTCTGAAGACCTGGATCCAAGTTCTGACTTTTCCCCCTGAC
AGCTGTGTGACCTTCGTGAAGTCGCCAAACCTCTCTGAGCCCCAGTCATTGCTAGTAAGACCTGCCTTTG
AGTTGGTATGATGTTCAAGTTAGATAACAAAATGTTTATACCCATTAGAACAGAGAATAAATAGAACTAC
ATTTCTTGCA

Figure 8K

SEQ ID NO:12
>gi|402766667|ref|NM_001266017.2| Macaca mulatta serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA

CAGGACAATGCCATCTTCTGTCTCATGGGGCGTCCTCCTGCTGGCAGGCCTGTGCTGCCTGCTCCCCGGC
TCTCTGGCTGAGGATCCCCAGGGAGATGCTGCCCAGAAGACGGATACATCCCACCATGATCAGGACCACC
CAACCCTCAACAAGATCACCCCCAGCCTGGCTGAGTTCGGCTTCAGCCTATACCGCCAGCTGGCACACCA
GTCCAACAGCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGG
ACCAAGGCTGACACTCACAGTGAAATCCTGGAGGGCCTGAATTTCAACGTCACGGAGATTCCGGAGGCTC
AGGTCCATGAAGGCTTCCAGGAACTCCTCCATACCCTCAACAAGCCAGACAGCCAGCTCCAGCTGACCAC
CGGCAACGGCCTGTTCCTCAACAAGAGCCTGAAGGTAGTGGATAAGTTTTTGGAGGATGTCAAAAAACTG
TACCACTCAGAAGCCTTCTCTGTCAACTTTGAGGACACCGAAGAGGCCAAGAAACAGATCAACAATTACG
TGGAGAAGGAAACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCT
GGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGACGTTGAGGCCACCAAGGAAGAGGAC
TTCCACGTGGACCAGGCGACCACCGTGAAGGTGCCCATGATGAGGCGTTTAGGCATGTTTAACATCTACC
ACTGTGAGAAGCTGTCCAGCTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCT
GCCTGATGAGGGGAAACTGCAGCACCTGGAAAATGAACTCACCCATGATATCATCACCAAGTTCCTGGAA
AATGAAAACAGCAGGTCTGCCAACTTACATTTACCCAGACTGGCCATTACTGGAACCTATGATCTGAAGA
CAGTCCTGGGCCACCTGGGTATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCGGGGATCACGGAGGA
GGCACCCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGATGAGAAAGGGACTGAAGCT
GCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATTCCCCCCGAGGTCAAGTTCAACAAACCCTTTG
TCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAGAA
ATAACTGCCTGTCACTCCTCAGCCCCTCCCCTCCATCCCTGGCCCCCTCCCTGAATGACAT

Figure 8L

SEQ ID NO:13
>gi|297298519|ref|XM_001099255.2| PREDICTED: Macaca mulatta serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1, transcript variant 6 (SERPINA1), mRNA

GCCCAGTCTTGTGTCTGCCTGGCAATGGGCAAGGCCCCTTCCTGCCCAAGCTCCCCGCCCCTCCCCAACC
TATTGCCTCCGCCACCCGCCACCCGAGGCCAACTTCCTGGGTGGGCAGGAACTGGGCCCTGTGCCCAGGG
CGTGCACTGCCTCCACGCAGCAACCCTCAGAGTACTGAGCTGAGCAAAGGAGGAGGAGGGGATCAGCACT
CTGAGGAAGGCCTAGCCACTGCTGCTGCCAGGAATTCCAGGGCGGCATCAGTCTTCAGCATCAGGCATTT
CGGGGTGAATTAGTAAATGGTAGATCTTGCTACCAGTGGAACAGCCGCTAAGGATTCTGCAGTGAGAGCA
GAGGGCCAGCAAAGTGGTACTCTCCCAGCGACTGGCTGACTCACGCCACCCCCTCCACCTTGGACGCAGG
ACACTGTGGTTTCTGAGCCAGGTACAATGACTCCTTTTGGTACGTGCAGTGGAGGCTGTATGCTGCTCAG
GCAGAGCGTCCGGACAGCGTGGGCGGGCGACTCAGCGCCCAGCCTGTGAACTTAGTCCCTGTTTGCTCCT
CCGGTAACTGGGGTGATCTTGGTTAATATTCACCAGCAGCCTCCCCCGTTGCCCCTCTGCACCCACTGCT
TAAATACGGACAAGGACAGGGCTCTGTCTCCTCAGCCTCAGGCACCACCACTGACCTGGGACGGTGAATC
GACAATGCCATCTTCTGTCTCATGGGGCGTCCTCCTGCTGGCAGGCCTGTGCTGCCTGCTCCCCGGCTCT
CTGGCTGAGGATCCCCAGGGAGATGCTGCCCAGAAGACGGATACATCCCACCATGATCAGGACCACCCAA
CCCTCAACAAGATCACCCCCAGCCTGGCTGAGTTCGGCTTCAGCCTATACCGCCAGCTGGCACACCAGTC
CAACAGCACCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGACC
AAGGCTGACACTCACAGTGAAATCCTGGAGGGCCTGAATTTCAACGTCACGGAGATTCCGGAGGCTCAGG
TCCATGAAGGCTTCCAGGAACTCCTCCATACCCTCAACAAGCCAGACAGCCAGCTCCAGCTGACCACCGG
CAACGGCCTGTTCCTCAACAAGAGCCTGAAGGTAGTGGATAAGTTTTTGGAGGATGTCAAAAAACTGTAC
CACTCAGAAGCCTTCTCTGTCAACTTTGAGGACACCGAAGAGGCCAAGAAACAGATCAACAATTACGTGG
AGAAGGAAACTCAAGGGAAAATTGTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGCTCTGGT
GAATTACATCTTCTTTAAAGGCAAATGGGAGAGACCCTTTGACGTTGAGGCCACCAAGGAAGAGGACTTC
CACGTGGACCAGGCGACCACCGTGAAGGTGCCCATGATGAGGCGTTTAGGCATGTTTAACATCTACCACT
GTGAGAAGCTGTCCAGCTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCTTCCTGCC
TGATGAGGGGAAACTGCAGCACCTGGAAAATGAACTCACCCATGATATCATCACCAAGTTCCTGGAAAAT
GAAAACAGCAGGTCTGCCAACTTACATTTACCCAGACTGGCCATTACTGGAACCTATGATCTGAAGACAG
TCCTGGGCCACCTGGGTATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCGGGGATCACGGAGGAGGC
ACCCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGATGAGAAAGGGACTGAAGCTGCT
GGGGCCATGTTTTTAGAGGCCATACCCATGTCTATTCCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCT
TCTTAATGATTGAACAAAATACCAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAGAAATA
ACTGCCTGTCACTCCTCAGCCCCTCCCCTCCATCCCTGGCCCCCTCCCTGAATGACATTAAAGAAGGGTT
GAGCTGGTCCCTGCCTGCGTGTGTGACTGCAAAC

Figure 8M

SEQ ID NO:14
>gi|297298520|ref|XM_001099044.2| PREDICTED: Macaca mulatta serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1, transcript variant 4 (SERPINA1), mRNA

TCTTGTGTCTGCCTGGCAATGGGCAAGGCCCCTTCCTGCCCAAGCTCCCCGCCCCTCCCCAACCTATTGC
CTCCGCCACCCGCCACCCGAGGCCAACTTCCTGGGTGGGCAGGAACTGGGCCCTGTGCCCAGGGCGTGCA
CTGCCTCCACGCAGCAACCCTCAGAGTACTGAGCTGAGCAAAGGAGGAGGAGGGGATCAGCACTCTGAGG
AAGGCCTAGCCACTGCTGCTGCCAGGAATTCCAGGACAATGCCATCTTCTGTCTCATGGGGCGTCCTCCT
GCTGGCAGGCCTGTGCTGCCTGCTCCCCGGCTCTCTGGCTGAGGATCCCCAGGGAGATGCTGCCCAGAAG
ACGGATACATCCCACCATGATCAGGACCACCCAACCCTCAACAAGATCACCCCCAGCCTGGCTGAGTTCG
GCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAATATCTTCTTCTCCCCAGTGAGCAT
CGCTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACAGTGAAATCCTGGAGGGCCTG
AATTTCAACGTCACGGAGATTCCGGAGGCTCAGGTCCATGAAGGCTTCCAGGAACTCCTCCATACCCTCA
ACAAGCCAGACAGCCAGCTCCAGCTGACCACCGGCAACGGCCTGTTCCTCAACAAGAGCCTGAAGGTAGT
GGATAAGTTTTTGGAGGATGTCAAAAAACTGTACCACTCAGAAGCCTTCTCTGTCAACTTTGAGGACACC
GAAGAGGCCAAGAAACAGATCAACAATTACGTGGAGAAGGAAACTCAAGGGAAAATTGTGGATTTGGTCA
AGGAGCTTGACAGAGACACAGTTTTTGCTCTGGTGAATTACATCTTCTTTAAAGGCAAATGGGAGAGACC
CTTTGACGTTGAGGCCACCAAGGAAGAGGACTTCCACGTGGACCAGGCGACCACCGTGAAGGTGCCCATG
ATGAGGCGTTTAGGCATGTTTAACATCTACCACTGTGAGAAGCTGTCCAGCTGGGTGCTGCTGATGAAAT
ACCTGGGCAATGCCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAACTGCAGCACCTGGAAAATGAACT
CACCCATGATATCATCACCAAGTTCCTGGAAAATGAAAACAGCAGGTCTGCCAACTTACATTTACCCAGA
CTGGCCATTACTGGAACCTATGATCTGAAGACAGTCCTGGGCCACCTGGGTATCACTAAGGTCTTCAGCA
ATGGGGCTGACCTCTCGGGGATCACGGAGGAGGCACCCCTGAAGCTCTCCAAGGCCGTGCATAAGGCTGT
GCTGACCATCGATGAGAAAGGGACTGAAGCTGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATT
CCCCCCGAGGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATACCAAGTCTCCCCTCT
TCATGGGAAAAGTGGTGAATCCCACCCAGAAATAACTGCCTGTCACTCCTCAGCCCCTCCCCTCCATCCC
TGGCCCCCTCCCTGAATGACATTAAAGAAGGGTTGAGCTGGTCCCTGCCTGCGTGTGTGACTGCAAAC

Figure 8N

SEQ ID NO:15
Reverse Complement of SEQ ID NO:1
TGCAAGAAATGTAGTTCTATTTATTCTCTGTTCTAATGGGTATAAACATTTTGTTATCTAACTTGAACATCATA
CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCTGCTGGTGAATATTAACCAAGGTCACCCCAGTTATCGGAGGAG
CAAACAGGGGCTAAGTCCACTGGCTGGGATCTGAGTCGCCCGCCTACGCTGCCCGGACGCTTTGCCTGGGCAGT
GTACAGCTTCCACTGCACTTACCGAAAGGAGTCATTGT

Figure 8O

SEQ ID NO:16
Reverse Complement of SEQ ID NO:2
TGCAAGAAATGTAGTTCTATTTATTCTCTGTTCTAATGGGTATAAACATTTTGTTATCTAACTTGAACATCATA
CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCCTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCTGTCTCTTCTGGCAGGCACAGGAGAGTGGCCTGAAGGC
TGGCAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCTGGCAGCAGCAGCGGCTAGGCCTTCCTCGGAGGCCCGA
CCCCCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAGGGTTGCTGCGTGGAGGCAGTGCATGCCCTGGGCACAG
TGCCCAGTTCCTGCCCA

Figure 8P

SEQ ID NO:17
Reverse Complement of SEQ ID NO:3
TGCAAGAAATGTAGTTCTATTTATTCTCTGTTCTAATGGGTATAAACATTTTGTTATCTAACTTGAACATCATA
CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCTGCGAAAGGAGTCATTGTACCTGGCTCAGAAACCACAGCGTCC
TGTGTCCAAGGTGGAGGGGGTGGCGTGAGTCAGACAGTCTCTGGGAGAGTACCACTTAGCTGGCCCTCTGCTCT
CACTGCAGAATCCTTAGTGGCTGTTCCACTGGTAGCAAGATCTACCATTTACTGAGTCACCCCAAAATGCCTGA
TGCTGAAGACTTACTGCCGCCCTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCTGTCTCTTCTGGCAGGCACA
GGAGAGTGGCCTGAAGGCTGGCAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCTGGCAGCAGCAGCGGCTAGG
CCTTCCTCGGAGGCCCGACCCCCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAGGGTTGCTGCGTGGAGGCAG
TGCATGCCCTGGGCACAGTGCCCAGTTCCTGCCCA

Figure 8Q

SEQ ID NO:18
Reverse Complement of SEQ ID NO:4
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CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCCTGTGGAACTGAGTGAGCAGCAGCAGCAATGTCCCACCTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCT
GTCTCTTCTGGCAGGCACAGGAGAGTGGCCTGAAGGCTGGCAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCT
GGCAGCAGCAGCGGCTAGGCCTTCCTCGGAGGCCCGACCCCCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAG
GGTTGCTGCGTGGAGGCAGTGCATGCCCTGGGCACAGTGCCCAGTTCCTGCCCA

Figure 8R

SEQ ID NO:19
Reverse Complement of SEQ ID NO:5
TGCAAGAAATGTAGTTCTATTTATTCTCTGTTCTAATGGGTATAAACATTTTGTTATCTAACTTGAACATCATA
CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
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ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCTGCTGGCTCAGAAACCACAGCGTCCTGTGTCCAAGGTGGAGGG
GGTGGCGTGAGTCAGACAGTCTCTGGGAGAGTACCACTTAGCTGGCCCTCTGCTCTCACTGCAGAATCCTTAGT
GGCTGTTCCACTGGTAGCAAGATCTACCATTTACTGAGTCACCCCAAAATGCCTGATGCTGAAGACTTACTGCC
GCCCTGTGGAACTGAGTGAGCAGCAGCAGCAATGTCCCACCTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCT
GTCTCTTCTGGCAGGCACAGGAGAGTGGCCTGAAGGCTGGCAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCT
GGCAGCAGCAGCGGCTAGGCCTTCCTCGGAGGCCCGACCCCCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAG
GGTTGCTGCGTGGAGGCAGTGCATGCCCTGGGCACAGTGCCCAGTTCCTGCCCA

Figure 8S

SEQ ID NO:20
Reverse Complement of SEQ ID NO:6
TGCAAGAAATGTAGTTCTATTTATTCTCTGTTCTAATGGGTATAAACATTTTGTTATCTAACTTGAACATCATA
CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCTGCTGTGGAACTGAGTGAGCAGCAGCAGCAATGTCCCACCTTT
CCTGCTCTCCTCAAGCTCTCCTCAAGCTCTGTCTCTTCTGGCAGGCACAGGAGAGTGGCCTGAAGGCTGGCAGG
AGGTTGCCGCCCCTCCAACCTGGAATTCCTGGCAGCAGCAGCGGCTAGGCCTTCCTCGGAGGCCCGACCCCCTC
CTCCTTCTTGGTTCAGCTCAGGACTCTGAGGGTTGCTGCGTGGAGGCAGTGCATGCCCTGGGCACAGTGCCCAG
TTCCTGCCCA

Figure 8T

SEQ ID NO:21
Reverse Complement of SEQ ID NO:7
TGCAAGAAATGTAGTTCTATTTATTCTCTGTTCTAATGGGTATAAACATTTTGTTATCTAACTTGAACATCATA
CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCTGCTGGCTCAGAAACCACAGCGTCCTGTGTCCAAGGTGGAGGG
GGTGGCGTGAGTCAGACAGTCTCTGGGAGAGTACCACTTAGCTGGCCCTCTGCTCTCACTGCAGAATCCTTAGT
GGCTGTTCCACTGGTAGCAAGATCTACCATTTACTGAGTCACCCCAAAATGCCTGATGCTGAAGACTTACTGCC
GCCCTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCTGTCTCTTCTGGCAGGCACAGGAGAGTGGCCTGAAGGC
TGGCAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCTGGCAGCAGCAGCGGCTAGGCCTTCCTCGGAGGCCCGA
CCCCCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAGGGTTGCTGCGTGGAGGCAGTGCATGCCCTGGGCACAG
TGCCCAGTTCCTGCCCA

Figure 8U

SEQ ID NO:22
Reverse Complement of SEQ ID NO:8
TGCAAGAAATGTAGTTCTATTTATTCTCTGTTCTAATGGGTATAAACATTTTGTTATCTAACTTGAACATCATA
CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCTGGCTCAGAAACCACAGCGTCCTGTGTCCAAGGTGGAGGGGGT
GGCGTGAGTCAGACAGTCTCTGGGAGAGTACCACTTAGCTGGCCCTCTGCTCTCACTGCAGAATCCTTAGTGGC
TGTTCCACTGGTAGCAAGATCTACCATTTACTGAGTCACCCCAAAATGCCTGATGCTGAAGACTTACTGCCGCC
CTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCTGTCTCTTCTGGCAGGCACAGGAGAGTGGCCTGAAGGCTGG
CAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCTGGCAGCAGCAGCGGCTAGGCCTTCCTCGGAGGCCCGACCC
CCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAGGGTTGCTGCGTGGAGGCAGTGCATGCCCTGGGCACAGTGC
CCAGTTCCTGCCCA

Figure 8V

SEQ ID NO:23
Reverse Complement of SEQ ID NO:9
TGCAAGAAATGTAGTTCTATTTATTCTCTGTTCTAATGGGTATAAACATTTTGTTATCTAACTTGAACATCATA
CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCGAAAGGAGTCATTGTACCTGGCTCAGAAACCACAGCGTCCTGT
GTCCAAGGTGGAGGGGGTGGCGTGAGTCAGACAGTCTCTGGGAGAGTACCACTTAGCTGGCCCTCTGCTCTCAC
TGCAGAATCCTTAGTGGCTGTTCCACTGGTAGCAAGATCTACCATTTACTGAGTCACCCCAAAATGCCTGATGC
TGAAGACTTACTGCCGCCCTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCTGTCTCTTCTGGCAGGCACAGGA
GAGTGGCCTGAAGGCTGGCAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCTGGCAGCAGCAGCGGCTAGGCCT
TCCTCGGAGGCCCGACCCCCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAGGGTTGCTGCGTGGAGGCAGTGC
ATGCCCTGGGCACAGTGCCCAGTTCCTGCCCA

Figure 8W

SEQ ID NO:24
Reverse Complement of SEQ ID NO:10
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CCAACTCAAAGGCAGGTCTTACTAGCAATGACTGGGGCTCAGAGAGGTTTGGCGACTTCACGAAGGTCACACAG
CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCTGCTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCTGTCTCTT
CTGGCAGGCACAGGAGAGTGGCCTGAAGGCTGGCAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCTGGCAGCA
GCAGCGGCTAGGCCTTCCTCGGAGGCCCGACCCCCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAGGGTTGCT
GCGTGGAGGCAGTGCATGCCCTGGGCACAGTGCCCAGTTCCTGCCCA

Figure 8X

SEQ ID NO:25
Reverse Complement of SEQ ID NO:11
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CTGTCAGGGGGAAAAGTCAGAACTTGGATCCAGGTCTTCAGACTCTCAGGTCTGGTGTCATCCTAGGGGGCTTG
GTGATGGCCATATCTTTAATGTATTTGTGGAGAGTGAAAGGCTGTCAGTGAGTAAGCTTAAGAGAACAGGAGAC
TTGTGTGGGAAACAGTCGGTATCCATTGATTAGACTGAATCATGTAGAATTGCTAATTTCACCATTTTGAACTA
TCGAAATCACTATTTGGTATGACTCAACCTCATCCTTTAAGTACACATTCATGACAGTGAGTGGTTAGACAGTG
ATTCCTAGATTAGTTTGGGATGGGGCAGTGCCTTCCATAGGACAAGGCCATTCCTGGTAGAGACGGAGGGAGCA
GGCTGTCCTTCAGCTAGGGGCCCAGGGGACTTCCTGGCTGCTGTGTCCTTTAGCAGGGCCTTGGAGGATGGAAG
GACTCTCCTGGCCCTTACCACAGGGGCTATTCAGGAACAGCCTCCTGCCGTGGCACTGGAGCTGCGGTGGCCCT
CTGAAGACTGCAGGGACAGCAACAGGCACAAAGAAGTCAGGCTGCATGTGGCCCCAGTCGGGACTCAGAGGAGG
AAAGGGAGGGGTTGCGGGGGTCAATGGGTGATGTGCTTCCTCTCCCATAGCTGAGGAGTCCTTGCAATGGCCTT
CCTGAGCCATCAGCAGGCCTATGGCCATGTGACTAGGGAGGAGAAGGGATATAGGGTAATGGTCTTCTGGGGCC
TGCTGGGCCTGGTCAAGTCTGAGGAGGAGATAGAGAAAACAAAGCAGAGACCCTCCTCTTCATCTGGGGAGAAG
GGACCTGATTCTAAACGGAGATATGTGAGGCTTTCTGGGGCAGCGATGGAAGGACAAGGACAGAATAGGTGTCC
TTGTTGCCCCATGGAGAATGGGCTTCAGGAAGAATCTGCCTCAGTCATTTTCCAGAAGTGCCTGAGAGGTGCAG
GGCCCGAGTCTGGTTAGGTGACAGCGGGTCAAGAGGAGGACATTGTCCTCTCTCTTGTGTTGCTGCAGATGCCA
CAAAACTGGGCCACGGCACGATCAGGCAGTTCTGGGGCCCCCAGGAGGGCAGCCTTGGGGTGGGCACAGCCAGC
CCTGGCAGGATGAGCAACTCTGGGTGGGGGGGAGTGGGGGATGAGCAGGGGGACATGAAGATGCTTGGTGGAGC
CTGGGGTCATGGCTGGTATCTGGTTCCTCCCCTGTGATTCCTTCTTGGGGACTCCAAGACAGGACAAGGAAGAC
TGGAGCCCTCCAGAAACAGATGGGCCCAGGTCCGTAAGCTGAGGATTCAGTCCCCCCTGGATTCAAGCCCAGCA
TGTGCCTACCCAGCCAGATGCTCCATGAACACAGTTCAGGGGGCCCGAAGACAGCACTGTTACCTGGAGCCCAC
ATACAGCCTCAGCAGGCAAAGGGAGACTCAGAGAAAACATGGGAGGGATTTACAGTCACATGCAGGCAGGGACC
AGCTCAACCCTTCTTTAATGTCATCCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGTTGAGGAGCGAGAGGCAG
TTATTTTTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGA
CAAAGGGTTTGTTGAACTTGACCTCGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCT
TCAGTCCCTTTCTCGTCGATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCTGT
GACCCCGGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATGCCCAGTTGACCCAGGACGCTCTTCAGATCAT
AGGTTCCAGTAATGGACAGTTTGGGTAAATGTAAGCTGGCAGACCTTCTGTCTTCATTTTCCAGGAACTTGGTG
ATGATATCGTGGGTGAGTTCATTTTCCAGGTGCTGTAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGC
ATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTTACAGTGCTGGATGTTAAACATGCCTAAAC
GCTTCATCATAGGCACCTTCACGGTGGTCACCTGGTCCACGTGGAAGTCCTCTTCCTCGGTGTCCTTGACTTCA
AAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTT
GACCAAATCCACAATTTTCCCTTGAGTACCCTTCTCCACGTAATCGTTGATCTGTTTCTTGGCCTCTTCGGTGT
CCCCGAAGTTGACAGTGAAGGCTTCTGAGTGGTACAACTTTTTAACATCCTCCAAAAACTTATCCACTAGCTTC
AGGCCCTCGCTGAGGAACAGGCCATTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTGGTTGAGGGTACGGAG
GAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTGAGGTTGAAATTCAGGCCCTCCAGGATTT
CATCGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAG
ATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGAT
CTTGTTGAAGGTTGGGTGATCCTGATCATGGTGGGATGTATCTGTCTTCTGGGCAGCATCTCCCTGGGGATCCT
CAGCCAGGGAGACAGGGACCAGGCAGCACAGGCCTGCCAGCAGGAGGATGCCCCACGAGACAGAAGACGGCATT
GTCGATTCACTGTCCCAGGTCAGTGGTGGTGCCTGAAGCTGAGGAGACAGGGCCCTGTCCTCGTCCGTATTTAA
GCAGTGGATCCAGAGGGGCAACGGGGGAGGCTTTCCTGCTCTCCTCAAGCTCTCCTCAAGCTCTGTCTCTTCTG
GCAGGCACAGGAGAGTGGCCTGAAGGCTGGCAGGAGGTTGCCGCCCCTCCAACCTGGAATTCCTGGCAGCAGCA
GCGGCTAGGCCTTCCTCGGAGGCCCGACCCCCTCCTCCTTCTTGGTTCAGCTCAGGACTCTGAGGGTTGCTGCG
TGGAGGCAGTGCATGCCCTGGGCACAGTGCCCAGTTCCTGCCCA

Figure 8Y

SEQ ID NO:26
Reverse Complement of SEQ ID NO:12
ATGTCATTCAGGGAGGGGGCCAGGGATGGAGGGGAGGGGCTGAGGAGTGACAGGCAGTTATTTCTGGGTGGGAT
TCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTTGTTCAATCATTAAGAAGACAAAGGGTTTGTTGAAC
TTGACCTCGGGGGGAATAGACATGGGTATGGCCTCTAAAAACATGGCCCCAGCAGCTTCAGTCCCTTTCTCATC
GATGGTCAGCACAGCCTTATGCACGGCCTTGGAGAGCTTCAGGGGTGCCTCCTCCGTGATCCCCGAGAGGTCAG
CCCCATTGCTGAAGACCTTAGTGATACCCAGGTGGCCCAGGACTGTCTTCAGATCATAGGTTCCAGTAATGGCC
AGTCTGGGTAAATGTAAGTTGGCAGACCTGCTGTTTTCATTTTCCAGGAACTTGGTGATGATATCATGGGTGAG
TTCATTTTCCAGGTGCTGCAGTTTCCCCTCATCAGGCAGGAAGAAGATGGCGGTGGCATTGCCCAGGTATTTCA
TCAGCAGCACCCAGCTGGACAGCTTCTCACAGTGGTAGATGTTAAACATGCCTAAACGCCTCATCATGGGCACC
TTCACGGTGGTCGCCTGGTCCACGTGGAAGTCCTCTTCCTTGGTGGCCTCAACGTCAAAGGGTCTCTCCCATTT
GCCTTTAAAGAAGATGTAATTCACCAGAGCAAAAACTGTGTCTCTGTCAAGCTCCTTGACCAAATCCACAATTT
TCCCTTGAGTTTCCTTCTCCACGTAATTGTTGATCTGTTTCTTGGCCTCTTCGGTGTCCTCAAAGTTGACAGAG
AAGGCTTCTGAGTGGTACAGTTTTTTGACATCCTCCAAAAACTTATCCACTACCTTCAGGCTCTTGTTGAGGAA
CAGGCCGTTGCCGGTGGTCAGCTGGAGCTGGCTGTCTGGCTTGTTGAGGGTATGGAGGAGTTCCTGGAAGCCTT
CATGGACCTGAGCCTCCGGAATCTCCGTGACGTTGAAATTCAGGCCCTCCAGGATTTCACTGTGAGTGTCAGCC
TTGGTCCCCAGGGAGAGCATTGCAAAGGCTGTAGCGATGCTCACTGGGGAGAAGAAGATATTGGTGCTGTTGGA
CTGGTGTGCCAGCTGGCGGTATAGGCTGAAGCCGAACTCAGCCAGGCTGGGGGTGATCTTGTTGAGGGTTGGGT
GGTCCTGATCATGGTGGGATGTATCCGTCTTCTGGGCAGCATCTCCCTGGGGATCCTCAGCCAGAGAGCCGGGG
AGCAGGCAGCACAGGCCTGCCAGCAGGAGGACGCCCCATGAGACAGAAGATGGCATTGTCCTG

Figure 8Z

SEQ ID NO:27
Reverse Complement of SEQ ID NO:13
GTTTGCAGTCACACACGCAGGCAGGGACCAGCTCAACCCTTCTTTAATGTCATTCAGGGAGGGGGCCAGGGATG
GAGGGGAGGGGCTGAGGAGTGACAGGCAGTTATTTCTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGA
CTTGGTATTTTGTTCAATCATTAAGAAGACAAAGGGTTTGTTGAACTTGACCTCGGGGGGAATAGACATGGGTA
TGGCCTCTAAAAACATGGCCCCAGCAGCTTCAGTCCCTTTCTCATCGATGGTCAGCACAGCCTTATGCACGGCC
TTGGAGAGCTTCAGGGGTGCCTCCTCCGTGATCCCCGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATACC
CAGGTGGCCCAGGACTGTCTTCAGATCATAGGTTCCAGTAATGGCCAGTCTGGGTAAATGTAAGTTGGCAGACC
TGCTGTTTTCATTTTCCAGGAACTTGGTGATGATATCATGGGTGAGTTCATTTTCCAGGTGCTGCAGTTTCCCC
TCATCAGGCAGGAAGAAGATGGCGGTGGCATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTC
ACAGTGGTAGATGTTAAACATGCCTAAACGCCTCATCATGGGCACCTTCACGGTGGTCGCCTGGTCCACGTGGA
AGTCCTCTTCCTTGGTGGCCTCAACGTCAAAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGA
GCAAAAACTGTGTCTCTGTCAAGCTCCTTGACCAAATCCACAATTTTCCCTTGAGTTTCCTTCTCCACGTAATT
GTTGATCTGTTTCTTGGCCTCTTCGGTGTCCTCAAAGTTGACAGAGAAGGCTTCTGAGTGGTACAGTTTTTTGA
CATCCTCCAAAAACTTATCCACTACCTTCAGGCTCTTGTTGAGGAACAGGCCGTTGCCGGTGGTCAGCTGGAGC
TGGCTGTCTGGCTTGTTGAGGGTATGGAGGAGTTCCTGGAAGCCTTCATGGACCTGAGCCTCCGGAATCTCCGT
GACGTTGAAATTCAGGCCCTCCAGGATTTCACTGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGG
CTGTAGCGATGCTCACTGGGGAGAAGAAGATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTG
AAGCCGAACTCAGCCAGGCTGGGGGTGATCTTGTTGAGGGTTGGGTGGTCCTGATCATGGTGGGATGTATCCGT
CTTCTGGGCAGCATCTCCCTGGGGATCCTCAGCCAGAGAGCCGGGGAGCAGGCAGCACAGGCCTGCCAGCAGGA
GGACGCCCCATGAGACAGAAGATGGCATTGTCGATTCACCGTCCCAGGTCAGTGGTGGTGCCTGAGGCTGAGGA
GACAGAGCCCTGTCCTTGTCCGTATTTAAGCAGTGGGTGCAGAGGGGCAACGGGGGAGGCTGCTGGTGAATATT
AACCAAGATCACCCCAGTTACCGGAGGAGCAAACAGGGACTAAGTTCACAGGCTGGGCGCTGAGTCGCCCGCCC
ACGCTGTCCGGACGCTCTGCCTGAGCAGCATACAGCCTCCACTGCACGTACCAAAAGGAGTCATTGTACCTGGC
TCAGAAACCACAGTGTCCTGCGTCCAAGGTGGAGGGGGTGGCGTGAGTCAGCCAGTCGCTGGGAGAGTACCACT
TTGCTGGCCCTCTGCTCTCACTGCAGAATCCTTAGCGGCTGTTCCACTGGTAGCAAGATCTACCATTTACTAAT
TCACCCCGAAATGCCTGATGCTGAAGACTGATGCCGCCCTGGAATTCCTGGCAGCAGCAGTGGCTAGGCCTTCC
TCAGAGTGCTGATCCCCTCCTCCTCCTTTGCTCAGCTCAGTACTCTGAGGGTTGCTGCGTGGAGGCAGTGCACG
CCCTGGGCACAGGGCCCAGTTCCTGCCCACCCAGGAAGTTGGCCTCGGGTGGCGGGTGGCGGAGGCAATAGGTT
GGGGAGGGGCGGGGAGCTTGGGCAGGAAGGGGCCTTGCCCATTGCCAGGCAGACACAAGACTGGGC

Figure 8AA

SEQ ID NO:28
Reverse Complement of SEQ ID NO:14
GTTTGCAGTCACACACGCAGGCAGGGACCAGCTCAACCCTTCTTTAATGTCATTCAGGGAGGGGGCCAGGGATG
GAGGGGAGGGGCTGAGGAGTGACAGGCAGTTATTTCTGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGA
CTTGGTATTTTGTTCAATCATTAAGAAGACAAAGGGTTTGTTGAACTTGACCTCGGGGGGAATAGACATGGGTA
TGGCCTCTAAAAACATGGCCCCAGCAGCTTCAGTCCCTTTCTCATCGATGGTCAGCACAGCCTTATGCACGGCC
TTGGAGAGCTTCAGGGGTGCCTCCTCCGTGATCCCCGAGAGGTCAGCCCCATTGCTGAAGACCTTAGTGATACC
CAGGTGGCCCAGGACTGTCTTCAGATCATAGGTTCCAGTAATGGCCAGTCTGGGTAAATGTAAGTTGGCAGACC
TGCTGTTTTCATTTTCCAGGAACTTGGTGATGATATCATGGGTGAGTTCATTTTCCAGGTGCTGCAGTTTCCCC
TCATCAGGCAGGAAGAAGATGGCGGTGGCATTGCCCAGGTATTTCATCAGCAGCACCCAGCTGGACAGCTTCTC
ACAGTGGTAGATGTTAAACATGCCTAAACGCCTCATCATGGGCACCTTCACGGTGGTCGCCTGGTCCACGTGGA
AGTCCTCTTCCTTGGTGGCCTCAACGTCAAAGGGTCTCTCCCATTTGCCTTTAAAGAAGATGTAATTCACCAGA
GCAAAAACTGTGTCTCTGTCAAGCTCCTTGACCAAATCCACAATTTTCCCTTGAGTTTCCTTCTCCACGTAATT
GTTGATCTGTTTCTTGGCCTCTTCGGTGTCCTCAAAGTTGACAGAGAAGGCTTCTGAGTGGTACAGTTTTTTGA
CATCCTCCAAAAACTTATCCACTACCTTCAGGCTCTTGTTGAGGAACAGGCCGTTGCCGGTGGTCAGCTGGAGC
TGGCTGTCTGGCTTGTTGAGGGTATGGAGGAGTTCCTGGAAGCCTTCATGGACCTGAGCCTCCGGAATCTCCGT
GACGTTGAAATTCAGGCCCTCCAGGATTTCACTGTGAGTGTCAGCCTTGGTCCCCAGGGAGAGCATTGCAAAGG
CTGTAGCGATGCTCACTGGGGAGAAGAAGATATTGGTGCTGTTGGACTGGTGTGCCAGCTGGCGGTATAGGCTG
AAGCCGAACTCAGCCAGGCTGGGGGTGATCTTGTTGAGGGTTGGGTGGTCCTGATCATGGTGGGATGTATCCGT
CTTCTGGGCAGCATCTCCCTGGGGATCCTCAGCCAGAGAGCCGGGGAGCAGGCAGCACAGGCCTGCCAGCAGGA
GGACGCCCCATGAGACAGAAGATGGCATTGTCCTGGAATTCCTGGCAGCAGCAGTGGCTAGGCCTTCCTCAGAG
TGCTGATCCCCTCCTCCTCCTTTGCTCAGCTCAGTACTCTGAGGGTTGCTGCGTGGAGGCAGTGCACGCCCTGG
GCACAGGGCCCAGTTCCTGCCCACCCAGGAAGTTGGCCTCGGGTGGCGGGTGGCGGAGGCAATAGGTTGGGGAG
GGGCGGGGAGCTTGGGCAGGAAGGGGCCTTGCCCATTGCCAGGCAGACACAAGA

Figure 8AB