

COSII Marker C2_At2g37240, 1.0 cM, Chr. 9

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Primer Name	Primer Sequence (5' to 3')
LM9-F1	TCCTTTGTCGCATAAGAGCTGATTATC
LM9-R1	ACAAGTGCGACTCCTGCTGCATCC

902h LM9F1-R1: 515 bp:

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1      TCCTTTGTCG CATAAGAGCT GATTATCTTG CAGCTGAGAA GGTAATGCTT CTTCTTGACT
61     ACATTTACGA ATGTTATCAT GTTTTTCTTC CATGTGTTCT GCTGAAACTA TCCCAAAGCT
121    GACTAATGTA TTTCCAGGTC CAAATGACTT GTCTTAGTAT CCTTGTTTGA TGTTGGTGAG
181    TTAAGTCGTG GGAATAACAT AAGTTGCAGT GTCTACTATA ACGTACATAT CATAGTTTAC
241    AGACCATACT TTCCATAGGA AGCATTCTCT CTACCTCCCA AGGTAGAGGT GAAGTCTTCA
301    TGAACACTAC CCTCCCTAGA TCCCATTGTG GGGATTAGAC TGAGTATGTT GTCGTTTTAA
361    TTCAGATTTA TGTTATCTTC AGTGCGTTAA AAAAGTTATT CTAACCACAC CGATGACTGT
421    GCACATATCC TTAAGTTCCA CCATTACTAC AGTTTACATC CTTATACTGT TTTCTGTTCA
481    CAGGATAAGA TGGATGCAGC AGGAGTCGCA CTTGT
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Blast Search

No Match

SGN BAC Clone Search

No Match

Comparison With Other Breeding Lines

Both 902h and Cerasiforme produced good sequence with both the forward and reverse primers. Upon alignment they matched identically. Therefore, there are no SNP or INDEL that differentiate the begomovirus resistant genotypes from the susceptible at this location on chromosome 9.