Figure 1: A-2X35S/CPMV-HT/H5 Indonesia/NOS (Construct number 489)

Figure 1A

IF-H5A-I-05.s1+3c SEQ ID NO: 2

AAATTTGTCGGGCCCATGGAGAAAATAGTGCTTCTTCTTGC

Figure 1B

IF-H5dTm.r SEQ ID NO: 3

ACTAAAGAAAATAGGCCTTTAAATGCAAATTCTGCATTGTAACGATCCAT

Figure 1C

Schematic representation of construct 1191. SacII and StuI restriction enzyme sites used for plasmid linearization are annotated on the representation.

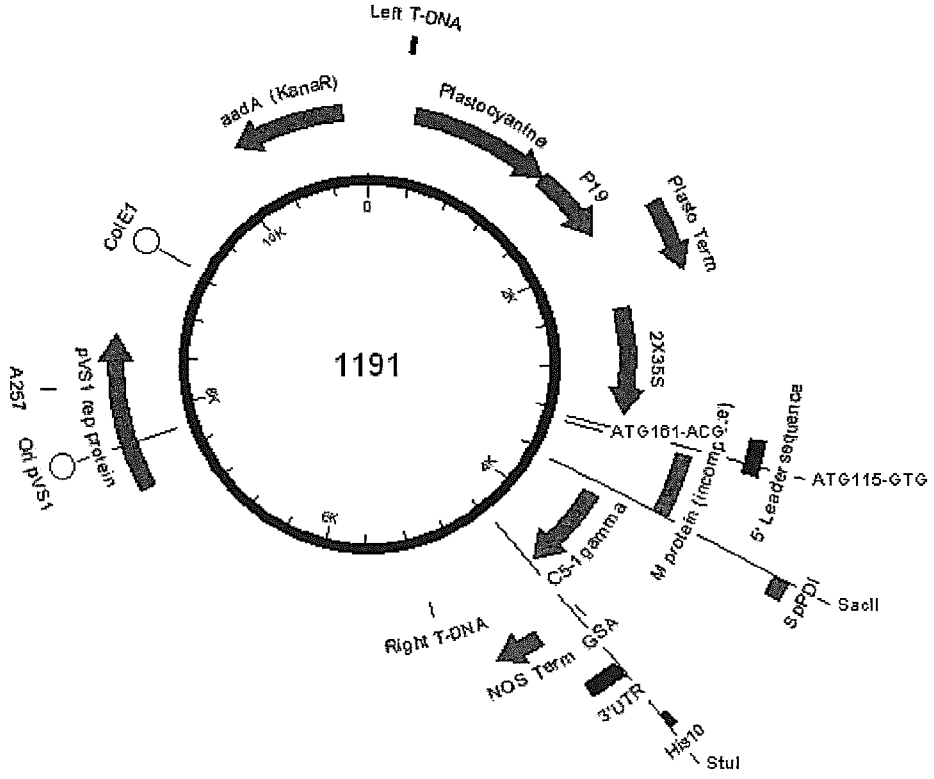


Figure 1D

Construct 1191 from left to right t-DNA borders (underlined). 2X35S/CPMV-HT/NOS with Plastocyanine-P19-Plastocyanine silencing inhibitor expression cassette (SEQ ID NO: 4)

TGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACATTGCGGACG
TTTTTAATGTACTGAATTAACGCCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTC
AAAAACCATAAAAGTTTAAGTTAGCAAGTGTGTACATTTTTACTTGAACAAAAATATTCACCTA
CTACTGTTATAAATCATTATTAAACATTAGAGTAAAGAAATATGGATGATAAGAACAAGAGTAG
TGATATTTTGACAACAATTTTGTTGCAACATTTGAGAAAATTTTGTTGTTCTCTCTTTTCATTG
GTCAAAAACAATAGAGAGAGAAAAAGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGA
GAAAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATTGAGGAATTTGACAAAAGC
TACACAAATAAGGGTTAATTGCTGTAAATAAATAAGGATGACGCATTAGAGAGATGTACCATTA
GAGAATTTTTGGCAAGTCATTAAAAAGAAAGAATAAATTATTTTTAAAATTAAAAGTTGAGTCA
TTTGATTAAACATGTGATTATTTAATGAATTGATGAAAGAGTTGGATTAAAGTTGTATTAGTAA
TTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCCTATATATTGCCCCATAGAGTC
AGTTAACTCATTTTTATATTTCATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCCAA
AAAAAAAAAACGGTATATTTACTAAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCCGTA
GGAGGATAACATCCAATCCAACCAATCACAACAATCCTGATGAGATAACCCACTTTAAGCCCAC
GCATCTGTGGCACATCTACATTATCTAAATCACACATTCTTCCACACATCTGAGCCACACAAAA
ACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACACTTTGTGAGTCTACACTTTGATT
CCCTTCAAACACATACAAAGAGAAGAGACTAATTAATTAATTAATCATCTTGAGAGAAAATGGA
ACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCA
GGAGGTACCACTTCTCCCTTCAAACTTCCTGACGAAAGTCCGAGTTGGACTGAGTGGCGGCTAC
ATAACGATGAGACGAATTCGAATCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGG
GAAAGTTGTATTTAAGAGATATCTCAGATACGACAGGACGGAAGCTTCACTGCACAGAGTCCTT
GGATCTTGGACGGGAGATTCGGTTAACTATGCAGCATCTCGATTTTTCGGTTTCGACCAGATCG
GATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTCGCGAACTCT
TCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCCAATCGAA
GTGGAAAGTAATGTATCAAGAGGATGCCCTGAAGGTACTCAAACCTTCGAAAAAGAAAGCGAGT
AAGTTAAAATGCTTCTTCGTCTCCTATTTATAATATGGTTTGTTATTGTTAATTTTGTTCTTGT
AGAAGAGCTTAATTAATCGTTGTTGTTATGAAATACTATTTGTATGAGATGAACTGGTGTAATG
TAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCCTCCATAACTAACTAGACATGAAG
ACCTGCCGCGTACAATTGTCTTATATTTGAACAACTAAAATTGAACATCTTTTGCCACAACTTT
ATAAGTGGTTAATATAGCTCAAATATATGGTCAAGTTCAATAGATTAATAATGGAAATATCAGT
TATCGAAATTCATTAACAATCAACTTAACGTTATTAACTACTAATTTTATATCATCCCCTTTGA
TAAATGATAGTACACCAATTAGGAAGGAGCATGCTCGCCTAGGAGATTGTCGTTTCCCGCCTTC
AGTTTGCAAGCTGCTCTAGCCGTGTAGCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGGAAT
TACTAGCGCGTGTCGACAAGCTTGCATGCCGGTCAACATGGTGGAGCACGACACACTTGTCTAC
TCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGG
TAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGT
GGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGAT
GCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAG
ACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACT
TGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAA
CAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGA
AGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGT

TGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAA
AAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAA
GGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCA
TTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAACCCGAACCAA
ACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGA
GCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGA
AATCAAAGATCTCTTTGTGGACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTC
TTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCTGGAGGCTGCTGTTCAGCCCCATACATTACT
TGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTTGACGAGGTATTGTT
GCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGA
AACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCC
AAATTTGTCGGGCCCGCGGATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTT
GTGTTGGTTCCTTCTCAGATCTTCGCCTGCAGGCTCCTCAGCCAAAACGACACCCCCATCTGTC
TATCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCA
AGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCA
CACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCC
AGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGG
ACAAGAAAATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATC
ATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTC
ACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATG
ATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTC
AGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAGCGATCGCTCACCATC
ACCATCACCATCACCATCACCATTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGG
TGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTA
ATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATT
TTATTAAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGT
TCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCA
TATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTAT
GAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATA
TAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCTCTAGAGTC
TCAAGCTTGGCGCGCCCACGTGACTAGTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGA
AAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAAT
AGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGCTAGA
GCAGCTTGAGCTTGGATCAGATTGTCGTTTCCCGCCTTCAGTTTAAACTATCAGTGTTTGACAG
GATATATTGGCGGGTAAACCTAAGAGAAAAGAGCGTTTA

Figure 1E

Expression cassette number 489 from 2X35S promoter to NOS terminator. H5 from influenza A/Indonesia/5/2005 (H5N1) is underlined. SEQ ID NO: 5

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAG
ACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTG
CCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCAT
CATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGAC
CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGA
TTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTC
TCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGAT
TCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAA
ATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAA
GATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGC
AAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCA
AGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTT
TGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTT
AAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCG
GCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGC
GGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTT
GCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGC
AATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGA
TTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGG
AGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGGAGAAAATAGTGC
TTCTTCTTGCAATAGTCAGTCTTGTTAAAAGTGATCAGATTTGCATTGGTTACCATGCAAACAA
TTCAACAGAGCAGGTTGACACAATCATGGAAAAGAACGTTACTGTTACACATGCCCAAGACATA
CTGGAAAAGACACACAACGGGAAGCTCTGCGATCTAGATGGAGTGAAGCCTCTAATTTTAAGAG
ATTGTAGTGTAGCTGGATGGCTCCTCGGGAACCCAATGTGTGACGAATTCATCAATGTACCGGA
ATGGTCTTACATAGTGGAGAAGGCCAATCCAACCAATGACCTCTGTTACCCAGGGAGTTTCAAC
GACTATGAAGAACTGAAACACCTATTGAGCAGAATAAACCATTTTGAGAAAATTCAAATCATCC
CCAAAAGTTCTTGGTCCGATCATGAAGCCTCATCAGGAGTTAGCTCAGCATGTCCATACCTGGG
AAGTCCCTCCTTTTTTAGAAATGTGGTATGGCTTATCAAAAAGAACAGTACATACCCAACAATA
AAGAAAAGCTACAATAATACCAACCAAGAGGATCTTTTGGTACTGTGGGGAATTCACCATCCTA
ATGATGCGGCAGAGCAGACAAGGCTATATCAAAACCCAACCACCTATATTTCCATTGGGACATC
AACACTAAACCAGAGATTGGTACCAAAAATAGCTACTAGATCCAAAGTAAACGGGCAAAGTGGA
AGGATGGAGTTCTTCTGGACAATTTTAAAACCTAATGATGCAATCAACTTCGAGAGTAATGGAA
ATTTCATTGCTCCAGAATATGCATACAAAATTGTCAAGAAAGGGGACTCAGCAATTATGAAAAG
TGAATTGGAATATGGTAACTGCAACACCAAGTGTCAAACTCCAATGGGGGCGATAAACTCTAGT
ATGCCATTCCACAACATACACCCTCTCACCATCGGGGAATGCCCCAAATATGTGAAATCAAACA
GATTAGTCCTTGCAACAGGGCTCAGAAATAGCCCTCAAAGAGAGAGCAGAAGAAAAAAGAGAGG
ACTATTTGGAGCTATAGCAGGTTTTATAGAGGGAGGATGGCAGGGAATGGTAGATGGTTGGTAT
GGGTACCACCATAGCAATGAGCAGGGGAGTGGGTACGCTGCAGACAAAGAATCCACTCAAAAGG
CAATAGATGGAGTCACCAATAAGGTCAACTCAATCATTGACAAAATGAACACTCAGTTTGAGGC
CGTTGGAAGGGAATTTAATAACTTAGAAAGGAGAATAGAGAATTTAAACAAGAAGATGGAAGAC
GGGTTTCTAGATGTCTGGACTTATAATGCCGAACTTCTGGTTCTCATGGAAAATGAGAGAACTC
TAGACTTTCATGACTCAAATGTTAAGAACCTCTACGACAAGGTCCGACTACAGCTTAGGGATAA

TGCAAAGGAGCTGGGTAACGGTTGTTTCGAGTTCTATCACAAATGTGATAATGAATGTATGGAA
AGTATAAGAAACGGAACGTACAACTATCCGCAGTATTCAGAAGAAGCAAGATTAAAAAGAGAGG
AAATAAGTGGGGTAAAATTGGAATCAATAGGAACTTACCAAATACTGTCAATTTATTCAACAGT
GGCGAGTTCCCTAGCACTGGCAATCATGATGGCTGGTCTATCTTTATGGATGTGCTCCAATGGA
TCGTTACAATGCAGAATTTGCATTTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCG
GTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTT
AATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAAT
TTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCG
TTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATC
ATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTA
TGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAAT
ATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 1F

Amino acid sequence of H5 from influenza A/Indonesia/5/2005 (H5N1) SEQ ID NO: 6

MEKIVLLLAIVSLVKSDQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDLDGVK
PLILRDCSVAGWLLGNPMCDEFINVPEWSYIVEKANPTNDLCYPGSFNDYEELKHLLSRINHFE
KIQIIPKSSWSDHEASSGVSSACPYLGSPSFFRNVVWLIKKNSTYPTIKKSYNNTNQEDLLVLW
GIHHPNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIATRSKVNGQSGRMEFFWTILKPNDAIN
FESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAINSSMPFHNIHPLTIGECPK
YVKSNRLVLATGLRNSPQRESRRKKRGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQGSGYAADK
ESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLM
ENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESIRNGTYNYPQYSEEA
RLKREEISGVKLESIGTYQILSIYSTVASSLALAIMMAGLSLWMCSNGSLQCRICI

Figure 1G nucleotide sequence encoding H5 from influenza A/Indonesia/5/2005 (H5N1) SEQ ID NO: 42)

ATGGAGAAAATAGTGCTTCTTCTTGCAATAGTCAGTCTTGTTAAAAGTGATCAGATTTGCATTG
GTTACCATGCAAACAATTCAACAGAGCAGGTTGACACAATCATGGAAAAGAACGTTACTGTTAC
ACATGCCCAAGACATACTGGAAAAGACACACAACGGGAAGCTCTGCGATCTAGATGGAGTGAAG
CCTCTAATTTTAAGAGATTGTAGTGTAGCTGGATGGCTCCTCGGGAACCCAATGTGTGACGAAT
TCATCAATGTACCGGAATGGTCTTACATAGTGGAGAAGGCCAATCCAACCAATGACCTCTGTTA
CCCAGGGAGTTTCAACGACTATGAAGAACTGAAACACCTATTGAGCAGAATAAACCATTTTGAG
AAAATTCAAATCATCCCCAAAAGTTCTTGGTCCGATCATGAAGCCTCATCAGGAGTTAGCTCAG
CATGTCCATACCTGGGAAGTCCCTCCTTTTTTAGAAATGTGGTATGGCTTATCAAAAAGAACAG
TACATACCCAACAATAAAGAAAAGCTACAATAATACCAACCAAGAGGATCTTTTGGTACTGTGG
GGAATTCACCATCCTAATGATGCGGCAGAGCAGACAAGGCTATATCAAAACCCAACCACCTATA
TTTCCATTGGGACATCAACACTAAACCAGAGATTGGTACCAAAAATAGCTACTAGATCCAAAGT
AAACGGGCAAAGTGGAAGGATGGAGTTCTTCTGGACAATTTTAAAACCTAATGATGCAATCAAC
TTCGAGAGTAATGGAAATTTCATTGCTCCAGAATATGCATACAAAATTGTCAAGAAAGGGGACT
CAGCAATTATGAAAAGTGAATTGGAATATGGTAACTGCAACACCAAGTGTCAAACTCCAATGGG
GGCGATAAACTCTAGTATGCCATTCCACAACATACACCCTCTCACCATCGGGGAATGCCCCAAA
TATGTGAAATCAAACAGATTAGTCCTTGCAACAGGGCTCAGAAATAGCCCTCAAAGAGAGAGCA
GAAGAAAAAAGAGAGGACTATTTGGAGCTATAGCAGGTTTTATAGAGGGAGGATGGCAGGGAAT
GGTAGATGGTTGGTATGGGTACCACCATAGCAATGAGCAGGGGAGTGGGTACGCTGCAGACAAA
GAATCCACTCAAAAGGCAATAGATGGAGTCACCAATAAGGTCAACTCAATCATTGACAAAATGA
ACACTCAGTTTGAGGCCGTTGGAAGGGAATTTAATAACTTAGAAAGGAGAATAGAGAATTTAAA
CAAGAAGATGGAAGACGGGTTTCTAGATGTCTGGACTTATAATGCCGAACTTCTGGTTCTCATG
GAAAATGAGAGAACTCTAGACTTTCATGACTCAAATGTTAAGAACCTCTACGACAAGGTCCGAC
TACAGCTTAGGGATAATGCAAAGGAGCTGGGTAACGGTTGTTTCGAGTTCTATCACAAATGTGA
TAATGAATGTATGGAAAGTATAAGAAACGGAACGTACAACTATCCGCAGTATTCAGAAGAAGCA
AGATTAAAAAGAGAGGAAATAAGTGGGGTAAAATTGGAATCAATAGGAACTTACCAAATACTGT
CAATTTATTCAACAGTGGCGAGTTCCCTAGCACTGGCAATCATGATGGCTGGTCTATCTTTATG
GATGTGCTCCAATGGATCGTTACAATGCAGAATTTGCATTTAA

Figure 2: B-2X35S/CPMV HT/M2 New Caledonia/NOS (Construct number 1261)

Figure 2A

IF-S1-M1+M2ANC.c (SEQ ID NO:7)

AAATTTGTCGGGCCCATGAGTCTTCTAACCGAGGTCGAAACG

Figure 2B

IF-S1-4-M2ANC.r (SEQ ID NO: 8)

ACTAAAGAAAATAGGCCTTTACTCCAGCTCTATGCTGACAAAA

Figure 2C

Synthesized M2 gene (corresponding to nt 1-26 joined to 715-982 from Genbank accession number DQ508860) (SEQ ID NO: 9)

ATGAGTCTTCTAACCGAGGTCGAAACGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGATT
CAAGTGATCCTCTTGTTGTTGCCGCAAGTATAATTGGGATTGTGCACCTGATATTGTGGATTAT
TGATCGCCTTTTTTCCAAAAGCATTTATCGTATCTTTAAACACGGTTTAAAAAGAGGGCCTTCT
ACGGAAGGAGTACCAGAGTCTATGAGGGAAGAATATCGAGAGGAACAGCAGAATGCTGTGGATG
CTGACGATGGTCATTTTGTCAGCATAGAGCTGGAGTAA

Figure 2D

Expression cassette number 1261 from 2X35S promoter to NOS terminator. M2 from influenza A/New Caledonia/20/1999 (H1N1) is underlined. (SEQ ID NO: 10)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAG
ACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTG
CCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCAT
CATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGAC
CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGA
TTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTC
TCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGAT
TCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAA
ATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAA
GATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGC
AAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCA

AGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTT
TGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTT
AAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCG
GCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGC
GGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTT
GCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGC
AATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGA
TTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGG
AGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGAGTCTTCTAACCG
AGGTCGAAACGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGATTCAAGTGATCCTCTTGT
TGTTGCCGCAAGTATAATTGGGATTGTGCACCTGATATTGTGGATTATTGATCGCCTTTTTTCC
AAAAGCATTTATCGTATCTTTAAACACGGTTTAAAAAGAGGGCCTTCTACGGAAGGAGTACCAG
AGTCTATGAGGGAAGAATATCGAGAGGAACAGCAGAATGCTGTGGATGCTGACGATGGTCATTT
TGTCAGCATAGAGCTGGAGTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTG
CATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTT
CTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTAT
TAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAA
ACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATA
ATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGA
TGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGC
GCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 2E

Amino acid sequence of M2 from influenza A/New Caledonia/20/1999 (H1N1) (SEQ ID NO: 11)

MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPS
TEGVPESMREEYREEQQNAVDADDGHFVSIELE

Figure 3: C-2X35S/CPMV-HT/M2 Puerto Rico/NOS (Construct number 859)

Figure 3A

Synthesized M2 gene (corresponding to nt 26-51 joined to nt 740-1007 from Genebank accession number EF467824) (SEQ ID NO: 12)

ATGAGTCTTCTAACCGAGGTCGAAACGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTT
CAAGTGATCCTCTCACTATTGCCGCAAATATCATTGGGATCTTGCACTTGACATTGTGGATTCT
TGATCGTCTTTTTTTCAAATGCATTTACCGTCGCTTTAAATACGGACTGAAAGGAGGGCCTTCT
ACGGAAGGAGTGCCAAAGTCTATGAGGGAAGAATATCGAAAGGAACAGCAGAGTGCTGTGGATG
CTGACGATGGTCATTTTGTCAGCATAGAGCTGGAGTAA

Figure 3B

Expression cassette number 859 from 2X35S promoter to NOS terminator. M2 from Influenza A/Puerto Rico/8/1934 (H1N1) is underlined. (SEQ ID NO: 13)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAG
ACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTG
CCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCAT
CATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGAC
CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGA
TTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTC
TCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGAT
TCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAA
ATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAA
GATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGC
AAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCA
AGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTT
TGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTT
AAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCG
GCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGC
GGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTT
GCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGC
AATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGA
TTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGG
AGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGAGTCTTCTAACCG
AGGTCGAAACGCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCAC
TATTGCCGCAAATATCATTGGGATCTTGCACTTGACATTGTGGATTCTTGATCGTCTTTTTTTC
AAATGCATTTACCGTCGCTTTAAATACGGACTGAAAGGAGGGCCTTCTACGGAAGGAGTGCCAA
AGTCTATGAGGGAAGAATATCGAAAGGAACAGCAGAGTGCTGTGGATGCTGACGATGGTCATTT
TGTCAGCATAGAGCTGGAGTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTG
CATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTT

CTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTAT
TAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAA
ACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATA
ATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGA
TGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGC
GCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 3C

Amino acid sequence of M2 from influenza A/Puerto Rico/8/1934 (H1N1) (SEQ ID NO:14)

MSLLTEVETPIRNEWGCRCNGSSDPLTIAANIIGILHLTLWILDRLFFKCIYRRFKYGLKGGPS
TEGVPKSMREEYRKEQQSAVDADDGHFVSIELE

Figiure 4: G-2X35S/CPMV-HT/PDISP/HA B Brisbane/NOS into BeYDV+Replicase amplification system (Construct number 1008)

Figure 4A

Schematic representation of construct 1194. SacII and StuI restriction enzyme sites used for plasmid linearization are annotated on the representation.

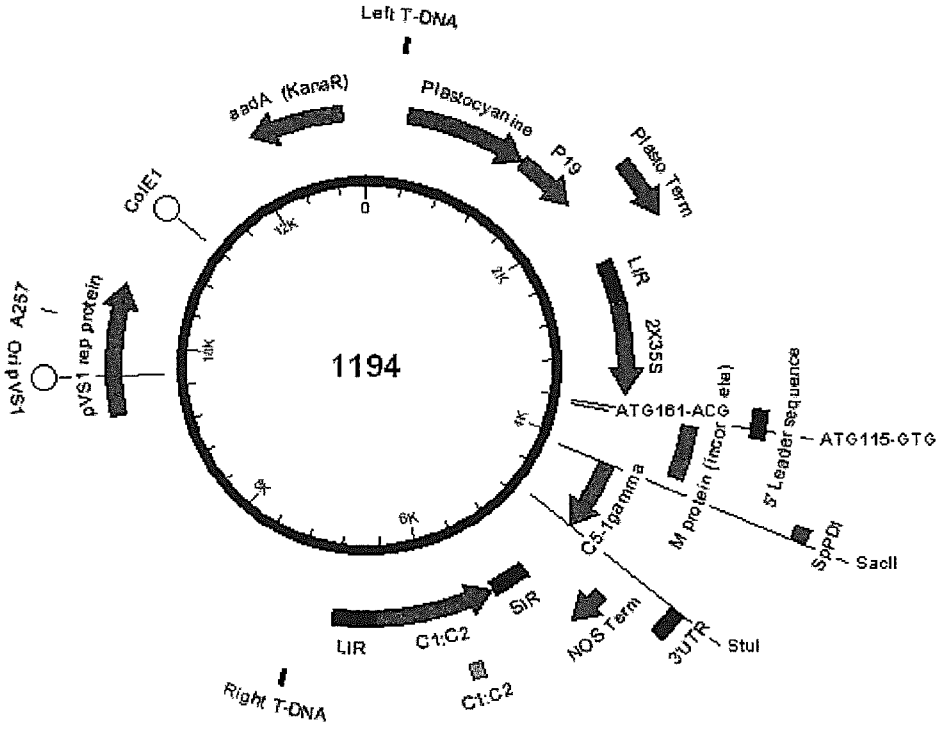


Figure 4B

Construct 1194 from left to right t-DNA borders (underlined). 2X35S/CPMV-HT/PDISP/NOS into BeYDV+Replicase amplification system with Plastocyanine-P19-Plastocyanine silencing inhibitor expression cassette (SEQ ID NO: 31)

TGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACATTGCGGACG
TTTTTAATGTACTGAATTAACGCCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTC
AAAAACCATAAAAGTTTAAGTTAGCAAGTGTGTACATTTTTACTTGAACAAAAATATTCACCTA
CTACTGTTATAAATCATTATTAAACATTAGAGTAAAGAAATATGGATGATAAGAACAAGAGTAG
TGATATTTTGACAACAATTTTGTTGCAACATTTGAGAAAATTTTGTTGTTCTCTCTTTTCATTG
GTCAAAAACAATAGAGAGAGAAAAAGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGA
GAAAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATTGAGGAATTTGACAAAAGC

TACACAAATAAGGGTTAATTGCTGTAAATAAATAAGGATGACGCATTAGAGAGATGTACCATTA
GAGAATTTTTGGCAAGTCATTAAAAAGAAAGAATAAATTATTTTTAAAATTAAAAGTTGAGTCA
TTTGATTAAACATGTGATTATTTAATGAATTGATGAAAGAGTTGGATTAAAGTTGTATTAGTAA
TTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCCTATATATTGCCCCATAGAGTC
AGTTAACTCATTTTTATATTTCATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCCAA
AAAAAAAAAACGGTATATTTACTAAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCCGTA
GGAGGATAACATCCAATCCAACCAATCACAACAATCCTGATGAGATAACCCACTTTAAGCCCAC
GCATCTGTGGCACATCTACATTATCTAAATCACACATTCTTCCACACATCTGAGCCACACAAAA
ACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACACTTTGTGAGTCTACACTTTGATT
CCCTTCAAACACATACAAAGAGAAGAGACTAATTAATTAATTAATCATCTTGAGAGAAAATGGA
ACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCA
GGAGGTACCACTTCTCCCTTCAAACTTCCTGACGAAAGTCCGAGTTGGACTGAGTGGCGGCTAC
ATAACGATGAGACGAATTCGAATCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGG
GAAAGTTGTATTTAAGAGATATCTCAGATACGACAGGACGGAAGCTTCACTGCACAGAGTCCTT
GGATCTTGGACGGGAGATTCGGTTAACTATGCAGCATCTCGATTTTTCGGTTTCGACCAGATCG
GATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTCGCGAACTCT
TCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCCAATCGAA
GTGGAAAGTAATGTATCAAGAGGATGCCCTGAAGGTACTCAAACCTTCGAAAAAGAAAGCGAGT
AAGTTAAAATGCTTCTTCGTCTCCTATTTATAATATGGTTTGTTATTGTTAATTTTGTTCTTGT
AGAAGAGCTTAATTAATCGTTGTTGTTATGAAATACTATTTGTATGAGATGAACTGGTGTAATG
TAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCCTCCATAACTAACTAGACATGAAG
ACCTGCCGCGTACAATTGTCTTATATTTGAACAACTAAAATTGAACATCTTTTGCCACAACTTT
ATAAGTGGTTAATATAGCTCAAATATATGGTCAAGTTCAATAGATTAATAATGGAAATATCAGT
TATCGAAATTCATTAACAATCAACTTAACGTTATTAACTACTAATTTTATATCATCCCCTTTGA
TAAATGATAGTACACCAATTAGGAAGGAGCATGCTCGCCTAGGAGATTGTCGTTTCCCGCCTTC
AGTTTGCAAGCTGCTCTAGCCGTGTAGCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGGAAT
TACTAGCGCGTGTCGACACGCGTGGCGCGCCCTAGCAGAAGGCATGTTGTTGTGACTCCGAGGG
GTTGCCTCAAACTCTATCTTATAACCGGCGTGGAGGCATGGAGGCAAGGGCATTTTGGTAATTT
AAGTAGTTAGTGGAAAATGACGTCATTTACTTAAAGACGAAGTCTTGCGACAAGGGGGGCCCAC
GCCGAATTTTAATATTACCGGCGTGGCCCCACCTTATCGCGAGTGCTTTAGCACGAGCGGTCCA
GATTTAAAGTAGAAAAGTTCCCGCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATAC
GATGTGATGGTATTTGATAAAGCGTATATTGTATCAGGTATTTCCGTCGGATACGAATTATTCG
TACAAGCTTCTTAAGCCGGTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCA
AAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAA
CCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGT
GGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACA
GTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCAC
GTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAA
AATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATAT
CCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAA
GGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCT
GCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTC
CAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACA
ATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTAT
TAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAA
CTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACG
TTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTC

TTTGTGGACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGT
CTTGGGAAAAGAAAGCTTGCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTG
CTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTT
TCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCC
CGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGC
CCATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCA
GATCTTCGCCGCGGCTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTGGAT
CTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAGCC
AGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTG
CAGTCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGA
CCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAG
GGATTGTGGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCTTCCCC
CCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACA
TCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGC
TCAGACGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATC
ATGCACCAGGACTGGCTCAATGGCAAGGAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATT
CGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAAT
TTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTA
ATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGAT
CGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTA
TCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATT
TATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAA
ATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCTCTAGA
GTCTCAAGCTTGGCGCGGGGTACCGAGCTCGAATTCCGAGTGTACTTCAAGTCAGTTGGAAATC
AATAAAATGATTATTTTATGAATATATTTCATTGTGCAAGTAGATAGAAATTACATATGTTACA
TAACACACGAAATAAACAAAAAAACACAATCCAAAACAAACACCCCAAACAAAATAACACTATA
TATATCCTCGTATGAGGAGAGGCACGTTCAGTGACTCGACGATTCCCGAGCAAAAAAAGTCTCC
CCGTCACACATATAGTGGGTGACGCAATTATCTTCAAAGTAATCCTTCTGTTGACTTGTCATTG
ATAACATCCAGTCTTCGTCAGGATTGCAAAGAATTATAGAAGGGATCCCACCTTTTATTTTCTT
CTTTTTTCCATATTTAGGGTTGACAGTGAAATCAGACTGGCAACCTATTAATTGCTTCCACAAT
GGGACGAACTTGAAGGGGATGTCGTCGATGATATTATAGGTGGCGTGTTCATCGTAGTTGGTGA
AGTCGATGGTCCCGTTCCAGTAGTTGTGTCGCCCGAGACTTCTAGCCCAGGTGGTCTTTCCGGT
ACGAGTTGGTCCGCAGATGTAGAGGCTGGGGTGTCTGACCCCAGTCCTTCCCTCATCCTGGTTA
GATCGGCCATCCACTCAAGGTCAGATTGTGCTTGATCGTAGGAGACAGGATGTATGAAAGTGTA
GGCATCGATGCTTACATGATATAGGTGCGTCTCTCTCCAGTTGTGCAGATCTTCGTGGCAGCGG
AGATCTGATTCTGTGAAGGGCGACACGTACTGCTCAGGTTGTGGAGGAAATAATTTGTTGGCTG
AATATTCCAGCCATTGAAGCTTTGTTGCCCATTCATGAGGGAATTCTTCTTTGATCATGTCAAG
ATACTCCTCCTTAGACGTTGCAGTCTGGATAATAGTTCGCCATCGTGCGTCAGATTTGCGAGGA
GAGACCTTATGATCTCGGAAATCTCCTCTGGTTTTAATATCTCCGTCCTTTGATATGTAATCAA
GGACTTGTTTAGAGTTTCTAGCTGGCTGGATATTAGGGTGATTTCCTTCAAAATCGAAAAAAGA
AGGATCCCTAATACAAGGTTTTTTATCAAGCTGGATAAGAGCATGATAGTGGGTAGTGCCATCT
TGATGAAGCTCAGAAGCAACACCAAGGAAGAAAATAAGAAAAGGTGTGAGTTTCTCCCAGAGAA
ACTGGAATAAATCATCTCTTTGAGATGAGCACTTGGGGTAGGTAAGGAAAACATATTTAGATTG
GAGTCTGAAGTTCTTGCTAGCAGAAGGCATGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCT
ATCTTATAACCGGCGTGGAGGCATGGAGGCAAGGGCATTTTGGTAATTTAAGTAGTTAGTGGAA
AATGACGTCATTTACTTAAAGACGAAGTCTTGCGACAAGGGGGGCCCACGCCGAATTTTAATAT
TACCGGCGTGGCCCCACCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTTAAAGTAGAAA

AGTTCCCGCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTT
GATGGAGCGTATATTGTATCAGGTATTTCCGTCGGATACGAATTATTCGTACGGCCGGCCACTA
GTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATC
GCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCC
TTCCCAACAGTTGCGCAGCCTGAATGGCGAATGCTAGAGCAGCTTGAGCTTGGATCAGATTGTC
GTTTCCCGCCTTCAGTTTAAACTATCAGTGTTTGACAGGATATATTGGCGGGTAAACCTAAGAG
AAAAGAGCGTTTA

Figure 4C

Expression cassette number 1008 from BeYDV left LIR to BeYDV right LIR. PDISP/HA from influenza B/Brisbane/60/2008 is underlined (SEQ ID NO: 32)

CTAGCAGAAGGCATGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCTATCTTATAACCGGCGT
GGAGGCATGGAGGCAAGGGCATTTTGGTAATTTAAGTAGTTAGTGGAAAATGACGTCATTTACT
TAAAGACGAAGTCTTGCGACAAGGGGGGCCCACGCCGAATTTTAATATTACCGGCGTGGCCCCA
CCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTTAAAGTAGAAAAGTTCCCGCCCACTAG
GGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTTGATAAAGCGTATATTG
TATCAGGTATTTCCGTCGGATACGAATTATTCGTACAAGCTTCTTAAGCCGGTCAACATGGTGG
AGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAAT
TGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGT
CACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAG
GAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAG
GAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAAC
ATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAA
GGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGC
TATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGC
GATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCAC
CCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATG
TGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCT
ATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAA
CGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCT
CTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAAC
GTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGCGGCGCCATTAAAT
AACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCTGGAGGCTGCT
GTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTT
CTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAG
AAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTA
AGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGGCGAAAAACGTTGCGATTTTCGGCTT
ATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGAATCTGCACTGGAATA
ACATCGTCAAACTCACCACATGTCGTCAAAACTGCTACTCAAGGGGAGGTCAATGTGACTGGTG
TAATACCACTGACAACAACACCCACCAAATCTCATTTTGCAAATCTCAAAGGAACAGAAACCAG
GGGGAAACTATGCCCAAAATGCCTCAACTGCACAGATCTGGACGTAGCCTTGGGCAGACCAAAA
TGCACGGGGAAAATACCCTCGGCAAGAGTTTCAATACTCCATGAAGTCAGACCTGTTACATCTG
GGTGCTTTCCTATAATGCACGACAGAACAAAAATTAGACAGCTGCCTAACCTTCTCCGAGGATA
CGAACATATCAGGTTATCAACCCATAACGTTATCAATGCAGAAAATGCACCAGGAGGACCCTAC

AAAATTGGAACCTCAGGGTCTTGCCCTAACATTACCAATGGAAACGGATTTTTCGCAACAATGG
CTTGGGCCGTCCCAAAAAACGACAAAAACAAAACAGCAACAAATCCATTAACAATAGAAGTACC
ATACATTTGTACAGAAGGAGAAGACCAAATTACCGTTTGGGGGTTCCACTCTGACAACGAGACC
CAAATGGCAAAGCTCTATGGGGACTCAAAGCCCCAGAAGTTCACCTCATCTGCCAACGGAGTGA
CCACACATTACGTTTCACAGATTGGTGGCTTCCCAAATCAAACAGAAGACGGAGGACTACCACA
AAGTGGTAGAATTGTTGTTGATTACATGGTGCAAAAATCTGGGAAAACAGGAACAATTACCTAT
CAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTGCGCAAGTGGCAGGAGCAAGGTAATAAAAG
GATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTCCACGAAAAATACGGTGGATTAAACAAAAG
CAAGCCTTACTACACAGGGGAACATGCAAAGGCCATAGGAAATTGCCCAATATGGGTGAAAACA
CCCTTGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGCAAAACTATTAAAGGAAAGGGGTT
TCTTCGGAGCTATTGCTGGTTTCTTAGAAGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGG
ATACACATCCCATGGGGCACATGGAGTAGCGGTGGCAGCAGACCTTAAGAGCACTCAAGAGGCC
ATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTGAGCTGGAAGTAAAGAATCTTCAAAGAC
TAAGCGGTGCCATGGATGAACTCCACAACGAAATACTAGAACTAGATGAGAAAGTGGATGATCT
CAGAGCTGATACAATAAGCTCACAAATAGAACTCGCAGTCCTGCTTTCCAATGAAGGAATAATA
AACAGTGAAGATGAACATCTCTTGGCGCTTGAAAGAAAGCTGAAGAAAATGCTGGGCCCCTCTG
CTGTAGAGATAGGGAATGGATGCTTTGAAACCAAACACAAGTGCAACCAGACCTGTCTCGACAG
AATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTCTCCCCACCTTTGATTCACTGAATATT
ACTGCTGCATCTTTAAATGACGATGGATTGGATAATCATACTATACTGCTTTACTACTCAACTG
CTGCCTCCAGTTTGGCTGTAACACTGATGATAGCTATCTTTGTTGTTTATATGGTCTCCAGAGA
CAATGTTTCTTGCTCCATCTGTCTATAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTC
GGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATT
TAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAA
TTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATC
GTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTAT
CATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTT
ATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAA
TATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCTCTAGAG
TCTCAAGCTTGGCGCGGGGTACCGAGCTCGAATTCCGAGTGTACTTCAAGTCAGTTGGAAATCA
ATAAAATGATTATTTTATGAATATATTTCATTGTGCAAGTAGATAGAAATTACATATGTTACAT
AACACACGAAATAAACAAAAAAACACAATCCAAAACAAACACCCCAAACAAAATAACACTATAT
ATATCCTCGTATGAGGAGAGGCACGTTCAGTGACTCGACGATTCCCGAGCAAAAAAAGTCTCCC
CGTCACACATATAGTGGGTGACGCAATTATCTTCAAAGTAATCCTTCTGTTGACTTGTCATTGA
TAACATCCAGTCTTCGTCAGGATTGCAAAGAATTATAGAAGGGATCCCACCTTTTATTTTCTTC
TTTTTTCCATATTTAGGGTTGACAGTGAAATCAGACTGGCAACCTATTAATTGCTTCCACAATG
GGACGAACTTGAAGGGGATGTCGTCGATGATATTATAGGTGGCGTGTTCATCGTAGTTGGTGAA
GTCGATGGTCCCGTTCCAGTAGTTGTGTCGCCCGAGACTTCTAGCCCAGGTGGTCTTTCCGGTA
CGAGTTGGTCCGCAGATGTAGAGGCTGGGGTGTCTGACCCCAGTCCTTCCCTCATCCTGGTTAG
ATCGGCCATCCACTCAAGGTCAGATTGTGCTTGATCGTAGGAGACAGGATGTATGAAAGTGTAG
GCATCGATGCTTACATGATATAGGTGCGTCTCTCTCCAGTTGTGCAGATCTTCGTGGCAGCGGA
GATCTGATTCTGTGAAGGGCGACACGTACTGCTCAGGTTGTGGAGGAAATAATTTGTTGGCTGA
ATATTCCAGCCATTGAAGCTTTGTTGCCCATTCATGAGGGAATTCTTCTTTGATCATGTCAAGA
TACTCCTCCTTAGACGTTGCAGTCTGGATAATAGTTCGCCATCGTGCGTCAGATTTGCGAGGAG
AGACCTTATGATCTCGGAAATCTCCTCTGGTTTTAATATCTCCGTCCTTTGATATGTAATCAAG
GACTTGTTTAGAGTTTCTAGCTGGCTGGATATTAGGGTGATTTCCTTCAAAATCGAAAAAAGAA
GGATCCCTAATACAAGGTTTTTTATCAAGCTGGATAAGAGCATGATAGTGGGTAGTGCCATCTT
GATGAAGCTCAGAAGCAACACCAAGGAAGAAAATAAGAAAAGGTGTGAGTTTCTCCCAGAGAAA

CTGGAATAAATCATCTCTTTGAGATGAGCACTTGGGGTAGGTAAGGAAAACATATTTAGATTGG
AGTCTGAAGTTCTTGCTAGCAGAAGGCATGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCTA
TCTTATAACCGGCGTGGAGGCATGGAGGCAAGGGCATTTTGGTAATTTAAGTAGTTAGTGGAAA
ATGACGTCATTTACTTAAAGACGAAGTCTTGCGACAAGGGGGGCCCACGCCGAATTTTAATATT
ACCGGCGTGGCCCCACCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTTAAAGTAGAAAA
GTTCCCGCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTTG
ATGGAGCGTATATTGTATCAGGTATTTCCGTCGGATACGAATTATTCGTAC

Figure 5: I-2X35S/CPMV-HT/PDISP/HA_B_Brisbane with deleted proteolytic loop/NOS into BeYDV+Replicase amplification system (Construct number 1059)

Figure 5A,

1039+1059.r (SEQ ID NO: 38)

CTTCCCATCCTCCACCAGGAGGTCTATATTTGGTTCCATTGGCCAGCTTCAA

Figure 5B

1039+1059.c (SEQ ID NO: 39)

CAAATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCAC

Figure 5C,

Expression cassette number 1059 from BeYDV left LIR to BeYDV right LIR. PDISP/HA from influenza B/Brisbane/60/2008 with deleted proteolytic loop is underlined. (SEQ ID NO: 40)

CTAGCAGAAGGCATGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCTATCTTATAACCGGCGT
GGAGGCATGGAGGCAAGGGCATTTTGGTAATTTAAGTAGTTAGTGGAAAATGACGTCATTTACT
TAAAGACGAAGTCTTGCGACAAGGGGGGCCCACGCCGAATTTTAATATTACCGGCGTGGCCCCA
CCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTTAAAGTAGAAAAGTTCCCGCCCACTAG
GGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTTGATAAAGCGTATATTG
TATCAGGTATTTCCGTCGGATACGAATTATTCGTACAAGCTTCTTAAGCCGGTCAACATGGTGG
AGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAAT
TGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGT
CACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAG
GAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAG
GAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAAC

ATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAA
GGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGC
TATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGC
GATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCAC
CCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATG
TGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCT
ATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAA
CGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCT
CTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAAC
GTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGCGGCGCCATTAAAT
AACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCTGGAGGCTGCT
GTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTT
CTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAG
AAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTA
AGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGGCGAAAAACGTTGCGATTTTCGGCTT
ATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGAATCTGCACTGGAATA
ACATCGTCAAACTCACCACATGTCGTCAAAACTGCTACTCAAGGGGAGGTCAATGTGACTGGTG
TAATACCACTGACAACAACACCCACCAAATCTCATTTTGCAAATCTCAAAGGAACAGAAACCAG
GGGGAAACTATGCCCAAAATGCCTCAACTGCACAGATCTGGACGTAGCCTTGGGCAGACCAAAA
TGCACGGGGAAAATACCCTCGGCAAGAGTTTCAATACTCCATGAAGTCAGACCTGTTACATCTG
GGTGCTTTCCTATAATGCACGACAGAACAAAAATTAGACAGCTGCCTAACCTTCTCCGAGGATA
CGAACATATCAGGTTATCAACCCATAACGTTATCAATGCAGAAAATGCACCAGGAGGACCCTAC
AAAATTGGAACCTCAGGGTCTTGCCCTAACATTACCAATGGAAACGGATTTTTCGCAACAATGG
CTTGGGCCGTCCCAAAAAACGACAAAAACAAAACAGCAACAAATCCATTAACAATAGAAGTACC
ATACATTTGTACAGAAGGAGAAGACCAAATTACCGTTTGGGGGTTCCACTCTGACAACGAGACC
CAAATGGCAAAGCTCTATGGGGACTCAAAGCCCCAGAAGTTCACCTCATCTGCCAACGGAGTGA
CCACACATTACGTTTCACAGATTGGTGGCTTCCCAAATCAAACAGAAGACGGAGGACTACCACA
AAGTGGTAGAATTGTTGTTGATTACATGGTGCAAAAATCTGGGAAAACAGGAACAATTACCTAT
CAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTGCGCAAGTGGCAGGAGCAAGGTAATAAAAG
GATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTCCACGAAAAATACGGTGGATTAAACAAAAG
CAAGCCTTACTACACAGGGGAACATGCAAAGGCCATAGGAAATTGCCCAATATGGGTGAAAACA
CCCTTGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTG
CAGGTTGGCACGGATACACATCCCATGGGGCACATGGAGTAGCGGTGGCAGCAGACCTTAAGAG
CACTCAAGAGGCCATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTGAGCTGGAAGTAAAG
AATCTTCAAAGACTAAGCGGTGCCATGGATGAACTCCACAACGAAATACTAGAACTAGATGAGA
AAGTGGATGATCTCAGAGCTGATACAATAAGCTCACAAATAGAACTCGCAGTCCTGCTTTCCAA
TGAAGGAATAATAAACAGTGAAGATGAACATCTCTTGGCGCTTGAAAGAAAGCTGAAGAAAATG
CTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATGCTTTGAAACCAAACACAAGTGCAACCAGA
CCTGTCTCGACAGAATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTCTCCCCACCTTTGA
TTCACTGAATATTACTGCTGCATCTTTAAATGACGATGGATTGGATAATCATACTATACTGCTT
TACTACTCAACTGCTGCCTCCAGTTTGGCTGTAACACTGATGATAGCTATCTTTGTTGTTTATA
TGGTCTCCAGAGACAATGTTTCTTGCTCCATCTGTCTATAAAGGCCTATTTTCTTTAGTTTGAA
TTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTT
ATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACAC
AAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTAT
CGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTC
TTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATG

CATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCG
ATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTAC
TAGATCTCTAGAGTCTCAAGCTTGGCGCGGGGTACCGAGCTCGAATTCCGAGTGTACTTCAAGT
CAGTTGGAAATCAATAAAATGATTATTTTATGAATATATTTCATTGTGCAAGTAGATAGAAATT
ACATATGTTACATAACACACGAAATAAACAAAAAAACACAATCCAAAACAAACACCCCAAACAA
AATAACACTATATATATCCTCGTATGAGGAGAGGCACGTTCAGTGACTCGACGATTCCCGAGCA
AAAAAAGTCTCCCCGTCACACATATAGTGGGTGACGCAATTATCTTCAAAGTAATCCTTCTGTT
GACTTGTCATTGATAACATCCAGTCTTCGTCAGGATTGCAAAGAATTATAGAAGGGATCCCACC
TTTTATTTTCTTCTTTTTTCCATATTTAGGGTTGACAGTGAAATCAGACTGGCAACCTATTAAT
TGCTTCCACAATGGGACGAACTTGAAGGGGATGTCGTCGATGATATTATAGGTGGCGTGTTCAT
CGTAGTTGGTGAAGTCGATGGTCCCGTTCCAGTAGTTGTGTCGCCCGAGACTTCTAGCCCAGGT
GGTCTTTCCGGTACGAGTTGGTCCGCAGATGTAGAGGCTGGGGTGTCTGACCCCAGTCCTTCCC
TCATCCTGGTTAGATCGGCCATCCACTCAAGGTCAGATTGTGCTTGATCGTAGGAGACAGGATG
TATGAAAGTGTAGGCATCGATGCTTACATGATATAGGTGCGTCTCTCTCCAGTTGTGCAGATCT
TCGTGGCAGCGGAGATCTGATTCTGTGAAGGGCGACACGTACTGCTCAGGTTGTGGAGGAAATA
ATTTGTTGGCTGAATATTCCAGCCATTGAAGCTTTGTTGCCCATTCATGAGGGAATTCTTCTTT
GATCATGTCAAGATACTCCTCCTTAGACGTTGCAGTCTGGATAATAGTTCGCCATCGTGCGTCA
GATTTGCGAGGAGAGACCTTATGATCTCGGAAATCTCCTCTGGTTTTAATATCTCCGTCCTTTG
ATATGTAATCAAGGACTTGTTTAGAGTTTCTAGCTGGCTGGATATTAGGGTGATTTCCTTCAAA
ATCGAAAAAAGAAGGATCCCTAATACAAGGTTTTTTATCAAGCTGGATAAGAGCATGATAGTGG
GTAGTGCCATCTTGATGAAGCTCAGAAGCAACACCAAGGAAGAAAATAAGAAAAGGTGTGAGTT
TCTCCCAGAGAAACTGGAATAAATCATCTCTTTGAGATGAGCACTTGGGGTAGGTAAGGAAAAC
ATATTTAGATTGGAGTCTGAAGTTCTTGCTAGCAGAAGGCATGTTGTTGTGACTCCGAGGGGTT
GCCTCAAACTCTATCTTATAACCGGCGTGGAGGCATGGAGGCAAGGGCATTTTGGTAATTTAAG
TAGTTAGTGGAAAATGACGTCATTTACTTAAAGACGAAGTCTTGCGACAAGGGGGGCCCACGCC
GAATTTTAATATTACCGGCGTGGCCCCACCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGAT
TTAAAGTAGAAAAGTTCCCGCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGAT
GTGATGGTATTTGATGGAGCGTATATTGTATCAGGTATTTCCGTCGGATACGAATTATTCGTAC

Figure 5D

Amino acid sequence of PDISP/HA from influenza B/Brisbane/60/2008 with deleted proteolytic loop (SEQ ID NO: 41)

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSH
FANLKGTETRGKLCPKCLNCTDLDVALGRPKCTGKIPSARVSILHEVRPVTSGCFPIMHDRTKI
RQLPNLLRGYEHIRLSTHNVINAENAPGGPYKIGTSGSCPNITNGNGFFATMAWAVPKNDKNKT
ATNPLTIEVPYICTEGEDQITVWGFHSDNETQMAKLYGDSKPQKFTSSANGVTTHYVSQIGGFP
NQTEDGGLPQSGRIVVDYMVQKSGKTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCL
HEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAH
GVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISS
QIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFD
AGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMIAIFVVYMVSRDNVSCSIC
L

Figure 5E nucleotide sequence of PDISP/HA from influenza B/Brisbane/60/2008 with deleted proteolytic loop (SEQ ID NO: 43)

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGA
TCTTCGCCGATCGAATCTGCACTGGAATAACATCGTCAAACTCACCACATGTCGTCAAAACTGC
TACTCAAGGGGAGGTCAATGTGACTGGTGTAATACCACTGACAACAACACCCACCAAATCTCAT
TTTGCAAATCTCAAAGGAACAGAAACCAGGGGGAAACTATGCCCAAAATGCCTCAACTGCACAG
ATCTGGACGTAGCCTTGGGCAGACCAAAATGCACGGGGAAAATACCCTCGGCAAGAGTTTCAAT
ACTCCATGAAGTCAGACCTGTTACATCTGGGTGCTTTCCTATAATGCACGACAGAACAAAAATT
AGACAGCTGCCTAACCTTCTCCGAGGATACGAACATATCAGGTTATCAACCCATAACGTTATCA
ATGCAGAAAATGCACCAGGAGGACCCTACAAAATTGGAACCTCAGGGTCTTGCCCTAACATTAC
CAATGGAAACGGATTTTTCGCAACAATGGCTTGGGCCGTCCCAAAAAACGACAAAAACAAAACA
GCAACAAATCCATTAACAATAGAAGTACCATACATTTGTACAGAAGGAGAAGACCAAATTACCG
TTTGGGGGTTCCACTCTGACAACGAGACCCAAATGGCAAAGCTCTATGGGGACTCAAAGCCCCA
GAAGTTCACCTCATCTGCCAACGGAGTGACCACACATTACGTTTCACAGATTGGTGGCTTCCCA
AATCAAACAGAAGACGGAGGACTACCACAAAGTGGTAGAATTGTTGTTGATTACATGGTGCAAA
AATCTGGGAAAACAGGAACAATTACCTATCAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTG
CGCAAGTGGCAGGAGCAAGGTAATAAAAGGATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTC
CACGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCA
TAGGAAATTGCCCAATATGGGTGAAAACACCCTTGAAGCTGGCCAATGGAACCAAATATAGACC
TCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCCCATGGGGCACAT
GGAGTAGCGGTGGCAGCAGACCTTAAGAGCACTCAAGAGGCCATAAACAAGATAACAAAAAATC
TCAACTCTTTGAGTGAGCTGGAAGTAAAGAATCTTCAAAGACTAAGCGGTGCCATGGATGAACT
CCACAACGAAATACTAGAACTAGATGAGAAAGTGGATGATCTCAGAGCTGATACAATAAGCTCA
CAAATAGAACTCGCAGTCCTGCTTTCCAATGAAGGAATAATAAACAGTGAAGATGAACATCTCT
TGGCGCTTGAAAGAAAGCTGAAGAAAATGCTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATG
CTTTGAAACCAAACACAAGTGCAACCAGACCTGTCTCGACAGAATAGCTGCTGGTACCTTTGAT
GCAGGAGAATTTTCTCTCCCCACCTTTGATTCACTGAATATTACTGCTGCATCTTTAAATGACG
ATGGATTGGATAATCATACTATACTGCTTTACTACTCAACTGCTGCCTCCAGTTTGGCTGTAAC
ACTGATGATAGCTATCTTTGTTGTTTATATGGTCTCCAGAGACAATGTTTCTTGCTCCATCTGT
CTATAA

Figure 6: B-2X35S/CPMV-HT/HA B Wisconsin/NOS into BeYDV(m)+Replicase amplification system (Construct number 1462)

Figure 6A, SEQ ID NO: 49
IF-HAB110.S1+3c

AAATTTGTCGGGCCCATGAAGGCAATAATTGTACTACTCATGGTAG

Figure 6B, SEQ ID NO: 50
IF-HAB110.s1-4r

ACTAAAGAAAATAGGCCTTTATAGACAGATGGAGCATGAAACGTTGTCTCTG

Figure 6C, SEQ ID NO: 51
Synthesized HA B Wisconsin (Genbank accession number JN993010)

ATGAAGGCAATAATTGTACTACTCATGGTAGTAACATCCAATGCAGATCGAATCTGCACTGGGA
TAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTGG
CGTGATACCACTGACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACC
AGAGGGAAACTATGCCCGGACTGTCTCAACTGTACAGATCTGGATGTGGCCTTGGGCAGGCCAA
TGTGTGTGGGGACCACACCTTCTGCTAAAGCTTCAATACTCCACGAGGTCAGACCTGTTACATC
CGGGTGCTTTCCTATAATGCACGACAGAACAAAAATCAGGCAACTACCCAATCTTCTCAGAGGA
TATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAAAAAGCACCAGGAGGACCCT
ACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAAATCGGATTTTTTGCAACAAT
GGCTTGGGCTGTCCCAAAGGACAACTACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCA
TACATTTGTACAGAAGGGGAAGACCAAATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCC
AAATGAAGAGCCTCTATGGAGACTCAAATCCTCAAAAGTTCACCTCATCTGCTAATGGAGTAAC
CACACATTATGTTTCTCAGATTGGCGACTTCCCAGATCAAACAGAAGACGGAGGACTACCACAA
AGCGGCAGAATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTATC
AAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGG
GTCATTGCCTTTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGC
AAGCCTTACTACACAGGAGAACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTAAAAACAC
CTTTGAAGCTTGCCAATGGAACCAAATATAGACCTCCTGCAAAACTATTGAAGGAAAGGGGTTT
CTTCGGAGCTATTGCTGGTTTCCTAGAAGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGA
TACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCAGACCTTAAGAGTACACAAGAAGCTA
TAAATAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAACCTTCAAAGACT
AAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTC
AGAGCTGACACTATAAGCTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAA
ACAGTGAAGACGAGCATCTATTGGCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGC
TGTAGACATAGGAAACGGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAGACAGG
ATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCATTGAACATTA
CTGCTGCATCTTTAAATGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGC
TGCTTCTAGTTTGGCTGTAACATTAATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGAC
AACGTTTCATGCTCCATCTGTCTATAA

Figure 6D
Schematic representation of construct 193. SacII and StuI restriction enzyme sites used for plasmid linearization are annotated on the representation.

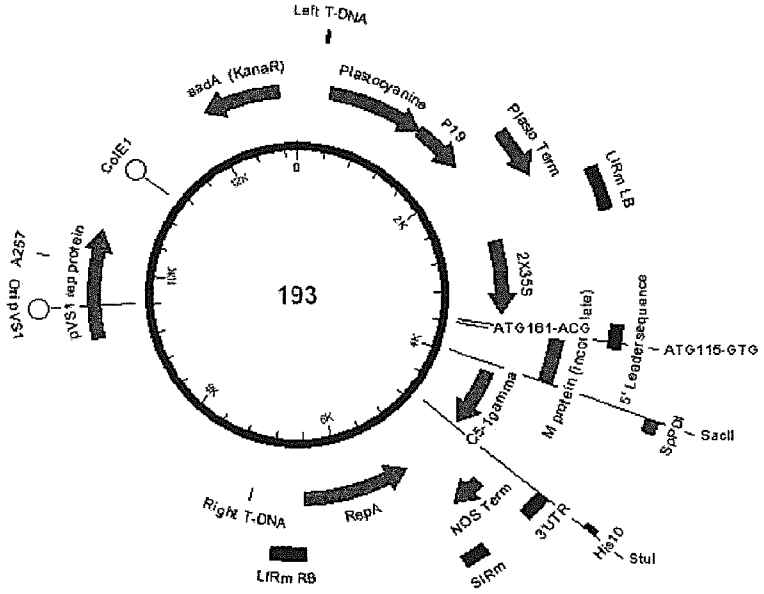


Figure 6E, SEQ ID NO: 52
Construct 193 from left to right t-DNA borders (underlined). 2X35S/CPMV-HT/NOS into BeYDV(m)+Replicase amplification system with Plastocyanine-P19-Plastocyanine silencing inhibitor expression cassette

TGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACATTGCGGACG
TTTTTAATGTACTGAATTAACGCCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTC
AAAAACCATAAAAGTTTAAGTTAGCAAGTGTGTACATTTTTACTTGAACAAAAATATTCACCTA
CTACTGTTATAAATCATTATTAAACATTAGAGTAAAGAAATATGGATGATAAGAACAAGAGTAG
TGATATTTTGACAACAATTTTGTTGCAACATTTGAGAAAATTTTGTTGTTCTCTCTTTTCATTG
GTCAAAAACAATAGAGAGAGAAAAAGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGA
GAAAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATTGAGGAATTTGACAAAAGC
TACACAAATAAGGGTTAATTGCTGTAAATAAATAAGGATGACGCATTAGAGAGATGTACCATTA
GAGAATTTTTGGCAAGTCATTAAAAAGAAAGAATAAATTATTTTTAAAATTAAAAGTTGAGTCA
TTTGATTAAACATGTGATTATTTAATGAATTGATGAAAGAGTTGGATTAAAGTTGTATTAGTAA
TTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCCTATATATTGCCCCATAGAGTC
AGTTAACTCATTTTTATATTTCATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCCAA
AAAAAAAAAACGGTATATTTACTAAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCCGTA
GGAGGATAACATCCAATCCAACCAATCACAACAATCCTGATGAGATAACCCACTTTAAGCCCAC
GCATCTGTGGCACATCTACATTATCTAAATCACACATTCTTCCACACATCTGAGCCACACAAAA
ACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACACTTTGTGAGTCTACACTTTGATT

CCCTTCAAACACATACAAAGAGAAGAGACTAATTAATTAATTAATCATCTTGAGAGAAAATGGA
ACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCA
GGAGGTACCACTTCTCCCTTCAAACTTCCTGACGAAAGTCCGAGTTGGACTGAGTGGCGGCTAC
ATAACGATGAGACGAATTCGAATCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGG
GAAAGTTGTATTTAAGAGATATCTCAGATACGACAGGACGGAAGCTTCACTGCACAGAGTCCTT
GGATCTTGGACGGGAGATTCGGTTAACTATGCAGCATCTCGATTTTTCGGTTTCGACCAGATCG
GATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTCGCGAACTCT
TCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCCAATCGAA
GTGGAAAGTAATGTATCAAGAGGATGCCCTGAAGGTACTCAAACCTTCGAAAAAGAAAGCGAGT
AAGTTAAAATGCTTCTTCGTCTCCTATTTATAATATGGTTTGTTATTGTTAATTTTGTTCTTGT
AGAAGAGCTTAATTAATCGTTGTTGTTATGAAATACTATTTGTATGAGATGAACTGGTGTAATG
TAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCCTCCATAACTAACTAGACATGAAG
ACCTGCCGCGTACAATTGTCTTATATTTGAACAACTAAAATTGAACATCTTTTGCCACAACTTT
ATAAGTGGTTAATATAGCTCAAATATATGGTCAAGTTCAATAGATTAATAATGGAAATATCAGT
TATCGAAATTCATTAACAATCAACTTAACGTTATTAACTACTAATTTTATATCATCCCCTTTGA
TAAATGATAGTACACCAATTAGGAAGGAGCATGCTCGCCTAGGAGATTGTCGTTTCCCGCCTTC
AGTTTGCAAGCTGCTCTAGCCGTGTAGCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGGAAT
TACTAGCGCGTGTCGAGACGCGTTGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCTATCTTA
TAACCGGCGTGGAGGCATGGAGGCAGGGGTATTTTGGTCATTTTAATAGATAGTGGAAAATGAC
GTGGAATTTACTTAAAGACGAAGTCTTTGCGACAAGGGGGGGCCCACGCCGAATTTAATATTAC
CGGCGTGGCCCCCCCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTTAAAGTAGAAAATT
TCCCGCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTTGGT
CGACAAGCTTGCATGCCGGTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCA
AAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAA
CCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGT
GGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACA
GTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCAC
GTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAA
AATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATAT
CCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAA
GGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCT
GCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTC
CAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACA
ATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTAT
TAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAA
CTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACG
TTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTC
TTTGTGGACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGT
CTTGGGAAAAGAAAGCTTGCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTG
CTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTT
TCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCC
CGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGC
CCGCGGATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTT
CTCAGATCTTCGCCTGCAGGCTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCC
CTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCC
TGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCT
GTCCTGCAGTCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCA

GCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT
GCCCAGGGATTGTGGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATC
TTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGG
TAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCA
CACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTT
CCCATCATGCACCAGGACTGGCTCAATGGCAAGGAGCGATCGCTCACCATCACCATCACCATCA
CCATCACCATTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTAT
GTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAG
CTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAA
AAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGC
AATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTT
GAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTT
ATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACT
AGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCTCTAGAGTCTCAAGCTTGGCGC
GCCATAAAATGATTATTTTATGAATATATTTCATTGTGCAAGTAGATAGAAATTACATATGTTA
CATAACACACGAAATAAACAAAAAAAGACAATCCAAAAACAAACACCCCAAAAAAAATAATCAC
TTTAGATAAACTCGTATGAGGAGAGGCACGTTCAGTGACTCGACGATTCCCGAGCAAAAAAAGT
CTCCCCGTCACACATATAGTGGGTGACGCAATTATCTTTAAAGTAATCCTTCTGTTGACTTGTC
ATTGATAACATCCAGTCTTCGTCAGGATTGCAAAGAATTATAGAAGGGATCCCACCTTTTATTT
TCTTCTTTTTTCCATATTTAGGGTTGACAGTGAAATCAGACTGGCAACCTATTAATTGCTTCCA
CAATGGGACGAACTTGAAGGGGATGTCGTCGATGATATTATAGGTGGCGTGTTCATCGTAGTTG
GTGAAATCGATGGTACCGTTCCAATAGTTGTGTCGTCCGAGACTTCTAGCCCAGGTGGTCTTTC
CGGTACGAGTTGGTCCGCAGATGTAGAGGCTGGGGTGTCGGATTCCATTCCTTCCATTGTCCTG
GTTAAATCGGCCATCCATTCAAGGTCAGATTGAGCTTGTTGGTATGAGACAGGATGTATGTAAG
TATAAGCGTCTATGCTTACATGGTATAGATGGGTTTCCCTCCAGGAGTGTAGATCTTCGTGGCA
GCGAAGATCTGATTCTGTGAAGGGCGACACATACGGTTCAGGTTGTGGAGGGAATAATTTGTTG
GCTGAATATTCCAGCCATTGAAGTTTTGTTGCCCATTCATGAGGGAATTCTTCCTTGATCATGT
CAAGATATTCCTCCTTAGACGTTGCAGTCTGGATAATAGTTCTCCATCGTGCGTCAGATTTGCG
AGGAGAGACCTTATGATCTCGGAAATCTCCTCTGGTTTTAATATCTCCGTCCTTTGATATGTAA
TCAAGGACTTGTTTAGAGTTTCTAGCTGGCTGGATATTAGGGTGATTTCCTTCAAAATCGAAAA
AAGAAGGATCCCTAATACAAGGTTTTTTATCAAGCTGGAGAAGAGCATGATAGTGGGTAGTGCC
ATCTTGATGAAGCTCAGAAGCAACACCAAGGAAGAAAATAAGAAAAGGTGTGAGTTTCTCCCAG
AGAAACTGGAATAAATCATCTCTTTGAGATGAGCACTTGGGATAGGTAAGGAAAACATATTTAG
ATTGGAGTCTGAAGTTCTTACTAGCAGAAGGCATGTTGTTGTGACTCCGAGGGGTTGCCTCAAA
CTCTATCTTATAACCGGCGTGGAGGCATGGAGGCAGGGGTATTTTGGTCATTTTAATAGATAGT
GGAAAATGACGTGGAATTTACTTAAAGACGAAGTCTTTGCGACAAGGGGGGGCCCACGCCGAAT
TTAATATTACCGGCGTGGCCCCCCCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTTAAA
GTAGAAAATTTCCCGCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGAT
GGTATTTGACTAGTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTA
CCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCG
CACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGCTAGAGCAGCTTGAGCTTG
GATCAGATTGTCGTTTCCCGCCTTCAGTTTAAACTATCAGTGTTTGACAGGATATATTGGCGGG
TAAACCTAAGAGAAAAGAGCGTTTA

Figure 6F, SEQ ID NO: 53
Expression cassette number 1462 from 2X35S promoter to NOS terminator. HA from influenza B/Wisconsin/1/2010 is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAG
ACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTG
CCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCAT
CATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGAC
CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGA
TTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTC
TCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGAT
TCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAA
ATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAA
GATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGC
AAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCA
AGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTT
TGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTT
AAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCG
GCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGC
GGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTT
GCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGC
AATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGA
TTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGG
AGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGAAGGCAATAATTG
TACTACTCATGGTAGTAACATCCAATGCAGATCGAATCTGCACTGGGATAACATCTTCAAACTC
ACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTGGCGTGATACCACTGACA
ACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAGGGAAACTATGCC
CGGACTGTCTCAACTGTACAGATCTGGATGTGGCCTTGGGCAGGCCAATGTGTGTGGGGACCAC
ACCTTCTGCTAAAGCTTCAATACTCCACGAGGTCAGACCTGTTACATCCGGGTGCTTTCCTATA
ATGCACGACAGAACAAAAATCAGGCAACTACCCAATCTTCTCAGAGGATATGAAAATATCAGGT
TATCAACCCAAAACGTTATCGATGCAGAAAAAGCACCAGGAGGACCCTACAGACTTGGAACCTC
AGGATCTTGCCCTAACGCTACCAGTAAAATCGGATTTTTTGCAACAATGGCTTGGGCTGTCCCA
AAGGACAACTACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAAG
GGGAAGACCAAATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAGCCTCTA
TGGAGACTCAAATCCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCT
CAGATTGGCGACTTCCCAGATCAAACAGAAGACGGAGGACTACCACAAAGCGGCAGAATTGTTG
TTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTATCAAAGAGGTGTTTTGTT
GCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCATTGCCTTTAATT
GGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAG
GAGAACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTAAAAACACCTTTGAAGCTTGCCAA
TGGAACCAAATATAGACCTCCTGCAAAACTATTGAAGGAAAGGGGTTTCTTCGGAGCTATTGCT
GGTTTCCTAGAAGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCTCACGGAG
CACATGGAGTGGCAGTGGCGGCAGACCTTAAGAGTACACAAGAAGCTATAAATAAGATAACAAA
AAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAACCTTCAAAGACTAAGTGGTGCCATGGAT
GAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGACACTATAA
GCTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGACGAGCA
TCTATTGGCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGACATAGGAAAC

GGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCT
TTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCATTGAACATTACTGCTGCATCTTTAAA
TGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGCTGCTTCTAGTTTGGCT
GTAACATTAATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGACAACGTTTCATGCTCCA
TCTGTCTATAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGT
TTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCT
CCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAAAA
AAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAA
TAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGA
ATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTAT
GATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAG
GATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 6G, SEQ ID NO: 54
Amino acid sequence of HA from influenza B/Wisconsin/1/2010

MKAIIVLLMVVTSNADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTRT
RGKLCPDCLNCTDLDVALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLPNLLRG
YENIRLSTQNVIDAEKAPGGPYRLGTSGSCPNATSKIGFFATMAWAVPKDNYKNATNPLTVEVP
YICTEGEDQITVWGFHSDNKTQMKSLYGDSNPQKFTSSANGVTTHYVSQIGDFPDQTEDGGLPQ
SGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKS
KPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPAKLLKERGFFGAIAGFLEGGWEGMIAGWHG
YTSHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDL
RADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSAVDIGNGCFETKHKCNQTCLDR
IAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMLAIFIVYMVSRD
NVSCSICL*

Figure 6H
Schematic representation of construct number 1462

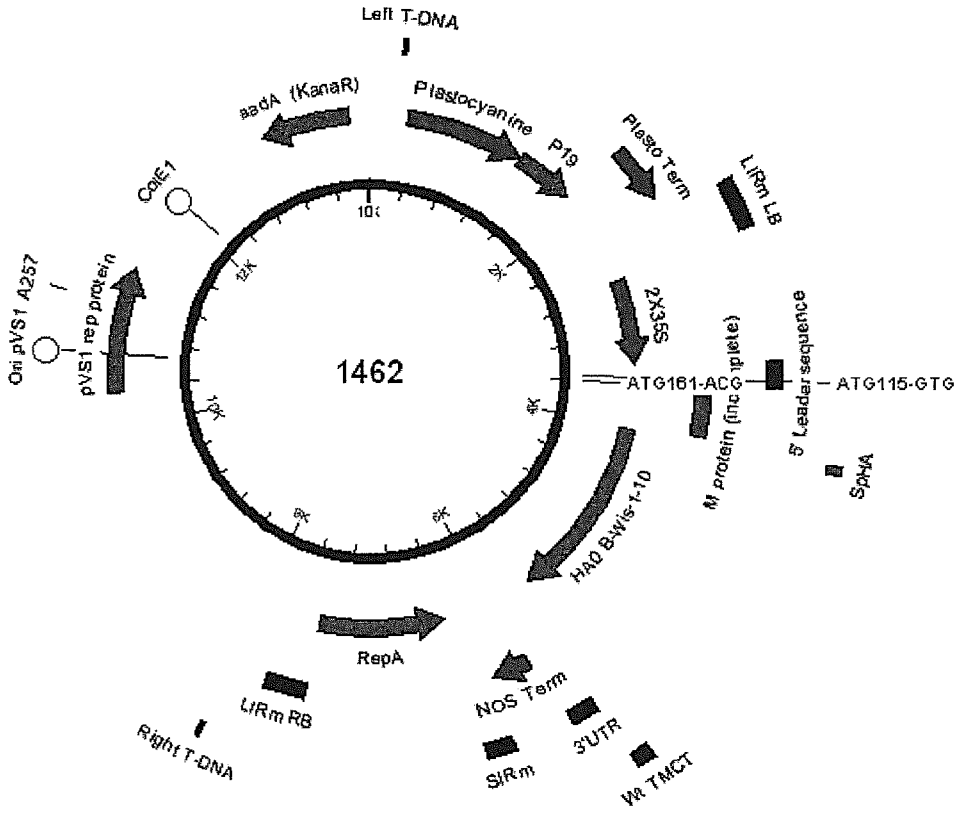


Figure 7: C-2X35S/CPMV-HT/HA B Wisconsin with deleted proteolytic loop/NOS into BeYDV(m)+Replicase amplification system (Construct number 1467)

Figure 7A, SEQ ID NO: 55
HAB110(PrL-).r

TCCTTCCCATCCTCCACCAGGAGGTCTATATTTGGTTCCATTGGCAAGCTTCAAAG

Figure 7B, SEQ ID NO: 56
HAB110(PrL-).c

ATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGA

Figure 7C, SEQ ID NO: 57
Expression cassette number 1467 from 2X35S promoter to NOS terminator. HA from influenza B/Wisconsin/1/2010 with deleted proteolytic loop is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAG
ACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTG
CCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCAT
CATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGAC
CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGA
TTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTC
TCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGAT
TCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAA
ATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAA
GATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGC
AAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCA
AGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTT
TGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTT
AAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCG
GCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGC
GGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTT
GCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGC
AATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGA
TTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGG
AGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGAAGGCAATAATTG
TACTACTCATGGTAGTAACATCCAATGCAGATCGAATCTGCACTGGGATAACATCTTCAAACTC
ACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTGGCGTGATACCACTGACA
ACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAGGGAAACTATGCC
CGGACTGTCTCAACTGTACAGATCTGGATGTGGCCTTGGGCAGGCCAATGTGTGTGGGGACCAC
ACCTTCTGCTAAAGCTTCAATACTCCACGAGGTCAGACCTGTTACATCCGGGTGCTTTCCTATA
ATGCACGACAGAACAAAAATCAGGCAACTACCCAATCTTCTCAGAGGATATGAAAATATCAGGT
TATCAACCCAAAACGTTATCGATGCAGAAAAAGCACCAGGAGGACCCTACAGACTTGGAACCTC
AGGATCTTGCCCTAACGCTACCAGTAAAATCGGATTTTTTGCAACAATGGCTTGGGCTGTCCCA
AAGGACAACTACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAAG
GGGAAGACCAAATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAGCCTCTA

TGGAGACTCAAATCCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCT
CAGATTGGCGACTTCCCAGATCAAACAGAAGACGGAGGACTACCACAAAGCGGCAGAATTGTTG
TTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTATCAAAGAGGTGTTTTGTT
GCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCATTGCCTTTAATT
GGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAG
GAGAACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTAAAAACACCTTTGAAGCTTGCCAA
TGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATAC
ACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCAGACCTTAAGAGTACACAAGAAGCTATAA
ATAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAACCTTCAAAGACTAAG
TGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGA
GCTGACACTATAAGCTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACA
GTGAAGACGAGCATCTATTGGCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGT
AGACATAGGAAACGGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAGACAGGATA
GCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCATTGAACATTACTG
CTGCATCTTTAAATGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGCTGC
TTCTAGTTTGGCTGTAACATTAATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGACAAC
GTTTCATGCTCCATCTGTCTATAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTG
TGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAAT
TTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTT
ATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTC
AAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATA
TAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGA
GATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATA
GCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 7D, SEQ ID NO: 58
Amino acid sequence of HA from influenza B/Wisconsin/1/2010 with deleted proteolytic loop

MKAIIVLLMVVTSNADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTRT
RGKLCPDCLNCTDLDVALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLPNLLRG
YENIRLSTQNVIDAEKAPGGPYRLGTSGSCPNATSKIGFFATMAWAVPKDNYKNATNPLTVEVP
YICTEGEDQITVWGFHSDNKTQMKSLYGDSNPQKFTSSANGVTTHYVSQIGDFPDQTEDGGLPQ
SGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKS
KPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKS
TQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSN
EGIINSEDEHLLALERKLKKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFD
SLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMLAIFIVYMVSRDNVSCSICL*

Figure 7E
Schematic representation of construct number 1467

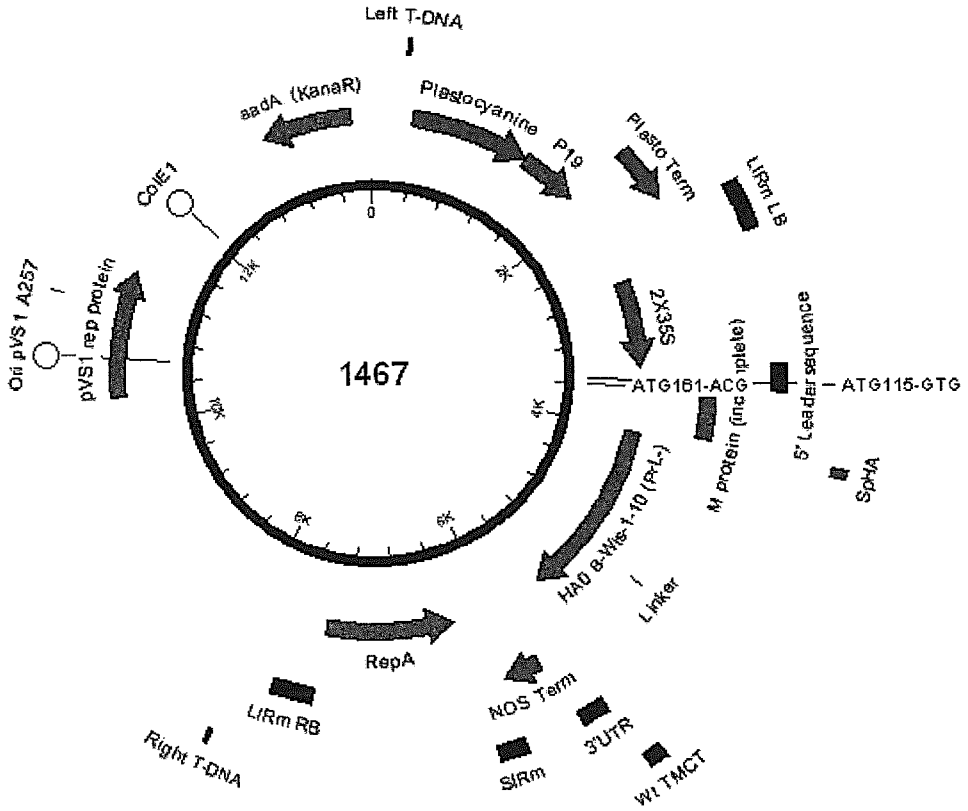


Figure 8: A-2X35S/CPMV-HT/PDISP/HA B Brisbane with deleted proteolytic loop/NOS (Construct number 1039)

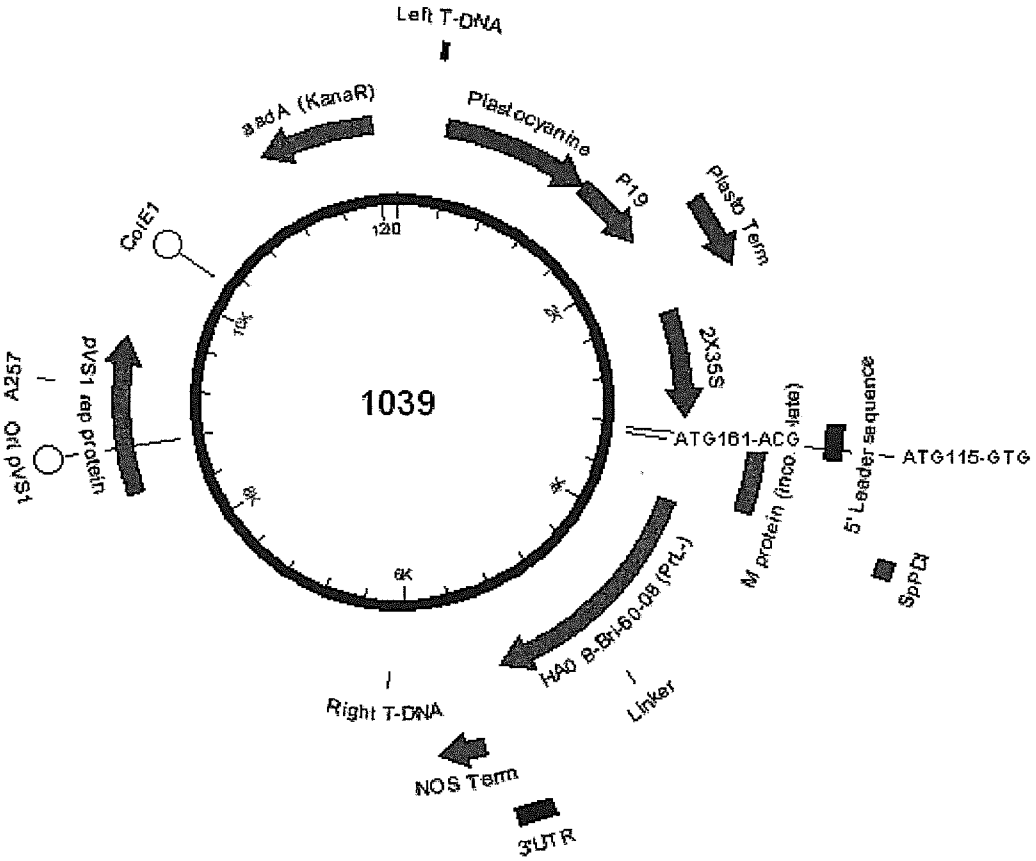
Figure 8A (SEQ ID NO: 15)

Expression cassette number 1039 from 2X35S promoter to Nos terminator. PDISP/HA from influenza B/Brisbane/60/2008 with deleted proteolytic loop is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAG
ACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTG
CCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCAT
CATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGAC
CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGA
TTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTC
TCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGAT
TCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAA
ATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAA
GATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGC
AAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCA
AGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTT
TGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTT
AAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCG
GCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGC
GGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTT
GCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGC
AATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGA
TTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGG
AGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGGCGAAAAACGTTG
CGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGAAT
CTGCACTGGAATAACATCGTCAAACTCACCACATGTCGTCAAAACTGCTACTCAAGGGGAGGTC
AATGTGACTGGTGTAATACCACTGACAACAACACCCACCAAATCTCATTTTGCAAATCTCAAAG
GAACAGAAACCAGGGGGAAACTATGCCCAAAATGCCTCAACTGCACAGATCTGGACGTAGCCTT
GGGCAGACCAAAATGCACGGGGAAAATACCCTCGGCAAGAGTTTCAATACTCCATGAAGTCAGA
CCTGTTACATCTGGGTGCTTTCCTATAATGCACGACAGAACAAAAATTAGACAGCTGCCTAACC
TTCTCCGAGGATACGAACATATCAGGTTATCAACCCATAACGTTATCAATGCAGAAAATGCACC
AGGAGGACCCTACAAAATTGGAACCTCAGGGTCTTGCCCTAACATTACCAATGGAAACGGATTT
TTCGCAACAATGGCTTGGGCCGTCCCAAAAAACGACAAAAACAAAACAGCAACAAATCCATTAA
CAATAGAAGTACCATACATTTGTACAGAAGGAGAAGACCAAATTACCGTTTGGGGGTTCCACTC
TGACAACGAGACCCAAATGGCAAAGCTCTATGGGGACTCAAAGCCCCAGAAGTTCACCTCATCT
GCCAACGGAGTGACCACACATTACGTTTCACAGATTGGTGGCTTCCCAAATCAAACAGAAGACG
GAGGACTACCACAAAGTGGTAGAATTGTTGTTGATTACATGGTGCAAAAATCTGGGAAAACAGG
AACAATTACCTATCAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTGCGCAAGTGGCAGGAGC
AAGGTAATAAAAGGATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTCCACGAAAAATACGGTG
GATTAAACAAAAGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCATAGGAAATTGCCCAAT
ATGGGTGAAAACACCCTTGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGG
GAAGGAATGATTGCAGGTTGGCACGGATACACATCCCATGGGGCACATGGAGTAGCGGTGGCAG
CAGACCTTAAGAGCACTCAAGAGGCCATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTGA

GCTGGAAGTAAAGAATCTTCAAAGACTAAGCGGTGCCATGGATGAACTCCACAACGAAATACTA
GAACTAGATGAGAAAGTGGATGATCTCAGAGCTGATACAATAAGCTCACAAATAGAACTCGCAG
TCCTGCTTTCCAATGAAGGAATAATAAACAGTGAAGATGAACATCTCTTGGCGCTTGAAAGAAA
GCTGAAGAAAATGCTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATGCTTTGAAACCAAACAC
AAGTGCAACCAGACCTGTCTCGACAGAATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTC
TCCCCACCTTTGATTCACTGAATATTACTGCTGCATCTTTAAATGACGATGGATTGGATAATCA
TACTATACTGCTTTACTACTCAACTGCTGCCTCCAGTTTGGCTGTAACACTGATGATAGCTATC
TTTGTTGTTTATATGGTCTCCAGAGACAATGTTTCTTGCTCCATCTGTCTATAAAGGCCTATTT
TCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGC
TCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCT
TCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAAGACCGGGAATTCG
ATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAAT
CCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAA
TTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATA
CATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTG
TCATCTATGTTACTAGAT

Figure 8B,
Schematic representation of construct number 1039



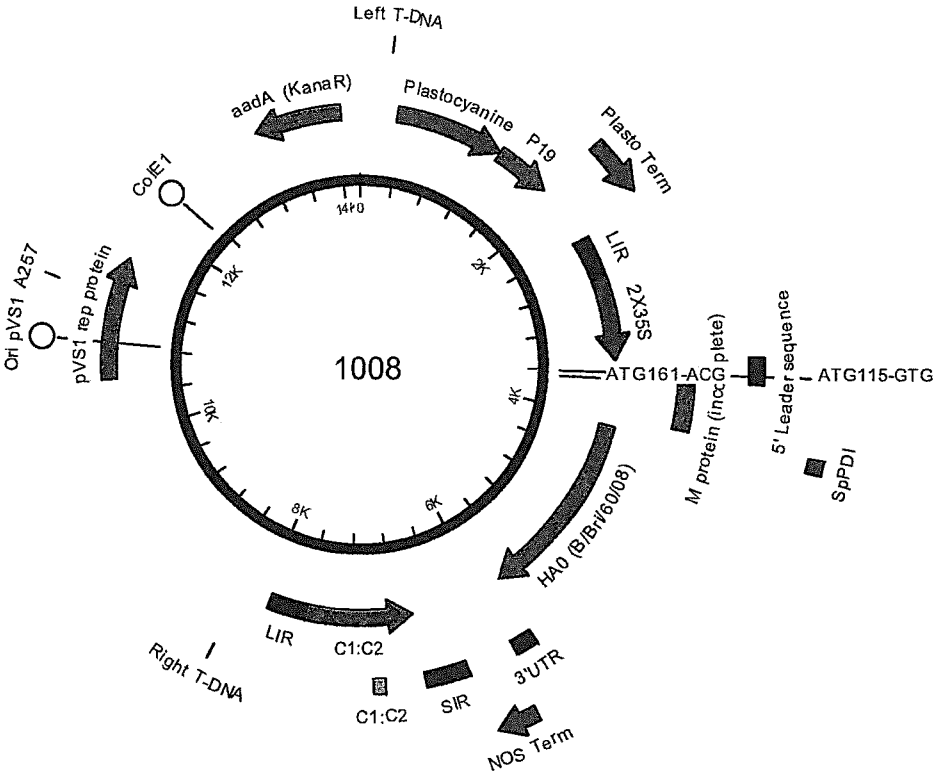


Figure 9

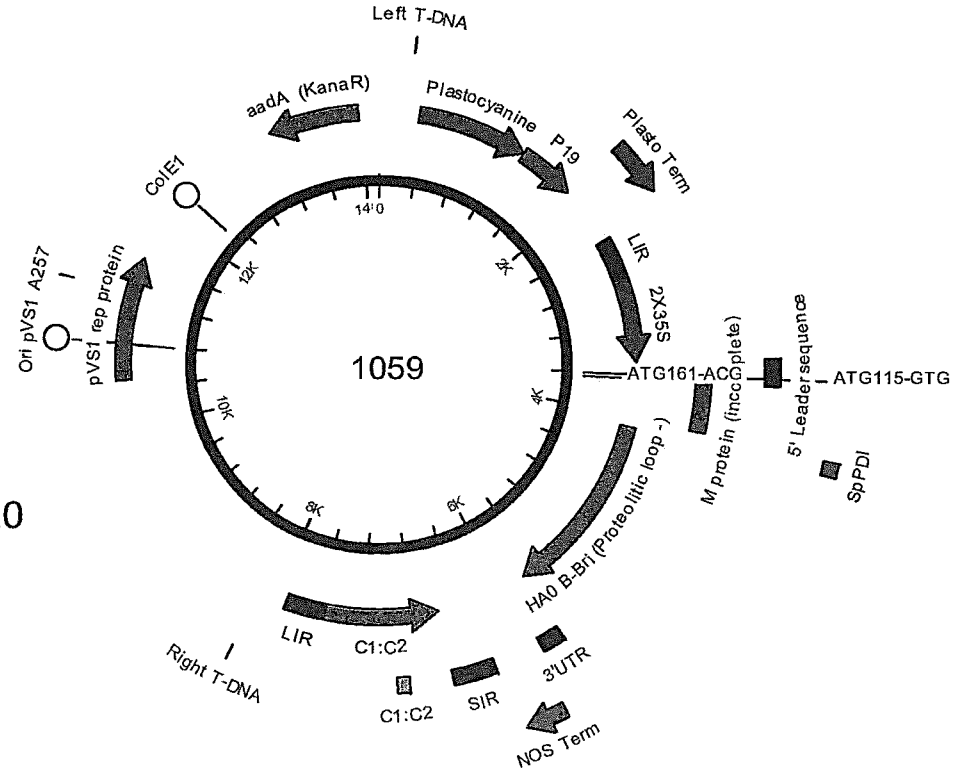


Figure 10

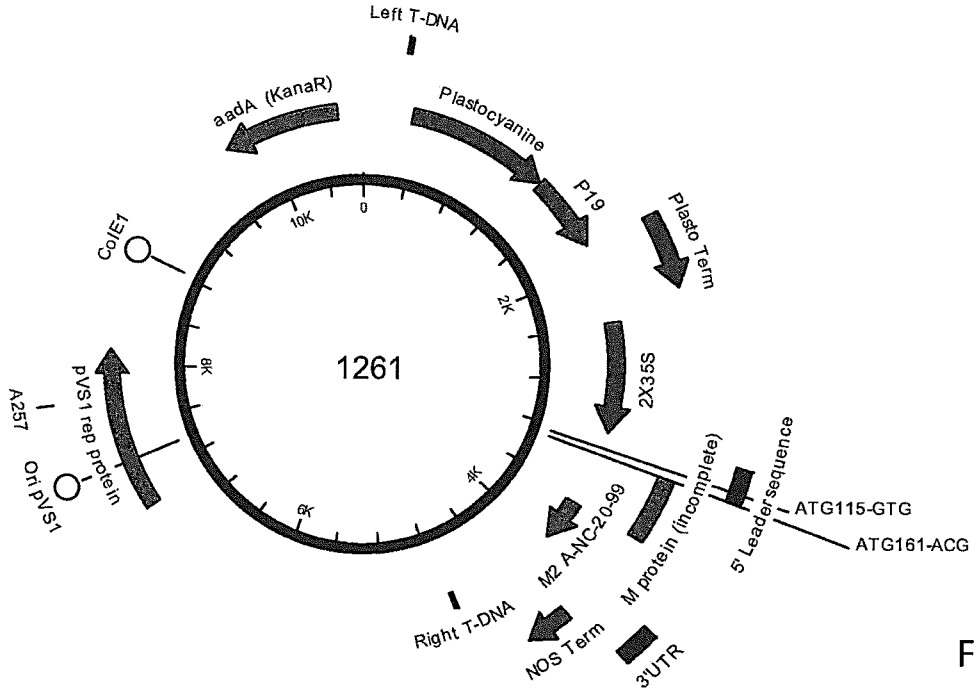


Figure 11

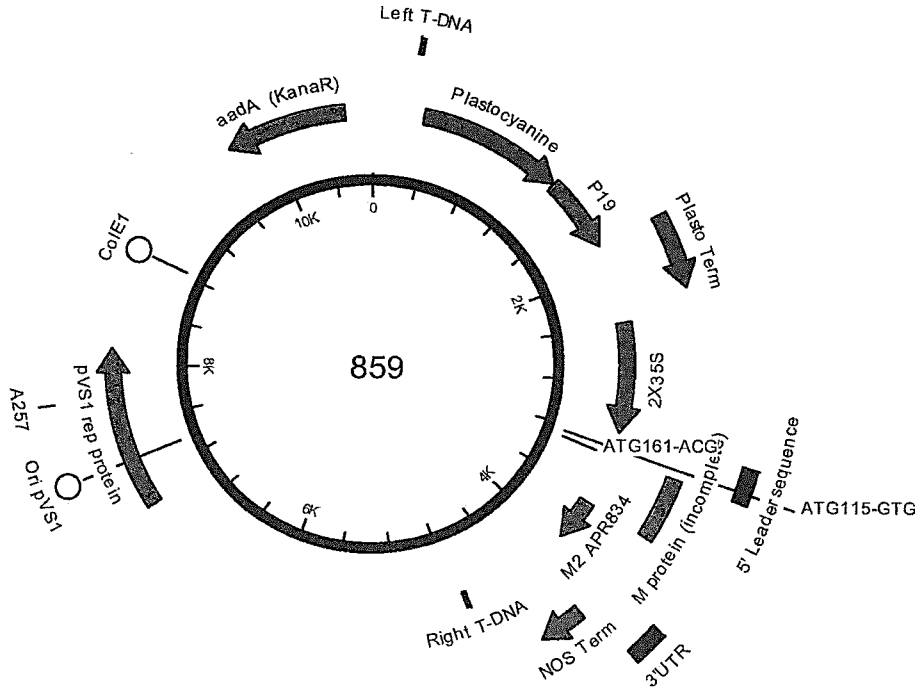


Figure12

Figure 13A

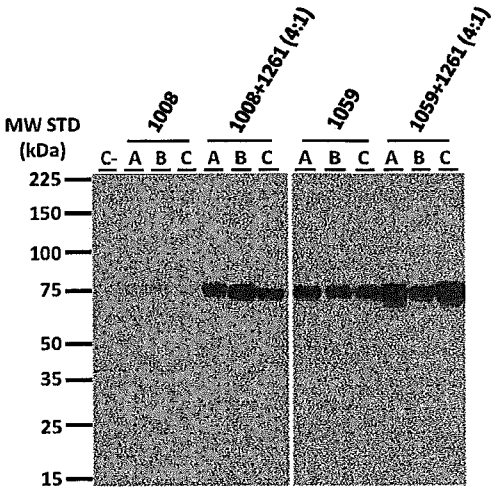


Figure 13B

Construct number	Hemagglutination capacity (HA units / mg protein)[a]
1008	533
1008 + 1261 (4:1)	3200
1059	4267
1059 + 1261 (4:1)	34133

[a] Inverse of the smallest amount of total protein required for positive hemagglutination reaction in a final volume of 200 µl.

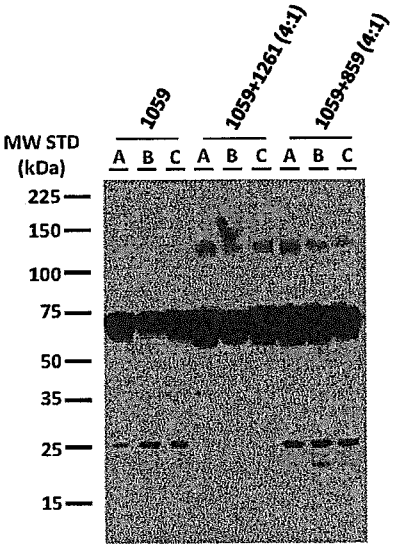

1059
1059+1261 (4:1)
1059+859 (4:1)
MW STD
(kDa)
A B C A B C A B C
225
150
100
75
50
35
25
15

Figure 14

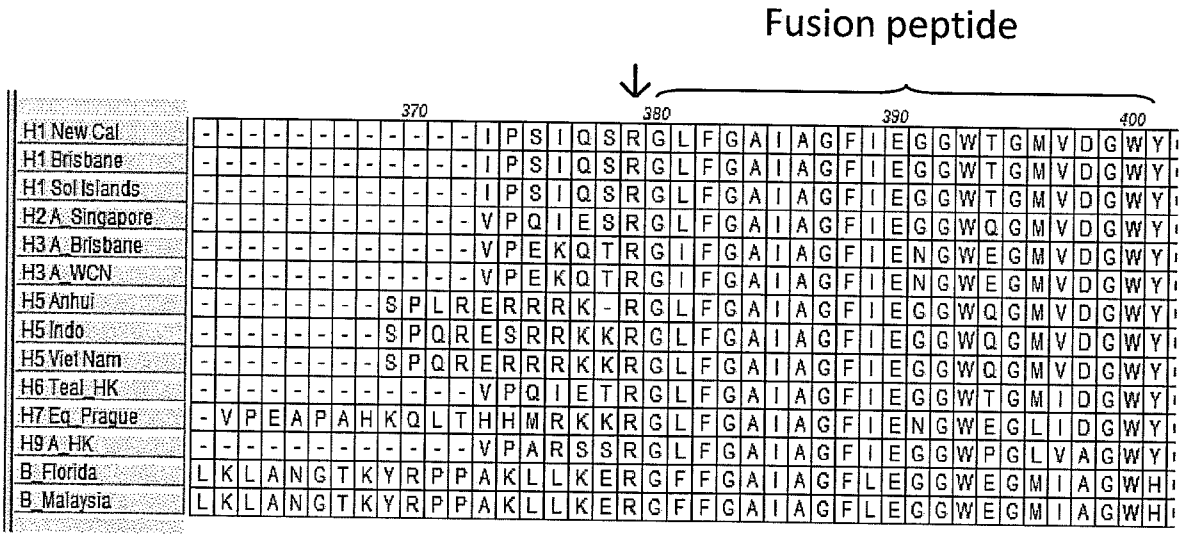

Fusion peptide
370
380
390
400
H1 New Cal
H1 Brisbane
H1 Sol Islands
H2 A_Singapore
H3 A_Brisbane
H3 A_WCN
H5 Anhui
H5 Indo
H5 Viet Nam
H6 Teal_HK
H7 Eq_Prague
H9 A_HK
B_Florida
B_Malaysia

Figure 15

Figure 16A

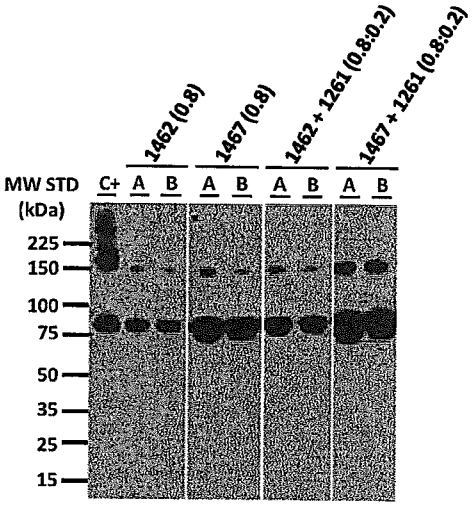


Figure 16B

Construct number	Hemagglutination capacity (HA titer)[a]
1462 (0.8)	136 ± 48
1467 (0.8)	2660 ± 384
1462 + 1261 (0.8:0.2)	941 ± 192
1467 + 1261 (0.8:0.2)	4344 ± 1536

[a] Inverse of the highest dilution capable of agglutinating red blood cells.

Figure 17A

Construct number	Regulatory elements	BeYDV	Proteolytic loop	M2 co-expression	Hemagglutination capacity (HA unit/ml)
1008	CPMV-HT	Yes	Present	No	1216
1008 + 1261	CPMV-HT	Yes	Present	Yes	5696
1039	CPMV-HT	No	Removed	No	141
1039 + 1261	CPMV-HT	No	Removed	Yes	2944
1059	CPMV-HT	Yes	Removed	No	10197
1059 + 1261	CPMV-HT	Yes	Removed	Yes	43008

Figure 17B

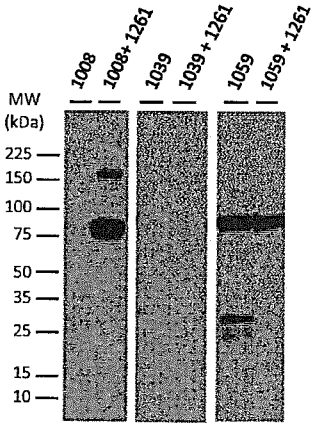


Figure 18A

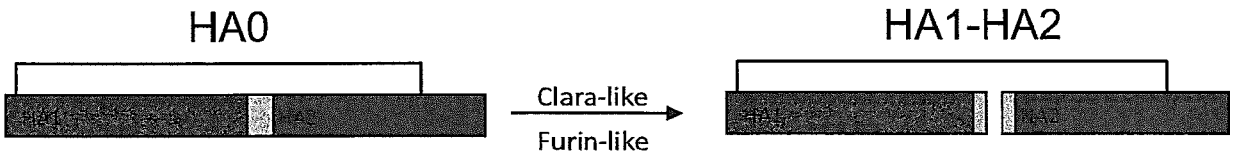


Figure 18B

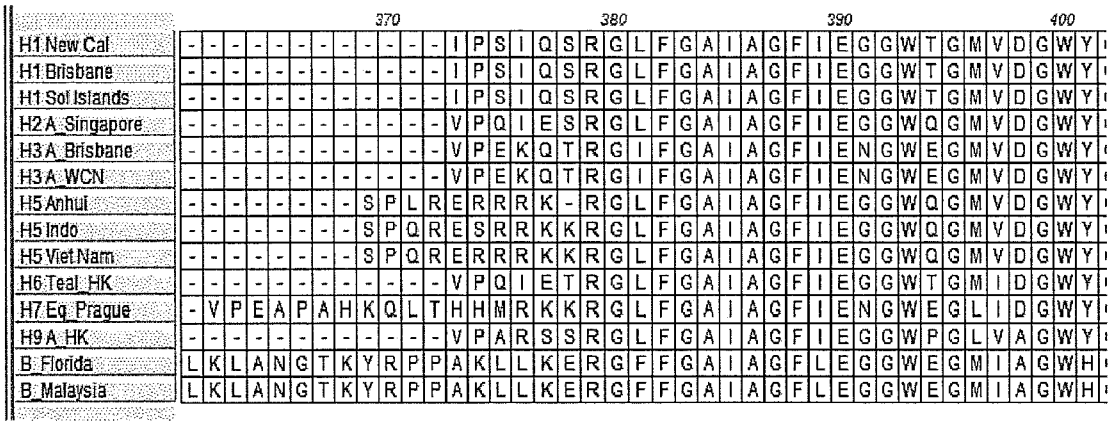


Figure 18C

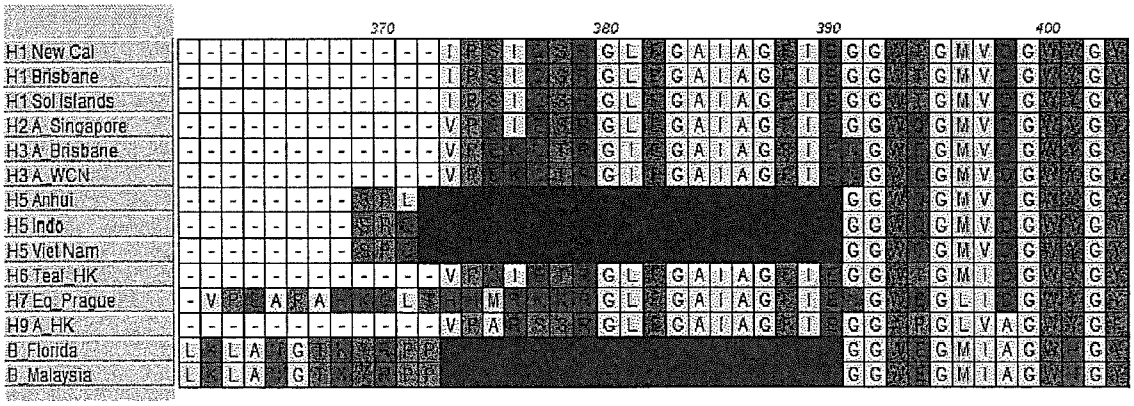
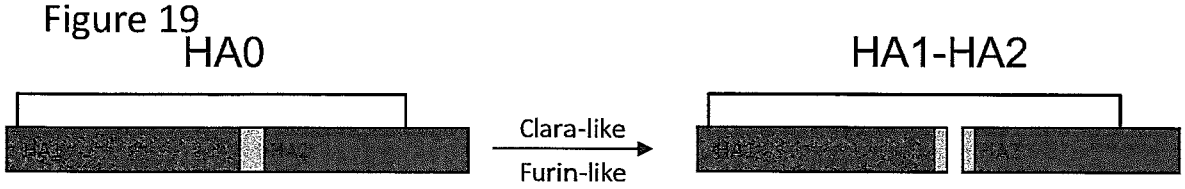


Figure 19



Strain	Natural sequence	Abolition of precursor cleavage site
H5/Indo	TGLRNSPQ**RESRRKKR**↓GLF	TGLRNSPQ**TETR**↓GLF TGLRNSPQ**TETQ**GLF

Figure 20

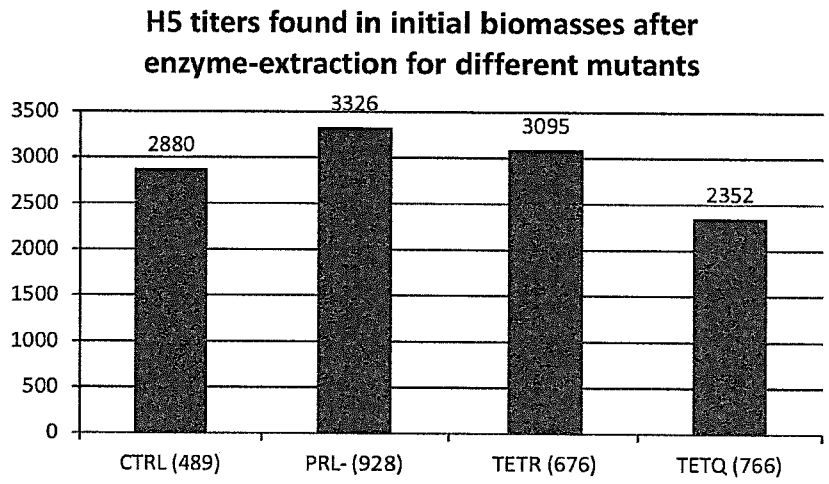

H5 titers found in initial biomasses after enzyme-extraction for different mutants
3500
3000
2500
2000
1500
1000
500
0
2880
3326
3095
2352
CTRL (489)
PRL- (928)
TETR (676)
TETQ (766)

Figure 21: Deletions/replacement approaches for type B HA

Figure 21 A

Primary sequence of the native B/Brisbane/60/2008 (SEQ ID NO: 16)

DRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSHFANLKGTETRGKLCPKCLNCTDLD
VALGRPKCTGKIPSARVSILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYEHIRLSTHNVINAE
NAPGGPYKIGTSGSCPNITNGNGFFATMAWAVPKNDKNKTATNPLTIEVPYICTEGEDQITVWG
FHSDNETQMAKLYGDSKPQKFTSSANGVTTHYVSQIGGFPNQTEDGGLPQSGRIVVDYMVQKSG
KTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGN
CPIWVKTPLKLANGTKYRPPAKLLKERGFFGAIAGFLEGGWEGMIAGWHGYTSHGAHGVAVAAD
LKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVL
LSNEGIINSEDEHLLALERKLKKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFDAGEFSLP
TFDSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMIAIFVVYMVSRDNVSCSICL

Figure 21 B

Δ proteolytic loop of type B HA (SEQ ID NO:17)

DRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSHFANLKGTETRGKLCPKCLNCTDLD
VALGRPKCTGKIPSARVSILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYEHIRLSTHNVINAE
NAPGGPYKIGTSGSCPNITNGNGFFATMAWAVPKNDKNKTATNPLTIEVPYICTEGEDQITVWG
FHSDNETQMAKLYGDSKPQKFTSSANGVTTHYVSQIGGFPNQTEDGGLPQSGRIVVDYMVQKSG
KTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGN
CPIWVKTPLKLANGTKYRPP-*GG*-
GWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNE
ILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSAVEIGNGCFET
KHKCNQTCLDRIAAGTFDAGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMI
AIFVVYMVSRDNVSCSICL

Figure 21 C

Replacement of cleavage site of type B HA by a linker (SEQ ID NO:18)

DRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSHFANLKGTETRGKLCPKCLNCTDLD
VALGRPKCTGKIPSARVSILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYEHIRLSTHNVINAE
NAPGGPYKIGTSGSCPNITNGNGFFATMAWAVPKNDKNKTATNPLTIEVPYICTEGEDQITVWG
FHSDNETQMAKLYGDSKPQKFTSSANGVTTHYVSQIGGFPNQTEDGGLPQSGRIVVDYMVQKSG
KTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGN
CPIWVKTPLKLANGTKYR *-GSSSGSSSG-*
GFFGAIAGFLEGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQ
RLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLGP
SAVEIGNGCFETKHKCNQTCLDRIAAGTFDAGEFSLPTFDSLNITAASLNDDGLDNHTILLYYS
TAASSLAVTLMIAIFVVYMVSRDNVSCSICL

Figure 21 D

Deletions/replacement approaches for H3

Primary sequence of the native H3 A/Perth/16/2009 (SEQ ID NO:19

QKLPGNDNSTATLCLGHHAVPNGTIVKTITNDQIEVTNATELVQSSSTGEICDSPHQILDGKNC
TLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNESFNWT
GVTQNGTSSACIRRSKNSFFSRLNWLTHLNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKDQI
FLYAQASGRITVSTKRSQQTVSPNIGSRPRVRNIPSRISIYWTIVKPGDILLINSTGNLIAPRG
YFKIRSGKSSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGM
RNVPEKQTRGIFGAIAGFIENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRL
IGKTNEKFHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLF
EKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTYDHDVYRDEALNNRFQIKGVELKSGYK
DWILWISFAISCFLLCVALLGFIMWACQKGNIRCNICI

Figure 21 E

Δ proteolytic loop H3 (in BeYDV, 1096) (SEQ ID NO:20)

QKLPGNDNSTATLCLGHHAVPNGTIVKTITNDQIEVTNATELVQSSSTGEICDSPHQILDGKNC
TLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNESFNWT
GVTQNGTSSACIRRSKNSFFSRLNWLTHLNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKDQI
FLYAQASGRITVSTKRSQQTVSPNIGSRPRVRNIPSRISIYWTIVKPGDILLINSTGNLIAPRG
YFKIRSGKSSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGM
-GS-
GAIAGFIENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIE
KEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLRENAE
DMGNGCFKIYHKCDNACIGSIRNGTYDHDVYRDEALNNRFQIKGVELKSGYKDWILWISFAISC
FLLCVALLGFIMWACQKGNIRCNICI

Figure 21 F

Replacement of cleavage site of H3 by a linker (in BeYDV, 1097) (SEQ ID NO:21)

QKLPGNDNSTATLCLGHHAVPNGTIVKTITNDQIEVTNATELVQSSSTGEICDSPHQILDGKNC
TLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNESFNWT
GVTQNGTSSACIRRSKNSFFSRLNWLTHLNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKDQI
FLYAQASGRITVSTKRSQQTVSPNIGSRPRVRNIPSRISIYWTIVKPGDILLINSTGNLIAPRG
YFKIRSGKSSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGM
-GSSGSSGSS-
GIFGAIAGFIENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFH
QIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLRE
NAEDMGNGCFKIYHKCDNACIGSIRNGTYDHDVYRDEALNNRFQIKGVELKSGYKDWILWISFA
ISCFLLCVALLGFIMWACQKGNIRCNICI

FIGURE 22

Lane #	Sample	Description
1	496-59-001A	H5/Indo CTRL (# 489)
2	496-59-001B	H5/Indo CTRL (# 489)
3	496-59-002A	H5/Indo PRL- (# 928)
4	496-59-002B	H5/Indo PRL- (# 928)
5	496-59-003A	H5/Indo TETR (# 676)
6	496-59-003B	H5/Indo TETR (# 676)
7	496-59-004A	H5/Indo TETQ (# 766)
8	496-59-004B	H5/Indo TETQ (# 766)
9	MW	
10	C+	H5 25 ng

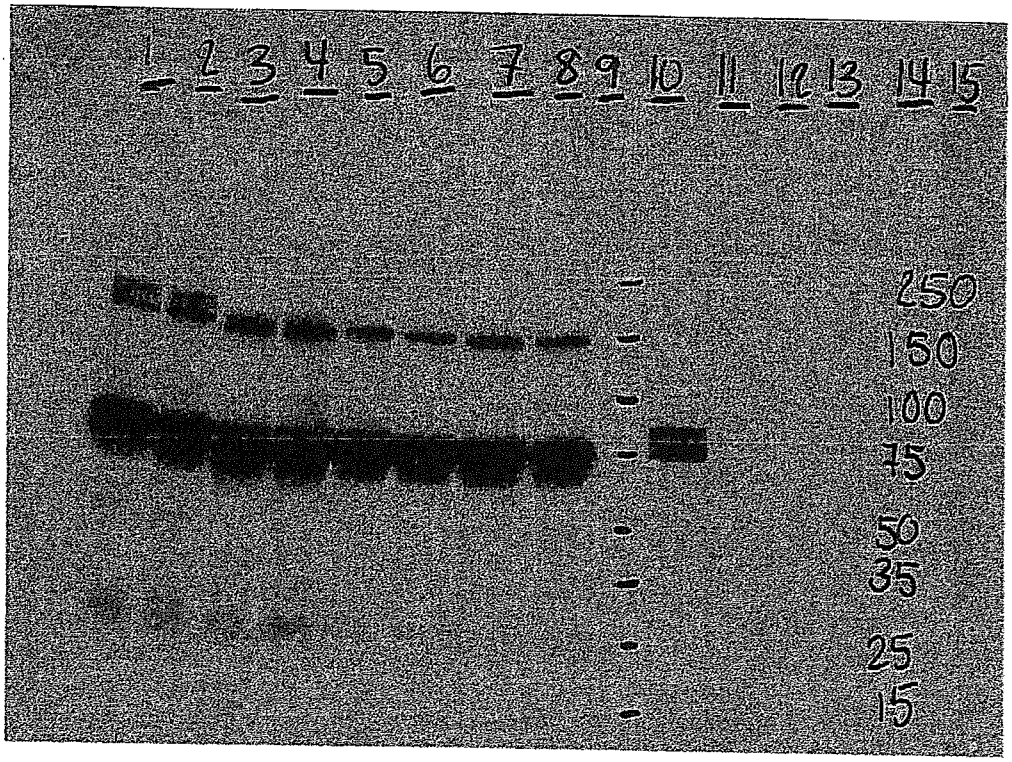


Figure 23: A-2X35S/CPMV-HT/H5 from A/Indonesia/5/2005 with TETR cleavage site mutation (Construct number 676)

Figure 23A, SEQ ID NO : 74 MutCleavage-H5(Indo).r

TAGTCCTCTTGTCTCTGTTTGAGGGCTATTTCTGAGCCCTGTTGC

Figure 23B, SEQ ID NO : 75 MutCleavage-H5(Indo).c

TAGCCCTCAAACAGAGACAAGAGGACTATTTGGAGCTATAGCAGG

Figure 23C, SEQ ID NO : 76

Expression cassette number 676 from 2X35S promoter to NOS terminator. H5 from influenza A/Indonesia/5/2005 (H5N1) TETR cleavage site mutant is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTC
AGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCG
GATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGC
TCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGA
CAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTC
CAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTT
GTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTT
TCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACT
TTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAA
GGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACC
CACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATT
GATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGAC
CCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTT
TTGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATC
TCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAG
ATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTT
TGTGGACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGT
GGTCTTGGGAAAAGAAAGCTTGCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTA
CGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTTGACGAGGTATTGTT
GCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTC
TTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTA
TATTCTGCCCAAATTTGTCGGGCCCATGGAGAAAATAGTGCTTCTTCTTGCAATAGTCA
GTCTTGTTAAAAGTGATCAGATTTGCATTGGTTACCATGCAAACAATTCAACAGAGCAG

GTTGACACAATCATGGAAAAGAACGTTACTGTTACACATGCCCAAGACATACTGGAAAA
GACACACAACGGGAAGCTCTGCGATCTAGATGGAGTGAAGCCTCTAATTTTAAGAGATT
GTAGTGTAGCTGGATGGCTCCTCGGGAACCCAATGTGTGACGAATTCATCAATGTACCG
GAATGGTCTTACATAGTGGAGAAGGCCAATCCAACCAATGACCTCTGTTACCCAGGGAG
TTTCAACGACTATGAAGAACTGAAACACCTATTGAGCAGAATAAACCATTTTGAGAAAA
TTCAAATCATCCCCAAAAGTTCTTGGTCCGATCATGAAGCCTCATCAGGAGTTAGCTCA
GCATGTCCATACCTGGGAAGTCCCTCCTTTTTTAGAAATGTGGTATGGCTTATCAAAAA
GAACAGTACATACCCAACAATAAAGAAAAGCTACAATAATACCAACCAAGAGGATCTTT
TGGTACTGTGGGGAATTCACCATCCTAATGATGCGGCAGAGCAGACAAGGCTATATCAA
AACCCAACCACCTATATTTCCATTGGGACATCAACACTAAACCAGAGATTGGTACCAAA
AATAGCTACTAGATCCAAAGTAAACGGGCAAAGTGGAAGGATGGAGTTCTTCTGGACAA
TTTTAAAACCTAATGATGCAATCAACTTCGAGAGTAATGGAAATTTCATTGCTCCAGAA
TATGCATACAAAATTGTCAAGAAAGGGGACTCAGCAATTATGAAAAGTGAATTGGAATA
TGGTAACTGCAACACCAAGTGTCAAACTCCAATGGGGGCGATAAACTCTAGTATGCCAT
TCCACAACATACACCCTCTCACCATCGGGGAATGCCCCAAATATGTGAAATCAAACAGA
TTAGTCCTTGCAACAGGGCTCAGAAATAGCCCTCAAACAGAGACAAGAGGACTATTTGG
AGCTATAGCAGGTTTTATAGAGGGAGGATGGCAGGGAATGGTAGATGGTTGGTATGGGT
ACCACCATAGCAATGAGCAGGGGAGTGGGTACGCTGCAGACAAAGAATCCACTCAAAAG
GCAATAGATGGAGTCACCAATAAGGTCAACTCAATCATTGACAAAATGAACACTCAGTT
TGAGGCCGTTGGAAGGGAATTTAATAACTTAGAAAGGAGAATAGAGAATTTAAACAAGA
AGATGGAAGACGGGTTTCTAGATGTCTGGACTTATAATGCCGAACTTCTGGTTCTCATG
GAAAATGAGAGAACTCTAGACTTTCATGACTCAAATGTTAAGAACCTCTACGACAAGGT
CCGACTACAGCTTAGGGATAATGCAAAGGAGCTGGGTAACGGTTGTTTCGAGTTCTATC
ACAAATGTGATAATGAATGTATGGAAAGTATAAGAAACGGAACGTACAACTATCCGCAG
TATTCAGAAGAAGCAAGATTAAAAAGAGAGGAAATAAGTGGGGTAAAATTGGAATCAAT
AGGAACTTACCAAATACTGTCAATTTATTCAACAGTGGCGAGTTCCCTAGCACTGGCAA
TCATGATGGCTGGTCTATCTTTATGGATGTGCTCCAATGGATCGTTACAATGCAGAATT
TGCATTTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTA
TGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTT
TGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTT
ATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGAT
CGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGAT
GATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCA
TGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATAC
GCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATC
TATGTTACTAGAT

Figure 23D, SEQ ID NO : 77

Amino acid sequence of H5 from influenza A/Indonesia/5/2005 (H5N1) TETR cleavage site mutant.

MEKIVLLLAIVSLVKSDQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCD
LDGVKPLILRDCSVAGWLLGNPMCDEFINVPEWSYIVEKANPTNDLCYPGSFNDYEELK
HLLSRINHFEKIQIIPKSSWSDHEASSGVSSACPYLGSPSFFRNVVWLIKKNSTYPTIK
KSYNNTNQEDLLVLWGIHHPNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIATRSKVN
GQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQ
TPMGAINSSMPFHNIHPLTIGECPKYVKSNRLVLATGLRNSPQTETRGLFGAIAGFIEG
GWQGMVDGWYGYHHSNEQGSGYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFN
NLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNA
KELGNGCFEFYHKCDNECMESIRNGTYNYPQYSEEARLKREEISGVKLESIGTYQILSI
YSTVASSLALAIMMAGLSLWMCSNGSLQCRICI

Figure 23E

Schematic representation of construct number 676.

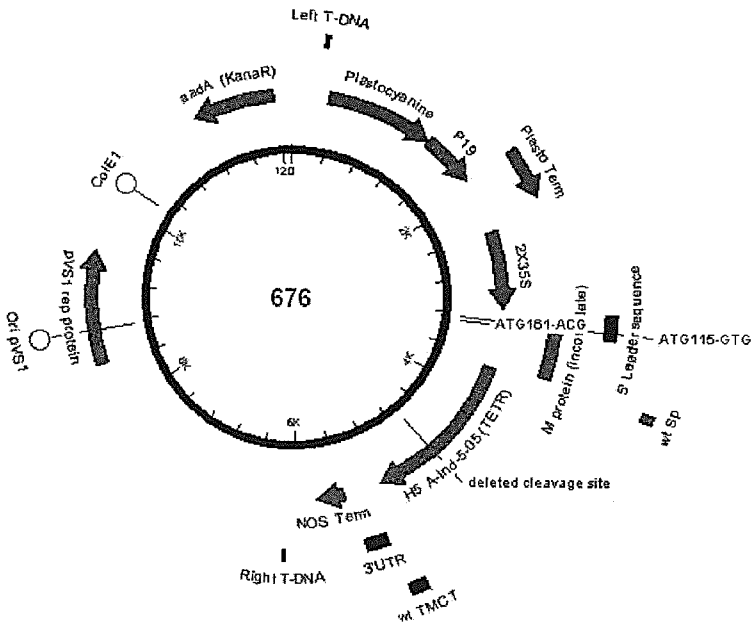


Figure 24: B-2X35S/CPMV-HT/H5 from A/Indonesia/5/2005 with TETQ cleavage site mutation (Construct number 766)

Figure 24A, SEQ ID NO : 78 H5I505_TETQ.r

TCCAAATAGTCCTTGTGTCTCTGTTTGAGGGCTATTTCTGAGCCCTGT

Figure 24B, SEQ ID NO : 79 H5I505_TETQ.c

AAATAGCCCTCAAACAGAGACACAAGGACTATTTGGAGCTATAGCAGG

Figure 24C, SEQ ID NO : 80

Expression cassette number 766 from 2X35S promoter to NOS terminator. H5 from influenza A/Indonesia/5/2005 (H5N1) TETQ cleavage site mutant is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTC
AGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCG
GATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGC
TCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGA
CAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTC
CAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTT
GTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTT
TCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACT
TTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAA
GGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACC
CACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATT
GATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGAC
CCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTT
TTGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATC
TCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAG
ATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTT
TGTGGACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGT
GGTCTTGGGAAAAGAAAGCTTGCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTA
CGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTTGACGAGGTATTGTT
GCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTC
TTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTA
TATTCTGCCCAAATTTGTCGGGCCCATGGAGAAAATAGTGCTTCTTCTTGCAATAGTCA
GTCTTGTTAAAAGTGATCAGATTTGCATTGGTTACCATGCAAACAATTCAACAGAGCAG

GTTGACACAATCATGGAAAAGAACGTTACTGTTACACATGCCCAAGACATACTGGAAAA
GACACACAACGGGAAGCTCTGCGATCTAGATGGAGTGAAGCCTCTAATTTTAAGAGATT
GTAGTGTAGCTGGATGGCTCCTCGGGAACCCAATGTGTGACGAATTCATCAATGTACCG
GAATGGTCTTACATAGTGGAGAAGGCCAATCCAACCAATGACCTCTGTTACCCAGGGAG
TTTCAACGACTATGAAGAACTGAAACACCTATTGAGCAGAATAAACCATTTTGAGAAAA
TTCAAATCATCCCCAAAAGTTCTTGGTCCGATCATGAAGCCTCATCAGGAGTTAGCTCA
GCATGTCCATACCTGGGAAGTCCCTCCTTTTTTTAGAAATGTGGTATGGCTTATCAAAAA
GAACAGTACATACCCAACAATAAAGAAAAGCTACAATAATACCAACCAAGAGGATCTTT
TGGTACTGTGGGGAATTCACCATCCTAATGATGCGGCAGAGCAGACAAGGCTATATCAA
AACCCAACCACCTATATTTCCATTGGGACATCAACACTAAACCAGAGATTGGTACCAAA
AATAGCTACTAGATCCAAAGTAAACGGGCAAAGTGGAAGGATGGAGTTCTTCTGGACAA
TTTTAAAACCTAATGATGCAATCAACTTCGAGAGTAATGGAAATTTCATTGCTCCAGAA
TATGCATACAAAATTGTCAAGAAAGGGGACTCAGCAATTATGAAAAGTGAATTGGAATA
TGGTAACTGCAACACCAAGTGTCAAACTCCAATGGGGGCGATAAACTCTAGTATGCCAT
TCCACAACATACACCCTCTCACCATCGGGGAATGCCCCAAATATGTGAAATCAAACAGA
TTAGTCCTTGCAACAGGGCTCAGAAATAGCCCTCAAACAGAGACACAAGGACTATTTGG
AGCTATAGCAGGTTTTATAGAGGGAGGATGGCAGGGAATGGTAGATGGTTGGTATGGGT
ACCACCATAGCAATGAGCAGGGGAGTGGGTACGCTGCAGACAAAGAATCCACTCAAAAG
GCAATAGATGGAGTCACCAATAAGGTCAACTCAATCATTGACAAAATGAACACTCAGTT
TGAGGCCGTTGGAAGGGAATTTAATAACTTAGAAAGGAGAATAGAGAATTTAAACAAGA
AGATGGAAGACGGGTTTCTAGATGTCTGGACTTATAATGCCGAACTTCTGGTTCTCATG
GAAAATGAGAGAACTCTAGACTTTCATGACTCAAATGTTAAGAACCTCTACGACAAGGT
CCGACTACAGCTTAGGGATAATGCAAAGGAGCTGGGTAACGGTTGTTTCGAGTTCTATC
ACAAATGTGATAATGAATGTATGGAAAGTATAAGAAACGGAACGTACAACTATCCGCAG
TATTCAGAAGAAGCAAGATTAAAAAGAGAGGAAATAAGTGGGGTAAAATTGGAATCAAT
AGGAACTTACCAAATACTGTCAATTTATTCAACAGTGGCGAGTTCCCTAGCACTGGCAA
TCATGATGGCTGGTCTATCTTTATGGATGTGCTCCAATGGATCGTTACAATGCAGAATT
TGCATTTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTA
TGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTT
TGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTT
ATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGAT
CGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGAT
GATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCA
TGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATAC
GCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATC
TATGTTACTAGAT

Figure 24D, SEQ ID NO : 81

Amino acid sequence of H5 from influenza A/Indonesia/5/2005 (H5N1) TETQ cleavage site mutant.

MEKIVLLLAIVSLVKSDQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCD
LDGVKPLILRDCSVAGWLLGNPMCDEFINVPEWSYIVEKANPTNDLCYPGSFNDYEELK
HLLSRINHFEKIQIIPKSSWSDHEASSGVSSACPYLGSPSFFRNVVWLIKKNSTYPTIK
KSYNNTNQEDLLVLWGIHHPNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIATRSKVN
GQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQ
TPMGAINSSMPFHNIHPLTIGECPKYVKSNRLVLATGLRNSPQTETQGLFGAIAGFIEG
GWQGMVDGWYGYHHSNEQGSGYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFN
NLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNA
KELGNGCFEFYHKCDNECMESIRNGTYNYPQYSEEARLKREEISGVKLESIGTYQILSI
YSTVASSLALAIMMAGLSLWMCSNGSLQCRICI

Figure 24E

Schematic representation of construct number 766.

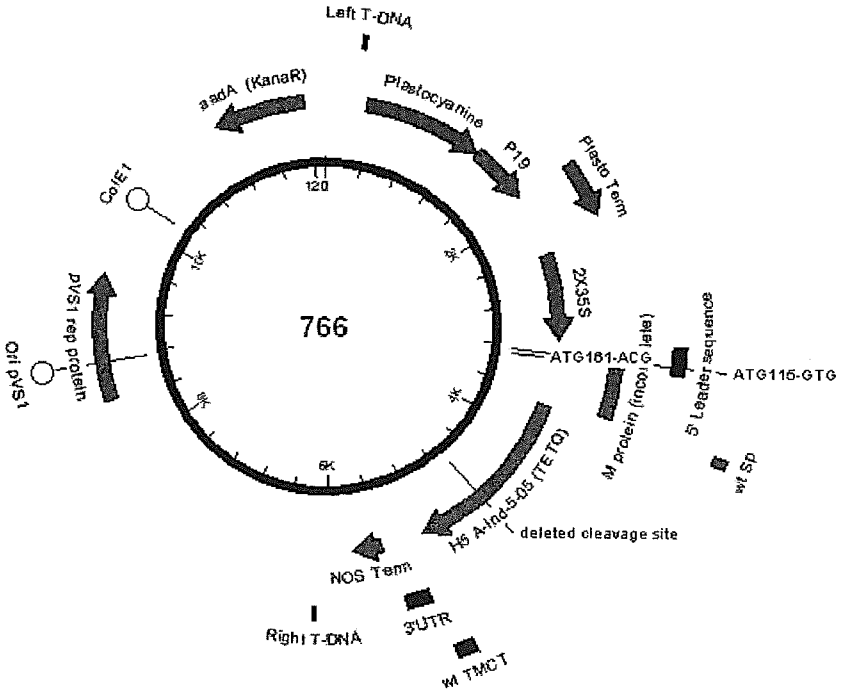


Figure 25: C-2X35S/CPMV-HT/H5 from A/Indonesia/5/2005 with deleted proteolytic loop (Construct number 928)

Figure 25A, SEQ ID NO : 82 H5I505(PrL-).r

CTGCCATCCTCCGCCAGGGCTATTTCTGAGCCCTGTTGCAAGGACTAATC

Figure 25B, SEQ ID NO : 83 H5I505(PrL-).c

GAAATAGCCCTGGCGGAGGATGGCAGGGAATGGTAGATGGTTGGTATGGGTA

Figure 25C, SEQ ID NO : 84

Expression cassette number 928 from 2X35S promoter to NOS terminator. H5 from influenza A/Indonesia/5/2005 (H5N1) with deleted proteolytic loop is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTC
AGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCG
GATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGC
TCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGA
CAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTC
CAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTT
GTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTT
TCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACT
TTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAA
GGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACC
CACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATT
GATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGAC
CCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTT
TTGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATC
TCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAG
ATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTT
TGTGGACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGT
GGTCTTGGGAAAAGAAAGCTTGCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTA
CGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTTGACGAGGTATTGTT
GCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTC
TTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTA
TATTCTGCCCAAATTTGTCGGGCCCATGGAGAAAATAGTGCTTCTTCTTGCAATAGTCA
GTCTTGTTAAAAGTGATCAGATTTGCATTGGTTACCATGCAAACAATTCAACAGAGCAG

GTTGACACAATCATGGAAAAGAACGTTACTGTTACACATGCCCAAGACATACTGGAAAA
GACACACAACGGGAAGCTCTGCGATCTAGATGGAGTGAAGCCTCTAATTTTAAGAGATT
GTAGTGTAGCTGGATGGCTCCTCGGGAACCCAATGTGTGACGAATTCATCAATGTACCG
GAATGGTCTTACATAGTGGAGAAGGCCAATCCAACCAATGACCTCTGTTACCCAGGGAG
TTTCAACGACTATGAAGAACTGAAACACCTATTGAGCAGAATAAACCATTTTGAGAAAA
TTCAAATCATCCCCAAAAGTTCTTGGTCCGATCATGAAGCCTCATCAGGAGTTAGCTCA
GCATGTCCATACCTGGGAAGTCCCTCCTTTTTTAGAAATGTGGTATGGCTTATCAAAAA
GAACAGTACATACCCAACAATAAAGAAAAGCTACAATAATACCAACCAAGAGGATCTTT
TGGTACTGTGGGGAATTCACCATCCTAATGATGCGGCAGAGCAGACAAGGCTATATCAA
AACCCAACCACCTATATTTCCATTGGGACATCAACACTAAACCAGAGATTGGTACCAAA
AATAGCTACTAGATCCAAAGTAAACGGGCAAAGTGGAAGGATGGAGTTCTTCTGGACAA
TTTTAAAACCTAATGATGCAATCAACTTCGAGAGTAATGGAAATTTCATTGCTCCAGAA
TATGCATACAAAATTGTCAAGAAAGGGGACTCAGCAATTATGAAAAGTGAATTGGAATA
TGGTAACTGCAACACCAAGTGTCAAACTCCAATGGGGGCGATAAACTCTAGTATGCCAT
TCCACAACATACACCCTCTCACCATCGGGGAATGCCCCAAATATGTGAAATCAAACAGA
TTAGTCCTTGCAACAGGGCTCAGAAATAGCCCTGGCGGAGGATGGCAGGGAATGGTAGA
TGGTTGGTATGGGTACCACCATAGCAATGAGCAGGGGAGTGGGTACGCTGCAGACAAAG
AATCCACTCAAAAGGCAATAGATGGAGTCACCAATAAGGTCAACTCAATCATTGACAAA
ATGAACACTCAGTTTGAGGCCGTTGGAAGGGAATTTAATAACTTAGAAAGGAGAATAGA
GAATTTAAACAAGAAGATGGAAGACGGGTTTCTAGATGTCTGGACTTATAATGCCGAAC
TTCTGGTTCTCATGGAAAATGAGAGAACTCTAGACTTTCATGACTCAAATGTTAAGAAC
CTCTACGACAAGGTCCGACTACAGCTTAGGGATAATGCAAAGGAGCTGGGTAACGGTTG
TTTCGAGTTCTATCACAAATGTGATAATGAATGTATGGAAAGTATAAGAAACGGAACGT
ACAACTATCCGCAGTATTCAGAAGAAGCAAGATTAAAAAGAGAGGAAATAAGTGGGGTA
AAATTGGAATCAATAGGAACTTACCAAATACTGTCAATTTATTCAACAGTGGCGAGTTC
CCTAGCACTGGCAATCATGATGGCTGGTCTATCTTTATGGATGTGCTCCAATGGATCGT
TACAATGCAGAATTTGCATTTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTC
GGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATG
TAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAA
AAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTT
ATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTT
GCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAAT
TAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAAT
TATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCG
CGCGCGGTGTCATCTATGTTACTAGAT

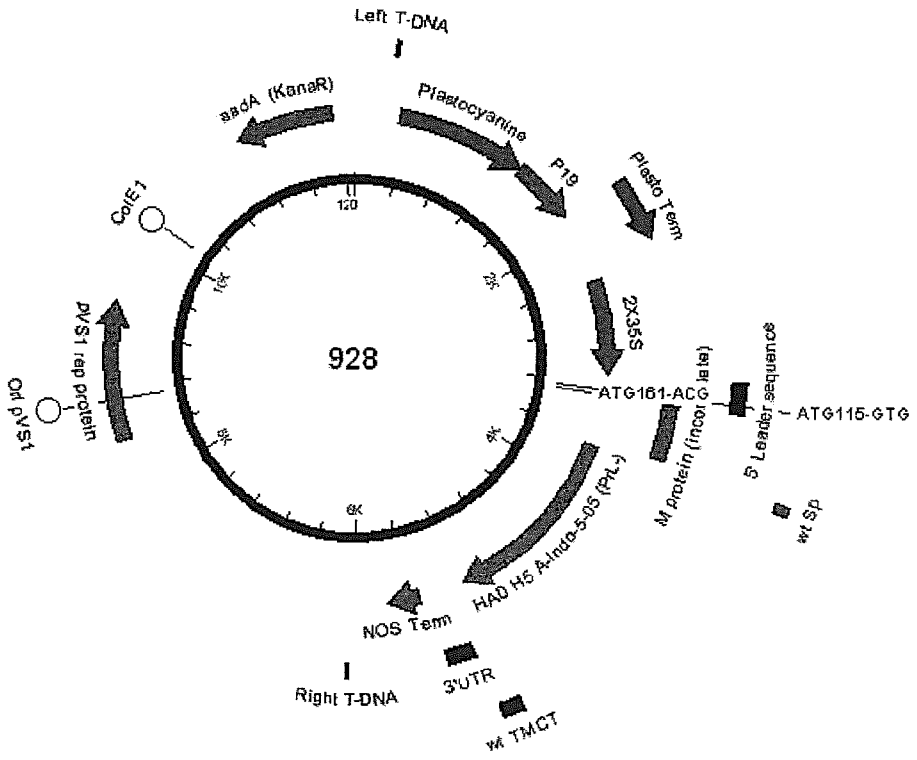
Figure 25D, SEQ ID NO : 85

Amino acid sequence of H5 from influenza A/Indonesia/5/2005 (H5N1) with deleted proteolytic loop.

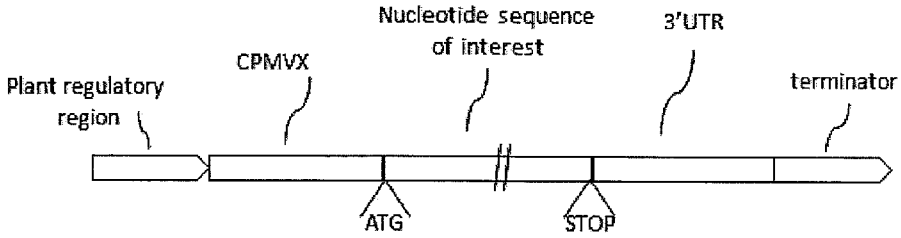
MEKIVLLLAIVSLVKSDQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCD
LDGVKPLILRDCSVAGWLLGNPMCDEFINVPEWSYIVEKANPTNDLCYPGSFNDYEELK
HLLSRINHFEKIQIIPKSSWSDHEASSGVSSACPYLGSPSFFRNVVWLIKKNSTYPTIK
KSYNNTNQEDLLVLWGIHHPNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIATRSKVN
GQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQ
TPMGAINSSMPFHNIHPLTIGECPKYVKSNRLVLATGLRNSPGGGWQGMVDGWYGYHHS
NEQGSGYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMED
GFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCD
NECMESIRNGTYNYPQYSEEARLKREEISGVKLESIGTYQILSIYSTVASSLALAIMMA
GLSLWMCSNGSLQCRICI

Figure 25E

Schematic representation of construct number 928.



Construct comprising CPMV 160



Construct comprising CPMV 160+

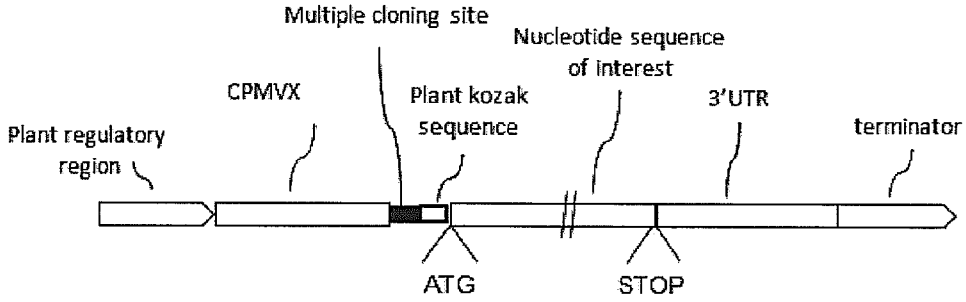


Figure 26A

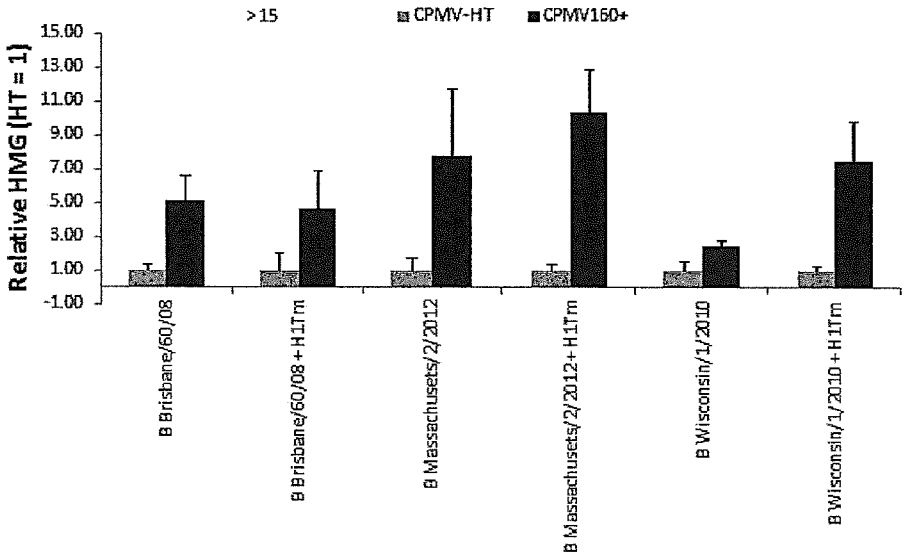


Figure 26B

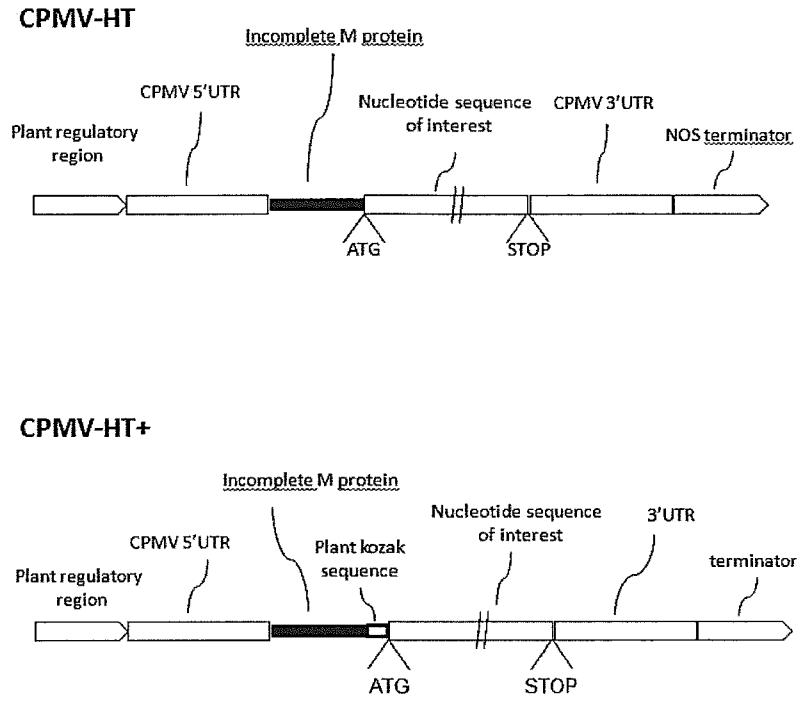


Figure 27A

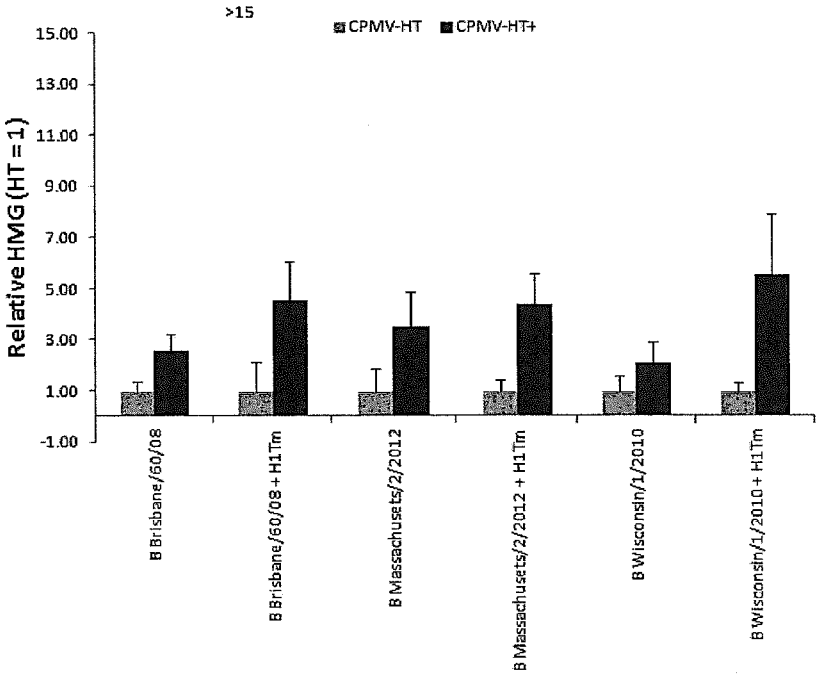
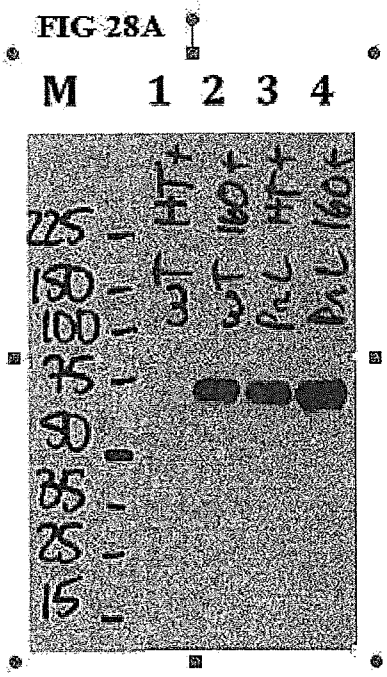


Figure 27B

FIG 28A



28B

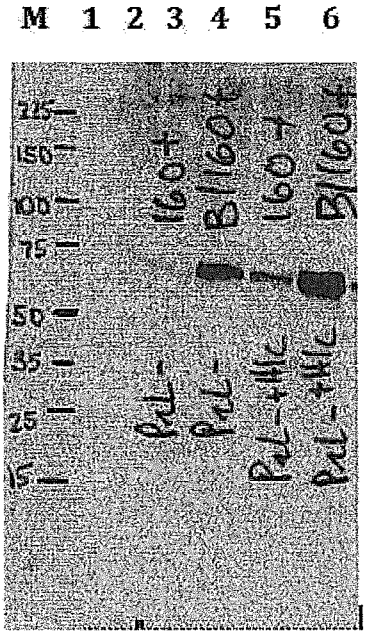


FIG 28C

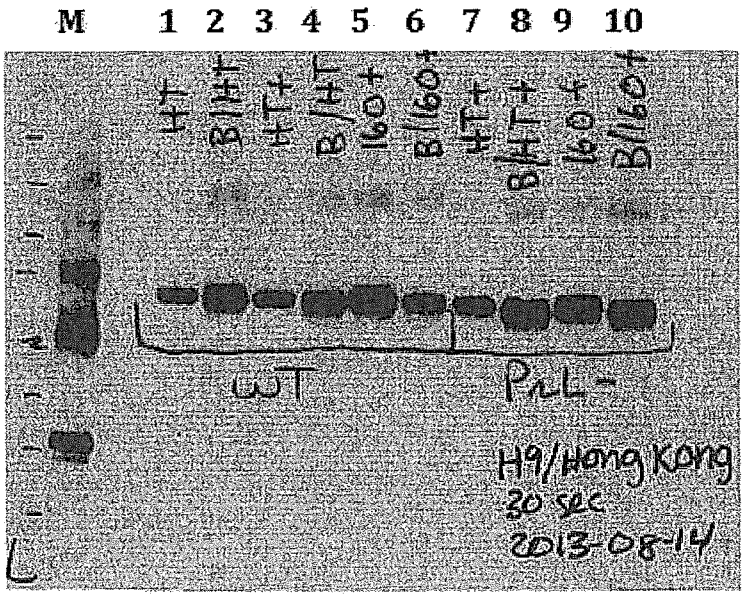


FIG 28D

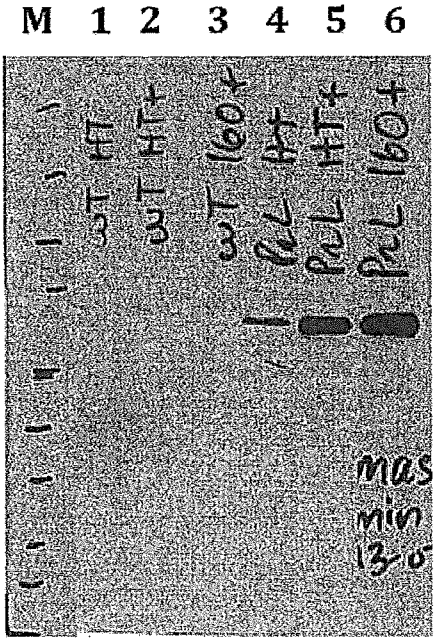
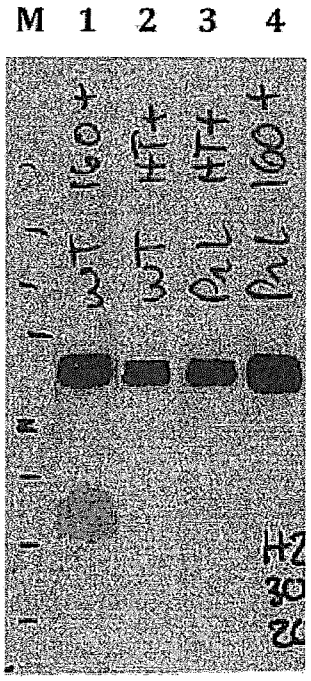


FIG 28E



28F

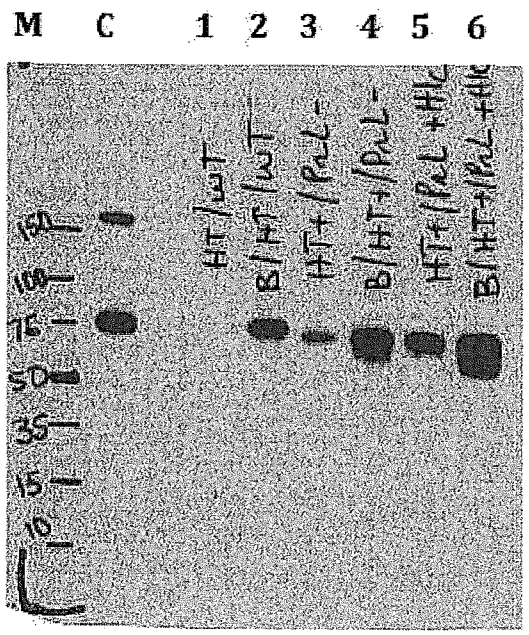
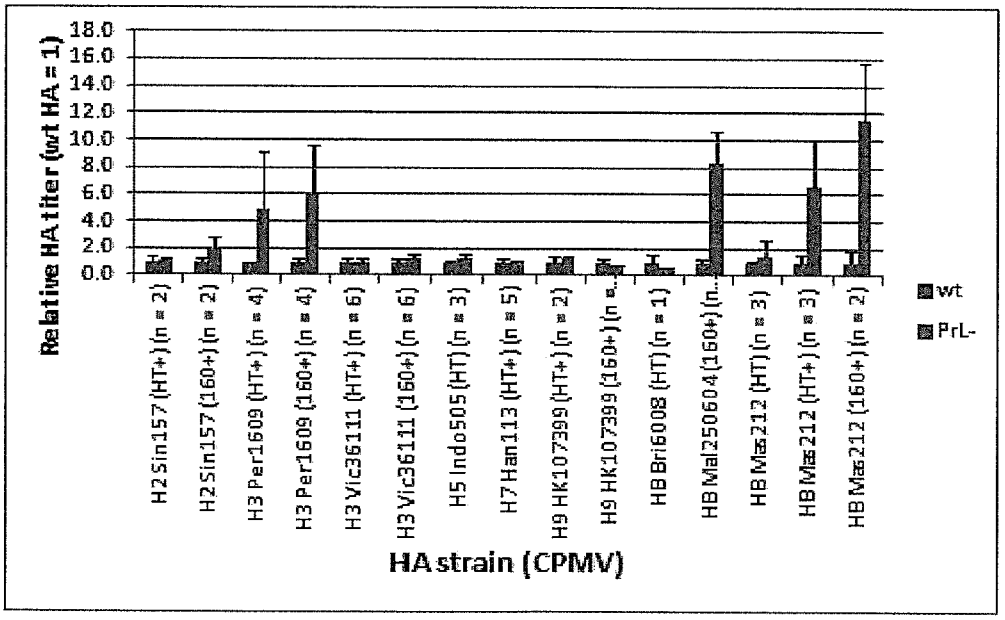


FIG. 29A



F-2X35S/CPMV-HT/PDISP/HA B Brisbane/NOS (Construct number 1029)

Figure 30A

IF-S2+S4-B Bris.c (SEQ ID NO: 86)

TCTCAGATCTTCGCCGATCGAATCTGCACTGGAATAACAT

Figure 30B

IF-S1a4-B Bris.r (SEQ ID NO: 87)

ACTAAAGAAAATAGGCCTTTATAGACAGATGGAGCAAGAAACA

Figure 30C

Synthesized HA B Brisbane gene (corresponding to nt 34-1791 from Genbank accession number FJ766840) (SEQ ID NO: 88)

ATGAAGGCAATAATTGTACTACTCATGGTAGTAACATCCAATGCAGATCGAATCTGCACTGGAA
TAACATCGTCAAACTCACCACATGTCGTCAAAACTGCTACTCAAGGGGAGGTCAATGTGACTGG
TGTAATACCACTGACAACAACACCCACCAAATCTCATTTTGCAAATCTCAAAGGAACAGAAACC
AGGGGGAAACTATGCCCAAAATGCCTCAACTGCACAGATCTGGACGTAGCCTTGGGCAGACCAA
AATGCACGGGGAAAATACCCTCGGCAAGAGTTTCAATACTCCATGAAGTCAGACCTGTTACATC
TGGGTGCTTTCCTATAATGCACGACAGAACAAAAATTAGACAGCTGCCTAACCTTCTCCGAGGA
TACGAACATATCAGGTTATCAACCCATAACGTTATCAATGCAGAAAATGCACCAGGAGGACCCT
ACAAAATTGGAACCTCAGGGTCTTGCCCTAACATTACCAATGGAAACGGATTTTTCGCAACAAT
GGCTTGGGCCGTCCCAAAAAACGACAAAAACAAAACAGCAACAAATCCATTAACAATAGAAGTA
CCATACATTTGTACAGAAGGAGAAGACCAAATTACCGTTTGGGGGTTCCACTCTGACAACGAGA
CCCAAATGGCAAAGCTCTATGGGGACTCAAAGCCCCAGAAGTTCACCTCATCTGCCAACGGAGT
GACCACACATTACGTTTCACAGATTGGTGGCTTCCCAAATCAAACAGAAGACGGAGGACTACCA
CAAAGTGGTAGAATTGTTGTTGATTACATGGTGCAAAAATCTGGGAAAACAGGAACAATTACCT
ATCAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTGCGCAAGTGGCAGGAGCAAGGTAATAAA
AGGATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTCCACGAAAAATACGGTGGATTAAACAAA
AGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCATAGGAAATTGCCCAATATGGGTGAAAA
CACCCTTGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGCAAAACTATTAAAGGAAAGGGG
TTTCTTCGGAGCTATTGCTGGTTTCTTAGAAGGAGGATGGGAAGGAATGATTGCAGGTTGGCAC
GGATACACATCCCATGGGGCACATGGAGTAGCGGTGGCAGCAGACCTTAAGAGCACTCAAGAGG
CCATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTGAGCTGGAAGTAAAGAATCTTCAAAG
ACTAAGCGGTGCCATGGATGAACTCCACAACGAAATACTAGAACTAGATGAGAAAGTGGATGAT
CTCAGAGCTGATACAATAAGCTCACAAATAGAACTCGCAGTCCTGCTTTCCAATGAAGGAATAA
TAAACAGTGAAGATGAACATCTCTTGGCGCTTGAAAGAAAGCTGAAGAAAATGCTGGGCCCCTC
TGCTGTAGAGATAGGGAATGGATGCTTTGAAACCAAACACAAGTGCAACCAGACCTGTCTCGAC
AGAATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTCTCCCCACCTTTGATTCACTGAATA

TTACTGCTGCATCTTTAAATGACGATGGATTGGATAATCATACTATACTGCTTTACTACTCAAC
TGCTGCCTCCAGTTTGGCTGTAACACTGATGATAGCTATCTTTGTTGTTTATATGGTCTCCAGA
GACAATGTTTCTTGCTCCATCTGTCTATAA

Figure 30D

Expression cassette number 1029 from 2X35S promoter to NOS terminator. PDISP/HA from influenza B/Brisbane/60/2008 is underlined. (SEQ ID NO: 89)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAG
ACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTG
CCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCAT
CATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGAC
CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGA
TTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTC
TCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGAT
TCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAA
ATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAA
GATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGC
AAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCA
AGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTT
TGATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTT
AAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCG
GCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACACGTAGTGC
GGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTT
GCTGGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGC
AATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGA
TTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAACTTGG
AGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCATGGCGAAAAACGTTG
CGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGAAT
CTGCACTGGAATAACATCGTCAAACTCACCACATGTCGTCAAAACTGCTACTCAAGGGGAGGTC
AATGTGACTGGTGTAATACCACTGACAACAACACCCACCAAATCTCATTTTGCAAATCTCAAAG
GAACAGAAACCAGGGGGAAACTATGCCCAAAATGCCTCAACTGCACAGATCTGGACGTAGCCTT
GGGCAGACCAAAATGCACGGGGAAAATACCCTCGGCAAGAGTTTCAATACTCCATGAAGTCAGA
CCTGTTACATCTGGGTGCTTTCCTATAATGCACGACAGAACAAAAATTAGACAGCTGCCTAACC
TTCTCCGAGGATACGAACATATCAGGTTATCAACCCATAACGTTATCAATGCAGAAAATGCACC
AGGAGGACCCTACAAAATTGGAACCTCAGGGTCTTGCCCTAACATTACCAATGGAAACGGATTT
TTCGCAACAATGGCTTGGGCCGTCCCAAAAAACGACAAAAACAAAACAGCAACAAATCCATTAA
CAATAGAAGTACCATACATTTGTACAGAAGGAGAAGACCAAATTACCGTTTGGGGGTTCCACTC
TGACAACGAGACCCAAATGGCAAAGCTCTATGGGGACTCAAAGCCCCAGAAGTTCACCTCATCT
GCCAACGGAGTGACCACACATTACGTTTCACAGATTGGTGGCTTCCCAAATCAAACAGAAGACG
GAGGACTACCACAAAGTGGTAGAATTGTTGTTGATTACATGGTGCAAAAATCTGGGAAAACAGG
AACAATTACCTATCAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTGCGCAAGTGGCAGGAGC
AAGGTAATAAAAGGATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTCCACGAAAAATACGGTG
GATTAAACAAAAGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCATAGGAAATTGCCCAAT
ATGGGTGAAAACACCCTTGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGCAAAACTATTA
AAGGAAAGGGGTTTCTTCGGAGCTATTGCTGGTTTCTTAGAAGGAGGATGGGAAGGAATGATTG

CAGGTTGGCACGGATACACATCCCATGGGGCACATGGAGTAGCGGTGGCAGCAGACCTTAAGAG
CACTCAAGAGGCCATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTGAGCTGGAAGTAAAG
AATCTTCAAAGACTAAGCGGTGCCATGGATGAACTCCACAACGAAATACTAGAACTAGATGAGA
AAGTGGATGATCTCAGAGCTGATACAATAAGCTCACAAATAGAACTCGCAGTCCTGCTTTCCAA
TGAAGGAATAATAAACAGTGAAGATGAACATCTCTTGGCGCTTGAAAGAAAGCTGAAGAAAATG
CTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATGCTTTGAAACCAAACACAAGTGCAACCAGA
CCTGTCTCGACAGAATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTCTCCCCACCTTTGA
TTCACTGAATATTACTGCTGCATCTTTAAATGACGATGGATTGGATAATCATACTATACTGCTT
TACTACTCAACTGCTGCCTCCAGTTTGGCTGTAACACTGATGATAGCTATCTTTGTTGTTTATA
TGGTCTCCAGAGACAATGTTTCTTGCTCCATCTGTCTATAAAGGCCTATTTTCTTTAGTTTGAA
TTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTT
ATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACAC
AAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTAT
CGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTC
TTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATG
CATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCG
ATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTAC
TAGAT

Figure 30E,

Amino acid sequence of PDISP/HA from influenza
B/Brisbane/60/2008 SEQ ID NO: 90

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSH
FANLKGTETRGKLCPKCLNCTDLDVALGRPKCTGKIPSARVSILHEVRPVTSGCFPIMHDRTKI
RQLPNLLRGYEHIRLSTHNVINAENAPGGPYKIGTSGSCPNITNGNGFFATMAWAVPKNDKNKT
ATNPLTIEVPYICTEGEDQITVWGFHSDNETQMAKLYGDSKPQKFTSSANGVTTHYVSQIGGFP
NQTEDGGLPQSGRIVVDYMVQKSGKTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCL
HEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPAKLLKERGFFGAIAGFLEGG
WEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEI
LELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSAVEIGNGCFETK
HKCNQTCLDRIAAGTFDAGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMIA
IFVVYMVSRDNVSCSICL

Fig. 30F

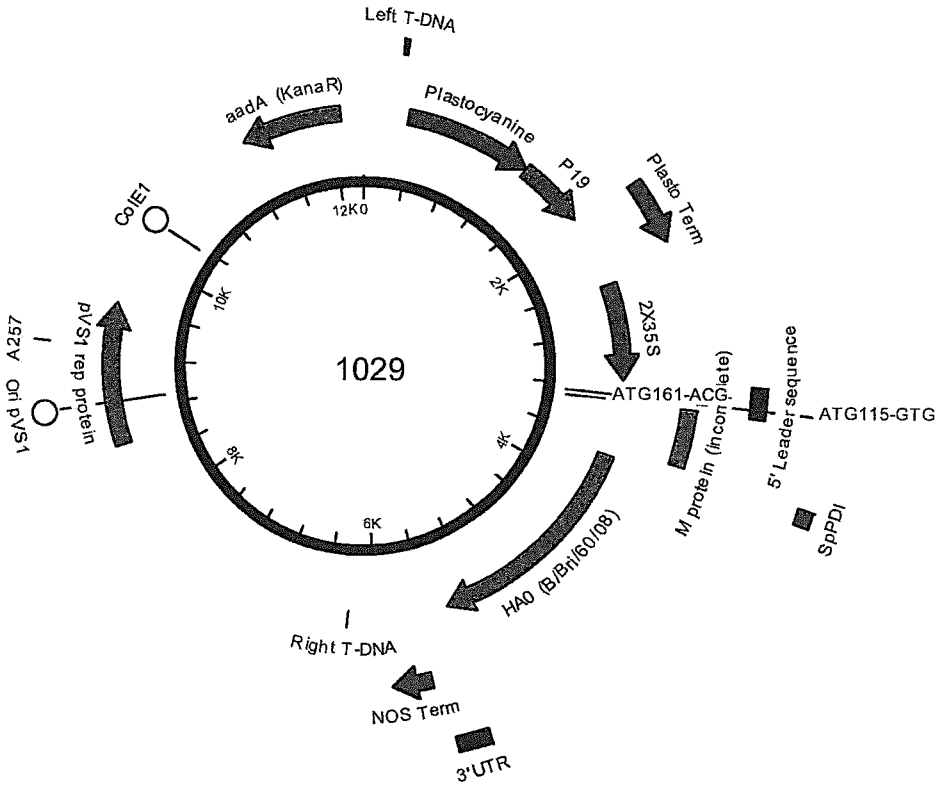

Left T-DNA
aadA (KanaR)
Plastocyanine
P19
Plasto Term
2X35S
ATG161-ACG
ATG115-GTG
5' Leader sequence
M protein (incomplete)
SpPDI
HA0 (B/Bri/60/08)
Right T-DNA
NOS Term
3'UTR
ColE1
pVS1 rep protein
pVS1 Ori
A257
1029
12K0
2K
4K
6K
8K
10K

Fig 31

K- 2X35S/CPMV HT (construct no 1039) and HT* (construct no 1829) for PDISP/HA B Brisbane (PrL-)

Figure 31A, SEQ ID NO : 91 Nucleotide sequence of PDISP/HA B Brisbane (PrL-).

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGA
TCTTCGCCGATCGAATCTGCACTGGAATAACATCGTCAAACTCACCACATGTCGTCAAAACTGC
TACTCAAGGGGAGGTCAATGTGACTGGTGTAATACCACTGACAACAACACCCACCAAATCTCAT
TTTGCAAATCTCAAAGGAACAGAAACCAGGGGGAAACTATGCCCAAAATGCCTCAACTGCACAG
ATCTGGACGTAGCCTTGGGCAGACCAAAATGCACGGGGAAAATACCCTCGGCAAGAGTTTCAAT
ACTCCATGAAGTCAGACCTGTTACATCTGGGTGCTTTCCTATAATGCACGACAGAACAAAAATT
AGACAGCTGCCTAACCTTCTCCGAGGATACGAACATATCAGGTTATCAACCCATAACGTTATCA
ATGCAGAAAATGCACCAGGAGGACCCTACAAAATTGGAACCTCAGGGTCTTGCCCTAACATTAC
CAATGGAAACGGATTTTTCGCAACAATGGCTTGGGCCGTCCCAAAAAACGACAAAAACAAAACA
GCAACAAATCCATTAACAATAGAAGTACCATACATTTGTACAGAAGGAGAAGACCAAATTACCG
TTTGGGGGTTCCACTCTGACAACGAGACCCAAATGGCAAAGCTCTATGGGGACTCAAAGCCCCA
GAAGTTCACCTCATCTGCCAACGGAGTGACCACACATTACGTTTCACAGATTGGTGGCTTCCCA
AATCAAACAGAAGACGGAGGACTACCACAAAGTGGTAGAATTGTTGTTGATTACATGGTGCAAA
AATCTGGGAAAACAGGAACAATTACCTATCAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTG
CGCAAGTGGCAGGAGCAAGGTAATAAAAGGATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTC
CACGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCA
TAGGAAATTGCCCAATATGGGTGAAAACACCCTTGAAGCTGGCCAATGGAACCAAATATAGACC
TCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCCCATGGGGCACAT
GGAGTAGCGGTGGCAGCAGACCTTAAGAGCACTCAAGAGGCCATAAACAAGATAACAAAAAATC
TCAACTCTTTGAGTGAGCTGGAAGTAAAGAATCTTCAAAGACTAAGCGGTGCCATGGATGAACT
CCACAACGAAATACTAGAACTAGATGAGAAAGTGGATGATCTCAGAGCTGATACAATAAGCTCA
CAAATAGAACTCGCAGTCCTGCTTTCCAATGAAGGAATAATAAACAGTGAAGATGAACATCTCT
TGGCGCTTGAAAGAAAGCTGAAGAAAATGCTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATG
CTTTGAAACCAAACACAAGTGCAACCAGACCTGTCTCGACAGAATAGCTGCTGGTACCTTTGAT
GCAGGAGAATTTTCTCTCCCCACCTTTGATTCACTGAATATTACTGCTGCATCTTTAAATGACG
ATGGATTGGATAATCATACTATACTGCTTTACTACTCAACTGCTGCCTCCAGTTTGGCTGTAAC
ACTGATGATAGCTATCTTTGTTGTTTATATGGTCTCCAGAGACAATGTTTCTTGCTCCATCTGT
CTATAA

Figure 31B, SEQ ID NO :92

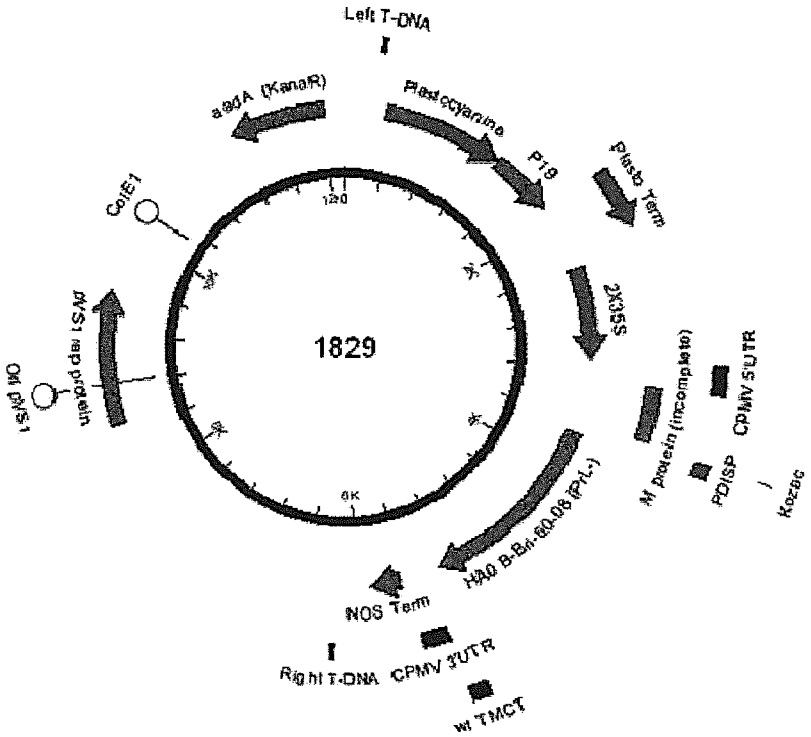
Amino acid sequence of PDISP/HA B Brisbane (PrL-).

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSH
FANLKGTETRGKLCPKCLNCTDLDVALGRPKCTGKIPSARVSILHEVRPVTSGCFPIMHDRTKI
RQLPNLLRGYEHIRLSTHNVINAENAPGGPYKIGTSGSCPNITNGNGFFATMAWAVPKNDKNKT
ATNPLTIEVPYICTEGEDQITVWGFHSDNETQMAKLYGDSKPQKFTSSANGVTTHYVSQIGGFP
NQTEDGGLPQSGRIVVDYMVQKSGKTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCL

HEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAH
GVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISS
QIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFD
AGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMIAIFVVYMVSRDNVSCSIC
L*

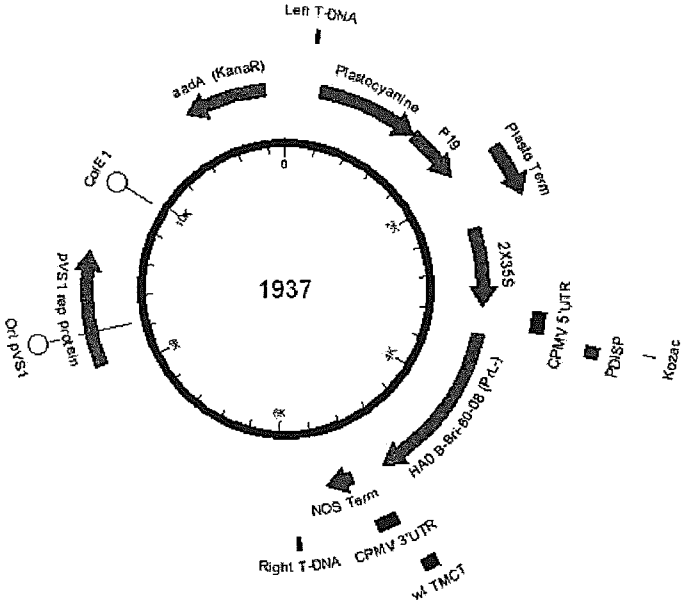
Figure 31C

Schematic representation of construct number 1829 (2X35S/CPMV HT*)



2X35S/CPMV HT (construct no 1039) and HT*(-Mprot) (construct no 1937) for PDISP/HA B Brisbane (PrL-)

Figure 32A
Schematic representation of construct number 1937 (2X35S/CPMV HT*(-Mprot))



2X35S/CPMV HT (construct no 1067) and HT*(-Mprot) (construct no 1977) for PDISP/HA B Brisbane (PrL-)+H1 California TMCT

Figure 33A, SEQ ID NO :95

Nucleotide sequence of PDISP/HA B Brisbane (PrL-)+H1 California TMCT.

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGA
ATCTGCACTGGAATAACATCGTCAAACTCACCACATGTCGTCAAAACTGCTACTCAAGGGGAGGTCAATGTGACTG
GTGTAATACCACTGACAACAACACCCACCAAATCTCATTTTGCAAATCTCAAAGGAACAGAAACCAGGGGGAAAC
TATGCCCAAAATGCCTCAACTGCACAGATCTGGACGTAGCCTTGGGCAGACCAAAATGCACGGGGAAAATACCCT
CGGCAAGAGTTTCAATACTCCATGAAGTCAGACCTGTTACATCTGGGTGCTTTCCTATAATGCACGACAGAACAAA
AATTAGACAGCTGCCTAACCTTCTCCGAGGATACGAACATATCAGGTTATCAACCCATAACGTTATCAATGCAGAA
AATGCACCAGGAGGACCCTACAAAATTGGAACCTCAGGGTCTTGCCCTAACATTACCAATGGAAACGGATTTTTCG
CAACAATGGCTTGGGCCGTCCCAAAAAACGACAAAAACAAAACAGCAACAAATCCATTAACAATAGAAGTACCA
TACATTTGTACAGAAGGAGAAGACCAAATTACCGTTTGGGGGTTCCACTCTGACAACGAGACCCAAATGGCAAAG
CTCTATGGGGACTCAAAGCCCCAGAAGTTCACCTCATCTGCCAACGGAGTGACCACACATTACGTTTCACAGATTG
GTGGCTTCCCAAATCAAACAGAAGACGGAGGACTACCACAAAGTGGTAGAATTGTTGTTGATTACATGGTGCAAA
AATCTGGGAAAACAGGAACAATTACCTATCAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTGCGCAAGTGGCA
GGAGCAAGGTAATAAAAGGATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTCCACGAAAAATACGGTGGATTAA
ACAAAAGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCATAGGAAATTGCCCAATATGGGTGAAAACACCCT
TGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGAT
ACACATCCCATGGGGCACATGGAGTAGCGGTGGCAGCAGACCTTAAGAGCACTCAAGAGGCCATAAACAAGATA
ACAAAAAAATCTCAACTCTTTGAGTGAGCTGGAAGTAAAGAATCTTCAAAGACTAAGCGGTGCCATGGATGAACTC
CACAACGAAATACTAGAACTAGATGAGAAAGTGGATGATCTCAGAGCTGATACAATAAGCTCACAAATAGAACTC
GCAGTCCTGCTTTCCAATGAAGGAATAATAAACAGTGAAGATGAACATCTCTTGGCGCTTGAAAGAAAGCTGAAG
AAAATGCTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATGCTTTGAAACCAAACACAAGTGCAACCAGACCTGT
CTCGACAGAATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTCTCCCCACCTTTGATTCACTGAATATTACTGC
TGCATCTTTAAATGACGATGGATTGGATAATTACCAGATTTTGGCGATCTATTCAACTGTCGCCAGTTCATTGGTAC
TGGTAGTCTCCCTGGGGGCAATCAGTTTCTGGATGTGCTCTAATGGGTCTCTACAGTGTAGAATATGTATTTAA

Figure 33B, SEQ ID NO : 96

Amino acid sequence of PDISP/HA B Brisbane (PrL-)+H1 California TMCT.

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSHFANLKGTETRGKLCPKC
LNCTDLDVALGRPKCTGKIPSARVSILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYEHIRLSTHNVINAENAPGGPYKIG
TSGSCPNITNGNGFFATMAWAVPKNDKNKTATNPLTIEVPYICTEGEDQITVWGFHSDNETQMAKLYGDSKPQKFTSSA
NGVTTHYVSQIGGFPNQTEDGGLPQSGRIVVDYMVQKSGKTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCL
HEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQ
EAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKK
MLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFDAGEFSLPTFDSLNITAASLNDDGLDNYQILAIYSTVASSLVLVVSL
GAISFWMCSNGSLQCRICI*

Figure 33C
Schematic representation of construct number 1067 (2X35S/CPMV HT)

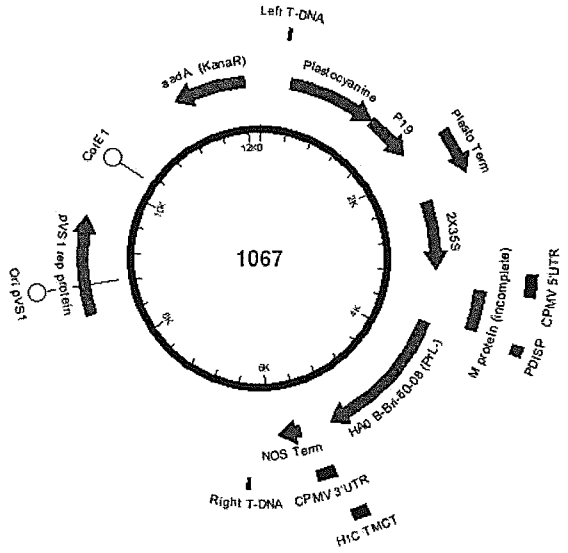
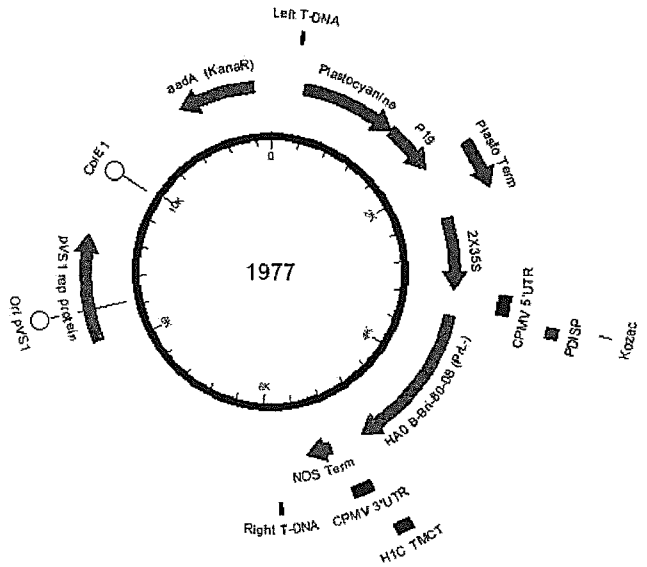


Figure 33D
Schematic representation of construct number 1977 (2X35S/CPMV HT*(-Mprot))



2X35S/CPMV HT (construct no 2072) and HT*(-Mprot) (construct no 2050) for PDISP/HA B Massachussetts (PrL-)

Figure 34A SEQ ID NO : 97
Nucleotide sequence of PDISP/HA B Massachussetts (PrL-).

```
ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCG
AATCTGCACTGGGATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTG
GTGTGATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAAGACCAGAGGGAAACTA
TGCCCAGACTGTCTCAACTGTACAGATCTGGATGTGGCCCTGGGCAGGCCAATGTGTGTGGGAACTACACCTTCTGC
GAAAGCTTCAATACTTCACGAAGTCAGACCTGTTACATCCGGGTGCTTCCCTATAATGCACGACAGAACAAAAATCA
GGCAACTAGCCAATCTTCTCAGAGGATATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAAAAGGCA
CCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAAAGCGGATTTTTCGCAACAAT
GGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCATTAACAGTAGAAGTACCATACATTTGTGCAG
AAGGGGAAGACCAAATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATGGAGACTCA
AATCCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCTCAGATTGGCGGCTTCCCAGATCA
AACAGAAGACGGAGGACTACCACAAAGCGGCAGAATTGTCGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAA
CAATTGTCTATCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGG
TCCTTGCCTTTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACAC
AGGAGAACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTGAAAACACCTTTGAAGCTTGCCAATGGAACCAAAT
ATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCTCACGGAGCACATGGAGTG
GCAGTTGCTGCAGACCTTAAGAGCACACAAGAAGCTATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTGAGCT
AGAAGTAAAGAATCTTCAAAGGCTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAG
TGGATGACCTCAGAGCTGACACTATAAGTTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAAC
AGTGAAGACGAGCATCTATTGGCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGACATAGGAAA
TGGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAG
AGTTTTCTCTCCCCACTTTTGATTCATTGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACCATACT
ATACTGCTCTATTACTCAACTGCTGCTTCTAGTTTGGCTGTAACATTGATGCTAGCTATTTTTATTGTTTATATGGT
CTCCAGAGACAACGTTTCATGCTCCATCTGTCTATAA
```

Figure 34B, SEQ ID NO : 98
Amino acid sequence of PDISP/HA B Massachussetts (PrL-).

```
MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTKTRGKL
CPDCLNCTDLDVALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLANLLRGYENIRLSTQNVIDAEKA
PGGPYRLGTSGSCPNATSKSGFFATMAWAVPKDNNKNATNPLTVEVPYICAEGEDQITVWGFHSDNKTQMKNLYGDS
NPQKFTSSANGVTTHYVSQIGGFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKG
SLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGV
AVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIIN
SEDEHLLALERKLKKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNHT
ILLYYSTAASSLAVTLMLAIFIVYMVSRDNVSCSICL*
```

Figure 34C
Schematic representation of construct number 2072 (2X35S/CPMV HT)

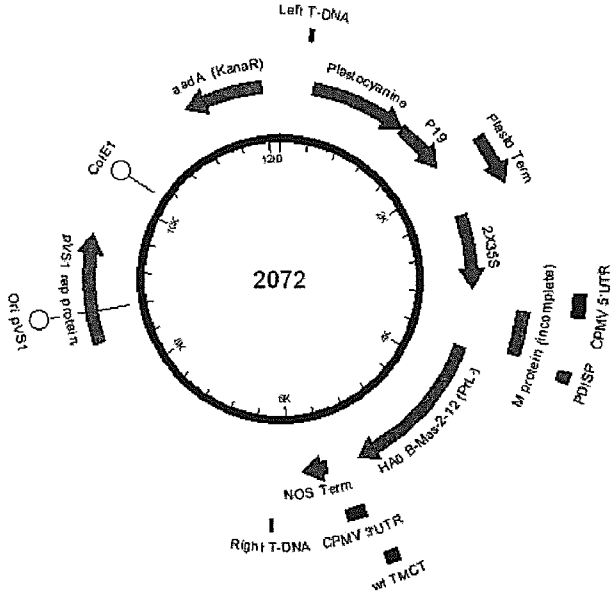
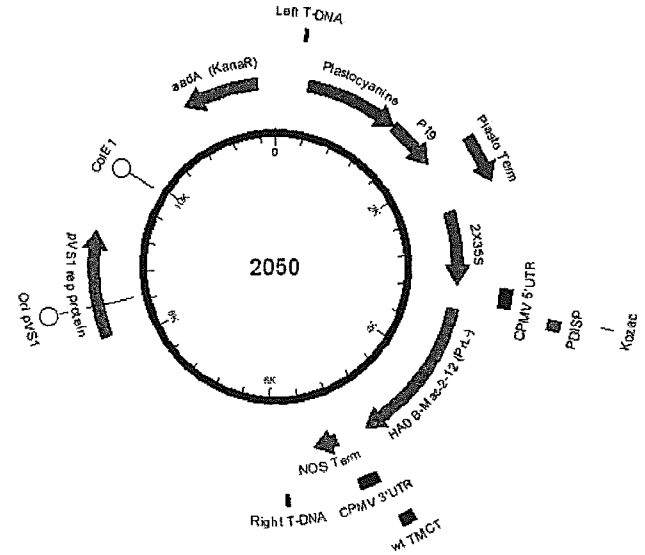


Figure 34D
Schematic representation of construct number 2050 (2X35S/CPMV HT*(-Mprot))



2X35S/CPMV HT (construct no 2074) and HT*(-Mprot) (construct no 2060) for PDISP/HA B Massachussetts (PrL-)+H1 California TMCT

Figure 35A SEQ ID NO : 99
Nucleotide sequence of PDISP/HA B Massachussetts (PrL-)+H1 California TMCT.

```
ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCG
AATCTGCACTGGGATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTG
GTGTGATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAAGACCAGAGGGAAACTA
TGCCCAGACTGTCTCAACTGTACAGATCTGGATGTGGCCCTGGGCAGGCCAATGTGTGTGGGAACTACACCTTCTGC
GAAAGCTTCAATACTTCACGAAGTCAGACCTGTTACATCCGGGTGCTTCCCTATAATGCACGACAGAACAAAAATCA
GGCAACTAGCCAATCTTCTCAGAGGATATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAAAAGGCA
CCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAAAGCGGATTTTTCGCAACAAT
GGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCATTAACAGTAGAAGTACCATACATTTGTGCAG
AAGGGGAAGACCAAATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATGGAGACTCA
AATCCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCTCAGATTGGCGGCTTCCCAGATCA
AACAGAAGACGGAGGACTACCACAAAGCGGCAGAATTGTCGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAA
CAATTGTCTATCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGG
TCCTTGCCTTTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACAC
AGGAGAACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTGAAAACACCTTTGAAGCTTGCCAATGGAACCAAAT
ATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCTCACGGAGCACATGGAGTG
GCAGTTGCTGCAGACCTTAAGAGCACACAAGAAGCTATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTGAGCT
AGAAGTAAAGAATCTTCAAAGGCTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAG
TGGATGACCTCAGAGCTGACACTATAAGTTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAAC
AGTGAAGACGAGCATCTATTGGCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGACATAGGAAA
TGGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAG
AGTTTTCTCTCCCCACTTTTGATTCATTGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACTACCAG
ATTTTGGCGATCTATTCAACTGTCGCCAGTTCATTGGTACTGGTAGTCTCCCTGGGGGCAATCAGTTTCTGGATGTG
CTCTAATGGGTCTCTACAGTGTAGAATATGTATTTAA
```

Figure 35B, SEQ ID NO :100
Amino acid sequence of PDISP/HA B Massachussetts (PrL-)+H1 California TMCT.

```
MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTKTRGKL
CPDCLNCTDLDVALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLANLLRGYENIRLSTQNVIDAEKA
PGGPYRLGTSGSCPNATSKSGFFATMAWAVPKDNNKNATNPLTVEVPYICAEGEDQITVWGFHSDNKTQMKNLYGDS
NPQKFTSSANGVTTHYVSQIGGFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKG
SLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGV
AVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIIN
SEDEHLLALERKLKKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNYQ
ILAIYSTVASSLVLVVSLGAISFWMCSNGSLQCRICI*
```

Figure 35C
Schematic representation of construct number 2074 (2X35S/CPMV HT)

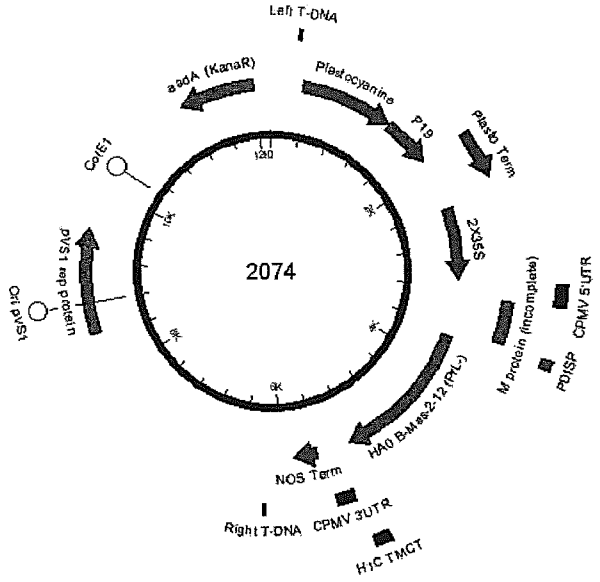
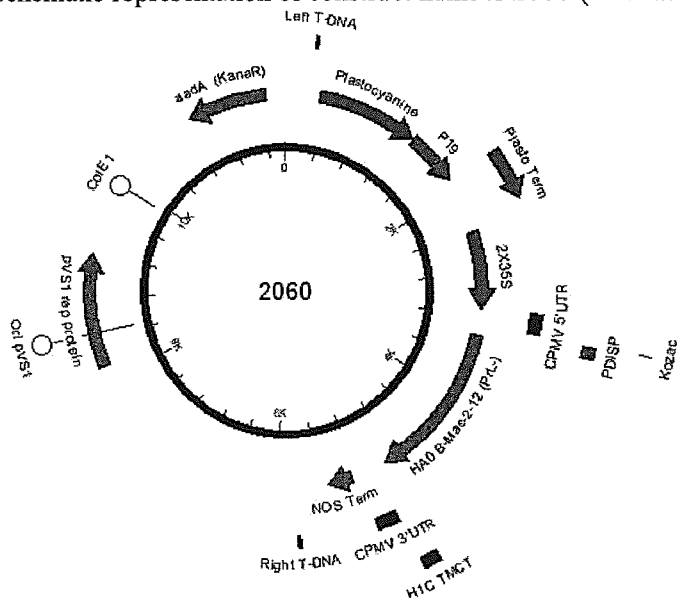


Figure 35D
Schematic representation of construct number 2060 (2X35S/CPMV HT*(-Mprot))



2X35S/CPMV HT (construct no 1445), HT*(-Mprot) (construct no 1820) and HT(fl5'UTR) (construct no 1975) for HA B Wisconsin (PrL-)

Figure 36A, SEQ ID NO : 101
Nucleotide sequence of HA B Wisconsin (PrL-).

```
ATGAAGGCAATAATTGTACTACTCATGGTAGTAACATCCAATGCAGATCGAATCTGCACTGGGATAACATCTTCAAA
CTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTGGCGTGATACCACTGACAACAACACCAA
CAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAGGGAAACTATGCCCGGACTGTCTCAACTGTACAGAT
CTGGATGTGGCCTTGGGCAGGCCAATGTGTGTGGGGACCACACCTTCTGCTAAAGCTTCAATACTCCACGAGGTCAG
ACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAAAATCAGGCAACTACCCAATCTTCTCAGAGGAT
ATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAAAAAGCACCAGGAGGACCCTACAGACTTGGAACC
TCAGGATCTTGCCCTAACGCTACCAGTAAAATCGGATTTTTTGCAACAATGGCTTGGGCTGTCCCAAAGGACAACTA
CAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAAGGGGAAGACCAAATTACTGTTTGGG
GGTTCCATTCAGATAACAAAACCCAAATGAAGAGCCTCTATGGAGACTCAAATCCTCAAAAGTTCACCTCATCTGCT
AATGGAGTAACCACACATTATGTTTCTCAGATTGGCGACTTCCCAGATCAAACAGAAGACGGAGGACTACCACAAAG
CGGCAGAATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTATCAAAGAGGTGTTTTGT
TGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCATTGCCTTTAATTGGTGAAGCAGAT
TGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATGCAAAAGCCATAGGAAA
TTGCCCAATATGGGTAAAAACACCTTTGAAGCTTGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAG
GAATGATTGCAGGTTGGCACGGATACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCAGACCTTAAGAGTACA
CAAGAAGCTATAAATAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAACCTTCAAAGACTAAG
TGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGACACTATAA
GCTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGACGAGCATCTATTGGCACTT
GAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGACATAGGAAACGGATGCTTCGAAACCAAACACAAATG
CAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCAT
TGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGCTGCT
TCTAGTTTGGCTGTAACATTAATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGACAACGTTTCATGCTCCAT
CTGTCTATAA
```

Figure 36B, SEQ ID NO : 102
Amino acid sequence of HA B Wisconsin (PrL-).

```
MKAIIVLLMVVTSNADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTRTRGKLCPDCLNCTD
LDVALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYENIRLSTQNVIDAEKAPGGPYRLGT
SGSCPNATSKIGFFATMAWAVPKDNYKNATNPLTVEVPYICTEGEDQITVWGFHSDNKTQMKSLYGDSNPQKFTSSA
NGVTTHYVSQIGDFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEAD
CLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKST
QEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLAL
ERKLKKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAA
SSLAVTLMLAIFIVYMVSRDNVSCSICL*
```

Figure 36C
Schematic representation of construct number 1445 (2X35S/CPMV HT)

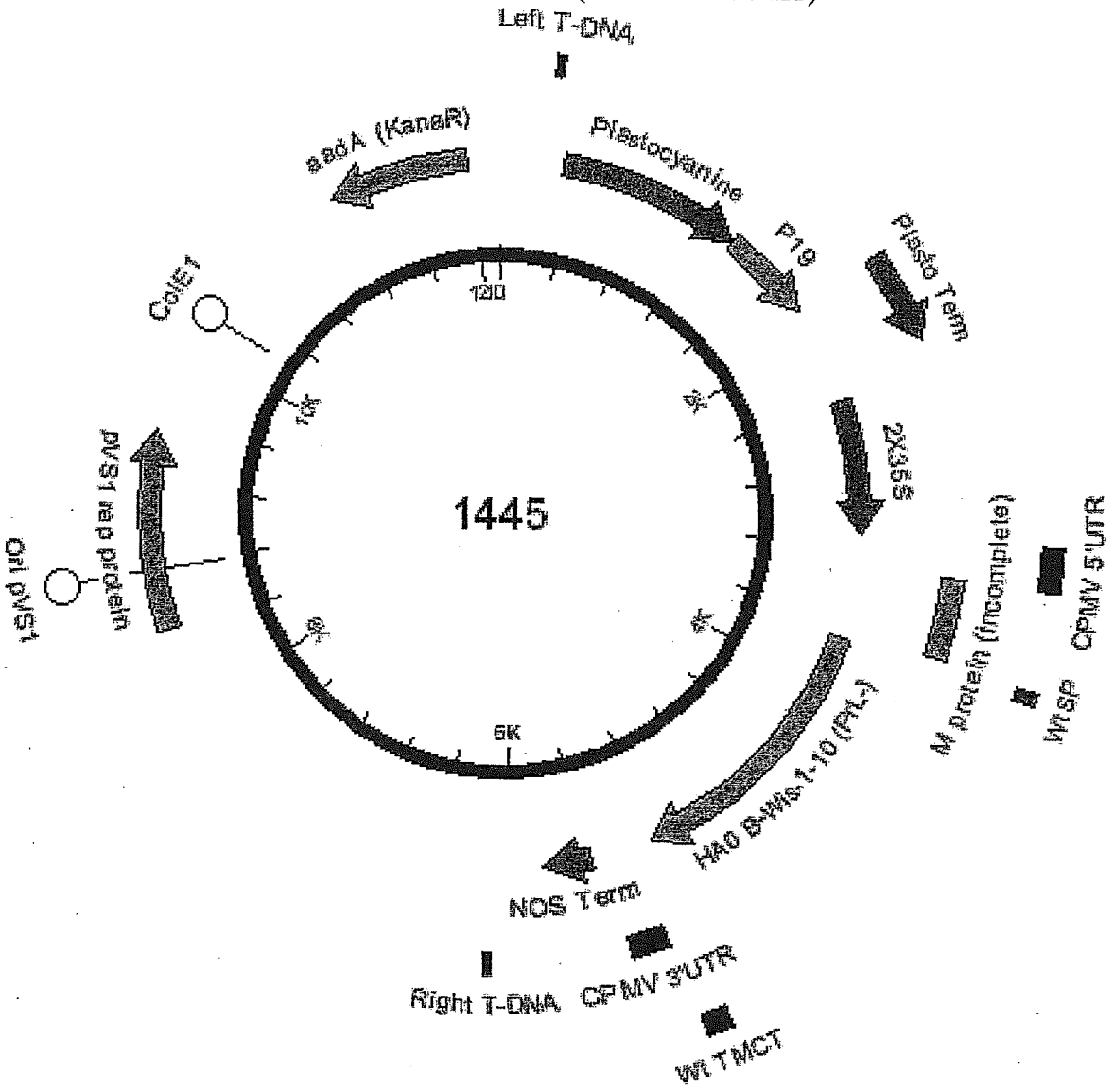


Figure 36D
Schematic representation of construct number 1820 (2X35S/CPMV HT*(-Mprot))

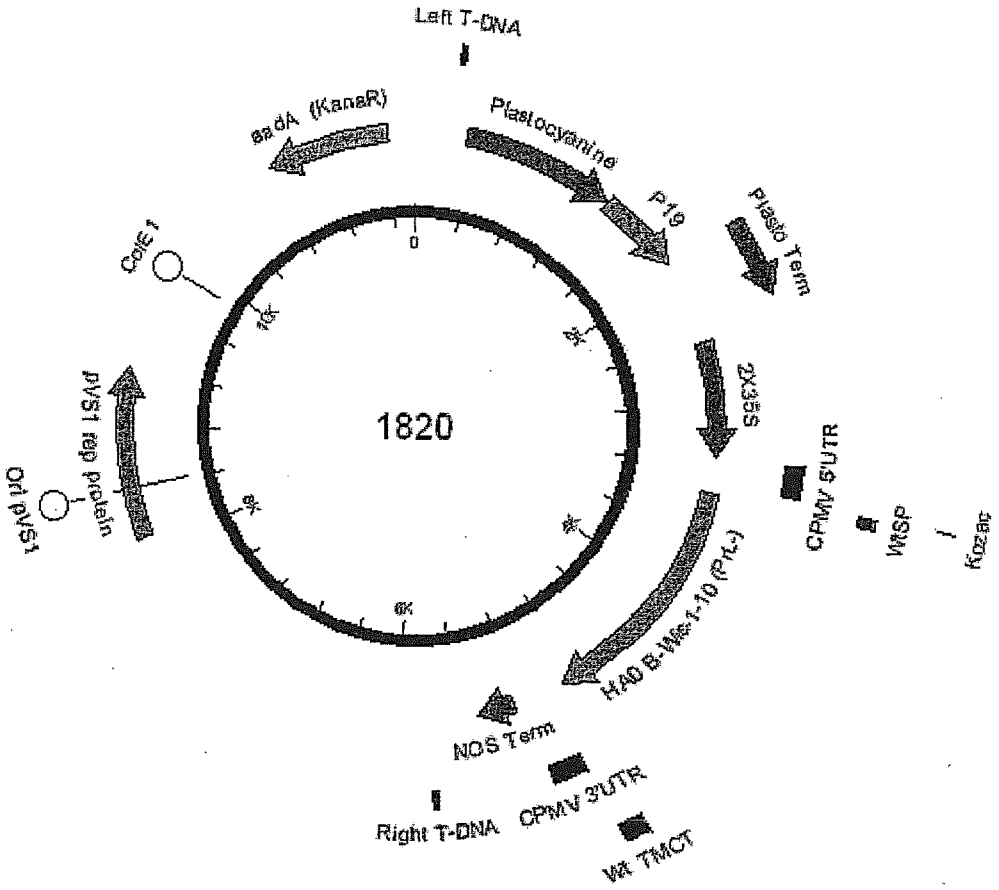
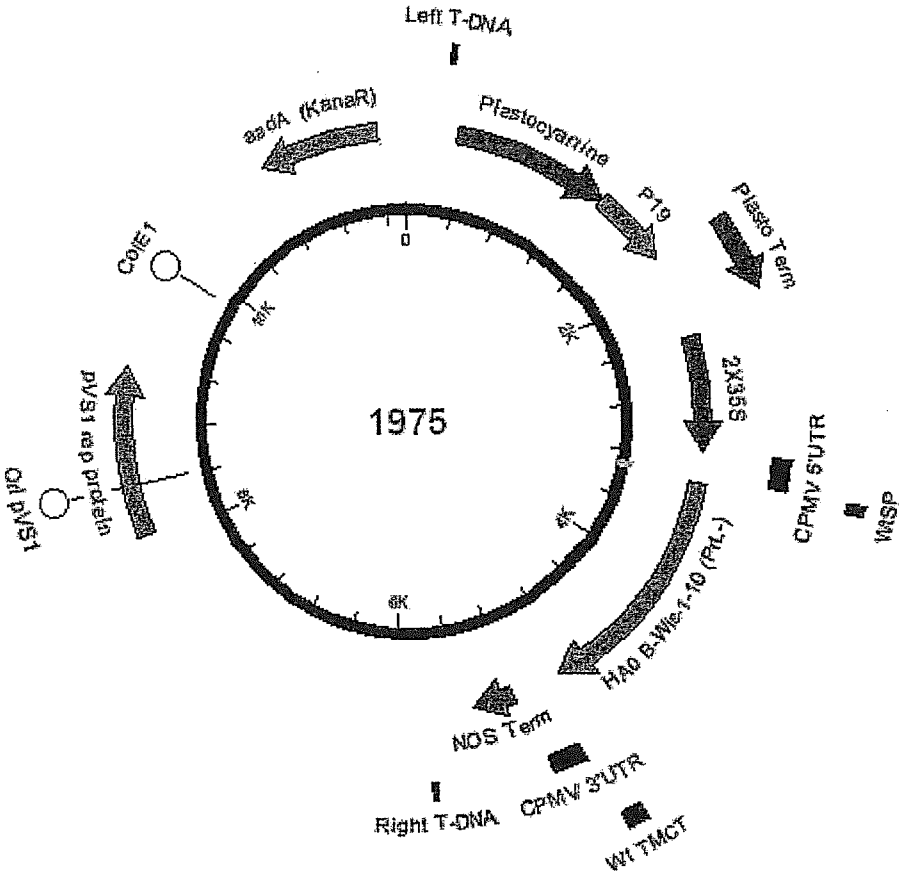


Figure 36E
Schematic representation of construct number 1975 (2X35S/CPMV HT*(fl5'UTR))



2X35S/CPMV HT (construct no 1454) and HT*(-Mprot) (construct no 1893) for HA B Wisconsin (PrL-)+H1 California TMCT

Figure 37A, SEQ ID NO : 103
Nucleotide sequence of HA B Wisconsin (PrL-)+H1 California TMCT

```
ATGAAGGCAATAATTGTACTACTCATGGTAGTAACATCCAATGCAGATCGAATCTGCACTGGGATAACATCTTCAAA
CTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTGGCGTGATACCACTGACAACAACACCAA
CAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAGGGAAACTATGCCCGGACTGTCTCAACTGTACAGAT
CTGGATGTGGCCTTGGGCAGGCCAATGTGTGTGGGGACCACACCTTCTGCTAAAGCTTCAATACTCCACGAGGTCAG
ACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAAAATCAGGCAACTACCCAATCTTCTCAGAGGAT
ATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAAAAAGCACCAGGAGGACCCTACAGACTTGGAACC
TCAGGATCTTGCCCTAACGCTACCAGTAAAATCGGATTTTTTGCAACAATGGCTTGGGCTGTCCCAAAGGACAACTA
CAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAAGGGGAAGACCAAATTACTGTTTGGG
GGTTCCATTCAGATAACAAAACCCAAATGAAGAGCCTCTATGGAGACTCAAATCCTCAAAAGTTCACCTCATCTGCT
AATGGAGTAACCACACATTATGTTTCTCAGATTGGCGACTTCCCAGATCAAACAGAAGACGGAGGACTACCACAAAG
CGGCAGAATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTATCAAAGAGGTGTTTTGT
TGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCATTGCCTTTAATTGGTGAAGCAGAT
TGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATGCAAAAGCCATAGGAAA
TTGCCCAATATGGGTAAAAACACCTTTGAAGCTTGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAG
GAATGATTGCAGGTTGGCACGGATACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCAGACCTTAAGAGTACA
CAAGAAGCTATAAATAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAACCTTCAAAGACTAAG
TGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGACACTATAA
GCTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGACGAGCATCTATTGGCACTT
GAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGACATAGGAAACGGATGCTTCGAAACCAAACACAAATG
CAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCAT
TGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACTACCAGATTTTGGCGATCTATTCAACTGTCGCC
AGTTCATTGGTACTGGTAGTCTCCCTGGGGGCAATCAGTTTCTGGATGTGCTCTAATGGGTCTCTACAGTGTAGAAT
ATGTATTTAA
```

Figure 37B, SEQ ID NO : 104
Amino acid sequence of HA B Wisconsin (PrL-)+H1 California TMC.

```
MKAIIVLLMVVTSNADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTRTRGKLCPDCLNCTD
LDVALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYENIRLSTQNVIDAEKAPGGPYRLGT
SGSCPNATSKIGFFATMAWAVPKDNYKNATNPLTVEVPYICTEGEDQITVWGFHSDNKTQMKSLYGDSNPQKFTSSA
NGVTTHYVSQIGDFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEAD
CLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKST
QEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLAL
ERKLKKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNYQILAIYSTVA
SSLVLVVSLGAISFWMCSNGSLQCRICI*
```

Figure 37C
Schematic representation of construct number 1454 (2X35S/CPMV HT)

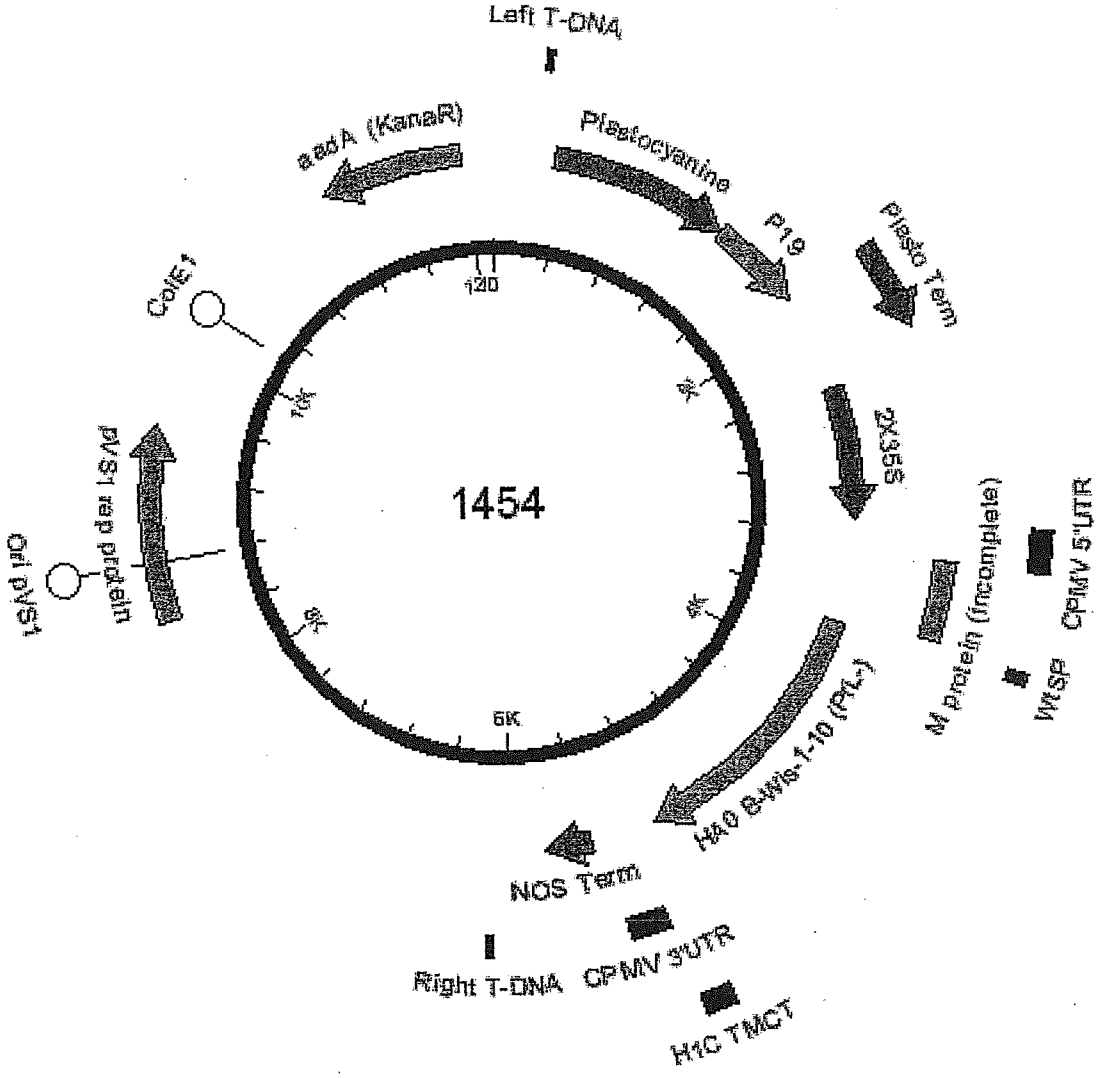
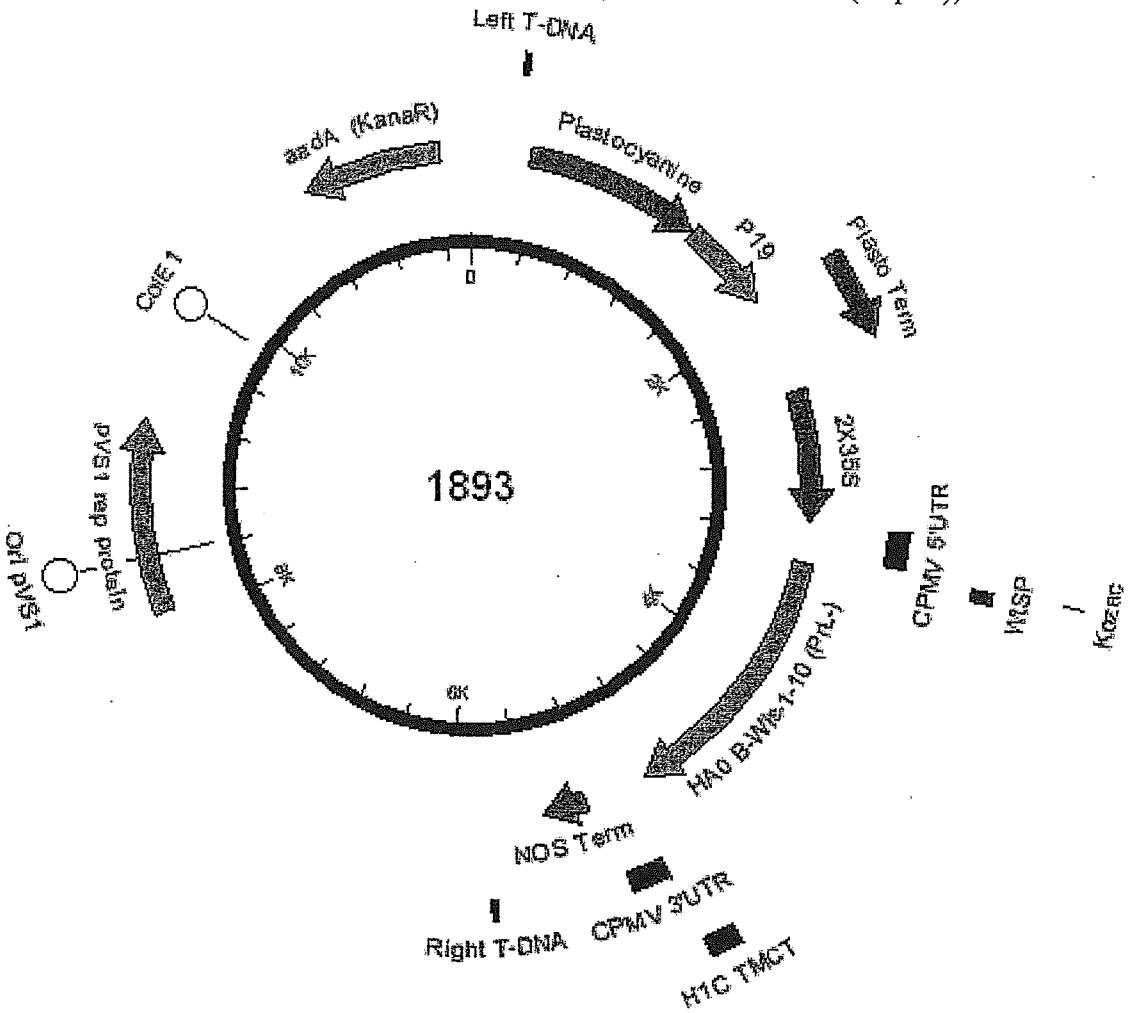


Figure 37D
Schematic representation of construct number 1893 (2X35S/CPMV HT*(-Mprot))



L- 2X35S/CPMV HT (construct no 1067) and HT* (construct no 1875) for PDISP/HA B Brisbane (PrL-)+H1 California TMCT

Figure 38A, SEQ ID NO : 105

Nucleotide sequence of PDISP/HA B Brisbane (PrL-)+H1 California TMCT.

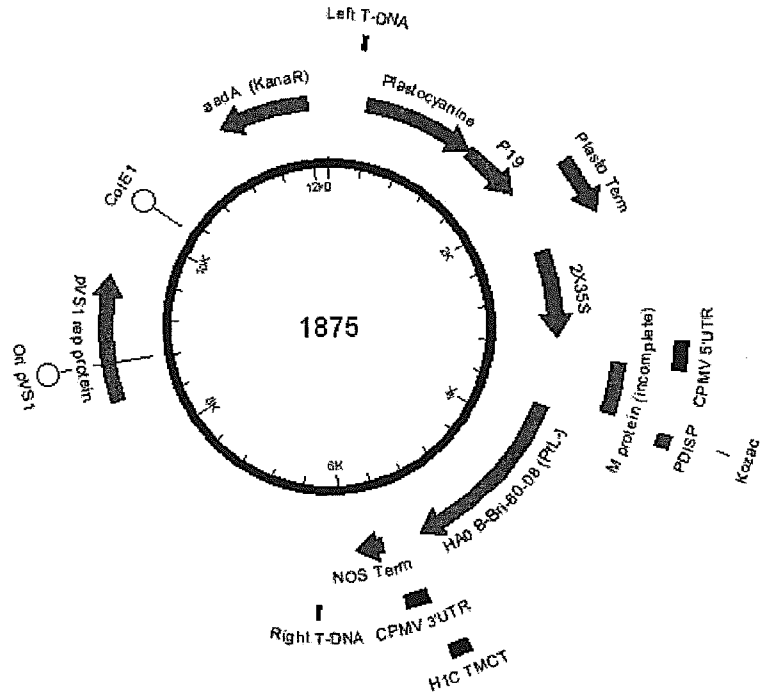
ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGA
ATCTGCACTGGAATAACATCGTCAAACTCACCACATGTCGTCAAAACTGCTACTCAAGGGGAGGTCAATGTGACTG
GTGTAATACCACTGACAACAACACCCACCAAATCTCATTTTGCAAATCTCAAAGGAACAGAAACCAGGGGGAAAC
TATGCCCAAAATGCCTCAACTGCACAGATCTGGACGTAGCCTTGGGCAGACCAAAATGCACGGGGAAAATACCCT
CGGCAAGAGTTTCAATACTCCATGAAGTCAGACCTGTTACATCTGGGTGCTTTCCTATAATGCACGACAGAACAAA
AATTAGACAGCTGCCTAACCTTCTCCGAGGATACGAACATATCAGGTTATCAACCCATAACGTTATCAATGCAGAA
AATGCACCAGGAGGACCCTACAAAATTGGAACCTCAGGGTCTTGCCCTAACATTACCAATGGAAACGGATTTTTCG
CAACAATGGCTTGGGCCGTCCCAAAAAACGACAAAAACAAAACAGCAACAAATCCATTAACAATAGAAGTACCA
TACATTTGTACAGAAGGAGAAGACCAAATTACCGTTTGGGGGTTCCACTCTGACAACGAGACCCAAATGGCAAAG
CTCTATGGGGACTCAAAGCCCCAGAAGTTCACCTCATCTGCCAACGGAGTGACCACACATTACGTTTCACAGATTG
GTGGCTTCCCAAATCAAACAGAAGACGGAGGACTACCACAAAGTGGTAGAATTGTTGTTGATTACATGGTGCAAA
AATCTGGGAAAACAGGAACAATTACCTATCAAAGGGGTATTTTATTGCCTCAAAAGGTGTGGTGCGCAAGTGGCA
GGAGCAAGGTAATAAAAGGATCCTTGCCTTTAATTGGAGAAGCAGATTGCCTCCACGAAAAATACGGTGGATTAA
ACAAAAGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCATAGGAAATTGCCCAATATGGGTGAAAACACCCT
TGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGAT
ACACATCCCATGGGGCACATGGAGTAGCGGTGGCAGCAGACCTTAAGAGCACTCAAGAGGCCATAAACAAGATA
ACAAAAAATCTCAACTCTTTGAGTGAGCTGGAAGTAAAGAATCTTCAAAGACTAAGCGGTGCCATGGATGAACTC
CACAACGAAATACTAGAACTAGATGAGAAAGTGGATGATCTCAGAGCTGATACAATAAGCTCACAAATAGAACTC
GCAGTCCTGCTTTCCAATGAAGGAATAATAAACAGTGAAGATGAACATCTCTTGGCGCTTGAAAGAAAGCTGAAG
AAAATGCTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATGCTTTGAAACCAAACACAAGTGCAACCAGACCTGT
CTCGACAGAATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTCTCCCCACCTTTGATTCACTGAATATTACTGC
TGCATCTTTAAATGACGATGGATTGGATAATTACCAGATTTTGGCGATCTATTCAACTGTCGCCAGTTCATTGGTAC
TGGTAGTCTCCCTGGGGGCAATCAGTTTCTGGATGTGCTCTAATGGGTCTCTACAGTGTAGAATATGTATTTAA

Figure 38B, SEQ ID NO : 106

Amino acid sequence of PDISP/HA B Brisbane (PrL-)+H1 California TMCT.

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSHFANLKGTETRGKLCPKC
LNCTDLDVALGRPKCTGKIPSARVSILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYEHIRLSTHNVINAENAPGGPYKIG
TSGSCPNITNGNGFFATMAWAVPKNDKNKTATNPLTIEVPYICTEGEDQITVWGFHSDNETQMAKLYGDSKPQKFTSSA
NGVTTHYVSQIGGFPNQTEDGGLPQSGRIVVDYMVQKSGKTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCL
HEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQ
EAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKK
MLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFDAGEFSLPTFDSLNITAASLNDDGLDNYQILAIYSTVASSLVLVVSL
GAISFWMCSNGSLQCRICI*

Figure 38C
Schematic representation of construct number 1875 (2X35S/CPMV HT*)



M- 2X35S/CPMV HT (construct no 2072) and HT* (construct no 2052) for PDISP/HA B Massachussetts (PrL-)

Figure 39A, SEQ ID NO : 107

Nucleotide sequence of PDISP/HA B Massachussetts (PrL-).

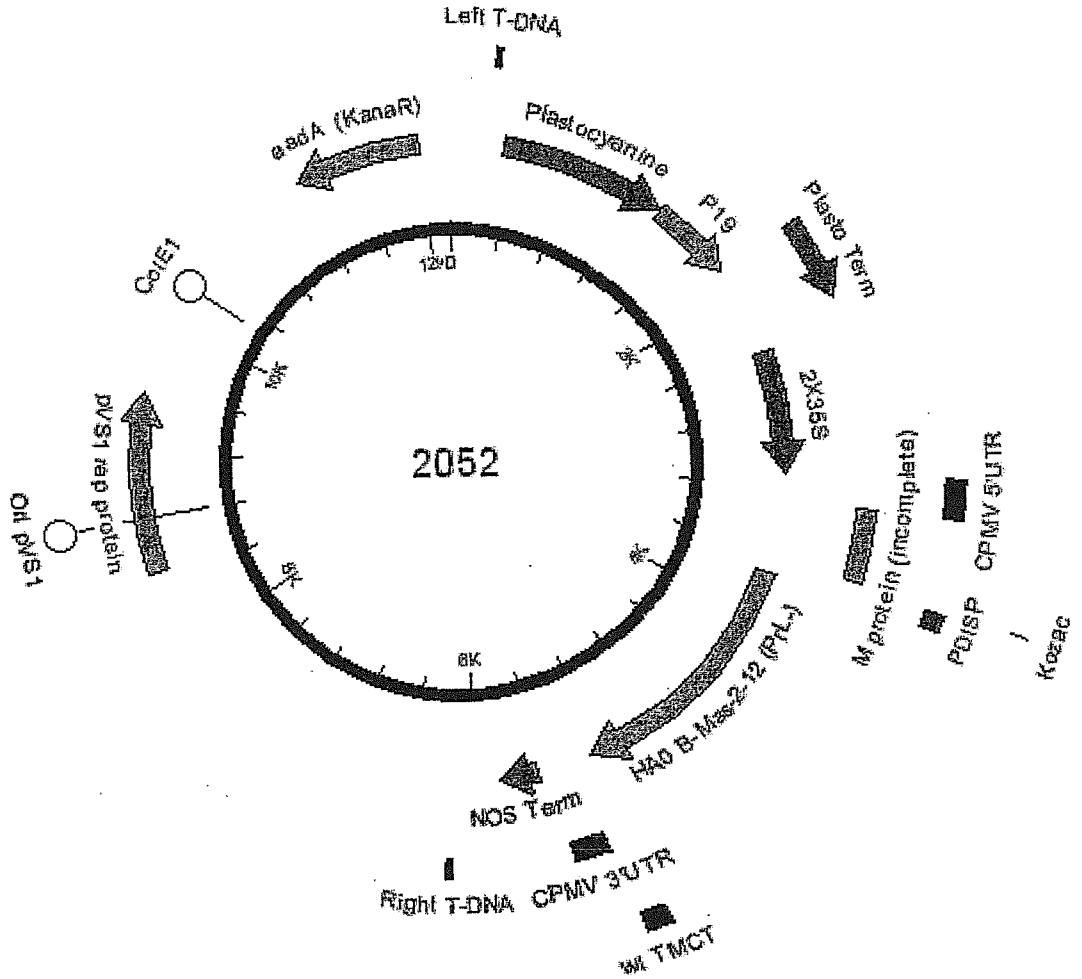
ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGA
ATCTGCACTGGGATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTG
GTGTGATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAAGACCAGAGGGAAAC
TATGCCCAGACTGTCTCAACTGTACAGATCTGGATGTGGCCCTGGGCAGGCCAATGTGTGTGGGAACTACACCTTC
TGCGAAAGCTTCAATACTTCACGAAGTCAGACCTGTTACATCCGGGTGCTTCCCTATAATGCACGACAGAACAAAA
ATCAGGCAACTAGCCAATCTTCTCAGAGGATATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAA
AAGGCACCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAAAGCGGATTTTTC
GCAACAATGGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCATTAACAGTAGAAGTACCATAC
ATTTGTGCAGAAGGGGAAGACCAAATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTC
TATGGAGACTCAAATCCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCTCAGATTGGCG
GCTTCCCAGATCAAACAGAAGACGGAGGACTACCACAAAGCGGCAGAATTGTCGTTGATTACATGATGCAAAAAC
CTGGGAAAACAGGAACAATTGTCTATCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGA
GCAAAGTAATAAAAGGGTCCTTGCCTTTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACA
AAAGCAAGCCTTACTACACAGGAGAACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTGAAAACACCTTTGA
AGCTTGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACA
CATCTCACGGAGCACATGGAGTGGCAGTTGCTGCAGACCTTAAGAGCACACAAGAAGCTATAAACAAGATAACAA
AAAATCTCAACTCTTTGAGTGAGCTAGAAGTAAAGAATCTTCAAAGGCTAAGTGGTGCCATGGATGAACTCCACA
ACGAAATACTCGAGCTGGATGAGAAAGTGGATGACCTCAGAGCTGACACTATAAGTTCACAAATAGAACTTGCAG
TCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGACGAGCATCTATTGGCACTTGAGAGAAAACTAAAGAAAA
TGCTGGGTCCCTCTGCTGTAGACATAGGAAATGGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAG
ACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAGTTTTCTCTCCCCACTTTTGATTCATTGAACATTACTGCTGCA
TCTTTAAATGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGCTGCTTCTAGTTTGGCTGTAAC
ATTGATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGACAACGTTTCATGCTCCATCTGTCTATAA

Figure 39B, SEQ ID NO :108

Amino acid sequence of PDISP/HA B Massachussetts (PrL-).

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTKTRGKLCPDC
LNCTDLDVALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLANLLRGYENIRLSTQNVIDAEKAPGGPYRL
GTSGSCPNATSKSGFFATMAWAVPKDNNKNATNPLTVEVPYICAEGEDQITVWGFHSDNKTQMKNLYGDSNPQKFTSS
ANGVTTHYVSQIGGFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEAD
CLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKS
TQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKL
KKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAASSLAVTL
MLAIFIVYMVSRDNVSCSICL*

Figure 39C
Schematic representation of construct number 2052 (2X35S/CPMV HT*)



N- 2X35S/CPMV HT (construct no 2074) and HT* (construct no 2062) for PDISP/HA B Massachussetts (PrL-)+H1 California TMCT

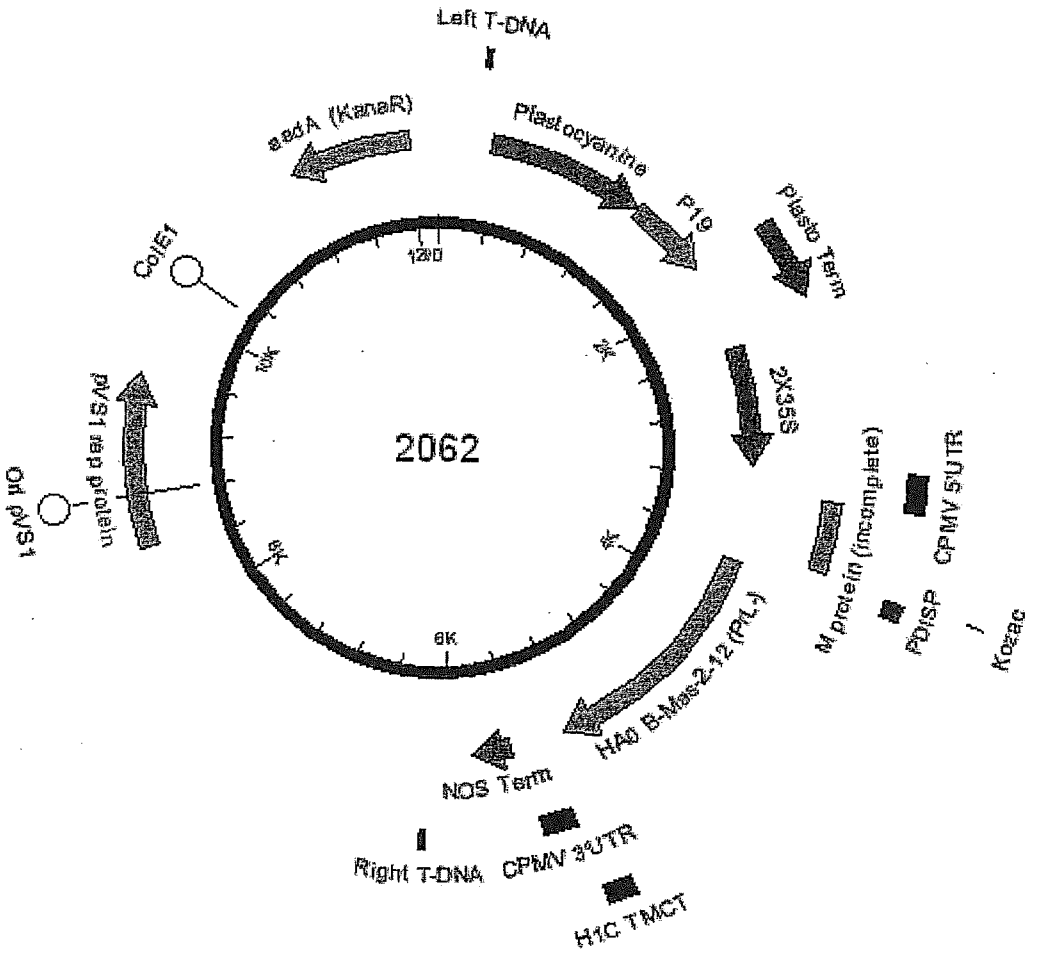
Figure 40A, SEQ ID NO : 109
Nucleotide sequence of PDISP/HA B Massachussetts (PrL-)+H1 California TMCT.

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGA
ATCTGCACTGGGATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTG
GTGTGATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAAGACCAGAGGGAAAC
TATGCCCAGACTGTCTCAACTGTACAGATCTGGATGTGGCCCTGGGCAGGCCAATGTGTGTGGGAACTACACCTTC
TGCGAAAGCTTCAATACTTCACGAAGTCAGACCTGTTACATCCGGGTGCTTCCCTATAATGCACGACAGAACAAAA
ATCAGGCAACTAGCCAATCTTCTCAGAGGATATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAA
AAGGCACCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAAAGCGGATTTTTC
GCAACAATGGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCATTAACAGTAGAAGTACCATAC
ATTTGTGCAGAAGGGGAAGACCAAATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTC
TATGGAGACTCAAATCCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCTCAGATTGGCG
GCTTCCCAGATCAAACAGAAGACGGAGGACTACCACAAAGCGGCAGAATTGTCGTTGATTACATGATGCAAAAAC
CTGGGAAAACAGGAACAATTGTCTATCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGA
GCAAAGTAATAAAAGGGTCCTTGCCTTTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACA
AAAGCAAGCCTTACTACACAGGAGAACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTGAAAACACCTTTGA
AGCTTGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACA
CATCTCACGGAGCACATGGAGTGGCAGTTGCTGCAGACCTTAAGAGCACACAAGAAGCTATAAACAAGATAACAA
AAAATCTCAACTCTTTGAGTGAGCTAGAAGTAAAGAATCTTCAAAGGCTAAGTGGTGCCATGGATGAACTCCACA
ACGAAATACTCGAGCTGGATGAGAAAGTGGATGACCTCAGAGCTGACACTATAAGTTCACAAATAGAACTTGCAG
TCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGACGAGCATCTATTGGCACTTGAGAGAAAACTAAAGAAAA
TGCTGGGTCCCTCTGCTGTAGACATAGGAAATGGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAG
ACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAGTTTTCTCTCCCCACTTTGATTCATTGAACATTACTGCTGCA
TCTTTAAATGATGATGGATTGGATAACTACCAGATTTTGGCGATCTATTCAACTGTCGCCAGTTCATTGGTACTGGT
AGTCTCCCTGGGGGCAATCAGTTTCTGGATGTGCTCTAATGGGTCTCTACAGTGTAGAATATGTATTTAA

Figure 40B, SEQ ID NO : 110
Amino acid sequence of PDISP/HA B Massachussetts (PrL-)+H1 California TMCT.

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTKTRGKLCPDC
LNCTDLDVALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLANLLRGYENIRLSTQNVIDAEKAPGGPYRL
GTSGSCPNATSKSGFFATMAWAVPKDNNKNATNPLTVEVPYICAEGEDQITVWGFHSDNKTQMKNLYGDSNPQKFTSS
ANGVTTHYVSQIGGFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEAD
CLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKS
TQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKL
KKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNYQILAIYSTVASSLVLVV
SLGAISFWMCSNGSLQCRICI*

Figure 40C Schematic representation of construct number 2062 (2X35S/CPMV HT*)



O- 2X35S/CPMV HT (construct no 1445), HT* (construct no 1839), HT*(-Mprot) (construct no 1820) and HT(fl5'UTR) (construct no 1975) for HA B Wisconsin (PrL-)

Figure 41A, SEQ ID NO :111
Nucleotide sequence of HA B Wisconsin (PrL-).

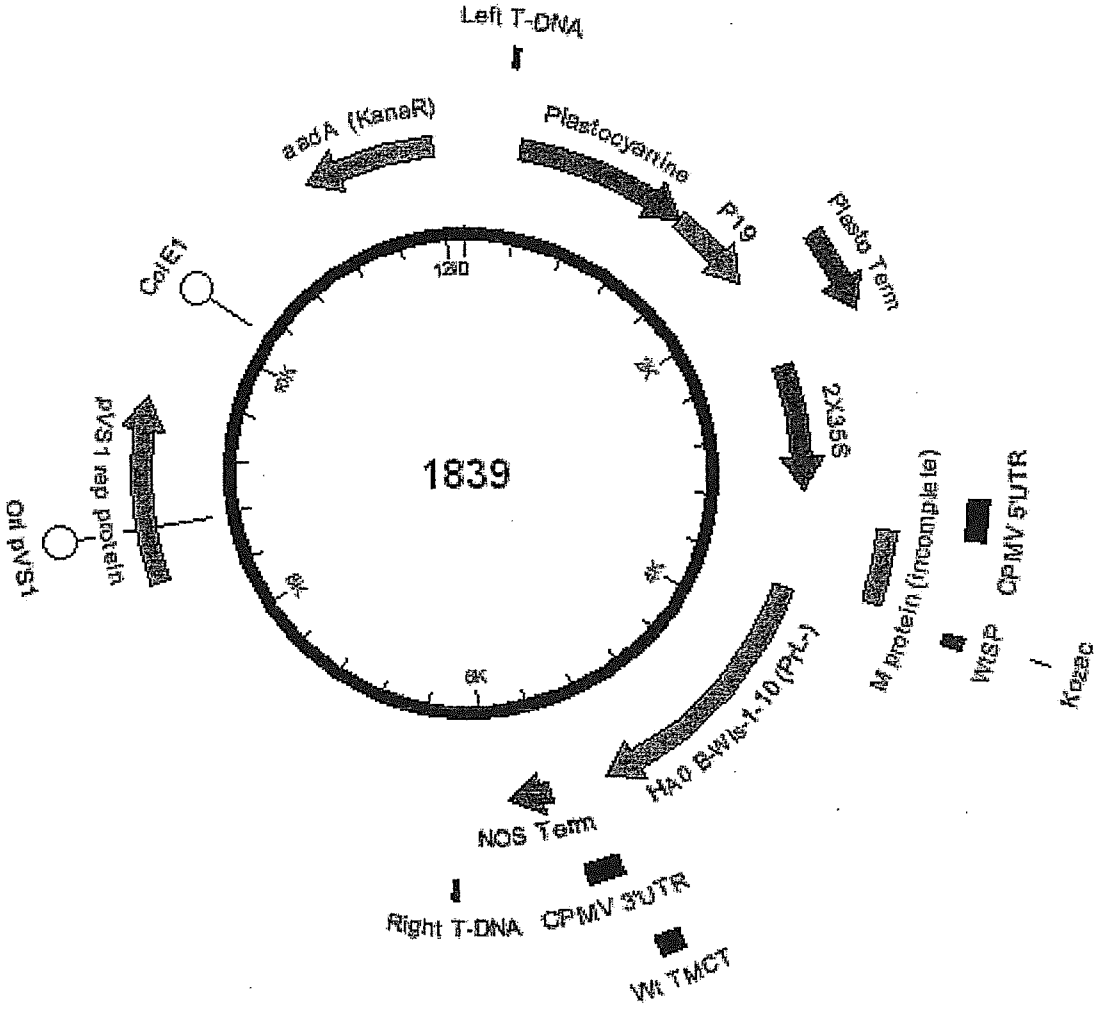
ATGAAGGCAATAATTGTACTACTCATGGTAGTAACATCCAATGCAGATCGAATCTGCACTGGGATAACATCTTCAA
ACTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTGGCGTGATACCACTGACAACAACAC
CAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAGGGAAACTATGCCCGGACTGTCTCAACTGTA
CAGATCTGGATGTGGCCTTGGGCAGGCCAATGTGTGTGGGGACCACACCTTCTGCTAAAGCTTCAATACTCCACGA
GGTCAGACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAAAATCAGGCAACTACCCAATCTTCTC
AGAGGATATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAAAAAGCACCAGGAGGACCCTACAGA
CTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAAATCGGATTTTTTGCAACAATGGCTTGGGCTGTCCCAA
AGGACAACTACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAAGGGGAAGACCAA
ATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAGCCTCTATGGAGACTCAAATCCTCAAAAGT
TCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCTCAGATTGGCGACTTCCCAGATCAAACAGAAGACGG
AGGACTACCACAAAGCGGCAGAATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTA
TCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCATTGCC
TTTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGA
ACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTAAAAACACCTTTGAAGCTTGCCAATGGAACCAAATATAG
ACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCTCACGGAGCACATGGAGTGGC
AGTGGCGGCAGACCTTAAGAGTACACAAGAAGCTATAAATAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCT
AGAAGTAAAGAACCTTCAAAGACTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAA
AGTGGATGATCTCAGAGCTGACACTATAAGCTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATA
AACAGTGAAGACGAGCATCTATTGGCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGACATA
GGAAACGGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAAT
GCAGGAGAATTTTCTCTCCCCACTTTTGATTCATTGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAA
CCATACTATACTGCTCTATTACTCAACTGCTGCTTCTAGTTTGGCTGTAACATTAATGCTAGCTATTTTTATTGTTTA
TATGGTCTCCAGAGACAACGTTTCATGCTCCATCTGTCTATAA

Figure 41B, SEQ ID NO : 112
Amino acid sequence of HA B Wisconsin (PrL-).

MKAIIVLLMVVTSNADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTRTRGKLCPDCLNCTDLDV
ALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYENIRLSTQNVIDAEKAPGGPYRLGTSGSCPN
ATSKIGFFATMAWAVPKDNYKNATNPLTVEVPYICTEGEDQITVWGFHSDNKTQMKSLYGDSNPQKFTSSANGVTTHY
VSQIGDFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGG
LNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKIT
KNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSA
VDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMLAIFIVY
MVSRDNVSCSICL*

Figure 41C

Schematic representation of construct number 1839 (2X35S/CPMV HT*)



P- 2X35S/CPMV HT (construct no 1454) and HT* (construct no 1860) for HA B Wisconsin (PrL-)+H1 California TMCT

Figure 42A, SEQ ID NO : 113

Nucleotide sequence of HA B Wisconsin (PrL-)+H1 California TMCT

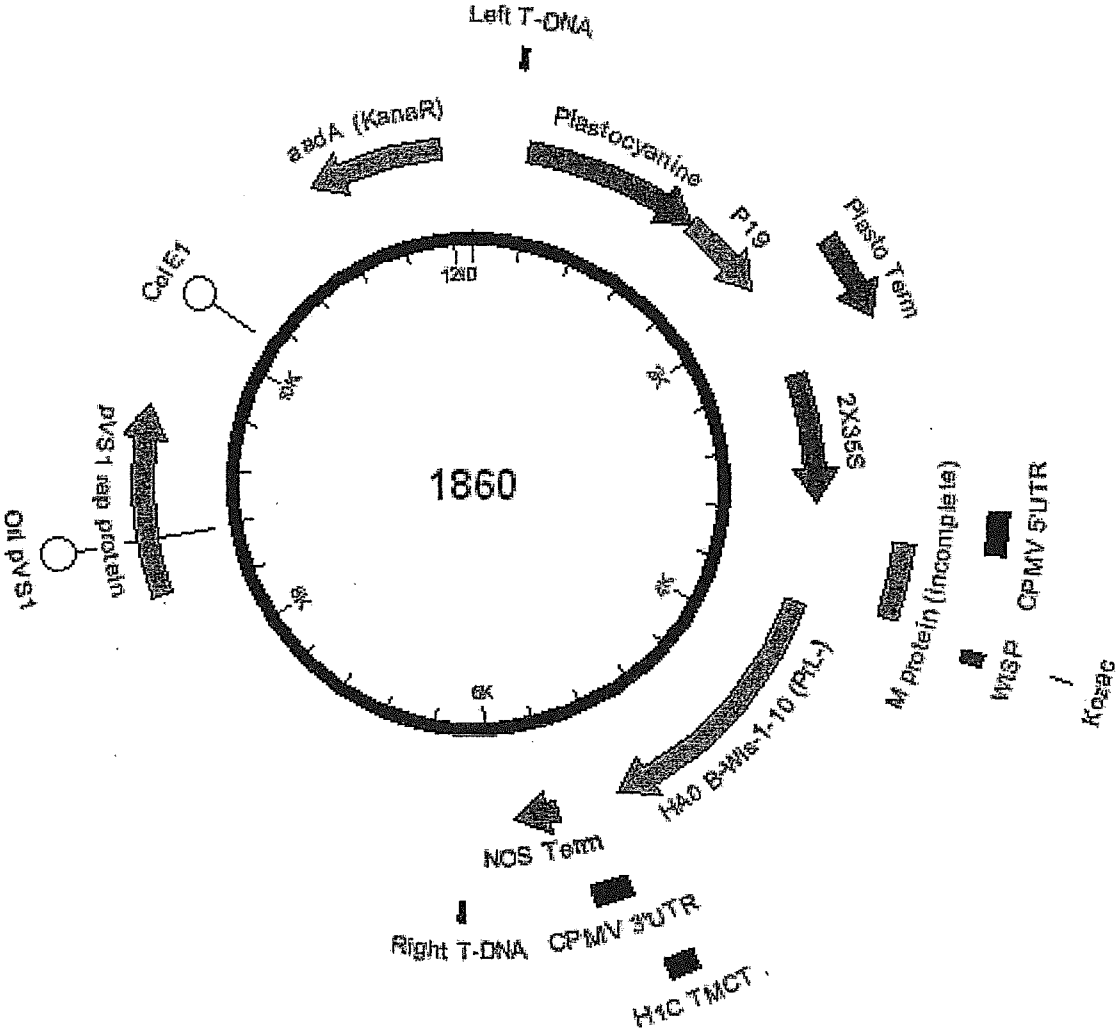
ATGAAGGCAATAATTGTACTACTCATGGTAGTAACATCCAATGCAGATCGAATCTGCACTGGGATAACATCTTCAA
ACTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTGGCGTGATACCACTGACAACAACAC
CAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAGGGAAACTATGCCCGGACTGTCTCAACTGTA
CAGATCTGGATGTGGCCTTGGGCAGGCCAATGTGTGTGGGGACCACACCTTCTGCTAAAGCTTCAATACTCCACGA
GGTCAGACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAAAATCAGGCAACTACCCAATCTTCTC
AGAGGATATGAAAATATCAGGTTATCAACCCAAAACGTTATCGATGCAGAAAAAGCACCAGGAGGACCCTACAGA
CTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAAATCGGATTTTTTGCAACAATGGCTTGGGCTGTCCCAA
AGGACAACTACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAAGGGGAAGACCAA
ATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAGCCTCTATGGAGACTCAAATCCTCAAAAGT
TCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCTCAGATTGGCGACTTCCCAGATCAAACAGAAGACGG
AGGACTACCACAAAGCGGCAGAATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTA
TCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCATTGCC
TTTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGA
ACATGCAAAAGCCATAGGAAATTGCCCAATATGGGTAAAAACACCTTTGAAGCTTGCCAATGGAACCAAATATAG
ACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCTCACGGAGCACATGGAGTGGC
AGTGGCGGCAGACCTTAAGAGTACACAAGAAGCTATAAATAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCT
AGAAGTAAAGAACCTTCAAAGACTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAA
AGTGGATGATCTCAGAGCTGACACTATAAGCTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATA
AACAGTGAAGACGAGCATCTATTGGCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGACATA
GGAAACGGATGCTTCGAAACCAAACACAAATGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAAT
GCAGGAGAATTTTCTCTCCCCACTTTTGATTCATTGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAA
CTACCAGATTTTGGCGATCTATTCAACTGTCGCCAGTTCATTGGTACTGGTAGTCTCCCTGGGGGCAATCAGTTTCT
GGATGTGCTCTAATGGGTCTCTACAGTGTAGAATATGTATTTAA

Figure 42B, SEQ ID NO : 114

Amino acid sequence of HA B Wisconsin (PrL-)+H1 California TMC.

MKAIIVLLMVVTSNADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTRTRGKLCPDCLNCTDLDV
ALGRPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLPNLLRGYENIRLSTQNVIDAEKAPGGPYRLGTSGSCPN
ATSKIGFFATMAWAVPKDNYKNATNPLTVEVPYICTEGEDQITVWGFHSDNKTQMKSLYGDSNPQKFTSSANGVTTHY
VSQIGDFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGG
LNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKIT
KNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSA
VDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNYQILAIYSTVASSLVLVVSLGAISFW
MCSNGSLQCRICI*

Figure 42C
Schematic representation of construct number 1860 (2X35S/CPMV HT*)



2X35S/CPMV HT (construct no 489), HT*(-Mprot) (construct no 1880) and HT(fl5'UTR) (construct no 1885) for H5 Indonesia

Figure 43A

Nucleotide sequence of native H5 Indonesia. (SEQ ID NO: 115)

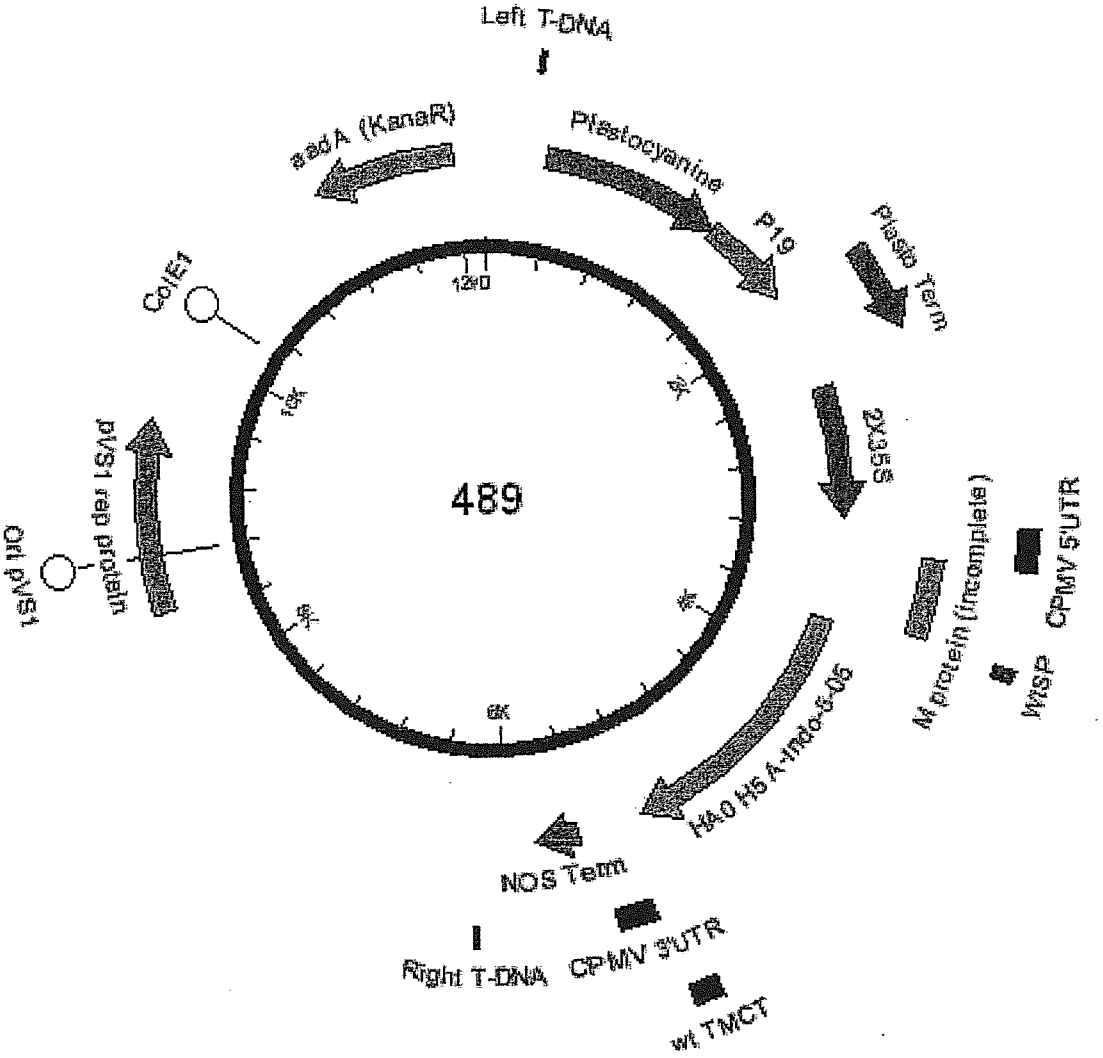
ATGGAGAAAATAGTGCTTCTTCTTGCAATAGTCAGTCTTGTTAAAAGTGATCAGATTTGCATTGGTTACCATGCAAA
CAATTCAACAGAGCAGGTTGACACAATCATGGAAAAGAACGTTACTGTTACACATGCCCAAGACATACTGGAAAAGA
CACACAACGGGAAGCTCTGCGATCTAGATGGAGTGAAGCCTCTAATTTTAAGAGATTGTAGTGTAGCTGGATGGCTC
CTCGGGAACCCAATGTGTGACGAATTCATCAATGTACCGGAATGGTCTTACATAGTGGAGAAGGCCAATCCAACCAA
TGACCTCTGTTACCCAGGGAGTTTCAACGACTATGAAGAACTGAAACACCTATTGAGCAGAATAAACCATTTTGAGA
AAATTCAAATCATCCCCAAAAGTTCTTGGTCCGATCATGAAGCCTCATCAGGAGTTAGCTCAGCATGTCCATACCTG
GGAAGTCCCTCCTTTTTTAGAAATGTGGTATGGCTTATCAAAAAGAACAGTACATACCCAACAATAAAGAAAAGCTA
CAATAATACCAACCAAGAGGATCTTTTGGTACTGTGGGGAATTCACCATCCTAATGATGCGGCAGAGCAGACAAGGC
TATATCAAAACCCAACCACCTATATTTCCATTGGGACATCAACACTAAACCAGAGATTGGTACCAAAAATAGCTACT
AGATCCAAAGTAAACGGGCAAAGTGGAAGGATGGAGTTCTTCTGGACAATTTTAAAACCTAATGATGCAATCAACTT
CGAGAGTAATGGAAATTTCATTGCTCCAGAATATGCATACAAAATTGTCAAGAAAGGGGACTCAGCAATTATGAAAA
GTGAATTGGAATATGGTAACTGCAACACCAAGTGTCAAACTCCAATGGGGGCGATAAACTCTAGTATGCCATTCCAC
AACATACACCCTCTCACCATCGGGGAATGCCCCAAATATGTGAAATCAAACAGATTAGTCCTTGCAACAGGGCTCAG
AAATAGCCCTCAAAGAGAGAGCAGAAGAAAAAAGAGAGGACTATTTGGAGCTATAGCAGGTTTTATAGAGGGAGGAT
GGCAGGGAATGGTAGATGGTTGGTATGGGTACCACCATAGCAATGAGCAGGGGAGTGGGTACGCTGCAGACAAAGAA
TCCACTCAAAAGGCAATAGATGGAGTCACCAATAAGGTCAACTCAATCATTGACAAAATGAACACTCAGTTTGAGGC
CGTTGGAAGGGAATTTAATAACTTAGAAAGGAGAATAGAGAATTTAAACAAGAAGATGGAAGACGGGTTTCTAGATG
TCTGGACTTATAATGCCGAACTTCTGGTTCTCATGGAAAATGAGAGAACTCTAGACTTTCATGACTCAAATGTTAAG
AACCTCTACGACAAGGTCCGACTACAGCTTAGGGATAATGCAAAGGAGCTGGGTAACGGTTGTTTCGAGTTCTATCA
CAAATGTGATAATGAATGTATGGAAAGTATAAGAAACGGAACGTACAACTATCCGCAGTATTCAGAAGAAGCAAGAT
TAAAAAGAGAGGAAATAAGTGGGGTAAAATTGGAATCAATAGGAACTTACCAAATACTGTCAATTTATTCAACAGTG
GCGAGTTCCCTAGCACTGGCAATCATGATGGCTGGTCTATCTTTATGGATGTGCTCCAATGGATCGTTACAATGCAG
AATTTGCATTTAA

Figure 43B

Amino acid sequence of native H5 Indonesia. (SEQ ID NO: 116)

MEKIVLLLAIVSLVKSDQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDLDGVKPLILRDCSVAGWL
LGNPMCDEFINVPEWSYIVEKANPTNDLCYPGSFNDYEELKHLLSRINHFEKIQIIPKSSWSDHEASSGVSSACPYL
GSPSFFRNVVWLIKKNSTYPTIKKSYNNTNQEDLLVLWGIHHPNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIAT
RSKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGDSAIMKSELEYGNCNTKCQTPMGAINSSMPFH
NIHPLTIGECPKYVKSNRLVLATGLRNSPQRESRRKKRGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQGSGYAADKE
STQKAIDGVTNKVNSIIDKMNTQFEAVGREFNNLERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVK
NLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESIRNGTYNYPQYSEEARLKREEISGVKLESIGTYQILSIYSTV
ASSLALAIMMAGLSLWMCSNGSLQCRICI*

Figure 43C
Schematic representation of construct number 489 (2X35S/CPMV HT)



2X35S/CPMV-HT*(-Mprot)/ PDISP/H3 Victoria/ NOS (Construct number 1800)

Figure 44A
IF**(SacII)-PDI.s1+4c
ACAGGGCCCAATACCGCGGAGAAAATGGCGAAAAACGTTGCGATTTTCGGCT (SEQ ID NO: 117)

Figure 44B
IF-H3V36111.s1-4r
ACTAAAGAAAATAGGCCTTCAAATGCAAATGTTGCACCTAATGTTGCCCTT (SEQ ID NO: 118)

Figure 44C
Nucleotide sequence of PDISP/H3 Victoria. (SEQ ID NO: 119)
ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCCAAAA
ACTTCCTGGAAATGACAACAGCACGGCAACGCTGTGCCTTGGGCACCATGCAGTACCAAACGGAACGATAGTGAAAA
CAATCACGAATGACCAAATTGAAGTTACTAATGCTACTGAGCTGGTTCAGAATTCCTCAATAGGTGAAATATGCGAC
AGTCCTCATCAGATCCTTGATGGAGAAAACTGCACACTAATAGATGCTCTATTGGGAGACCCTCAGTGTGATGGCTT
CCAAAATAAGAAATGGGACCTTTTTGTTGAACGAAGCAAAGCCTACAGCAACTGTTACCCTTATGATGTGCCGGATT
ATGCCTCCCTTAGGTCACTAGTTGCCTCATCCGGCACACTGGAGTTTAACAATGAAAGCTTCAATTGGACTGGAGTC
ACTCAAAACGGAACAAGTTCTGCTTGCATAAGGAGATCTAATAATAGTTTCTTTAGTAGATTAAATTGGTTGACCCA
CTTAAACTTCAAATACCCAGCATTGAACGTGACTATGCCAAACAATGAACAATTTGACAAATTGTACATTTGGGGGG
TTCACCACCCGGGTACGGACAAGGACCAAATCTTCCTGTATGCTCAATCATCAGGAAGAATCACAGTATCTACCAAA
AGAAGCCAACAAGCTGTAATCCCGAATATCGGATCTAGACCCAGAATAAGGAATATCCCTAGCAGAATAAGCATCTA
TTGGACAATAGTAAAACCGGGAGACATACTTTTGATTAACAGCACAGGGAATCTAATTGCTCCTAGGGGTTACTTCA
AAATACGAAGTGGGAAAAGCTCAATAATGAGATCAGATGCACCCATTGGCAAATGCAATTCTGAATGCATCACTCCA
AATGGAAGCATTCCCAATGACAAACCATTCCAAAATGTAAACAGGATCACATACGGGGCCTGTCCCAGATATGTTAA
GCAAAGCACTCTGAAATTGGCAACAGGAATGCGAAATGTACCAGAGAAACAAACTAGAGGCATATTTGGCGCAATAG
CGGGTTTCATAGAAAATGGTTGGGAGGGAATGGTGGATGGTTGGTACGGTTTCAGGCATCAAAATTCTGAGGGAAGA
GGACAAGCAGCAGATCTCAAAAGCACTCAAGCAGCAATCGATCAAATCAATGGGAAGCTGAATCGATTGATCGGGAA
AACCAACGAGAAATTCCATCAGATTGAAAAAGAATTCTCAGAAGTCGAAGGGAGAATTCAGGACCTTGAGAAATATG
TTGAGGACACTAAAATAGATCTCTGGTCATACAACGCGGAGCTTCTTGTTGCCCTGGAGAACCAACATACAATTGAT
CTAACTGACTCAGAAATGAACAAACTGTTTGAAAAAACAAAGAAGCAACTAAGGGAAAATGCTGAGGATATGGGCAA
TGGTTGTTTCAAAATATACCACAAATGTGACAATGCCTGCATAGGATCAATCAGAAATGGAACTTATGACCACGATG
TATACAGAGATGAAGCATTAAACAACCGGTTCCAGATCAAGGGAGTTGAGCTGAAGTCAGGGTACAAAGATTGGATC
CTATGGATTTCCTTTGCCATATCATGTTTTTTGCTTTGTGTTGCTTTGTTGGGGTTCATCATGTGGGCCTGCCAAAA
GGGCAACATTAGGTGCAACATTTGCATTTGA

Figure 44D
Schematic representation of construct 2171. SacII and StuI restriction enzyme sites used for plasmid linearization are annotated on the representation.

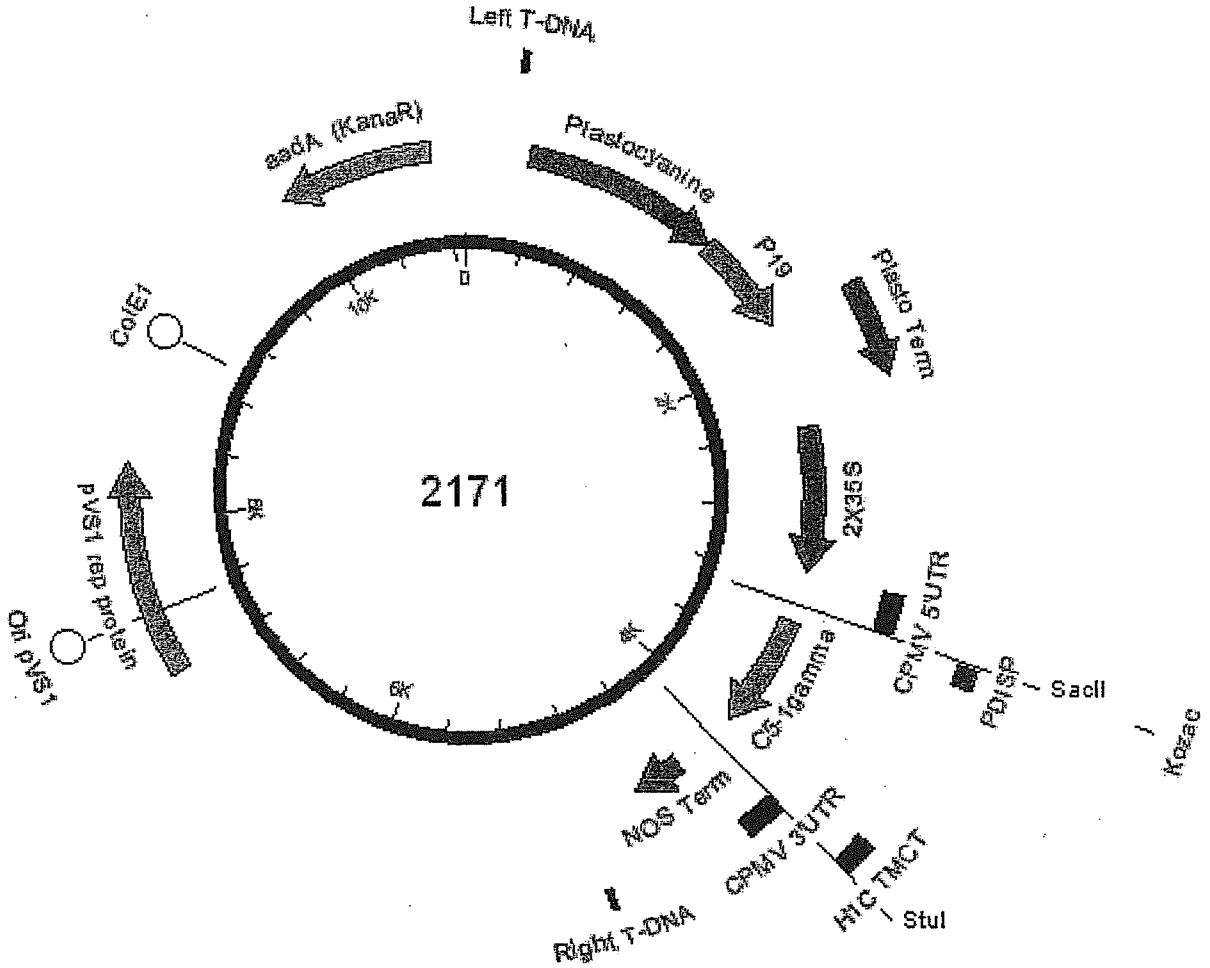


Figure 44E

Construct 2171 from left to right t-DNA borders (underlined). 2X35S/CPMV-HT*(-Mprot)/NOS with Plastocyanine-P19-Plastocyanine silencing inhibitor expression cassette (SEQ ID NO: 120)

TGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACATTGCGGACGTTTTTAATGTACT
GAATTAACGCCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTCAAAAACCATAAAAGTTTAAGTTAGCA
AGTGTGTACATTTTTACTTGAACAAAAATATTCACCTACTACTGTTATAAATCATTATTAAACATTAGAGTAAAGAA
ATATGGATGATAAGAACAAGAGTAGTGATATTTTGACAACAATTTTGTTGCAACATTTGAGAAAATTTTGTTGTTCT
CTCTTTTCATTGGTCAAAAACAATAGAGAGAGAAAAAGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGAG
AAAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATTGAGGAATTTGACAAAAGCTACACAAATAAGGG
TTAATTGCTGTAAATAAATAAGGATGACGCATTAGAGAGATGTACCATTAGAGAATTTTTGGCAAGTCATTAAAAAG
AAAGAATAAATTATTTTTAAAATTAAAAGTTGAGTCATTTGATTAAACATGTGATTATTTAATGAATTGATGAAAGA
GTTGGATTAAAGTTGTATTAGTAATTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCCTATATATTGC
CCCATAGAGTCAGTTAACTCATTTTTATATTTCATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCCAAAA
AAAAAAAACGGTATATTTACTAAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCCGTAGGAGGATAACATCCA
ATCCAACCAATCACAACAATCCTGATGAGATAACCCACTTTAAGCCCACGCATCTGTGGCACATCTACATTATCTAA
ATCACACATTCTTCCACACATCTGAGCCACACAAAAACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACA
CTTTGTGAGTCTACACTTTGATTCCCTTCAAACACATACAAAGAGAAGAGACTAATTAATTAATCATCTTGAG
AGAAAATGGAACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCAGGA
GGTACCACTTCTCCCTTCAAACTTCCTGACGAAAGTCCGAGTTGGACTGAGTGGCGGCTACATAACGATGAGACGAA
TTCGAATCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGGGAAAGTTGTATTTAAGAGATATCTCAGAT
ACGACAGGACGGAAGCTTCACTGCACAGAGTCCTTGGATCTTGGACGGGAGATTCGGTTAACTATGCAGCATCTCGA
TTTTTCGGTTTCGACCAGATCGGATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTC
GCGAACTCTTCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCCAATCGAAGTGG
AAAGTAATGTATCAAGAGGATGCCCTGAAGGTACTCAAACCTTCGAAAAAGAAAGCGAGTAAGTTAAAATGCTTCTT
CGTCTCCTATTTATAATATGGTTTGTTATTGTTAATTTTGTTCTTGTAGAAGAGCTTAATTAATCGTTGTTGTTATG
AAATACTATTTGTATGAGATGAACTGGTGTAATGTAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCCTC
CATAACTAACTAGACATGAAGACCTGCCGCGTACAATTGTCTTATATTTGAACAACTAAAATTGAACATCTTTTGCC
ACAACTTTATAAGTGGTTAATATAGCTCAAATATATGGTCAAGTTCAATAGATTAATAATGGAAATATCAGTTATCG
AAATTCATTAACAATCAACTTAACGTTATTAACTACTAATTTTATATCATCCCCTTTGATAAATGATAGTACACCAA
TTAGGAAGGAGCATGCTCGCCTAGGAGATTGTCGTTTCCCGCCTTCAGTTTGCAAGCTGCTCTAGCCGTGTAGCCAA
TACGCAAACCGCCTCTCCCCGCGCGTTGGGAATTACTAGCGCGTGTCGACAAGCTTGCATGCCGGTCAACATGGTGG
AGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAA
CAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAA
GGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTC
CCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGAT
TGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAG
GGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTA
TTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGAT
GCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCAC
GTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAG
ACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACG
TGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTG
CGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAGGGCCCAATACCGCGGAGAAAATGGCGAAA
AACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGACGTCACTCCTCAG
CCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGGGA
TGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACAC
CTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCG
AGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTGTGGT
TGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCAC
CATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGT
TTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTC
AGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAGACGTCCAGATTTTGGCGATCTATTCAACTGTC
GCCAGTTCATTGGTACTGGTAGTCTCCCTGGGGGCAATCAGTTTCTGGATGTGCTCTAATGGGTCTCTACAGTGTAG
AATATGTATTTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGG
TTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCA

GCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGA
CCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCAT
ATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTA
TGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCG
CGCGCGGTGTCATCTATGTTACTAGATCTCTAGAGTCTCAAGCTTGGCGCGCCCACGTGACTAGTGGCACTGGCCGT
CGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCA
GCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGCTAGAGC
AGCTTGAGCTTGGATCAGATTGTCGTTTCCCGCCTTCAGTTTAAACTATCAGTGTTTGACAGGATATATTGGCGGGT
AAACCTAAGAGAAAAGAGCGTTTA

Figure 44F

Expression cassette number 1800 from 2X35S promoter to NOS terminator. PDISP/H3 Victoria nucleotide sequence is underlined. SEQ ID NO: 121

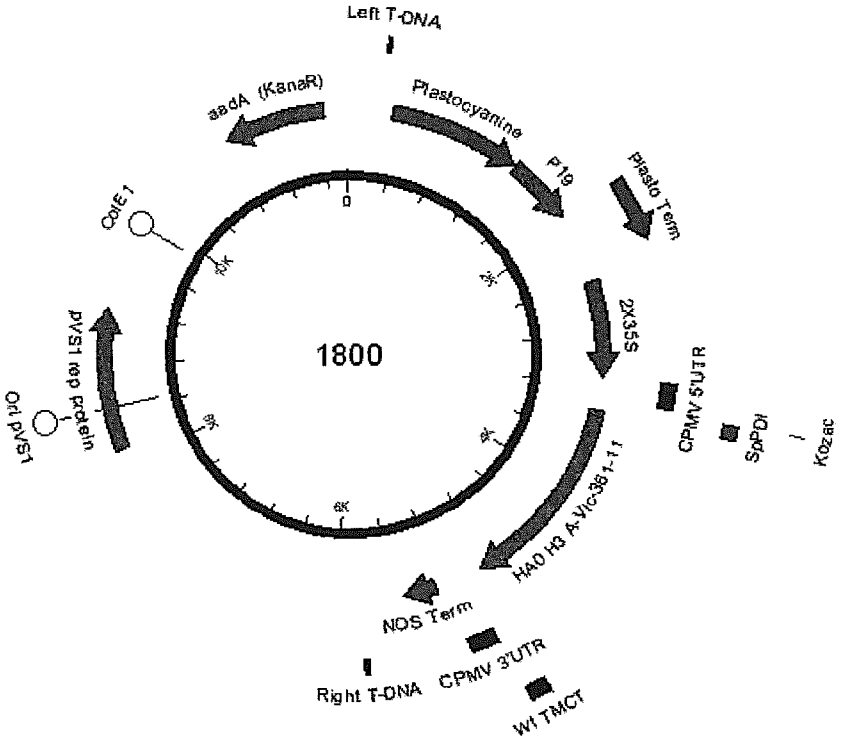
GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTT
TCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAG
GTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCC
CCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCA
CGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATAT
CCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGC
CATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCAT
CGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAAT
CCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAA
AAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTG
CGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAGGGCCCAATACCGCGGAGAAAATGGCGAAAAACGTTGCG
ATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCCAAAAACTTCCTGGAAATGACAACAGCACGGC
AACGCTGTGCCTTGGGCACCATGCAGTACCAAACGGAACGATAGTGAAAACAATCACGAATGACCAAATTGAAGTTACTAATGCTA
CTGAGCTGGTTCAGAATTCCTCAATAGGTGAAATATGCGACAGTCCTCATCAGATCCTTGATGGAGAAAACTGCACACTAATAGAT
GCTCTATTGGGAGACCCTCAGTGTGATGGCTTCCAAAATAAGAAATGGGACCTTTTTGTTGAACGAAGCAAAGCCTACAGCAACTG
TTACCCTTATGATGTGCCGGATTATGCCTCCCTTAGGTCACTAGTTGCCTCATCCGGCACACTGGAGTTTAACAATGAAAGCTTCA
ATTGGACTGGAGTCACTCAAAACGGAACAAGTTCTGCTTGCATAAGGAGATCTAATAATAGTTTCTTTAGTAGATTAAATTGGTTG
ACCCACTTAAACTTCAAATACCCAGCATTGAACGTGACTATGCCAAACAATGAACAATTTGACAAATTGTACATTTGGGGGGTTCA
CCACCCGGGTACGGACAAGGACCAAATCTTCCTGTATGCTCAATCATCAGGAAGAATCACAGTATCTACCAAAAGAAGCCAACAAG
CTGTAATCCCGAATATCGGATCTAGACCCAGAATAAGGAATATCCCTAGCAGAATAAGCATCTATTGGACAATAGTAAAACCGGGA
GACATACTTTTGATTAACAGCACAGGGAATCTAATTGCTCCTAGGGGTTACTTCAAAATACGAAGTGGGAAAAGCTCAATAATGAG
ATCAGATGCACCCATTGGCAAATGCAATTCTGAATGCATCACTCCAAATGGAAGCATTCCCAATGACAAACCATTCCAAAATGTAA
ACAGGATCACATACGGGGCCTGTCCCAGATATGTTAAGCAAAGCACTCTGAAATTGGCAACAGGAATGCGAAATGTACCAGAGAAA
CAAACTAGAGGCATATTTGGCGCAATAGCGGGTTTCATAGAAAATGGTTGGGAGGGAATGGTGGATGGTTGGTACGGTTTCAGGCA
TCAAAATTCTGAGGGAAGAGGACAAGCAGCAGATCTCAAAAGCACTCAAGCAGCAATCGATCAAATCAATGGGAAGCTGAATCGAT
TGATCGGGAAAACCAACGAGAAATTCCATCAGATTGAAAAAGAATTCTCAGAAGTCGAAGGGAGAATTCAGGACCTTGAGAAATAT
GTTGAGGACACTAAAATAGATCTCTGGTCATACAACGCGGAGCTTCTTGTTGCCCTGGAGAACCAACATACAATTGATCTAACTGA
CTCAGAAATGAACAAACTGTTTGAAAAAACAAAGAAGCAACTAAGGGAAAATGCTGAGGATATGGGCAATGGTTGTTTCAAAATAT
ACCACAAATGTGACAATGCCTGCATAGGATCAATCAGAAATGGAACTTATGACCACGATGTATACAGAGATGAAGCATTAAACAAC
CGGTTCCAGATCAAGGGAGTTGAGCTGAAGTCAGGGTACAAAGATTGGATCCTATGGATTTCCTTTGCCATATCATGTTTTTTGCT
TTGTGTTGCTTTGTTGGGGTTCATCATGTGGGCCTGCCAAAAGGGCAACATTAGGTGCAACATTTGCATTTGAAGGCCTATTTTCT
TTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAAT
TTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAA
AAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGT
TGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTA
TGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAA
TTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 44G

Amino acid sequence of PDISP/H3 Victoria (SEQ ID NO: 122)

MAKNVAIFGLLFSLLVLVPSQIFAQKLPGNDNSTATLCLGHHAVPNGTIVKTITNDQIEVTNATELVQNSSIGEICDSPHQILDGE
NCTLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNESFNWTGVTQNGTSSACIRRSNNSFF
SRLNWLTHLNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKDQIFLYAQSSGRITVSTKRSQQAVIPNIGSRPRIRNIPSRISIYW
TIVKPGDILLINSTGNLIAPRGYFKIRSGKSSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQSTLKLATGM
RNVPEKQTRGIFGAIAGFIENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIEKEFSEVEGRI
QDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTYDHDVYR
DEALNNRFQIKGVELKSGYKDWILWISFAISCFLLCVALLGFIMWACQKGNIRCNICI*

Figure 44H
Schematic representation of construct number 1800



2X3B-2X35S/CPMV-HT*/ PDISP/H3 Victoria/ NOS (Construct number 1819)

Figure 45A
IF(SacII)-Kozac_PDI.c
GTCGGGCCCAATACCGCGGAGAAAATGGCGAAAAACGTTGCGATTTTC (SEQ ID NO.: 123)

Figure 45B
IF-H3V36111.s1-4r
ACTAAAGAAAATAGGCCTTCAAATGCAAATGTTGCACCTAATGTTGCCCTT (SEQ ID NO: 124)

Figure 45C
Schematic representation of construct 2181. SacII and StuI restriction enzyme sites used for plasmid linearization are annotated on the representation.

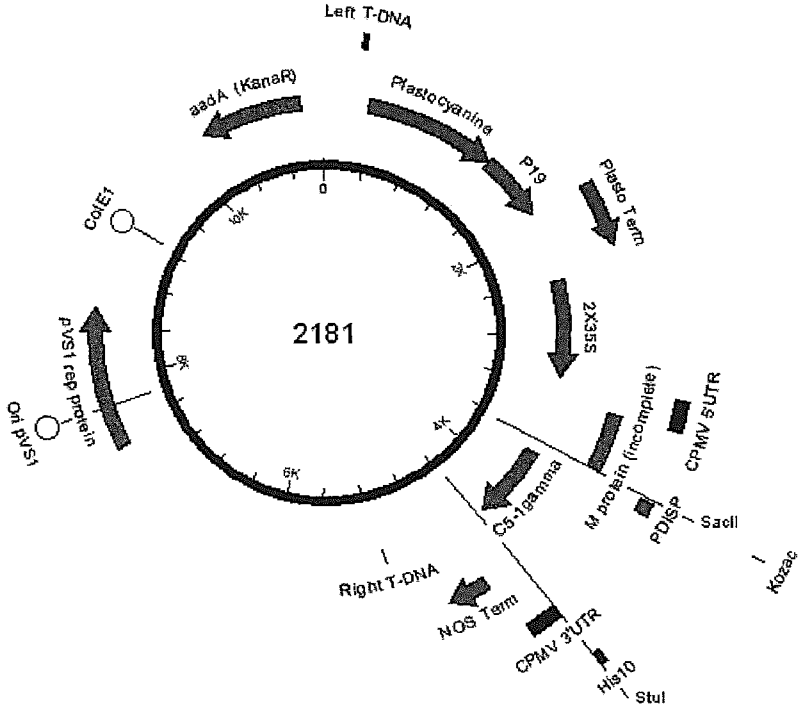


Figure 45D,
Construct 2181 from left to right t-DNA borders (underlined). 2X35S/CPMV-HT*/NOS with Plastocyanine-P19-Plastocyanine silencing inhibitor expression cassette (SEQ ID NO: 125)
TGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACATTGCGGACGTTTTTAATGTACTGAATTAACG
CCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTCAAAAACCATAAAAGTTTAAGTTAGCAAGTGTGTACATTTTTACT
TGAACAAAAATATTCACCTACTACTGTTATAAATCATTATTAAACATTAGAGTAAAGAAATATGGATGATAAGAACAAGAGTAGTG
ATATTTTGACAACAATTTTGTTGCAACATTTGAGAAAATTTTGTTGTTCTCTCTTTTCATTGGTCAAAAACAATAGAGAGAGAAAA
AGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGAGAAAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATT
GAGGAATTTGACAAAAGCTACACAAATAAGGGTTAATTGCTGTAAATAAATAAGGATGACGCATTAGAGAGATGTACCATTAGAGA
ATTTTTGGCAAGTCATTAAAAAGAAAGAATAAATTATTTTTAAAATTAAAAGTTGAGTCATTTGATTAAACATGTGATTATTTAAT
GAATTGATGAAAGAGTTGGATTAAAGTTGTATTAGTAATTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCCTATAT

ATTGCCCCATAGAGTCAGTTAACTCATTTTTATATTTCATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCCAAAAAAAA
AAAACGGTATATTTACTAAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCCGTAGGAGGATAACATCCAATCCAACCAATCA
CAACAATCCTGATGAGATAACCCACTTTAAGCCCACGCATCTGTGGCACATCTACATTATCTAAATCACACATTCTTCCACACATC
TGAGCCACACAAAAACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACACTTTGTGAGTCTACACTTTGATTCCCTTCAA
ACACATACAAAGAGAAGAGACTAATTAATTAATTAATCATCTTGAGAGAAAATGGAACGAGCTATACAAGGAAACGACGCTAGGGA
ACAAGCTAACAGTGAACGTTGGGATGGAGGATCAGGAGGTACCACTTCTCCCTTCAAACTTCCTGACGAAAGTCCGAGTTGGACTG
AGTGGCGGCTACATAACGATGAGACGAATTCGAATCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGGGAAAGTTGTA
TTTAAGAGATATCTCAGATACGACAGGACGGAAGCTTCACTGCACAGAGTCCTTGGATCTTGGACGGGAGATTCGGTTAACTATGC
AGCATCTCGATTTTTCGGTTTCGACCAGATCGGATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGT
CGCGAACTCTTCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCCAATCGAAGTGGAAAGTAAT
GTATCAAGAGGATGCCCTGAAGGTACTCAAACCTTCGAAAAAGAAAGCGAGTAAGTTAAAATGCTTCTTCGTCTCCTATTTATAAT
ATGGTTTGTTATTGTTAATTTTGTTCTTGTAGAAGAGCTTAATTAATCGTTGTTGTTATGAAATACTATTTGTATGAGATGAACTG
GTGTAATGTAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCCTCCATAACTAACTAGACATGAAGACCTGCCGCGTACA
ATTGTCTTATATTTGAACAACTAAAATTGAACATCTTTTGCCACAACTTTATAAGTGGTTAATATAGCTCAAATATATGGTCAAGT
TCAATAGATTAATAATGGAAATATCAGTTATCGAAATTCATTAACAATCAACTTAACGTTATTAACTACTAATTTTATATCATCCC
CTTTGATAAATGATAGTACACCAATTAGGAAGGAGCATGCTCGCCTAGGAGATTGTCGTTTCCCGCCTTCAGTTTGCAAGCTGCTC
TAGCCGTGTAGCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGGAATTACTAGCGCGTGTCGACAAGCTTGCATGCCGGTCAACA
TGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAA
AGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTC
CTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCA
CGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACA
CTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAA
CCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATT
GCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAA
AAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTA
TCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAA
CGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGC
GATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGGACAC
GTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCTGGAGGCTGCTGT
TCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTTGACGAGGTATTGTTGCCT
GTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGTTTTCGAA
CTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCAATACCGCGGAGAAAATGGCGAAAAACGTTGCG
ATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGACGTCACTCCTCAGCCAAAACGACACCCCCAT
CTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAG
CCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCT
GAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAGG
TGGACAAGAAAATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCTTCCCC
CCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGT
CCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCAACAGCACTTTCCGCT
CAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAGCGATCGCTCACCATCACCATCACCATCACCATCACC
ATTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGT
GTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTT
TATTAAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTT
CTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGT
AATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAG
CGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCTCTAGAGTCTCAAGCTTGGCGCGCCCACGTGACT
AGTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTT
TCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGCTAGAGCAGC
TTGAGCTTGGATCAGATTGTCGTTTCCCGCCTTCAGTTTAAACTATCAGTGTTTGACAGGATATATTGGCGGGTAAACCTAAGAGA
AAAGAGCGTTTA

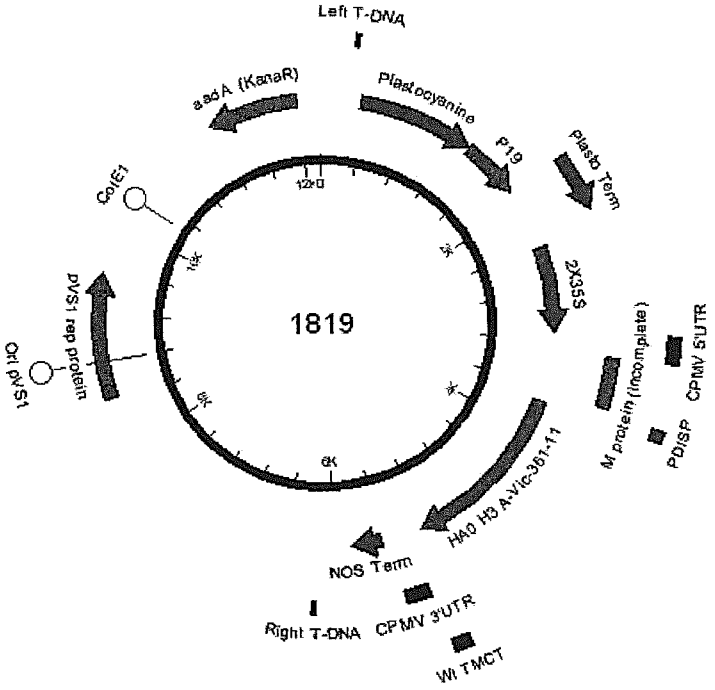
Figure 45E

Expression cassette number 1819 from 2X35S promoter to NOS terminator. PDISP/H3 Victoria nucleotide sequence is underlined. (SEQ ID NO: 126)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTT
TCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAG
GTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCC
CCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCA
CGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATAT
CCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGC
CATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCAT
CGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAAT

CCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAA
AAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTG
CGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTG
TGGACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCTGGAGG
CTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTTGACGAGGTATT
GTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGAAACAGAGTTTTCCCGTGGT
TTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCAATACCGCGGAGAAAATGGCGAAAAA
CGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCCAAAAACTTCCTGGAAATGACAACA
GCACGGCAACGCTGTGCCTTGGGCACCATGCAGTACCAAACGGAACGATAGTGAAAACAATCACGAATGACCAAATTGAAGTTACT
AATGCTACTGAGCTGGTTCAGAATTCCTCAATAGGTGAAATATGCGACAGTCCTCATCAGATCCTTGATGGAGAAAACTGCACACT
AATAGATGCTCTATTGGGAGACCCTCAGTGTGATGGCTTCCAAAATAAGAAATGGGACCTTTTTGTTGAACGAAGCAAAGCCTACA
GCAACTGTTACCCTTATGATGTGCCGGATTATGCCTCCCTTAGGTCACTAGTTGCCTCATCCGGCACACTGGAGTTTAACAATGAA
AGCTTCAATTGGACTGGAGTCACTCAAAACGGAACAAGTTCTGCTTGCATAAGGAGATCTAATAATAGTTTCTTTAGTAGATTAAA
TTGGTTGACCCACTTAAACTTCAAATACCCAGCATTGAACGTGACTATGCCAAACAATGAACAATTTGACAAATTGTACATTTGGG
GGGTTCACCACCCGGGTACGGACAAGGACCAAATCTTCCTGTATGCTCAATCATCAGGAAGAATCACAGTATCTACCAAAAGAAGC
CAACAAGCTGTAATCCCGAATATCGGATCTAGACCCAGAATAAGGAATATCCCTAGCAGAATAAGCATCTATTGGACAATAGTAAA
ACCGGGAGACATACTTTTGATTAACAGCACAGGGAATCTAATTGCTCCTAGGGGTTACTTCAAAATACGAAGTGGGAAAAGCTCAA
TAATGAGATCAGATGCACCCATTGGCAAATGCAATTCTGAATGCATCACTCCAAATGGAAGCATTCCCAATGACAAACCATTCCAA
AATGTAAACAGGATCACATACGGGGCCTGTCCCAGATATGTTAAGCAAAGCACTCTGAAATTGGCAACAGGAATGCGAAATGTACC
AGAGAAACAAACTAGAGGCATATTTGGCGCAATAGCGGGTTTCATAGAAAATGGTTGGGAGGGAATGGTGGATGGTTGGTACGGTT
TCAGGCATCAAAATTCTGAGGGAAGAGGACAAGCAGCAGATCTCAAAAGCACTCAAGCAGCAATCGATCAAATCAATGGGAAGCTG
AATCGATTGATCGGGAAAACCAACGAGAAATTCCATCAGATTGAAAAAGAATTCTCAGAAGTCGAAGGGAGAATTCAGGACCTTGA
GAAATATGTTGAGGACACTAAAATAGATCTCTGGTCATACAACGCGGAGCTTCTTGTTGCCCTGGAGAACCAACATACAATTGATC
TAACTGACTCAGAAATGAACAAACTGTTTGAAAAAACAAAGAAGCAACTAAGGGAAAATGCTGAGGATATGGGCAATGGTTGTTTC
AAAATATACCACAAATGTGACAATGCCTGCATAGGATCAATCAGAAATGGAACTTATGACCACGATGTATACAGAGATGAAGCATT
AAACAACCGGTTCCAGATCAAGGGAGTTGAGCTGAAGTCAGGGTACAAAGATTGGATCCTATGGATTTCCTTTGCCATATCATGTT
TTTTGCTTTGTGTTGCTTTGTTGGGGTTCATCATGTGGGCCTGCCAAAAGGGCAACATTAGGTGCAACATTTGCATTTGAAGGCCT
ATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTT
ATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAA
AAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGA
ATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACG
TTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTA
GGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 45F
Schematic representation of construct number 1819



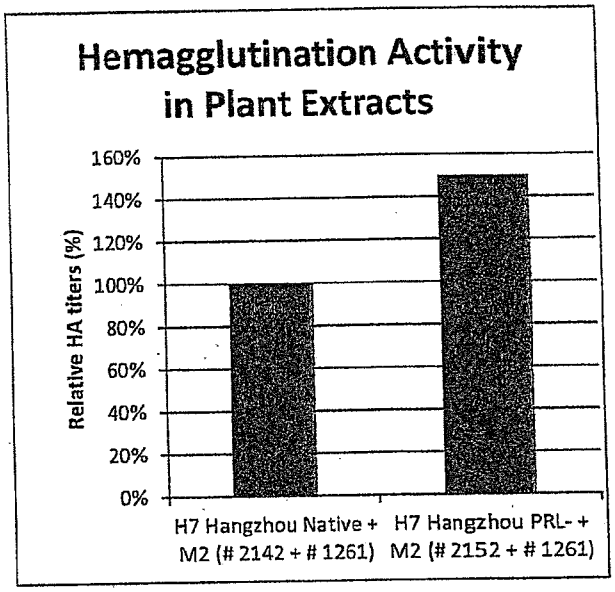
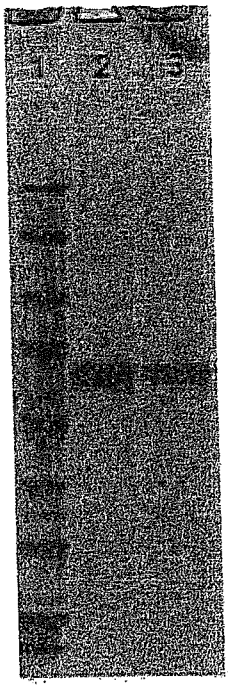


Figure 46A

Figure 46C



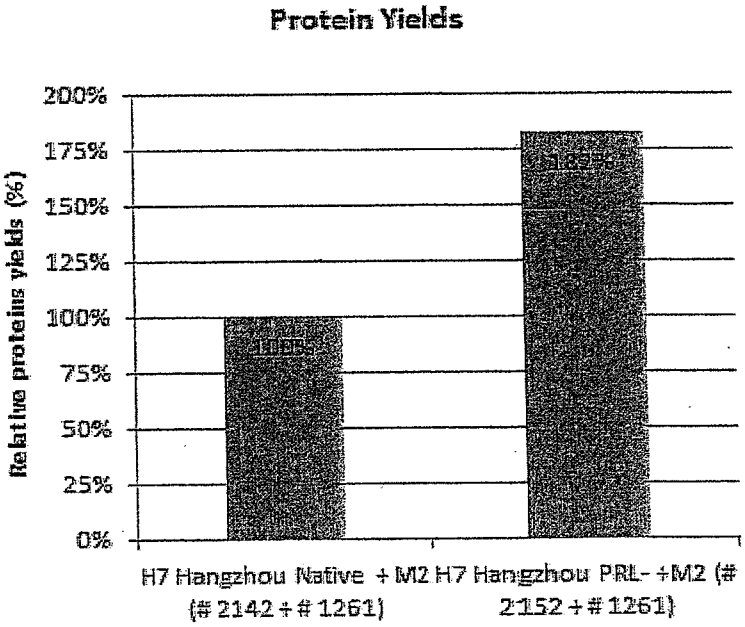


Figure 46B

Fig. 47A

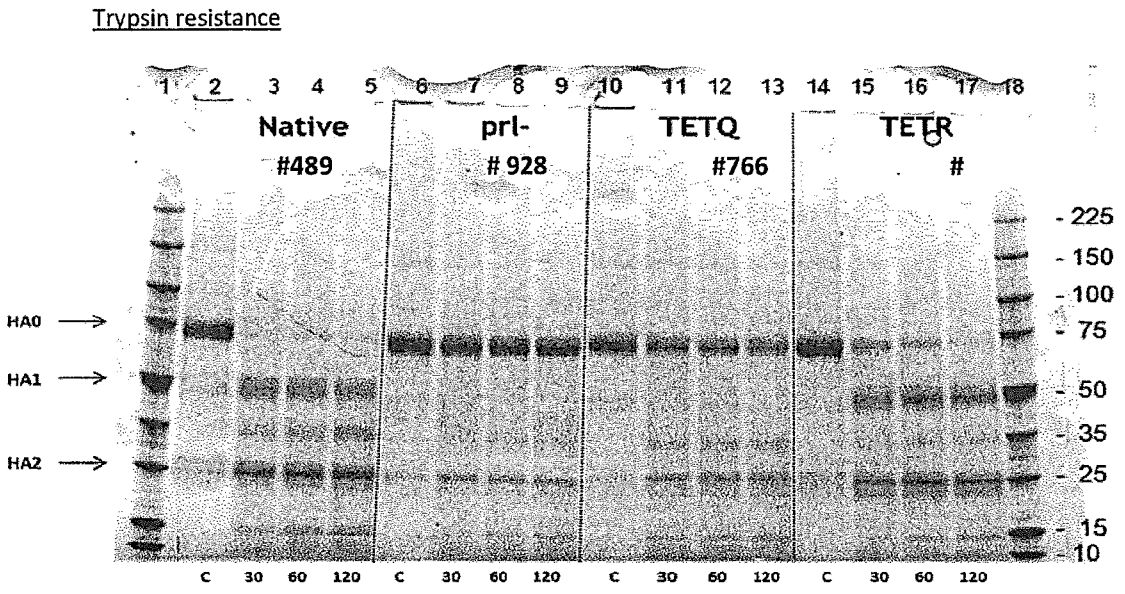
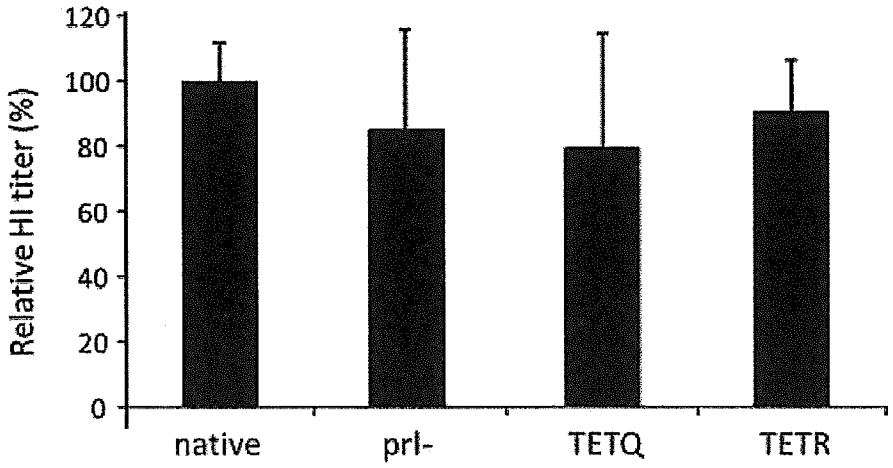


Fig. 47B



2X35S/CPMV HT+/ PDISP/H2 Singapore/ NOS (Construct number 2220)

Figure 48A, SEQ ID NO: 127

IF**-H2S157.s1-6r

ACTAAAGAAAATAGGCCTTCATATGCAGATCCTGCACTGCAGAGACCCGT

Figure 48B, SEQ ID NO: 128

Nucleotide sequence of PDISP/H2 Singapore.

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGACCAAA
TATGCATTGGATACCATGCCAATAATTCCACAGAGAAGGTCGACACAATTCTAGAGCGGAACGTCACTGTGACTCATGC
CAAGGACATTCTTGAGAAGACCCATAACGGAAAGTTATGCAAACTAAACGGAATCCCTCCACTTGAACTAGGGGACTGT
AGCATTGCCGGATGGCTCCTTGGAAATCCAGAATGTGATAGGCTTCTAAGTGTGCCAGAATGGTCCTATATAATGGAGA
AAGAAAACCCGAGAGACGGTTTGTGTTATCCAGGCAGCTTCAATGATTATGAAGAATTGAAACATCTCCTCAGCAGCGT
GAAACATTTCGAGAAAGTAAAGATTCTGCCCAAAGATAGATGGACACAGCATACAACAACTGGAGGTTCACGGGCCTGC
GCGGTGTCTGGTAATCCATCATTCTTCAGGAACATGGTCTGGCTGACAAAGAAAGAATCAAATTATCCGGTTGCCAAAG
GATCGTACAACAATACAAGCGGAGAACAAATGCTAATAATTTGGGGGGTGCACCATCCCAATGATGAGACAGAACAAAG
AACATTGTACCAGAATGTGGGAACCTATGTTTCCGTAGGCACATCAACATTGAACAAAAGGTCAACCCCAGACATAGCA
ACAAGGCCTAAAGTGAATGGACTAGGAAGTAGAATGGAGTTCTCTTGGACCCTATTGGATATGTGGGACACCATAAATT
TTGAGAGTACTGGTAATCTAATTGCACCAGAGTATGGATTCAAAATATCGAAAAGAGGTAGTTCAGGGATCATGAAAAC
AGAAGGAACACTTGAGAACTGTGAGACCAAATGCCAAACTCCTTTGGGAGCAATAAATACAACATTGCCTTTTCACAAT
GTCCACCCACTGACAATAGGTGAGTGCCCCAAATATGTAAAATCGGAGAAGTTGGTCTTAGCAACAGGACTAAGGAATG
TTCCCCAGATTGAATCAAGAGGATTGTTTGGGGCAATAGCTGGTTTTATAGAAGGAGGATGGCAAGGAATGGTTGATGG
TTGGTATGGATACCATCACAGCAATGACCAGGGATCAGGGTATGCAGCAGACAAAGAATCCACTCAAAAGGCATTTGAT
GGAATCACCAACAAGGTAAATTCTGTGATTGAAAAGATGAACACCCAATTTGAAGCTGTTGGGAAAGAGTTCAGTAACT
TAGAGAGAAGACTGGAGAACTTGAACAAAAAGATGGAAGACGGGTTTCTAGATGTGTGGACATACAATGCTGAGCTTCT
AGTTCTGATGGAAAATGAGAGGACACTTGACTTTCATGATTCTAATGTCAAGAATCTGTATGATAAAGTCAGAATGCAG
CTGAGAGACAACGTCAAAGAACTAGGAAATGGATGTTTTGAATTTTATCACAAATGTGATGATGAATGCATGAATAGTG
TGAAAAACGGGACGTATGATTATCCCAAGTATGAAGAAGAGTCTAAACTAAATAGAAATGAAATCAAAGGGGTAAAATT
GAGCAGCATGGGGGTTTATCAAATCCTTGCCATTTATGCTACAGTAGCAGGTTCTCTGTCACTGGCAATCATGATGGCT
GGGATCTCTTTCTGGATGTGCTCCAACGGGTCTCTGCAGTGCAGGATCTGCATATGA

Figure 48C, SEQ ID NO: 129

Expression cassette number 2220 from 2X35S promoter to NOS terminator. PDISP/H2 Singapore nucleotide sequence is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTG
AGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGAT
AGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGAC
AGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAG
TGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCA
AAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTT
ATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATG
CCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTC
TTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCT
TCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAA
ACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGA
TCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTG
GACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCT
GGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCT
TGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGA

AACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCC
AATACCGCGGAGAAAATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGA
TCTTCGCGGACCAAATATGCATTGGATACCATGCCAATAATTCCACAGAGAAGGTCGACACAATTCTAGAGCGGAACGT
CACTGTGACTCATGCCAAGGACATTCTTGAGAAGACCCATAACGGAAAGTTATGCAAACTAAACGGAATCCCTCCACTT
GAACTAGGGGACTGTAGCATTGCCGGATGGCTCCTTGGAAATCCAGAATGTGATAGGCTTCTAAGTGTGCCAGAATGGT
CCTATATAATGGAGAAAGAAAACCCGAGAGACGGTTTGTGTTATCCAGGCAGCTTCAATGATTATGAAGAATTGAAACA
TCTCCTCAGCAGCGTGAAACATTTCGAGAAAGTAAAGATTCTGCCCAAAGATAGATGGACACAGCATACAACAACTGGA
GGTTCACGGGCCTGCGCGGTGTCTGGTAATCCATCATTCTTCAGGAACATGGTCTGGCTGACAAAGAAAGAATCAAATT
ATCCGGTTGCCAAAGGATCGTACAACAATACAAGCGGAGAACAAATGCTAATAATTTGGGGGGTGCACCATCCCAATGA
TGAGACAGAACAAAGAACATTGTACCAGAATGTGGGAACCTATGTTTCCGTAGGCACATCAACATTGAACAAAAGGTCA
ACCCCAGACATAGCAACAAGGCCTAAAGTGAATGGACTAGGAAGTAGAATGGAGTTCTCTTGGACCCTATTGGATATGT
GGGACACCATAAATTTTGAGAGTACTGGTAATCTAATTGCACCAGAGTATGGATTCAAAATATCGAAAAGAGGTAGTTC
AGGGATCATGAAAACAGAAGGAACACTTGAGAACTGTGAGACCAAATGCCAAACTCCTTTGGGAGCAATAAATACAACA
TTGCCTTTTCACAATGTCCACCCACTGACAATAGGTGAGTGCCCCAAATATGTAAAATCGGAGAAGTTGGTCTTAGCAA
CAGGACTAAGGAATGTTCCCCAGATTGAATCAAGAGGATTGTTTGGGGCAATAGCTGGTTTTATAGAAGGAGGATGGCA
AGGAATGGTTGATGGTTGGTATGGATACCATCACAGCAATGACCAGGGATCAGGGTATGCAGCAGACAAAGAATCCACT
CAAAAGGCATTTGATGGAATCACCAACAAGGTAAATTCTGTGATTGAAAAGATGAACACCCAATTTGAAGCTGTTGGGA
AAGAGTTCAGTAACTTAGAGAGAAGACTGGAGAACTTGAACAAAAAGATGGAAGACGGGTTTCTAGATGTGTGGACATA
CAATGCTGAGCTTCTAGTTCTGATGGAAAATGAGAGGACACTTGACTTTCATGATTCTAATGTCAAGAATCTGTATGAT
AAAGTCAGAATGCAGCTGAGAGACAACGTCAAAGAACTAGGAAATGGATGTTTTGAATTTTATCACAAATGTGATGATG
AATGCATGAATAGTGTGAAAAACGGGACGTATGATTATCCCAAGTATGAAGAAGAGTCTAAACTAAATAGAAATGAAAT
CAAAGGGGTAAAATTGAGCAGCATGGGGGTTTATCAAATCCTTGCCATTTATGCTACAGTAGCAGGTTCTCTGTCACTG
GCAATCATGATGGCTGGGATCTCTTTCTGGATGTGCTCCAACGGGTCTCTGCAGTGCAGGATCTGCATATGAAGGCCTA
TTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTT
TATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAAT
TTTATTAAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCA
ATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCAT
GTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAAT
ACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

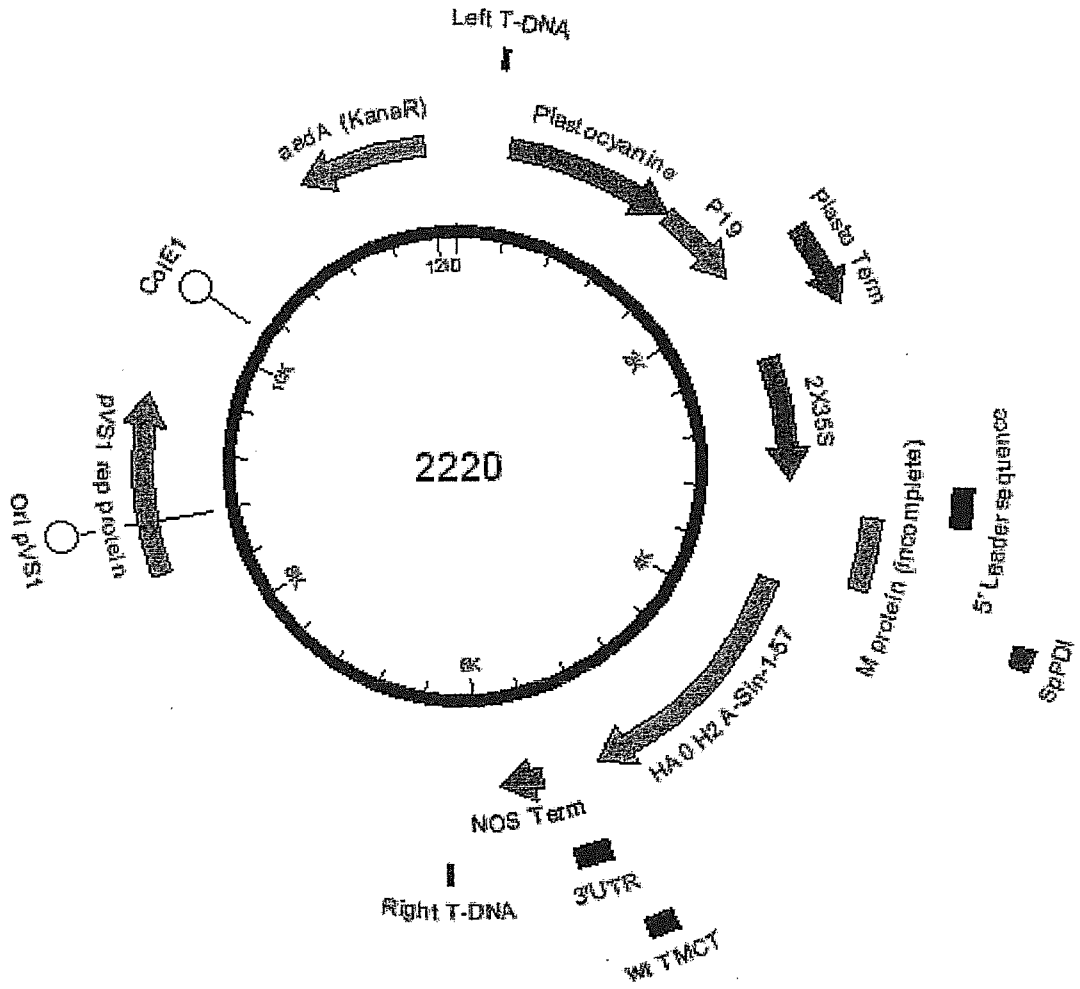
Figure 48D, SEQ ID NO: 130

Amino acid sequence of PDISP/H2 Singapore

MAKNVAIFGLLFSLLVLVPSQIFADQICIGYHANNSTEKVDTILERNVTVTHAKDILEKTHNGKLCKLNGIPPLELGDC
SIAGWLLGNPECDRLLSVPEWSYIMEKENPRDGLCYPGSFNDYEELKHLLSSVKHFEKVKILPKDRWTQHTTTGGSRAC
AVSGNPSFFRNMVWLTKKESNYPVAKGSYNNTSGEQMLIIWGVHHPNDETEQRTLYQNVGTYVSVGTSTLNKRSTPDIA
TRPKVNGLGSRMEFSWTLLDMWDTINFESTGNLIAPEYGFKISKRGSSGIMKTEGTLENCETKCQTPLGAINTTLPFHN
VHPLTIGECPKYVKSEKLVLATGLRNVPQIESRGLFGAIAGFIEGGWQGMVDGWYGYHHSNDQGSGYAADKESTQKAFD
GITNKVNSVIEKMNTQFEAVGKEFSNLERRLENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQ
LRDNVKELGNGCFEFYHKCDDECMNSVKNGTYDYPKYEEESKLNRNEIKGVKLSSMGVYQILAIYATVAGSLSLAIMMA
GISFWMCSNGSLQCRICI*

Figure 48E

Schematic representation of construct number 2220



2X35S/CPMV HT+/ PDISP/H2 Singapore with deleted proteolytic loop/ NOS (Construct number 2221)

Figure 49A, SEQ ID NO: 131

H2S157(Prl-).r

TGCCATCCTCCGCCGGGAACATTCCTTAGTCCTGTTGCTAAGACCAAC

Figure 49B, SEQ ID NO: 132

H2S157(Prl-).c

AGGAATGTTCCCGGCGGAGGATGGCAAGGAATGGTTGATGGTTGGTATGG

Figure 49C, SEQ ID NO: 133

Expression cassette number 2221 from 2X35S promoter to NOS terminator. PDISP/H2 Singapore with deleted proteolytic loop nucleotide sequence is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTG
AGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGAT
AGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGAC
AGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAG
TGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCA
AAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTT
ATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATG
CCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTC
TTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCT
TCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAA
ACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGA

TCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTG
GACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCT
GGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCT
TGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGA
AACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCC
AATACCGCGGAGAAAATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGA
TCTTCGCGGACCAAATATGCATTGGATACCATGCCAATAATTCCACAGAGAAGGTCGACACAATTCTAGAGCGGAACGT
CACTGTGACTCATGCCAAGGACATTCTTGAGAAGACCCATAACGGAAAGTTATGCAAACTAAACGGAATCCCTCCACTT
GAACTAGGGGACTGTAGCATTGCCGGATGGCTCCTTGGAAATCCAGAATGTGATAGGCTTCTAAGTGTGCCAGAATGGT
CCTATATAATGGAGAAAGAAAACCCGAGAGACGGTTTGTGTTATCCAGGCAGCTTCAATGATTATGAAGAATTGAAACA
TCTCCTCAGCAGCGTGAAACATTTCGAGAAAGTAAAGATTCTGCCCAAAGATAGATGGACACAGCATACAACAACTGGA
GGTTCACGGGCCTGCGCGGTGTCTGGTAATCCATCATTCTTCAGGAACATGGTCTGGCTGACAAAGAAAGAATCAAATT
ATCCGGTTGCCAAAGGATCGTACAACAATACAAGCGGAGAACAAATGCTAATAATTTGGGGGGTGCACCATCCCAATGA
TGAGACAGAACAAAGAACATTGTACCAGAATGTGGGAACCTATGTTTCCGTAGGCACATCAACATTGAACAAAAGGTCA
ACCCCAGACATAGCAACAAGGCCTAAAGTGAATGGACTAGGAAGTAGAATGGAGTTCTCTTGGACCCTATTGGATATGT
GGGACACCATAAATTTTGAGAGTACTGGTAATCTAATTGCACCAGAGTATGGATTCAAAATATCGAAAAGAGGTAGTTC
AGGGATCATGAAAACAGAAGGAACACTTGAGAACTGTGAGACCAAATGCCAAACTCCTTTGGGAGCAATAAATACAACA
TTGCCTTTTCACAATGTCCACCCACTGACAATAGGTGAGTGCCCCAAATATGTAAAATCGGAGAAGTTGGTCTTAGCAA
CAGGACTAAGGAATGTTCCCGGCGGAGGATGGCAAGGAATGGTTGATGGTTGGTATGGATACCATCACAGCAATGACCA
GGGATCAGGGTATGCAGCAGACAAAGAATCCACTCAAAAGGCATTTGATGGAATCACCAACAAGGTAAATTCTGTGATT
GAAAAGATGAACACCCAATTTGAAGCTGTTGGGAAAGAGTTCAGTAACTTAGAGAGAAGACTGGAGAACTTGAACAAAA
AGATGGAAGACGGGTTTCTAGATGTGTGGACATACAATGCTGAGCTTCTAGTTCTGATGGAAAATGAGAGGACACTTGA
CTTTCATGATTCTAATGTCAAGAATCTGTATGATAAAGTCAGAATGCAGCTGAGAGACAACGTCAAAGAACTAGGAAAT
GGATGTTTTGAATTTTATCACAAATGTGATGATGAATGCATGAATAGTGTGAAAAACGGGACGTATGATTATCCCAAGT
ATGAAGAAGAGTCTAAACTAAATAGAAATGAAATCAAAGGGGTAAAATTGAGCAGCATGGGGGTTTATCAAATCCTTGC
CATTTATGCTACAGTAGCAGGTTCTCTGTCACTGGCAATCATGATGGCTGGGATCTCTTTCTGGATGTGCTCCAACGGG
TCTCTGCAGTGCAGGATCTGCATATGAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATG
TTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGT
CGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAG
CTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGAT
TATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTT
TTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTAT
CGCGCGCGGTGTCATCTATGTTACTAGAT

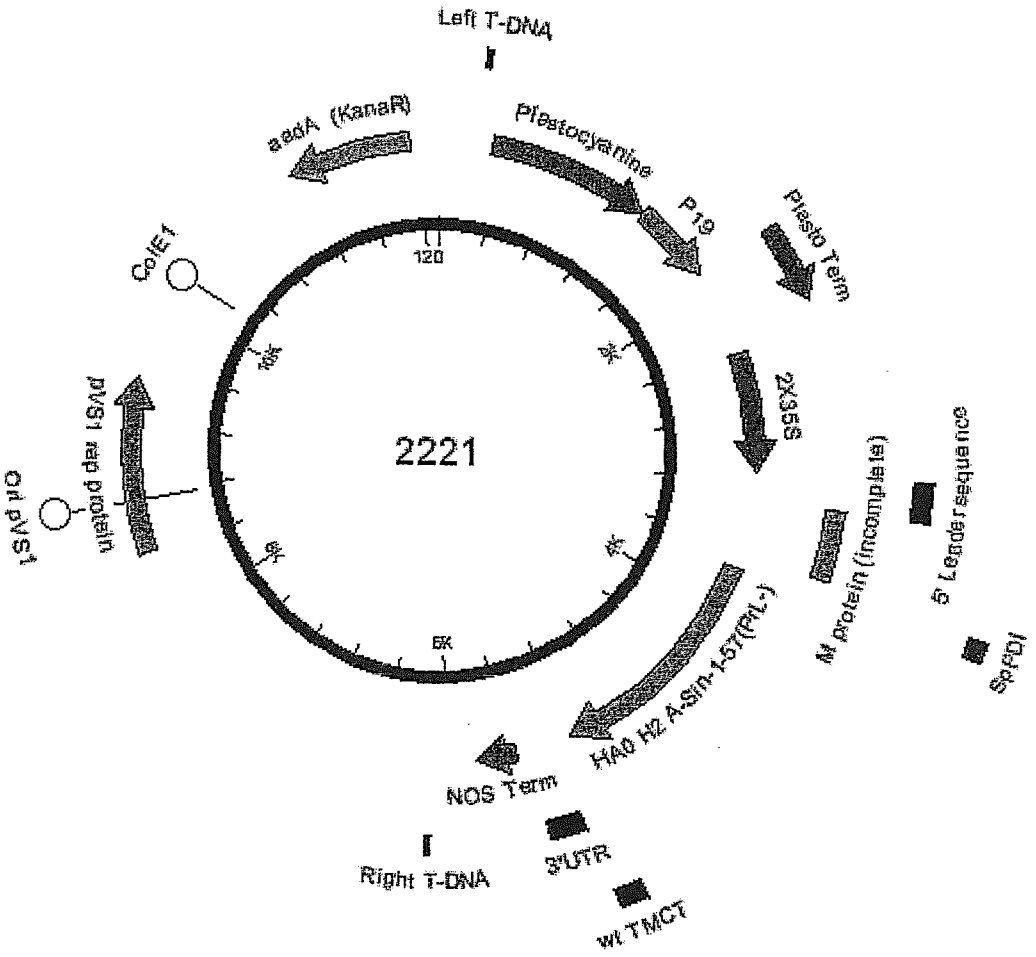
Figure 49D, SEQ ID NO: 134

Amino acid sequence of PDISP/H2 Singapore with deleted proteolytic loop

MAKNVAIFGLLFSLLVLVPSQIFADQICIGYHANNSTEKVDTILERNVTVTHAKDILEKTHNGKLCKLNGIPPLELGDCSIAGWLLGNPECD
RLLSVPEWSYIMEKENPRDGLCYPGSFNDYEELKHLLSSVKHFEKVKILPKDRWTQHTTTGGSRACAVSGNPSFFRNMVWLTKKESNYP
VAKGSYNNTSGEQMLIIWGVHHPNDETEQRTLYQNVGTYVSVGTSTLNKRSTPDIATRPKVNGLGSRMEFSWTLLDMWDTINFESTG
NLIAPEYGFKISKRGSSGIMKTEGTLENCETKCQTPLGAINTTLPFHNVHPLTIGECPKYVKSEKLVLATGLRNVPGGGWQGMVDGWYG
YHHSNDQGSGYAADKESTQKAFDGITNKVNSVIEKMNTQFEAVGKEFSNLERRLENLNKKMEDGFLDVWTYNAELLVLMENERTLDF
HDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMNSVKNGTYDYPKYEEESKLNRNEIKGVKLSSMGVYQILAIYATVAGSLSL
AIMMAGISFWMCSNGSLQCRICI*

Figure 49E

Schematic representation of construct number 2221



PDISP/H2 Singapore (Construct number 2222) and PDISP/H2 Singapore with deleted proteolytic loop (Construct number 2223) in 2X35S/CPMV 160+/NOS expression system

Figure 50A, SEQ ID NO: 135

Expression cassette number 2222 from 2X35S promoter to NOS terminator. PDISP/H2 Singapore nucleotide sequence is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTG
AGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGAT
AGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGAC
AGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAG
TGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCA
AAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTT
ATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATG
CCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTC
TTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCT
TCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAA
ACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGA
TCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAGGGCCCAATACCGCGGAGAAAATGGCGAAAAACGTTGCGAT
TTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGACCAAATATGCATTGGATACCATGCC
AATAATTCCACAGAGAAGGTCGACACAATTCTAGAGCGGAACGTCACTGTGACTCATGCCAAGGACATTCTTGAGAAGA
CCCATAACGGAAAGTTATGCAAACTAAACGGAATCCCTCCACTTGAACTAGGGGACTGTAGCATTGCCGGATGGCTCCT
TGGAAATCCAGAATGTGATAGGCTTCTAAGTGTGCCAGAATGGTCCTATATAATGGAGAAAGAAAACCCGAGAGACGGT
TTGTGTTATCCAGGCAGCTTCAATGATTATGAAGAATTGAAACATCTCCTCAGCAGCGTGAAACATTTCGAGAAAGTAA
AGATTCTGCCCAAAGATAGATGGACACAGCATACAACAACTGGAGGTTCACGGGCCTGCGCGGTGTCTGGTAATCCATC
ATTCTTCAGGAACATGGTCTGGCTGACAAAGAAAGAATCAAATTATCCGGTTGCCAAAGGATCGTACAACAATACAAGC
GGAGAACAAATGCTAATAATTTGGGGGGTGCACCATCCCAATGATGAGACAGAACAAAGAACATTGTACCAGAATGTGG
GAACCTATGTTTCCGTAGGCACATCAACATTGAACAAAAGGTCAACCCCAGACATAGCAACAAGGCCTAAAGTGAATGG
ACTAGGAAGTAGAATGGAGTTCTCTTGGACCCTATTGGATATGTGGGACACCATAAATTTTGAGAGTACTGGTAATCTA

ATTGCACCAGAGTATGGATTCAAAATATCGAAAAGAGGTAGTTCAGGGATCATGAAAACAGAAGGAACACTTGAGAACT
GTGAGACCAAATGCCAAACTCCTTTGGGAGCAATAAATACAACATTGCCTTTTCACAATGTCCACCCACTGACAATAGG
TGAGTGCCCCAAATATGTAAAATCGGAGAAGTTGGTCTTAGCAACAGGACTAAGGAATGTTCCCCAGATTGAATCAAGA
GGATTGTTTGGGGCAATAGCTGGTTTTATAGAAGGAGGATGGCAAGGAATGGTTGATGGTTGGTATGGATACCATCACA
GCAATGACCAGGGATCAGGGTATGCAGCAGACAAAGAATCCACTCAAAAGGCATTTGATGGAATCACCAACAAGGTAAA
TTCTGTGATTGAAAAGATGAACACCCAATTTGAAGCTGTTGGGAAAGAGTTCAGTAACTTAGAGAGAAGACTGGAGAAC
TTGAACAAAAAGATGGAAGACGGGTTTCTAGATGTGTGGACATACAATGCTGAGCTTCTAGTTCTGATGGAAAATGAGA
GGACACTTGACTTTCATGATTCTAATGTCAAGAATCTGTATGATAAAGTCAGAATGCAGCTGAGAGACAACGTCAAAGA
ACTAGGAAATGGATGTTTTGAATTTTATCACAAATGTGATGATGAATGCATGAATAGTGTGAAAAACGGGACGTATGAT
TATCCCAAGTATGAAGAAGAGTCTAAACTAAATAGAAATGAAATCAAAGGGGTAAAATTGAGCAGCATGGGGGTTTATC
AAATCCTTGCCATTTATGCTACAGTAGCAGGTTCTCTGTCACTGGCAATCATGATGGCTGGGATCTCTTTCTGGATGTG
CTCCAACGGGTCTCTGCAGTGCAGGATCTGCATATGAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTG
CATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTG
TTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATT
CGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTC
TTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTAT
GAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAG
GATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 50B, SEQ ID NO: 136

Expression cassette number 2223 from 2X35S promoter to NOS terminator. PDISP/H2 Singapore with deleted proteolytic loop nucleotide sequence is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTG
AGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGAT
AGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGAC
AGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAG
TGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCA
AAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTT
ATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATG
CCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTC
TTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCT
TCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAA
ACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGA
TCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAGGGCCCAATACCGCGGAGAAAATGGCGAAAAACGTTGCGAT
TTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGACCAAATATGCATTGGATACCATGCC
AATAATTCCACAGAGAAGGTCGACACAATTCTAGAGCGGAACGTCACTGTGACTCATGCCAAGGACATTCTTGAGAAGA
CCCATAACGGAAAGTTATGCAAACTAAACGGAATCCCTCCACTTGAACTAGGGGACTGTAGCATTGCCGGATGGCTCCT
TGGAAATCCAGAATGTGATAGGCTTCTAAGTGTGCCAGAATGGTCCTATATAATGGAGAAAGAAAACCCGAGAGACGGT
TTGTGTTATCCAGGCAGCTTCAATGATTATGAAGAATTGAAACATCTCCTCAGCAGCGTGAAACATTTCGAGAAAGTAA
AGATTCTGCCCAAAGATAGATGGACACAGCATACAACAACTGGAGGTTCACGGGCCTGCGCGGTGTCTGGTAATCCATC
ATTCTTCAGGAACATGGTCTGGCTGACAAAGAAAGAATCAAATTATCCGGTTGCCAAAGGATCGTACAACAATACAAGC
GGAGAACAAATGCTAATAATTTGGGGGGTGCACCATCCCAATGATGAGACAGAACAAAGAACATTGTACCAGAATGTGG
GAACCTATGTTTCCGTAGGCACATCAACATTGAACAAAAGGTCAACCCCAGACATAGCAACAAGGCCTAAAGTGAATGG
ACTAGGAAGTAGAATGGAGTTCTCTTGGACCCTATTGGATATGTGGGACACCATAAATTTTGAGAGTACTGGTAATCTA
ATTGCACCAGAGTATGGATTCAAAATATCGAAAAGAGGTAGTTCAGGGATCATGAAAACAGAAGGAACACTTGAGAACT
GTGAGACCAAATGCCAAACTCCTTTGGGAGCAATAAATACAACATTGCCTTTTCACAATGTCCACCCACTGACAATAGG
TGAGTGCCCCAAATATGTAAAATCGGAGAAGTTGGTCTTAGCAACAGGACTAAGGAATGTTCCCGGCGGAGGATGGCAA
GGAATGGTTGATGGTTGGTATGGATACCATCACAGCAATGACCAGGGATCAGGGTATGCAGCAGACAAAGAATCCACTC
AAAAGGCATTTGATGGAATCACCAACAAGGTAAATTCTGTGATTGAAAAGATGAACACCCAATTTGAAGCTGTTGGGAA
AGAGTTCAGTAACTTAGAGAGAAGACTGGAGAACTTGAACAAAAAGATGGAAGACGGGTTTCTAGATGTGTGGACATAC
AATGCTGAGCTTCTAGTTCTGATGGAAAATGAGAGGACACTTGACTTTCATGATTCTAATGTCAAGAATCTGTATGATA
AAGTCAGAATGCAGCTGAGAGACAACGTCAAAGAACTAGGAAATGGATGTTTTGAATTTTATCACAAATGTGATGATGA
ATGCATGAATAGTGTGAAAAACGGGACGTATGATTATCCCAAGTATGAAGAAGAGTCTAAACTAAATAGAAATGAAATC

AAAGGGGTAAAATTGAGCAGCATGGGGGTTTATCAAATCCTTGCCATTTATGCTACAGTAGCAGGTTCTCTGTCACTGG
CAATCATGATGGCTGGGATCTCTTTCTGGATGTGCTCCAACGGGTCTCTGCAGTGCAGGATCTGCATATGAAGGCCTAT
TTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTT
ATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATT
TTATTAAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAA
TAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATG
TAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATA
CGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 50C

Schematic representation of construct number 2222

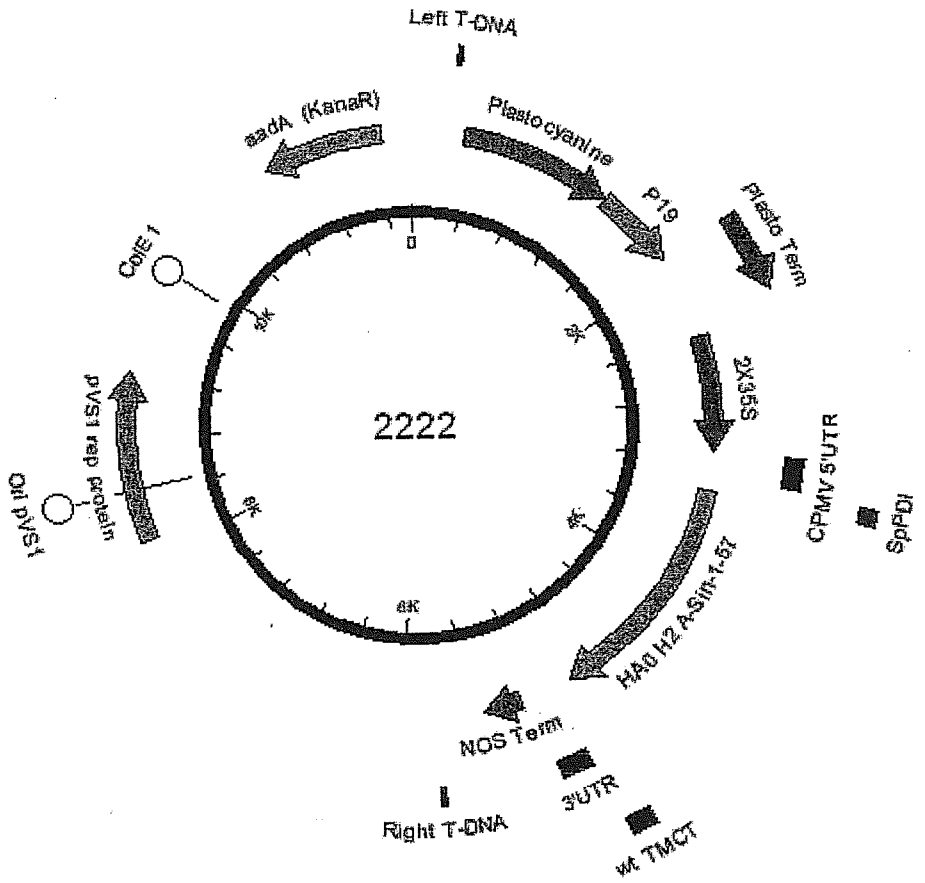
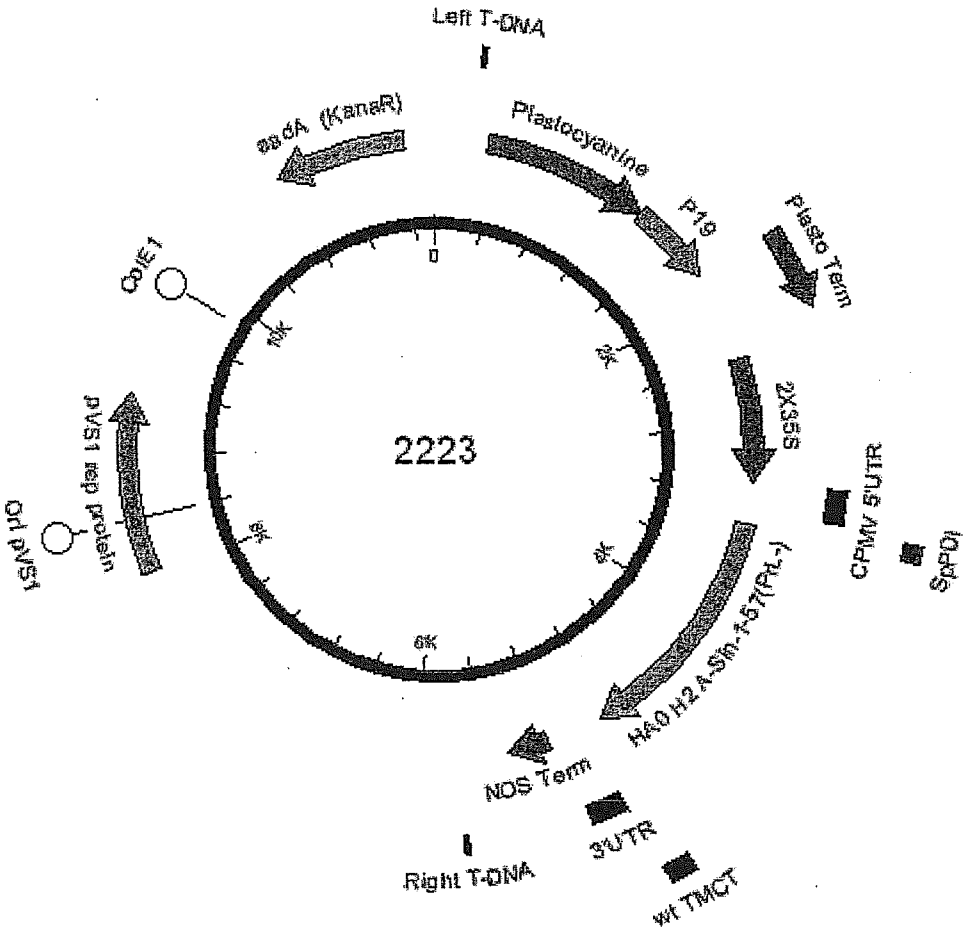


Figure 50D

Schematic representation of construct number 2223



2X35S/CPMV HT+ (construct no 2019) and 160+ (construct no 2139) for PDISP/H3 Perth

Figure 51A, SEQ ID NO: 137

Nucleotide sequence of PDISP/H3 Perth

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGCAAAAAC
TTCCTGGAAATGACAACAGCACGGCAACGCTGTGCCTTGGGCACCATGCAGTACCAAACGGAACGATAGTGAAAACAAT
CACGAATGACCAAATTGAAGTTACTAATGCTACTGAGCTGGTTCAGAGTTCCTCAACAGGTGAAATATGCGACAGTCCT
CATCAGATCCTTGATGGAAAAAACTGCACACTAATAGATGCTCTATTGGGAGACCCTCAGTGTGATGGCTTCCAAAATA
AGAAATGGGACCTTTTTGTTGAACGCAGCAAAGCCTACAGCAACTGTTACCCTTATGATGTGCCGGATTATGCCTCCCT
TAGGTCACTAGTTGCCTCATCCGGCACACTGGAGTTTAACAATGAAAGCTTCAATTGGACTGGAGTCACTCAAAACGGA
ACAAGCTCTGCTTGCATAAGGAGATCTAAAAACAGTTTCTTTAGTAGATTGAATTGGTTGACCCACTTAAACTTCAAAT
ACCCAGCATTGAACGTGACTATGCCAAACAATGAACAATTTGACAAATTGTACATTTGGGGGGTTCACCACCCGGGTAC
GGACAAAGACCAAATCTTCCTGTATGCTCAAGCATCAGGAAGAATCACAGTCTCTACCAAAAGAAGCCAACAAACCGTA
AGCCCGAATATCGGATCTAGACCCAGAGTAAGGAATATCCCTAGCAGAATAAGCATCTATTGGACAATAGTAAAACCGG
GAGACATACTTTTGATTAACAGCACAGGGAATCTAATTGCTCCTAGGGGTTACTTCAAAATACGAAGTGGGAAAAGCTC
AATAATGAGATCAGATGCACCCATTGGCAAATGCAATTCTGAATGCATCACTCCAAATGGAAGCATTCCCAATGACAAA
CCATTCCAAAATGTAAACAGGATCACATACGGGGCCTGTCCCAGATATGTTAAGCAAAACACTCTGAAATTGGCAACAG
GGATGCGAAATGTACCAGAGAAACAAACTAGAGGCATATTTGGCGCAATCGCGGGTTTCATAGAAAATGGTTGGGAGGG
AATGGTGGATGGTTGGTACGGTTTCAGGCATCAAAATTCTGAGGGAAGAGGACAAGCAGCAGATCTCAAAAGCACTCAA
GCAGCAATCGATCAAATCAATGGGAAGCTGAATAGATTGATCGGGAAAACCAACGAGAAATTCCATCAGATTGAAAAAG
AATTCTCAGAAGTCGAAGGGAGAATTCAGGACCTTGAGAAATATGTTGAGGACACTAAAATAGATCTCTGGTCATACAA
CGCGGAGCTTCTTGTTGCCCTGGAGAACCAACATACAATTGATCTAACTGACTCAGAAATGAACAAACTGTTTGAAAAA
ACAAAGAAGCAACTGAGGGAAAATGCTGAGGATATGGGCAATGGTTGTTTCAAAATATACCACAAATGTGACAATGCCT
GCATAGGATCAATCAGAAATGGAACTTATGACCACGATGTATACAGAGATGAAGCATTAAACAACCGGTTTCAGATCAA
GGGAGTTGAGCTGAAGTCAGGGTACAAAGATTGGATCCTATGGATTTCCTTTGCCATATCATGTTTTTTGCTTTGTGTT
GCTTTGTTGGGGTTCATCATGTGGGCCTGCCAAAAAGGCAACATTAGGTGCAACATTTGCATTTGA

Figure 51B, SEQ ID NO: 138

IF**-H3P1609.S1-6r

ACTAAAGAAAATAGGCCTTCAAATGCAAATGTTGCACCTAATGTTGCCTT

Figure 51C, SEQ ID NO: 139

Amino acid sequence of PDISP/H3 Perth

MAKNVAIFGLLFSLLVLVPSQIFAQKLPGNDNSTATLCLGHHAVPNGTIVKTITNDQIEVTNATELVQSSSTGEICDSP
HQILDGKNCTLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNESFNWTGVTQNG
TSSACIRRSKNSFFSRLNWLTHLNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKDQIFLYAQASGRITVSTKRSQQTV
SPNIGSRPRVRNIPSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGKSSIMRSDAPIGKCNSECITPNGSIPNDK
PFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGFIENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQ
AAIDQINGKLNRLIGKTNEKFHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEK
TKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTYDHDVYRDEALNNRFQIKGVELKSGYKDWILWISFAISCFLLCV
ALLGFIMWACQKGNIRCNICI*

Figure 51D

Schematic representation of construct number 2019

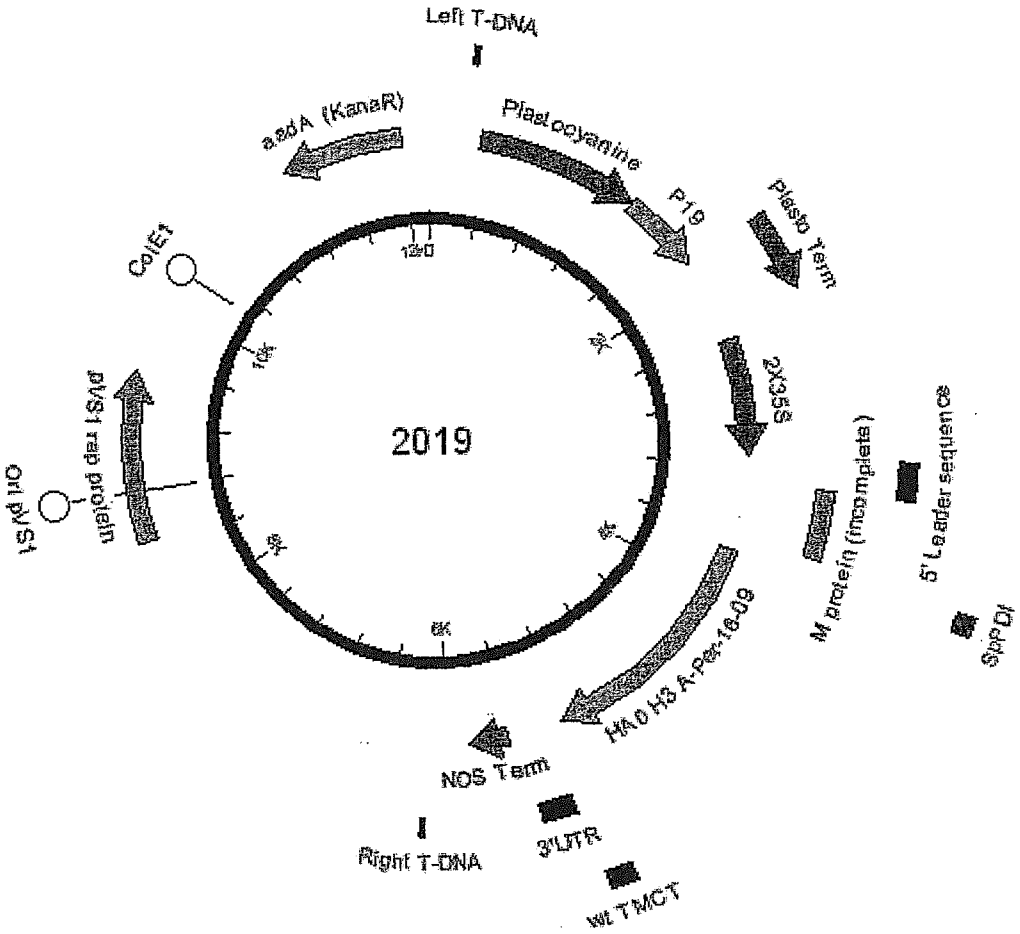
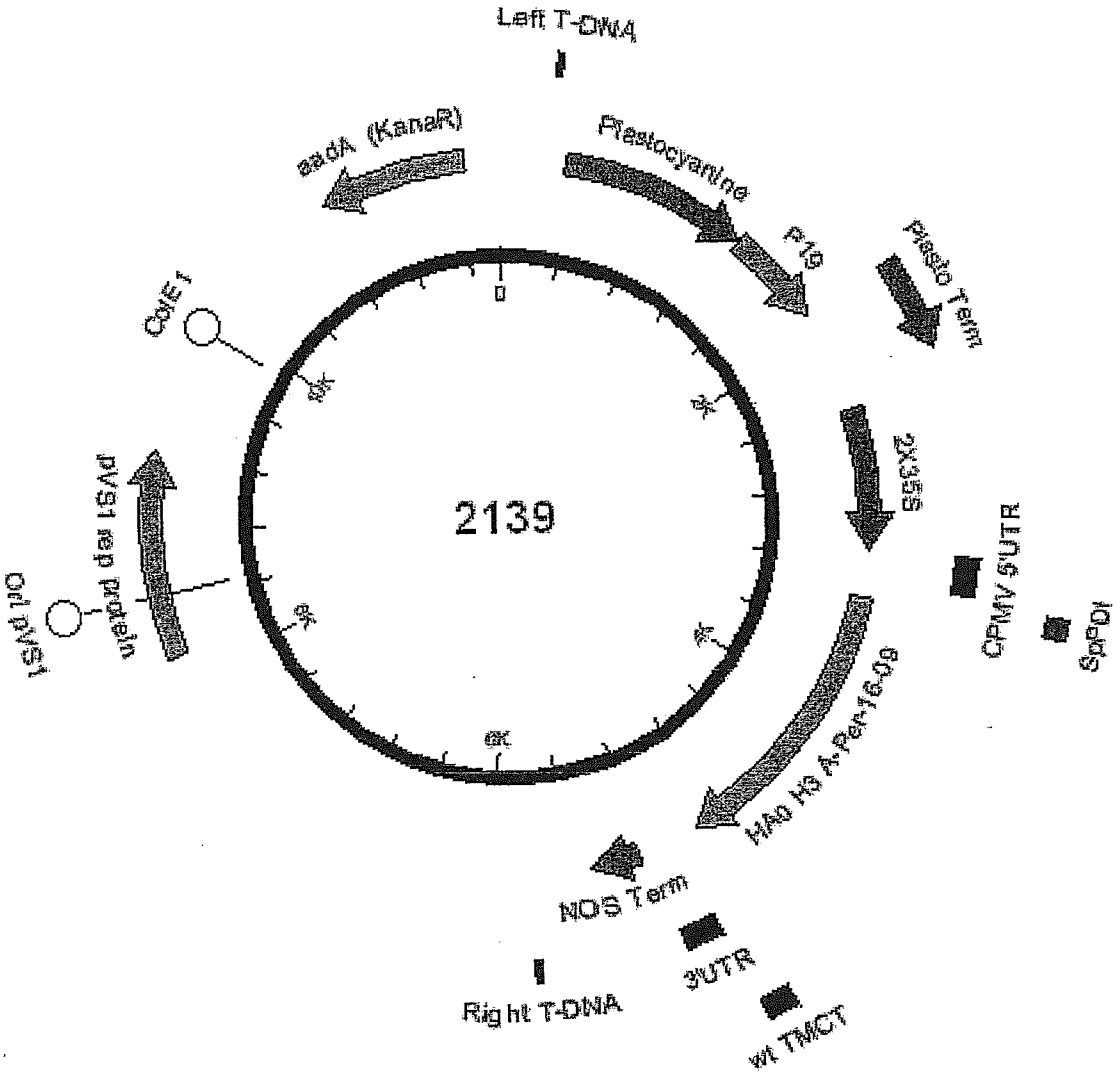


Figure 51E

Schematic representation of construct number 2139



2X35S/CPMV HT+ (construct no 2039) and 160+ (construct no 2159) for PDISP/H3 Perth with deleted proteolytic loop

Figure 52A, SEQ ID NO: 140

Nucleotide sequence of PDISP/H3 Perth with deleted proteolytic loop

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGCAAAAAC
TTCCTGGAAATGACAACAGCACGGCAACGCTGTGCCTTGGGCACCATGCAGTACCAAACGGAACGATAGTGAAAACAAT
CACGAATGACCAAATTGAAGTTACTAATGCTACTGAGCTGGTTCAGAGTTCCTCAACAGGTGAAATATGCGACAGTCCT
CATCAGATCCTTGATGGAAAAAACTGCACACTAATAGATGCTCTATTGGGAGACCCTCAGTGTGATGGCTTCCAAAATA
AGAAATGGGACCTTTTTGTTGAACGCAGCAAAGCCTACAGCAACTGTTACCCTTATGATGTGCCGGATTATGCCTCCCT
TAGGTCACTAGTTGCCTCATCCGGCACACTGGAGTTTAACAATGAAAGCTTCAATTGGACTGGAGTCACTCAAAACGGA
ACAAGCTCTGCTTGCATAAGGAGATCTAAAAACAGTTTCTTTAGTAGATTGAATTGGTTGACCCACTTAAACTTCAAAT
ACCCAGCATTGAACGTGACTATGCCAAACAATGAACAATTTGACAAATTGTACATTTGGGGGGTTCACCACCCGGGTAC
GGACAAAGACCAAATCTTCCTGTATGCTCAAGCATCAGGAAGAATCACAGTCTCTACCAAAAGAAGCCAACAAACCGTA
AGCCCGAATATCGGATCTAGACCCAGAGTAAGGAATATCCCTAGCAGAATAAGCATCTATTGGACAATAGTAAAACCGG
GAGACATACTTTTGATTAACAGCACAGGGAATCTAATTGCTCCTAGGGGTTACTTCAAAATACGAAGTGGGAAAAGCTC
AATAATGAGATCAGATGCACCCATTGGCAAATGCAATTCTGAATGCATCACTCCAAATGGAAGCATTCCCAATGACAAA
CCATTCCAAAATGTAAACAGGATCACATACGGGGCCTGTCCCAGATATGTTAAGCAAAACACTCTGAAATTGGCAACAG
GGATGCGAAATGTACCAGGCGGAGGTTGGGAGGGAATGGTGGATGGTTGGTACGGTTTCAGGCATCAAAATTCTGAGGG
AAGAGGACAAGCAGCAGATCTCAAAAGCACTCAAGCAGCAATCGATCAAATCAATGGGAAGCTGAATAGATTGATCGGG
AAAACCAACGAGAAATTCCATCAGATTGAAAAAGAATTCTCAGAAGTCGAAGGGAGAATTCAGGACCTTGAGAAATATG
TTGAGGACACTAAAATAGATCTCTGGTCATACAACGCGGAGCTTCTTGTTGCCCTGGAGAACCAACATACAATTGATCT
AACTGACTCAGAAATGAACAAACTGTTTGAAAAAACAAAGAAGCAACTGAGGGAAAATGCTGAGGATATGGGCAATGGT
TGTTTCAAAATATACCACAAATGTGACAATGCCTGCATAGGATCAATCAGAAATGGAACTTATGACCACGATGTATACA
GAGATGAAGCATTAAACAACCGGTTTCAGATCAAGGGAGTTGAGCTGAAGTCAGGGTACAAAGATTGGATCCTATGGAT
TTCCTTTGCCATATCATGTTTTTTGCTTTGTGTTGCTTTGTTGGGGTTCATCATGTGGGCCTGCCAAAAAGGCAACATT
AGGTGCAACATTTGCATTTGA

Figure 52B, SEQ ID NO: 141

H3P1609(Prl-)#2.r

CCCTCCCAACCTCCGCCTGGTACATTTCGCATCCCTGTTGCCAATTTC

Figure 52C, SEQ ID NO: 142

H3P1609(Prl-)#2.c

AATGTACCAGGCGGAGGTTGGGAGGGAATGGTGGATGGTTGGTACGGT

Figure 52D, SEQ ID NO: 143

Amino acid sequence of PDISP/H3 Perth with deleted proteolytic loop

MAKNVAIFGLLFSLLVLVPSQIFAQKLPGNDNSTATLCLGHHAVPNGTIVKTITNDQIEVTNATELVQSSSTGEICDSP
HQILDGKNCTLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNESFNWTGVTQNG
TSSACIRRSKNSFFSRLNWLTHLNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKDQIFLYAQASGRITVSTKRSQQTV
SPNIGSRPRVRNIPSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGKSSIMRSDAPIGKCNSECITPNGSIPNDK
PFQNVNRITYGACPRYVKQNTLKLATGMRNVPGGGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIG
KTNEKFHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLRENAEDMGNG
CFKIYHKCDNACIGSIRNGTYDHDVYRDEALNNRFQIKGVELKSGYKDWILWISFAISCFLLCVALLGFIMWACQKGNI
RCNICI*

Figure 52E

Schematic representation of construct number 2039

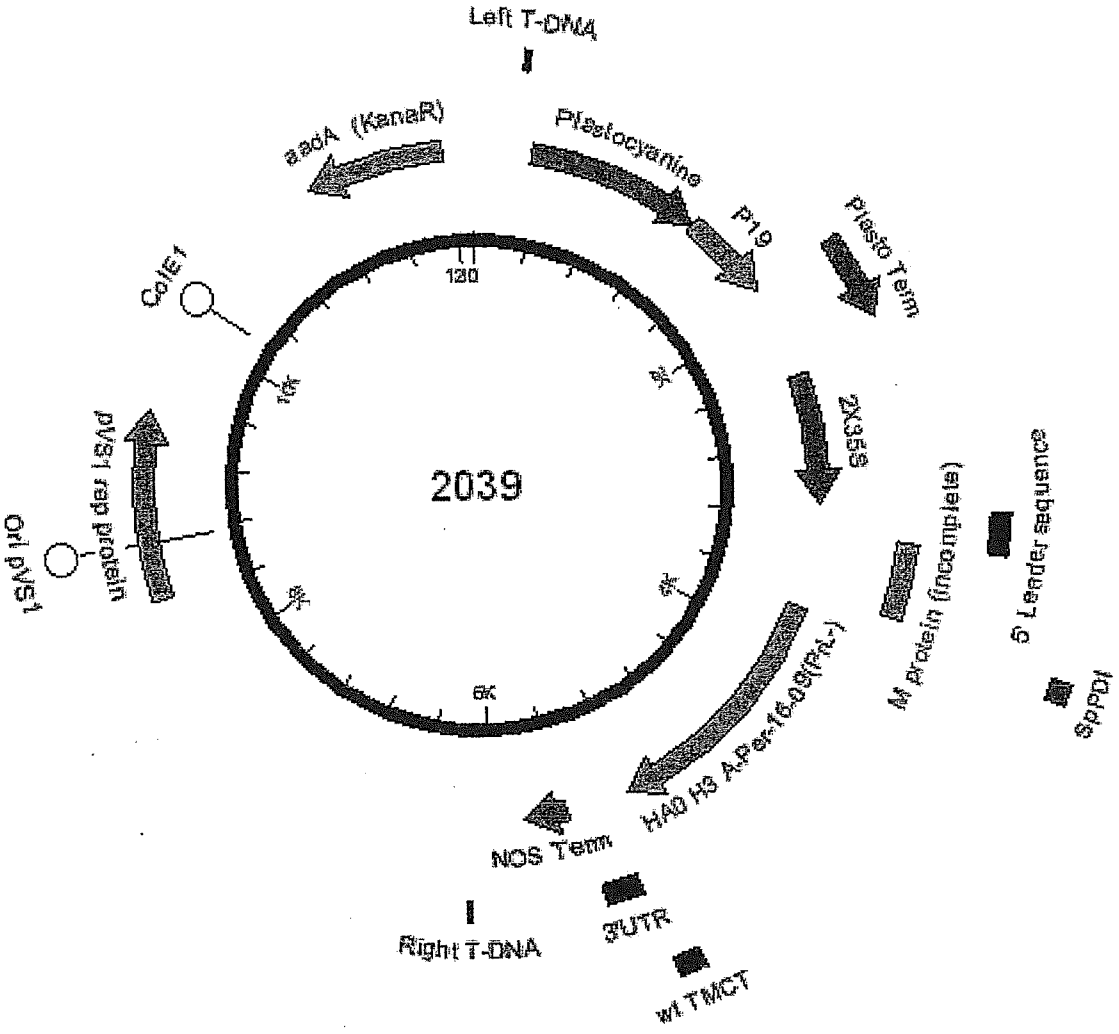
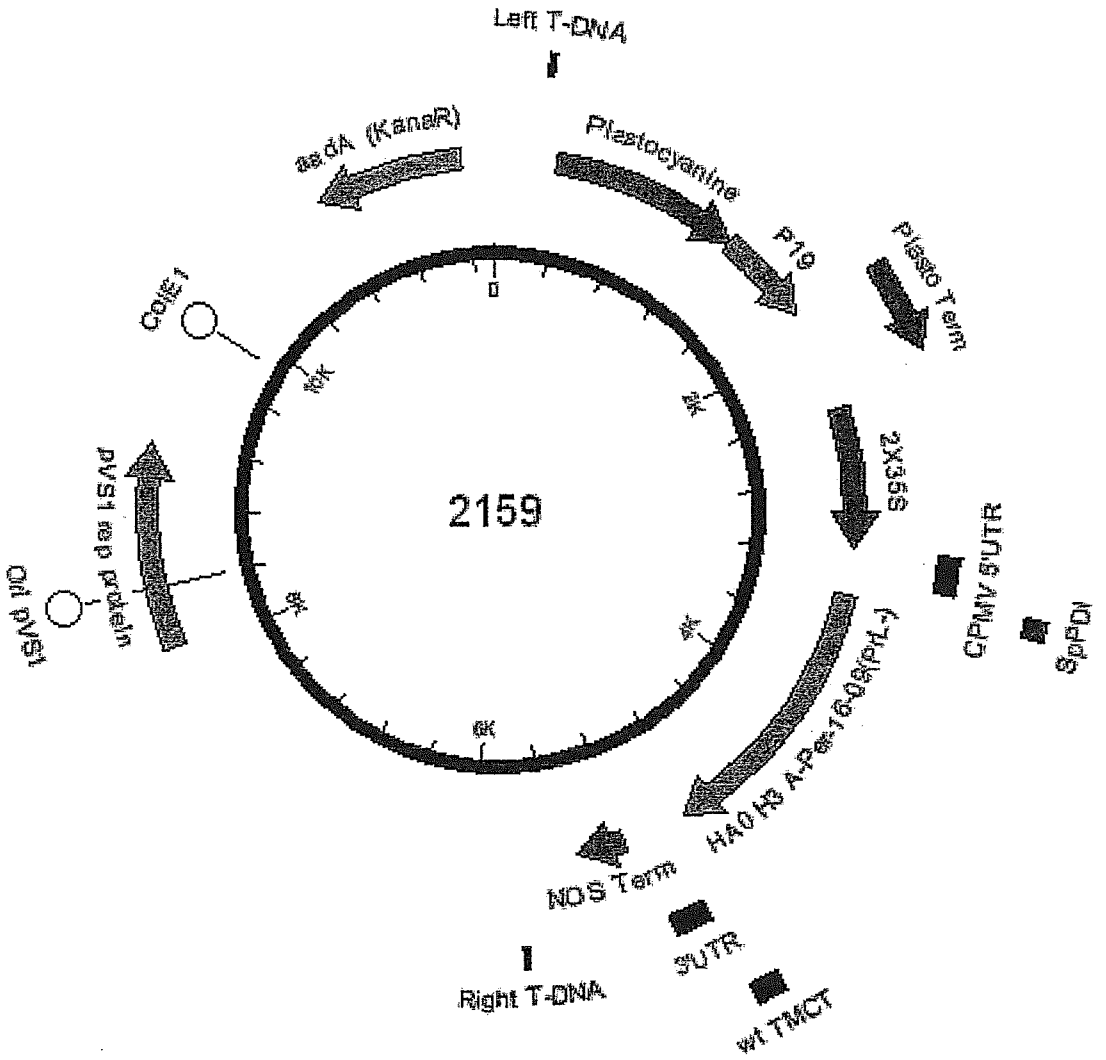


Figure 52F

Schematic representation of construct number 2159



2X35S/CPMV HT+ (construct no 2230) and 160+ (construct no 2250) for PDISP/H3 Victoria with deleted proteolytic loop

Figure 53A, SEQ ID NO: 144

Nucleotide sequence of PDISP/H3 Victoria with deleted proteolytic loop

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGCAAAAACTTCCTGGAA
ATGACAACAGCACGGCAACGCTGTGCCTTGGGCACCATGCAGTACCAAACGGAACGATAGTGAAAACAATCACGAATGACCAAA
TTGAAGTTACTAATGCTACTGAGCTGGTTCAGAATTCCTCAATAGGTGAAATATGCGACAGTCCTCATCAGATCCTTGATGGAGAA
AACTGCACACTAATAGATGCTCTATTGGGAGACCCTCAGTGTGATGGCTTCCAAAATAAGAAATGGGACCTTTTTGTTGAACGAAG
CAAAGCCTACAGCAACTGTTACCCTTATGATGTGCCGGATTATGCCTCCCTTAGGTCACTAGTTGCCTCATCCGGCACACTGGAGTT
TAACAATGAAAGCTTCAATTGGACTGGAGTCACTCAAAACGGAACAAGTTCTGCTTGCATAAGGAGATCTAATAATAGTTTCTTTA
GTAGATTAAATTGGTTGACCCACTTAAACTTCAAATACCCAGCATTGAACGTGACTATGCCAAACAATGAACAATTTGACAAATTG
TACATTTGGGGGGTTCACCACCCGGGTACGGACAAGGACCAAATCTTCCTGTATGCTCAATCATCAGGAAGAATCACAGTATCTAC
CAAAAGAAGCCAACAAGCTGTAATCCCGAATATCGGATCTAGACCCAGAATAAGGAATATCCCTAGCAGAATAAGCATCTATTGG
ACAATAGTAAAACCGGGAGACATACTTTTGATTAACAGCACAGGGAATCTAATTGCTCCTAGGGGTTACTTCAAAATACGAAGTG
GGAAAAGCTCAATAATGAGATCAGATGCACCCATTGGCAAATGCAATTCTGAATGCATCACTCCAAATGGAAGCATTCCCAATGA
CAAACCATTCCAAAATGTAAACAGGATCACATACGGGGCCTGTCCCAGATATGTTAAGCAAAGCACTCTGAAATTGGCAACAGGA
ATGCGAAATGTACCAGGCGGAGGTTGGGAGGGAATGGTGGATGGTTGGTACGGTTTCAGGCATCAAAATTCTGAGGGAAGAGG
ACAAGCAGCAGATCTCAAAAGCACTCAAGCAGCAATCGATCAAATCAATGGGAAGCTGAATCGATTGATCGGGAAAACCAACGA
GAAATTCCATCAGATTGAAAAAGAATTCTCAGAAGTCGAAGGGAGAATTCAGGACCTTGAGAAATATGTTGAGGACACTAAAATA
GATCTCTGGTCATACAACGCGGAGCTTCTTGTTGCCCTGGAGAACCAACATACAATTGATCTAACTGACTCAGAAATGAACAAACT
GTTTGAAAAAACAAAGAAGCAACTAAGGGAAAATGCTGAGGATATGGGCAATGGTTGTTTCAAAATATACCACAAATGTGACAAT
GCCTGCATAGGATCAATCAGAAATGGAACTTATGACCACGATGTATACAGAGATGAAGCATTAAACAACCGGTTCCAGATCAAGG
GAGTTGAGCTGAAGTCAGGGTACAAAGATTGGATCCTATGGATTTCCTTTGCCATATCATGTTTTTTGCTTTGTGTTGCTTTGTTGG
GGTTCATCATGTGGGCCTGCCAAAAGGGCAACATTAGGTGCAACATTTGCATTTGA

Figure 53B, SEQ ID NO: 145

H3V36111(Prl-).r

CCCTCCCAACCTCCGCCTGGTACATTTCGCATTCCTGTTGCCAATTTC

Figure 53C, SEQ ID NO: 146

H3V36111(Prl-).c

AATGTACCAGGCGGAGGTTGGGAGGGAATGGTGGATGGTTGGTACGGT

Figure 53D, SEQ ID NO: 147

Amino acid sequence of PDISP/H3 Victoria with deleted proteolytic loop

MAKNVAIFGLLFSLLVLVPSQIFAQKLPGNDNSTATLCLGHHAVPNGTIVKTITNDQIEVTNATELVQNSSIGEICDSPHQILDGENCTLID
ALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNESFNWTGVTQNGTSSACIRRSNNSFFSRLNWLTH
LNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKDQIFLYAQSSGRITVSTKRSQQAVIPNIGSRPRIRNIPSRISIYWTIVKPGDILLINST
GNLIAPRGYFKIRSGKSSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQSTLKLATGMRNVPGGGWEGMVDGWY
GFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDS
EMNKLFEKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTYDHDVYRDEALNNRFQIKGVELKSGYKDWILWISFAISCFLLCVALL
GFIMWACQKGNIRCNICI*

Figure 53E

Schematic representation of construct number 2230

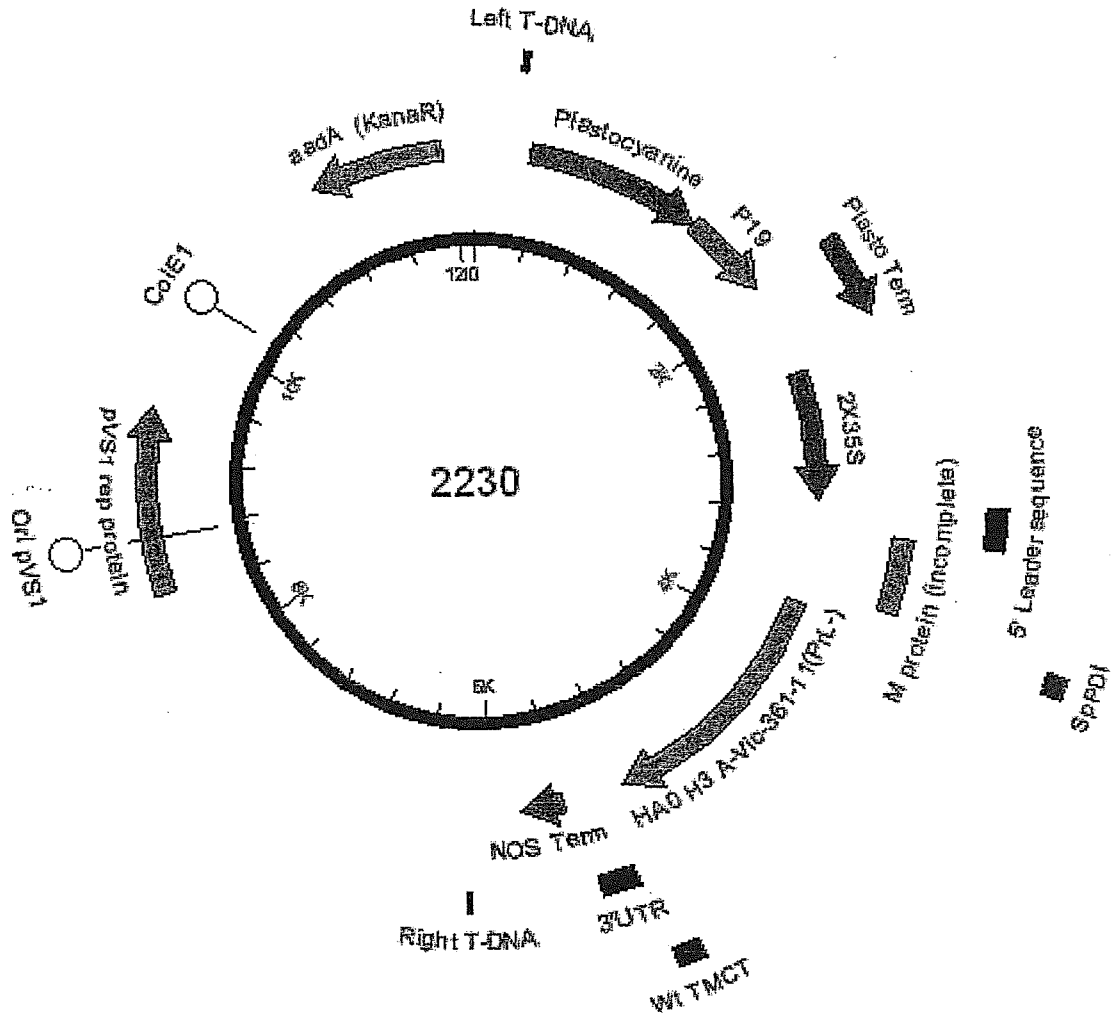
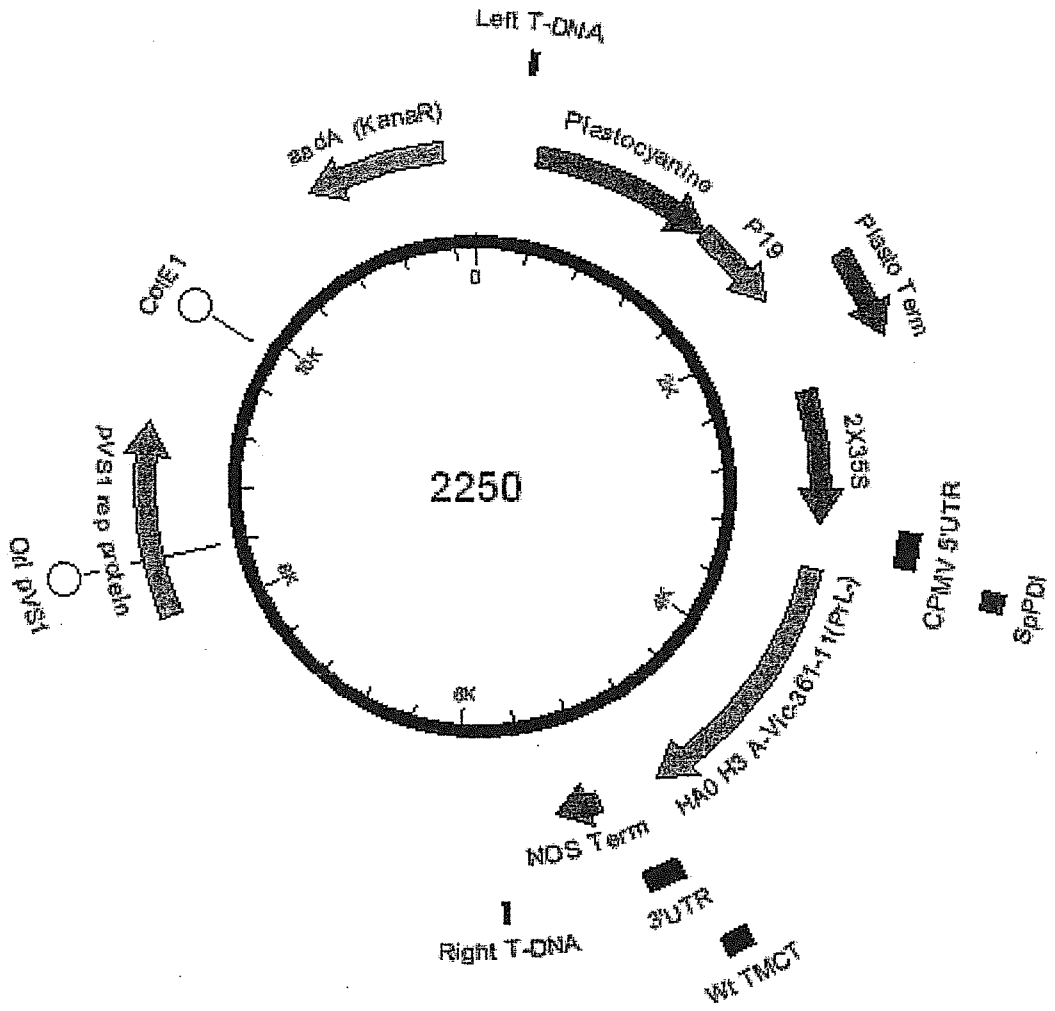


Figure 53F

Schematic representation of construct number 2250



2X35S/CPMV HT+/PDISP/H7 Hangzhou/NOS (Construct no 2142)

Figure 54A, SEQ ID NO: 148

Nucleotide sequence of PDISP/H7 Hangzhou

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGACAAAATCTGCCTCG
GACATCATGCCGTGTCAAACGGAACCAAAGTAAACACATTAACTGAAAGAGGAGTGGAAGTCGTCAATGCAACTGAAACAGTGG
AACGAACAAACATCCCCAGGATCTGCTCAAAAGGGAAAAGGACAGTTGACCTCGGTCAATGTGGACTCCTGGGGACAATCACTG
GACCACCTCAATGTGACCAATTCCTAGAATTTTCAGCCGATTTAATTATTGAGAGGCGAGAAGGAAGTGATGTCTGTTATCCTGGG
AAATTCGTGAATGAAGAAGCTCTGAGGCAAATTCTCAGAGAATCAGGCGGAATTGACAAGGAAGCAATGGGATTCACATACAGT
GGAATAAGAACTAATGGAGCAACCAGTGCATGTAGGAGATCAGGATCTTCATTCTATGCAGAAATGAAATGGCTCCTGTCAAACA
CAGATAATGCTGCATTCCCGCAGATGACTAAGTCATATAAAAATACAAGAAAAAGCCCAGCTCTAATAGTATGGGGGATCCATCA
TTCCGTATCAACTGCAGAGCAAACCAAGCTATATGGGAGTGGAAACAAACTGGTGACAGTTGGGAGTTCTAATTATCAACAATCT
TTTGTACCGAGTCCAGGAGCGAGACCACAAGTTAATGGTATATCTGGAAGAATTGACTTTCATTGGCTAATGCTAAATCCCAATGA
TACAGTCACTTTCAGTTTCAATGGGGCTTTCATAGCTCCAGACCGTGCAAGCTTCCTGAGAGGAAAATCTATGGGAATCCAGAGTG
GAGTACAGGTTGATGCCAATTGTGAAGGGGACTGCTATCATAGTGGAGGGACAATAATAAGTAACTTGCCATTTCAGAACATAGA
TAGCAGGGCAGTTGGAAAATGTCCGAGATATGTTAAGCAAAGGAGTCTGCTGCTAGCAACAGGGATGAAGAATGTTCCTGAGAT
TCCAAAGGGAAGAGGCCTATTTGGTGCTATAGCGGGTTTCATTGAAAATGGATGGGAAGGCCTAATTGATGGTTGGTATGGTTTC
AGACACCAGAATGCACAGGGAGAGGGAACTGCTGCAGATTACAAAAGCACTCAATCGGCAATTGATCAAATAACAGGAAAATTA
AACCGGCTTATAGAAAAAACCAACCAACAATTTGAGTTGATCGACAATGAATTCAATGAGGTAGAGAAGCAAATCGGTAATGTGA
TAAATTGGACCAGAGATTCTATAACAGAAGTGTGGTCATACAATGCTGAACTCTTGGTAGCAATGGAGAACCAGCATACAATTGA
TCTGGCTGATTCAGAAATGGACAAACTGTACGAACGAGTGAAAAGACAGCTGAGAGAGAATGCTGAAGAAGATGGCACTGGTTG
CTTTGAAATATTTCACAAGTGTGATGATGACTGTATGGCCAGTATTAGAAATAACACCTATGATCACAGCAAATACAGGGAAGAG
GCAATGCAAAATAGAATACAGATTGACCCAGTCAAACTAAGCAGCGGCTACAAAGATGTGATACTTTGGTTTAGCTTCGGGGCAT
CATGTTTCATACTTCTAGCCATTGTAATGGGCCTTGTCTTCATATGTGTAAAGAATGGAAACATGCGGTGCACTATTTGTATATAA

Figure 54B, SEQ ID NO: 149

IF*-H7H113.s1-6r

ACTAAAGAAAATAGGCCTTTATATACAAATAGTGCACCGCATGTTTCCAT

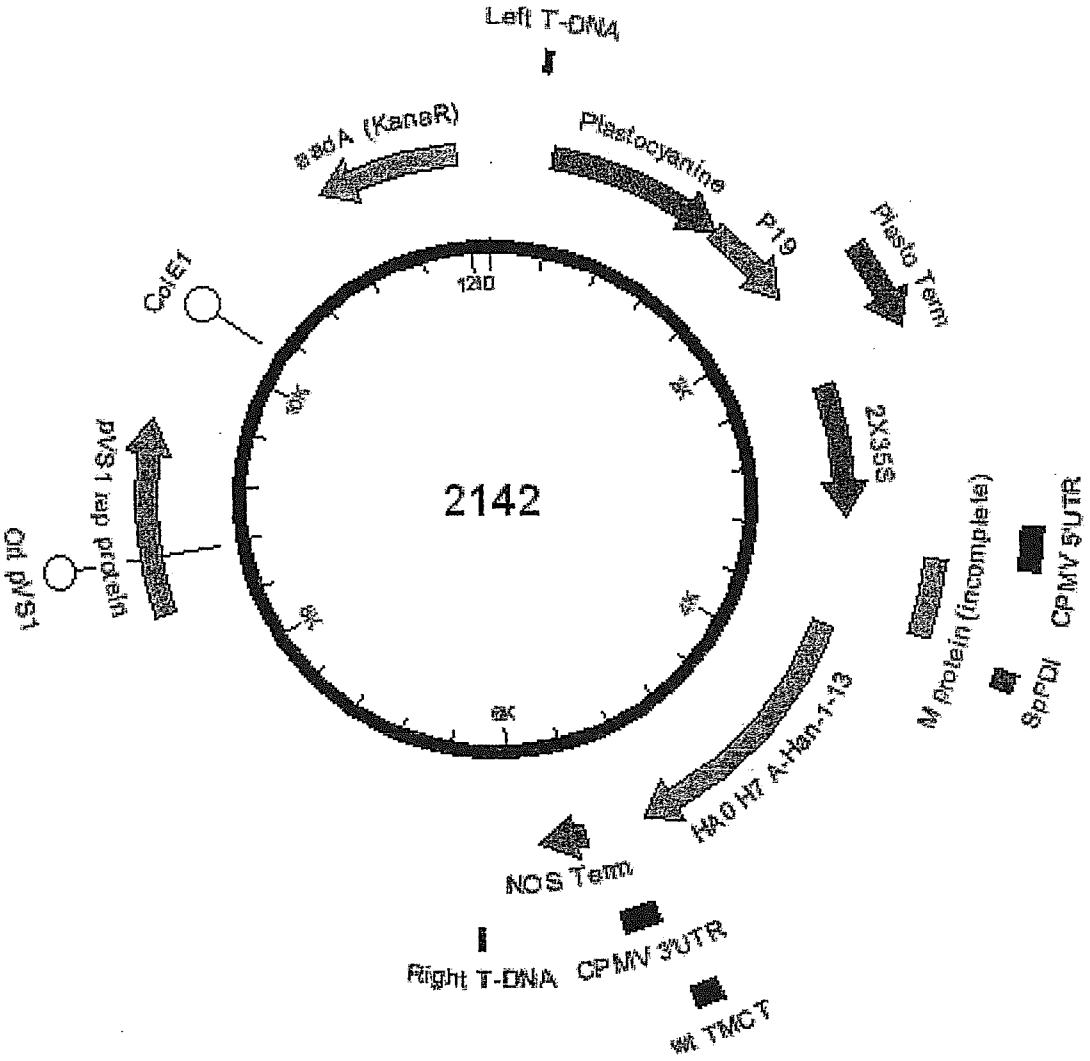
Figure 54C, SEQ ID NO: 150

Amino acid sequence of PDISP/H7 Hangzhou

MAKNVAIFGLLFSLLVLVPSQIFADKICLGHHAVSNGTKVNTLTERGVEVVNATETVERTNIPRICSKGKRTVDLGQCGLLGTITGPPQCD
QFLEFSADLIIERREGSDVCYPGKFVNEEALRQILRESGGIDKEAMGFTYSGIRTNGATSACRRSGSSFYAEMKWLLSNTDNAAFPQMTK
SYKNTRKSPALIVWGIHHSVSTAEQTKLYGSGNKLVTVGSSNYQQSFVPSPGARPQVNGISGRIDFHWLMLNPNDTVTFSFNGAFIAPD
RASFLRGKSMGIQSGVQVDANCEGDCYHSGGTIISNLPFQNIDSRAVGKCPRYVKQRSLLLATGMKNVPEIPKGRGLFGAIAGFIENGW
EGLIDGWYGFRHQNAQGEGTAADYKSTQSAIDQITGKLNRLIEKTNQQFELIDNEFNEVEKQIGNVINWTRDSITEVWSYNAELLVAME
NQHTIDLADSEMDKLYERVKRQLRENAEEDGTGCFEIFHKCDDDCMASIRNNTYDHSKYREEAMQNRIQIDPVKLSSGYKDVILWFSFG
ASCFILLAIVMGLVFICVKNGNMRCTICI*

Figure 54D

Schematic representation of construct number 2142



2X35S/CPMV HT+/PDISP/H7 Hangzhou with deleted proteolytic loop/NOS (Construct no 2152)

Figure 55A, SEQ ID NO: 151

Nucleotide sequence of PDISP/H7 Hangzhou with deleted proteolytic loop

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGACAAAATCTGCCTCG
GACATCATGCCGTGTCAAACGGAACCAAAGTAAACACATTAACTGAAAGAGGAGTGGAAGTCGTCAATGCAACTGAAACAGTGG
AACGAACAAACATCCCCAGGATCTGCTCAAAAGGGAAAAGGACAGTTGACCTCGGTCAATGTGGACTCCTGGGGACAATCACTG
GACCACCTCAATGTGACCAATTCCTAGAATTTTCAGCCGATTTAATTATTGAGAGGCGAGAAGGAAGTGATGTCTGTTATCCTGGG
AAATTCGTGAATGAAGAAGCTCTGAGGCAAATTCTCAGAGAATCAGGCGGAATTGACAAGGAAGCAATGGGATTCACATACAGT
GGAATAAGAACTAATGGAGCAACCAGTGCATGTAGGAGATCAGGATCTTCATTCTATGCAGAAATGAAATGGCTCCTGTCAAACA
CAGATAATGCTGCATTCCCGCAGATGACTAAGTCATATAAAAATACAAGAAAAAGCCCAGCTCTAATAGTATGGGGGATCCATCA
TTCCGTATCAACTGCAGAGCAAACCAAGCTATATGGGAGTGGAAACAAACTGGTGACAGTTGGGAGTTCTAATTATCAACAATCT
TTTGTACCGAGTCCAGGAGCGAGACCACAAGTTAATGGTATATCTGGAAGAATTGACTTTCATTGGCTAATGCTAAATCCCAATGA
TACAGTCACTTTCAGTTTCAATGGGGCTTTCATAGCTCCAGACCGTGCAAGCTTCCTGAGAGGAAAATCTATGGGAATCCAGAGTG
GAGTACAGGTTGATGCCAATTGTGAAGGGGACTGCTATCATAGTGGAGGGACAATAATAAGTAACTTGCCATTTCAGAACATAGA
TAGCAGGGCAGTTGGAAAATGTCCGAGATATGTTAAGCAAAGGAGTCTGCTGCTAGCAACAGGGATGAAGAATGTTCCTGGCGG
ATGGGAAGGCCTAATTGATGGTTGGTATGGTTTCAGACACCAGAATGCACAGGGAGAGGGAACTGCTGCAGATTACAAAAGCAC
TCAATCGGCAATTGATCAAATAACAGGAAAATTAAACCGGCTTATAGAAAAAACCAACCAACAATTTGAGTTGATCGACAATGAA
TTCAATGAGGTAGAGAAGCAAATCGGTAATGTGATAAATTGGACCAGAGATTCTATAACAGAAGTGTGGTCATACAATGCTGAAC
TCTTGGTAGCAATGGAGAACCAGCATACAATTGATCTGGCTGATTCAGAAATGGACAAACTGTACGAACGAGTGAAAAGACAGCT
GAGAGAGAATGCTGAAGAAGATGGCACTGGTTGCTTTGAAATATTTCACAAGTGTGATGATGACTGTATGGCCAGTATTAGAAAT
AACACCTATGATCACAGCAAATACAGGGAAGAGGCAATGCAAAATAGAATACAGATTGACCCAGTCAAACTAAGCAGCGGCTAC
AAAGATGTGATACTTTGGTTTAGCTTCGGGGCATCATGTTTCATACTTCTAGCCATTGTAATGGGCCTTGTCTTCATATGTGTAAAG
AATGGAAACATGCGGTGCACTATTTGTATATAA

Figure 55B, SEQ ID NO: 152

H7H113(PrL-).r

CCTTCCCATCCGCCAGGAACATTCTTCATCCCTGTTGCTAGCAGCAGAC

Figure 55C, SEQ ID NO: 153

H7H113(PrL-).c

AGAATGTTCCTGGCGGATGGGAAGGCCTAATTGATGGTTGGTATGGTT

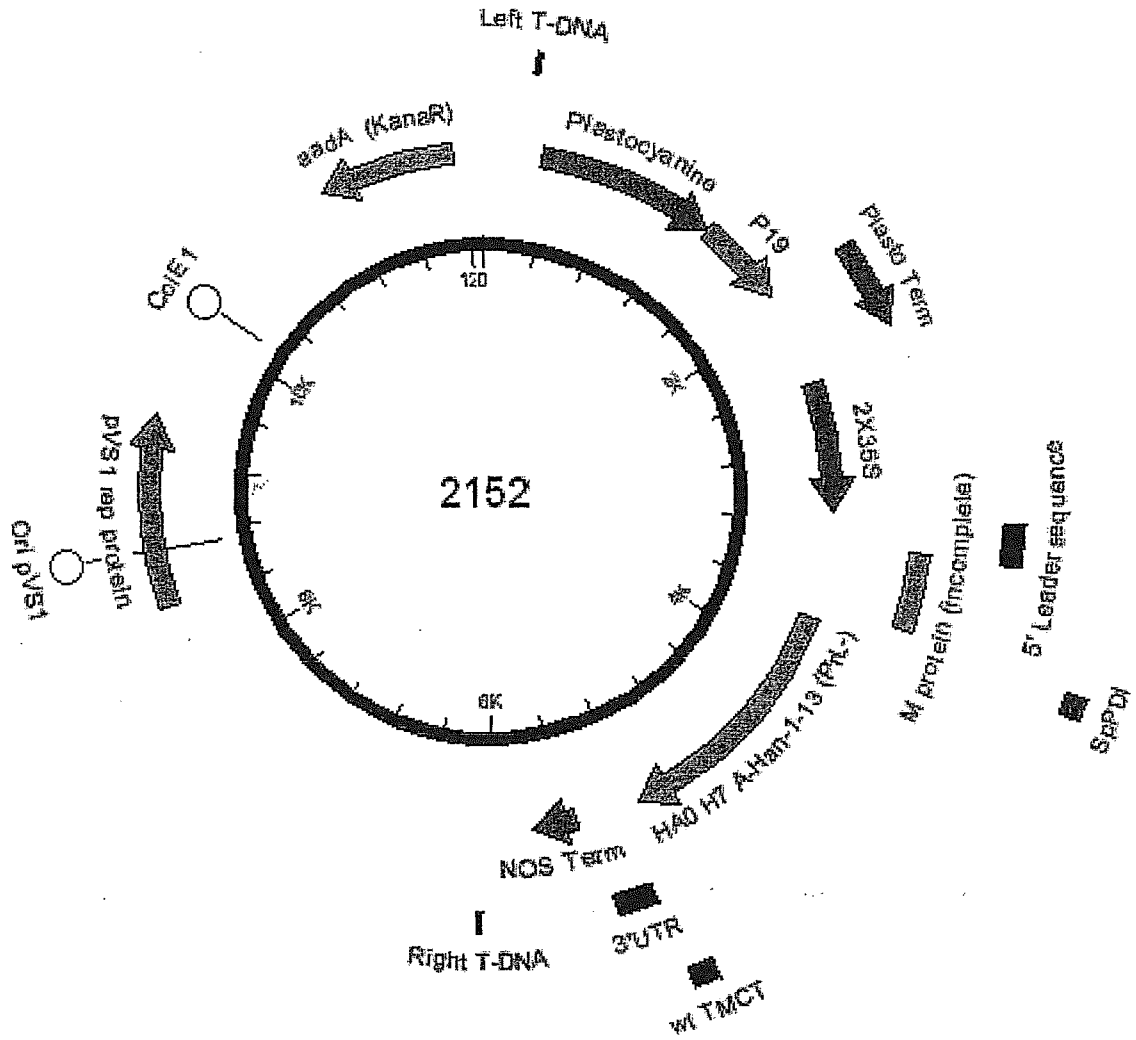
Figure 55D, SEQ ID NO: 154

Amino acid sequence of PDISP/H7 Hangzhou with deleted proteolytic loop

MAKNVAIFGLLFSLLVLVPSQIFADKICLGHHAVSNGTKVNTLTERGVEVVNATETVERTNIPRICSKGKRTVDLGQCGLLGTITGPPQCD
QFLEFSADLIIERREGSDVCYPGKFVNEEALRQILRESGGIDKEAMGFTYSGIRTNGATSACRRSGSSFYAEMKWLLSNTDNAAFPQMTK
SYKNTRKSPALIVWGIHHSVSTAEQTKLYGSGNKLVTVGSSNYQQSFVPSPGARPQVNGISGRIDFHWLMLNPNDTVTFSFNGAFIAPD
RASFLRGKSMGIQSGVQVDANCEGDCYHSGGTIISNLPFQNIDSRAVGKCPRYVKQRSLLLATGMKNVPGGWEGLIDGWYGFRHQNA
QGEGTAADYKSTQSAIDQITGKLNRLIEKTNQQFELIDNEFNEVEKQIGNVINWTRDSITEVWSYNAELLVAMENQHTIDLADSEMDKL
YERVKRQLRENAEEDGTGCFEIFHKCDDDCMASIRNNTYDHSKYREEAMQNRIQIDPVKLSSGYKDVILWFSFGASCFILLAIVMGLVFIC
VKNGNMRCTICI*

Figure 55E

Schematic representation of construct number 2152



2X35S/CPMV HT+ (construct no 2224) and 160+ (construct no 2226) for PDISP/H9 Hong Kong

Figure 56A, SEQ ID NO: 155

Nucleotide sequence of PDISP/H9 Hong Kong

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGATAAAATCTGCATCG
GCCACCAGTCAACAAACTCCACAGAAACTGTGGACACGCTAACAGAAACCAATGTTCCTGTGACACATGCCAAAGAATTGCTCCAC
ACAGAGCATAATGGAATGCTGTGTGCAACAAGCCTGGGACATCCCCTCATTCTAGACACATGCACTATTGAAGGACTAGTCTATG
GCAACCCTTCTTGTGACCTGCTGTTGGGAGGAAGAGAATGGTCCTACATCGTCGAAAGATCATCAGCTGTAAATGGAACGTGTTA
CCCTGGGAATGTAGAAAACCTAGAGGAACTCAGGACACTTTTTAGTTCCGCTAGTTCCTACCAAAGAATCCAAATCTTCCCAGACA
CAACCTGGAATGTGACTTACACTGGAACAAGCAGAGCATGTTCAGGTTCATTCTACAGGAGTATGAGATGGCTGACTCAAAAGAG
CGGTTTTTACCCTGTTCAAGACGCCCAATACACAAATAACAGGGGAAAGAGCATTCTTTTCGTGTGGGGCATACATCACCCACCCA
CCTATACCGAGCAAACAAATTTGTACATAAGAAACGACACAACAACAAGCGTGACAACAGAAGATTTGAATAGGACCTTCAAACC
AGTGATAGGGCCAAGGCCCCTTGTCAATGGTCTGCAGGGAAGAATTGATTATTATTGGTCGGTACTAAAACCAGGCCAAACATTG
CGAGTACGATCCAATGGGAATCTAATTGCTCCATGGTATGGACACGTTCTTTCAGGAGGGAGCCATGGAAGAATCCTGAAGACTG
ATTTAAAAGGTGGTAATTGTGTAGTGCAATGTCAGACTGAAAAAGGTGGCTTAAACAGTACATTGCCATTCCACAATATCAGTAAA
TATGCATTTGGAACCTGCCCCAAATATGTAAGAGTTAATAGTCTCAAACTGGCAGTCGGTCTGAGGAACGTGCCTGCTAGATCAA
GTAGAGGACTATTTGGAGCCATAGCTGGATTCATAGAAGGAGGTTGGCCAGGACTAGTCGCTGGCTGGTATGGTTTCCAGCATTC
AAATGATCAAGGGGTTGGTATGGCTGCAGATAGGGATTCAACTCAAAAGGCAATTGATAAAATAACATCCAAGGTGAATAATATA
GTCGACAAGATGAACAAGCAATATGAAATAATTGATCATGAATTTAGTGAGGTTGAAACTAGACTCAATATGATCAATAATAAGA
TTGATGACCAAATACAAGACGTATGGGCATATAATGCAGAATTGCTAGTACTACTTGAAAATCAAAAAACACTCGATGAGCATGA
TGCGAACGTGAACAATCTATATAACAAGGTGAAGAGGGCACTGGGCTCCAATGCTATGGAAGATGGGAAAGGCTGTTTCGAGCT
ATACCATAAATGTGATGATCAGTGCATGGAAACAATTCGGAACGGGACCTATAATAGGAGAAAGTATAGAGAGGAATCAAGACT
AGAAAGGCAGAAAATAGAGGGGGTTAAGCTGGAATCTGAGGGAACTTACAAAATCCTCACCATTTATTCGACTGTCGCCTCATCT
CTTGTGCTTGCAATGGGGTTTGCTGCCTTCCTGTTCTGGGCCATGTCCAATGGATCTTGCAGATGCAACATTTGTATATAA

Figure 56B, SEQ ID NO: 156

IF**-H9HK107399.S1-6r

ACTAAAGAAAATAGGCCTTTATATACAAATGTTGCATCTGCAAGATCCAT

Figure 56C, SEQ ID NO: 157

Amino acid sequence of PDISP/H9 Hong Kong

MAKNVAIFGLLFSLLVLVPSQIFADKICIGHQSTNSTETVDTLTETNVPVTHAKELLHTEHNGMLCATSLGHPLILDTCTIEGLVYGNPSCD
LLLGGREWSYIVERSSAVNGTCYPGNVENLEELRTLFSSASSYQRIQIFPDTTWNVTYTGTSRACSGSFYRSMRWLTQKSGFYPVQDAQ
YTNNRGKSILFVWGIHHPPTYTEQTNLYIRNDTTTSVTTEDLNRTFKPVIGPRPLVNGLQGRIDYYWSVLKPGQTLRVRSNGNLIAPWYG
HVLSGGSHGRILKTDLKGGNCVVQCQTEKGGLNSTLPFHNISKYAFGTCPKYVRVNSLKLAVGLRNVPARSSRGLFGAIAGFIEGGWPGL
VAGWYGFQHSNDQGVGMAADRDSTQKAIDKITSKVNNIVDKMNKQYEIIDHEFSEVETRLNMINNKIDDQIQDVWAYNAELLVLLEN
QKTLDEHDANVNNLYNKVKRALGSNAMEDGKGCFELYHKCDDQCMETIRNGTYNRRKYREESRLERQKIEGVKLESEGTYKILTIYSTVA
SSLVLAMGFAAFLFWAMSNGSCRCNICI*

Figure 56D

Schematic representation of construct number 2224

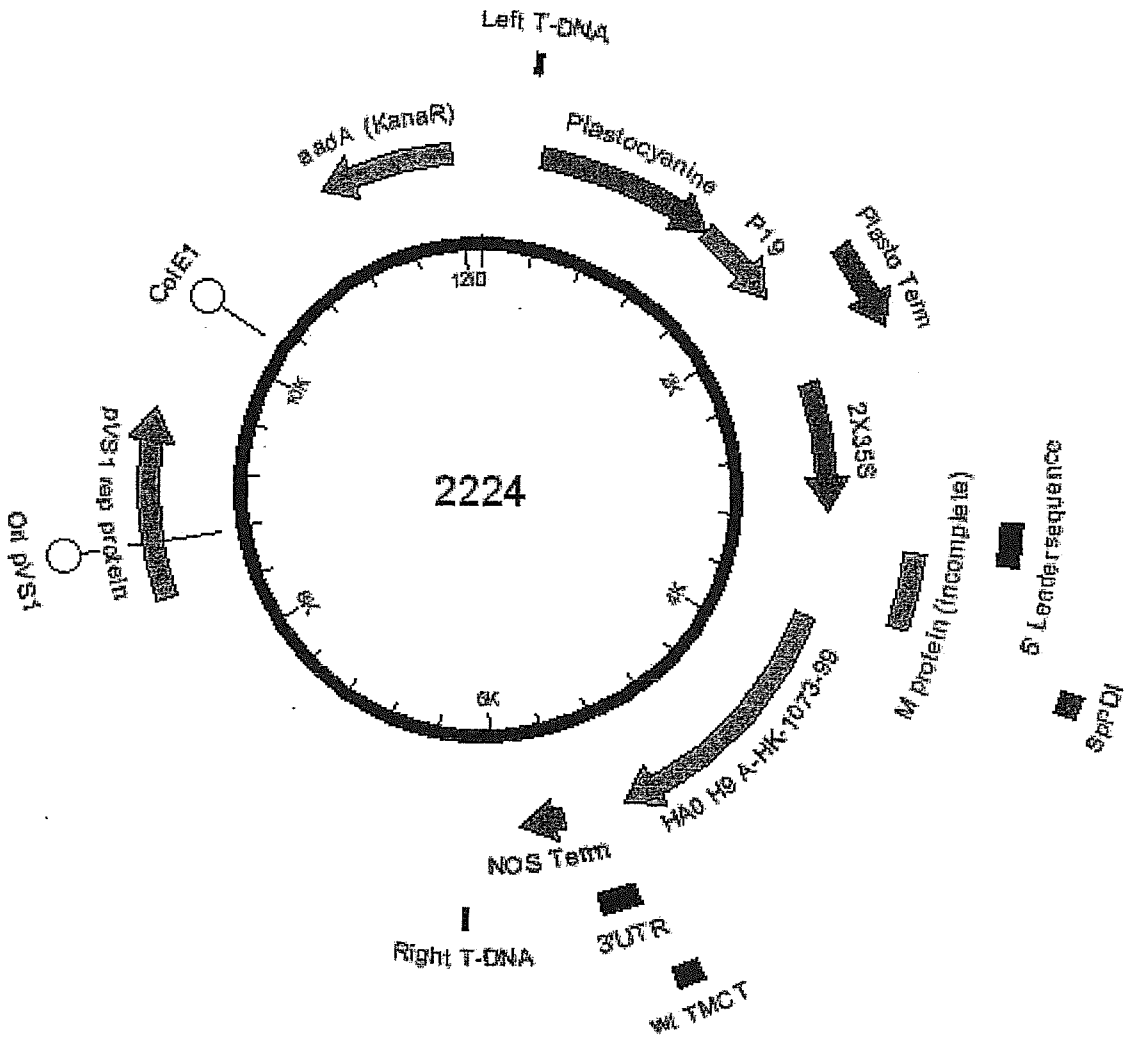
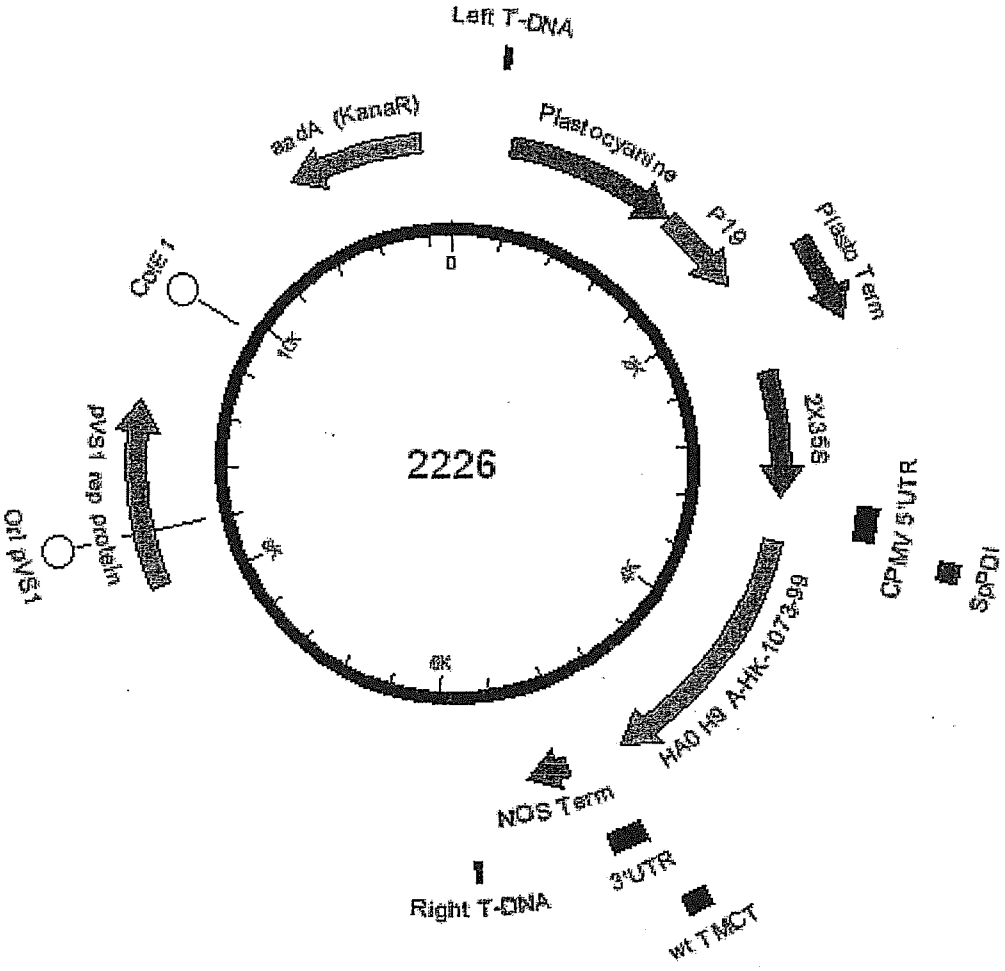


Figure 56E

Schematic representation of construct number 2226



2X35S/CPMV HT+ (construct no 2225) and 160+ (construct no 2227) for PDISP/H9 Hong Kong with deleted proteolytic loop

Figure 57A, SEQ ID NO: 158

Nucleotide sequence of PDISP/H9 Hong Kong with deleted proteolytic loop

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGATAAAATCTGCATCG
GCCACCAGTCAACAAACTCCACAGAAACTGTGGACACGCTAACAGAAACCAATGTTCCTGTGACACATGCCAAAGAATTGCTCCAC
ACAGAGCATAATGGAATGCTGTGTGCAACAAGCCTGGGACATCCCCTCATTCTAGACACATGCACTATTGAAGGACTAGTCTATG
GCAACCCTTCTTGTGACCTGCTGTTGGGAGGAAGAGAATGGTCCTACATCGTCGAAAGATCATCAGCTGTAAATGGAACGTGTTA
CCCTGGGAATGTAGAAAACCTAGAGGAACTCAGGACACTTTTTAGTTCCGCTAGTTCCTACCAAAGAATCCAAATCTTCCCAGACA
CAACCTGGAATGTGACTTACACTGGAACAAGCAGAGCATGTTCAGGTTCATTCTACAGGAGTATGAGATGGCTGACTCAAAAGAG
CGGTTTTTACCCTGTTCAAGACGCCCAATACACAAATAACAGGGGAAAGAGCATTCTTTTCGTGTGGGGCATACATCACCCACCCA
CCTATACCGAGCAAACAAATTTGTACATAAGAAACGACACAACAACAAGCGTGACAACAGAAGATTTGAATAGGACCTTCAAACC
AGTGATAGGGCCAAGGCCCCTTGTCAATGGTCTGCAGGGAAGAATTGATTATTATTGGTCGGTACTAAAACCAGGCCAAACATTG
CGAGTACGATCCAATGGGAATCTAATTGCTCCATGGTATGGACACGTTCTTTCAGGAGGGAGCCATGGAAGAATCCTGAAGACTG
ATTTAAAAGGTGGTAATTGTGTAGTGCAATGTCAGACTGAAAAAGGTGGCTTAAACAGTACATTGCCATTCCACAATATCAGTAAA
TATGCATTTGGAACCTGCCCCAAATATGTAAGAGTTAATAGTCTCAAACTGGCAGTCGGTCTGAGGAACGTGCCTGGCGGAGGTT
GGCCAGGACTAGTCGCTGGCTGGTATGGTTTCCAGCATTCAAATGATCAAGGGGTTGGTATGGCTGCAGATAGGGATTCAACTCA
AAAGGCAATTGATAAAATAACATCCAAGGTGAATAATATAGTCGACAAGATGAACAAGCAATATGAAATAATTGATCATGAATTT
AGTGAGGTTGAAACTAGACTCAATATGATCAATAATAAGATTGATGACCAAATACAAGACGTATGGGCATATAATGCAGAATTGC
TAGTACTACTTGAAAATCAAAAAACACTCGATGAGCATGATGCGAACGTGAACAATCTATATAACAAGGTGAAGAGGGCACTGG
GCTCCAATGCTATGGAAGATGGGAAAGGCTGTTTCGAGCTATACCATAAATGTGATGATCAGTGCATGGAAACAATTCGGAACGG
GACCTATAATAGGAGAAAGTATAGAGAGGAATCAAGACTAGAAAGGCAGAAAATAGAGGGGGTTAAGCTGGAATCTGAGGGAA
CTTACAAAATCCTCACCATTTATTCGACTGTCGCCTCATCTCTTGTGCTTGCAATGGGGTTTGCTGCCTTCCTGTTCTGGGCCATGTC
CAATGGATCTTGCAGATGCAACATTTGTATATAA

Figure 57B, SEQ ID NO: 159

H9HK107399(Prl-).r

GTCCTGGCCAACCTCCGCCAGGCACGTTCCTCAGACCGACTGCCAGTT

Figure 57C, SEQ ID NO: 160

H9HK107399(Prl-).c

GGAACGTGCCTGGCGGAGGTTGGCCAGGACTAGTCGCTGGCTGGTATG

Figure 57D, SEQ ID NO: 161

Amino acid sequence of PDISP/H9 Hong Kong with deleted proteolytic loop

MAKNVAIFGLLFSLLVLVPSQIFADKICIGHQSTNSTETVDTLTETNVPVTHAKELLHTEHNGMLCATSLGHPLILDTCTIEGLVYGNPSCD
LLLGGREWSYIVERSSAVNGTCYPGNVENLEELRTLFSSASSYQRIQIFPDTTWNVTYTGTSRACSGSFYRSMRWLTQKSGFYPVQDAQ
YTNNRGKSILFVWGIHHPPTYTEQTNLYIRNDTTTSVTTEDLNRTFKPVIGPRPLVNGLQGRIDYYWSVLKPGQTLRVRSNGNLIAPWYG
HVLSGGSHGRILKTDLKGGNCVVQCQTEKGGLNSTLPFHNISKYAFGTCPKYVRVNSLKLAVGLRNVPGGGWPGLVAGWYGFQHSND
QGVGMAADRDSTQKAIDKITSKVNNIVDKMNKQYEIIDHEFSEVETRLNMINNKIDDQIQDVWAYNAELLVLLENQKTLDEHDANVN
NLYNKVKRALGSNAMEDGKGCFELYHKCDDQCMETIRNGTYNRRKYREESRLERQKIEGVKLESEGTYKILTIYSTVASSLVLAMGFAAF
LFWAMSNGSCRCNICI*

Figure 57E

Schematic representation of construct number 2225

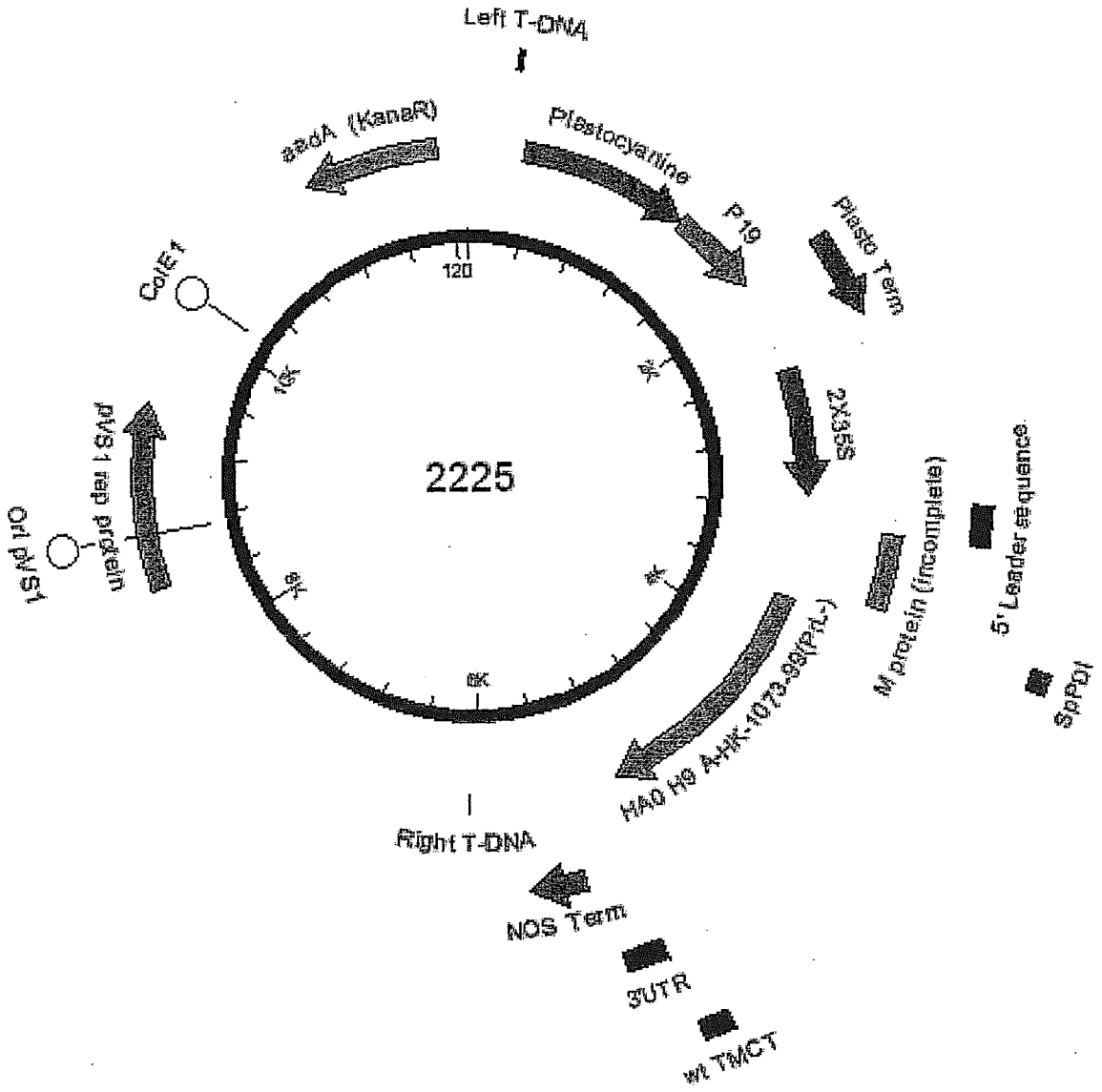
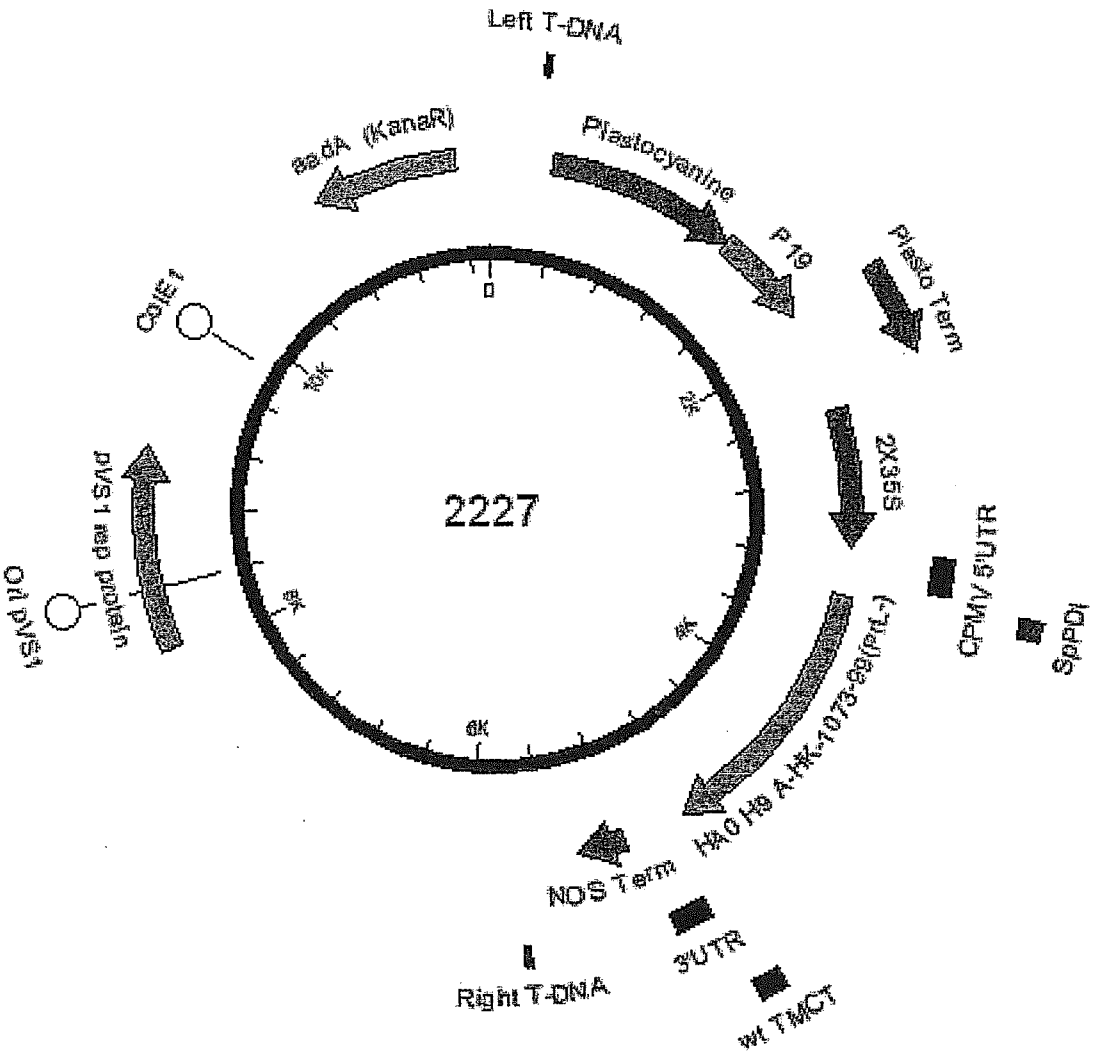


Figure 57F

Schematic representation of construct number 2227



2X35S/CPMV 160+/PDISP/HA B Malaysia/NOS (Construct no 2013)

Figure 58A, SEQ ID NO: 162

Nucleotide sequence of PDISP/HA B Malaysia

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGATCGAATCTGCACTG
GGATAACATCGTCAAACTCACCACATGTTGTCAAAACTGCTACTCAAGGGGAGGTCAATGTGACTGGTGTAATACCACTGACAAC
AACACCCACCAAATCTCATTTTGCAAATCTCAAAGGAACAGAAACCAGAGGGAAACTATGCCCAAAATGCCTCAACTGCACAGATC
TGGACGTGGCCTTGGGCAGACCAAAATGCACGGGGAACATACCCTCGGCAAGAGTTTCAATACTCCATGAAGTCAGACCTGTTAC
ATCTGGGTGCTTTCCTATAATGCACGACAGAACAAAAATTAGACAGCTGCCTAAACTTCTCAGAGGATACGAACATATCAGGTTAT
CAACTCATAACGTTATCAATGCAGAAAATGCACCAGGAGGACCCTACAAAATTGGAACCTCAGGGTCTTGCCCTAACGTTACCAAT
GGAAACGGATTTTTCGCAACAATGGCTTGGGCCGTCCCAAAAAACGACAACAACAAAACAGCAACAAATTCATTAACAATAGAAG
TACCATACATTTGTACAGAAGGAGAAGACCAAATTACCGTTTGGGGGTTCCACTCTGATAACGAAACCCAAATGGCAAAGCTCTAT
GGGGACTCAAAGCCCCAGAAGTTCACCTCATCTGCCAACGGAGTGACCACACATTACGTTTCACAGATTGGTGGCTTCCCAAATCA
AACAGAAGACGGAGGACTACCACAAAGCGGTAGAATTGTTGTTGATTACATGGTGCAAAAATCTGGGAAAACAGGAACAATTAC
CTATCAAAGAGGTATTTTATTGCCTCAAAAAGTGTGGTGCGCAAGTGGCAGGAGCAAGGTAATAAAAGGATCGTTGCCTTTAATT
GGAGAAGCAGATTGCCTCCACGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCATA
GGAAATTGCCCAATATGGGTGAAAACACCCTTGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGCAAAACTATTAAAGGAAA
GGGGTTTCTTCGGAGCTATTGCTGGTTTCTTAGAAGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCCCATG
GGGCACATGGAGTAGCGGTGGCAGCAGACCTTAAGAGCACTCAAGAGGCCATAAACAAGATAACAAAAAATCTCAACTCTTTGA
GTGAGCTGGAAGTAAAGAATCTTCAAAGACTAAGCGGTGCCATGGATGAACTCCACAACGAAATACTAGAACTAGACGAGAAAG
TGGATGATCTCAGAGCTGATACAATAAGCTCACAAATAGAACTCGCAGTCCTGCTTTCCAATGAAGGAATAATAAACAGTGAAGA
TGAGCATCTCTTGGCGCTTGAAAGAAAGCTGAAGAAAATGCTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATGCTTTGAAACC
AAACACAAGTGCAACCAGACCTGTCTCGACAGAATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCA
CTGAATATTACTGCTGCATCTTTAAATGACGATGGATTGGATAATCATACTATACTGCTTTACTACTCAACTGCTGCCTCCAGTTTG
GCTGTAACATTGATGATAGCTATCTTTGTTGTTTATATGGTCTCCAGAGACAATGTTTCTTGCTCCATCTGTCTATAA

Figure 58B, SEQ ID NO: 163

IF**-HBM250604.S1-6r

ACTAAAGAAAATAGGCCTTTATAGACAGATGGAGCAAGAAACATTGTCTC

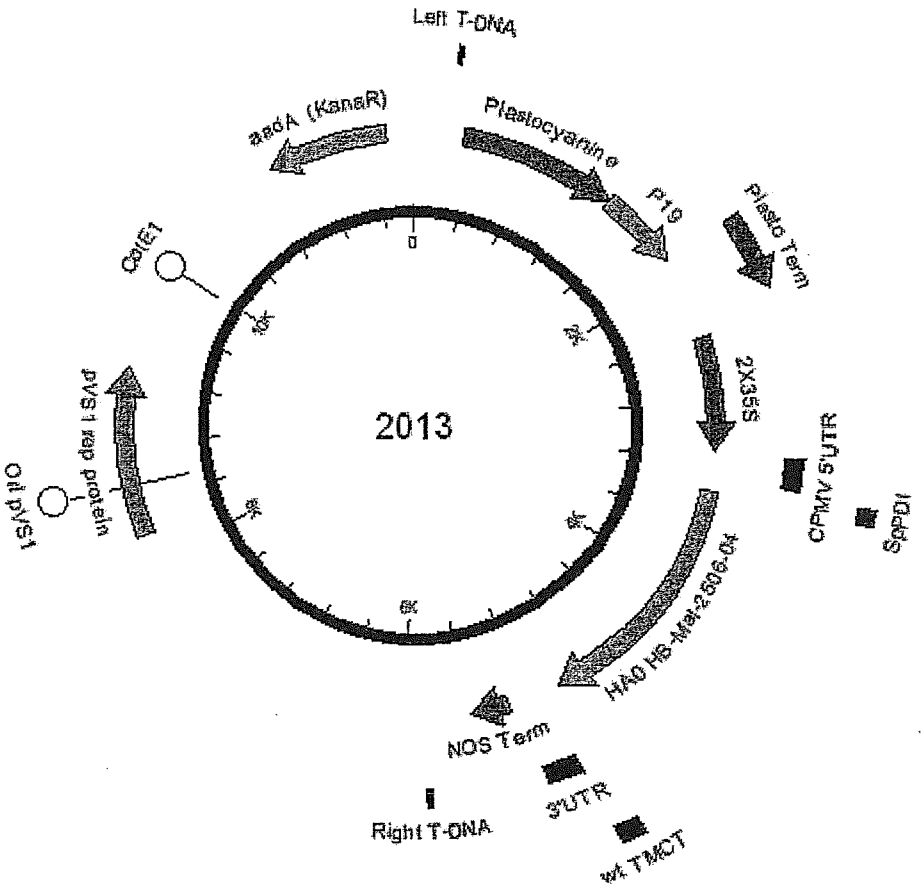
Figure 58C, SEQ ID NO: 164

Amino acid sequence of PDISP/HA B Malaysia

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSHFANLKGTETRGKLCPKCLNCTDLDVALG
RPKCTGNIPSARVSILHEVRPVTSGCFPIMHDRTKIRQLPKLLRGYEHIRLSTHNVINAENAPGGPYKIGTSGSCPNVTNGNGFFATMAW
AVPKNDNNKTATNSLTIEVPYICTEGEDQITVWGFHSDNETQMAKLYGDSKPQKFTSSANGVTTHYVSQIGGFPNQTEDGGLPQSGRI
VVDYMVQKSGKTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTK
YRPPAKLLKERGFFGAIAGFLEGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEIL
ELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFDAGEFSLPTFDSLN
ITAASLNDDGLDNHTILLYYSTAASSLAVTLMIAIFVVYMVSRDNVSCSICL*

Figure 58D

Schematic representation of construct number 2013



2X35S/CPMV 160+/PDISP/HA B Malaysia with deleted proteolytic loop/NOS (Construct no 2014)

Figure 59A, SEQ ID NO: 165

Nucleotide sequence of PDISP/HA B Malaysia with deleted proteolytic loop

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGATCGAA
TCTGCACTGGGATAACATCGTCAAACTCACCACATGTTGTCAAAACTGCTACTCAAGGGGAGGTCAATGTGACTGGTGT
AATACCACTGACAACAACACCCACCAAATCTCATTTTGCAAATCTCAAAGGAACAGAAACCAGAGGGAAACTATGCCCA
AAATGCCTCAACTGCACAGATCTGGACGTGGCCTTGGGCAGACCAAAATGCACGGGGAACATACCCTCGGCAAGAGTTT
CAATACTCCATGAAGTCAGACCTGTTACATCTGGGTGCTTTCCTATAATGCACGACAGAACAAAAATTAGACAGCTGCC
TAAACTTCTCAGAGGATACGAACATATCAGGTTATCAACTCATAACGTTATCAATGCAGAAAATGCACCAGGAGGACCC
TACAAAATTGGAACCTCAGGGTCTTGCCCTAACGTTACCAATGGAAACGGATTTTTCGCAACAATGGCTTGGGCCGTCC
CAAAAAACGACAACAACAAAACAGCAACAAATTCATTAACAATAGAAGTACCATACATTTGTACAGAAGGAGAAGACCA
AATTACCGTTTGGGGGTTCCACTCTGATAACGAAACCCAAATGGCAAAGCTCTATGGGGACTCAAAGCCCCAGAAGTTC
ACCTCATCTGCCAACGGAGTGACCACACATTACGTTTCACAGATTGGTGGCTTCCCAAATCAAACAGAAGACGGAGGAC
TACCACAAAGCGGTAGAATTGTTGTTGATTACATGGTGCAAAAATCTGGGAAAACAGGAACAATTACCTATCAAAGAGG
TATTTTATTGCCTCAAAAAGTGTGGTGCGCAAGTGGCAGGAGCAAGGTAATAAAAGGATCGTTGCCTTTAATTGGAGAA
GCAGATTGCCTCCACGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGGGAACATGCAAAGGCCATAG
GAAATTGCCCAATATGGGTGAAAACACCCTTGAAGCTGGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGA
AGGAATGATTGCAGGTTGGCACGGATACACATCCCATGGGGCACATGGAGTAGCGGTGGCAGCAGACCTTAAGAGCACT
CAAGAGGCCATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTGAGCTGGAAGTAAAGAATCTTCAAAGACTAAGCG
GTGCCATGGATGAACTCCACAACGAAATACTAGAACTAGACGAGAAAGTGGATGATCTCAGAGCTGATACAATAAGCTC
ACAAATAGAACTCGCAGTCCTGCTTTCCAATGAAGGAATAATAAACAGTGAAGATGAGCATCTCTTGGCGCTTGAAAGA
AAGCTGAAGAAAATGCTGGGCCCCTCTGCTGTAGAGATAGGGAATGGATGCTTTGAAACCAAACACAAGTGCAACCAGA
CCTGTCTCGACAGAATAGCTGCTGGTACCTTTGATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCACTGAATATTAC
TGCTGCATCTTTAAATGACGATGGATTGGATAATCATACTATACTGCTTTACTACTCAACTGCTGCCTCCAGTTTGGCT
GTAACATTGATGATAGCTATCTTTGTTGTTTATATGGTCTCCAGAGACAATGTTTCTTGCTCCATCTGTCTATAA

Figure 59B, SEQ ID NO: 166

HBM250604(PrL-).r

CATTCCTTCCCATCCTCCACCAGGAGGTCTATATTTGGTTCCATTGGC

Figure 59C, SEQ ID NO: 167

HBM250604(PrL-).c

AGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGA

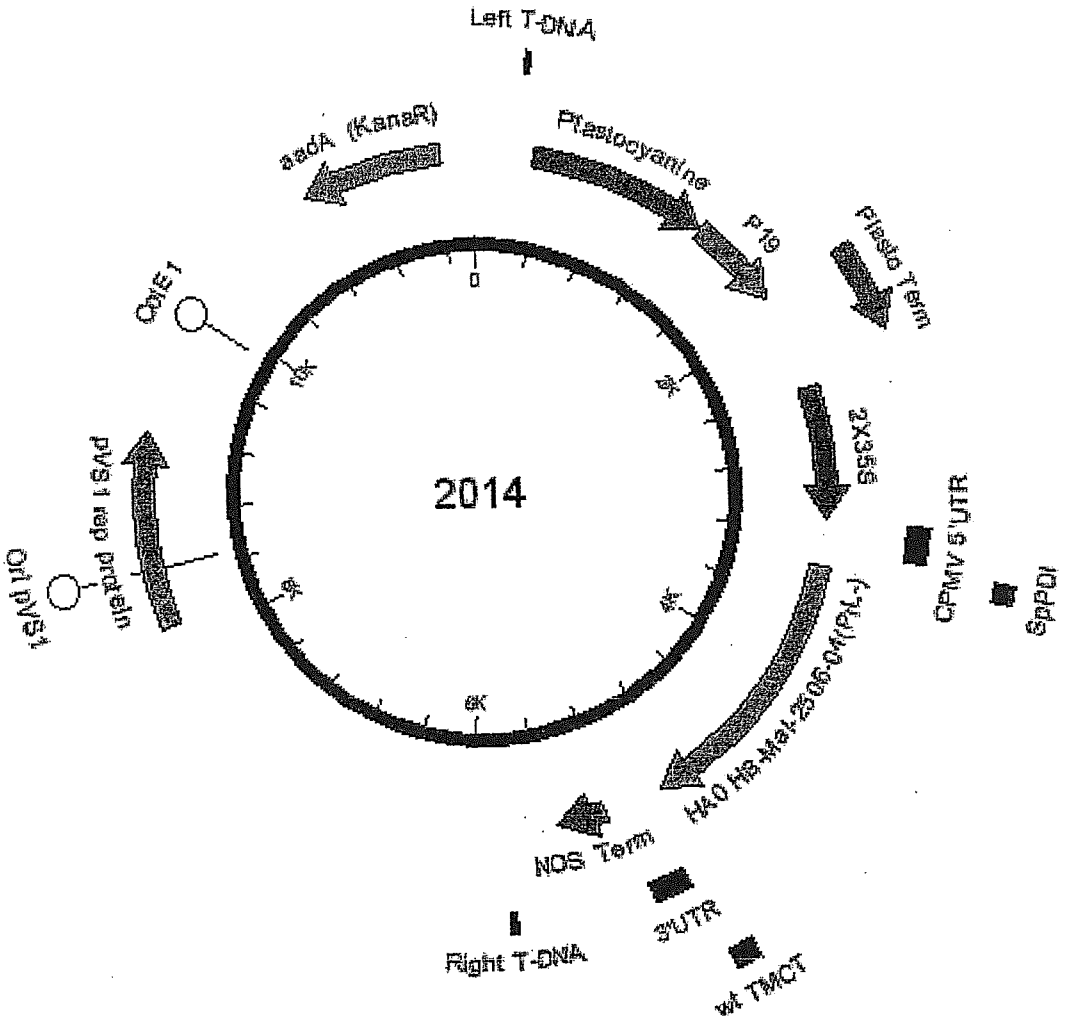
Figure 59D, SEQ ID NO: 168

Amino acid sequence of PDISP/HA B Malaysia with deleted proteolytic loop

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSHFANLKGTETRGKLCPKCLNCTDLDVALG
RPKCTGNIPSARVSILHEVRPVTSGCFPIMHDRTKIRQLPKLLRGYEHIRLSTHNVINAENAPGGPYKIGTSGSCPNVTNGNGFFATMAW
AVPKNDNNKTATNSLTIEVPYICTEGEDQITVWGFHSDNETQMAKLYGDSKPQKFTSSANGVTTHYVSQIGGFPNQTEDGGLPQSGRI
VVDYMVQKSGKTGTITYQRGILLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTK
YRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISS
QIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFDAGEFSLPTFDSLNITAASLNDDGLDNHT
ILLYYSTAASSLAVTLMIAIFVVYMVSRDNVSCSICL*

Figure 59E

Schematic representation of construct number 2014



2X35S/CPMV HT (construct no 2070), HT+ (construct no 2080) and 160+ (-Mprot) (construct no 2090) for PDISP/HA B Massachusetts

Figure 60A, SEQ ID NO: 169

Nucleotide sequence of PDISP/HA B Massachusetts

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCCGATCGAATCTGCACTG
GGATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCTACTCAAGGGGAGGTCAATGTGACTGGTGTGATACCACTAACAAC
AACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAAGACCAGAGGGAAACTATGCCCAGACTGTCTCAACTGTACAGATC
TGGATGTGGCCCTGGGCAGGCCAATGTGTGTGGGAACTACACCTTCTGCGAAAGCTTCAATACTTCACGAAGTCAGACCTGTTAC
ATCCGGGTGCTTCCCTATAATGCACGACAGAACAAAAATCAGGCAACTAGCCAATCTTCTCAGAGGATATGAAAATATCAGGTTAT

CAACCCAAAACGTTATCGATGCAGAAAAGGCACCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAG
TAAAAGCGGATTTTTCGCAACAATGGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCATTAACAGTAGAAGTA
CCATACATTTGTGCAGAAGGGGAAGACCAAATTACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATG
GAGACTCAAATCCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACATTATGTTTCTCAGATTGGCGGCTTCCCAGATCAAA
CAGAAGACGGAGGACTACCACAAAGCGGCAGAATTGTCGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCT
ATCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCCTTGCCTTTAATTGG
TGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATGCAAAAGCCATAGG
AAATTGCCCAATATGGGTGAAAACACCTTTGAAGCTTGCCAATGGAACCAAATATAGACCTCCTGCAAAACTATTAAAGGAAAGG
GGTTTCTTCGGAGCTATTGCTGGTTTCCTAGAAGGAGGATGGGAAGGAATGATTGCAGGTTGGCACGGATACACATCTCACGGA
GCACATGGAGTGGCAGTTGCTGCAGACCTTAAGAGCACACAAGAAGCTATAAACAAGATAACAAAAAATCTCAACTCTTTGAGTG
AGCTAGAAGTAAAGAATCTTCAAAGGCTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGG
ATGACCTCAGAGCTGACACTATAAGTTCACAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGACGA
GCATCTATTGGCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGACATAGGAAATGGATGCTTCGAAACCAAA
CACAAATGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAGTTTTCTCTCCCCACTTTTGATTCATTG
AACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGCTGCTTCTAGTTTGGCTG
TAACATTGATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGACAACGTTTCATGCTCCATCTGTCTATAA

Figure 60B, SEQ ID NO: 170

Amino acid sequence of PDISP/HA B Massachusetts

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTKTRGKLCPDCLNCTDLDVALG
RPMCVGTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLANLLRGYENIRLSTQNVIDAEKAPGGPYRLGTSGSCPNATSKSGFFATMA
WAVPKDNNKNATNPLTVEVPYICAEGEDQITVWGFHSDNKTQMKNLYGDSNPQKFTSSANGVTTHYVSQIGGFPDQTEDGGLPQSG
RIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLAN
GTKYRPPAKLLKERGFFGAIAGFLEGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELH
NEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTF
DSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMLAIFIVYMVSRDNVSCSICL*

Figure 60C

Schematic representation of construct number 2070

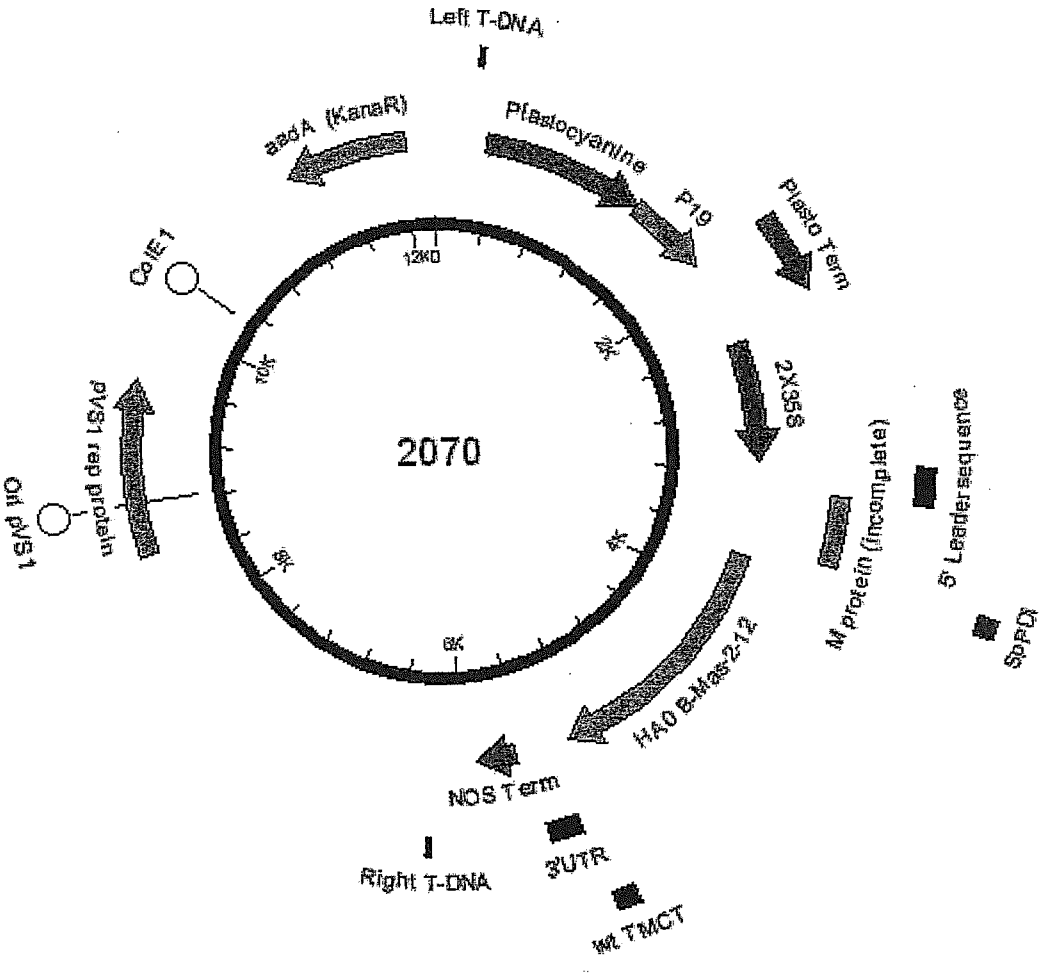


Figure 60D

Schematic representation of construct number 2080

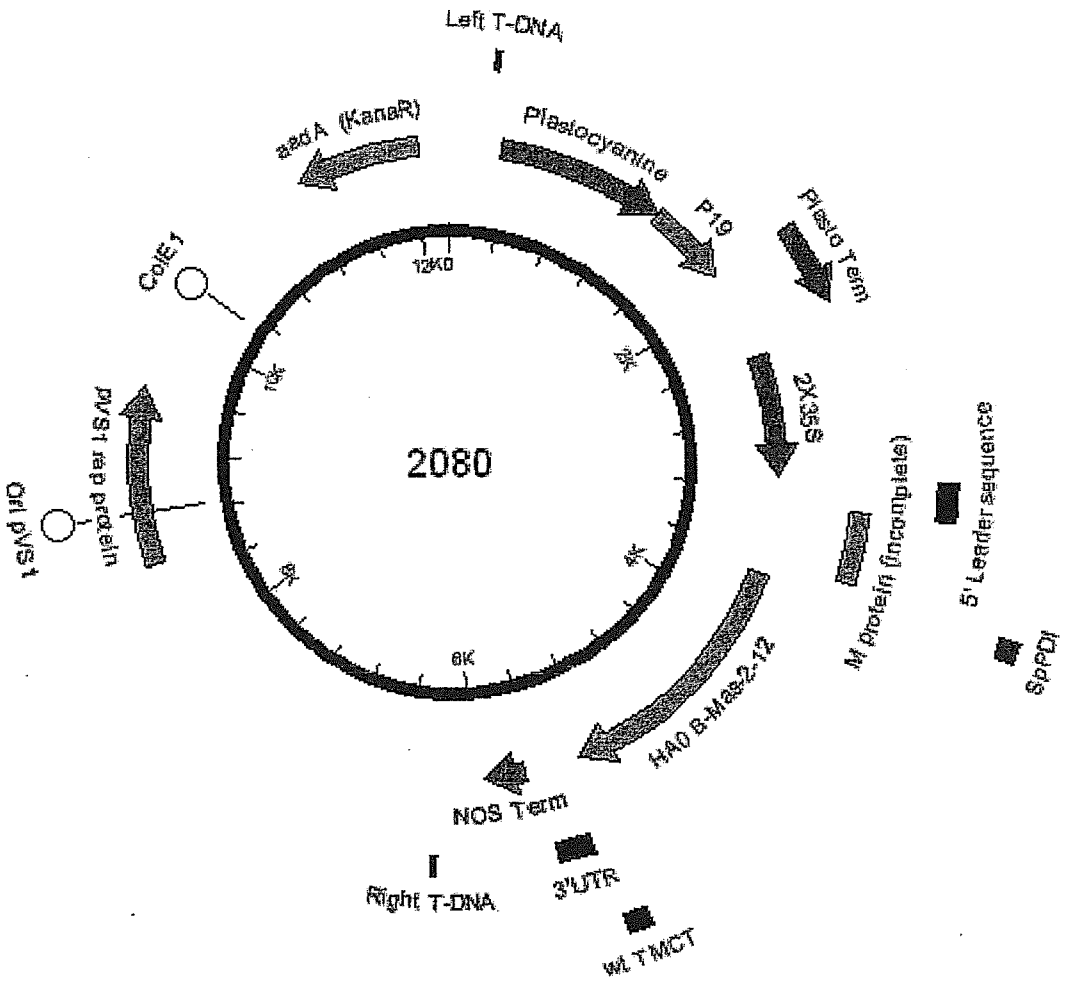
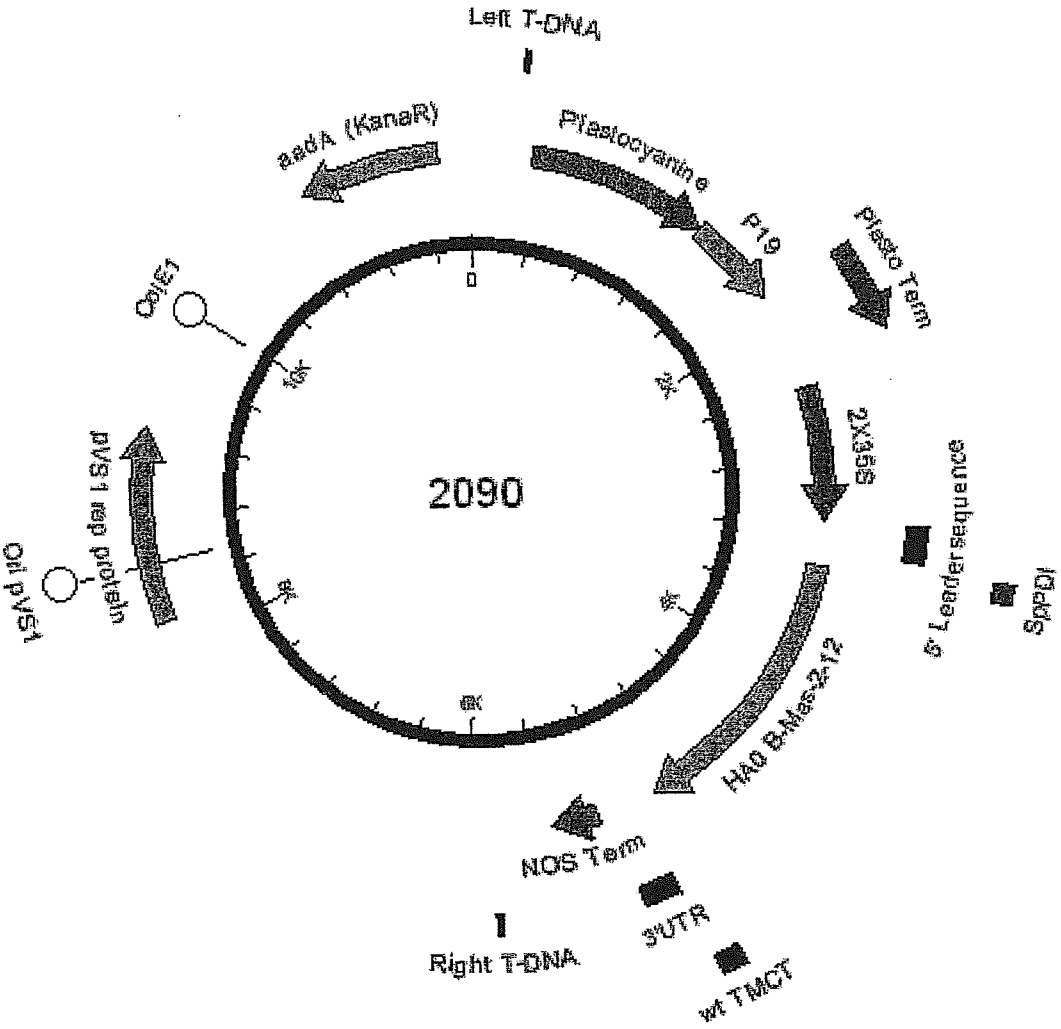


Figure 60E

Schematic representation of construct number 2090



2X35S/CPMV HT+/ PDISP/B Florida with proteolytic loop deleted/ NOS (Construct number 2102) and 2X35S/CPMV HT+/ BeYDV/PDISP/B Florida with proteolytic loop deleted/ NOS (Construct number 2104)

Fig 61A SEQ ID NO: 190

HBF406(PrL-).r (construct 2102 and 2104)

TCCTTCCCATCCTCCACCAGGAGGTCTATATTTGGTTCCATTGGCGAGCTTCAAAG

Fig 61B SEQ ID NO: 191

HBF406(PrL-).c (construct 2102 and 2104)

ATATAGACCTCCTGGTGGAGGATGGGAAGGAATGATTGCAGGCTGGCACGGA

Fig 61C SEQ ID NO: 192

IF*-HBF406.s1-6r (construct 2102 and 2104)

ACTAAAGAAAATAGGCCTTTATAGACAGATGGAGCATGAAACGTTGTCTC

Fig 61D SEQ ID NO: 193

Nucleotide sequence of PDISP/HA B Florida with deleted proteolytic loop (construct 2102 and 2104)

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGATCGAA
TCTGCACTGGAATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCCACTCAAGGGGAGGTCAATGTGACTGGTGT
GATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAGGGAAACTATGCCCA
GACTGTCTCAACTGCACAGATCTGGATGTGGCTTTGGGCAGACCAATGTGTGTGGGGACCACACCTTCGGCGAAGGCTT
CAATACTCCACGAAGTCAAACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAAAATCAGGCAACTACC
CAATCTTCTCAGAGGATATGAAAATATCAGGCTATCAACCCAAAACGTCATCGATGCGGAAAAGGCACCAGGAGGACCC
TACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAGAGCGGATTTTTCGCAACAATGGCTTGGGCTGTCC
CAAAGGACAACAACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAAGGGGAAGACCAAAT
CACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATGGAGACTCAAATCCTCAAAAGTTCACC
TCATCTGCTAATGGAGTAACCACACACTATGTTTCTCAGATTGGCAGCTTCCCAGATCAAACAGAAGACGGAGGACTAC
CACAAAGCGGCAGGATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTACCAAAGAGGTGT
TTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCCTTGCCTTTAATTGGTGAAGCA
GATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATGCAAAAGCCATAGGAA
ATTGCCCAATATGGGTGAAAACACCTTTGAAGCTCGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAGG
AATGATTGCAGGCTGGCACGGATACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCGGACCTTAAGAGTACGCAA
GAAGCTATAAACAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAATCTTCAAAGACTAAGTGGTG
CCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGACACTATAAGCTCGCA
AATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGATGAGCATCTATTGGCACTTGAGAGAAAA
CTAAAGAAAATGCTGGGTCCCTCTGCTGTAGAGATAGGAAATGGATGCTTCGAAACCAAACACAAGTGCAACCAGACCT
GCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCACTGAACATTACTGC
TGCATCTTTAAATGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGCTGCTTCTAGTTTGGCTGTA
ACATTGATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGACAACGTTTCATGCTCCATCTGTCTATAA

Fig 61E SEQ ID NO: 194

Amino acid sequence of PDISP/HA B Florida with deleted proteolytic loop (construct 2102 and 2104)

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTRTRGKLCP
DCLNCTDLDVALGRPMCVGTTPSAKASILHEVKPVTSGCFPIMHDRTKIRQLPNLLRGYENIRLSTQNVIDAEKAPGGP
YRLGTSGSCPNATSKSGFFATMAWAVPKDNNKNATNPLTVEVPYICTEGEDQITVWGFHSDNKTQMKNLYGDSNPQKFT
SSANGVTTHYVSQIGSFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEA

DCLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQ
EAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERK
LKKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNHTILLYYSTAASSLAV
TLMLAIFIVYMVSRDNVSCSICL*

Fig 61F SEQ ID NO: 195

Expression cassette number 2102 from 2X35S promoter to NOS terminator. PDISP/ HA B Florida with deleted proteolytic loop nucleotide sequence is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTG
AGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGAT
AGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGAC
AGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAG
TGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCA
AAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTT
ATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATG
CCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTC
TTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCT
TCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAA
ACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGA
TCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTG
GACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCT
GGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCT
TGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGA
AACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCC
AATACCGCGGAGAAAATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGA
TCTTCGCGGATCGAATCTGCACTGGAATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCCACTCAAGGGGAGGT
CAATGTGACTGGTGTGATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGA
GGGAAACTATGCCCAGACTGTCTCAACTGCACAGATCTGGATGTGGCTTTGGGCAGACCAATGTGTGTGGGGACCACAC
CTTCGGCGAAGGCTTCAATACTCCACGAAGTCAAACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAA
AATCAGGCAACTACCCAATCTTCTCAGAGGATATGAAAATATCAGGCTATCAACCCAAAACGTCATCGATGCGGAAAAG
GCACCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAGAGCGGATTTTTCGCAACAA
TGGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGA
AGGGGAAGACCAAATCACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATGGAGACTCAAAT
CCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACACTATGTTTCTCAGATTGGCAGCTTCCCAGATCAAACAG
AAGACGGAGGACTACCACAAAGCGGCAGGATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGT
CTACCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCCTTGCCT
TTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATG
CAAAAGCCATAGGAAATTGCCCAATATGGGTGAAAACACCTTTGAAGCTCGCCAATGGAACCAAATATAGACCTCCTGG
TGGAGGATGGGAAGGAATGATTGCAGGCTGGCACGGATACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCGGAC
CTTAAGAGTACGCAAGAAGCTATAAACAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAATCTTC
AAAGACTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGA
CACTATAAGCTCGCAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGATGAGCATCTATTG
GCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGAGATAGGAAATGGATGCTTCGAAACCAAACACA
AGTGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTC
ACTGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGCTGCT
TCTAGTTTGGCTGTAACATTGATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGACAACGTTTCATGCTCCATCT
GTCTATAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTG
TGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACA
CAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCG
TTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTG
AATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGC
AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTAT
GTTACTAGAT

Fig 61G

Schematic representation of construct number 2102

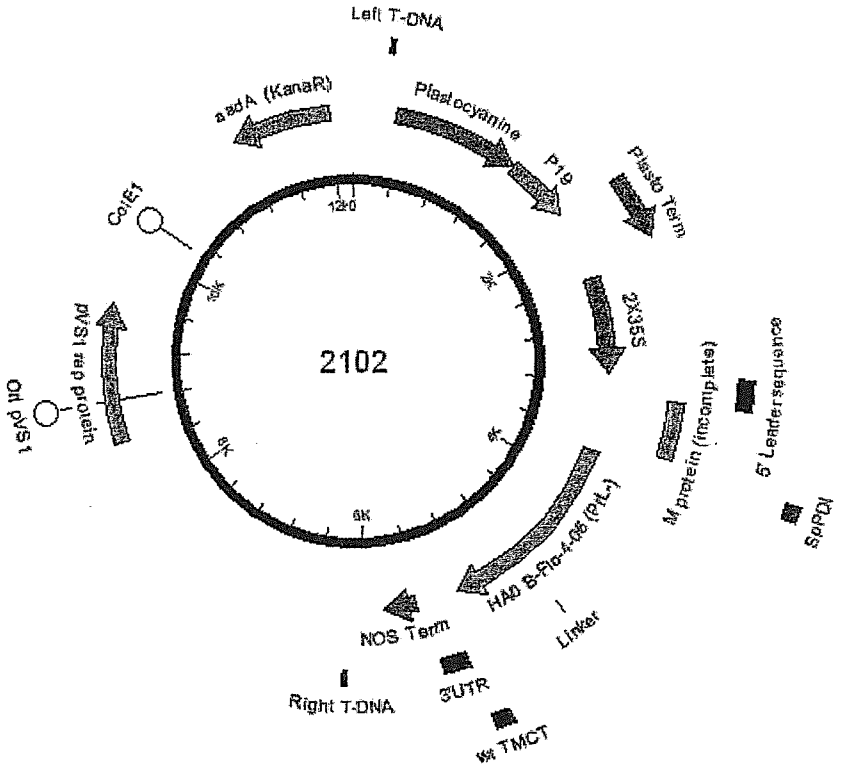


Fig 61H SEQ ID NO: 196

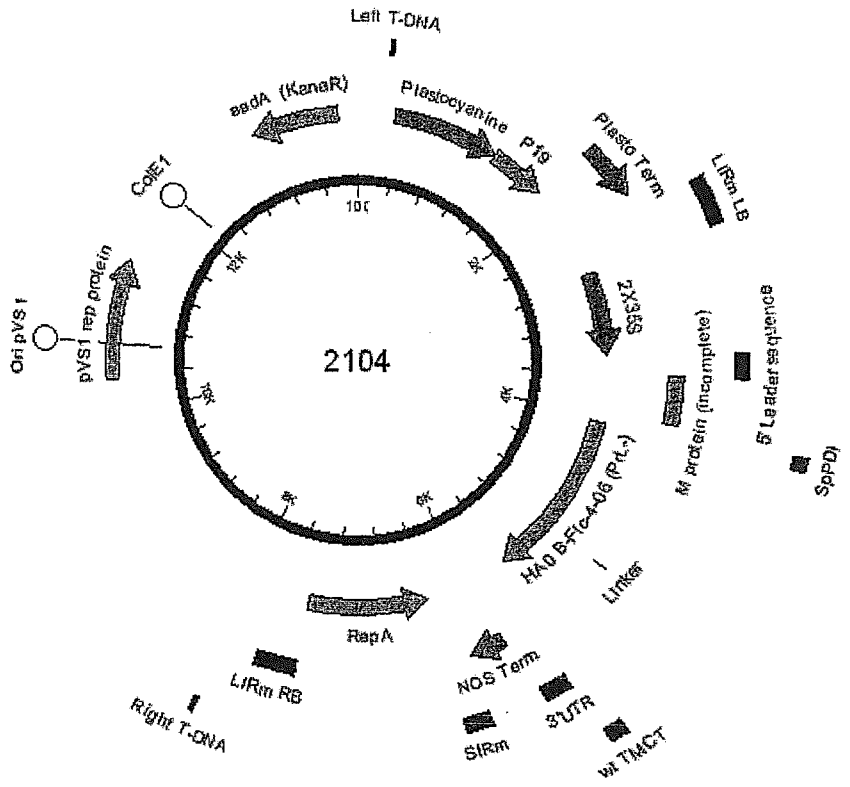
Expression cassette number 2104 from left to right LIR. PDISP/ HA B Florida with deleted proteolytic loop nucleotide sequence is underlined.

TGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCTATCTTATAACCGGCGTGGAGGCATGGAGGCAGGGGTATTTTGGT
CATTTTAATAGATAGTGGAAAATGACGTGGAATTTACTTAAAGACGAAGTCTTTGCGACAAGGGGGGGCCCACGCCGAA
TTTAATATTACCGGCGTGGCCCCCCCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTTAAAGTAGAAAATTTCCC
GCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTTGGTCGACAAGCTTGCATGCCGG
TCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGA
GACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATA
GTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACA
GTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGT
GGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAA
AGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTA
TTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGC
CTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCT
TCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTT
CCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAA
CCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGAT
CTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGG
ACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCTG
GAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTT
GACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGAA
ACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCA
ATACCGCGGAGAAAATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGAT
CTTCGCGGATCGAATCTGCACTGGAATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCCACTCAAGGGGAGGTC
AATGTGACTGGTGTGATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAG
GGAAACTATGCCCAGACTGTCTCAACTGCACAGATCTGGATGTGGCTTTGGGCAGACCAATGTGTGTGGGGACCACACC
TTCGGCGAAGGCTTCAATACTCCACGAAGTCAAACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAAA

ATCAGGCAACTACCCAATCTTCTCAGAGGATATGAAAATATCAGGCTATCAACCCAAAACGTCATCGATGCGGAAAAGG
CACCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAGAGCGGATTTTTCGCAACAAT
GGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAA
GGGGAAGACCAAATCACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATGGAGACTCAAATC
CTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACACTATGTTTCTCAGATTGGCAGCTTCCCAGATCAAACAGA
AGACGGAGGACTACCACAAAGCGGCAGGATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTC
TACCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCCTTGCCTT
TAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATGC
AAAAGCCATAGGAAATTGCCCAATATGGGTGAAAACACCTTTGAAGCTCGCCAATGGAACCAAATATAGACCTCCTGGT
GGAGGATGGGAAGGAATGATTGCAGGCTGGCACGGATACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCGGACC
TTAAGAGTACGCAAGAAGCTATAAACAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAATCTTCA
AAGACTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGAC
ACTATAAGCTCGCAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGATGAGCATCTATTGG
CACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGAGATAGGAAATGGATGCTTCGAAACCAAACACAA
GTGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCA
CTGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACCATACTATACTGCTCTATTACTCAACTGCTGCTT
CTAGTTTGGCTGTAACATTGATGCTAGCTATTTTTATTGTTTATATGGTCTCCAGAGACAACGTTTCATGCTCCATCTG
TCTATAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGT
GCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACAC
AAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGT
TCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGA
ATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCA
ATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATG
TTACTAGATCTCTAGAGTCTCAAGCTTGGCGCGCCATAAAATGATTATTTTATGAATATATTTCATTGTGCAAGTAGAT
AGAAATTACATATGTTACATAACACACGAAATAAACAAAAAAAAGACAATCCAAAAACAAACACCCCAAAAAAAATAATC
ACTTTAGATAAACTCGTATGAGGAGAGGCACGTTCAGTGACTCGACGATTCCCGAGCAAAAAAAGTCTCCCCGTCACAC
ATATAGTGGGTGACGCAATTATCTTTAAAGTAATCCTTCTGTTGACTTGTCATTGATAACATCCAGTCTTCGTCAGGAT
TGCAAAGAATTATAGAAGGGATCCCACCTTTTATTTTCTTCTTTTTTCCATATTTAGGGTTGACAGTGAAATCAGACTG
GCAACCTATTAATTGCTTCCACAATGGGACGAACTTGAAGGGGATGTCGTCGATGATATTATAGGTGGCGTGTTCATCG
TAGTTGGTGAAATCGATGGTACCGTTCCAATAGTTGTGTCGTCCGAGACTTCTAGCCCAGGTGGTCTTTCCGGTACGAG
TTGGTCCGCAGATGTAGAGGCTGGGGTGTCGGATTCCATTCCTTCCATTGTCCTGGTTAAATCGGCCATCCATTCAAGG
TCAGATTGAGCTTGTTGGTATGAGACAGGATGTATGTAAGTATAAGCGTCTATGCTTACATGGTATAGATGGGTTTCCC
TCCAGGAGTGTAGATCTTCGTGGCAGCGAAGATCTGATTCTGTGAAGGGCGACACATACGGTTCAGGTTGTGGAGGGAA
TAATTTGTTGGCTGAATATTCCAGCCATTGAAGTTTTGTTGCCCATTCATGAGGGAATTCTTCCTTGATCATGTCAAGA
TATTCCTCCTTAGACGTTGCAGTCTGGATAATAGTTCTCCATCGTGCGTCAGATTTGCGAGGAGAGACCTTATGATCTC
GGAAATCTCCTCTGGTTTTAATATCTCCGTCCTTTGATATGTAATCAAGGACTTGTTTAGAGTTTCTAGCTGGCTGGAT
ATTAGGGTGATTTCCTTCAAAATCGAAAAAAGAAGGATCCCTAATACAAGGTTTTTTATCAAGCTGGAGAAGAGCATGA
TAGTGGGTAGTGCCATCTTGATGAAGCTCAGAAGCAACACCAAGGAAGAAAATAAGAAAAGGTGTGAGTTTCTCCCAGA
GAAACTGGAATAAATCATCTCTTTGAGATGAGCACTTGGGATAGGTAAGGAAAACATATTTAGATTGGAGTCTGAAGTT
CTTACTAGCAGAAGGCATGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCTATCTTATAACCGGCGTGGAGGCATGGA
GGCAGGGGTATTTTGGTCATTTTAATAGATAGTGGAAAATGACGTGGAATTTACTTAAAGACGAAGTCTTTGCGACAAG
GGGGGGCCCACGCCGAATTTAATATTACCGGCGTGGCCCCCCCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTT
AAAGTAGAAAATTTCCCGCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTTG

Fig 61l

Schematic representation of construct number 2104



2X35S/CPMV HT+/ PDISP/B Florida +H1 California TMCT with proteolytic loop deleted / NOS (Construct number 2106) and 2X35S/CPMV HT+/ BeYDV/PDISP/B Florida +H1 California TMCT with proteolytic loop deleted/ NOS (Construct number 2108)

FIG 62A SEQ ID NO: 197

IF-H1cTMCT.S1-4r (Construct 2106 and 2108)

ACTAAAGAAAATAGGCCTTTAAATACATATTCTACACTGTAGAGAC

FIG 62B SEQ ID NO: 198

Nucleotide sequence of PDISP/HA B Florida+H1Cal TMCT with deleted proteolytic loop (construct 2106 and 2108)

ATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGATCTTCGCGGATCGAA
TCTGCACTGGAATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCCACTCAAGGGGAGGTCAATGTGACTGGTGT
GATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAGGGAAACTATGCCCA
GACTGTCTCAACTGCACAGATCTGGATGTGGCTTTGGGCAGACCAATGTGTGTGGGGACCACACCTTCGGCGAAGGCTT
CAATACTCCACGAAGTCAAACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAAAATCAGGCAACTACC
CAATCTTCTCAGAGGATATGAAAATATCAGGCTATCAACCCAAAACGTCATCGATGCGGAAAAGGCACCAGGAGGACCC
TACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAGAGCGGATTTTTCGCAACAATGGCTTGGGCTGTCC
CAAAGGACAACAACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAAGGGGAAGACCAAAT
CACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATGGAGACTCAAATCCTCAAAAGTTCACC
TCATCTGCTAATGGAGTAACCACACACTATGTTTCTCAGATTGGCAGCTTCCCAGATCAAACAGAAGACGGAGGACTAC
CACAAAGCGGCAGGATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTCTACCAAAGAGGTGT
TTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCCTTGCCTTTAATTGGTGAAGCA
GATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATGCAAAAGCCATAGGAA
ATTGCCCAATATGGGTGAAAACACCTTTGAAGCTCGCCAATGGAACCAAATATAGACCTCCTGGTGGAGGATGGGAAGG
AATGATTGCAGGCTGGCACGGATACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCGGACCTTAAGAGTACGCAA

GAAGCTATAAACAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAATCTTCAAAGACTAAGTGGTG
CCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGACACTATAAGCTCGCA
AATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGATGAGCATCTATTGGCACTTGAGAGAAAA
CTAAAGAAAATGCTGGGTCCCTCTGCTGTAGAGATAGGAAATGGATGCTTCGAAACCAAACACAAGTGCAACCAGACCT
GCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTGATTCACTGAACATTACTGC
TGCATCTTTAAATGATGATGGATTGGATAACTACCAGATTTTGGCGATCTATTCAACTGTCGCCAGTTCATTGGTACTG
GTAGTCTCCCTGGGGGCAATCAGTTTCTGGATGTGCTCTAATGGGTCTCTACAGTGTAGAATATGTATTTAA

FIG 62C SEQ ID NO: 199

Amino acid sequence of PDISP/HA B Florida+H1Cal TMCT with deleted proteolytic loop (construct 2106 and 2108)

MAKNVAIFGLLFSLLVLVPSQIFADRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTRTRGKLCP
DCLNCTDLDVALGRPMCVGTTPSAKASILHEVKPVTSGCFPIMHDRTKIRQLPNLLRGYENIRLSTQNVIDAEKAPGGP
YRLGTSGSCPNATSKSGFFATMAWAVPKDNNKNATNPLTVEVPYICTEGEDQITVWGFHSDNKTQMKNLYGDSNPQKFT
SSANGVTTHYVSQIGSFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEA
DCLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPGGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQ
EAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERK
LKKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNYQILAIYSTVASSLVL
VVSLGAISFWMCSNGSLQCRICI*

FIG 62D SEQ ID NO: 200

Expression cassette number 2106 from 2X35S promoter to NOS terminator. PDISP/ HA B Florida+H1Cal TMCT with deleted proteolytic loop nucleotide sequence is underlined.

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTG
AGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGAT
AGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGAC
AGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAG
TGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCA
AAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTT
ATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATG
CCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTC
TTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCT
TCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAA
ACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGA
TCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTG
GACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCT
GGAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCT
TGACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGA
AACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCC
AATACCGCGGAGAAAATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGA
TCTTCGCGGATCGAATCTGCACTGGAATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCCACTCAAGGGGAGGT
CAATGTGACTGGTGTGATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGA
GGGAAACTATGCCCAGACTGTCTCAACTGCACAGATCTGGATGTGGCTTTGGGCAGACCAATGTGTGTGGGGACCACAC
CTTCGGCGAAGGCTTCAATACTCCACGAAGTCAAACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAA
AATCAGGCAACTACCCAATCTTCTCAGAGGATATGAAAATATCAGGCTATCAACCCAAAACGTCATCGATGCGGAAAAG
GCACCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAGAGCGGATTTTTCGCAACAA
TGGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGA
AGGGGAAGACCAAATCACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATGGAGACTCAAAT
CCTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACACTATGTTTCTCAGATTGGCAGCTTCCCAGATCAAACAG
AAGACGGAGGACTACCACAAAGCGGCAGGATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGT
CTACCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCCTTGCCT
TTAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATG

CAAAAGCCATAGGAAATTGCCCAATATGGGTGAAAACACCTTTGAAGCTCGCCAATGGAACCAAATATAGACCTCCTGG
TGGAGGATGGGAAGGAATGATTGCAGGCTGGCACGGATACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCGGAC
CTTAAGAGTACGCAAGAAGCTATAAACAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAATCTTC
AAAGACTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGA
CACTATAAGCTCGCAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGATGAGCATCTATTG
GCACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGAGATAGGAAATGGATGCTTCGAAACCAAACACA
AGTGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTC
ACTGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACTACCAGATTTTGGCGATCTATTCAACTGTCGCC
AGTTCATTGGTACTGGTAGTCTCCCTGGGGGCAATCAGTTTCTGGATGTGCTCTAATGGGTCTCTACAGTGTAGAATAT
GTATTTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTG
TGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACA
CAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCG
TTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTG
AATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGC
AATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTAT
GTTACTAGAT

FIG 62E

Schematic representation of construct number 2106

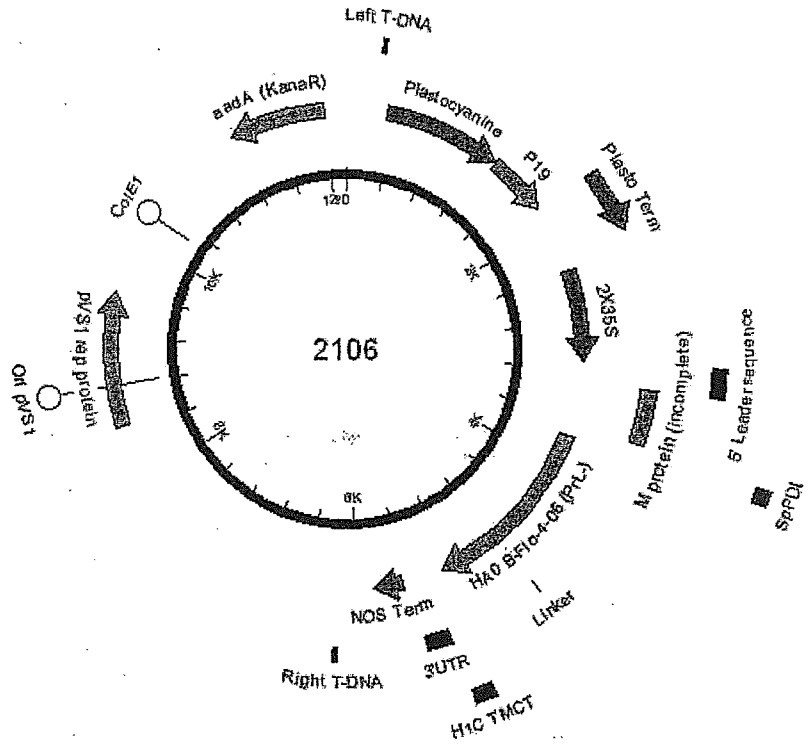


FIG 62F SEQ ID NO: 201

Expression cassette number 2108 from left to right LIR. PDISP/ HA B Florida+H1Cal TMCT with deleted proteolytic loop nucleotide sequence is underlined.

TGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCTATCTTATAACCGGCGTGGAGGCATGGAGGCAGGGGTATTTTGGT
CATTTTAATAGATAGTGGAAAATGACGTGGAATTTACTTAAAGACGAAGTCTTTGCGACAAGGGGGGGCCCACGCCGAA
TTTAATATTACCGGCGTGGCCCCCCCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTTAAAGTAGAAAATTTCCC
GCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTTGGTCGACAAGCTTGCATGCCGG
TCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGA
GACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATA
GTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACA
GTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGT
GGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAA
AGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTA
TTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGC
CTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCT
TCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTT
CCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAA
CCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGAT
CTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAACGTTTTCTTTCACTGAAGCGAAATCAAAGATCTCTTTGTGG
ACACGTAGTGCGGCGCCATTAAATAACGTGTACTTGTCCTATTCTTGTCGGTGTGGTCTTGGGAAAAGAAAGCTTGCTG
GAGGCTGCTGTTCAGCCCCATACATTACTTGTTACGATTCTGCTGACTTTCGGCGGGTGCAATATCTCTACTTCTGCTT
GACGAGGTATTGTTGCCTGTACTTCTTTCTTCTTCTTCTTGCTGATTGGTTCTATAAGAAATCTAGTATTTTCTTTGAA
ACAGAGTTTTCCCGTGGTTTTCGAACTTGGAGAAAGATTGTTAAGCTTCTGTATATTCTGCCCAAATTTGTCGGGCCCA
ATACCGCGGAGAAAATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGTGTTGGTTCCTTCTCAGAT
CTTCGCGGATCGAATCTGCACTGGAATAACATCTTCAAACTCACCTCATGTGGTCAAAACAGCCACTCAAGGGGAGGTC
AATGTGACTGGTGTGATACCACTAACAACAACACCAACAAAATCTTATTTTGCAAATCTCAAAGGAACAAGGACCAGAG
GGAAACTATGCCCAGACTGTCTCAACTGCACAGATCTGGATGTGGCTTTGGGCAGACCAATGTGTGTGGGGACCACACC
TTCGGCGAAGGCTTCAATACTCCACGAAGTCAAACCTGTTACATCCGGGTGCTTTCCTATAATGCACGACAGAACAAAA
ATCAGGCAACTACCCAATCTTCTCAGAGGATATGAAAATATCAGGCTATCAACCCAAAACGTCATCGATGCGGAAAAGG
CACCAGGAGGACCCTACAGACTTGGAACCTCAGGATCTTGCCCTAACGCTACCAGTAAGAGCGGATTTTTCGCAACAAT
GGCTTGGGCTGTCCCAAAGGACAACAACAAAAATGCAACGAACCCACTAACAGTAGAAGTACCATACATTTGTACAGAA
GGGGAAGACCAAATCACTGTTTGGGGGTTCCATTCAGATAACAAAACCCAAATGAAGAACCTCTATGGAGACTCAAATC
CTCAAAAGTTCACCTCATCTGCTAATGGAGTAACCACACACTATGTTTCTCAGATTGGCAGCTTCCCAGATCAAACAGA
AGACGGAGGACTACCACAAAGCGGCAGGATTGTTGTTGATTACATGATGCAAAAACCTGGGAAAACAGGAACAATTGTC
TACCAAAGAGGTGTTTTGTTGCCTCAAAAGGTGTGGTGCGCGAGTGGCAGGAGCAAAGTAATAAAAGGGTCCTTGCCTT
TAATTGGTGAAGCAGATTGCCTTCATGAAAAATACGGTGGATTAAACAAAAGCAAGCCTTACTACACAGGAGAACATGC
AAAAGCCATAGGAAATTGCCCAATATGGGTGAAAACACCTTTGAAGCTCGCCAATGGAACCAAATATAGACCTCCTGGT
GGAGGATGGGAAGGAATGATTGCAGGCTGGCACGGATACACATCTCACGGAGCACATGGAGTGGCAGTGGCGGCGGACC
TTAAGAGTACGCAAGAAGCTATAAACAAGATAACAAAAAATCTCAATTCTTTGAGTGAGCTAGAAGTAAAGAATCTTCA
AAGACTAAGTGGTGCCATGGATGAACTCCACAACGAAATACTCGAGCTGGATGAGAAAGTGGATGATCTCAGAGCTGAC
ACTATAAGCTCGCAAATAGAACTTGCAGTCTTGCTTTCCAACGAAGGAATAATAAACAGTGAAGATGAGCATCTATTGG
CACTTGAGAGAAAACTAAAGAAAATGCTGGGTCCCTCTGCTGTAGAGATAGGAAATGGATGCTTCGAAACCAAACACAA
GTGCAACCAGACCTGCTTAGACAGGATAGCTGCTGGCACCTTTAATGCAGGAGAATTTTCTCTCCCCACTTTTGATTCA
CTGAACATTACTGCTGCATCTTTAAATGATGATGGATTGGATAACTACCAGATTTTGGCGATCTATTCAACTGTCGCCA
GTTCATTGGTACTGGTAGTCTCCCTGGGGGCAATCAGTTTCTGGATGTGCTCTAATGGGTCTCTACAGTGTAGAATATG
TATTTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGT
GCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACAC
AAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAGACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGT
TCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGA
ATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCA
ATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATG
TTACTAGATCTCTAGAGTCTCAAGCTTGGCGCGCCATAAAATGATTATTTTATGAATATATTTCATTGTGCAAGTAGAT
AGAAATTACATATGTTACATAACACACGAAATAAACAAAAAAAGACAATCCAAAAACAAACACCCCAAAAAAAATAATC

ACTTTAGATAAACTCGTATGAGGAGAGGCACGTTCAGTGACTCGACGATTCCCGAGCAAAAAAAGTCTCCCCGTCACAC
ATATAGTGGGTGACGCAATTATCTTTAAAGTAATCCTTCTGTTGACTTGTCATTGATAACATCCAGTCTTCGTCAGGAT
TGCAAAGAATTATAGAAGGGATCCCACCTTTTATTTTCTTCTTTTTTCCATATTTAGGGTTGACAGTGAAATCAGACTG
GCAACCTATTAATTGCTTCCACAATGGGACGAACTTGAAGGGGATGTCGTCGATGATATTATAGGTGGCGTGTTCATCG
TAGTTGGTGAAATCGATGGTACCGTTCCAATAGTTGTGTCGTCCGAGACTTCTAGCCCAGGTGGTCTTTCCGGTACGAG
TTGGTCCGCAGATGTAGAGGCTGGGGTGTCGGATTCCATTCCTTCCATTGTCCTGGTTAAATCGGCCATCCATTCAAGG
TCAGATTGAGCTTGTTGGTATGAGACAGGATGTATGTAAGTATAAGCGTCTATGCTTACATGGTATAGATGGGTTTCCC
TCCAGGAGTGTAGATCTTCGTGGCAGCGAAGATCTGATTCTGTGAAGGGCGACACATACGGTTCAGGTTGTGGAGGGAA
TAATTTGTTGGCTGAATATTCCAGCCATTGAAGTTTTGTTGCCCATTCATGAGGGAATTCTTCCTTGATCATGTCAAGA
TATTCCTCCTTAGACGTTGCAGTCTGGATAATAGTTCTCCATCGTGCGTCAGATTTGCGAGGAGAGACCTTATGATCTC
GGAAATCTCCTCTGGTTTTAATATCTCCGTCCTTTGATATGTAATCAAGGACTTGTTTAGAGTTTCTAGCTGGCTGGAT
ATTAGGGTGATTTCCTTCAAAATCGAAAAAAGAAGGATCCCTAATACAAGGTTTTTTATCAAGCTGGAGAAGAGCATGA
TAGTGGGTAGTGCCATCTTGATGAAGCTCAGAAGCAACACCAAGGAAGAAAATAAGAAAAGGTGTGAGTTTCTCCCAGA
GAAACTGGAATAAATCATCTCTTTGAGATGAGCACTTGGGATAGGTAAGGAAAACATATTTAGATTGGAGTCTGAAGTT
CTTACTAGCAGAAGGCATGTTGTTGTGACTCCGAGGGGTTGCCTCAAACTCTATCTTATAACCGGCGTGGAGGCATGGA
GGCAGGGGTATTTTGGTCATTTTAATAGATAGTGGAAAATGACGTGGAATTTACTTAAAGACGAAGTCTTTGCGACAAG
GGGGGGCCCACGCCGAATTTAATATTACCGGCGTGGCCCCCCCTTATCGCGAGTGCTTTAGCACGAGCGGTCCAGATTT
AAAGTAGAAAATTTCCCGCCCACTAGGGTTAAAGGTGTTCACACTATAAAAGCATATACGATGTGATGGTATTTG

FIG 62G

Schematic representation of construct number 2108

