```
                            FLAG
E1_FLAG-mA3   ATGGACTACAAAGACGATGACGACAAGGGACCATTCTGTCTGGGATGCAGCCATCGCAAA
isoform_2     -----------------------ATGGGACCATTCTGTCTGGGATGCAGCCATCGCAAA
isoform_1     -----------------------ATGGGACCATTCTGTCTGGGATGCAGCCATCGCAAA
                                     *:*********************************


E1_FLAG-mA3   TGCTATTCACCGATCAGAAACCTGATATCTCAAGAAACATTCAAGTTCCACTTTAAGAAC
isoform_2     TGCTATTCACCGATCAGAAACCTGATATCTCAAGAAACATTCAAGTTCCACTTTAAGAAC
isoform_1     TGCTATTCACCGATCAGAAACCTGATATCTCAAGAAACATTCAAGTTCCACTTTAAGAAC
              ************************************************************


E1_FLAG-mA3   CTAGGCTATGCCAAAGGCCGGAAAGATACCTTCTTGTGCTATGAAGTGACTAGAAAGGAC
isoform_2     CTAGGCTATGCCAAAGGCCGGAAAGATACCTTCTTGTGCTATGAAGTGACTAGAAAGGAC
isoform_1     CTAGGCTATGCCAAAGGCCGGAAAGATACCTTCTTGTGCTATGAAGTGACTAGAAAGGAC
              ************************************************************


E1_FLAG-mA3   TGCGATTCACCCGTCTCCCTTCACCATGGGGTCTTTAAGAACAAGGACAACATCCACGCT
isoform_2     TGCGATTCACCCGTCTCCCTTCACCATGGGGTCTTTAAGAACAAGGACAACATCCACGCT
isoform_1     TGCGATTCACCCGTCTCCCTTCACCATGGGGTCTTTAAGAACAAGGACAACATCCACGCT
              ************************************************************


E1_FLAG-mA3   GAAATCTGCTTTTTATACTGGTTCCATGACAAAGTACTGAAAGTGCTGTCTCCGAGAGAA
isoform_2     GAAATCTGCTTTTTATACTGGTTCCATGACAAAGTACTGAAAGTGCTGTCTCCGAGAGAA
isoform_1     GAAATCTGCTTTTTATACTGGTTCCATGACAAAGTACTGAAAGTGCTGTCTCCGAGAGAA
              ************************************************************


E1_FLAG-mA3   GAGTTCAAGATCACCTGGTATATGTCCTGGAGCCCCTGTTTCGAATGTGCAGAGCAGATA
isoform_2     GAGTTCAAGATCACCTGGTATATGTCCTGGAGCCCCTGTTTCGAATGTGCAGAGCAGATA
isoform_1     GAGTTCAAGATCACCTGGTATATGTCCTGGAGCCCCTGTTTCGAATGTGCAGAGCAGATA
              ************************************************************


E1_FLAG-mA3   GTAAGGTTCCTGGCTACACACCACAACCTGAGCCTGGACATCTTCAGCTCCCGCCTCTAC
isoform_2     GTAAGGTTCCTGGCTACACACCACAACCTGAGCCTGGACATCTTCAGCTCCCGCCTCTAC
isoform_1     GTAAGGTTCCTGGCTACACACCACAACCTGAGCCTGGACATCTTCAGCTCCCGCCTCTAC
              ************************************************************


E1_FLAG-mA3   AACGTACAGGACCCAGAAACCCAGCAGAATCTTTGCAGGCTGGTTCAGGAAGGAGCCCAG
isoform_2     AACGTACAGGACCCAGAAACCCAGCAGAATCTTTGCAGGCTGGTTCAGGAAGGAGCCCAG
isoform_1     AACGTACAGGACCCAGAAACCCAGCAGAATCTTTGCAGGCTGGTTCAGGAAGGAGCCCAG
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E1_FLAG-mA3    GTGGCTGCCATGGACCTATACGAATTTAAAAAGTGTTGGAAGAAGTTTGTGGACAATGGT
isoform_2      GTGGCTGCCATGGACCTATACGAATTTAAAAAGTGTTGGAAGAAGTTTGTGGACAATGGT
isoform_1      GTGGCTGCCATGGACCTATACGAATTTAAAAAGTGTTGGAAGAAGTTTGTGGACAATGGT
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E1_FLAG-mA3    GGCAGGCGATTCAGGCCTTGGAAAAGACTGCTTACAAATTTTAGATACCAGGATTCTAAG
isoform_2      GGCAGGCGATTCAGGCCTTGGAAAAGACTGCTTACAAATTTTAGATACCAGGATTCTAAG
isoform_1      GGCAGGCGATTCAGGCCTTGGAAAAGACTGCTTACAAATTTTAGATACCAGGATTCTAAG
               ************************************************************


E1_FLAG-mA3    CTTCAGGAGATTCTGAG-------------------------------------------
isoform_2      CTTCAGGAGATTCTGAG-------------------------------------------
isoform_1      CTTCAGGAGATTCTGAGACCTTGCTACATCTCGGTCCCTTCCAGCTCTTCATCCACTCTG
               *****************


E1_FLAG-mA3    ---------------------------------------------------------GCGA
isoform_2      ---------------------------------------------------------GCGA
isoform_1      TCAAATATCTGTCTAACAAAAGGTCTCCCAGAGACGAGGTTCTGGGTGGAGGGCAGGCGA
                                                                        ****


E1_FLAG-mA3    ATGGACCCGCTAAGTGAAGAGGAATTTTACTCGCAGTTTTACAACCAACGAGTCAAGCAT
isoform_2      ATGGACCCGCTAAGTGAAGAGGAATTTTACTCGCAGTTTTACAACCAACGAGTCAAGCAT
isoform_1      ATGGACCCGCTAAGTGAAGAGGAATTTTACTCGCAGTTTTACAACCAACGAGTCAAGCAT
               ************************************************************


E1_FLAG-mA3    CTCTGCTACTACCACCGCATGAAGCCCTATCTATGCTACCAGCTGGAGCAGTTCAATGGC
isoform_2      CTCTGCTACTACCACCGCATGAAGCCCTATCTATGCTACCAGCTGGAGCAGTTCAATGGC
isoform_1      CTCTGCTACTACCACCGCATGAAGCCCTATCTATGCTACCAGCTGGAGCAGTTCAATGGC
               ************************************************************


E1_FLAG-mA3    CAAGCGCCACTCAAAGGCTGCCTGCTAAGCGAGAAAGGCAAACAGCATGCAGAAATCCTC
isoform_2      CAAGCGCCACTCAAAGGCTGCCTGCTAAGCGAGAAAGGCAAACAGCATGCAGAAATCCTC
isoform_1      CAAGCGCCACTCAAAGGCTGCCTGCTAAGCGAGAAAGGCAAACAGCATGCAGAAATCCTC
               ************************************************************


E1_FLAG-mA3    TTCCTTGATAAGATTCGGTCCATGGAGCTGAGCCAAGTGACAATCACCTGCTACCTCACC
isoform_2      TTCCTTGATAAGATTCGGTCCATGGAGCTGAGCCAAGTGACAATCACCTGCTACCTCACC
isoform_1      TTCCTTGATAAGATTCGGTCCATGGAGCTGAGCCAAGTGACAATCACCTGCTACCTCACC
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E1_FLAG-mA3    TGGAGCCCCTGCCCAAACTGTGCCTGGCAACTGGCGGCATTCAAAAGGGATCGTCCAGAT
isoform_2      TGGAGCCCCTGCCCAAACTGTGCCTGGCAACTGGCGGCATTCAAAAGGGATCGTCCAGAT
isoform_1      TGGAGCCCCTGCCCAAACTGTGCCTGGCAACTGGCGGCATTCAAAAGGGATCGTCCAGAT
               ************************************************************


E1_FLAG-mA3    CTAATTCTGCATATCTACACCTCCCGCCTGTATTTCCACTGGAAGAGGCCCTTCCAGAAG
isoform_2      CTAATTCTGCATATCTACACCTCCCGCCTGTATTTCCACTGGAAGAGGCCCTTCCAGAAG
isoform_1      CTAATTCTGCATATCTACACCTCCCGCCTGTATTTCCACTGGAAGAGGCCCTTCCAGAAG
               ************************************************************


E1_FLAG-mA3    GGGCTGTGTTCTCTGTGGCAATCAGGGATCCTGGTGGACGTCATGGACCTCCCACAGTTT
isoform_2      GGGCTGTGTTCTCTGTGGCAATCAGGGATCCTGGTGGACGTCATGGACCTCCCACAGTTT
isoform_1      GGGCTGTGTTCTCTGTGGCAATCAGGGATCCTGGTGGACGTCATGGACCTCCCACAGTTT
               ************************************************************


E1_FLAG-mA3    ACTGACTGCTGGACAAACTTTGTGAACCCGAAAAGGCCGTTTTGGCCATGGAAAGGATTG
isoform_2      ACTGACTGCTGGACAAACTTTGTGAACCCGAAAAGGCCGTTTTGGCCATGGAAAGGATTG
isoform_1      ACTGACTGCTGGACAAACTTTGTGAACCCGAAAAGGCCGTTTTGGCCATGGAAAGGATTG
               ************************************************************


E1_FLAG-mA3    GAGATAATCAGCAGGCGCACACAAAGGCGGCTCCGCAGGATCAAGGAGTCCTGGGGTCTG
isoform_2      GAGATAATCAGCAGGCGCACACAAAGGCGGCTCCGCAGGATCAAGGAGTCCTGGGGTCTG
isoform_1      GAGATAATCAGCAGGCGCACACAAAGGCGGCTCCGCAGGATCAAGGAGTCCTGGGGTCTG
               ************************************************************


E1_FLAG-mA3    CAAGATTTGGTGAATGACTTTGGAAACCTACAGCTTGGACCCCCGATGTCTTGA
isoform_2      CAAGATTTGGTGAATGACTTTGGAAACCTACAGCTTGGACCCCCGATGTCTTGA
isoform_1      CAAGATTTGGTGAATGACTTTGGAAACCTACAGCTTGGACCCCCGATGTCTTGA
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Figure S5. Sequence analysis of the entire coding region of *Apobec3* cDNA cloned from E1 spleen cells. Spleen cell mRNA was prepared from E1 mouse, reverse transcribed as described for Figure S2, and the *Apobec3* cDNA was amplified by using primers specific for 5' and 3' UTRs of the FLAG-tagged mA3 allele (5'-CAGAAAATGCAACCCCAGCGC-3' and 5'-CATGCACAACTTAATCTTGTCTTTC-3', respectively) and Pfu Turbo DNA Polymerase (Agilent Technologies, Santa Clara, California, U.S.A.). The amplified fragment was cloned into pCR-Blunt II-TOPO plasmid using the Zero Blunt TOPO PCR Cloning Kit (Invitorogen, Thermo Fisher Scientific) and sequenced as described [9]. The resultant DNA sequence was aligned with the consensus isoform 1 (NCBI Reference Sequence: NM_001160415.1) and isoform 2 (NCBI Reference Sequence: NM_030255.3) sequences using the Clustal W (https://www.genome.jp/tools-bin/clustalw).