

Figure 1. DNA Sequence of the Insert and Adjacent Genomic DNA in MON 87705

The following DNA sequence (13243 bp) represents the consensus sequence of the overlapping PCR products spanning the insert in MON 87705. Base pairs 1-3279 (underlined) represent soybean genomic DNA flanking the 5' end of the insert. Base pairs 3280-10530 represent the inserted DNA, which corresponds to bases 7840 to 6652 in the plasmid PV-GMPQ/HT4404. The arrangement of the elements in MON 87705 is such that the gene suppression elements of T-DNA I and T-DNA II are inverted repeats. However, T-DNA I and T-DNA II are spatially separate in the plasmid. Base pairs 10531-13243 (double underlined) represents soybean genomic DNA flanking the 3' end of the insert. Base pairs 906-3279 (bold) and 10535-12908 (bold) represent the 2374 bases that were most likely duplicated from the 3' end of the insert during transformation. Base 2402 (larger font; bold) represents the single nucleotide change ('T') in the 5' duplicated 2374 base pair region compared to the corresponding base 12031('A') from the 3' end of the insert.

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1  ATTAGTACAA GTGTATGTGG ATGATATCAT TTTTGGTGCT ACTAATGAAA TGCTCTATGA
61 AGATTTTTTCT AAGTTAATGC AAAGTGAAGT TGAAATGAGC ATGATGGGAG AGCTAAAATT
121 CTTCTTTTGA CTGCAAATAA AGCAAACACC CCAAGGCATT TACATTCATC AGACCAAGTA
181 TGTGAAAAAT TAGTTGAAGA AGTTCAACAT AAGTGATGAA AAAGAGATGA AGACTTTTAT
241 GCATCCCACT ACACATCTTG GACTGGATGA GGAATCAATG AAGGTGGACG TGACTCAATA
301 CAAAGCAATG ATTGGATCAC TGCTCTATCT TAATGCTTCT AGGCCTTATA TAATTTTTAG
361 TGTTTTATTA TGTGCAAGAT TCCAAAAGGA ACCAAGGGAA GTTCATTTAA CTGCAGTTAA
421 ACCTATATTC TAATATTTAA TTAGAAGTCA TAACCTTGGT CTTATGCTTA AGAGAAGAGA
481 TAGTTTCAGA CTCATGAGCT ATTGAGATGT GGACTATGTT GGTGATAAAG TCGAAAGAAA
541 AAGTACAAGT GGAAGTTGTC ACTTTATAGG TGGCAACTTA GTCAGTTGGA TATGGAAGAA
601 GTAGGGATCA ACTACATTGT TCACTGCTGA AGTAGAATGC GTGTCAGTAG CCATGGAGGT
661 TACCCTCGAC ATTGAAGACC CCAAGAAATA GGTTCAAAGT TTTGGAATC CACAGGGTCA
721 GAGCACAAGT GCAAGTTTCA AGTATCAAGG CAGCAACGAA GCTATATCGT AGGTAGGGGA
781 GTTTAGTGGT ACCAATAATG CCCAAACACC CACTGGTGGG ACTCAAAATC TACAAGGGGA
841 GAGCAGAATG TCTTCTACAT CATCAATATC CAAACCAAGA TTCTCAAGAC CGTGAAACAA
901 AGGATCTCAG GGTGTTGTTA TCACTGCGGT TTGGCCTTTG GGCCAAGGCA CCGTTGTCCT
961 GAAAAAATA TGAGAGTTGT AATACTCGCT AAGGATGAGT AGATTAATGA AGACGGGGAG
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1261 ATTATATGAG ATTGGGGGAT AGTAACCGCA AATCCACTCA AGGATGTTGT AAGAACTTAA
1321 AAAATAGTTG GGAGCTTATA CCATGGTAGG ATATTTCTAT CTATTTAAGT TGGGAGGAGT
1381 GGACCTAATT ATTGGAGTTG CTTAGTTGGA AACATTGGGA GAAATTAAGG TGAATTGGAG
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1561 ATGATGTTCA TGTTGTGGGT AATTGAAAGC AACTATGTGG AACAAATTGA TTTAACAAAG
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1681 AGGGTTTACC ACCATCTAGA GAGGTTGATC ACAAGATTGC AATTAAGTCC GGGGCATATC
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1801 TGGTTGAGAT GTTATGATTG GGGATTATTA GACTAAGCAA TAGCTCCTAT TCTAGCCAG
1861 TAATTTTGGT AAAAAGGAAA GATGGAAGTT GACGATTATG TATGGATTAT CAGGCTTTAA

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2101 GATTAACAAA CACCCCGACC ACGTTCCAAT GAGCTATGAA TGCCACACTG AAACCGTTCC
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2221 CCCATTTGGA TCATTTGAGT TAGGTGTTGG CCAGGTTATT AGAACATTAT TTCTTCACAA
2281 ATGTTTTTAA AAAAAATGT AGTTTTGGTC AAATTAAGGC GGGTTGCTTA GGGCACGTTA
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4561 AACATTGGTT TCGGATTCAA CGCTATAAAT AAAACCACTC TCGTTGCTGA TTCCATTTAT
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4681 CGTACCCTTA GATCGTTCTT TTTCTTTTTT GTCTGCTGAT CGTTGCTCAT ATTATTTTGA
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5101	GCTCGCTTAG	CTCAGATGAT	AGAGCACCAC	AATTTTTGTG	GTAGAAATCG	GTTTGACTCC
5161	GATAGCGGCT	TTTTACTATG	ATTGTTTTGT	GTTAAAGATG	ATTTTCATAA	TGGTTATATA
5221	TGTCTACTGT	TTTTATTGAT	TCAATATTTG	ATTGTTCTTT	TTTTTGCAGA	TTTGTTGACC
5281	AGAGATCTAC	CATGGCGCAA	GTTAGCAGAA	TCTGCAATGG	TGTGCAGAAC	CCATCTCTTA
5341	TCTCCAATCT	CTCGAAATCC	AGTCAACGCA	AATCTCCCTT	ATCGGTTTCT	CTGAAGACGC
5401	AGCAGCATCC	ACGAGCTTAT	CCGATTTTCG	CGTCGTGGGG	ATTGAAGAAG	AGTGGGATGA
5461	CGTTAATTGG	CTCTGAGCTT	CGTCCTCTTA	AGGTCATGTC	TTCTGTTTTT	ACGGCGTGCA
5521	TGCTTCACGG	TGCAAGCAGC	CGTCCAGCAA	CTGCTCGTAA	GTCCTCTGGT	CTTTCTGGAA
5581	CCGTCCGTAT	TCCAGGTGAC	AAGTCTATCT	CCCACAGGTC	CTTCATGTTT	GGAGGTCTCG
5641	CTAGCGGTGA	AACTCGTATC	ACCGGTCTTT	TGGAAGGTGA	AGATGTTATC	AACACTGGTA
5701	AGGCTATGCA	AGCTATGGGT	GCCAGAATCC	GTAAGGAAGG	TGATACTTGG	ATCATTGATG
5761	GTGTTGGTAA	CGGTGGACTC	CTTGCTCCTG	AGGCTCCTCT	CGATTTCCGG	AACGCTGCAA
5821	CTGGTTGCCG	TTTGACTATG	GGTCTTGTTG	GTGTTTACGA	TTTCGATAGC	ACTTTCATTG
5881	GTGACGCTTC	TCTCACTAAG	CGTCCAATGG	GTCGTGTGTT	GAACCCACTT	CGCGAAATGG
5941	GTGTGCAGGT	GAAGTCTGAA	GACGGTGATC	GTCTTCCAGT	TACCTTGCGT	GGACCAAAGA
6001	CTCCAACGCC	AATCACCTAC	AGGGTACCTA	TGGCTTCCGC	TCAAGTGAAG	TCCGCTGTTT
6061	TGCTTGCTGG	TCTCAACACC	CCAGGTATCA	CCACTGTTAT	CGAGCCAATC	ATGACTCGTG
6121	ACCACACTGA	AAAGATGCTT	CAAGGTTTTG	GTGCTAACCT	TACCGTTGAG	ACTGATGCTG
6181	ACGGTGTGCG	TACCATCCGT	CTTGAAGGTC	GTGGTAAGCT	CACCGGTCAA	GTGATTGATG
6241	TTCCAGGTGA	TCCATCCTCT	ACTGCTTTCC	CATTGGTTGC	TGCCTTGCTT	GTTCCAGGTT
6301	CCGACGTCAC	CATCCTTAAC	GTTTTGATGA	ACCCAACCCG	TACTGGTCTC	ATCTTGACTC
6361	TGCAGGAAAT	GGGTGCCGAC	ATCGAAGTGA	TCAACCCACG	TCTTGCTGGT	GGAGAAGACG
6421	TGGCTGACTT	GCGTGTTTCG	TCTTCTACTT	TGAAGGGTGT	TACTGTTCCA	GAAGACCGTG
6481	CTCCTTCTAT	GATCGACGAG	TATCCAATTC	TCGCTGTTGC	AGCTGCATTC	GCTGAAGGTG
6541	CTACCGTTAT	GAACGGTTTG	GAAGAATCTC	GTGTTAAGGA	AAGCGACCGT	CTTCTCGCTG
6601	TCGCAAACGG	TCTCAAGCTC	AACGGTGTTG	ATTGCGATGA	AGGTGAGACT	TCTCTCGTCG
6661	TGCGTGCTCG	TCCTGACGGT	AAGGGTCTCG	GTAACGCTTC	TGGAGCAGCT	GTCGCTACCC
6721	ACCTCGATCA	CCGTATCGCT	ATGAGCTTCC	TCGTTATGGG	TCTCGTTTCT	GAAAACCCTG
6781	TTACTGTTGA	TGATGCTACT	ATGATCGCTA	CTAGCTTCCC	AGAGTTCATG	GATTTGATGG
6841	CTGGTCTTGG	AGCTAAGATC	GAAGTCTCCG	ACACTAAGGC	TGCTTGATGA	GCTCAAGAAT
6901	TCGAGCTCGG	TACCGGATCC	TAAGATCTTA	GGATCCTCTA	GCTAGAGCTT	TCGTTCTGAT
6961	CATCGGTTTC	GACAACGTTT	GTCAAGTTCA	ATGCATCAGT	TTCATTGCGC	ACACACCAGA
7021	ATCCTACTGA	GTTTGAGTAT	TATGGCATTG	GGAAAATGTT	TTTTCTTGTA	CCATTTGTTG
7081	TGCTTGTAAT	TTACTGTGTT	TTTTATTTCG	TTTTCGCTAT	CGAACTGTGA	AATGGAAATG
7141	GATGGAGAAG	AGTTAATGAA	TGATATGGTC	CTTTTGTTCA	TTCTCAAATT	AATATTATTT
7201	GTTTTTTTCT	TTATTTGTTG	TGTGTTGAAT	TTGAAATTAT	AAGAGATATG	CAAACATTTT
7261	GTTTTGAGTA	AAAATGTGTC	AAATCGTGGC	CTCTAATGAC	CGAAGTTAAT	ATGAGGAGTA
7321	AAACACTTGT	AGTTGTACCA	TTATGCTTAT	TCAGTAGGCA	ACAAATATAT	TTTCAGACCT
7381	AGAAAAGCTG	CAAATGTTAC	TGAATACAAG	TATGTCCTCT	TGTGTTTTAG	ACATTTATGA
7441	ACTTTCCTTT	ATGTAATTTT	CCAGAATCCT	TGTCAGATTC	TAATCATTGC	TTTATAATTA
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7561	TGCCAATTGA	TTGACAACAT	GCATCAATCG	ACCTGCAGCC	ACTCGAAGCG	CCCCAACCCG
7621	GGGGCCTATA	TGGCCCGGTC	CGGCGGCCGC	GGTACGGTCG	ACTCTAGAGG	ATCCCCGGCA
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7921	GTGTCCATTG	CATTTGACTA	TGTGGATAGT	GTTTTGATCC	AGGCCTCCAT	TTGCCGCTTA
7981	TTAATTAATT	TGGTAACAGT	CCGTACTAAT	CAGTTACTTA	TCCTTCCTCC	ATCATAATTA
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