```
CLUSTAL O(1.2.4) multiple sequence alignment: E4P


Human           CACCTGTGGTCCTAGTTATTCAGGAGGCTGAGGGAGAAGAATCACTGGAGGCTAGGATTT     60
Rhesus          CACCTGTGGTCCTAGTTATTCAGGAGGCTGAGGGAGAGGAATCACTG----GAAGGATTT     56
Patas           CACCTGTGGTCCTAGTTATTCAGGAGGCTGAGGGAGAGGAATCACTGGAGCCCAGGATTT     60
AGM             CACCTGTGGTCCTAGTTATTCAGGAGGCTGAGGGAGAGGAATCACTGGAGCCCAGGATTT     60
                ************************************* *********      *******

Human           CCAGGCTGTAGTGAGCCATGATTGTGCTATTTCACTCCAGCTTGGGTGACAGGGTGAGAT     120
Rhesus          CCAGGCTGTAGTGAGCCATGATTGTGTTATTGCACTCCAGAGTGGGTGACAGGGTGAGAT     116
Patas           CCAGGCTGTAGTGAGCCATGATTGTGTTATTGCACTCCAGAGTGGGTGACAGGGTGAGAT     120
AGM             CCAGGCTGTAGTGAGCCATGATTGTGTTATTGCACTCCAGAGTGGGTGACAGGGTGAGAT     120
                ************************** **** ********  ******************

Human           CCTGTGTCTAAAAAGAATAATAACAATAATAATAAACATTATCTCACACAACGAGGAATC     180
Rhesus          CCTGTCTCTAAAAATAATAATAACGATCACAATACACACTATCTCACACAATGAGGAACT     176
Patas           CCTGTCTCTAAAAATAATAATAACGATCACAATACACACTATCTCACACAATGAGGAACT     180
AGM             CCTGTCTCTAAAAATAATAATAACGATCACAATACACACTATCTCACACAATGAGGAACT     180
                ***** ******** ********* ** * **** *** ************ ******
                                                           RUNX3
Human           CAGGAGCAGTCTTGCTGAGTAGTTCTGGCACAGGGTTGCTCATGAGGTTGCTGCTGAGGT     240
Rhesus          CAGGAGCAGTCTTGCTGAGTAGTTCTGGCACAGGGTCGCTCATGAGGTTGCTGCTGAGGT     236
Patas           CAGGAGCAGTCTTGCTGAGTAGTTCTGGCACAGGGTCGCTCATGAGGTTGCTGCTGAGGT     240
AGM             CAGGAGCAGTCTTGCTGAGTAGTTCTGGCACAGGGTCGCTCATGAGGTTGCTGCTGAGGT     240
                ************************************ ***********************

Human           GAGGGTCAGGTCTGGAGCCATCTGAAGGCTGGGATGGGGCTGGAGATTCTGCCTCCAAGA     300
Rhesus          GTGGGCCAGGCCAGGAGCCATCTGAAGGCTGGGATGGGGCTGGAGGATCTGCCTCCAAGA     296
Patas           GTGGGCCAGGCCAGGAGCCATCGGAAGGCTGGGATGGGGCTGGAGGATCTGCCTCCAAGA     300
AGM             GTGGGCCAGGCCAGGAGCCATTGGAAGGCTGGGATGGGGCTGGAGGATCTGCCTCCAAGA     300
                * *** **** * ********  **********************  *************

Human           CAGCTCACTCGGGAGGCTGTCGGCCAGAGGCCTTAACTCCTCCCTGT-GTGGGTGTCTTT     359
Rhesus          CAGCTCCCTTGGGAGGTTGTGGGCCAGAGGCCTTAGCGCCTCCCTGCGTTGGGCGTCTTT     356
Patas           CAGCTGCCCTGGGAGGTTGTGGGCCAGAGGCCTTAGCACCTCCCTGC-TTGGGCGTCTTT     359
AGM             CAGCTGCCCTGGGAAGTTGTGGGCCAGAGGCCTTAGCACCTCCCTGC-TTGGGCGTCTTT     359
                *****  *  **** * *** ************** * ********   **** ******

Human           ATGGGGCCTCTCACAACACGACACAGCAACTGGCTTCCCCCAGAGGGACAGCGTGGAAAA     419
Rhesus          ATGGGGCCTCTCACAACATGACACAGCAACTGGCTTCCCCCAGAGGGACAGCGTGGACAA     416
Patas           ATGGGGCCTCTCACAACACCACACGGCAACTGGCTTCCCTCAGAGGGACAGCGTGGACAA     419
AGM             ATGGGGCCTCTCACAACACCACACAGCAACTGGCTTCCCTCAGAGGGACAGCGTGGACAA     419
                ******************  **** ************** ***************** **
                                                  LEF1/TCF
Human           GACAAAAGCTACCACATCTTTATTTCAAGATTAGATTTGATCTTGAAAGCAACGTGCCAT     479
Rhesus          GACAAAAGCTACCATGTCTT----------------TTGATCTGGAAAACAACATACCAT     460
Patas           GACAAAAGCTACCATGTCTTTATTTCAAGATTGAATTTGATCTTGAAAACAACATACCAT     479
AGM             GACAAAAGCTACCATGTCTTTATTTCAAGATTGAATTTGATCTTGAAAACAACATACCAT     479
                **************  ****                ******* **** **** * ****

Human           AATTTCTGCCCTATTCTATTGATCACAGAGACCAACCTGGTGCAAGCAGGAGGGGGCAAT     539
Rhesus          GATTTCTGCCCTATTCTATTGGTCACAGAGACCAACCTGGTGCAAGCAGGAGGGGGCAAT     520
Patas           GATTTCTGCCCTATTCTATTGGTCACAGAGACCAACCTGGTGCAAGCAGGAGGGGGCAAT     539
AGM             GATTTCTGCCCTATTCTATTGGTCACAGAGACCAACCTGGTGCAAGCAGGAGGGGGCAAT     539
                 ******************** **************************************

Human           GCAAGGGTGTGAACTGAGGGAGACAGGAGTCACTGGGGGCCATCTTGCAGCCTGGCTGTC     599
Rhesus          GCAAGGGTGTGAACGGAGGGAGACAGGAGTCACTGGGGGCCATCTTGCAGCCTGGCTGTC     580
Patas           GCAAGGGTGTGAACGGAGGGAGACAGGAGTCACTGGGGGCCATCTTGCAGCCTGGCTGTC     599
AGM             GCAAGGGTGTGAACGGAGGGAGACAGGAGTCACTGGGAGCCATCTTGCAGCCTGGCTGTC     599
                ************** ********************** **********************

Human           AGAGTGGGGAGCAGTGCCTGAAACAGAGATAGGCCAAGAGACGGGAAGGGACGTCTCTGA     659
Rhesus          AGAGTGGGGAGCAGTGCCTGAAACAGGGATAGGCCAAGAGAGGAGAAGGGACCCCTCTGA     640
Patas           AGAGTGGAGAGCAGTGCCTGAAACAGGGATAGGCCAAGAGAGGAGAAGGGACCCCTCCGA     659
AGM             AGAGTGGAGAGCAGTGCCTGAAACAGGGATAGGCCAAGAGAGGAGAAGGGACCCCTCCGA     659
                ******* ****************** ************** * ********  *** **

Human           GCATCTCCATCCCCAGCCCTCTTCTCTTGTCCACTCTCCAGAAGTTCTGGAAGCCAAGTG     719
Rhesus          GCATCTCCATCCCCAGCTGTCTTCTCTTGTCCACTCTCGAGAAGTTCTGGAAGCCAAGTG     700
Patas           GCATCTCCATCCCCAGCCATCTTCTCTTGTCCACTCTCGAGAAGTTCTGGAAGCCAAGTG     719
AGM             GCATCTCCATCCCCAGCCATCTTCTCTTGTCCACTCTCGAGAAGTTCTGGAAGCCAAGTG     719
                *****************  ******************* *********************

Human           AGGTCCAGGGCCTTGGCAAGTCGAGTGTGTGAGGTAGGAGGCCATACTGTGCACATTCAG     779
Rhesus          AGGTCTAGGGCCCTGGCAAGTCGAGTGTGTGAGGTAGAAGGCCGTACTGTGCACACTCAG     760
Patas           AGGTCTAGGGCCCTGGCAAGTCGAGTGTGTGAGGTAGGAGGCCGTACTGTGCACACTCAG     779
AGM             AGGTCTAGGGCCCTGGCAAGTCGAGTGTGTGAGGTAGGAGGCCGTACTGTGCACACTCAG     779
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            ***** ****** ************************ ***** *********** ****

Human       CCTTGGAGTCGGGTTTGCCAGCGGTTCCCCTACCCCTGACGTGGTCTTCTCAGCTCCATA    839
Rhesus      CCCTGGAGTCGGGTTTGCCAGCTGTTCCCCTACCCGTGACCTGGTCTTCTCAGCTCCATA    820
Patas       CCTTGGAGTCGGGTTTGCCAGCCGTTCCCCTACCCGTGACCTGGTCTTCTCAGCTCCATA    839
AGM         CCCTGGAGTCGGGTTTGCCAGCCGTTCCCCTACCCGTGACCTGGTCTTCTCAGCTCCATA    839
            ** ******************* ************ **** *******************

Human       GTGCAGAGGAGGAGCCTCTGCAGGCCCAGAAATTTCCCTGCCCACCTCCCCTACCAGGTA    899
Rhesus      GCGCAGAGGAGGAGCCTCTGCAGGCCCAGAAATGTCCTTGCCCACCTCCCCTACCTGGTA    880
Patas       GCGCAGAGGAGGAGCCTCTGCAGGCCCAGAAATGTCCTTGCCCACCTCCCCTGCCTGGTA    899
AGM         GCGCAGAGGAGGAGCCTCTGCAGGCCCAGAAATGTCCTTGCCCACCTCCCCTGCCTGGTA    899
            * ******************************* *** ************** ** ****
                                                      LEF1/TCF
Human       GAGATGTTAGGGTTCAGGCCTGAGCCCCTGCTGCTATCCCTCCTTCAAAGGAGGAGATCA    959
Rhesus      GAGATGTTAGGGTTCAGGCCTGAGCCCCTGCTGCTATCCCTCCTTCAAAGGAGGAGATCA    940
Patas       GAGATGTTAGGGTTCAGGCCTGAGCCCCTGCTGCTATCCCTCCTTCAAAGGAGGAGATCA    959
AGM         GAGATGTTAGGGTTCAGGCCTGAGCCCCTGCTGCTATCCCTCCTTCAAAGGAGGAGATCA    959
            ************************************************************
                                                           LEF1/TCF
Human       AGGAGCTTAGGGTCCCCCGCACAGGCCCACCCCAGGGTGGGGTTCTTCCTTTGAAGGGAA    1019
Rhesus      AGGAGCTTAGGATCCCCTGCACAGGCCCACCCCAGGGTGGGGTTCTTCCTTTGAAGGGAG    1000
Patas       AGGAGCTTAGGATCCCCTGCACAGGCCCACCCCAGGGTCGGGTTCTTCCTTTGAAGGGAA    1019
AGM         AGGAGCTTAGGATCCCCTGCACAGGCCCACCCCAGGGTGGGGTTCTTCCTTTGAAGGGAA    1019
            *********** ***** ******************** ********************
                                                 RUNX1
Human       TTGCTTTGGGGTGGGGTCGGTTCTATCTGCTCCACTCTGTGGCTGACAGTTTCTCCAAGG    1079
Rhesus      TGGGTTTGGGGTAGGGTCGGTTCTATCTGTTCTACTCTGTGGCTGACAGTTTCTCCAAGG    1060
Patas       TGGGTTTGGGGTAGGGTCGGTTCTATCTGTTCTACTCTGTGGCTGACAGTTTCTCCAAGG    1079
AGM         TGGGTTTGGGGTAGGGTCGGTTCTATCTGTTCTACTCTGTGGCTGACAGTTTCTCCAAGG    1079
            * * ******** **************** ** ***************************
                  ZEB
Human       GGCTGCAGGTGTCAGCTGTCTGAGCCCGGGCTGAGCTCTGAAACGTGCCTACTCAAACTT    1139
Rhesus      GGCTGCAGGTGTCAGCTGTCTGAGGCCAGCCTGAGCTCTGAAATGTGCCTACTCAAACTT    1120
Patas       GGCTGCAGGTGTCAGCTGTCTGAGCCCAGCCCGAGCTCTGAAATGTGCCTACTCAAACTT    1139
AGM         GGCTGCAGGTGTCAGCTGTCTGAGCCCAGCCTGAGCTCTGAAATGTGCCTACTCAAACTT    1139
            ************************ ** * * *********** ****************

Human       CCCGTGGGGTAGGGGAGGCCCAGAACCACCCTCTGAGAGTGGCAAAAAGTGGTCCTGGAG    1199
Rhesus      CCA-TGGGGTGAGGGAGGCCCAGAACCACCCTCTGAGAGTGGCAACAAGTGGTCCTGCAG    1179
Patas       CCCGTGGGGTGAGGGAGGCCCAGAACCACCCTCTGAGAGTGGCAACAAGTGGTCCTGCAG    1199
AGM         CCCGTGGGGTGAGGGAGGCCCAGAACCACCCTCTGAGAGTGGCAACAAGTGGTCCTGCAG    1199
            **  ******  ********************************* *********** **

Human       CCAGGGGAAATGTGGATGGGGTAGA-1224
Rhesus      CCAGGGGAAATGTGGATGGGGTAGAC1205
Patas       CCAGGGGAAATGTGGATGGGGTAGAC1225
AGM         CCAGGGGAAATGTGGATGGGGTAGAC1225
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CLUSTAL O(1.2.4) multiple sequence alignment: TSS

                                                    ELF/ETS
Patas       ----GGGGCCGGCCCAGGCCTAGGGTGTGGAGGAACCTCGCCATCGGGCTTCCTGTCTCT    56
AGM         ----GGGGCCGGCCCAGGCCTAGGGTATGGAGGAGCCTCGCCATCGGGCTTCCTGTCTCT    56
Rhesus      ----GGGGCCGGCCCAGGCCTAGGGTGTGGAGGAGCCTCGCCATCGGGCTTCCTGTCTCT    56
Human       GTTTGGGGCCGGCCCAGGCCTAGGGTGTGGAGGAGCCTTGCCATCGGGCTTCCTGTCTCT    60
                ********************** ******* *** *********************
                                         TCF-1
Patas       CTTCATTTAAGCACGACTCTGCAGAAGGAACAAAGCACCCTCCCCACTGGGCTCCTGGTT    116
AGM         CTTCATTTAAGCACGACTCTGCAGAAGGAACAAAGCACCCTCCCCACTGGGCTCCTGGTT    116
Rhesus      CTTCATTTAAGCACGACTCTGCAGAAGGAACAAAGCACCCTCCCCACTGGGCTCCTGGTT    116
Human       CTTCATTTAAGCACGACTCTGCAGAAGGAACAAAGCACCCTCCCCACTGGGCTCCTGGTT    120
            ************************************************************

Patas       GCAAAGCTCCAAGTCCTCACACAGATACACTTGT  150
AGM         GCAAAGCTCCAAGTCCTCACACAGATACACTTGT  150
Rhesus      GCAAAGCTCCAAGTCCTCATACAGATACACTTGT  150
Human       GCAGAGCTCCAAGTCCTCACACAGATACGC----  150
            *** *************** ******** *
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CLUSTAL O(1.2.4) multiple sequence alignment: S4


Human       CGGTTCCCCCGATGTGGGTGTCTGAGGCGAAGAAGAGGATGGCGGAGGTTGCAGCCACCA     60
Rhesus      CGGTTCCCCCGATGTGGGTGTCTGAGGCGAAGAAGAGGATGGCGGAGGTTGCAGCCACCA     60
Patas       CGGTTCCCCCGATGTGGGTGTCTGAGGCGAAGAAGAGGATGGCGGAGGTTGCAGCCACCA     60
AGM         CGGTTCCCCCGATGTGGGTGTCTGAGGCGAAGAAGAGGATGGCGGAGGTTGCAGCCACCA     60
            ************************************************************
             RUNX3
Human       ACCACAAGAGTTCCTTAGAGGGGTCACAGTCTCTAGGAAGTTTATAGGAAGCTAGTCAGC     120
Rhesus      ACCACAAGAGTTCCTTAGAGGGGTCACAGTCTCTAGGAAGTTTATAGGAAGCCAGTCAGC     120
Patas       ACCACAAGAGTTCCTTAGAGGGGTCACAGTCTCTAGGAAGTTTCTAGGAAGCCAGTCAGC     120
AGM         ACCACAAGAGTTCCTTAGAGGGGTCACAGTCTCTAGGAAGTTTCTAGGAAGCCAGTCAGC     120
            ******************************************* ******** *******

Human       AGTAGAGAGGGTGAACGCGGTGGGGCACATCCCGCGGCTGGGCTTGAGTGGGCTGCTTGG     180
Rhesus      AGTAGAGAGGGTGAACGCGGTGGGGCACATCCCGCGGCTGGGCTTGAGTGGGCTGCTTGG     180
Patas       AGTAGAGAGGGTGAACGCGGTGGGGCACATCCCGCGGCTGGGCTCGAGTGGGCTGCTTGG     180
AGM         AGTAGAGAGTGTGAACGCGGTGGGGCACATCCCGCGGCTGGGCTCGAGTGGGCTGCTTGG     180
            ********* ********************************** ***************
                              LEF1
Human       GGGTTATGGGGAGAAGATAAAAGTGCCTGTGGGACCACAGACTCTCGCTGTGGTGGAGCT     240
Rhesus      GGGTTATGGAGAGAAGATAAAAGTGCCTGTGGGACCACAGACTCTTGCTGTGGTGGAGCT     240
Patas       GGGTTATGGAGAGAAGATAAAAGTGCCTGTGGGACCACAGACTCTCGCTGTGGTGGAGCT     240
AGM         GGGTTATGGAGAGAAGATAAAAGTGCCTGTGGGACCACAGACTCTCGCTGTGGTGGAGCT     240
            ********* *********************************** **************

Human       GGGCCCTCTTACCCTCCCAAGCCTCGCCCCTCATCCCATCCCTGGGGGCCAGGGGTGAGG     300
Rhesus      GGGCCCTCTTACCCTCCCAAGCCTCGCTCCTCATCCCATCCCTGGGGGCCAGGGGTGAGG     300
Patas       GGGCCCTCTTACCCTCCCAAGCCTCGCTCCTCGTCCCATCCCTGGGGGCCAGAGGTGAGG     300
AGM         GGGCCCTCTTACCCTCCCAAGCCTCACTCCTCGTCCCATCCCTGGGGGCCAGGGGTGAGG     300
            ************************* * **** ******************* *******
                      RUNX3
Human       GCGGCAGGAACCTCAAGGCTCTGAGAAAGTGCGTGGTGTGTGTTGCCATTTTGGTCTCTT     360
Rhesus      GCGGCAGGAACCTCAAGGCTCTGAGAGAGTGCGTGGTATGTGTTGCCATTTTGGTCTCAT     360
Patas       GCGGCAGGAACCTCAAGGCTCTGAGAGAGTGCGTGGTGTGTGTTGCCATTTTGGTCTCAT     360
AGM         GCGGCAGGAACCTCAAGGCTCTGAGAGAGTGCGTGGTGTGTGTTGCCATTTTGGTCTCAT     360
            ************************** ********** ******************** *

Human       CTCTTTCTCAGTCTCTCTTTGCCTCACTTTGGATCTATGCTCTGTGCATCTGTCTT-        416
Rhesus      CTCTTTCTCAGTCTCTCTTTGCCTCACTTTGGATCTATGCTCTGTGCATCTGTCTTG        417
Patas       CTCTTTCTCAGTCTCTCTTTGCCTCACTTTGGATCTGTGCTCTGTGCATCTGTCTTG        417
AGM         CTCTTTCTCAGTCTCTCTTTGCCTCACTTTGGATCTGTGCTCTGTGCATCTGTCTTG        417
            ************************************ *******************
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CLUSTAL O(1.2.4) multiple sequence alignment: E4M

                                          ELK/ETS
Human           AGGCCAGGAGGACTGTGTACAGACCGGAAGGAGCTAGAGCTTAGTGGCAGCCTGAGAGGG     60
Rhesus          -GGCCAGGAGGCCCGTGTACAGACCGGAAGCAGCTAGAGCTTAGTGGCAGCTGGAGAGGG     59
Patas           -GGCCAGGAGGCCTGTGTACAGACCAGAAGCAGCTAGAGCTTAGTGGCAGCTGGAGAGGG     59
AGM             -GGCCAGGAGGCCTGTGTACAGACCGGAAGCAGCTAGAGCTTAGTGGCAGCTGGAGAGGG     59
                 ********** * *********** **** ********************  *******

Human           GAAGCTGAAAAAGGAGAAGAGGCAAGGGGCATTCCAGGGGAGCCCGGGAGAGCCAGCACG     120
Rhesus          GAAGATTATAAAGGAGGAGAGGCAAGGGGCATTCCAGGGGAGCCCGGGAGAGCCAGCATG     119
Patas           GAAGATTATAAAGGAGGAGAGGCAAGGGGCATTCCAGGGGAGCCTGGGAGAGCCAGCACG     119
AGM             GAAGATTATAAAGGAGGAGAGGCAAGGGGCATTCCAGGGGAGCCTGGGAGAGCCAGCACG     119
                **** * * ******* *************************** ************* *

Human           GCCGCCTGGTATATGAGGCAAAGAGGAAGACAGACACAGACACAGGGAGCTGCAGGCTGG     180
Rhesus          ACCTCCTGGCATATGAGGCACAGAGGAAGACAGACACAGACACAGGGAGCTGCAGGCTGG     179
Patas           ACCTCCTGGCATATGAGGCACAGAGGAAGACAGACACAGACACAGGGAGCTGCAGGCTGG     179
AGM             ACCTCCTGGCATATGAGGCACAGAGGAAGACAGACACAGACACAGGGAGCTGCAGGCTGG     179
                 ** ***** ********** ***************************************

Human           GGGCATAAGCTGGGGGCTGGGAAGCATAGATACAGAAATGCACAGATGTGAGCTGAGAAG     240
Rhesus          GGGCATAAGCTGGGGGCTGGGAAGCATAGATACAGAAATGCACAGATGTGAGCTGAGAAG     239
Patas           GGGCATAAGCTGGGGGCTGGGAAGCACAGATACAGAAATGCACAGATGTGAGCTGCGAAG     239
AGM             GGGCATAAGCTGGGGGCTGGGAAGCACAGATACAGAAATGCACAGATGTGAGCTGAGAAG     239
                ************************** **************************** ****

Human           CAAGGAGGGAGAGAGAGAG----ACAGAAAGAGAGAGAGAGACGTGCCAGGGCTTGAGGG     296
Rhesus          CAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAAAGAGAGAGACGTGCTAGGGCTTGAGGG     299
Patas           CAAGCAGAGAGAGAGAGAGA------GAGAGAGAGAGAGAGACGTGCTAGGGCTTGAGGG     293
AGM             CAAGCAGAGAGAGAGAG------------AGAGAGAGAGAGACGTGCTAGGGCTTGAGGG     287
                **** ** *********            *** ************** ************

Human           ACCAGAGAGCCCTCCCAGCCTCTCTCGGAGTGCTGGTATACAGGATGCTACCGTACTAGG     356
Rhesus          ACCAGAGAGCCCTCCCAACCTCTCTCGGAGTGCTGGTCTACAGGATGCTGCTGTACTAGC     359
Patas           ACCAGAGAGCCCTCCCAACCTCTCTCGGAGTGCTGGTCTACAGGATGCTACCGTACTAGG     353
AGM             ACCAGAGAGCCCTCCCAACCTTTCTCGGAGTGCTGGTCTACAGGATGCTACCGTACTAGG     347
                ***************** *** *************** *********** * *******
                                                   TCF/LEF
Human           GTAAGACACCTCTGGGGACGCTGAGTATGGGAATCAAAGGCCAGATCTCTGGGGTGGCAG     416
Rhesus          GTAAGGCACCTCTGGGGACGCTGAGTATGGGAATCAAAGGCCGGATCTCTGTGGTGGCAG     419
Patas           GTAAGGCACCTCTGGGGACGCTGAGTATGGGAATCAAAGGCCAGATCTCTGCGGTGGCAG     413
AGM             GTAAGGCACCTCTGGGGACGCTGAGTATGGGAATCAAAGGCCAGATCTCTGCAGTGGCAG     407
                ***** ************************************ ********  *******
                                                        RUNX1
Human           CGGAAGCCCAAAGCACCAAAGCAAGCATGCTGGAAACCCACAGCCTCCTCCACTTAGCAG     476
Rhesus          CGGAAGCCCAAAGCACCAAAGCAAGCATGCTGGAAACCCACAGCCTCCTCCACTTAGCAG     479
Patas           CGGAAGCCCAAAGCACCAAAGCAAGCATGCTGGAAACCCACAGCCTCCTCCACTTAGCAG     473
AGM             CGGAAGCCCAAAGCACCAAAGCAAGCATGCTAGAAACCCACAGCCTCCTCCACTTAGCAG     467
                ******************************* ****************************

Human           AGCCTTGGGGTGAGATGAGGCAGAACAGGGAGCTGGAGGCAGGGAGGTGGCTGTCTGCAC     536
Rhesus          AGCCTTGGGGTGAGATGAGGCGGAACAGGGAGCTGGAGGCAGGGAGGTGGCTGTCTGCAC     539
Patas           AGCCTTGGGGTGAGATGAGGCGGAACAGGGAGCTGGAGGCAGGGAGGTGGCTGTCTGCAC     533
AGM             AGCCTTGGGGTGAGATGAAGCGGAACAGGGAGCTGGAGGCAGGGAGGTGGCTGTCTGCAC     527
                ***************** ** ***************************************

Human           ATACCTCAGGACCATGGAGCTGGGGGAGTCAAAACAGCCACCATATGGGGAAGGGTCAAG     596
Rhesus          AGACCTCAGGACCATGGAGCAGGGGGAGTCAAAACAGCCACCATGTGGGGAAGGGTCAAG     599
Patas           AGACCTCAGGACCATGGAGCAGGGGGAGTCAAAACAGCCACCATGTGGGGAAGGGTCAAG     593
AGM             AGACCTCAGGACCATGGAGCAGGGGGAGTCAAAACAGCCACCATGTGGGGAAGGGTCAAG     587
                * ****************** ************************ **************

Human           AATGCCTCTAGTCTTCCCCAGGCATCTTATCAGGGTAAGCTGAATTTGGACCCCAGAGAA     656
Rhesus          AATGCCTCTAGTCTTCCCCAGGCATCTTATCAGGGTAAGCTGGATTTGGACCCCAGAGAA     659
Patas           AATGCCTCTAGTCTTCCCCAGGCATCTTATCAGGGTAAGCTGGATTTGGACCCCAGAGAA     653
AGM             AATGCCTCTAGTCTTCCCCAGGCATCTTATCAGGGTAAGCTGGATTTGGACCCCAGAGAA     647
                ****************************************** *****************

Human           GGGATATCGTTTATGGAGACTTCCCCTCTTTCATCCCCTGCTCACCAAGGACC  709
Rhesus          GGGATATCCTATATGGAGACTTCCCCTCTTTCACTCCCTGTTCACCAAG----  708
Patas           GGGATATCCTATATGGAGACTTCCCCTCTTTCACTCCCTGCTCACCAAG----  702
AGM             GGGATATCCTATATGGAGACTTCCCCTCTTTCACTCCCTGCTCACCAAG----  696
                ******** * **********************  ***** ********
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Supplementary figure 1. DNA sequence alignments determined by ClustalX of CD4 regulatory regions in humans, rhesus macaque, Patas, and AGM. Bases highlighted in yellow represent sequences conservation in natural host species that have diverged from progressive hosts of HIV-1/SIV. Regions denoted in red represent transcription factor binding motifs predicted from the JASPAR database.