

**Table S1.** Multiple alignment of FLAG-tagged EFEMP1 wildtype (E1) and variant (E2 – E18) protein sequences.

E1	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E4	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E9	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E10	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E2	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E3	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E5	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E8	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E6	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E7	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E11	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCK-----
E13	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E14	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E15	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E18	MDYKDDDDKLKALFLMTLIALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDECDIVPDAKGGMKCVNHGGYLCLPKTAQIIV
E1	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E4	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E9	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E10	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEVQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E2	-----
E3	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E5	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E8	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E6	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E7	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E11	-----
E13	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E14	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E15	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E18	NNEQPQQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFIRRNPADPQRIPSNPSHRIQCAAGYEQS
E1	EHNVCQDIDECTAGTHNCRADQVICINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E4	EHNVCQDIDECTAGTHNCRDQVICINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E9	EHNVCQDIDECTAGTHNCRDQVICINLRGSFACQCPPGYQKRGDQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E10	EHNVCQDIDECTAGTHNCRADQVICINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E2	-----DIDECTAGTHNCRADQVICINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E3	EHNVCQDIDECTAGTHNCRADQVICINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E5	EHNVCQDIDECTAGTHNCRADQVICINLRGSFACQCPPGYQKRGDQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E8	EHNVCQDIDECTAGTHNCRDQVICINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E6	EHNVCQK-----DIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E7	EHNVCQK-----DIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E11	-----DIDECTAGTHNCRADQVICINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCV
E13	EHNVCQDIDECTAGTHNCRADQVICINLRGSFACQCPPGYQKRGEQCV-----
E14	EHNVCQDIDECTAGTHNCRDQVICINLRGSFACQCPPGYQKRGEQCV-----
E15	EHNVCQDIDECTAGTHNCRADQVICINLRGSFACQCPPGYQKRGDQCV-----
E18	EHNVCQ-----
E1	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E4	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E9	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E10	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E2	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E3	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E5	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E8	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E6	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E7	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E11	DINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDEDECRTSSYLQYQCVNEPGKFSCMCPPQGYQVVRSRRTCQDINECET
E13	-----
E14	-----
E15	-----
E18	-----

E1	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCVCPVSNAMELPCRELQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFR	
E4	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCVCPVSNAMELPCRELQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFR	
E9	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCVCPVSNAMELPCRELQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFR	
E10	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCVCPVSNAMELPCRELQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFR	
E2	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCVCPVSNAMELPCRELQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFR	
E3	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCV-----	
E5	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCV-----	
E8	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCV-----	
E6	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCV-----	
E7	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCVCPVSNAMELPCRELQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFR	
E11	TNECREDEMWCNYHGGFRCYPRNPCQDPYILT PENRCV-----	
E13	-----	
E14	-----	
E15	-----	
E18	-----	
E1	IKSGNENGEFYLRQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVRLTIIIVGPFSF	501 aa
E4	IKSGNENGEFYLRQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVRLTIIIVGPFSF	501 aa
E9	IKSGNENGEFYLRQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVRLTIIIVGPFSF	501 aa
E10	IKSGNENGEFYLRQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVRLTIIIVGPFSF	501 aa
E2	IKSGNENGEFYLRQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVRLTIIIVGPFSF	408 aa
E3	-----	386 aa
E5	-----	386 aa
E8	-----	386 aa
E6	-----	346 aa
E7	IKSGNENGEFYLRQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVRLTIIIVGPFSF	461 aa
E11	-----	258 aa
E13	-----	221 aa
E14	-----	221 aa
E15	-----	221 aa
E18	-----	180 aa

FLAG sequence was underlined in wild-type, mutations and insertions were shown by black and grey highlight, respectively, and deletion by dash. The sequence length was indicated at the end of each sequence.

**Table S2.** Multiple alignment of FLAG-tagged EFEMP1 wildtype and variant nucleotide sequences.

E1 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E4 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E9 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E10 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAGTCAGACTGGCGAATAACTTGTCA  
E2 -----  
E3 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E5 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E8 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E6 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E7 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E11 -----  
E13 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E14 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E15 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
E18 AGTGTGCCCCGGGGGTGTTTGTGCCAGTCGCTGCAGTCGAGGCCCTGAAATGCAGACTGGCGAATAACTTGTCA  
  
E1 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E4 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E9 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E10 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E2 -----  
E3 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E5 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E8 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E6 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E7 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E11 -----  
E13 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E14 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E15 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
E18 GGAACCCAGCTGACCCTCAGCGCATTCCCTCCAACCCCTCCACCGTATCCAGTGTGCAGCAGGCTACGAGCAAAGTG  
  
E1 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E4 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E9 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E10 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E2 -----GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E3 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E5 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E8 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E6 TGCAAGCTT  
E7 TGCAAGCTT  
E11 -----CTTGACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E13 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E14 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E15 TGCCAA---GACATAGACGAGTGCACTGCAGGGACGCACAACGTAGAGCAGACCAAGTGTGCATCAATT  
E18 TGCCAA**TAA**  
  
E1 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E4 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E9 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E10 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E2 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E3 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E5 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E8 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E6 -----GACATAGATGAATGTACCAT  
E7 -----GACATAGATGAATGTACCAT  
E11 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E13 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E14 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E15 TCAGTGCCCTCCTGGATATCAGAACCGAGGGGAGCAGTCGCTAGACATAGATGAATGTACCAT  
E18 -----



E1 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E4 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E9 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E10 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E2 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E3 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E5 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E8 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E6 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E7 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E11 GAAATGTGTTGAATTATCATGGCGGCTTCCGTTATCCACGAAATCCTGTCAGAATCCCTACATTCTAACACCAGAGAACCGATG  
E13 -----  
E14 -----  
E15 -----  
E18 -----

E1 TGTTGCCAGTCTCAAATGCCATGTGCCGAGAACTGCCCCAGTCATAAGTCACAAATACATGAGCATTGATAGGTCTGTGC  
E4 TGTTGCCAGTCTCAAATGCCATGTGCCGAGAACTGCCCCAGTCATAAGTCACAAATACATGAGCATTGATAGGTCTGTGC  
E9 TGTTGCCAGTCTCAAATGCCATGTGCCGAGAACTGCCCCAGTCATAAGTCACAAATACATGAGCATTGATAGGTCTGTGC  
E10 TGTTGCCAGTCTCAAATGCCATGTGCCGAGAACTGCCCCAGTCATAAGTCACAAATACATGAGCATTGATAGGTCTGTGC  
E2 TGTTGCCAGTCTCAAATGCCATGTGCCGAGAACTGCCCCAGTCATAAGTCACAAATACATGAGCATTGATAGGTCTGTGC  
E3 TGTTAA-----  
E5 TGTTAA-----  
E8 TGTTAA-----  
E6 TGTTAA-----  
E7 TGTTGCCAGTCTCAAATGCCATGTGCCGAGAACTGCCCCAGTCATAAGTCACAAATACATGAGCATTGATAGGTCTGTGC  
E11 TGTTAA-----  
E13 -----  
E14 -----  
E15 -----  
E18 -----

E1 CATCAGACATCTTCCAGATAACAGGCCACAACATTATGCCAACACCATAACTTTCGGATTAAATCTGAAATGAAATGGAGAG  
E4 CATCAGACATCTTCCAGATAACAGGCCACAACATTATGCCAACACCATAACTTTCGGATTAAATCTGAAATGAAATGGAGAG  
E9 CATCAGACATCTTCCAGATAACAGGCCACAACATTATGCCAACACCATAACTTTCGGATTAAATCTGAAATGAAATGGAGAG  
E10 CATCAGACATCTTCCAGATAACAGGCCACAACATTATGCCAACACCATAACTTTCGGATTAAATCTGAAATGAAATGGAGAG  
E2 CATCAGACATCTTCCAGATAACAGGCCACAACATTATGCCAACACCATAACTTTCGGATTAAATCTGAAATGAAATGGAGAG  
E3 -----  
E5 -----  
E8 -----  
E6 -----  
E7 CATCAGACATCTTCCAGATAACAGGCCACAACATTATGCCAACACCATAACTTTCGGATTAAATCTGAAATGAAATGGAGAG  
E11 -----  
E13 -----  
E14 -----  
E15 -----  
E18 -----

E1 TTCTACCTACGACAAACAAGTCTGTAAGTCAATGCTTGTGCTCGTGAAGTCATTATCAGGACCAAGAGAACATATCGTGACCTGGA  
E4 TTCTACCTACGACAAACAAGTCTGTAAGTCAATGCTTGTGCTCGTGAAGTCATTATCAGGACCAAGAGAACATATCGTGACCTGGA  
E9 TTCTACCTACGACAAACAAGTCTGTAAGTCAATGCTTGTGCTCGTGAAGTCATTATCAGGACCAAGAGAACATATCGTGACCTGGA  
E10 TTCTACCTACGACAAACAAGTCTGTAAGTCAATGCTTGTGCTCGTGAAGTCATTATCAGGACCAAGAGAACATATCGTGACCTGGA  
E2 TTCTACCTACGACAAACAAGTCTGTAAGTCAATGCTTGTGCTCGTGAAGTCATTATCAGGACCAAGAGAACATATCGTGACCTGGA  
E3 -----  
E5 -----  
E8 -----  
E6 -----  
E7 TTCTACCTACGACAAACAAGTCTGTAAGTCAATGCTTGTGCTCGTGAAGTCATTATCAGGACCAAGAGAACATATCGTGACCTGGA  
E11 -----  
E13 -----  
E14 -----  
E15 -----  
E18 -----

E1	GATGCTGACAGTCAGCAGTATA <u>AGGGACCTTCCGACAAGCTCTGTGTTAAGATTGACAATAATAGTGGGCCATTTCA</u> TTTAG	1506 bp
E4	GATGCTGACAGTCAGCAGTATA <u>AGGGACCTTCCGACAAGCTCTGTGTTAAGATTGACAATAATAGTGGGCCATTTCA</u> TTTAG	1506 bp
E9	GATGCTGACAGTCAGCAGTATA <u>AGGGACCTTCCGACAAGCTCTGTGTTAAGATTGACAATAATAGTGGGCCATTTCA</u> TTTAG	1506 bp
E10	GATGCTGACAGTCAGCAGTATA <u>AGGGACCTTCCGACAAGCTCTGTGTTAAGATTGACAATAATAGTGGGCCATTTCA</u> TTTAG	1506 bp
E2	GATGCTGACAGTCAGCAGTATA <u>AGGGACCTTCCGACAAGCTCTGTGTTAAGATTGACAATAATAGTGGGCCATTTCA</u> TTTAG	1227 bp
E3	-----	1161 bp
E5	-----	1161 bp
E8	-----	1161 bp
E6	-----	1041 bp
E7	GATGCTGACAGTCAGCAGTATA <u>AGGGACCTTCCGACAAGCTCTGTGTTAAGATTGACAATAATAGTGGGCCATTTCA</u> TTTAG	1386 bp
E11	-----	777 bp
E13	-----	666 bp
E14	-----	666 bp
E15	-----	666 bp
E18	-----	543 bp

FLAG sequence was underlined in wild-type, mutations and insertions were shown by black and grey highlight, respectively, deletion by dash, and stop codon by boldface. The sequence length was indicated at the end of each sequence.