

# Annex 3

Sequence Analysis of PCR Products from  
Episomally Replicating CaMV DNA in GM  
*Arabidopsis thaliana*

**Sequence analysis of PCR products of the CaMV gene II through gene III junction region, of episomally replicating CaMV DNAs.** The additional sequences are shown in colour with the matching sequence highlighted. The dark green regions are from the right flanking vector sequence while the yellow regions are from the left flanking vector sequence. The deleted regions are indicated by dashed lines over the sequences of gene II (II\_H7) or gene III (III\_H7). The *XhoI* site at which the CaMV genome had been split (CTCGAG) is shown highlighted above. Episomal replicating DNAs from 316B plants came from plant samples subjected to CMV-infection (E316-6), drought stress (E316-7), or no stress (E316-10 and -11). Episomal replicating DNAs from line 318-1 plants came from drought stressed (E318-1) and non stressed plants (E318-3, -4, -5, -6 and -7). Line 318-1 plants extracted at flowering in Table 9 have the suffix F after the clone number (e.g, E-3181F). Other letters refer to PCR bands (t, m and b, for top, middle and bottom) or different clones of the same PCR products (a and b).

|             | 10         | 20         | 30         | 40         | 50         | 60         |
|-------------|------------|------------|------------|------------|------------|------------|
| E316-7.     | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E316-11.    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E316-6.     | CAAAGCCCTT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E316-10.    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| Vector_DNA. | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-3Fa    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-3Fb    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTA---CTG | CAAAAAACAT |
| E318-4      | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-4Fta   | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-4Ftb   | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-4Fma   | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGCCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-4Fmb   | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-4Fba   | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-4Fbb   | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-6Fa    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | -----      | -----      | -----      |
| E318-6Fb    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| II_H7.      | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-5      | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-5Fa    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-5Fb    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| E318-1Fa    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | -----      | -----      | -----      |
| E318-1Fb    | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | -----      | -----      | -----      |
| E318-7      | CAAAGACCCT | TCGGAGTCCA | AATCAAAAAA | CCCGTCAGTT | TTTAATACTG | CAAAAAACAT |
| no_match.   | -----      | -----      | -----      | -----      | -----      | -----      |
| III_H7.     | -----      | -----      | -----      | -----      | -----      | -----      |

  

|             | 70         | 80         | 90         | 100        | 110        | 120        |
|-------------|------------|------------|------------|------------|------------|------------|
| E316-7.     | TTTTAAGAGT | AGTTGGGT-- | -----      | -----      | -----      | -----      |
| E316-11.    | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E316-6.     | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E316-10.    | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| vector_DNA. | -----      | -----      | CTCGAG     | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E318-3Fa    | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E318-3Fb    | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E318-4      | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E318-4Fta   | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E318-4Ftb   | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E318-4Fma   | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E318-4Fmb   | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |
| E318-4Fba   | TTTTAAGAGT | AGGGGGTTG  | ATTACT     | -----      | -----      | -----      |
| E318-4Fbb   | TTTTAAGAGT | AGGGGGTTG  | ATTACT     | -----      | -----      | -----      |
| E318-6Fa    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-6Fb    | TTTTAAG--- | -----      | -----      | -----      | -----      | -----      |
| II_H7.      | TTTTAAGAGT | AGGGGGTTG  | ATTACT     | -----      | -----      | -----      |
| E318-5      | TTTTAAG--- | -----      | -----      | -----      | -----      | -----      |
| E318-5Fa    | TTTTAAG--- | -----      | -----      | -----      | -----      | -----      |
| E318-5Fb    | TTTTAAG--- | -----      | -----      | -----      | -----      | -----      |
| E318-1Fa    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-1Fb    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-7      | TTTTAAGAGT | AGGGGGTTG  | ATTACTCGAG | GTCGACGGTA | TCGATAAGCT | TGATATCGAA |

# The Insertion of Cauliflower Mosaic Virus into Host Genomes During Natural Viral Infections

|             |            |                |               |             |            |            |
|-------------|------------|----------------|---------------|-------------|------------|------------|
| no_match.   | -----      | -----          | -----         | -----       | -----      | -----      |
| III_H7.     | -----      | -----          | -----         | -----       | -----      | -----      |
|             |            | 130            | 140           | 150         | 160        | 170        |
| E316-7.     | -----      | -----          | -----         | -----       | -----      | -----      |
| E316-11.    | TTCTGTCAGC | CCGGGGGATC     | CACTAGTTCT    | AGAG        | -----      | -----      |
| E316-6.     | TTCTGTCAGC | CCGGGGGATC     | CACTAGTTCT    | AGAGCGGCCG  | CCACCGCGGT | GGAGCTCCAG |
| E316-10.    | TTCTGTCAGC | CCGGGGGATC     | CACTAGTTCT    | AGAGCGGCCG  | CCACCGCGGT | GGAGCTCCAG |
| vector_DNA. | TTCTGTCAGC | CCGGGGGATC     | CACTAGTTCT    | AGAGCGGCCG  | CCACCGCGGT | GGAGCTCCAG |
| E318-3Fa    | TTCT       | -----          | -----         | -----       | -----      | -----      |
| E318-3Fb    | TTCT       | -----          | -----         | -----       | -----      | -----      |
| E318-4      | TTCTGTCAGC | CCGGGGGATC     | -----         | -----       | -----      | -----      |
| E318-4Fta   | TTCTGTCAGC | CCGGGGGATC     | CACTAGTTCT    | TGA         | -----      | -----      |
| E318-4Ftb   | TTCTGTCAGC | CCGGGGGATC     | CACTAGTTCT    | TGA         | -----      | -----      |
| E318-4Fma   | TTCTGTCAGC | CCGGG          | -----         | -----       | -----      | -----      |
| E318-4Fmb   | TTCTGTCAGC | CCGGGGGATC     | CACTAGTTCT    | TGA         | -----      | -----      |
| E318-4Fba   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4Fbb   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-6Fa    | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-6Fb    | -----      | -----          | -----         | -----       | -----      | -----      |
| II_H7.      | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-5      | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-5Fa    | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-5Fb    | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-1Fa    | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-1Fb    | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-7      | TTCTGTCAGC | CCGGGGGATC     | CACTA         | -----       | -----      | -----      |
| no_match.   | -----      | -----          | -----         | -----       | -----      | -----      |
| III_H7.     | -----      | -----          | -----         | -----       | -----      | -----      |
|             |            | 190            | 200           | 210         | 220        | 230        |
| E316-7.     | -----      | -----          | ACC GGGCCCCCC | TCGAGCCAAC  | TAAAGGAAGT | AAAATCCCTT |
| E316-11.    | -----      | -----          | -----         | CGAGCCAAC   | TAAAGGAAGT | AAAATCCCTT |
| E316-6.     | CTTTTGTGAA | TTGGGTACCG     | GGCCCCCCC     | TCGAGCCAAC  | TAAAGGAAGT | AAAATCCCTT |
| E316-10.    | CTTTTGT    | -----          | -----         | -----       | -----      | -----      |
| vector_DNA. | CTTTTGT    | -----          | -----         | -----       | -----      | -----      |
| E318-3Fa    | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-3Fb    | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4      | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4Fta   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4Ftb   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4Fma   | -----      | -----          | CCCCC         | TCGAGCCAAC  | TAAAGGAAGT | AAAATCCCTT |
| E318-4Fmb   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4Fba   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4Fbb   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-6Fa    | -----      | -----          | -----         | TC TAGCCAAC | TAAAGGAAGT | AAAATCCCTT |
| 318b-6Fb    | -----      | -----          | -----         | -----       | ---GAAGT   | AAAATCCCTT |
| II_H7.      | -----      | -----          | -----         | CGAGCCAAC   | TAAAGGAAGT | AAAATCCCTT |
| E318-5      | -----      | -----          | -----         | -----       | ---GAAGT   | AAAATCCCTT |
| E318-5Fa    | -----      | -----          | -----         | -----       | ---GAAGT   | AAAATCCCTT |
| E318-5Fb    | -----      | -----          | -----         | -----       | ---GAAGT   | AAAATCCCTT |
| E318-1Fa    | -----      | -----          | -----         | TC TAGCCAAC | TAAAGGAAGT | AAAATCCCTT |
| E318-1Fb    | -----      | -----          | -----         | TC TAGCCAAC | TAAAGGAAGT | AAAATCCCTT |
| E318-7      | -----      | -----          | -----         | -----       | -----      | -----      |
| no_match.   | -----      | GAA TTGGGTACCG | GGCCCCCCC     | -----       | -----      | -----      |
| III_H7.     | -----      | -----          | -----         | -----       | -----      | -----      |
|             |            | 250            | 260           | 270         | 280        | 290        |
| E316-7.     | TTAGAAGCTC | AAAATACTAG     | AATTAATAAT    | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |
| E316-11.    | TTAGAAGCTC | AAAATACTAG     | AATTAATAAT    | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |
| E316-6.     | TTAGAAGCTC | AAAATACTAG     | AATTAATAAT    | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |
| E316-10.    | -----      | -----          | -----         | -----       | -----      | -----      |
| vector_DNA. | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-3Fa    | -----      | -----          | -----         | -----       | -----      | --TAGATAAT |
| E318-3Fb    | -----      | -----          | -----         | -----       | -----      | --TAGATAAT |
| E318-4      | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4Fta   | -----      | -----          | T ATTCTTTAAT  | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |
| E318-4Ftb   | -----      | -----          | T ATTCTTTAAT  | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |
| E318-4Fma   | TTAGAAGCTC | AAAATACTAG     | AATTAATAAT    | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |
| E318-4Fmb   | -----      | -----          | T ATTCTTTAAT  | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |
| E318-4Fba   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-4Fbb   | -----      | -----          | -----         | -----       | -----      | -----      |
| E318-6Fa    | TTAGAAGCTC | AAAATACTAG     | AATTAATAAT    | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |
| E318-6Fb    | TTAGAAGCTC | AAAATACTAG     | AATTAATAAT    | CTAGAAAATG  | CAATTCAATC | CTTAGATAAT |

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II_H7.          TTAGAAGCTC AAAATACTAG AATTAAAAAT CTAGAAAATG CAATTCAATC CTTAGATAAT
E318-5         TTAGAAGCTC AAAATACTAG AATTAAAAAT CTAGAAAATG CAATTCAATC CTTAGATAAT
E318-5Fa      TTAGAAGCTC AAAATACTAG AATTAAAAAT CTAGAAAATG CAATTCAATC CTTAGATAAT
E318-5Fb      TTAGAAGCTC AAAATACTAG AATTAAAAAT CTAGAAAATG CAATTCAATC CTTAGATAAT
E318-1Fa      TTAGAAGCTC AAAATACTAG AATTAAAAAT CTAGAAAATG CAATTCAATC CTTAGATAAT
E318-1Fb      TTAGAAGCTC AAAATACTAG AATTAAAAAT CT-GAAAATG CAATTCAATC CTTAGATAAT
E318-7        -----
III_H7.        -----
    
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          310          320          330          340          350          360
E316-7.    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E316-11.   AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E316-6.    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E316-10.   -----
Vector_DNA. -----
E318-3Fa    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-3Fb    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-4      -----
E318-4Fta   AAGATTGAAC CAAAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-4Ftb   AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-4Fma   AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-4Fmb   AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-4Fba   -----
E318-4Fbb   -----
E318-6Fa    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-6Fb    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
II_H7.      AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-5      AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA -----
E318-5Fa    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-5Fb    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-1Fa    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-1Fb    AAGATTGAAC CAGAGCCCTT AACTAAAGAA GAAGTTAAAG AGCTAAAAGA ATCGATTAAC
E318-7      -----
III_H7.     -----
    
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          370          380          390          400          410          420
E316-7.    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E316-11.   TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E316-6.    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E316-10.   TTTAGTGAGG GTTAATTGCG CGCTTGGCGT AATC-----A TGGCTAATCT TAATCAAATC
Vector_DNA. TTTAGTGAGG GTTAATTGCG CGCTTGGCGT AATC-----A TGGCTAATCT TAATCAAATC
E318-3Fa    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-3Fb    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-4      -----
E318-4Fta   TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-4Ftb   TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-4Fma   TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-4Fmb   TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-4Fba   TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-4Fbb   TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-6Fa    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-6Fb    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
II_H7.      TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A -----
E318-5      -----
E318-5Fa    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-5Fb    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-1Fa    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-1Fb    TCGATCAAAG AAGGATTAAG GAATATTATT GGCTGAA--A TGGCTAATCT TAATCAAATC
E318-7      -----
III_H7.     -----
    
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          430          440          450          460          470          480
E316-7.    CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E316-11.   CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E316-6.    CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E316-10.   CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E318-3Fa    CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E318-3Fb    CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E318-4      -----
E318-4Fta   CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E318-4Ftb   CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E318-4Fma   CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E318-4Fmb   CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
E318-4Fba   CAGAAAGAAG TCTCTGAAAT CCTCAGTGAC CAAAAATCCA TGAAATCGGA TATAAAAGCT
    
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|           |            |            |            |            |            |            |
|-----------|------------|------------|------------|------------|------------|------------|
| E318-4Fbb | CAGAAAGAAG | TCTCTGAAAT | CCTCAGTGAC | CAAAAATCCA | TGAAATCGGA | TATAAAAGCT |
| E318-6Fa  | CAGAAAGAAG | TCTCTGAAAT | CCTCAGTGAC | CAAAAATCCA | TGAAATCGGA | TATAAAAGCT |
| E318-6Fb  | CAGAAAGAAG | TCTCTGAAAT | CCTCAGTGAC | CAAAAATCCA | TGAAATCGGA | TATAAAAGCT |
| II_H7.    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-5    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-5Fa  | CAGAAAGAAG | TCTCTGAAAT | CCTCAGTGAC | CAAAAATCCA | TGAAATCGGA | TATAAAAGCT |
| E318-5Fb  | CAGAAAGAAG | TCTCTGAAAT | CCTCAGTGAC | CAAAAATCCA | TGAAATCGGA | TATAAAAGCT |
| E318-1Fa  | CAGAAAGAAG | TCTCTGAAAT | CCTCAGTGAC | CAAAAATCCA | TGAAATCGGA | TATAAAAGCT |
| E318-1Fb  | CAGAAAGAAG | TCTCTGAAAT | CCTCAGTGAC | CAAAAATCCA | TGAAATCGGA | TATAAAAGCT |
| E318-7    | -----      | -----      | -----      | -----      | -----      | -----      |
| III_H7.   | CAGAAAGAAG | TCTCTGAAAT | CCTCAGTGAC | CAAAAATCCA | TGAAATCGGA | TATAAAAGCT |

|           |            |            |            |            |            |            |
|-----------|------------|------------|------------|------------|------------|------------|
|           | 490        | 500        | 510        | 520        | 530        | 540        |
| E316-7.   | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E316-11.  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E316-6.   | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E316-10.  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-3Fa  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-3Fb  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-4    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-4Fta | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-4Ftb | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-4Fma | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-4Fmb | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-4Fba | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-4FBb | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-6Fa  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-6Fb  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| II_H7.    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-5    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-5Fa  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-5Fb  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-1Fa  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-1Fb  | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |
| E318-7    | -----      | -----      | -----      | -----      | -----      | -----      |
| III_H7.   | ATCTTAGAAT | TGCTAGGATC | CCAAAATCCT | ACTAAAGAAA | GCTTAGAAGC | CGTTGCAGCG |

|           |            |            |            |            |            |            |
|-----------|------------|------------|------------|------------|------------|------------|
|           | 550        | 560        | 570        | 580        | 590        | 600        |
| E316-7.   | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E316-11.  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E316-6.   | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CCTGTAACAA | AGAGATATTA |
| E316-10.  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-3Fa  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-3Fb  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-4    | -----      | -----      | -----      | -----      | -----      | -GAAGCCTTA |
| E318-4Fta | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-4Ftb | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-4Fma | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-4Fmb | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-4Fba | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-4FBb | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-6Fa  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-6Fb  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| II_H7.    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-5    | -----      | -----      | -----      | -----      | -----      | -----      |
| E318-5Fa  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-5Fb  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-1Fa  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-1Fb  | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |
| E318-7    | -----      | -----      | -----      | -----      | -----      | -----      |
| III_H7.   | AAAATCGTTA | ATGACTTAAC | CAAGCTCATC | AATGATTGTC | CTTGTAACAA | AGAGATATTA |

|           |            |            |            |            |            |             |
|-----------|------------|------------|------------|------------|------------|-------------|
|           | 610        | 620        | 630        | 640        | 650        | 660         |
| E316-7.   | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E316-11.  | GAAGCCCTTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E316-6.   | GAAGCCCTTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E316-10.  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E318-3Fa  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E318-3Fb  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E318-4    | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E318-4Fta | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E318-4Ftb | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E318-4Fma | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |
| E318-4Fmb | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCCAA |

The Insertion of Cauliflower Mosaic Virus into Host Genomes During Natural Viral Infections

|                  |            |            |            |            |            |            |
|------------------|------------|------------|------------|------------|------------|------------|
| <b>E318-4Fba</b> | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |
| <b>E318-4Fbb</b> | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |
| <b>E318-6Fa</b>  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |
| <b>E318-6Fb</b>  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |
| <b>II_H7.</b>    | -----      | -----      | -----      | -----      | -----      | -----      |
| <b>E318-5</b>    | -----      | -----      | -----      | -----      | -----      | -----      |
| <b>E318-5Fa</b>  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |
| <b>E318-5Fb</b>  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |
| <b>E318-1Fa</b>  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |
| <b>E318-1Fb</b>  | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |
| <b>E318-7</b>    | -----      | -----      | -----      | -----      | -----AAG   | AAAAAGGCAA |
| <b>III_H7.</b>   | GAAGCC-TTA | GGCAATCAGC | CTAAAGAGCA | ACTAATAGAA | CAACCTAAAG | AAAAAGGCAA |

|                  |            |            |            |            |            |            |       |
|------------------|------------|------------|------------|------------|------------|------------|-------|
|                  |            | 670        | 680        | 690        | 700        | 710        | 720   |
| <b>E316-7.</b>   | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E316-11.</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAAGAAATG | AAGAATTAGG |       |
| <b>E316-6.</b>   | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTACG |       |
| <b>E316-10.</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAAGAAATG | AAGAATTAGG |       |
| <b>E318-3Fa</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-3Fb</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-4</b>    | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-4Fta</b> | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-4Ftb</b> | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-4Fma</b> | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-4Fmb</b> | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-4Fba</b> | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-4Fbb</b> | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-6Fa</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-6Fb</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>II_H7.</b>    | -----      | -----      | -----      | -----      | -----      | -----      | ----- |
| <b>E318-5</b>    | -----      | -----      | -----      | -----      | -----TG    | AAGAATTAGG |       |
| <b>E318-5Fa</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-5Fb</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-1Fa</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-1Fb</b>  | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>E318-7</b>    | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |
| <b>III_H7.</b>   | AGGCCTTAAT | CTAGGAAAAT | ATACTTACCC | CAATTACGGC | GTAGGAAATG | AAGAATTAGG |       |