

CT90, 66 or 76cM, Chromosome 6

Christopher Martin and Douglas Maxwell, University of Wisconsin Madison
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Primer Name	Primer Sequence (5'-3-)
CMCT90-F1	CCTTCAGGATACTTCACTTTGCG
CMCT90-R2	GGATGAGGATCAGGCTTTCAGG

HUJ-VF_CMCT90F1-R2: 598 bp;

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1      TTTCTCAATC TCTCTACCAA TTGATTCAGG GATGAACTTT GCTACCAACT CCTTCAGGTC
61     ACAGGAACTT GCTTGGTTTC TCATGATCTC AACCATCTTG CGACGGATCT AACACAATAA
121    GACAAACATG CTGATAAGTA ATCAAAACTA TACCTGCCAC GTAGATATTT TTCAGATAAG
181    TAAATAAGTG CAATCAAGTA TAAAATACCA CCAACCTGAC GGATCTGGCT GCTCTGAGCA
241    TAACATGTAC GCTTCTGTTG GTTTGGACGC TTCTTTGTAA AAGCAATGCA GAACATCCTA
301    AGAGTGTAGC TATCTGTAGT CTTGACATCC ACATGAGCCT CAATCAAAGT CTGCCACTTG
361    CGCACCAGAG ACCTCAACTT GTCTGTTGTG AAGTCCATCC CCTGAAGATA GCCAACAATA
421    AAGTTATTTA TTTTCTCAA AACAAAGTCA AATTCCATCC ATAAAAATAG CTATACTCCA
481    GTCTTGTGAA GAAATTATAG CGTAAAAGAA TCATCATACA TGGAAGTTTG TGAGGACATT
541    CCTCCCTTGC ACATCTTCTG CTCTCAAGCG GATCTTCCTG AAAGCCTGAT CCTCATCC
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Gc171_CMCT90F1-R2: 660 bp;

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1      CCTTCAGGAT ACTTCACTTT GCGAATATAA ACATTTTGGG GTGGAAAAAT GCTTGAAGTA
61     GCTTTCTCAA TCTCTCTACC AATTGATTCA GGGATGAACT TTGCTACCAA CTCCTTCAGG
121    TCACAGGAAC TTGCTTGGTT TCTCATGATC TCAACCATCT TGCGACGGAT CTAACACAAT
181    AAGACAAACA TGCTGATAAG TAATCAAAAC TATACCTGCC ACGTAGATAT TTTTCAGATA
241    AGTAAATAAG TGCAATCAAG TATAAAATAC CACCAACCTG ACGGATCTGG CTGCTCTGAG
301    CATAACATGT ACGCTTCTGT TGGTTTGGAC GCTTCTTTGT AAAAGCAATG CAGAACATCC
361    TAAGAGTGTA GCTATCTGTA GTCTTGACAT CCACATGAGC CTCAATCAA GTCTGCCACT
421    TGCGCACCAG AGACCTCAAC TTGTCTGTTG TGAAGTCCAT CCCCTGAAGA TAGCCAACAA
481    TAAAGTTATT TATTTTCTC AAAACAAAGT CAAATTCCAT CCATAAAAAAT AGCTATACTC
541    CAGTCTTGTG AAGAAATTAT AGCGTAAAAG AATCATCATA CATGGAAGTT TGTGAGGACA
601    TTCCTCCCTT GCACATCTTC TGCTCTCAAG CGGATCTTCC TGAAAGCCTG ATCCTCATCC
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Summary

Partial sequences for both plants were obtained with the forward and reverse primers. The reverse primer's sequence for HUJBF was not of a high quality, and thus it does not extend as far 5' as does the sequence for Gc171. However, the forward sequence was excellent, and the sequence listed above is believed to be 100% accurate. Upon alignment, HUJBF and Gc171 sequences matched identically. Therefore, Gc171 has no introgression from a wild species in this region of chromosome 6. In addition, this area is not the location of the Ty4 gene.