

COSII Marker C2_At3g01160, 83.4 cM, Chr. 2

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Primer Name	Primer Sequence (5' to 3')
BG2F-8	TCTGAAGAAGCTGAAGCAAGTAGAGC
BG2R-8	TGCCAACTGACGAGCATAAGCTGC

902BG-F8-R8: 398 bp:

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1      TCTGAAGAAG CTGAAGCAAG TAGAGCAGAG CTTGAGCTAT TACTTGCAGA TGACAAAGGA
61     GGAGACCCTA ACTTGAAGGG TTACAACATG AAACCTAAAA AGGCGAAGGG GAAGAAGGGT
121    AAAGGAACTC CAGTAGAGGA CAAGTTGCCA ACTATAGATT ATGAAGATCC ACGGTTTTTCA
181    TCTCTCTTTA AATCACACCT CTTTGCATTG GACCCACAG ATCCTCAGTT CAAACGGTAT
241    TTCCCATCTT GTTTACACCA ATTTCTTGTT TGTGCTTGTA AACAGAACTG GTCTGGCGTT
301    TTCCCAATTC CAAAACAAAG CCTGCTTGCT CTTTTCATTG GTTTACAGGT ATCTATTTTG
361    GTTTTTGCAG GAGTGCAGCT TATGCTCGTC AGTTGGCA
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Blast Search

No Match

SGN BAC Clone Search

The search produced a 100% identity with:

Clone name : LE_HBa0159F19

Name:Tomato HindIII BAC Library

Organism: Solanum lycopersicum

Comparison With Other Breeding Lines

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