

COSII Marker C2-At5g67370, 129.0 cM, Chr. 2

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Primer Name	Primer Sequence (5' to 3')
BG2F-11	TGAAACCAGTCATTAATAATGCTGAAG
BG2R-11	AGTACTGTCCACCGGCCAATGC

902h BGF11-R11: 395 bp;

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1      TGAAACCAGT CATTAAAATG CTGAAGCAAA CGCTAGTTGG AACAGGGGCT TTGCTTGTTG
61     CAGCAGTCTC ATTATTCATA TTTGCAACAC CAGTAGAAGA TTTTTTCCGC AATACTTTCA
121    CAACAAACGA GAACTCATTG AGTTCCACCT CAACAAACAG CACAAATAAA CTAGGCATCA
181    GGTAATTCTA TTGAAAACCT AAGAAGTACA ATACTATAAA ATTTTCATGAG CTTACGTTGT
241    TTCGCTATGT AATTAAGGA AAGAAGAACT GTTGCCTTG CCACTGGAAG TCAAGGAGGA
301    CGATGATCTA GCAAAGCTG CCGCTGAAGC AGCTGATGGA AGGCCAGTTT ACTGCAGAGA
361    TAGGTATTAT CGTGCATTGG CCGGTGGACA GTACT
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Blast Search

No Match

SGN BAC Clone Search

The sequence matched the following BAC clone with 100% identity:

Clone name: LE_HBa0155D20

Name: Tomato: HindIII BAC Library

Organism: Solanum lycopersicum

Comparison With Other Breeding Lines

Cerasiforme, Gc9, and 902h each gave good sequence with both the forward and reverse primers. Upon alignment all of the sequences matched identically. Therefore, there are no SNP or INDEL that distinguish the begomovirus resistant genotypes from the susceptible at this location on chromosome two.